The Little Book of Algorithms

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Duc-Tam Nguyen

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A Friendly Guide from Numbers to Neural Networks

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The Cheatsheet

Page 1. Big Picture and Complexity

A quick reference for understanding algorithms, efficiency, and growth rates. Keep this sheet beside you as you read or code.

What Is an Algorithm?

An algorithm is a clear, step-by-step process that solves a problem.

Property	Description
Precise	Each step is unambiguous
Finite	Must stop after a certain number of steps
Effective	Every step is doable by machine or human
Deterministic	Same input, same output (usually)

Think of it like a recipe:

- Input: ingredients
- Steps: instructions
- Output: final dish

Core Qualities

Concept	Question to Ask
Correctness	Does it always solve the problem
Termination	Does it eventually stop
Complexity	How much time and space it needs
Clarity	Is it easy to understand and implement

Why Complexity Matters

Different algorithms grow differently as input size n increases.

Growth Rate	Example Algorithm	Effect When n Doubles
$O(1)$	Hash lookup	No change
$O(\log n)$	Binary search	Slight increase
$O(n)$	Linear scan	Doubled
$O(n \log n)$	Merge sort	Slightly more than $2\times$
$O(n^2)$	Bubble sort	Quadrupled
$O(2^n)$	Subset generation	Explodes
$O(n!)$	Brute-force permutations	Unusable beyond $n = 10$

Measuring Time and Space

Measure	Meaning	Example
Time Complexity	Number of operations	Loop from 1 to n: $O(n)$
Space Complexity	Memory usage (stack, heap, data structures)	Recursive call depth: $O(n)$

Simple rules:

- Sequential steps: sum of costs
- Nested loops: product of sizes
- Recursion: use recurrence relations

Common Patterns

Pattern	Cost Formula	Complexity
Single Loop (1 to n)	$T(n) = n$	$O(n)$
Nested Loops ($n \times n$)	$T(n) = n^2$	$O(n^2)$
Halving Each Step	$T(n) = \log_2 n$	$O(\log n)$
Divide and Conquer (2 halves)	$T(n) = 2T(n/2) + n$	$O(n \log n)$

Doubling Rule

Run algorithm for n and $2n$:

Observation	Likely Complexity
Constant time	$O(1)$
Time doubles	$O(n)$
Time quadruples	$O(n^2)$
Time × log factor	$O(n \log n)$

Tiny Code: Binary Search

```
def binary_search(arr, x):
    lo, hi = 0, len(arr) - 1
    while lo <= hi:
        mid = (lo + hi) // 2
        if arr[mid] == x:
            return mid
        elif arr[mid] < x:
            lo = mid + 1
        else:
            hi = mid - 1
    return -1
```

Complexity:

$$T(n) = T(n/2) + 1 \Rightarrow O(\log n)$$

Common Pitfalls

Issue	Tip
Off-by-one error	Check loop bounds carefully
Infinite loop	Ensure termination condition is reachable
Midpoint overflow (C/C++)	Use `mid = lo + (hi - lo) / 2`
Unsorted data in search	Binary search only works on sorted input

Quick Growth Summary

Type	Formula Example	Description
Constant	1	Fixed time
Logarithmic	$\log n$	Divide each time
Linear	n	Step through all items
Linearithmic	$n \log n$	Sort-like complexity
Quadratic	n^2	Double loop
Cubic	n^3	Triple nested loops
Exponential	2^n	All subsets
Factorial	$n!$	All permutations

Simple Rule of Thumb

Trace small examples by hand. Count steps, memory, and recursion depth. You'll see how growth behaves before running code.

Page 2. Recurrences and Master Theorem

This page helps you break down recursive algorithms and estimate their runtime using recurrences.

What Is a Recurrence?

A recurrence relation expresses a problem's cost $T(n)$ in terms of smaller subproblems.

Typical structure:

$$T(n) = a, T\left(\frac{n}{b}\right) + f(n)$$

where:

- a = number of subproblems
- b = factor by which input shrinks
- $f(n)$ = extra work per call (merge, combine, etc.)

Common Recurrences

Algorithm	Recurrence Form	Solution
Binary Search	$T(n) = T(n/2) + 1$	$O(\log n)$
Merge Sort	$T(n) = 2T(n/2) + n$	$O(n \log n)$
Quick Sort (avg)	$T(n) = 2T(n/2) + O(n)$	$O(n \log n)$
Quick Sort (worst)	$T(n) = T(n-1) + O(n)$	$O(n^2)$
Matrix Multiply	$T(n) = 8T(n/2) + O(n^2)$	$O(n^3)$
Karatsuba	$T(n) = 3T(n/2) + O(n)$	$O(n^{\log_2 3})$

Solving Recurrences

There are several methods to solve them:

Method	Description	Best For
Iteration	Expand step by step	Simple recurrences
Substitution	Guess and prove with induction	Verification
Recursion Tree	Visualize total work per level	Divide and conquer
Master Theorem	Shortcut for $T(n) = aT(n/b) + f(n)$	Standard forms

The Master Theorem

Given

$$T(n) = aT(n/b) + f(n)$$

Let

$$n^{\log_b a}$$

be the "critical term"

Case	Condition	Result
1	If $f(n) = O(n^{\log_b a - \varepsilon})$	$T(n) = \Theta(n^{\log_b a})$
2	If $f(n) = \Theta(n^{\log_b a} \log^k n)$	$T(n) = \Theta(n^{\log_b a} \log^{k+1} n)$
3	If $f(n) = \Omega(n^{\log_b a + \varepsilon})$ and regularity holds	$T(n) = \Theta(f(n))$

Examples

Algorithm	a	b	$f(n)$	Case	$T(n)$
Merge Sort	2	2	n	2	$\Theta(n \log n)$

Algorithm	a	b	$f(n)$	Case	$T(n)$
Binary Search	1	2	1	1	$\Theta(\log n)$
Strassen Multiply	7	2	n^2	2	$\Theta(n^{\log_2 7})$
Quick Sort (avg)	2	2	n	2	$\Theta(n \log n)$

Recursion Tree Visualization

Break cost into levels:

Example: $T(n) = 2T(n/2) + n$

Level	#Nodes	Work per Node	Total Work
0	1	n	n
1	2	$n/2$	n
2	4	$n/4$	n
...	...	...	...

Sum across $\log_2 n$ levels:

$$T(n) = n \log_2 n$$

Tiny Code: Fast Exponentiation

Compute a^n efficiently.

```
def power(a, n):
    res = 1
    while n > 0:
        if n % 2 == 1:
            res *= a
        a *= a
        n //= 2
    return res
```

Recurrence:

$$T(n) = T(n/2) + O(1) \Rightarrow O(\log n)$$

Iteration Method Example

Solve $T(n) = T(n/2) + n$

Expand:

$$T(n) = T(n/2) + n \quad = T(n/4) + n/2 + n \; = T(n/8) + n/4 + n/2 + n \quad = ... + n(1 + 1/2 + 1/4 + ...) \; = O(n)$$

Common Forms

Form	Result
$T(n) = T(n-1) + O(1)$	$O(n)$
$T(n) = T(n/2) + O(1)$	$O(\log n)$
$T(n) = 2T(n/2) + O(1)$	$O(n)$
$T(n) = 2T(n/2) + O(n)$	$O(n \log n)$
$T(n) = T(n/2) + O(n)$	$O(n)$

Quick Checklist

1. Identify a, b, and $f(n)$
2. Compare $f(n)$ to $n^{\log_b a}$
3. Apply correct case
4. Confirm assumptions (regularity)
5. State final complexity

Understanding recurrences helps you estimate performance before coding. Always look for subproblem count, size, and merge cost.

Page 3. Sorting at a Glance

Sorting is one of the most common algorithmic tasks. This page helps you quickly compare sorting methods, their complexity, stability, and when to use them.

Why Sorting Matters

Sorting organizes data so that searches, merges, and analyses become efficient. Many problems become simpler once the input is sorted.

Quick Comparison Table

Algorithm	Best Case	Average Case	Worst Case	Space	Stable	In-Place	Notes
Bubble Sort	$O(n)$	$O(n^2)$	$O(n^2)$	$O(1)$	Yes	Yes	Simple, educational
Selection Sort	$O(n^2)$	$O(n^2)$	$O(n^2)$	$O(1)$	No	Yes	Few swaps
Insertion Sort	$O(n)$	$O(n^2)$	$O(n^2)$	$O(1)$	Yes	Yes	Great for small/partial sort
Merge Sort	$O(n \log n)$	$O(n \log n)$	$O(n \log n)$	$O(n)$	Yes	No	Stable, divide and conquer
Quick Sort	$O(n \log n)$	$O(n \log n)$	$O(n^2)$	$O(\log n)$	No	Yes	Fast average, in place
Heap Sort	$O(n \log n)$	$O(n \log n)$	$O(n \log n)$	$O(1)$	No	Yes	Not stable
Counting Sort	$O(n + k)$	$O(n + k)$	$O(n + k)$	$O(n+k)$	Yes	No	Integer keys only
Radix Sort	$O(d(n + k))$	$O(d(n + k))$	$O(d(n + k))$	$O(n+k)$	Yes	No	Sort by digits
Bucket Sort	$O(n + k)$	$O(n + k)$	$O(n^2)$	$O(n)$	Yes	No	Uniform distribution needed

Choosing a Sorting Algorithm

Situation	Best Choice
Small array or nearly sorted data	Insertion Sort
Stable required, general case	Merge Sort or Timsort
In-place and fast on average	Quick Sort
Guarantee worst-case $O(n \log n)$	Heap Sort
Small integer keys or limited range	Counting or Radix
External sorting (large data)	External Merge Sort

Tiny Code: Insertion Sort

Simple and intuitive for beginners.

```
def insertion_sort(a):
    for i in range(1, len(a)):
```

```
        key = a[i]
        j = i - 1
        while j >= 0 and a[j] > key:
            a[j + 1] = a[j]
            j -= 1
        a[j + 1] = key
    return a
```

Complexity:

$$T(n) = O(n^2)$$

average,

$$O(n)$$

best (already sorted)

Divide and Conquer Sorts

Merge Sort

Splits list, sorts halves, merges results.

Recurrence:

$$T(n) = 2T(n/2) + O(n) = O(n \log n)$$

Tiny Code:

```
def merge_sort(a):
    if len(a) <= 1:
        return a
    mid = len(a)//2
    L = merge_sort(a[:mid])
    R = merge_sort(a[mid:])
    i = j = 0
    res = []
    while i < len(L) and j < len(R):
        if L[i] <= R[j]:
            res.append(L[i]); i += 1
        else:
            res.append(R[j]); j += 1
    res.extend(L[i:]); res.extend(R[j:])
    return res
```

Quick Sort

Pick pivot, partition, sort subarrays.

Recurrence:

$$T(n) = T(k) + T(n - k - 1) + O(n)$$

Average case:

$$O(n \log n)$$

Worst case:

$$O(n^2)$$

Tiny Code:

```
def quick_sort(a):
    if len(a) <= 1:
        return a
    pivot = a[len(a)//2]
    left  = [x for x in a if x < pivot]
    mid   = [x for x in a if x == pivot]
    right = [x for x in a if x > pivot]
    return quick_sort(left) + mid + quick_sort(right)
```

Stable vs Unstable

Property	Description	Example
Stable	Equal elements keep original order	Merge Sort, Insertion
Unstable	May reorder equal elements	Quick, Heap

Visualization Tips

Pattern	Description
Bubble	Compare and swap adjacent
Selection	Select min each pass
Insertion	Grow sorted region step by step
Merge	Divide, conquer, merge
Quick	Partition and recurse
Heap	Build heap, extract repeatedly

Summary Table

Type	Category	Complexity	Stable	Space
Simple	Bubble, Selection	$O(n^2)$	Varies	$O(1)$
Insertion	Incremental	$O(n^2)$	Yes	$O(1)$
Divide/Conquer	Merge, Quick	$O(n \log n)$	Merge yes	Merge no
Distribution	Counting, Radix	$O(n + k)$	Yes	$O(n + k)$
Hybrid	Timsort, IntroSort	$O(n \log n)$	Yes	Varies

When in doubt, start with Timsort (Python) or std::sort (C++) which adapt dynamically.

Page 4. Searching and Selection

Searching means finding what you need from a collection. Selection means picking specific elements such as the smallest, largest, or k-th element. This page summarizes both.

Searching Basics

Type	Description	Data Requirement	Complexity
Linear Search	Check one by one	None	$O(n)$
Binary Search	Divide range by 2 each step	Sorted	$O(\log n)$
Jump Search	Skip ahead fixed steps	Sorted	$O(\sqrt{n})$
Interpolation	Guess position based on value	Sorted, uniform	$O(\log \log n)$ avg
Exponential	Expand window, then binary search	Sorted	$O(\log n)$

Linear Search

Simple but slow for large inputs.

```
def linear_search(a, x):
    for i, v in enumerate(a):
        if v == x:
            return i
    return -1
```

Complexity:

$$T(n) = O(n)$$

Binary Search

Fast on sorted lists.

```python
def binary_search(a, x):
    lo, hi = 0, len(a) - 1
    while lo <= hi:
        mid = (lo + hi) // 2
        if a[mid] == x:
            return mid
        elif a[mid] < x:
            lo = mid + 1
        else:
            hi = mid - 1
    return -1
```

Complexity:

$$T(n) = T(n/2) + 1 \Rightarrow O(\log n)$$

Binary Search Variants

Variant	Goal	Return Value
Lower Bound	First index where $a[i] \geq x$	Position of first x
Upper Bound	First index where $a[i] > x$	Position of first $>$ x
Count Range	`upper_bound - lower_bound`	Count of x in sorted array

Common Binary Search Pitfalls

Problem	Fix
Infinite loop	Update bounds correctly
Off-by-one	Check mid inclusion carefully
Unsuitable for unsorted data	Sort or use hash-based search
Overflow (C/C++)	`mid = lo + (hi - lo) / 2`

Exponential Search

Used for unbounded or large sorted lists.

1. Check positions $1, 2, 4, 8, \ldots$ until $a[i] \geq x$
2. Binary search in last found interval

Complexity:

$$O(\log n)$$

Selection Problems

Find the k-th smallest or largest element.

Task	Example Use Case	Algorithm	Complexity
Min / Max	Smallest / largest element	Linear Scan	$O(n)$
k-th Smallest	Order statistic	Quickselect	Avg $O(n)$
Median	Middle element	Quickselect	Avg $O(n)$
Top-k Elements	Partial sort	Heap / Partition	$O(n \log k)$
Median of Medians	Worst-case linear selection	Deterministic	$O(n)$

Tiny Code: Quickselect (k-th smallest)

```
import random

def quickselect(a, k):
    if len(a) == 1:
        return a[0]
    pivot = random.choice(a)
    left  = [x for x in a if x < pivot]
    mid   = [x for x in a if x == pivot]
    right = [x for x in a if x > pivot]

    if k < len(left):
        return quickselect(left, k)
    elif k < len(left) + len(mid):
        return pivot
    else:
        return quickselect(right, k - len(left) - len(mid))
```

Complexity: Average $O(n)$, Worst $O(n^2)$

Tiny Code: Lower Bound

```
def lower_bound(a, x):
    lo, hi = 0, len(a)
    while lo < hi:
        mid = (lo + hi) // 2
        if a[mid] < x:
            lo = mid + 1
        else:
            hi = mid
    return lo
```

Hash-Based Searching

When order does not matter, hashing gives near constant lookup.

Operation	Average	Worst
Insert	$O(1)$	$O(n)$
Search	$O(1)$	$O(n)$
Delete	$O(1)$	$O(n)$

Best for large, unsorted collections.

Summary Table

Scenario	Recommended Approach	Complexity
Small array	Linear Search	$O(n)$
Large, sorted array	Binary Search	$O(\log n)$
Unbounded range	Exponential Search	$O(\log n)$
Need k-th smallest element	Quickselect	Avg $O(n)$
Many lookups	Hash Table	Avg $O(1)$

Quick Tips

- Always check whether data is sorted before applying binary search.
- Quickselect is great when you only need the k-th element, not a full sort.
- Use hash maps for fast lookups on unsorted data.

Page 5. Core Data Structures

Data structures organize data for efficient access and modification. Choosing the right one often makes an algorithm simple and fast.

Arrays and Lists

Structure	Access	Search	Insert End	Insert Middle	Delete	Notes
Static Array	$O(1)$	$O(n)$	N/A	$O(n)$	$O(n)$	Fixed size
Dynamic Array	$O(1)$	$O(n)$	Amortized $O(1)$	$O(n)$	$O(n)$	Auto-resizing
Linked List (S)	$O(n)$	$O(n)$	$O(1)$ head	$O(1)$ if node known	$O(1)$ if node known	Sequential access
Linked List (D)	$O(n)$	$O(n)$	$O(1)$ head/tail	$O(1)$ if node known	$O(1)$ if node known	Two-way traversal

- Singly linked lists: next pointer only
- Doubly linked lists: next and prev pointers
- Dynamic arrays use *doubling* to grow capacity

Tiny Code: Dynamic Array Resize (Python-like)

```
def resize(arr, new_cap):
    new = [None] * new_cap
    for i in range(len(arr)):
        new[i] = arr[i]
    return new
```

Doubling capacity keeps amortized append $O(1)$.

Stacks and Queues

Structure	Push	Pop	Peek	Notes
Stack (LIFO)	$O(1)$	$O(1)$	$O(1)$	Undo operations, recursion
Queue (FIFO)	$O(1)$	$O(1)$	$O(1)$	Scheduling, BFS

Structure	Push	Pop	Peek	Notes
Deque	$O(1)$	$O(1)$	$O(1)$	Insert/remove both ends

Tiny Code: Stack

```
stack = []
stack.append(x)   # push
x = stack.pop()   # pop
```

Tiny Code: Queue

```
from collections import deque

q = deque()
q.append(x)   # enqueue
x = q.popleft()  # dequeue
```

Priority Queue (Heap)

Stores elements so the smallest (or largest) is always on top.

Operation	Complexity
Insert	$O(\log n)$
Extract min	$O(\log n)$
Peek min	$O(1)$
Build heap	$O(n)$

Tiny Code:

```
import heapq
heap = []
heapq.heappush(heap, value)
x = heapq.heappop(heap)
```

Heaps are used in Dijkstra, Prim, and scheduling.

Hash Tables

Operation	Average	Worst	Notes
Insert	$O(1)$	$O(n)$	Hash collisions increase cost
Search	$O(1)$	$O(n)$	Good hash + low load factor helps
Delete	$O(1)$	$O(n)$	Usually open addressing or chaining

Key ideas:

- Compute index using hash function: `index = hash(key) % capacity`
- Resolve collisions by chaining or probing

Tiny Code: Hash Map (Simplified)

```
table = [[] for _ in range(8)]
def put(key, value):
    i = hash(key) % len(table)
    for kv in table[i]:
        if kv[0] == key:
            kv[1] = value
            return
    table[i].append([key, value])
```

Sets

A hash-based collection of unique elements.

Operation	Average Complexity
Add	$O(1)$
Search	$O(1)$
Remove	$O(1)$

Used for membership checks and duplicates removal.

Union-Find (Disjoint Set)

Keeps track of connected components. Two main operations:

- find(x): get representative of x
- union(a,b): merge sets of a and b

With path compression + union by rank → nearly $O(1)$.

Tiny Code:

```
class DSU:
    def __init__(self, n):
        self.p = list(range(n))
        self.r = [0]*n
    def find(self, x):
        if self.p[x] != x:
            self.p[x] = self.find(self.p[x])
        return self.p[x]
    def union(self, a, b):
        ra, rb = self.find(a), self.find(b)
        if ra == rb: return
        if self.r[ra] < self.r[rb]: ra, rb = rb, ra
        self.p[rb] = ra
        if self.r[ra] == self.r[rb]:
            self.r[ra] += 1
```

Summary Table

Category	Structure	Use Case
Sequence	Array, List	Ordered data
LIFO/FIFO	Stack, Queue	Recursion, scheduling
Priority	Heap	Best-first selection, PQ problems
Hash-based	Hash Table, Set	Fast lookups, uniqueness
Connectivity	Union-Find	Graph components, clustering

Quick Tips

- Choose array when random access matters.
- Choose list when insertions/deletions frequent.
- Choose stack or queue for control flow.

- Choose heap for priority.
- Choose hash table for constant lookups.
- Choose DSU for disjoint sets or graph merging.

Page 6. Graphs Quick Use

Graphs model connections between objects. They appear everywhere: maps, networks, dependencies, and systems. This page gives you a compact view of common graph algorithms.

Graph Basics

A graph has vertices (nodes) and edges (connections).

Type	Description
Undirected	Edges go both ways
Directed (Digraph)	Edges have direction
Weighted	Edges carry cost or distance
Unweighted	All edges cost 1

Representations

Representation	Space	Best For	Notes
Adjacency List	$O(V+E)$	Sparse graphs	Common in practice
Adjacency Matrix	$O(V^2)$	Dense graphs	Constant-time edge lookup
Edge List	$O(E)$	Edge-based algorithms	Easy to iterate over edges

Adjacency List Example (Python):

```
graph = {
    0: [(1, 2), (2, 5)],
    1: [(2, 1)],
    2: []
}
```

Each tuple `(neighbor, weight)` represents an edge.

Traversals

Breadth-First Search (BFS)

Visits layer by layer (good for shortest paths in unweighted graphs).

```
from collections import deque
def bfs(adj, s):
    dist = {s: 0}
    q = deque([s])
    while q:
        u = q.popleft()
        for v in adj[u]:
            if v not in dist:
                dist[v] = dist[u] + 1
                q.append(v)
    return dist
```

Complexity: $O(V + E)$

Depth-First Search (DFS)

Explores deeply before backtracking.

```
def dfs(adj, u, visited):
    visited.add(u)
    for v in adj[u]:
        if v not in visited:
            dfs(adj, v, visited)
```

Complexity: $O(V + E)$

Shortest Path Algorithms

Algorithm	Works On	Negative Edges	Complexity	Notes
BFS	Unweighted	No	$O(V + E)$	Shortest hops
Dijkstra	Weighted (nonneg)	No	$O((V + E) \log V)$	Uses priority queue
Bellman-Ford	Weighted	Yes	$O(VE)$	Detects negative cycles

Algorithm	Works On	Negative Edges	Complexity	Notes
Floyd-Warshall	All pairs	Yes	$O(V^3)$	DP approach

Tiny Code: Dijkstra's Algorithm

```
import heapq

def dijkstra(adj, s):
    INF = 1018
    dist = [INF] * len(adj)
    dist[s] = 0
    pq = [(0, s)]
    while pq:
        d, u = heapq.heappop(pq)
        if d != dist[u]:
            continue
        for v, w in adj[u]:
            nd = d + w
            if nd < dist[v]:
                dist[v] = nd
                heapq.heappush(pq, (nd, v))
    return dist
```

Topological Sort (DAGs only)

Orders nodes so every edge (u, v) goes from earlier to later.

Method	Idea	Complexity
DFS-based	Post-order stack reversal	$O(V + E)$
Kahn's Algo	Remove nodes with indegree 0	$O(V + E)$

Minimum Spanning Tree (MST)

Connect all nodes with minimum total weight.

Algorithm	Idea	Complexity	Notes
Kruskal	Sort edges, use Union-Find	$O(E \log E)$	Works well with edge list
Prim	Grow tree using PQ	$O(E \log V)$	Starts from any vertex

Tiny Code: Kruskal MST

```
def kruskal(edges, n):
    parent = list(range(n))
    def find(x):
        if parent[x] != x:
            parent[x] = find(parent[x])
        return parent[x]
    res = 0
    for w, u, v in sorted(edges):
        ru, rv = find(u), find(v)
        if ru != rv:
            res += w
            parent[rv] = ru
    return res
```

Strongly Connected Components (SCC)

Subsets where every node can reach every other. Use Kosaraju or Tarjan algorithm, both $O(V + E)$.

Cycle Detection

Graph Type	Method	Notes
Undirected	DFS with parent	Edge to non-parent visited
Directed	DFS with color/state	Back edge found = cycle

Summary Table

Task	Algorithm	Complexity	Notes
Visit all nodes	DFS / BFS	$O(V + E)$	Traversal

Task	Algorithm	Complexity	Notes
Shortest path (unweighted)	BFS	$O(V+E)$	Counts edges
Shortest path (weighted)	Dijkstra	$O(E \log V)$	No negative weights
Negative edges allowed	Bellman-Ford	$O(VE)$	Detects negative cycles
All-pairs shortest path	Floyd-Warshall	$O(V^3)$	DP matrix
MST	Kruskal / Prim	$O(E \log V)$	Minimal connection cost
DAG order	Topological Sort	$O(V+E)$	Only for DAGs

Quick Tips

- Use BFS for shortest path in unweighted graphs.
- Use Dijkstra if weights are nonnegative.
- Use Union-Find for Kruskal MST.
- Use Topological Sort for dependency resolution.
- Always check for negative edges before using Dijkstra.

Page 7. Dynamic Programming Quick Use

Dynamic Programming (DP) is about solving big problems by breaking them into overlapping subproblems and reusing their solutions. This page helps you see patterns quickly.

When to Use DP

You can usually apply DP if:

Symptom	Meaning
Optimal Substructure	Best solution uses best of subparts
Overlapping Subproblems	Same subresults appear again
Decision + Recurrence	State transitions can be defined

DP Styles

Style	Description	Example
Top-down (Memo)	Recursion + cache results	Fibonacci with memoization
Bottom-up (Tabular)	Iterative fill table	Knapsack table
Space-optimized	Reuse previous row/state	Rolling arrays

Fibonacci Example

Recurrence:

$$F(n) = F(n-1) + F(n-2), \quad F(0) = 0, F(1) = 1$$

Top-down (Memoization)

```python
def fib(n, memo={}):
    if n <= 1:
        return n
    if n not in memo:
        memo[n] = fib(n-1, memo) + fib(n-2, memo)
    return memo[n]
```

Bottom-up (Tabulation)

```python
def fib(n):
    dp = [0, 1]
    for i in range(2, n + 1):
        dp.append(dp[i-1] + dp[i-2])
    return dp[n]
```

Steps to Solve DP Problems

1. Define State Example: $dp[i]$ = best answer for first i items
2. Define Transition Example: $dp[i] = \max(dp[i-1], value[i] + dp[i - weight[i]])$
3. Set Base Cases Example: $dp[0] = 0$
4. Choose Order Bottom-up or Top-down
5. Return Answer Often $dp[n]$ or $dp[target]$

Common DP Categories

Category	Example Problems	State Form
Sequence	LIS, LCS, Edit Distance	$dp[i][j]$ over prefixes
Subset	Knapsack, Subset Sum	$dp[i][w]$ capacity-based
Partition	Palindrome Partitioning, Equal Sum	$dp[i]$ cut-based
Grid	Min Path Sum, Unique Paths	$dp[i][j]$ over cells
Counting	Coin Change Count, Stairs	Add ways from subproblems

Category	Example Problems	State Form
Interval	Matrix Chain, Burst Balloons	$dp[i][j]$ range subproblem
Bitmask	TSP, Assignment	$dp[mask][i]$ subset states
Digit	Count numbers with constraint	$dp[pos][tight][sum]$ digits
Tree	Rerooting, Subtree DP	$dp[u]$ over children

Classic Problems

Problem	State Definition	Transition
Climbing Stairs	$dp[i]$ = ways to reach step i	$dp[i] = dp[i-1] + dp[i-2]$
Coin Change (Count Ways)	$dp[x]$ = ways to make sum x	$dp[x] += dp[x - coin]$
0/1 Knapsack	$dp[w]$ = max value under weight w	$dp[w] = \max(dp[w], dp[w - w_i] + v_i)$
Longest Increasing Subseq.	$dp[i]$ = LIS ending at i	if $a[j] < a[i]$, $dp[i] = dp[j] + 1$
Edit Distance	$dp[i][j]$ = edit cost	min(insert,delete,replace)
Matrix Chain Multiplication	$dp[i][j]$ = min cost mult subchain	$dp[i][j] = \min_k(dp[i][k] + dp[k+1][j])$

Tiny Code: 0/1 Knapsack (1D optimized)

```
def knapsack(weights, values, W):
    dp = [0]*(W+1)
    for i in range(len(weights)):
        for w in range(W, weights[i]-1, -1):
            dp[w] = max(dp[w], dp[w-weights[i]] + values[i])
    return dp[W]
```

Sequence Alignment Example

Edit Distance Recurrence:

$$dp[i][j] = \begin{cases} dp[i-1][j-1], & \text{if } s[i] = t[j], \\ 1 + \min(dp[i-1][j],\ dp[i][j-1],\ dp[i-1][j-1]), & \text{otherwise.} \end{cases}$$

Optimization Techniques

Technique	When to Use	Example
Space Optimization	2D $\rightarrow$ 1D states reuse	Knapsack, LCS
Prefix/Suffix Precomp	Range aggregates	Sum/Min queries
Divide & Conquer DP	Monotonic decisions	Matrix Chain
Convex Hull Trick	Linear transition minima	DP on lines
Bitset DP	Large boolean states	Subset sum optimization

Debugging Tips

- Print partial `dp` arrays to see progress.
- Check base cases carefully.
- Ensure loops match transition dependencies.
- Always confirm the recurrence before coding.

Page 8. Mathematics for Algorithms Quick Use

Mathematics builds the foundation for algorithmic reasoning. This page collects essential formulas and methods every programmer should know.

Number Theory Essentials

Topic	Description	Formula / Idea
GCD (Euclidean)	Greatest common divisor	$gcd(a, b) = gcd(b, a$
Extended GCD	Solve $ax + by = gcd(a, b)$	Backtrack coefficients
LCM	Least common multiple	$lcm(a, b) = \frac{a \cdot b}{gcd(a,b)}$
Modular Addition	Add under modulo M	$(a + b) \bmod M$
Modular Multiply	Multiply under modulo M	$(a \cdot b) \bmod M$
Modular Inverse	$a^{-1} \bmod M$	$a^{M-2} \bmod M$ if M is prime
Modular Exponent	Fast exponentiation	Square and multiply
CRT	Combine congruences	Solve system $x \equiv a_i \pmod{m_i}$

Tiny Code (Modular Exponentiation):

```python
def modpow(a, n, M):
    res = 1
    while n:
        if n & 1:
            res = res * a % M
        a = a * a % M
        n >>= 1
    return res
```

Primality and Factorization

Algorithm	Use Case	Complexity	Notes
Trial Division	Small n	$O(\sqrt{n})$	Simple
Sieve of Eratosthenes	Generate primes	$O(n \log \log n)$	Classic prime sieve
Miller–Rabin	Probabilistic primality	$O(k \log^3 n)$	Fast for big n
Pollard Rho	Factor composite	$O(n^{1/4})$	Randomized
Sieve of Atkin	Faster variant	$O(n)$	Complex implementation

Combinatorics

Formula	Description
$n! = n \cdot (n-1) \cdots 1$	Factorial
$\binom{n}{k} = \frac{n!}{k!(n-k)!}$	Number of combinations
$P(n,k) = \frac{n!}{(n-k)!}$	Number of permutations
Pascal's Rule: $\binom{n}{k} = \binom{n-1}{k} + \binom{n-1}{k-1}$	Build Pascal's Triangle
Catalan: $C_n = \frac{1}{n+1}\binom{2n}{n}$	Parentheses counting

Tiny Code (nCr with factorials mod M):

```python
def nCr(n, r, fact, inv):
    return fact[n]*inv[r]%M*inv[n-r]%M
```

Probability Basics

Concept	Formula or Idea
Probability	$P(A) = \frac{\text{favorable}}{\text{total}}$
Complement	$P(\bar{A}) = 1 - P(A)$
Union	$P(A \cup B) = P(A) + P(B) - P(A \cap B)$
Conditional	$P(A\|B) = \frac{P(A \cap B)}{P(B)}$
Bayes' Theorem	$P(A\|B) = \frac{P(B\|A)P(A)}{P(B)}$
Expected Value	$E[X] = \sum x_i P(x_i)$
Variance	$Var(X) = E[X^2] - E[X]^2$

Linear Algebra Core

Operation	Formula / Method	Complexity
Gaussian Elimination	Solve $Ax = b$	$O(n^3)$
Determinant	Product of pivots	$O(n^3)$
Matrix Multiply	$(AB) * ij = \sum_k A * ikB_{kj}$	$O(n^3)$
Transpose	$A^T_{ij} = A_{ji}$	$O(n^2)$
LU Decomposition	$A = LU$ (lower, upper)	$O(n^3)$
Cholesky	$A = LL^T$ (symmetric pos. def.)	$O(n^3)$
Power Method	Dominant eigenvalue estimation	iterative

Tiny Code (Gaussian Elimination Skeleton):

```
for i in range(n):
    pivot = a[i][i]
    for j in range(i, n+1):
        a[i][j] /= pivot
    for k in range(n):
        if k != i:
            ratio = a[k][i]
            for j in range(i, n+1):
                a[k][j] -= ratio*a[i][j]
```

Fast Transforms

Transform	Use Case	Complexity	Notes
FFT	Polynomial convolution	$O(n \log n)$	Complex numbers
NTT	Modular convolution	$O(n \log n)$	Prime modulus
FWT (XOR)	XOR-based convolution	$O(n \log n)$	Subset DP

FFT Equation:

$$X_k = \sum_{n=0}^{N-1} x_n e^{-2\pi i k n / N}$$

Numerical Methods

Method	Purpose	Formula or Idea
Bisection	Root-finding	Midpoint halve until $f(x) = 0$
Newton–Raphson	Fast convergence	$x_{n+1} = x_n - \frac{f(x_n)}{f'(x_n)}$
Secant Method	Approx derivative	$x_{n+1} = x_n - f(x_n)\frac{x_n - x_{n-1}}{f(x_n) - f(x_{n-1})}$
Simpson's Rule	Integration	$\int_a^b f(x)dx \approx \frac{h}{3}(f(a) + 4f(m) + f(b))$

Optimization and Calculus

Concept	Formula / Idea
Derivative	$f'(x) = \lim_{h \to 0} \frac{f(x+h) - f(x)}{h}$
Gradient Descent	$x_{k+1} = x_k - \eta \nabla f(x_k)$
Lagrange Multipliers	$\nabla f = \lambda \nabla g$
Convex Function	$f(\lambda x + (1-\lambda)y) \leq \lambda f(x) + (1-\lambda) f(y)$

Tiny Code (Gradient Descent):

```
x = x0
for _ in range(1000):
    grad = df(x)
    x -= lr * grad
```

Algebraic Tricks

Topic	Formula / Use
Exponentiation	a^n via square-multiply
Polynomial Deriv.	$(ax^n)' = n \cdot ax^{n-1}$
Integration	$\int x^n dx = \frac{x^{n+1}}{n+1} + C$
Möbius Inversion	$f(n) = \sum_{d\|n} g(d) \implies g(n) = \sum_{d\|n} \mu(d) \cdot f(n/d)$

Quick Reference Table

Domain	Must-Know Algorithm
Number Theory	GCD, Mod Exp, CRT
Combinatorics	Pascal, Factorial, Catalan
Probability	Bayes, Expected Value
Linear Algebra	Gaussian Elimination
Transforms	FFT, NTT
Optimization	Gradient Descent

Page 9. Strings and Text Algorithms Quick Use

Strings are sequences of characters used in text search, matching, and transformation. This page gives quick references to classical and modern string techniques.

String Fundamentals

Concept	Description	Example
Alphabet	Set of symbols	`{a, b, c}`
String Length	Number of characters	`"hello"` $\to 5$
Substring	Continuous part of string	`"ell"` in `"hello"`
Subsequence	Ordered subset (not necessarily cont.)	`"hlo"` from `"hello"`
Prefix / Suffix	Starts / ends part of string	`"he"`, `"lo"`

Indexing: Most algorithms use 0-based indexing.

String Search Overview

Algorithm	Complexity	Description
Naive Search	$O(nm)$	Check all positions
KMP	$O(n+m)$	Prefix-suffix skip table
Z-Algorithm	$O(n+m)$	Precompute match lengths
Rabin–Karp	$O(n+m)$ avg	Rolling hash check
Boyer–Moore	$O(n/m)$ avg	Backward scan, skip mismatches

KMP Prefix Function

Compute prefix-suffix matches for pattern.

Step	Meaning
$pi[i]$	Longest proper prefix that is also suffix for $pattern[0:i]$

Tiny Code:

```
def prefix_function(p):
    pi = [0]*len(p)
    j = 0
    for i in range(1, len(p)):
        while j > 0 and p[i] != p[j]:
            j = pi[j-1]
        if p[i] == p[j]:
            j += 1
        pi[i] = j
    return pi
```

Search uses `pi` to skip mismatches.

Z-Algorithm

Computes length of substring starting at i matching prefix.

Step	Meaning
$Z[i]$	Longest substring starting at i matching prefix

Use `$S = pattern + '$' + text$` to find pattern occurrences.

Rabin–Karp Rolling Hash

Idea	Compute hash for window of text, slide, compare

Hash Function:

$$h(s) = (s_0 p^{n-1} + s_1 p^{n-2} + \cdots + s_{n-1}) \bmod M$$

Update efficiently when sliding one character.

Tiny Code:

```
def rolling_hash(s, base=257, mod=109+7):
    h = 0
    for ch in s:
        h = (h*base + ord(ch)) % mod
    return h
```

Advanced Pattern Matching

Algorithm	Use Case	Complexity
Boyer–Moore	Large alphabet	$O(n/m)$ avg
Sunday	Last char shift heuristic	$O(n)$ avg
Bitap	Approximate match	$O(nm/w)$
Aho–Corasick	Multi-pattern search	$O(n + z)$

Aho–Corasick Automaton

Build a trie from patterns and compute failure links.

Step	Description
Build Trie	Add all patterns
Failure Link	Fallback to next prefix
Output Link	Record pattern match

Tiny Code Sketch:

```python
from collections import deque

def build_ac(patterns):
    trie = [{}]
    fail = [0]
    for pat in patterns:
        node = 0
        for c in pat:
            node = trie[node].setdefault(c, len(trie))
            if node == len(trie):
                trie.append({})
                fail.append(0)
    # compute failure links
    q = deque()
    for c in trie[0]:
        q.append(trie[0][c])
    while q:
        u = q.popleft()
        for c, v in trie[u].items():
            f = fail[u]
            while f and c not in trie[f]:
                f = fail[f]
            fail[v] = trie[f].get(c, 0)
            q.append(v)
    return trie, fail
```

Suffix Structures

Structure	Purpose	Build Time
Suffix Array	Sorted list of suffix indices	$O(n \log n)$
LCP Array	Longest Common Prefix of suffix	$O(n)$
Suffix Tree	Trie of suffixes	$O(n)$ (Ukkonen)
Suffix Automaton	Minimal DFA of substrings	$O(n)$

Suffix Array Doubling Approach:

- Rank substrings of length 2^k
- Sort and merge using pairs of ranks

LCP via Kasai's Algorithm:

$$LCP[i] = \text{common prefix of } S[SA[i]:], S[SA[i-1]:]$$

Palindrome Detection

Algorithm	Description	Complexity
Manacher's Algorithm	Longest palindromic substring	$O(n)$
DP Table	Check substring palindrome	$O(n^2)$
Center Expansion	Expand around center	$O(n^2)$

Manacher's Core:

- Transform with separators (`#`)
- Track radius of palindrome around each center

Edit Distance Family

Algorithm	Description	Complexity
Levenshtein Distance	Insert/Delete/Replace	$O(nm)$
Damerau–Levenshtein	Add transposition	$O(nm)$
Hirschberg	Space-optimized LCS	$O(nm)$ time, $O(n)$ space

Recurrence:

$$dp[i][j] = \min \Big\{ dp[i-1][j] + 1 \; dp[i][j-1] + 1 \; dp[i-1][j-1] + (s_i \neq t_j)$$

Compression Techniques

Algorithm	Type	Idea
Huffman Coding	Prefix code	Shorter codes for frequent chars
Arithmetic Coding	Range encoding	Fractional interval representation
LZ77 / LZ78	Dictionary-based	Reuse earlier substrings
BWT + MTF + RLE	Block sorting	Group similar chars before coding

Huffman Principle: Shorter bit strings assigned to higher frequency symbols.

Hashing and Checksums

Algorithm	Use Case	Notes
CRC32	Error detection	Simple polynomial mod
MD5	Hash (legacy)	Not secure
SHA-256	Secure hash	Cryptographic
Rolling Hash	Substring compare	Used in Rabin–Karp

Quick Reference

Task	Algorithm	Complexity
Single pattern search	KMP / Z	$O(n + m)$
Multi-pattern search	Aho–Corasick	$O(n + z)$
Approximate search	Bitap / Wu–Manber	$O(kn)$
Substring queries	Suffix Array + LCP	$O(\log n)$
Palindromes	Manacher	$O(n)$
Compression	Huffman / LZ77	variable
Edit distance	DP table	$O(nm)$

Page 10. Geometry, Graphics, and Spatial Algorithms Quick Use

Geometry helps us solve problems about shapes, distances, and spatial relationships. This page summarizes core computational geometry techniques with simple formulas and examples.

Coordinate Basics

Concept	Description	Formula / Example
Point Distance	Distance between (x_1, y_1) and (x_2, y_2)	$d = \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$
Midpoint	Between two points	$(\frac{x_1+x_2}{2}, \frac{y_1+y_2}{2})$
Dot Product	Angle & projection	$\vec{a} \cdot \vec{b} = \|a\|\|b\| \cos\theta$
Cross Product (2D)	Signed area, orientation	$a \times b = a_x b_y - a_y b_x$
Orientation Test	CCW, CW, collinear check	$\text{sign}(a \times b)$

Tiny Code (Orientation Test):

```python
def orient(a, b, c):
    val = (b[0]-a[0])*(c[1]-a[1]) - (b[1]-a[1])*(c[0]-a[0])
    return 0 if val == 0 else (1 if val > 0 else -1)
```

Convex Hull

Find the smallest convex polygon enclosing all points.

Algorithm	Complexity	Notes
Graham Scan	$O(n \log n)$	Sort by angle, use stack
Andrew's Monotone	$O(n \log n)$	Sort by x, build upper/lower
Jarvis March	$O(nh)$	Wrap hull, h = hull size
Chan's Algorithm	$O(n \log h)$	Output-sensitive hull

Steps:

1. Sort points
2. Build lower hull
3. Build upper hull
4. Concatenate

Closest Pair of Points

Divide-and-conquer approach.

Step	Description
Split by x	Divide points into halves
Recurse and merge	Track min distance across strip

Complexity: $O(n \log n)$

Formula:

$$d(p, q) = \sqrt{(x_p - x_q)^2 + (y_p - y_q)^2}$$

Line Intersection

Two segments (p_1, p_2) and (q_1, q_2) intersect if:

1. Orientations differ
2. Segments overlap on line if collinear

Tiny Code:

```
def intersect(p1, p2, q1, q2):
    o1 = orient(p1, p2, q1)
    o2 = orient(p1, p2, q2)
    o3 = orient(q1, q2, p1)
    o4 = orient(q1, q2, p2)
    return o1 != o2 and o3 != o4
```

Polygon Area (Shoelace Formula)

For vertices (x_i, y_i) in order:

$$A = \frac{1}{2} \left| \sum_{i=0}^{n-1} (x_i y_{i+1} - x_{i+1} y_i) \right|$$

Tiny Code:

```
def area(poly):
    s = 0
    n = len(poly)
    for i in range(n):
        x1, y1 = poly[i]
        x2, y2 = poly[(i+1)%n]
        s += x1*y2 - x2*y1
    return abs(s)/2
```

Point in Polygon

Method	Idea	Complexity
Ray Casting	Count edge crossings	$O(n)$
Winding Number	Track signed rotations	$O(n)$
Convex Test	Check all orientations	$O(n)$

Ray Casting: Odd number of crossings → inside.

Rotating Calipers

Used for:

- Polygon diameter (farthest pair)
- Minimum bounding box
- Width and antipodal pairs

Idea: Sweep around convex hull using tangents. Complexity: $O(n)$ after hull.

Sweep Line Techniques

Problem	Method	Complexity
Closest Pair	Active set by y	$O(n \log n)$
Segment Intersection	Event-based sweeping	$O((n+k) \log n)$
Rectangle Union Area	Vertical edge events	$O(n \log n)$
Skyline Problem	Merge by height	$O(n \log n)$

Use balanced trees or priority queues for active sets.

Circle Geometry

Concept	Formula
Equation	$(x - x_c)^2 + (y - y_c)^2 = r^2$
Tangent Length	$\sqrt{d^2 - r^2}$
Two-Circle Intersection	Distance-based geometry

Spatial Data Structures

Structure	Use Case	Notes
KD-Tree	Nearest neighbor search	Axis-aligned splits
R-Tree	Range queries	Bounding boxes hierarchy
Quadtree	2D recursive subdivision	Graphics, collision detection
Octree	3D extension	Volumetric partitioning

Structure	Use Case	Notes
BSP Tree	Planar splits	Rendering, collision

Rasterization and Graphics

Algorithm	Purpose	Notes
Bresenham Line	Draw line integer grid	No floating point
Midpoint Circle	Circle rasterization	Symmetry exploitation
Scanline Fill	Polygon fill algorithm	Sort edges, horizontal sweep
Z-Buffer	Hidden surface removal	Per-pixel depth comparison
Phong Shading	Smooth lighting	Interpolate normals

Pathfinding in Space

Algorithm	Description	Notes
A*	Heuristic shortest path	$f(n) = g(n) + h(n)$
Theta*	Any-angle path	Shortcut-based
RRT / RRT*	Random exploration	Robotics planning
PRM	Probabilistic roadmap	Sampled graph
Visibility Graph	Connect visible points	Geometric planning

Quick Summary

Task	Algorithm	Complexity
Convex Hull	Graham / Andrew	$O(n \log n)$
Closest Pair	Divide and Conquer	$O(n \log n)$
Segment Intersection Detection	Sweep Line	$O(n \log n)$
Point in Polygon	Ray Casting	$O(n)$
Polygon Area	Shoelace Formula	$O(n)$
Nearest Neighbor Search	KD-Tree	$O(\log n)$
Pathfinding	A*	$O(E \log V)$

Tip

- Always sort points for geometry preprocessing.
- Use cross product for orientation tests.
- Prefer integer arithmetic when possible to avoid floating errors.

Page 11. Systems, Databases, and Distributed Algorithms Quick Use

Systems and databases rely on algorithms that manage memory, concurrency, persistence, and coordination. This page gives an overview of the most important ones.

Concurrency Control

Ensures correctness when multiple transactions or threads run at once.

Method	Idea	Notes
Two-Phase Locking (2PL)	Acquire locks, then release after commit	Guarantees serializability
Strict 2PL	Hold all locks until commit	Prevents cascading aborts
Conservative 2PL	Lock all before execution	Deadlock-free but less parallel
Timestamp Ordering	Order by timestamps	May abort late transactions
Multiversion CC (MVCC)	Readers get snapshots	Used in PostgreSQL, InnoDB
Optimistic CC (OCC)	Validate at commit	Best for low conflict workloads

Tiny Code: Timestamp Ordering

```
# Simplified
if write_ts[x] > txn_ts or read_ts[x] > txn_ts:
    abort()
else:
    write_ts[x] = txn_ts
```

Each object tracks read and write timestamps.

Deadlocks

Circular waits among transactions.

Detection | Build Wait-For Graph, detect cycle |
Prevention | Wait-Die (old waits) / Wound-Wait (young aborts) |

Detection Complexity: $O(V + E)$

Tiny Code (Wait-For Graph Cycle Check):

```
def has_cycle(graph):
    visited, stack = set(), set()
    def dfs(u):
        visited.add(u)
        stack.add(u)
        for v in graph[u]:
            if v not in visited and dfs(v): return True
            if v in stack: return True
        stack.remove(u)
        return False
    return any(dfs(u) for u in graph)
```

Logging and Recovery

Technique	Description	Notes
Write-Ahead Log	Log before data	Ensures durability
ARIES	Analysis, Redo, Undo phases	Industry standard
Checkpointing	Save consistent snapshot	Speeds recovery
Shadow Paging	Copy-on-write updates	Simpler but less flexible

Recovery after crash:

1. Analysis: find active transactions
2. Redo: reapply committed changes
3. Undo: revert uncommitted ones

Indexing

Accelerates lookups and range queries.

Index Type	Description	Notes
B-Tree / B+Tree	Balanced multiway tree	Disk-friendly
Hash Index	Exact match only	No range queries
GiST / R-Tree	Spatial data	Bounding box hierarchy
Inverted Index	Text search	Maps token to document list

B+Tree Complexity: $O(\log_B N)$ (B = branching factor)

Tiny Code (Binary Search in Index):

```
def search(node, key):
    i = bisect_left(node.keys, key)
    if i < len(node.keys) and node.keys[i] == key:
        return node.values[i]
    if node.is_leaf:
        return None
    return search(node.children[i], key)
```

Query Processing

Step	Description
Parsing	Build abstract syntax tree
Optimization	Reorder joins, pick indices
Execution Plan	Choose algorithm per operator
Execution	Evaluate iterators or pipelines

Common join strategies:

Join Type	Complexity	Notes
Nested Loop	$O(nm)$	Simple, slow
Hash Join	$O(n + m)$	Build + probe
Sort-Merge Join	$O(n \log n + m \log m)$	Sorted inputs

Caching and Replacement

Policy	Description	Notes
LRU	Evict least recently used	Simple, temporal locality
LFU	Evict least frequently used	Good for stable patterns
ARC / LIRS	Adaptive hybrid	Handles mixed workloads
Random	Random eviction	Simple, fair

Tiny Code (LRU using OrderedDict):

```
from collections import OrderedDict

class LRU:
    def __init__(self, cap):
        self.cap = cap
        self.cache = OrderedDict()
    def get(self, k):
        if k not in self.cache: return -1
        self.cache.move_to_end(k)
        return self.cache[k]
    def put(self, k, v):
        if k in self.cache: self.cache.move_to_end(k)
        self.cache[k] = v
        if len(self.cache) > self.cap: self.cache.popitem(last=False)
```

Distributed Systems Core

Problem	Description	Typical Solution
Consensus	Agree on value across nodes	Paxos, Raft
Leader Election	Pick coordinator	Bully, Raft
Replication	Maintain copies	Log replication
Partitioning	Split data	Consistent hashing
Membership	Detect nodes	Gossip protocols

Raft Consensus (Simplified)

Phase	Action
Election	Nodes vote, elect leader
Replication	Leader appends log entries

Phase	Action
Commitment	Once majority acknowledge

Safety: Committed entries never change. Liveness: New leader elected on failure.

Tiny Code Sketch:

```
if vote_request.term > term:
    term = vote_request.term
    voted_for = candidate
```

Consistent Hashing

Distributes keys across nodes smoothly.

Step	Description
Hash each node to ring	e.g. hash(node_id)
Hash each key	Find next node clockwise
Add/remove node	Only nearby keys move

Used in: Dynamo, Cassandra, Memcached.

Fault Tolerance Patterns

Pattern	Description	Example
Replication	Multiple copies	Primary-backup
Checkpointing	Save progress periodically	ML training
Heartbeats	Liveness detection	Cluster managers
Retry + Backoff	Handle transient failures	API calls
Quorum Reads/Writes	Require majority agreement	Cassandra

Distributed Coordination

Tool / Protocol	Description	Example Use
ZooKeeper	Centralized coordination	Locks, config
Raft	Distributed consensus	Log replication

Tool / Protocol	Description	Example Use
Etcd	Key-value store on Raft	Cluster metadata

Summary Table

Topic	Algorithm / Concept	Complexity	Notes
Locking	2PL, MVCC, OCC	varies	Transaction isolation
Deadlock	Wait-Die, Detection	$O(V + E)$	Graph-based check
Recovery	ARIES, WAL	varies	Crash recovery
Indexing	B+Tree, Hash Index	$O(\log N)$	Faster queries
Join	Hash / Sort-Merge	varies	Query optimization
Cache	LRU, LFU	$O(1)$	Data locality
Consensus	Raft, Paxos	$O(n)$ msg	Fault tolerance
Partitioning	Consistent Hashing	$O(1)$ avg	Scalability

Quick Tips

- Always ensure serializability in concurrency.
- Use MVCC for read-heavy workloads.
- ARIES ensures durability via WAL.
- For scalability, partition and replicate wisely.
- Consensus is required for shared state correctness.

Page 12. Algorithms for AI, ML, and Optimization Quick Use

This page gathers classical algorithms that power modern AI and machine learning systems, from clustering and classification to gradient-based learning and metaheuristics.

Classical Machine Learning Algorithms

Category	Algorithm	Core Idea	Complexity
Clustering	k-Means	Assign to nearest centroid, update centers	$O(nkt)$
Clustering	k-Medoids (PAM)	Representative points as centers	$O(k(n-k)^2)$
Clustering	Gaussian Mixture (EM)	Soft assignments via probabilities	$O(nkd)$ per iter

Category	Algorithm	Core Idea	Complexity
Classification	Naive Bayes	Apply Bayes rule with feature independence	$O(nd)$
Classification	Logistic Regression	Linear + sigmoid activation	$O(nd)$
Classification	SVM (Linear)	Maximize margin via convex optimization	$O(nd)$ approx
Classification	k-NN	Vote from nearest neighbors	$O(nd)$ per query
Trees	Decision Tree (CART)	Recursive splitting by impurity	$O(nd \log n)$
Projection	LDA / PCA	Find projection maximizing variance or class separation	$O(d^3)$

Tiny Code: k-Means

```
import random, math

def kmeans(points, k, iters=100):
    centroids = random.sample(points, k)
    for _ in range(iters):
        groups = [[] for _ in range(k)]
        for p in points:
            idx = min(range(k), key=lambda i: (p[0]-centroids[i][0])2 + (p[1]-centroids[i][1]
            groups[idx].append(p)
        new_centroids = []
        for g in groups:
            if g:
                x = sum(p[0] for p in g)/len(g)
                y = sum(p[1] for p in g)/len(g)
                new_centroids.append((x,y))
            else:
                new_centroids.append(random.choice(points))
        if centroids == new_centroids: break
        centroids = new_centroids
    return centroids
```

Linear Models

Model	Formula	Loss Function
Linear Regression	$\hat{y} = w^T x + b$	MSE: $\frac{1}{n}\sum(y - \hat{y})^2$
Logistic Regression	$\hat{y} = \sigma(w^T x + b)$	Cross-Entropy
Ridge Regression	Linear + L_2 penalty	$L = \text{MSE} + \lambda \lvert w \rvert^2$
Lasso Regression	Linear + L_1 penalty	$L = \text{MSE} + \lambda \lvert w \rvert_1$

Tiny Code (Gradient Descent for Linear Regression):

```
def train(X, y, lr=0.01, epochs=1000):
    w = [0]*len(X[0])
    b = 0
    for _ in range(epochs):
        for i in range(len(y)):
            y_pred = sum(w[j]*X[i][j] for j in range(len(w))) + b
            err = y_pred - y[i]
            for j in range(len(w)):
                w[j] -= lr * err * X[i][j]
            b -= lr * err
    return w, b
```

Decision Trees and Ensembles

Algorithm	Description	Notes
ID3 / C4.5 / CART	Split by info gain or Gini	Recursive, interpretable
Random Forest	Bagging + Decision Trees	Reduces variance
Gradient Boosting	Sequential residual fitting	XGBoost, LightGBM, CatBoost
AdaBoost	Weighted weak learners	Sensitive to noise

Impurity Measures:

- Gini: $1 - \sum p_i^2$
- Entropy: $-\sum p_i \log_2 p_i$

Support Vector Machines (SVM)

Finds a maximum margin hyperplane.

Objective:

$$\min_{w,b} \frac{1}{2}|w|^2 + C \sum \xi_i$$

subject to $y_i(w^T x_i + b) \geq 1 - \xi_i$

Kernel trick enables nonlinear separation:

$$K(x_i, x_j) = \phi(x_i) \cdot \phi(x_j)$$

Neural Network Fundamentals

Component	Description
Neuron	$y = \sigma(w \cdot x + b)$
Activation	Sigmoid, ReLU, Tanh
Loss	MSE, Cross-Entropy
Training	Gradient Descent + Backprop
Optimizers	SGD, Adam, RMSProp

Forward Propagation:

$$a^{(l)} = \sigma(W^{(l)} a^{(l-1)} + b^{(l)})$$

Backpropagation computes gradients layer by layer.

Gradient Descent Variants

Variant	Idea	Notes
Batch	Use all data each step	Stable but slow
Stochastic	Update per sample	Noisy, fast
Mini-batch	Group updates	Common practice
Momentum	Add velocity term	Faster convergence
Adam	Adaptive moment estimates	Most popular

Update Rule:

$$w = w - \eta \cdot \frac{\partial L}{\partial w}$$

Unsupervised Learning

Algorithm	Description	Notes
PCA	Variance-based projection	Eigen decomposition
ICA	Independent components	Signal separation

Algorithm	Description	Notes
t-SNE	Preserve local structure	Visualization only
Autoencoder	NN reconstruction model	Dimensionality red.

PCA Formula: Covariance $C = \frac{1}{n} X^T X$, eigenvectors of C are principal axes.

Probabilistic Models

Model	Description	Notes
Naive Bayes	Independence assumption	$P(y\|x) \propto P(y) \prod P(x_i\|y)$
HMM	Sequential hidden states	Viterbi for decoding
Markov Chains	Transition probabilities	$P(x_t\|x_{t-1})$
Gaussian Mixture	Soft clustering	EM algorithm

Optimization and Metaheuristics

Algorithm	Category	Notes
Gradient Descent	Convex Opt.	Differentiable objectives
Newton's Method	Second-order	Uses Hessian
Simulated Annealing	Prob. search	Escape local minima
Genetic Algorithm	Evolutionary	Population-based search
PSO (Swarm)	Collective move	Inspired by flocking behavior
Hill Climbing	Greedy search	Local optimization

Reinforcement Learning Core

Concept	Description	Example
Agent	Learner/decision maker	Robot, policy
Environment	Provides states, rewards	Game, simulation
Policy	Mapping state $\rightarrow$ action	$\pi(s) = a$
Value Function	Expected return	$V(s)$, $Q(s, a)$

Q-Learning Update:

$$Q(s,a) \leftarrow Q(s,a) + \alpha(r + \gamma \max_{a'} Q(s',a') - Q(s,a))$$

Tiny Code:

```
Q[s][a] += alpha * (r + gamma * max(Q[s_next]) - Q[s][a])
```

AI Search Algorithms

Algorithm	Description	Complexity	Notes
BFS	Shortest path unweighted	$O(V+E)$	Level order search
DFS	Deep exploration	$O(V+E)$	Backtracking
A* Search	Informed, uses heuristic	$O(E \log V)$	$f(n) = g(n) + h(n)$
IDA*	Iterative deepening A*	Memory efficient	Optimal if h admissible
Beam Search	Keep best k states	Approximate	NLP decoding

Evaluation Metrics

Task	Metric	Formula / Meaning
Classification	Accuracy, Precision, Recall	$\frac{TP}{TP+FP}$, $\frac{TP}{TP+FN}$
Regression	RMSE, MAE, R^2	Fit and error magnitude
Clustering	Silhouette Score	Cohesion vs separation
Ranking	MAP, NDCG	Order-sensitive

Confusion Matrix:

	Pred +	Pred -
Actual +	TP	FN
Actual -	FP	TN

Summary

Category	Algorithm Example	Notes
Clustering	k-Means, GMM	Unsupervised grouping
Classification	Logistic, SVM, Trees	Supervised labeling
Regression	Linear, Ridge, Lasso	Predict continuous value
Optimization	GD, Adam, Simulated Annealing	Minimize loss
Probabilistic	Bayes, HMM, EM	Uncertainty modeling
Reinforcement	Q-Learning, SARSA	Reward-based learning

The Plan

Chapter 1. Foundations of Algorithms

1. What Is an Algorithm?

#	Algorithm	Note
1	Euclid's GCD	Oldest known algorithm for greatest common divisor
2	Sieve of Eratosthenes	Generate primes efficiently
3	Binary Search	Divide and conquer search
4	Exponentiation by Squaring	Fast power computation
5	Long Division	Classic step-by-step arithmetic
6	Modular Addition Algorithm	Wrap-around arithmetic
7	Base Conversion Algorithm	Convert between number systems
8	Factorial Computation	Recursive and iterative approaches
9	Fibonacci Sequence	Recursive vs. dynamic computation
10	Tower of Hanoi	Recursive problem-solving pattern

2. Measuring Time and Space

#	Algorithm	Note
11	Counting Operations	Manual step-counting for complexity
12	Loop Analysis	Evaluate time cost of loops
13	Recurrence Expansion	Analyze recursive costs
14	Amortized Analysis	Average per-operation cost
15	Space Counting	Stack and heap tracking
16	Memory Footprint Estimator	Track per-variable usage
17	Time Complexity Table	Map O(1)…O(n^2)…O(2)
18	Space-Time Tradeoff	Cache vs. recomputation
19	Profiling Algorithm	Empirical time measurement
20	Benchmarking Framework	Compare algorithm performance

3. Big-O, Big-Theta, Big-Omega

#	Algorithm	Note
21	Growth Rate Comparator	Compare asymptotic behaviors
22	Dominant Term Extractor	Simplify runtime expressions
23	Limit-Based Complexity Test	Using limits for asymptotics
24	Summation Simplifier	Sum of arithmetic/geometric sequences
25	Recurrence Tree Method	Visualize recursive costs
26	Master Theorem Evaluator	Solve T(n) recurrences
27	Big-Theta Proof Builder	Bounding upper and lower limits
28	Big-Omega Case Finder	Best-case scenario analysis
29	Empirical Complexity Estimator	Measure via doubling experiments
30	Complexity Class Identifier	Match runtime to known class

4. Algorithmic Paradigms (Greedy, Divide and Conquer, DP)

#	Algorithm	Note
31	Greedy Coin Change	Local optimal step-by-step
32	Huffman Coding	Greedy compression tree
33	Merge Sort	Divide and conquer sort
34	Binary Search	Divide and conquer search
35	Karatsuba Multiplication	Recursive divide & conquer
36	Matrix Chain Multiplication	DP with substructure
37	Longest Common Subsequence	Classic DP problem
38	Rod Cutting	DP optimization
39	Activity Selection	Greedy scheduling
40	Optimal Merge Patterns	Greedy file merging

5. Recurrence Relations

#	Algorithm	Note
41	Linear Recurrence Solver	Closed-form for linear recurrences
42	Master Theorem	Divide-and-conquer complexity
43	Substitution Method	Inductive proof approach
44	Iteration Method	Expand recurrence step-by-step
45	Generating Functions	Transform recurrences
46	Matrix Exponentiation	Solve linear recurrences fast

#	Algorithm	Note
47	Recurrence to DP Table	Tabulation approach
48	Divide & Combine Template	Convert recurrence into algorithm
49	Memoized Recursive Solver	Store overlapping results
50	Characteristic Polynomial	Solve homogeneous recurrence

6. Searching Basics

#	Algorithm	Note
51	Linear Search	Sequential element scan
52	Binary Search	Midpoint halving
53	Jump Search	Block skip linear
54	Exponential Search	Doubling step size
55	Interpolation Search	Estimate position by value
56	Ternary Search	Divide into thirds
57	Fibonacci Search	Golden ratio search
58	Sentinel Search	Early termination optimization
59	Bidirectional Search	Meet-in-the-middle
60	Search in Rotated Array	Adapted binary search

7. Sorting Basics

#	Algorithm	Note
61	Bubble Sort	Adjacent swap sort
62	Selection Sort	Find minimum each pass
63	Insertion Sort	Incremental build sort
64	Shell Sort	Gap-based insertion
65	Merge Sort	Divide-and-conquer
66	Quick Sort	Partition-based
67	Heap Sort	Binary heap order
68	Counting Sort	Integer key distribution
69	Radix Sort	Digit-by-digit
70	Bucket Sort	Group into ranges

8. Data Structures Overview

#	Algorithm	Note
71	Stack Push/Pop	LIFO operations
72	Queue Enqueue/Dequeue	FIFO operations
73	Singly Linked List	Linear node chain
74	Doubly Linked List	Bidirectional traversal
75	Hash Table Insertion	Key-value indexing
76	Binary Search Tree Insert	Ordered node placement
77	Heapify	Build heap in-place
78	Union-Find Operations	Disjoint-set management
79	Graph Adjacency List Build	Sparse representation
80	Trie Insertion/Search	Prefix tree for strings

9. Graphs and Trees Overview

#	Algorithm	Note
81	DFS Traversal	Depth-first exploration
82	BFS Traversal	Level-order exploration
83	Topological Sort	DAG ordering
84	Minimum Spanning Tree	Kruskal/Prim overview
85	Dijkstra's Shortest Path	Weighted graph shortest route
86	Bellman-Ford	Handle negative edges
87	Floyd-Warshall	All-pairs shortest path
88	Union-Find for MST	Edge grouping
89	Tree Traversals	Inorder, Preorder, Postorder
90	LCA (Lowest Common Ancestor)	Common node in tree

10. Algorithm Design Patterns

#	Algorithm	Note
91	Brute Force	Try all possibilities
92	Greedy Choice	Local optimum per step
93	Divide and Conquer	Break and merge
94	Dynamic Programming	Reuse subproblems
95	Backtracking	Explore with undo
96	Branch and Bound	Prune search space
97	Randomized Algorithm	Inject randomness
98	Approximation Algorithm	Near-optimal solution
99	Online Algorithm	Step-by-step decision

#	Algorithm	Note
100	Hybrid Strategy	Combine paradigms

Chapter 2. Sorting and Searching

11. Elementary Sorting (Bubble, Insertion, Selection)

#	Algorithm	Note
101	Bubble Sort	Swap adjacent out-of-order elements
102	Improved Bubble Sort	Stop early if already sorted
103	Cocktail Shaker Sort	Bidirectional bubble pass
104	Selection Sort	Select smallest element each pass
105	Double Selection Sort	Find both min and max each pass
106	Insertion Sort	Insert each element into correct spot
107	Binary Insertion Sort	Use binary search for position
108	Gnome Sort	Simple insertion-like with swaps
109	Odd-Even Sort	Parallel-friendly comparison sort
110	Stooge Sort	Recursive quirky educational sort

12. Divide-and-Conquer Sorting (Merge, Quick, Heap)

#	Algorithm	Note
111	Merge Sort	Recursive divide and merge
112	Iterative Merge Sort	Bottom-up non-recursive version
113	Quick Sort	Partition-based recursive sort
114	Hoare Partition Scheme	Classic quicksort partition
115	Lomuto Partition Scheme	Simpler but less efficient
116	Randomized Quick Sort	Avoid worst-case pivot
117	Heap Sort	Heapify + extract max repeatedly
118	3-Way Quick Sort	Handle duplicates efficiently
119	External Merge Sort	Disk-based merge for large data
120	Parallel Merge Sort	Divide work among threads

13. Counting and Distribution Sorts (Counting, Radix, Bucket)

#	Algorithm	Note
121	Counting Sort	Count key occurrences
122	Stable Counting Sort	Preserve order of equals
123	Radix Sort (LSD)	Least significant digit first
124	Radix Sort (MSD)	Most significant digit first
125	Bucket Sort	Distribute into buckets
126	Pigeonhole Sort	Simple bucket variant
127	Flash Sort	Distribution with in-place correction
128	Postman Sort	Stable multi-key sort
129	Address Calculation Sort	Hash-like distribution
130	Spread Sort	Hybrid radix/quick strategy

14. Hybrid Sorts (IntroSort, Timsort)

#	Algorithm	Note
131	IntroSort	Quick + Heap fallback
132	TimSort	Merge + Insertion + Runs
133	Dual-Pivot QuickSort	Modern quicksort optimization
134	SmoothSort	Heap-like adaptive sort
135	Block Merge Sort	Cache-efficient merge variant
136	Adaptive Merge Sort	Adjusts to partially sorted data
137	PDQSort	Pattern-defeating quicksort
138	WikiSort	Stable in-place merge
139	GrailSort	In-place stable mergesort
140	Adaptive Hybrid Sort	Dynamically selects strategy

15. Special Sorts (Cycle, Gnome, Comb, Pancake)

#	Algorithm	Note
141	Cycle Sort	Minimal writes
142	Comb Sort	Shrinking gap bubble
143	Gnome Sort	Insertion-like with swaps
144	Cocktail Sort	Two-way bubble
145	Pancake Sort	Flip-based sorting
146	Bitonic Sort	Parallel network sorting
147	Odd-Even Merge Sort	Sorting network design
148	Sleep Sort	Uses timing as order key
149	Bead Sort	Simulates gravity

#	Algorithm	Note
150	Bogo Sort	Randomly permute until sorted

16. Linear and Binary Search

#	Algorithm	Note
151	Linear Search	Scan sequentially
152	Linear Search (Sentinel)	Guard element at end
153	Binary Search (Iterative)	Halve interval each loop
154	Binary Search (Recursive)	Halve interval via recursion
155	Binary Search (Lower Bound)	First >= target
156	Binary Search (Upper Bound)	First > target
157	Exponential Search	Double step size
158	Jump Search	Jump fixed steps then linear
159	Fibonacci Search	Golden-ratio style jumps
160	Uniform Binary Search	Avoid recomputing midpoints

17. Interpolation and Exponential Search

#	Algorithm	Note
161	Interpolation Search	Estimate index by value
162	Recursive Interpolation Search	Divide by estimated midpoint
163	Exponential Search	Double and binary refine
164	Doubling Search	Generic exponential pattern
165	Galloping Search	Used in TimSort merges
166	Unbounded Binary Search	Find bounds dynamically
167	Root-Finding Bisection	Search zero-crossing
168	Golden Section Search	Optimize unimodal function
169	Fibonacci Search (Optimum)	Similar to golden search
170	Jump + Binary Hybrid	Combined probing strategy

18. Selection Algorithms (Quickselect, Median of Medians)

#	Algorithm	Note
171	Quickselect	Partition-based selection
172	Median of Medians	Deterministic pivot

#	Algorithm	Note
173	Randomized Select	Random pivot version
174	Binary Search on Answer	Range-based selection
175	Order Statistics Tree	BST with rank queries
176	Tournament Tree Selection	Hierarchical comparison
177	Heap Select (Min-Heap)	Maintain top-k elements
178	Partial QuickSort	Sort partial prefix
179	BFPRT Algorithm	Linear-time selection
180	Kth Largest Stream	Streaming selection

19. Range Searching and Nearest Neighbor

#	Algorithm	Note
181	Binary Search Range	Find lower and upper bounds
182	Segment Tree Query	Sum/min/max over interval
183	Fenwick Tree Query	Efficient prefix sums
184	Interval Tree Search	Overlap queries
185	KD-Tree Search	Spatial nearest neighbor
186	R-Tree Query	Range search in geometry
187	Range Minimum Query (RMQ)	Sparse table approach
188	Mo's Algorithm	Offline query reordering
189	Sweep Line Range Search	Sort + scan technique
190	Ball Tree Nearest Neighbor	Metric-space search

20. Search Optimizations and Variants

#	Algorithm	Note
191	Binary Search with Tolerance	For floating values
192	Ternary Search	Unimodal optimization
193	Hash-Based Search	O(1) expected lookup
194	Bloom Filter Lookup	Probabilistic membership
195	Cuckoo Hash Search	Dual-hash relocation
196	Robin Hood Hashing	Equalize probe lengths
197	Jump Consistent Hashing	Stable hash assignment
198	Prefix Search in Trie	Auto-completion lookup
199	Pattern Search in Suffix Array	Fast substring lookup
200	Search in Infinite Array	Dynamic bound finding

Chapter 3. Data Structures in Action

21. Arrays, Linked Lists, Stacks, Queues

#	Algorithm	Note
201	Dynamic Array Resize	Doubling strategy for capacity
202	Circular Array Implementation	Wrap-around indexing
203	Singly Linked List Insert/Delete	Basic node manipulation
204	Doubly Linked List Insert/Delete	Two-way linkage
205	Stack Push/Pop	LIFO structure
206	Queue Enqueue/Dequeue	FIFO structure
207	Deque Implementation	Double-ended queue
208	Circular Queue	Fixed-size queue with wrap-around
209	Stack via Queue	Implement stack using two queues
210	Queue via Stack	Implement queue using two stacks

22. Hash Tables and Variants (Cuckoo, Robin Hood, Consistent)

#	Algorithm	Note
211	Hash Table Insertion	Key-value pair with modulo
212	Linear Probing	Resolve collisions sequentially
213	Quadratic Probing	Nonlinear probing sequence
214	Double Hashing	Alternate hash on collision
215	Cuckoo Hashing	Two-table relocation strategy
216	Robin Hood Hashing	Equalize probe length fairness
217	Chained Hash Table	Linked list buckets
218	Perfect Hashing	No-collision mapping
219	Consistent Hashing	Stable distribution across nodes
220	Dynamic Rehashing	Resize on load factor threshold

23. Heaps (Binary, Fibonacci, Pairing)

#	Algorithm	Note
221	Binary Heap Insert	Bubble-up maintenance
222	Binary Heap Delete	Heapify-down maintenance
223	Build Heap (Heapify)	Bottom-up O(n) build
224	Heap Sort	Extract max repeatedly

#	Algorithm	Note
225	Min Heap Implementation	For smallest element access
226	Max Heap Implementation	For largest element access
227	Fibonacci Heap Insert/Delete	Amortized efficient operations
228	Pairing Heap Merge	Lightweight mergeable heap
229	Binomial Heap Merge	Merge trees of equal order
230	Leftist Heap Merge	Maintain rank-skewed heap

24. Balanced Trees (AVL, Red-Black, Splay, Treap)

#	Algorithm	Note
231	AVL Tree Insert	Rotate to maintain balance
232	AVL Tree Delete	Balance after deletion
233	Red-Black Tree Insert	Color fix and rotations
234	Red-Black Tree Delete	Maintain invariants
235	Splay Tree Access	Move accessed node to root
236	Treap Insert	Priority-based rotation
237	Treap Delete	Randomized balance
238	Weight Balanced Tree	Maintain subtree weights
239	Scapegoat Tree Rebuild	Rebalance on size threshold
240	AA Tree	Simplified red-black variant

25. Segment Trees and Fenwick Trees

#	Algorithm	Note
241	Build Segment Tree	Recursive construction
242	Range Sum Query	Recursive or iterative query
243	Range Update	Lazy propagation technique
244	Point Update	Modify single element
245	Fenwick Tree Build	Incremental binary index
246	Fenwick Update	Update cumulative sums
247	Fenwick Query	Prefix sum retrieval
248	Segment Tree Merge	Combine child results
249	Persistent Segment Tree	Maintain history of versions
250	2D Segment Tree	For matrix range queries

26. Disjoint Set Union (Union-Find)

#	Algorithm	Note
251	Make-Set	Initialize each element
252	Find	Locate representative
253	Union	Merge two sets
254	Union by Rank	Attach smaller tree to larger
255	Path Compression	Flatten tree structure
256	DSU with Rollback	Support undo operations
257	DSU on Tree	Track subtree connectivity
258	Kruskal's MST	Edge selection with DSU
259	Connected Components	Group graph nodes
260	Offline Query DSU	Handle dynamic unions

27. Probabilistic Data Structures (Bloom, Count-Min, HyperLogLog)

#	Algorithm	Note
261	Bloom Filter Insert	Hash to bit array
262	Bloom Filter Query	Probabilistic membership check
263	Counting Bloom Filter	Support deletions via counters
264	Cuckoo Filter	Space-efficient alternative
265	Count-Min Sketch	Approximate frequency table
266	HyperLogLog	Cardinality estimation
267	Flajolet-Martin	Early probabilistic counting
268	MinHash	Estimate Jaccard similarity
269	Reservoir Sampling	Random k-sample stream
270	Skip Bloom Filter	Range queries on Bloom

28. Skip Lists and B-Trees

#	Algorithm	Note
271	Skip List Insert	Probabilistic layered list
272	Skip List Delete	Adjust pointers
273	Skip List Search	Jump via tower levels
274	B-Tree Insert	Split on overflow
275	B-Tree Delete	Merge on underflow
276	B+ Tree Search	Leaf-based sequential scan

#	Algorithm	Note
277	B+ Tree Range Query	Efficient ordered access
278	B* Tree	More space-efficient variant
279	Adaptive Radix Tree	Byte-wise branching
280	Trie Compression	Path compression optimization

29. Persistent and Functional Data Structures

#	Algorithm	Note
281	Persistent Stack	Keep all versions
282	Persistent Array	Copy-on-write segments
283	Persistent Segment Tree	Versioned updates
284	Persistent Linked List	Immutable nodes
285	Functional Queue	Amortized reverse lists
286	Finger Tree	Fast concat and split
287	Zipper Structure	Localized mutation
288	Red-Black Persistent Tree	Immutable balanced tree
289	Trie with Versioning	Historical string lookup
290	Persistent Union-Find	Time-travel connectivity

30. Advanced Trees and Range Queries

#	Algorithm	Note
291	Sparse Table Build	Static range min/max
292	Cartesian Tree	RMQ to LCA transformation
293	Segment Tree Beats	Handle complex queries
294	Merge Sort Tree	Range count queries
295	Wavelet Tree	Rank/select by value
296	KD-Tree	Multidimensional queries
297	Range Tree	Orthogonal range queries
298	Fenwick 2D Tree	Matrix prefix sums
299	Treap Split/Merge	Range-based treap ops
300	Mo's Algorithm on Tree	Offline subtree queries

Chapter 4. Graph Algorithms

31. Traversals (DFS, BFS, Iterative Deepening)

#	Algorithm	Note
301	Depth-First Search (Recursive)	Explore deeply before backtracking
302	Depth-First Search (Iterative)	Stack-based exploration
303	Breadth-First Search (Queue)	Level-order traversal
304	Iterative Deepening DFS	Combine depth-limit + completeness
305	Bidirectional BFS	Search from both ends
306	DFS on Grid	Maze solving / connected components
307	BFS on Grid	Shortest path in unweighted graph
308	Multi-Source BFS	Parallel layer expansion
309	Topological Sort (DFS-based)	DAG ordering
310	Topological Sort (Kahn's Algorithm)	In-degree tracking

32. Strongly Connected Components (Tarjan, Kosaraju)

#	Algorithm	Note
311	Kosaraju's Algorithm	Two-pass DFS
312	Tarjan's Algorithm	Low-link discovery
313	Gabow's Algorithm	Stack pair tracking
314	SCC DAG Construction	Condensed component graph
315	SCC Online Merge	Incremental condensation
316	Component Label Propagation	Iterative labeling
317	Path-Based SCC	DFS with path stack
318	Kosaraju Parallel Version	SCC via parallel DFS
319	Dynamic SCC Maintenance	Add/remove edges
320	SCC for Weighted Graph	Combine with edge weights

33. Shortest Paths (Dijkstra, Bellman-Ford, A*, Johnson)

#	Algorithm	Note
321	Dijkstra (Binary Heap)	Greedy edge relaxation
322	Dijkstra (Fibonacci Heap)	Improved priority queue
323	Bellman-Ford	Negative weights support
324	SPFA (Queue Optimization)	Faster average Bellman-Ford
325	A* Search	Heuristic-guided path
326	Floyd–Warshall	All-pairs shortest path
327	Johnson's Algorithm	All-pairs using reweighting
328	0-1 BFS	Deque-based shortest path
329	Dial's Algorithm	Integer weight buckets

#	Algorithm	Note
330	Multi-Source Dijkstra	Multiple starting points

34. Shortest Path Variants (0–1 BFS, Bidirectional, Heuristic A*)

#	Algorithm	Note
331	0–1 BFS	For edges with weight 0 or 1
332	Bidirectional Dijkstra	Meet in the middle
333	A* with Euclidean Heuristic	Spatial shortest path
334	ALT Algorithm	A* landmarks + triangle inequality
335	Contraction Hierarchies	Preprocessing for road networks
336	CH Query Algorithm	Shortcut-based routing
337	Bellman-Ford Queue Variant	Early termination
338	Dijkstra with Early Stop	Halt on target
339	Goal-Directed Search	Restrict expansion direction
340	Yen's K Shortest Paths	Enumerate multiple best paths

35. Minimum Spanning Trees (Kruskal, Prim, Borůvka)

#	Algorithm	Note
341	Kruskal's Algorithm	Sort edges + union-find
342	Prim's Algorithm (Heap)	Grow MST from seed
343	Prim's Algorithm (Adj Matrix)	Dense graph variant
344	Borůvka's Algorithm	Component merging
345	Reverse-Delete MST	Remove heavy edges
346	MST via Dijkstra Trick	For positive weights
347	Dynamic MST Maintenance	Handle edge updates
348	Minimum Bottleneck Spanning Tree	Max edge minimization
349	Manhattan MST	Grid graph optimization
350	Euclidean MST (Kruskal + Geometry)	Use Delaunay graph

36. Flows (Ford–Fulkerson, Edmonds–Karp, Dinic)

#	Algorithm	Note
351	Ford–Fulkerson	Augmenting path method
352	Edmonds–Karp	BFS-based Ford–Fulkerson

#	Algorithm	Note
353	Dinic's Algorithm	Level graph + blocking flow
354	Push–Relabel	Local preflow push
355	Capacity Scaling	Speed-up with capacity tiers
356	Cost Scaling	Min-cost optimization
357	Min-Cost Max-Flow (Bellman-Ford)	Costed augmenting paths
358	Min-Cost Max-Flow (SPFA)	Faster average
359	Circulation with Demands	Generalized flow formulation
360	Successive Shortest Path	Incremental min-cost updates

37. Cuts (Stoer–Wagner, Karger, Gomory–Hu)

#	Algorithm	Note
361	Stoer–Wagner Minimum Cut	Global min cut
362	Karger's Randomized Cut	Contract edges randomly
363	Karger–Stein	Recursive randomized cut
364	Gomory–Hu Tree	All-pairs min-cut
365	Max-Flow Min-Cut	Duality theorem application
366	Stoer–Wagner Repeated Phase	Multiple passes
367	Dynamic Min Cut	Maintain on edge update
368	Minimum s–t Cut (Edmonds–Karp)	Based on flow
369	Approximate Min Cut	Random sampling
370	Min k-Cut	Partition graph into k parts

38. Matchings (Hopcroft–Karp, Hungarian, Blossom)

#	Algorithm	Note
371	Bipartite Matching (DFS)	Simple augmenting path
372	Hopcroft–Karp	$O(E\sqrt{V})$ bipartite matching
373	Hungarian Algorithm	Weighted assignment
374	Kuhn–Munkres	Max-weight matching
375	Blossom Algorithm	General graph matching
376	Edmonds' Blossom Shrinking	Odd cycle contraction
377	Greedy Matching	Fast approximate
378	Stable Marriage (Gale–Shapley)	Stable pairing
379	Weighted b-Matching	Capacity-constrained
380	Maximal Matching	Local greedy maximal set

39. Tree Algorithms (LCA, HLD, Centroid Decomposition)

#	Algorithm	Note
381	Euler Tour LCA	Flatten tree to array
382	Binary Lifting LCA	Jump powers of two
383	Tarjan's LCA (Offline DSU)	Query via union-find
384	Heavy-Light Decomposition	Decompose paths
385	Centroid Decomposition	Recursive split on centroid
386	Tree Diameter (DFS Twice)	Farthest pair
387	Tree DP	Subtree-based optimization
388	Rerooting DP	Compute all roots' answers
389	Binary Search on Tree	Edge weight constraints
390	Virtual Tree	Build on query subset

40. Advanced Graph Algorithms and Tricks

#	Algorithm	Note
391	Topological DP	DP on DAG order
392	SCC Condensed Graph DP	Meta-graph processing
393	Eulerian Path	Trail covering all edges
394	Hamiltonian Path	NP-complete exploration
395	Chinese Postman	Eulerian circuit with repeats
396	Hierholzer's Algorithm	Construct Eulerian circuit
397	Johnson's Cycle Finding	Enumerate all cycles
398	Transitive Closure (Floyd–Warshall)	Reachability matrix
399	Graph Coloring (Backtracking)	Constraint satisfaction
400	Articulation Points & Bridges	Critical structure detection

Chapter 5. Dynamic Programming

41. DP Basics and State Transitions

#	Algorithm	Note
401	Fibonacci DP	Classic top-down vs bottom-up
402	Climbing Stairs	Count paths with small steps
403	Grid Paths	DP over 2D lattice
404	Min Cost Path	Accumulate minimal sums

#	Algorithm	Note
405	Coin Change (Count Ways)	Combinatorial sums
406	Coin Change (Min Coins)	Minimize step count
407	Knapsack 0/1	Select items under weight limit
408	Knapsack Unbounded	Repeatable items
409	Longest Increasing Subsequence (DP)	Subsequence optimization
410	Edit Distance (Levenshtein)	Measure similarity step-by-step

42. Classic Problems (Knapsack, Subset Sum, Coin Change)

#	Algorithm	Note
411	0/1 Knapsack	Value maximization under capacity
412	Subset Sum	Boolean feasibility DP
413	Equal Partition	Divide set into equal halves
414	Count of Subsets with Sum	Counting variant
415	Target Sum	DP with +/- transitions
416	Unbounded Knapsack	Reuse items
417	Fractional Knapsack	Greedy + DP comparison
418	Coin Change (Min Coins)	DP shortest path
419	Coin Change (Count Ways)	Combinatorial counting
420	Multi-Dimensional Knapsack	Capacity in multiple dimensions

43. Sequence Problems (LIS, LCS, Edit Distance)

#	Algorithm	Note
421	Longest Increasing Subsequence	$O(n^2)$ DP
422	LIS (Patience Sorting)	O(n log n) optimized
423	Longest Common Subsequence	Two-sequence DP
424	Edit Distance (Levenshtein)	Transform operations
425	Longest Palindromic Subsequence	Symmetric DP
426	Shortest Common Supersequence	Merge sequences
427	Longest Repeated Subsequence	DP with overlap
428	String Interleaving	Merge with order preservation
429	Sequence Alignment (Bioinformatics)	Gap penalties
430	Diff Algorithm (Myers/DP)	Minimal edit path

44. Matrix and Chain Problems

#	Algorithm	Note
431	Matrix Chain Multiplication	Parenthesization cost
432	Boolean Parenthesization	Count true outcomes
433	Burst Balloons	Interval DP
434	Optimal BST	Weighted search cost
435	Polygon Triangulation	DP over partitions
436	Matrix Path Sum	DP on 2D grid
437	Largest Square Submatrix	Dynamic growth check
438	Max Rectangle in Binary Matrix	Histogram + DP
439	Submatrix Sum Queries	Prefix sum DP
440	Palindrome Partitioning	DP with cuts

45. Bitmask DP and Traveling Salesman

#	Algorithm	Note
441	Traveling Salesman (TSP)	Visit all cities
442	Subset DP	Over subsets of states
443	Hamiltonian Path DP	State compression
444	Assignment Problem DP	Mask over tasks
445	Partition into Two Sets	Balanced load
446	Count Hamiltonian Cycles	Bitmask enumeration
447	Steiner Tree DP	Minimal connection of terminals
448	SOS DP (Sum Over Subsets)	Precompute sums
449	Bitmask Knapsack	State compression
450	Bitmask Independent Set	Graph subset optimization

46. Digit DP and SOS DP

#	Algorithm	Note
451	Count Numbers with Property	Digit-state transitions
452	Count Without Adjacent Duplicates	Adjacent constraints
453	Sum of Digits in Range	Carry-dependent states
454	Count with Mod Condition	DP over digit sum mod M
455	Count of Increasing Digits	Ordered constraint
456	Count with Forbidden Digits	Exclusion transitions
457	SOS DP Subset Sum	Sum over bitmask subsets

#	Algorithm	Note
458	SOS DP Superset Sum	Sum over supersets
459	XOR Basis DP	Combine digit and bit DP
460	Digit DP for Palindromes	Symmetric digit state

47. DP Optimizations (Divide & Conquer, Convex Hull Trick, Knuth)

#	Algorithm	Note
461	Divide & Conquer DP	Monotone decision property
462	Knuth Optimization	DP with quadrangle inequality
463	Convex Hull Trick	Linear recurrence min queries
464	Li Chao Tree	Segment-based hull maintenance
465	Slope Trick	Piecewise-linear optimization
466	Monotonic Queue Optimization	Sliding DP state
467	Bitset DP	Speed via bit-parallel
468	Offline DP Queries	Preprocessing state
469	DP + Segment Tree	Range-based optimization
470	Divide & Conquer Knapsack	Split-space DP

48. Tree DP and Rerooting

#	Algorithm	Note
471	Subtree Sum DP	Aggregate values
472	Diameter DP	Max path via child states
473	Independent Set DP	Choose or skip nodes
474	Vertex Cover DP	Tree constraint problem
475	Path Counting DP	Count root-leaf paths
476	DP on Rooted Tree	Bottom-up aggregation
477	Rerooting Technique	Compute for all roots
478	Distance Sum Rerooting	Efficient recomputation
479	Tree Coloring DP	Combinatorial counting
480	Binary Search on Tree DP	Monotonic transitions

49. DP Reconstruction and Traceback

#	Algorithm	Note
481	Reconstruct LCS	Backtrack table
482	Reconstruct LIS	Track predecessors
483	Reconstruct Knapsack	Recover selected items
484	Edit Distance Alignment	Trace insert/delete/substitute
485	Matrix Chain Parentheses	Rebuild parenthesization
486	Coin Change Reconstruction	Backtrack last used coin
487	Path Reconstruction DP	Trace minimal route
488	Sequence Reconstruction	Rebuild from states
489	Multi-Choice Reconstruction	Combine best subpaths
490	Traceback Visualization	Visual DP backtrack tool

50. Meta-DP and Optimization Templates

#	Algorithm	Note
491	State Compression Template	Represent subsets compactly
492	Transition Optimization Template	Precompute transitions
493	Space Optimization Template	Rolling arrays
494	Multi-Dimensional DP Template	Nested loops version
495	Decision Monotonicity	Optimization hint
496	Monge Array Optimization	Matrix property leverage
497	Divide & Conquer Template	Half-split recursion
498	Rerooting Template	Generalized tree DP
499	Iterative DP Pattern	Bottom-up unrolling
500	Memoization Template	Recursive caching skeleton

Chapter 6. Mathematics for Algorithms

51. Number Theory (GCD, Modular Arithmetic, CRT)

#	Algorithm	Note
501	Euclidean Algorithm	Compute gcd(a, b)
502	Extended Euclidean Algorithm	Solve ax + by = gcd(a, b)
503	Modular Addition	Add under modulo M
504	Modular Multiplication	Multiply under modulo M
505	Modular Exponentiation	Fast power mod M
506	Modular Inverse	Compute a^{-1} mod M
507	Chinese Remainder Theorem	Combine modular systems

#	Algorithm	Note
508	Binary GCD (Stein's Algorithm)	Bitwise gcd
509	Modular Reduction	Normalize residues
510	Modular Linear Equation Solver	Solve ax b (mod m)

52. Primality and Factorization (Miller–Rabin, Pollard Rho)

#	Algorithm	Note
511	Trial Division	Simple prime test
512	Sieve of Eratosthenes	Generate primes up to n
513	Sieve of Atkin	Faster sieve variant
514	Miller–Rabin Primality Test	Probabilistic primality
515	Fermat Primality Test	Modular power check
516	Pollard's Rho	Randomized factorization
517	Pollard's p−1 Method	Factor using smoothness
518	Wheel Factorization	Skip known composites
519	AKS Primality Test	Deterministic polynomial test
520	Segmented Sieve	Prime generation for large n

53. Combinatorics (Permutations, Combinations, Subsets)

#	Algorithm	Note
521	Factorial Precomputation	Build n! table
522	nCr Computation	Use Pascal's or factorials
523	Pascal's Triangle	Binomial coefficients
524	Multiset Combination	Repetition allowed
525	Permutation Generation	Lexicographic order
526	Next Permutation	STL-style increment
527	Subset Generation	Bitmask or recursion
528	Gray Code Generation	Single-bit flips
529	Catalan Number DP	Count valid parentheses
530	Stirling Numbers	Partition counting

54. Probability and Randomized Algorithms

#	Algorithm	Note
531	Monte Carlo Simulation	Approximate via randomness
532	Las Vegas Algorithm	Always correct, variable time
533	Reservoir Sampling	Uniform sampling from stream
534	Randomized QuickSort	Expected O(n log n)
535	Randomized QuickSelect	Random pivot
536	Birthday Paradox Simulation	Probability collision
537	Random Hashing	Reduce collision chance
538	Random Walk Simulation	State transitions
539	Coupon Collector Estimation	Expected trials
540	Markov Chain Simulation	Transition matrix sampling

55. Sieve Methods and Modular Math

#	Algorithm	Note
541	Sieve of Eratosthenes	Base prime sieve
542	Linear Sieve	O(n) sieve variant
543	Segmented Sieve	Range prime generation
544	SPF (Smallest Prime Factor) Table	Factorization via sieve
545	Möbius Function Sieve	Multiplicative function calc
546	Euler's Totient Sieve	Compute (n) for all n
547	Divisor Count Sieve	Count divisors efficiently
548	Modular Precomputation	Store inverses, factorials
549	Fermat Little Theorem	a^(p−1) 1 mod p
550	Wilson's Theorem	Prime test via factorial mod p

56. Linear Algebra (Gaussian Elimination, LU, SVD)

#	Algorithm	Note
551	Gaussian Elimination	Solve Ax = b
552	Gauss-Jordan Elimination	Reduced row echelon
553	LU Decomposition	Factor A into L · U
554	Cholesky Decomposition	A = L · L for SPD
555	QR Decomposition	Orthogonal factorization
556	Matrix Inversion (Gauss-Jordan)	Find A [1]
557	Determinant by Elimination	Product of pivots
558	Rank of Matrix	Count non-zero rows
559	Eigenvalue Power Method	Approximate dominant eigenvalue

#	Algorithm	Note
560	Singular Value Decomposition	A = UΣV

57. FFT and NTT (Fast Transforms)

#	Algorithm	Note
561	Discrete Fourier Transform (DFT)	$O(n^2)$ baseline
562	Fast Fourier Transform (FFT)	O(n log n) convolution
563	Cooley–Tukey FFT	Recursive divide and conquer
564	Iterative FFT	In-place bit reversal
565	Inverse FFT	Recover time-domain
566	Convolution via FFT	Polynomial multiplication
567	Number Theoretic Transform (NTT)	Modulo prime FFT
568	Inverse NTT	Modular inverse transform
569	Bluestein's Algorithm	FFT of arbitrary size
570	FFT-Based Multiplication	Big integer product

58. Numerical Methods (Newton, Simpson, Runge–Kutta)

#	Algorithm	Note
571	Newton–Raphson	Root finding via tangent
572	Bisection Method	Interval halving
573	Secant Method	Approximate derivative
574	Fixed-Point Iteration	x = f(x) convergence
575	Gaussian Quadrature	Weighted integration
576	Simpson's Rule	Piecewise quadratic integral
577	Trapezoidal Rule	Linear interpolation integral
578	Runge–Kutta (RK4)	ODE solver
579	Euler's Method	Step-by-step ODE
580	Gradient Descent (1D)	Numerical optimization

59. Mathematical Optimization (Simplex, Gradient, Convex)

#	Algorithm	Note
581	Simplex Method	Linear programming solver
582	Dual Simplex Method	Solve dual constraints

#	Algorithm	Note
583	Interior-Point Method	Convex optimization
584	Gradient Descent	Unconstrained optimization
585	Stochastic Gradient Descent	Sample-based updates
586	Newton's Method (Multivariate)	Quadratic convergence
587	Conjugate Gradient	Solve SPD systems
588	Lagrange Multipliers	Constrained optimization
589	KKT Conditions Solver	Convex constraint handling
590	Coordinate Descent	Sequential variable updates

60. Algebraic Tricks and Transform Techniques

#	Algorithm	Note
591	Polynomial Multiplication (FFT)	Fast convolution
592	Polynomial Inversion	Newton iteration
593	Polynomial Derivative	Term-wise multiply by index
594	Polynomial Integration	Divide by index+1
595	Formal Power Series Composition	Substitute series
596	Exponentiation by Squaring	Fast powering
597	Modular Exponentiation	Fast power mod M
598	Fast Walsh–Hadamard Transform	XOR convolution
599	Zeta Transform	Subset summation
600	Möbius Inversion	Recover original from sums

Chapter 7. Strings and Text Algorithms

61. String Matching (KMP, Z, Rabin–Karp, Boyer–Moore)

#	Algorithm	Note
601	Naive String Matching	Compare every position
602	Knuth–Morris–Pratt (KMP)	Prefix function skipping
603	Z-Algorithm	Match using Z-values
604	Rabin–Karp	Rolling hash comparison
605	Boyer–Moore	Backward skip based on mismatch
606	Boyer–Moore–Horspool	Simplified shift table
607	Sunday Algorithm	Last-character shift
608	Finite Automaton Matching	DFA-based matching
609	Bitap Algorithm	Bitmask approximate matching

#	Algorithm	Note
610	Two-Way Algorithm	Optimal linear matching

62. Multi-Pattern Search (Aho–Corasick)

#	Algorithm	Note
611	Aho–Corasick Automaton	Trie + failure links
612	Trie Construction	Prefix tree build
613	Failure Link Computation	BFS for transitions
614	Output Link Management	Handle overlapping patterns
615	Multi-Pattern Search	Find all keywords
616	Dictionary Matching	Find multiple substrings
617	Dynamic Aho–Corasick	Add/remove patterns
618	Parallel AC Search	Multi-threaded traversal
619	Compressed AC Automaton	Memory-optimized
620	Extended AC with Wildcards	Flexible matching

63. Suffix Structures (Suffix Array, Suffix Tree, LCP)

#	Algorithm	Note
621	Suffix Array (Naive)	Sort all suffixes
622	Suffix Array (Doubling)	O(n log n) rank-based
623	Kasai's LCP Algorithm	Longest common prefix
624	Suffix Tree (Ukkonen)	Linear-time online
625	Suffix Automaton	Minimal DFA of substrings
626	SA-IS Algorithm	O(n) suffix array
627	LCP RMQ Query	Range minimum for substring
628	Generalized Suffix Array	Multiple strings
629	Enhanced Suffix Array	Combine SA + LCP
630	Sparse Suffix Tree	Space-efficient variant

64. Palindromes and Periodicity (Manacher)

#	Algorithm	Note
631	Naive Palindrome Check	Expand around center
632	Manacher's Algorithm	O(n) longest palindrome

#	Algorithm	Note
633	Longest Palindromic Substring	Center expansion
634	Palindrome DP Table	Substring boolean matrix
635	Palindromic Tree (Eertree)	Track distinct palindromes
636	Prefix Function Periodicity	Detect repetition patterns
637	Z-Function Periodicity	Identify periodic suffix
638	KMP Prefix Period Check	Shortest repeating unit
639	Lyndon Factorization	Decompose string into Lyndon words
640	Minimal Rotation (Booth's Algorithm)	Lexicographically minimal shift

65. Edit Distance and Alignment

#	Algorithm	Note
641	Levenshtein Distance	Insert/delete/replace cost
642	Damerau–Levenshtein	Swap included
643	Hamming Distance	Count differing bits
644	Needleman–Wunsch	Global alignment
645	Smith–Waterman	Local alignment
646	Hirschberg's Algorithm	Memory-optimized alignment
647	Edit Script Reconstruction	Backtrack operations
648	Affine Gap Penalty DP	Varying gap cost
649	Myers Bit-Vector Algorithm	Fast edit distance
650	Longest Common Subsequence	Alignment by inclusion

66. Compression (Huffman, Arithmetic, LZ77, BWT)

#	Algorithm	Note
651	Huffman Coding	Optimal prefix tree
652	Canonical Huffman	Deterministic ordering
653	Arithmetic Coding	Interval probability coding
654	Shannon–Fano Coding	Early prefix method
655	Run-Length Encoding (RLE)	Repeat compression
656	LZ77	Sliding-window match
657	LZ78	Dictionary building
658	LZW	Variant used in GIF
659	Burrows–Wheeler Transform	Block reordering
660	Move-to-Front Encoding	Locality boosting transform

67. Cryptographic Hashes and Checksums

#	Algorithm	Note
661	Rolling Hash	Polynomial mod-based
662	CRC32	Cyclic redundancy check
663	Adler-32	Lightweight checksum
664	MD5	Legacy cryptographic hash
665	SHA-1	Deprecated hash function
666	SHA-256	Secure hash standard
667	SHA-3 (Keccak)	Sponge construction
668	HMAC	Keyed message authentication
669	Merkle Tree	Hierarchical hashing
670	Hash Collision Detection	Birthday bound simulation

68. Approximate and Streaming Matching

#	Algorithm	Note
671	K-Approximate Matching	Allow k mismatches
672	Bitap Algorithm	Bitwise dynamic programming
673	Landau–Vishkin Algorithm	Edit distance k
674	Filtering Algorithm	Fast approximate search
675	Wu–Manber	Multi-pattern approximate search
676	Streaming KMP	Online prefix updates
677	Rolling Hash Sketch	Sliding window hashing
678	Sketch-based Similarity	MinHash / LSH variants
679	Weighted Edit Distance	Weighted operations
680	Online Levenshtein	Dynamic stream update

69. Bioinformatics Alignment (Needleman–Wunsch, Smith–Waterman)

#	Algorithm	Note
681	Needleman–Wunsch	Global sequence alignment
682	Smith–Waterman	Local alignment
683	Gotoh Algorithm	Affine gap penalties
684	Hirschberg Alignment	Linear-space alignment
685	Multiple Sequence Alignment (MSA)	Progressive methods
686	Profile Alignment	Align sequence to profile

#	Algorithm	Note
687	Hidden Markov Model Alignment	Probabilistic alignment
688	BLAST	Heuristic local search
689	FASTA	Word-based alignment
690	Pairwise DP Alignment	General DP framework

70. Text Indexing and Search Structures

#	Algorithm	Note
691	Inverted Index Build	Word-to-document mapping
692	Positional Index	Store word positions
693	TF-IDF Weighting	Importance scoring
694	BM25 Ranking	Modern ranking formula
695	Trie Index	Prefix search structure
696	Suffix Array Index	Substring search
697	Compressed Suffix Array	Space-optimized
698	FM-Index	BWT-based compressed index
699	DAWG (Directed Acyclic Word Graph)	Shared suffix graph
700	Wavelet Tree for Text	Rank/select on sequences

Chapter 8. Geometry, Graphics, and Spatial Algorithms

71. Convex Hull (Graham, Andrew, Chan)

#	Algorithm	Note
701	Gift Wrapping (Jarvis March)	Wrap hull one point at a time
702	Graham Scan	Sort by angle, maintain stack
703	Andrew's Monotone Chain	Sort by x, upper + lower hull
704	Chan's Algorithm	Output-sensitive O(n log h)
705	QuickHull	Divide-and-conquer hull
706	Incremental Convex Hull	Add points one by one
707	Divide & Conquer Hull	Merge two partial hulls
708	3D Convex Hull	Extend to 3D geometry
709	Dynamic Convex Hull	Maintain hull with inserts
710	Rotating Calipers	Compute diameter, width, antipodal pairs

72. Closest Pair and Segment Intersection

#	Algorithm	Note
711	Closest Pair (Divide & Conquer)	Split, merge minimal distance
712	Closest Pair (Sweep Line)	Maintain active window
713	Brute Force Closest Pair	Check all $O(n^2)$ pairs
714	Bentley–Ottmann	Find all line intersections
715	Segment Intersection Test	Cross product orientation
716	Line Sweep for Segments	Event-based intersection
717	Intersection via Orientation	CCW test
718	Circle Intersection	Geometry of two circles
719	Polygon Intersection	Clip overlapping polygons
720	Nearest Neighbor Pair	Combine KD-tree + search

73. Line Sweep and Plane Sweep Algorithms

#	Algorithm	Note
721	Sweep Line for Events	Process sorted events
722	Interval Scheduling	Select non-overlapping intervals
723	Rectangle Union Area	Sweep edges to count area
724	Segment Intersection (Bentley–Ottmann)	Detect all crossings
725	Skyline Problem	Merge height profiles
726	Closest Pair Sweep	Maintain active set
727	Circle Arrangement	Sweep and count regions
728	Sweep for Overlapping Rectangles	Detect collisions
729	Range Counting	Count points in rectangle
730	Plane Sweep for Triangles	Polygon overlay computation

74. Delaunay and Voronoi Diagrams

#	Algorithm	Note
731	Delaunay Triangulation (Incremental)	Add points, maintain Delaunay
732	Delaunay (Divide & Conquer)	Merge triangulations
733	Delaunay (Fortune's Sweep)	O(n log n) construction
734	Voronoi Diagram (Fortune's)	Sweep line beachline
735	Incremental Voronoi	Update on insertion
736	Bowyer–Watson	Empty circle criterion

#	Algorithm	Note
737	Duality Transform	Convert between Voronoi/Delaunay
738	Power Diagram	Weighted Voronoi
739	Lloyd's Relaxation	Smooth Voronoi cells
740	Voronoi Nearest Neighbor	Region-based lookup

75. Point in Polygon and Polygon Triangulation

#	Algorithm	Note
741	Ray Casting	Count edge crossings
742	Winding Number	Angle sum method
743	Convex Polygon Point Test	Orientation checks
744	Ear Clipping Triangulation	Remove ears iteratively
745	Monotone Polygon Triangulation	Sweep line triangulation
746	Delaunay Triangulation	Optimal triangle quality
747	Convex Decomposition	Split into convex parts
748	Polygon Area (Shoelace Formula)	Signed area computation
749	Minkowski Sum	Add shapes geometrically
750	Polygon Intersection (Weiler–Atherton)	Clip overlapping shapes

76. Spatial Data Structures (KD, R-tree)

#	Algorithm	Note
751	KD-Tree Build	Recursive median split
752	KD-Tree Search	Axis-aligned query
753	Range Search KD-Tree	Orthogonal query
754	Nearest Neighbor KD-Tree	Closest point search
755	R-Tree Build	Bounding box hierarchy
756	R*-Tree	Optimized split strategy
757	Quad Tree	Spatial decomposition
758	Octree	3D spatial decomposition
759	BSP Tree (Binary Space Partition)	Split by planes
760	Morton Order (Z-Curve)	Spatial locality index

77. Rasterization and Scanline Techniques

#	Algorithm	Note
761	Bresenham's Line Algorithm	Efficient integer drawing
762	Midpoint Circle Algorithm	Circle rasterization
763	Scanline Fill	Polygon interior fill
764	Edge Table Fill	Sort edges by y
765	Z-Buffer Algorithm	Hidden surface removal
766	Painter's Algorithm	Sort by depth
767	Gouraud Shading	Vertex interpolation shading
768	Phong Shading	Normal interpolation
769	Anti-Aliasing (Supersampling)	Smooth jagged edges
770	Scanline Polygon Clipping	Efficient clipping

78. Computer Vision (Canny, Hough, SIFT)

#	Algorithm	Note
771	Canny Edge Detector	Gradient + hysteresis
772	Sobel Operator	Gradient magnitude filter
773	Hough Transform (Lines)	Accumulator for line detection
774	Hough Transform (Circles)	Radius-based accumulator
775	Harris Corner Detector	Eigenvalue-based corners
776	FAST Corner Detector	Intensity circle test
777	SIFT (Scale-Invariant Feature Transform)	Keypoint detection
778	SURF (Speeded-Up Robust Features)	Faster descriptor
779	ORB (Oriented FAST + BRIEF)	Binary robust feature
780	RANSAC	Robust model fitting

79. Pathfinding in Space (A*, RRT, PRM)

#	Algorithm	Note
781	A* Search	Heuristic pathfinding
782	Dijkstra for Grid	Weighted shortest path
783	Theta*	Any-angle pathfinding
784	Jump Point Search	Grid acceleration
785	RRT (Rapidly-Exploring Random Tree)	Random sampling tree
786	RRT*	Optimal variant with rewiring
787	PRM (Probabilistic Roadmap)	Graph sampling planner
788	Visibility Graph	Connect visible vertices
789	Potential Field Pathfinding	Gradient-based navigation

#	Algorithm	Note
790	Bug Algorithms	Simple obstacle avoidance

80. Computational Geometry Variants and Applications

#	Algorithm	Note
791	Convex Polygon Intersection	Clip convex sets
792	Minkowski Sum	Shape convolution
793	Rotating Calipers	Closest/farthest pair
794	Half-Plane Intersection	Feasible region
795	Line Arrangement	Count regions
796	Point Location (Trapezoidal Map)	Query region lookup
797	Voronoi Nearest Facility	Region query
798	Delaunay Mesh Generation	Triangulation refinement
799	Smallest Enclosing Circle	Welzl's algorithm
800	Collision Detection (SAT)	Separating axis theorem

Chapter 9. Systems, Databases, and Distributed Algorithms

81. Concurrency Control (2PL, MVCC, OCC)

#	Algorithm	Note
801	Two-Phase Locking (2PL)	Acquire-then-release locks
802	Strict 2PL	Hold locks until commit
803	Conservative 2PL	Prevent deadlocks via prelock
804	Timestamp Ordering	Schedule by timestamps
805	Multiversion Concurrency Control (MVCC)	Snapshot isolation
806	Optimistic Concurrency Control (OCC)	Validate at commit
807	Serializable Snapshot Isolation	Merge read/write sets
808	Lock-Free Algorithm	Atomic CAS updates
809	Wait-Die / Wound-Wait	Deadlock prevention policies
810	Deadlock Detection (Wait-for Graph)	Cycle detection in waits

82. Logging, Recovery, and Commit Protocols

#	Algorithm	Note
811	Write-Ahead Logging (WAL)	Log before commit
812	ARIES Recovery	Re-do/undo with LSNs
813	Shadow Paging	Copy-on-write persistence
814	Two-Phase Commit (2PC)	Coordinator-driven commit
815	Three-Phase Commit (3PC)	Non-blocking variant
816	Checkpointing	Save state for recovery
817	Undo Logging	Rollback uncommitted
818	Redo Logging	Reapply committed
819	Quorum Commit	Majority agreement
820	Consensus Commit	Combine 2PC + Paxos

83. Scheduling (Round Robin, EDF, Rate-Monotonic)

#	Algorithm	Note
821	First-Come First-Served (FCFS)	Sequential job order
822	Shortest Job First (SJF)	Optimal average wait
823	Round Robin (RR)	Time-slice fairness
824	Priority Scheduling	Weighted selection
825	Multilevel Queue	Tiered priority queues
826	Earliest Deadline First (EDF)	Real-time optimal
827	Rate Monotonic Scheduling (RMS)	Fixed periodic priority
828	Lottery Scheduling	Probabilistic fairness
829	Multilevel Feedback Queue	Adaptive behavior
830	Fair Queuing (FQ)	Flow-based proportional sharing

84. Caching and Replacement (LRU, LFU, CLOCK)

#	Algorithm	Note
831	LRU (Least Recently Used)	Evict oldest used
832	LFU (Least Frequently Used)	Evict lowest frequency
833	FIFO Cache	Simple queue eviction
834	CLOCK Algorithm	Approximate LRU
835	ARC (Adaptive Replacement Cache)	Mix of recency + frequency
836	Two-Queue (2Q)	Separate recent/frequent
837	LIRS (Low Inter-reference Recency Set)	Predict reuse distance
838	TinyLFU	Frequency sketch admission
839	Random Replacement	Simple stochastic policy

#	Algorithm	Note
840	Belady's Optimal	Evict farthest future use

85. Networking (Routing, Congestion Control)

#	Algorithm	Note
841	Dijkstra's Routing	Shortest path routing
842	Bellman–Ford Routing	Distance-vector routing
843	Link-State Routing (OSPF)	Global view routing
844	Distance-Vector Routing (RIP)	Local neighbor updates
845	Path Vector (BGP)	Route advertisement
846	Flooding	Broadcast to all nodes
847	Spanning Tree Protocol	Loop-free topology
848	Congestion Control (AIMD)	TCP window control
849	Random Early Detection (RED)	Queue preemptive drop
850	ECN (Explicit Congestion Notification)	Mark packets early

86. Distributed Consensus (Paxos, Raft, PBFT)

#	Algorithm	Note
851	Basic Paxos	Majority consensus
852	Multi-Paxos	Sequence of agreements
853	Raft	Log replication + leader election
854	Viewstamped Replication	Alternative consensus design
855	PBFT (Practical Byzantine Fault Tolerance)	Byzantine safety
856	Zab (Zookeeper Atomic Broadcast)	Broadcast + ordering
857	EPaxos	Leaderless fast path
858	VRR (Virtual Ring Replication)	Log around ring
859	Two-Phase Commit with Consensus	Transactional commit
860	Chain Replication	Ordered state replication

87. Load Balancing and Rate Limiting

#	Algorithm	Note
861	Round Robin Load Balancing	Sequential distribution
862	Weighted Round Robin	Proportional to weight

#	Algorithm	Note
863	Least Connections	Pick least loaded node
864	Consistent Hashing	Map requests stably
865	Power of Two Choices	Sample and choose lesser load
866	Random Load Balancing	Simple uniform random
867	Token Bucket	Rate-based limiter
868	Leaky Bucket	Steady flow shaping
869	Sliding Window Counter	Rolling time window
870	Fixed Window Counter	Resettable counter limiter

88. Search and Indexing (Inverted, BM25, WAND)

#	Algorithm	Note
871	Inverted Index Construction	Word → document list
872	Positional Index Build	Store term positions
873	TF-IDF Scoring	Term frequency weighting
874	BM25 Ranking	Modern scoring model
875	Boolean Retrieval	Logical AND/OR/NOT
876	WAND Algorithm	Efficient top-k retrieval
877	Block-Max WAND (BMW)	Early skipping optimization
878	Impact-Ordered Indexing	Sort by contribution
879	Tiered Indexing	Prioritize high-score docs
880	DAAT vs SAAT Evaluation	Document vs score-at-a-time

89. Compression and Encoding in Systems

#	Algorithm	Note
881	Run-Length Encoding (RLE)	Simple repetition encoding
882	Huffman Coding	Optimal variable-length code
883	Arithmetic Coding	Fractional interval coding
884	Delta Encoding	Store differences
885	Variable Byte Encoding	Compact integers
886	Elias Gamma Coding	Prefix integer encoding
887	Rice Coding	Unary + remainder scheme
888	Snappy	Fast block compression
889	Zstandard (Zstd)	Modern adaptive codec
890	LZ4	High-speed dictionary compressor

90. Fault Tolerance and Replication

#	Algorithm	Note
891	Primary–Backup Replication	One leader, one standby
892	Quorum Replication	Majority write/read rule
893	Chain Replication	Ordered consistency
894	Gossip Protocol	Epidemic state exchange
895	Anti-Entropy Repair	Periodic reconciliation
896	Erasure Coding	Redundant data blocks
897	Checksum Verification	Detect corruption
898	Heartbeat Monitoring	Liveness detection
899	Leader Election (Bully)	Highest ID wins
900	Leader Election (Ring)	Token-based rotation

Chapter 10. AI, ML, and Optimization

91. Classical ML (k-means, Naive Bayes, SVM, Decision Trees)

#	Algorithm	Note
901	k-Means Clustering	Partition by centroid iteration
902	k-Medoids (PAM)	Cluster by exemplars
903	Gaussian Mixture Model (EM)	Soft probabilistic clustering
904	Naive Bayes Classifier	Probabilistic feature independence
905	Logistic Regression	Sigmoid linear classifier
906	Perceptron	Online linear separator
907	Decision Tree (CART)	Recursive partition by impurity
908	ID3 Algorithm	Information gain splitting
909	k-Nearest Neighbors (kNN)	Distance-based classification
910	Linear Discriminant Analysis (LDA)	Projection for separation

92. Ensemble Methods (Bagging, Boosting, Random Forests)

#	Algorithm	Note
911	Bagging	Bootstrap aggregation
912	Random Forest	Ensemble of decision trees
913	AdaBoost	Weighted error correction
914	Gradient Boosting	Sequential residual fitting

#	Algorithm	Note
915	XGBoost	Optimized gradient boosting
916	LightGBM	Histogram-based leaf growth
917	CatBoost	Ordered boosting for categoricals
918	Stacking	Meta-model ensemble
919	Voting Classifier	Majority aggregation
920	Snapshot Ensemble	Averaged checkpoints

93. Gradient Methods (SGD, Adam, RMSProp)

#	Algorithm	Note
921	Gradient Descent	Batch full-gradient step
922	Stochastic Gradient Descent (SGD)	Sample-wise updates
923	Mini-Batch SGD	Tradeoff speed and variance
924	Momentum	Add velocity to descent
925	Nesterov Accelerated Gradient	Lookahead correction
926	AdaGrad	Adaptive per-parameter rate
927	RMSProp	Exponential moving average
928	Adam	Momentum + adaptive rate
929	AdamW	Decoupled weight decay
930	L-BFGS	Limited-memory quasi-Newton

94. Deep Learning (Backpropagation, Dropout, Normalization)

#	Algorithm	Note
931	Backpropagation	Gradient chain rule
932	Xavier/He Initialization	Scaled variance init
933	Dropout	Random neuron deactivation
934	Batch Normalization	Normalize per batch
935	Layer Normalization	Normalize per feature
936	Gradient Clipping	Prevent explosion
937	Early Stopping	Prevent overfitting
938	Weight Decay	Regularization via penalty
939	Learning Rate Scheduling	Dynamic LR adjustment
940	Residual Connections	Skip layer improvement

95. Sequence Models (Viterbi, Beam Search, CTC)

#	Algorithm	Note
941	Hidden Markov Model (Forward–Backward)	Probabilistic sequence model
942	Viterbi Algorithm	Most probable path
943	Baum–Welch	EM training for HMMs
944	Beam Search	Top-k path exploration
945	Greedy Decoding	Fast approximate decoding
946	Connectionist Temporal Classification (CTC)	Unaligned sequence training
947	Attention Mechanism	Weighted context aggregation
948	Transformer Decoder	Self-attention stack
949	Seq2Seq with Attention	Encoder-decoder framework
950	Pointer Network	Output index selection

96. Metaheuristics (GA, SA, PSO, ACO)

#	Algorithm	Note
951	Genetic Algorithm (GA)	Evolutionary optimization
952	Simulated Annealing (SA)	Temperature-controlled search
953	Tabu Search	Memory of forbidden moves
954	Particle Swarm Optimization (PSO)	Velocity-based search
955	Ant Colony Optimization (ACO)	Pheromone-guided path
956	Differential Evolution (DE)	Vector-based mutation
957	Harmony Search	Music-inspired improvisation
958	Firefly Algorithm	Brightness-attraction movement
959	Bee Colony Optimization	Explore-exploit via scouts
960	Hill Climbing	Local incremental improvement

97. Reinforcement Learning (Q-learning, Policy Gradients)

#	Algorithm	Note
961	Monte Carlo Control	Average returns
962	Temporal Difference (TD) Learning	Bootstrap updates
963	SARSA	On-policy TD learning
964	Q-Learning	Off-policy TD learning
965	Double Q-Learning	Reduce overestimation
966	Deep Q-Network (DQN)	Neural Q approximator

#	Algorithm	Note
967	REINFORCE	Policy gradient by sampling
968	Actor–Critic	Value-guided policy update
969	PPO (Proximal Policy Optimization)	Clipped surrogate objective
970	DDPG / SAC	Continuous action RL

98. Approximation and Online Algorithms

#	Algorithm	Note
971	Greedy Set Cover	ln(n)-approximation
972	Vertex Cover Approximation	Double-matching heuristic
973	Traveling Salesman Approximation	MST-based 2-approx
974	k-Center Approximation	Farthest-point heuristic
975	Online Paging (LRU)	Competitive analysis
976	Online Matching (Ranking)	Adversarial input resilience
977	Online Knapsack	Ratio-based acceptance
978	Competitive Ratio Evaluation	Bound worst-case performance
979	PTAS / FPTAS Schemes	Polynomial approximation
980	Primal–Dual Method	Approximate combinatorial optimization

99. Fairness, Causal Inference, and Robust Optimization

#	Algorithm	Note
981	Reweighting for Fairness	Adjust sample weights
982	Demographic Parity Constraint	Equalize positive rates
983	Equalized Odds	Align error rates
984	Adversarial Debiasing	Learn fair representations
985	Causal DAG Discovery	Graphical causal inference
986	Propensity Score Matching	Estimate treatment effect
987	Instrumental Variable Estimation	Handle confounders
988	Robust Optimization	Worst-case aware optimization
989	Distributionally Robust Optimization	Minimax over uncertainty sets
990	Counterfactual Fairness	Simulate do-interventions

100. AI Planning, Search, and Learning Systems

#	Algorithm	Note
991	Breadth-First Search (BFS)	Uninformed search
992	Depth-First Search (DFS)	Backtracking search
993	A* Search	Heuristic guided
994	Iterative Deepening A* (IDA*)	Memory-bounded heuristic
995	Uniform Cost Search	Expand by path cost
996	Monte Carlo Tree Search (MCTS)	Exploration vs exploitation
997	Minimax	Game tree evaluation
998	Alpha–Beta Pruning	Prune unneeded branches
999	STRIPS Planning	Action-based state transition
1000	Hierarchical Task Network (HTN)	Structured AI planning

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Chapter 1. Foundations of algorithms

1. What Is an Algorithm?

Let's start at the beginning. Before code, data, or performance, we need a clear idea of what an algorithm really is.

An algorithm is a clear, step-by-step procedure to solve a problem. Think of it like a recipe: you have inputs (ingredients), a series of steps (instructions), and an output (the finished dish).

At its core, an algorithm should be:

- Precise: every step is well defined and unambiguous
- Finite: it finishes after a limited number of steps
- Effective: each step is simple enough to carry out
- Deterministic (usually): the same input gives the same output

When you write an algorithm, you are describing how to get from question to answer, not just what the answer is.

Example: Sum from 1 to (n)

Suppose you want the sum of the numbers from 1 to (n).

Natural language steps

1. Set `total = 0`
2. For each `i` from `1` to `n`, add `i` to `total`
3. Return `total`

Pseudocode

```
Algorithm SumToN(n):
    total ← 0
    for i ← 1 to n:
        total ← total + i
    return total
```

C code

```c
int sum_to_n(int n) {
    int total = 0;
    for (int i = 1; i <= n; i++) {
        total += i;
    }
    return total;
}
```

Tiny Code

Try a quick run by hand with (n = 5):

- start `total = 0`
- add 1 → `total = 1`
- add 2 → `total = 3`
- add 3 → `total = 6`
- add 4 → `total = 10`
- add 5 → `total = 15`

Output is `15`.

You will also see this closed-form formula soon:

$$1 + 2 + 3 + \cdots + n = \frac{n(n+1)}{2}$$

Why It Matters

Algorithms are the blueprints of computation. Every program, from a calculator to an AI model, is built from algorithms. Computers are fast at following instructions. Algorithms give those instructions structure and purpose.

> Algorithms are the language of problem solving.

Try It Yourself

1. Write an algorithm to find the maximum number in a list
2. Write an algorithm to reverse a string
3. Describe your morning routine as an algorithm: list the inputs, the steps, and the final output

Tip: the best way to learn is to think in small, clear steps. Break a problem into simple actions you can execute one by one.

2. Measuring Time and Space

Now that you know what an algorithm is, it's time to ask a deeper question:

> How do we know if one algorithm is better than another?

It's not enough for an algorithm to be correct. It should also be efficient. We measure efficiency in two key ways: time and space.

Time Complexity

Time measures how long an algorithm takes to run, relative to its input size. We don't measure in seconds, because hardware speed varies. Instead, we count steps or operations.

Example:

```
for (int i = 0; i < n; i++) {
    printf("Hi\n");
}
```

This loop runs n times, so it has time complexity $O(n)$. The time grows linearly with input size.

Another example:

```
for (int i = 0; i < n; i++)
  for (int j = 0; j < n; j++)
    printf("*");
```

This runs $n \times n = n^2$ times, so it has $O(n^2)$ time complexity.

These Big-O symbols describe how runtime grows as the input grows.

Space Complexity

Space measures how much memory an algorithm uses.

Example:

```
int sum = 0;  // O(1) space
```

This uses a constant amount of memory, regardless of input size.

But if we allocate an array:

```
int arr[n];   // O(n) space
```

This uses space proportional to n.

Often, we trade time for space:

- Using a hash table speeds up lookups (more memory, less time)
- Using a streaming algorithm saves memory (less space, more time)

Tiny Code

Compare two ways to compute the sum from 1 to n:

Method 1: Loop

```
int sum_loop(int n) {
    int total = 0;
    for (int i = 1; i <= n; i++) total += i;
    return total;
}
```

Time: $O(n)$ Space: $O(1)$

Method 2: Formula

```
int sum_formula(int n) {
    return n * (n + 1) / 2;
}
```

Time: $O(1)$ Space: $O(1)$

Both are correct, but one is faster. Analyzing time and space helps you understand why.

Why It Matters

When data grows huge (millions or billions), small inefficiencies explode.

An algorithm that takes $O(n^2)$ time might feel fine for 10 elements, but impossible for 1,000,000.

Measuring time and space helps you:

- Predict performance
- Compare different solutions
- Optimize intelligently

It's your compass for navigating complexity.

Try It Yourself

1. Write a simple algorithm to find the minimum in an array. Estimate its time and space complexity.
2. Compare two algorithms that solve the same problem. Which one scales better?
3. Think of a daily task that feels like $O(n)$. Can you imagine one that's $O(1)$?

Understanding these measurements early makes every future algorithm more meaningful.

3. Big-O, Big-Theta, Big-Omega

Now that you can measure time and space, let's learn the language used to describe those measurements.

When we say an algorithm is $O(n)$, we're using asymptotic notation, a way to describe how an algorithm's running time or memory grows as input size n increases.

It's not about exact steps, but about how the cost scales for very large n.

The Big-O (Upper Bound)

Big-O answers the question: *"How bad can it get?"* It gives an upper bound on growth, the worst-case scenario.

If an algorithm takes at most $5n + 20$ steps, we write $O(n)$. We drop constants and lower-order terms because they don't matter at scale.

Common Big-O notations:

Name	Notation	Growth	Example
Constant	$O(1)$	Flat	Accessing array element
Logarithmic	$O(\log n)$	Very slow growth	Binary search
Linear	$O(n)$	Proportional	Single loop
Quadratic	$O(n^2)$	Grows quickly	Double loop
Exponential	$O(2^n)$	Explodes	Recursive subset generation

If your algorithm is $O(n)$, doubling input size roughly doubles runtime. If it's $O(n^2)$, doubling input size makes it about four times slower.

The Big-Theta (Tight Bound)

Big-Theta (Θ) gives a tight bound, when you know the algorithm's growth from above and below.

If runtime is roughly $3n + 2$, then $T(n) = \Theta(n)$. That means it's both $O(n)$ and $\Omega(n)$.

The Big-Omega (Lower Bound)

Big-Omega (Ω) answers: *"How fast can it possibly be?"* It's the best-case growth, the lower limit.

Example:

- Linear search: $\Omega(1)$ if the element is at the start
- $O(n)$ in the worst case if it's at the end

So we might say:

$$T(n) = \Omega(1), \quad T(n) = O(n)$$

Tiny Code

Let's see Big-O in action.

```
int sum_pairs(int n) {
    int total = 0;
    for (int i = 0; i < n; i++)         // O(n)
        for (int j = 0; j < n; j++)     // O(n)
            total += i + j;             // O(1)
    return total;
}
```

Total steps $n \times n = n^2$. So $T(n) = O(n^2)$.

If we added a constant-time operation before or after the loops, it wouldn't matter. Constants vanish in asymptotic notation.

Why It Matters

Big-O, Big-Theta, and Big-Omega let you talk precisely about performance. They are the grammar of efficiency.

When you can write:

> Algorithm A runs in $O(n \log n)$ time, $O(n)$ space

you've captured its essence clearly and compared it meaningfully.

They help you:

- Predict behavior at scale
- Choose better data structures
- Communicate efficiency in interviews and papers

It's not about exact timing, it's about growth.

Try It Yourself

1. Analyze this code:

   ```
   for (int i = 1; i <= n; i *= 2)
       printf("%d", i);
   ```

   What's the time complexity?

2. Write an algorithm that's $O(n \log n)$ (hint: merge sort).
3. Identify the best, worst, and average-case complexities for linear search and binary search.

Learning Big-O is like learning a new language, once you're fluent, you can see how code grows before you even run it.

4. Algorithmic Paradigms (Greedy, Divide and Conquer, DP)

Once you can measure performance, it's time to explore how algorithms are designed. Behind every clever solution is a guiding paradigm, a way of thinking about problems.

Three of the most powerful are:

1. Greedy Algorithms
2. Divide and Conquer
3. Dynamic Programming (DP)

Each represents a different mindset for problem solving.

1. Greedy Algorithms

A greedy algorithm makes the best local choice at each step, hoping it leads to a global optimum.

Think of it like:

> "Take what looks best right now, and don't worry about the future."

They are fast and simple, but not always correct. They only work when the greedy choice property holds.

Example: Coin Change (Greedy version) Suppose you want to make 63 cents using US coins (25, 10, 5, 1). The greedy approach:

- Take 25 $\rightarrow$ 38 left
- Take 25 $\rightarrow$ 13 left
- Take 10 $\rightarrow$ 3 left
- Take 1 $\times$ 3

This works here, but not always (try coins 1, 3, 4 for amount 6). Simple, but not guaranteed optimal.

Common greedy algorithms:

- Kruskal's Minimum Spanning Tree

- Prim's Minimum Spanning Tree
- Dijkstra's Shortest Path (non-negative weights)
- Huffman Coding

2. Divide and Conquer

This is a classic paradigm. You break the problem into smaller subproblems, solve each recursively, and then combine the results.

It's like splitting a task among friends, then merging their answers.

Formally:

$$T(n) = aT\left(\frac{n}{b}\right) + f(n)$$

Examples:

- Merge Sort: divide the array, sort halves, merge
- Quick Sort: partition around a pivot
- Binary Search: halve the range each step

Elegant and powerful, but recursion overhead can add cost if poorly structured.

3. Dynamic Programming (DP)

DP is for problems with overlapping subproblems and optimal substructure. You solve smaller subproblems once and store the results to avoid recomputation.

It's like divide and conquer with memory.

Example: Fibonacci Naive recursion is exponential. DP with memoization is linear.

```
int fib(int n) {
    if (n <= 1) return n;
    static int memo[1000] = {0};
    if (memo[n]) return memo[n];
    memo[n] = fib(n-1) + fib(n-2);
    return memo[n];
}
```

Efficient reuse, but requires insight into subproblem structure.

Tiny Code

Quick comparison using Fibonacci:

Naive (Divide and Conquer)

```
int fib_dc(int n) {
    if (n <= 1) return n;
    return fib_dc(n-1) + fib_dc(n-2);  // exponential
}
```

DP (Memoization)

```
int fib_dp(int n, int memo[]) {
    if (n <= 1) return n;
    if (memo[n]) return memo[n];
    return memo[n] = fib_dp(n-1, memo) + fib_dp(n-2, memo);
}
```

Why It Matters

Algorithmic paradigms give you patterns for design:

- Greedy: when local choices lead to a global optimum
- Divide and Conquer: when the problem splits naturally
- Dynamic Programming: when subproblems overlap

Once you recognize a problem's structure, you'll instantly know which mindset fits best.

Think of paradigms as templates for reasoning, not just techniques but philosophies.

Try It Yourself

1. Write a greedy algorithm to make change using coins [1, 3, 4] for amount 6. Does it work?
2. Implement merge sort using divide and conquer.
3. Solve Fibonacci both ways (naive vs DP) and compare speeds.
4. Think of a real-life task you solve greedily.

Learning paradigms is like learning styles of thought. Once you know them, every problem starts to look familiar.

5. Recurrence Relations

Every time you break a problem into smaller subproblems, you create a recurrence, a mathematical way to describe how the total cost grows.

Recurrence relations are the backbone of analyzing recursive algorithms. They tell us how much time or space an algorithm uses, based on the cost of its subproblems.

What Is a Recurrence?

A recurrence relation expresses $T(n)$, the total cost for input size n, in terms of smaller instances.

Example (Merge Sort):

$$T(n) = 2T(n/2) + O(n)$$

That means:

- It divides the problem into 2 halves ($2T(n/2)$)
- Merges results in $O(n)$ time

You will often see recurrences like:

- $T(n) = T(n-1) + O(1)$
- $T(n) = 2T(n/2) + O(n)$
- $T(n) = T(n/2) + O(1)$

Each one represents a different structure of recursion.

Example 1: Simple Linear Recurrence

Consider this code:

```
int count_down(int n) {
    if (n == 0) return 0;
    return 1 + count_down(n - 1);
}
```

This calls itself once for each smaller input:

$$T(n) = T(n-1) + O(1)$$

Solve it:

$$T(n) = O(n)$$

Because it runs once per level.

Example 2: Binary Recurrence

For binary recursion:

```
int sum_tree(int n) {
    if (n == 1) return 1;
    return sum_tree(n/2) + sum_tree(n/2) + 1;
}
```

Here we do two subcalls on $n/2$ and a constant amount of extra work:

$$T(n) = 2T(n/2) + O(1)$$

Solve it: $T(n) = O(n)$

Why? Each level doubles the number of calls but halves the size. There are $\log n$ levels, and total work adds up to $O(n)$.

Solving Recurrences

There are several ways to solve them:

- Substitution Method Guess the solution, then prove it by induction.
- Recursion Tree Method Expand the recurrence into a tree and sum the cost per level.
- Master Theorem Use a formula when the recurrence matches:

$$T(n) = aT(n/b) + f(n)$$

Master Theorem (Quick Summary)

If $T(n) = aT(n/b) + f(n)$, then:

- If $f(n) = O(n^{\log_b a - \epsilon})$, then $T(n) = \Theta(n^{\log_b a})$
- If $f(n) = \Theta(n^{\log_b a})$, then $T(n) = \Theta(n^{\log_b a} \log n)$
- If $f(n) = \Omega(n^{\log_b a + \epsilon})$, and the regularity condition holds, then $T(n) = \Theta(f(n))$

Example (Merge Sort): $a = 2$, $b = 2$, $f(n) = O(n)$

$$T(n) = 2T(n/2) + O(n) = O(n \log n)$$

Tiny Code

Let's write a quick recursive sum:

```
int sum_array(int arr[], int l, int r) {
    if (l == r) return arr[l];
    int mid = (l + r) / 2;
    return sum_array(arr, l, mid) + sum_array(arr, mid+1, r);
}
```

Recurrence:

$$T(n) = 2T(n/2) + O(1)$$

$\to O(n)$

If you added merging (like in merge sort), you would get $+O(n)$:

$\to O(n \log n)$

Why It Matters

Recurrence relations let you predict the cost of recursive solutions.

Without them, recursion feels like magic. With them, you can quantify efficiency.

They are key to understanding:

- Divide and Conquer
- Dynamic Programming
- Backtracking

Once you can set up a recurrence, solving it becomes a game of algebra and logic.

Try It Yourself

1. Write a recurrence for binary search. Solve it.
2. Write a recurrence for merge sort. Solve it.
3. Analyze this function:

```
void fun(int n) {
    if (n <= 1) return;
    fun(n/2);
    fun(n/3);
    fun(n/6);
}
```

   What's the recurrence? Approximate the complexity.

4. Expand $T(n) = T(n-1) + 1$ into its explicit sum.

Learning recurrences helps you see inside recursion. They turn code into equations.

6. Searching Basics

Before we sort or optimize, we need a way to find things. Searching is one of the most fundamental actions in computing, whether it's looking up a name, finding a key, or checking if something exists.

A search algorithm takes a collection (array, list, tree, etc.) and a target, and returns whether the target is present (and often its position).

Let's begin with two foundational techniques: Linear Search and Binary Search.

1. Linear Search

Linear search is the simplest method:

- Start at the beginning
- Check each element in turn
- Stop if you find the target

It works on any list, sorted or not, but can be slow for large data.

```c
int linear_search(int arr[], int n, int key) {
    for (int i = 0; i < n; i++) {
        if (arr[i] == key) return i;
    }
    return -1;
}
```

Example: If `arr = [2, 4, 6, 8, 10]` and `key = 6`, it finds it at index 2.

Complexity:

- Time: $O(n)$
- Space: $O(1)$

Linear search is simple and guaranteed to find the target if it exists, but slow when lists are large.

2. Binary Search

When the list is sorted, we can do much better. Binary search repeatedly divides the search space in half.

Steps:

1. Check the middle element
2. If it matches, you're done
3. If `target < mid`, search the left half
4. Else, search the right half

```c
int binary_search(int arr[], int n, int key) {
    int low = 0, high = n - 1;
    while (low <= high) {
        int mid = (low + high) / 2;
        if (arr[mid] == key) return mid;
        else if (arr[mid] < key) low = mid + 1;
        else high = mid - 1;
    }
    return -1;
}
```

Example: `arr = [2, 4, 6, 8, 10]`, `key = 8`

- mid = 6 → key > mid → search right half
- mid = 8 → found

Complexity:

- Time: $O(\log n)$
- Space: $O(1)$

Binary search is a massive improvement; doubling input only adds one extra step.

3. Recursive Binary Search

Binary search can also be written recursively:

```
int binary_search_rec(int arr[], int low, int high, int key) {
    if (low > high) return -1;
    int mid = (low + high) / 2;
    if (arr[mid] == key) return mid;
    else if (arr[mid] > key) return binary_search_rec(arr, low, mid - 1, key);
    else return binary_search_rec(arr, mid + 1, high, key);
}
```

Same logic, different structure. Both iterative and recursive forms are equally efficient.

4. Choosing Between Them

Method	Works On	Time	Space	Needs Sorting
Linear Search	Any list	O(n)	O(1)	No
Binary Search	Sorted list	O(log n)	O(1)	Yes

If data is unsorted or very small, linear search is fine. If data is sorted and large, binary search is far superior.

Tiny Code

Compare the steps: For $n = 16$:

- Linear search → up to 16 comparisons
- Binary search → $\log_2 16 = 4$ comparisons

That's a huge difference.

Why It Matters

Searching is the core of information retrieval. Every database, compiler, and system relies on it.

Understanding simple searches prepares you for:

- Hash tables (constant-time lookups)
- Tree searches (ordered structures)
- Graph traversals (structured exploration)

It's not just about finding values; it's about learning how data structure and algorithm design fit together.

Try It Yourself

1. Write a linear search that returns all indices where a target appears.
2. Modify binary search to return the first occurrence of a target in a sorted array.
3. Compare runtime on arrays of size 10, 100, 1000.
4. What happens if you run binary search on an unsorted list?

Search is the foundation. Once you master it, you'll recognize its patterns everywhere.

7. Sorting Basics

Sorting is one of the most studied problems in computer science. Why? Because order matters. It makes searching faster, patterns clearer, and data easier to manage.

A sorting algorithm arranges elements in a specific order (usually ascending or descending). Once sorted, many operations (like binary search, merging, or deduplication) become much simpler.

Let's explore the foundational sorting methods and the principles behind them.

1. What Makes a Sort Algorithm

A sorting algorithm should define:

- Input: a sequence of elements
- Output: the same elements, in sorted order
- Stability: keeps equal elements in the same order (important for multi-key sorts)
- In-place: uses only a constant amount of extra space

Different algorithms balance speed, memory, and simplicity.

2. Bubble Sort

Idea: repeatedly "bubble up" the largest element to the end by swapping adjacent pairs.

```
void bubble_sort(int arr[], int n) {
    for (int i = 0; i < n - 1; i++) {
        for (int j = 0; j < n - i - 1; j++) {
            if (arr[j] > arr[j + 1]) {
                int temp = arr[j];
                arr[j] = arr[j + 1];
                arr[j + 1] = temp;
            }
        }
    }
}
```

Each pass moves the largest remaining item to its final position.

- Time: $O(n^2)$
- Space: $O(1)$
- Stable: Yes

Simple but inefficient for large data.

3. Selection Sort

Idea: repeatedly select the smallest element and put it in the correct position.

```
void selection_sort(int arr[], int n) {
    for (int i = 0; i < n - 1; i++) {
        int min_idx = i;
        for (int j = i + 1; j < n; j++) {
            if (arr[j] < arr[min_idx]) min_idx = j;
        }
        int temp = arr[i];
        arr[i] = arr[min_idx];
        arr[min_idx] = temp;
    }
}
```

- Time: $O(n^2)$
- Space: $O(1)$

- Stable: No

Fewer swaps, but still quadratic in time.

4. Insertion Sort

Idea: build the sorted list one item at a time, inserting each new item in the right place.

```
void insertion_sort(int arr[], int n) {
    for (int i = 1; i < n; i++) {
        int key = arr[i];
        int j = i - 1;
        while (j >= 0 && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}
```

- Time: $O(n^2)$ (best case $O(n)$ when nearly sorted)
- Space: $O(1)$
- Stable: Yes

Insertion sort is great for small or nearly sorted datasets. It is often used as a base in hybrid sorts like Timsort.

5. Comparing the Basics

Algorithm	Best Case	Average Case	Worst Case	Stable	In-place
Bubble Sort	O(n)	O(n²)	O(n²)	Yes	Yes
Selection Sort	O(n²)	O(n²)	O(n²)	No	Yes
Insertion Sort	O(n)	O(n²)	O(n²)	Yes	Yes

All three are quadratic in time, but Insertion Sort performs best on small or partially sorted data.

Tiny Code

Quick check with `arr = [5, 3, 4, 1, 2]`:

Insertion Sort (step by step)

- Insert 3 before 5 → [3, 5, 4, 1, 2]
- Insert 4 → [3, 4, 5, 1, 2]
- Insert 1 → [1, 3, 4, 5, 2]
- Insert 2 → [1, 2, 3, 4, 5]

Sorted!

Why It Matters

Sorting is a gateway algorithm. It teaches you about iteration, swapping, and optimization.

Efficient sorting is critical for:

- Preprocessing data for binary search
- Organizing data for analysis
- Building indexes and ranking systems

It's the first step toward deeper concepts like divide and conquer and hybrid optimization.

Try It Yourself

1. Implement all three: bubble, selection, insertion
2. Test them on arrays of size 10, 100, 1000, and note timing differences
3. Try sorting an array that's already sorted. Which one adapts best?
4. Modify insertion sort to sort in descending order

Sorting may seem simple, but it's a cornerstone. Mastering it will shape your intuition for almost every other algorithm.

8. Data Structures Overview

Algorithms and data structures are two sides of the same coin. An algorithm is how you solve a problem. A data structure is where you store and organize data so that your algorithm can work efficiently.

You can think of data structures as containers, each one shaped for specific access patterns, trade-offs, and performance needs. Choosing the right one is often the key to designing a fast algorithm.

1. Why Data Structures Matter

Imagine you want to find a book quickly.

- If all books are piled randomly → you must scan every one ($O(n)$)
- If they're sorted on a shelf → you can use binary search ($O(\log n)$)
- If you have an index or catalog → you can find it instantly ($O(1)$)

Different structures unlock different efficiencies.

2. The Core Data Structures

Let's walk through the most essential ones:

Type	Description	Key Operations	Typical Use
Array	Fixed-size contiguous memory	Access ($O(1)$), Insert/Delete ($O(n)$)	Fast index access
Linked List	Sequence of nodes with pointers	Insert/Delete ($O(1)$), Access ($O(n)$)	Dynamic sequences
Stack	LIFO (last-in, first-out)	push(), pop() in $O(1)$	Undo, recursion
Queue	FIFO (first-in, first-out)	enqueue(), dequeue() in $O(1)$	Scheduling, buffers
Hash Table	Key-value pairs via hashing	Average $O(1)$, Worst $O(n)$	Lookup, caching
Heap	Partially ordered tree	Insert $O(\log n)$, Extract-Min $O(\log n)$	Priority queues
Tree	Hierarchical structure	Access $O(\log n)$ (balanced)	Sorted storage
Graph	Nodes + edges	Traversal $O(V + E)$	Networks, paths
Set / Map	Unique keys or key-value pairs	$O(\log n)$ or $O(1)$	Membership tests

Each comes with trade-offs. Arrays are fast but rigid, linked lists are flexible but slower to access, and hash tables are lightning-fast but unordered.

3. Abstract Data Types (ADTs)

An ADT defines what operations you can do, not how they're implemented. For example, a Stack ADT promises:

- `push(x)`

- `pop()`
- `peek()`

It can be implemented with arrays or linked lists, the behavior stays the same.

Common ADTs:

- Stack
- Queue
- Deque
- Priority Queue
- Map / Dictionary

This separation of interface and implementation helps design flexible systems.

4. The Right Tool for the Job

Choosing the correct data structure often decides the performance of your algorithm:

Problem	Good Choice	Reason
Undo feature	Stack	LIFO fits history
Scheduling tasks	Queue	FIFO order
Dijkstra's algorithm	Priority Queue	Extract smallest distance
Counting frequencies	Hash Map	Fast key lookup
Dynamic median	Heap + Heap	Balance two halves
Search by prefix	Trie	Fast prefix lookups

Good programmers don't just write code. They pick the right structure.

Tiny Code

Example: comparing array vs linked list

Array:

```
int arr[5] = {1, 2, 3, 4, 5};
printf("%d", arr[3]); // O(1)
```

Linked List:

```
struct Node { int val; struct Node* next; };
```

To get the 4th element, you must traverse $\rightarrow O(n)$

Different structures, different access costs.

Why It Matters

Every efficient algorithm depends on the right data structure.

- Searching, sorting, and storing all rely on structure
- Memory layout affects cache performance
- The wrong choice can turn $O(1)$ into $O(n^2)$

Understanding these structures is like knowing the tools in a workshop. Once you recognize their shapes, you'll instinctively know which to grab.

Try It Yourself

1. Implement a stack using an array. Then implement it using a linked list.
2. Write a queue using two stacks.
3. Try storing key-value pairs in a hash table (hint: mod by table size).
4. Compare access times for arrays vs linked lists experimentally.

Data structures aren't just storage. They are the skeletons your algorithms stand on.

9. Graphs and Trees Overview

Now that you've seen linear structures like arrays and linked lists, it's time to explore non-linear structures, graphs and trees. These are the shapes behind networks, hierarchies, and relationships.

They appear everywhere: family trees, file systems, maps, social networks, and knowledge graphs all rely on them.

1. Trees

A tree is a connected structure with no cycles. It's a hierarchy, and every node (except the root) has one parent.

- Root: the top node
- Child: a node directly connected below
- Leaf: a node with no children
- Height: the longest path from root to a leaf

A binary tree is one where each node has at most two children. A binary search tree (BST) keeps elements ordered:

- Left child $<$ parent $<$ right child

Basic operations:

- Insert
- Search
- Delete
- Traverse (preorder, inorder, postorder, level-order)

Example:

```
struct Node {
    int val;
    struct Node *left, *right;
};
```

Insert in BST:

```
struct Node* insert(struct Node* root, int val) {
    if (!root) return newNode(val);
    if (val < root->val) root->left = insert(root->left, val);
    else root->right = insert(root->right, val);
    return root;
}
```

2. Common Tree Types

Type	Description	Use Case
Binary Tree	Each node has 2 children	General hierarchy
Binary Search Tree	Left < Root < Right	Ordered data
AVL / Red-Black Tree	Self-balancing BST	Fast search/insert
Heap	Complete binary tree, parent or children	Priority queues
Trie	Tree of characters	Prefix search
Segment Tree	Tree over ranges	Range queries
Fenwick Tree	Tree with prefix sums	Efficient updates

Balanced trees keep height $O(\log n)$, guaranteeing fast operations.

3. Graphs

A graph generalizes the idea of trees. In graphs, nodes (vertices) can connect freely.

A graph is a set of vertices (V) and edges (E):

$$G = (V, E)$$

Directed vs Undirected:

- Directed: edges have direction (A $\rightarrow$ B)
- Undirected: edges connect both ways (A, B)

Weighted vs Unweighted:

- Weighted: each edge has a cost
- Unweighted: all edges are equal

Representation:

1. Adjacency Matrix: $n \times n$ matrix; entry $(i, j) = 1$ if edge exists
2. Adjacency List: array of lists; each vertex stores its neighbors

Example adjacency list:

```
vector<int> graph[n];
graph[0].push_back(1);
graph[0].push_back(2);
```

4. Common Graph Types

Graph Type	Description	Example
Undirected	Edges without direction	Friendship network
Directed	Arrows indicate direction	Web links
Weighted	Edges have costs	Road network
Cyclic	Contains loops	Task dependencies
Acyclic	No loops	Family tree
DAG (Directed Acyclic)	Directed, no cycles	Scheduling, compilers
Complete	All pairs connected	Dense networks
Sparse	Few edges	Real-world graphs

5. Basic Graph Operations

- Add Vertex / Edge
- Traversal: Depth-First Search (DFS), Breadth-First Search (BFS)
- Path Finding: Dijkstra, Bellman-Ford
- Connectivity: Union-Find, Tarjan (SCC)
- Spanning Trees: Kruskal, Prim

Each graph problem has its own flavor, from finding shortest paths to detecting cycles.

Tiny Code

Breadth-first search (BFS):

```
void bfs(int start, vector<int> graph[], int n) {
    bool visited[n];
    memset(visited, false, sizeof(visited));
    queue<int> q;
    visited[start] = true;
    q.push(start);
    while (!q.empty()) {
        int node = q.front(); q.pop();
        printf("%d ", node);
        for (int neighbor : graph[node]) {
            if (!visited[neighbor]) {
                visited[neighbor] = true;
                q.push(neighbor);
            }
```

```
        }
    }
}
```

This explores level by level, perfect for shortest paths in unweighted graphs.

Why It Matters

Trees and graphs model relationships and connections, not just sequences. They are essential for:

- Search engines (web graph)
- Compilers (syntax trees, dependency DAGs)
- AI (state spaces, decision trees)
- Databases (indexes, joins, relationships)

Understanding them unlocks an entire world of algorithms, from DFS and BFS to Dijkstra, Kruskal, and beyond.

Try It Yourself

1. Build a simple binary search tree and implement inorder traversal.
2. Represent a graph with adjacency lists and print all edges.
3. Write a DFS and BFS for a small graph.
4. Draw a directed graph with a cycle and detect it manually.

Graphs and trees move you beyond linear thinking. They let you explore *connections*, not just collections.

10. Algorithm Design Patterns

By now, you've seen what algorithms are and how they're analyzed. You've explored searches, sorts, structures, and recursion. The next step is learning patterns, reusable strategies that guide how you build new algorithms from scratch.

Just like design patterns in software architecture, algorithmic design patterns give structure to your thinking. Once you recognize them, many problems suddenly feel familiar.

1. Brute Force

Start simple. Try every possibility and pick the best result. Brute force is often your baseline, clear but inefficient.

Example: Find the maximum subarray sum by checking all subarrays.

- Time: $O(n^2)$
- Advantage: easy to reason about
- Disadvantage: explodes for large input

Sometimes, brute force helps you see the structure needed for a better approach.

2. Divide and Conquer

Split the problem into smaller parts, solve each, and combine. Ideal for problems with self-similarity.

Classic examples:

- Merge Sort $\rightarrow$ split and merge
- Binary Search $\rightarrow$ halve the search space
- Quick Sort $\rightarrow$ partition and sort

General form:

$$T(n) = aT(n/b) + f(n)$$

Use recurrence relations and the Master Theorem to analyze them.

3. Greedy

Make the best local decision at each step. Works only when local optimal choices lead to a global optimum.

Examples:

- Activity Selection
- Huffman Coding
- Dijkstra (for non-negative weights)

Greedy algorithms are simple and fast when they fit.

4. Dynamic Programming (DP)

When subproblems overlap, store results and reuse them. Think recursion plus memory.

Two main styles:

- Top-Down (Memoization): recursive with caching
- Bottom-Up (Tabulation): iterative filling table

Used in:

- Fibonacci numbers
- Knapsack
- Longest Increasing Subsequence (LIS)
- Matrix Chain Multiplication

DP transforms exponential recursion into polynomial time.

5. Backtracking

Explore all possibilities, but prune when constraints fail. It is brute force with early exits.

Perfect for:

- N-Queens
- Sudoku
- Permutation generation
- Subset sums

Backtracking builds solutions incrementally, abandoning paths that cannot lead to a valid result.

6. Two Pointers

Move two indices through a sequence to find patterns or meet conditions.

Common use:

- Sorted arrays (sum pairs, partitions)
- String problems (palindromes, sliding windows)
- Linked lists (slow and fast pointers)

Simple, but surprisingly powerful.

7. Sliding Window

Maintain a window over data, expand or shrink it as needed.

Used for:

- Maximum sum subarray (Kadane's algorithm)
- Substrings of length k
- Longest substring without repeating characters

Helps reduce $O(n^2)$ to $O(n)$ in sequence problems.

8. Binary Search on Answer

Sometimes, the input is not sorted, but the answer space is. If you can define a function `check(mid)` that is monotonic (true or false changes once), you can apply binary search on possible answers.

Examples:

- Minimum capacity to ship packages in D days
- Smallest feasible value satisfying a constraint

Powerful for optimization under monotonic conditions.

9. Graph-Based

Think in terms of nodes and edges, paths and flows.

Patterns include:

- BFS and DFS (exploration)
- Topological Sort (ordering)
- Dijkstra and Bellman-Ford (shortest paths)
- Union-Find (connectivity)
- Kruskal and Prim (spanning trees)

Graphs often reveal relationships hidden in data.

10. Meet in the Middle

Split the problem into two halves, compute all possibilities for each, and combine efficiently. Used in problems where brute force $O(2^n)$ is too large but $O(2^{n/2})$ is manageable.

Examples:

- Subset sum (divide into two halves)
- Search problems in combinatorics

A clever compromise between brute force and efficiency.

Tiny Code

Example: Two Pointers to find a pair sum

```c
int find_pair_sum(int arr[], int n, int target) {
    int i = 0, j = n - 1;
    while (i < j) {
        int sum = arr[i] + arr[j];
        if (sum == target) return 1;
        else if (sum < target) i++;
        else j--;
    }
    return 0;
}
```

Works in $O(n)$ for sorted arrays, elegant and fast.

Why It Matters

Patterns are mental shortcuts. They turn "blank page" problems into "I've seen this shape before."

Once you recognize the structure, you can choose a suitable pattern and adapt it. This is how top coders solve complex problems under time pressure, not by memorizing algorithms, but by seeing patterns.

Try It Yourself

1. Write a brute-force and a divide-and-conquer solution for maximum subarray sum. Compare speed.
2. Solve the coin change problem using both greedy and DP.
3. Implement N-Queens with backtracking.
4. Use two pointers to find the smallest window with a given sum.
5. Pick a problem you've solved before. Can you reframe it using a different design pattern?

The more patterns you practice, the faster you will map new problems to known strategies, and the more powerful your algorithmic intuition will become.

Chapter 2. Sorting and Searching

11. Elementary Sorting (Bubble, Insertion, Selection)

Before diving into advanced sorts like mergesort or heapsort, it's important to understand the elementary sorting algorithms , the building blocks. They're simple, intuitive, and great for learning how sorting works under the hood.

In this section, we'll cover three classics:

- Bubble Sort - swap adjacent out-of-order pairs- Selection Sort - select the smallest element each time- Insertion Sort - insert elements one by one in order These algorithms share (On^2) time complexity but differ in behavior and stability.

1. Bubble Sort

Idea: Compare adjacent pairs and swap if they're out of order. Repeat until the array is sorted. Each pass "bubbles" the largest element to the end.

Steps:

1. Compare `arr[j]` and `arr[j+1]`
2. Swap if `arr[j] > arr[j+1]`
3. Continue passes until no swaps are needed

Code:

```c
void bubble_sort(int arr[], int n) {
    for (int i = 0; i < n - 1; i++) {
        int swapped = 0;
        for (int j = 0; j < n - i - 1; j++) {
            if (arr[j] > arr[j + 1]) {
                int temp = arr[j];
                arr[j] = arr[j + 1];
                arr[j + 1] = temp;
                swapped = 1;
            }
        }
        if (!swapped) break;
    }
}
```

Complexity:

- Best: (O(n)) (already sorted)- Worst: (On^2)- Space: (O(1))- Stable: Yes Intuition: Imagine bubbles rising , after each pass, the largest "bubble" settles at the top.

2. Selection Sort

Idea: Find the smallest element and place it at the front.

Steps:

1. For each position `i`, find the smallest element in the remainder of the array
2. Swap it with `arr[i]`

Code:

```c
void selection_sort(int arr[], int n) {
    for (int i = 0; i < n - 1; i++) {
        int min_idx = i;
        for (int j = i + 1; j < n; j++) {
            if (arr[j] < arr[min_idx])
                min_idx = j;
        }
        int temp = arr[i];
        arr[i] = arr[min_idx];
        arr[min_idx] = temp;
    }
}
```

Complexity:

- Best: (On^2)- Worst: (On^2)- Space: (O(1))- Stable: No Intuition: Selection sort "selects" the next correct element and fixes it. It minimizes swaps but still scans all elements.

3. Insertion Sort

Idea: Build a sorted array one element at a time by inserting each new element into its correct position.

Steps:

1. Start from index 1
2. Compare with previous elements
3. Shift elements greater than key to the right
4. Insert key into the correct place

Code:

```
void insertion_sort(int arr[], int n) {
    for (int i = 1; i < n; i++) {
        int key = arr[i];
        int j = i - 1;
        while (j >= 0 && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}
```

Complexity:

- Best: (O(n)) (nearly sorted)- Worst: (On^2)- Space: (O(1))- Stable: Yes Intuition: It's like sorting cards in your hand , take the next card and slide it into the right place.

4. Comparing the Three

Algorithm	Best Case	Average Case	Worst Case	Stable	In-Place	Notes
Bubble Sort	O(n)	$O(n^2)$	$O(n^2)$	Yes	Yes	Early exit possible
Selection Sort	$O(n^2)$	$O(n^2)$	$O(n^2)$	No	Yes	Few swaps
Insertion Sort	O(n)	$O(n^2)$	$O(n^2)$	Yes	Yes	Great on small or nearly sorted data

Tiny Code

Let's see how insertion sort works on `[5, 3, 4, 1, 2]`:

- Start with 3 → insert before 5 → `[3, 5, 4, 1, 2]`- Insert 4 → `[3, 4, 5, 1, 2]`- Insert 1 → `[1, 3, 4, 5, 2]`- Insert 2 → `[1, 2, 3, 4, 5]` Sorted in five passes.

Why It Matters

Elementary sorts teach you:

- How comparisons and swaps drive order- The trade-off between simplicity and efficiency- How to reason about stability and adaptability While these aren't used for large datasets in practice, they're used *inside* hybrid algorithms like Timsort and IntroSort, which switch to insertion sort for small chunks.

Try It Yourself

1. Implement all three and print the array after each pass.
2. Test on arrays: already sorted, reversed, random, partially sorted.
3. Modify bubble sort to sort descending.
4. Try insertion sort on 10,000 elements and note its behavior.
5. Can you detect when the list is already sorted and stop early?

Start simple. Master these patterns. They'll be your foundation for everything from merge sort to radix sort.

12. Divide-and-Conquer Sorting (Merge, Quick, Heap)

Elementary sorts are great for learning, but their (On^2) runtime quickly becomes a bottleneck. To scale beyond small arrays, we need algorithms that divide problems into smaller parts, sort them independently, and combine the results.

This is the essence of divide and conquer , break it down, solve subproblems, merge solutions. In sorting, this approach yields some of the fastest general-purpose algorithms: Merge Sort, Quick Sort, and Heap Sort.

1. Merge Sort

Idea: Split the array in half, sort each half recursively, then merge the two sorted halves.

Merge sort is stable, works well with linked lists, and guarantees ($On \log n$) time.

Steps:

1. Divide the array into halves
2. Recursively sort each half
3. Merge two sorted halves into one

Code:

```
void merge(int arr[], int l, int m, int r) {
    int n1 = m - l + 1;
    int n2 = r - m;
    int L[n1], R[n2];
    for (int i = 0; i < n1; i++) L[i] = arr[l + i];
    for (int j = 0; j < n2; j++) R[j] = arr[m + 1 + j];
    int i = 0, j = 0, k = l;
    while (i < n1 && j < n2) {
        if (L[i] <= R[j]) arr[k++] = L[i++];
        else arr[k++] = R[j++];
    }
    while (i < n1) arr[k++] = L[i++];
    while (j < n2) arr[k++] = R[j++];
}

void merge_sort(int arr[], int l, int r) {
    if (l < r) {
        int m = (l + r) / 2;
        merge_sort(arr, l, m);
        merge_sort(arr, m + 1, r);
```

```
        merge(arr, l, m, r);
    }
}
```

Complexity:

- Time: ($On \log n$) (always)- Space: (O(n)) (temporary arrays)- Stable: Yes Merge sort is predictable, making it ideal for external sorting (like sorting data on disk).

2. Quick Sort

Idea: Pick a pivot, partition the array so smaller elements go left and larger go right, then recursively sort both sides.

Quick sort is usually the fastest in practice due to good cache locality and low constant factors.

Steps:

1. Choose a pivot (often middle or random)
2. Partition: move smaller elements to left, larger to right
3. Recursively sort the two partitions

Code:

```
int partition(int arr[], int low, int high) {
    int pivot = arr[high];
    int i = low - 1;
    for (int j = low; j < high; j++) {
        if (arr[j] < pivot) {
            i++;
            int tmp = arr[i]; arr[i] = arr[j]; arr[j] = tmp;
        }
    }
    int tmp = arr[i + 1]; arr[i + 1] = arr[high]; arr[high] = tmp;
    return i + 1;
}

void quick_sort(int arr[], int low, int high) {
    if (low < high) {
        int pi = partition(arr, low, high);
        quick_sort(arr, low, pi - 1);
        quick_sort(arr, pi + 1, high);
```

```
    }
}
```

Complexity:

- Best / Average: ($On \log n$)- Worst: (On^2) (bad pivot, e.g. sorted input with naive pivot)- Space: ($O\log n$) (recursion)- Stable: No (unless modified) Quick sort is often used in standard libraries due to its efficiency in real-world workloads.

3. Heap Sort

Idea: Turn the array into a heap, repeatedly extract the largest element, and place it at the end.

A heap is a binary tree where every parent is its children (max-heap).

Steps:

1. Build a max-heap
2. Swap the root (max) with the last element
3. Reduce heap size, re-heapify
4. Repeat until sorted

Code:

```c
void heapify(int arr[], int n, int i) {
    int largest = i;
    int l = 2 * i + 1;
    int r = 2 * i + 2;
    if (l < n && arr[l] > arr[largest]) largest = l;
    if (r < n && arr[r] > arr[largest]) largest = r;
    if (largest != i) {
        int tmp = arr[i]; arr[i] = arr[largest]; arr[largest] = tmp;
        heapify(arr, n, largest);
    }
}

void heap_sort(int arr[], int n) {
    for (int i = n / 2 - 1; i >= 0; i--)
        heapify(arr, n, i);
    for (int i = n - 1; i > 0; i--) {
        int tmp = arr[0]; arr[0] = arr[i]; arr[i] = tmp;
        heapify(arr, i, 0);
```

```
    }
}
```

Complexity:

- Time: ($On \log n$)- Space: (O(1))- Stable: No Heap sort is reliable and space-efficient but less cache-friendly than quicksort.

4. Comparison

Algorithm	Best Case	Average Case	Worst Case	Space	Stable	Notes
Merge Sort	O(n log n)	O(n log n)	O(n log n)	O(n)	Yes	Predictable, stable
Quick Sort	O(n log n)	O(n log n)	$O(n^2)$	O(log n)	No	Fast in practice
Heap Sort	O(n log n)	O(n log n)	O(n log n)	O(1)	No	In-place, robust

Each one fits a niche:

- Merge Sort → stability and guarantees- Quick Sort → speed and cache performance- Heap Sort → low memory usage and simplicity

Tiny Code

Try sorting `[5, 1, 4, 2, 8]` with merge sort:

1. Split → `[5,1,4]`, `[2,8]`
2. Sort each → `[1,4,5]`, `[2,8]`
3. Merge → `[1,2,4,5,8]`

Each recursive split halves the problem, yielding ($O \log n$) depth with (O(n)) work per level.

Why It Matters

Divide-and-conquer sorting is the foundation for efficient order processing. It introduces ideas you'll reuse in:

- Binary search (halving)- Matrix multiplication- Fast Fourier Transform- Dynamic programming These sorts teach how recursion, partitioning, and merging combine into scalable solutions.

Try It Yourself

1. Implement merge sort, quick sort, and heap sort.
2. Test all three on the same random array. Compare runtime.
3. Modify quick sort to use a random pivot.
4. Build a stable version of heap sort.
5. Visualize merge sort's recursion tree and merging process.

Mastering these sorts gives you a template for solving any divide-and-conquer problem efficiently.

13. Counting and Distribution Sorts (Counting, Radix, Bucket)

So far, we've seen comparison-based sorts like merge sort and quicksort. These rely on comparing elements and are bounded by the O(n log n) lower limit for comparisons.

But what if you don't need to compare elements directly , what if they're integers or values from a limited range?

That's where counting and distribution sorts come in. They exploit structure, not just order, to achieve linear-time sorting in the right conditions.

1. Counting Sort

Idea: If your elements are integers in a known range ([0, k)), you can count occurrences of each value, then reconstruct the sorted output.

Counting sort doesn't compare , it counts.

Steps:

1. Find the range of input (max value (k))
2. Count occurrences in a frequency array
3. Convert counts to cumulative counts
4. Place elements into their sorted positions

Code:

```
void counting_sort(int arr[], int n, int k) {
    int count[k + 1];
    int output[n];
    for (int i = 0; i <= k; i++) count[i] = 0;
    for (int i = 0; i < n; i++) count[arr[i]]++;
    for (int i = 1; i <= k; i++) count[i] += count[i - 1];
```

```
    for (int i = n - 1; i >= 0; i--) {
        output[count[arr[i]] - 1] = arr[i];
        count[arr[i]]--;
    }
    for (int i = 0; i < n; i++) arr[i] = output[i];
}
```

Example: arr = [4, 2, 2, 8, 3, 3, 1], k = 8 → count = [0,1,2,2,1,0,0,0,1] → cumulative = [0,1,3,5,6,6,6,6,7] → sorted = [1,2,2,3,3,4,8]

Complexity:

- Time: (O(n + k))- Space: (O(k))- Stable: Yes When to use:
- Input is integers- Range (k) not much larger than (n)

2. Radix Sort

Idea: Sort digits one at a time, from least significant (LSD) or most significant (MSD), using a stable sub-sort like counting sort.

Radix sort works best when all elements have fixed-length representations (e.g., integers, strings of equal length).

Steps (LSD method):

1. For each digit position (from rightmost to leftmost)
2. Sort all elements by that digit using a stable sort (like counting sort)

Code:

```
int get_max(int arr[], int n) {
    int mx = arr[0];
    for (int i = 1; i < n; i++)
        if (arr[i] > mx) mx = arr[i];
    return mx;
}

void counting_sort_digit(int arr[], int n, int exp) {
    int output[n];
    int count[10] = {0};
    for (int i = 0; i < n; i++)
        count[(arr[i] / exp) % 10]++;
    for (int i = 1; i < 10; i++)
```

```
        count[i] += count[i - 1];
    for (int i = n - 1; i >= 0; i--) {
        int digit = (arr[i] / exp) % 10;
        output[count[digit] - 1] = arr[i];
        count[digit]--;
    }
    for (int i = 0; i < n; i++)
        arr[i] = output[i];
}

void radix_sort(int arr[], int n) {
    int m = get_max(arr, n);
    for (int exp = 1; m / exp > 0; exp *= 10)
        counting_sort_digit(arr, n, exp);
}
```

Example: arr = [170, 45, 75, 90, 802, 24, 2, 66] → sort by 1s → 10s → 100s → final = [2, 24, 45, 66, 75, 90, 170, 802]

Complexity:

- Time: (O(d ×(n + b))), where
  - (d): number of digits - (b): base (10 for decimal)- Space: (O(n + b))- Stable: Yes When to use:
- Fixed-length numbers- Bounded digits (e.g., base 10 or 2)

3. Bucket Sort

Idea: Divide elements into buckets based on value ranges, sort each bucket individually, then concatenate.

Works best when data is uniformly distributed in a known interval.

Steps:

1. Create (k) buckets for value ranges
2. Distribute elements into buckets
3. Sort each bucket (often using insertion sort)
4. Merge buckets

Code:

```
void bucket_sort(float arr[], int n) {
    vector<float> buckets[n];
    for (int i = 0; i < n; i++) {
        int idx = n * arr[i]; // assuming 0 <= arr[i] < 1
        buckets[idx].push_back(arr[i]);
    }
    for (int i = 0; i < n; i++)
        sort(buckets[i].begin(), buckets[i].end());
    int idx = 0;
    for (int i = 0; i < n; i++)
        for (float val : buckets[i])
            arr[idx++] = val;
}
```

Complexity:

- Average: (O(n + k))- Worst: (On^2) (if all fall in one bucket)- Space: (O(n + k))- Stable: Depends on bucket sort method When to use:
- Real numbers uniformly distributed in ([0,1))

4. Comparison

Algorithm	Time	Space	Stable	Type	Best Use
Counting Sort	O(n + k)	O(k)	Yes	Non-comparison	Small integer range
Radix Sort	O(d(n + b))	O(n + b)	Yes	Non-comparison	Fixed-length numbers
Bucket Sort	O(n + k) avg	O(n + k)	Often	Distribution-based	Uniform floats

These algorithms achieve O(n) behavior when assumptions hold , they're specialized but incredibly fast when applicable.

Tiny Code

Let's walk counting sort on `arr = [4, 2, 2, 8, 3, 3, 1]`:

- Count occurrences → [1,2,2,1,0,0,0,1]- Cumulative count → positions- Place elements → [1,2,2,3,3,4,8] Sorted , no comparisons.

Why It Matters

Distribution sorts teach a key insight:

> If you know the structure of your data, you can sort faster than comparison allows.

They show how data properties , range, distribution, digit length , can drive algorithm design.

You'll meet these ideas again in:

- Hashing (bucketing)- Indexing (range partitioning)- Machine learning (binning, histogramming)

Try It Yourself

1. Implement counting sort for integers from 0 to 100.
2. Extend radix sort to sort strings by character.
3. Visualize bucket sort for values between 0 and 1.
4. What happens if you use counting sort on negative numbers? Fix it.
5. Compare counting vs quick sort on small integer arrays.

These are the first glimpses of linear-time sorting , harnessing knowledge about data to break the $(On \log n)$ barrier.

14. Hybrid Sorts (IntroSort, Timsort)

In practice, no single sorting algorithm is perfect for all cases. Some are fast on average but fail in worst cases (like Quick Sort). Others are consistent but slow due to overhead (like Merge Sort). Hybrid sorting algorithms combine multiple techniques to get the *best of all worlds* , practical speed, stability, and guaranteed performance.

Two of the most widely used hybrids in modern systems are IntroSort and Timsort , both power the sorting functions in major programming languages.

1. The Idea Behind Hybrid Sorting

Real-world data is messy: sometimes nearly sorted, sometimes random, sometimes pathological. A smart sorting algorithm should adapt to the data.

Hybrids switch between different strategies based on:

- Input size- Recursion depth- Degree of order- Performance thresholds So, the algorithm "introspects" or "adapts" while running.

2. IntroSort

IntroSort (short for *introspective sort*) begins like Quick Sort, but when recursion gets too deep , which means Quick Sort's worst case may be coming , it switches to Heap Sort to guarantee $(On \log n)$ time.

Steps:

1. Use Quick Sort as long as recursion depth $< 2 \log n$
2. If depth exceeds limit $\rightarrow$ switch to Heap Sort
3. For very small subarrays $\rightarrow$ switch to Insertion Sort

This triple combo ensures:

- Fast average case (Quick Sort)- Guaranteed upper bound (Heap Sort)- Efficiency on small arrays (Insertion Sort) Code Sketch:

```
void intro_sort(int arr[], int n) {
    int depth_limit = 2 * log(n);
    intro_sort_util(arr, 0, n - 1, depth_limit);
}

void intro_sort_util(int arr[], int begin, int end, int depth_limit) {
    int size = end - begin + 1;
    if (size < 16) {
        insertion_sort(arr + begin, size);
        return;
    }
    if (depth_limit == 0) {
        heap_sort_range(arr, begin, end);
        return;
    }
    int pivot = partition(arr, begin, end);
    intro_sort_util(arr, begin, pivot - 1, depth_limit - 1);
    intro_sort_util(arr, pivot + 1, end, depth_limit - 1);
}
```

Complexity:

- Average: $(On \log n)$- Worst: $(On \log n)$- Space: $(O \log n)$- Stable: No (depends on partition scheme) Used in:
- C++ STL's `std::sort`- Many systems where performance guarantees matter

3. Timsort

Timsort is a stable hybrid combining Insertion Sort and Merge Sort. It was designed to handle real-world data, which often has runs (already sorted segments).

Developed by Tim Peters (Python core dev), Timsort is now used in:

- Python's `sorted()` and `.sort()`- Java's `Arrays.sort()` for objects Idea:
- Identify runs , segments already ascending or descending- Reverse descending runs (to make them ascending)- Sort small runs with Insertion Sort- Merge runs with Merge Sort Timsort adapts beautifully to partially ordered data.

Steps:

1. Scan array, detect runs (sequences already sorted)
2. Push runs to a stack
3. Merge runs using a carefully balanced merge strategy

Pseudocode (simplified):

```
def timsort(arr):
    RUN = 32
    n = len(arr)

    # Step 1: sort small chunks
    for i in range(0, n, RUN):
        insertion_sort(arr, i, min((i + RUN - 1), n - 1))

    # Step 2: merge sorted runs
    size = RUN
    while size < n:
        for start in range(0, n, size * 2):
            mid = start + size - 1
            end = min(start + size * 2 - 1, n - 1)
            merge(arr, start, mid, end)
        size *= 2
```

Complexity:

- Best: (O(n)) (already sorted data)- Average: ($On \log n$)- Worst: ($On \log n$)- Space: (O(n))- Stable: Yes Key Strengths:
- Excellent for real-world, partially sorted data- Stable (keeps equal keys in order)- Optimized merges (adaptive merging)

4. Comparison

Algorithm	Base Methods	Stability	Best	Average	Worst	Real Use
IntroSort	Quick + Heap + Insertion	No	O(n log n)	O(n log n)	O(n log n)	C++ STL
Timsort	Merge + Insertion	Yes	O(n)	O(n log n)	O(n log n)	Python, Java

IntroSort prioritizes performance guarantees. Timsort prioritizes adaptivity and stability.

Both show that "one size fits all" sorting doesn't exist , great systems detect *what's going on* and adapt.

Tiny Code

Suppose we run Timsort on `[1, 2, 3, 7, 6, 5, 8, 9]`:

- Detect runs: `[1,2,3]`, `[7,6,5]`, `[8,9]`- Reverse `[7,6,5]` → `[5,6,7]`- Merge runs → `[1,2,3,5,6,7,8,9]` Efficient because it leverages the existing order.

Why It Matters

Hybrid sorts are the real-world heroes , they combine theory with practice. They teach an important principle:

> When one algorithm's weakness shows up, switch to another's strength.

These are not academic curiosities , they're in your compiler, your browser, your OS, your database. Understanding them means you understand how modern languages optimize fundamental operations.

Try It Yourself

1. Implement IntroSort and test on random, sorted, and reverse-sorted arrays.
2. Simulate Timsort's run detection on nearly sorted input.
3. Compare sorting speed of Insertion Sort vs Timsort for small arrays.
4. Add counters to Quick Sort and see when IntroSort should switch.
5. Explore Python's `sorted()` with different input shapes , guess when it uses merge vs insertion.

Hybrid sorts remind us: good algorithms adapt , they're not rigid, they're smart.

15. Special Sorts (Cycle, Gnome, Comb, Pancake)

Not all sorting algorithms follow the mainstream divide-and-conquer or distribution paradigms. Some were designed to solve niche problems, to illustrate elegant ideas, or simply to experiment with different mechanisms of ordering.

These special sorts, Cycle Sort, Gnome Sort, Comb Sort, and Pancake Sort, are fascinating not because they're the fastest, but because they reveal creative ways to think about permutation, local order, and in-place operations.

1. Cycle Sort

Idea: Minimize the number of writes. Cycle sort rearranges elements into cycles, placing each value directly in its correct position. It performs exactly as many writes as there are misplaced elements, making it ideal for flash memory or systems where writes are expensive.

Steps:

1. For each position `i`, find where `arr[i]` belongs (its rank).
2. If it's not already there, swap it into position.
3. Continue the cycle until the current position is correct.
4. Move to the next index.

Code:

```
void cycle_sort(int arr[], int n) {
    for (int cycle_start = 0; cycle_start < n - 1; cycle_start++) {
        int item = arr[cycle_start];
        int pos = cycle_start;

        for (int i = cycle_start + 1; i < n; i++)
            if (arr[i] < item) pos++;

        if (pos == cycle_start) continue;

        while (item == arr[pos]) pos++;
        int temp = arr[pos];
        arr[pos] = item;
        item = temp;

        while (pos != cycle_start) {
            pos = cycle_start;
            for (int i = cycle_start + 1; i < n; i++)
```

```
                if (arr[i] < item) pos++;
            while (item == arr[pos]) pos++;
            temp = arr[pos];
            arr[pos] = item;
            item = temp;
        }
    }
}
```

Complexity:

- Time: (On^2)- Writes: minimal (exactly n-c, where c = #cycles)- Stable: No Use Case: When minimizing writes is more important than runtime.

2. Gnome Sort

Idea: A simpler variation of insertion sort. Gnome sort moves back and forth like a "gnome" tidying flower pots: if two adjacent pots are out of order, swap and step back; otherwise, move forward.

Steps:

1. Start at index 1
2. If `arr[i] >= arr[i-1]`, move forward
3. Else, swap and step back (if possible)
4. Repeat until the end

Code:

```
void gnome_sort(int arr[], int n) {
    int i = 1;
    while (i < n) {
        if (i == 0 || arr[i] >= arr[i - 1]) i++;
        else {
            int temp = arr[i]; arr[i] = arr[i - 1]; arr[i - 1] = temp;
            i--;
        }
    }
}
```

Complexity:

- Time: (On^2)- Space: (O(1))- Stable: Yes Use Case: Educational simplicity. It's a readable form of insertion logic without nested loops.

3. Comb Sort

Idea: An improvement over Bubble Sort by introducing a gap between compared elements, shrinking it gradually. By jumping farther apart early, Comb Sort helps eliminate small elements that are "stuck" near the end.

Steps:

1. Start with gap = n
2. On each pass, shrink gap = gap / 1.3
3. Compare and swap items `gap` apart
4. Stop when gap = 1 and no swaps occur

Code:

```
void comb_sort(int arr[], int n) {
    int gap = n;
    int swapped = 1;
    while (gap > 1 || swapped) {
        gap = (gap * 10) / 13;
        if (gap == 9 || gap == 10) gap = 11;
        if (gap < 1) gap = 1;
        swapped = 0;
        for (int i = 0; i + gap < n; i++) {
            if (arr[i] > arr[i + gap]) {
                int temp = arr[i]; arr[i] = arr[i + gap]; arr[i + gap] = temp;
                swapped = 1;
            }
        }
    }
}
```

Complexity:

- Average: $(On \log n)$- Worst: (On^2)- Space: (O(1))- Stable: No Use Case: When a simple, in-place, nearly linear-time alternative to bubble sort is desired.

4. Pancake Sort

Idea: Sort an array using only one operation: flip (reversing a prefix). It's like sorting pancakes on a plate, flip the stack so the largest pancake goes to the bottom, then repeat for the rest.

Steps:

1. Find the maximum unsorted element
2. Flip it to the front
3. Flip it again to its correct position
4. Reduce the unsorted portion by one

Code:

```
void flip(int arr[], int i) {
    int start = 0;
    while (start < i) {
        int temp = arr[start];
        arr[start] = arr[i];
        arr[i] = temp;
        start++;
        i--;
    }
}

void pancake_sort(int arr[], int n) {
    for (int curr_size = n; curr_size > 1; curr_size--) {
        int mi = 0;
        for (int i = 1; i < curr_size; i++)
            if (arr[i] > arr[mi]) mi = i;
        if (mi != curr_size - 1) {
            flip(arr, mi);
            flip(arr, curr_size - 1);
        }
    }
}
```

Complexity:

- Time: (On^2)- Space: (O(1))- Stable: No Fun Fact: Pancake sort is the only known algorithm whose operations mimic a kitchen utensil, and inspired the Burnt Pancake Problem in combinatorics and genome rearrangement theory.

5. Comparison

Algorithm	Time	Space	Stable	Distinctive Trait
Cycle Sort	O(n²)	O(1)	No	Minimal writes
Gnome Sort	O(n²)	O(1)	Yes	Simple insertion-like behavior

Algorithm	Time	Space	Stable	Distinctive Trait
Comb Sort	O(n log n) avg	O(1)	No	Shrinking gap, improved bubble
Pancake Sort	$O(n^2)$	O(1)	No	Prefix reversals only

Each highlights a different design goal:

- Cycle: minimize writes- Gnome: simplify logic- Comb: optimize comparisons- Pancake: restrict operations

Tiny Code

Example (Pancake Sort on `[3, 6, 1, 9]`):

1. Max = 9 at index 3 → flip(3) → `[9,1,6,3]`
2. flip(3) → `[3,6,1,9]` (9 fixed)
3. Max = 6 → flip(1) → `[6,3,1,9]`
4. flip(2) → `[1,3,6,9]`

Sorted using only flips.

Why It Matters

Special sorts show there's more than one way to think about ordering. They're laboratories for exploring new ideas: minimizing swaps, limiting operations, or optimizing stability. Even if they're not the go-to in production, they deepen your intuition about sorting mechanics.

Try It Yourself

1. Implement each algorithm and visualize their operations step-by-step.
2. Measure how many writes Cycle Sort performs vs. others.
3. Compare Gnome and Insertion sort on nearly sorted arrays.
4. Modify Comb Sort's shrink factor, how does performance change?
5. Write Pancake Sort with printouts of every flip to see the "stack" in motion.

These quirky algorithms prove that sorting isn't just science, it's also art and experimentation.

16. Linear and Binary Search

Searching is the process of finding a target value within a collection of data. Depending on whether the data is sorted or unsorted, you'll use different strategies.

In this section, we revisit two of the most fundamental searching methods , Linear Search and Binary Search , and see how they underpin many higher-level algorithms and data structures.

1. Linear Search

Idea: Check each element one by one until you find the target. This is the simplest possible search and works on unsorted data.

Steps:

1. Start from index 0
2. Compare `arr[i]` with the target
3. If match, return index
4. If end reached, return -1

Code:

```
int linear_search(int arr[], int n, int key) {
    for (int i = 0; i < n; i++) {
        if (arr[i] == key) return i;
    }
    return -1;
}
```

Example: arr = [7, 2, 4, 9, 1], key = 9

- Compare 7, 2, 4, then 9 → found at index 3 Complexity:
- Time: (O(n))- Space: (O(1))- Best case: (O(1)) (first element)- Worst case: (O(n)) Pros:
- Works on any data (sorted or unsorted)- Simple to implement Cons:
- Inefficient on large arrays Use it when data is small or unsorted, or when simplicity matters more than speed.

2. Binary Search

Idea: If the array is sorted, you can repeatedly halve the search space. Compare the middle element to the target , if it's greater, search left; if smaller, search right.

Steps:

1. Find the midpoint
2. If `arr[mid] == key`, done
3. If `arr[mid] > key`, search left
4. If `arr[mid] < key`, search right
5. Repeat until range is empty

Iterative Version:

```
int binary_search(int arr[], int n, int key) {
    int low = 0, high = n - 1;
    while (low <= high) {
        int mid = (low + high) / 2;
        if (arr[mid] == key) return mid;
        else if (arr[mid] < key) low = mid + 1;
        else high = mid - 1;
    }
    return -1;
}
```

Recursive Version:

```
int binary_search_rec(int arr[], int low, int high, int key) {
    if (low > high) return -1;
    int mid = (low + high) / 2;
    if (arr[mid] == key) return mid;
    else if (arr[mid] > key)
        return binary_search_rec(arr, low, mid - 1, key);
    else
        return binary_search_rec(arr, mid + 1, high, key);
}
```

Example: arr = [1, 3, 5, 7, 9, 11], key = 7

- mid = 5 → key > mid → move right- mid = 7 → found Complexity:
- Time: (O$\log n$)- Space: (O(1)) (iterative) or (O$\log n$) (recursive)- Best case: (O(1)) (middle element) Requirements:

- Must be sorted- Must have random access (array, not linked list) Pros:
- Very fast for large sorted arrays- Foundation for advanced searches (e.g. interpolation, exponential) Cons:
- Needs sorted data- Doesn't adapt to frequent insertions/deletions

3. Binary Search Variants

Binary search is a *pattern* as much as a single algorithm. You can tweak it to find:

- First occurrence: move left if `arr[mid] == key`- Last occurrence: move right if `arr[mid] == key`- Lower bound: first index key- Upper bound: first index > key Example (Lower Bound):

```
int lower_bound(int arr[], int n, int key) {
    int low = 0, high = n;
    while (low < high) {
        int mid = (low + high) / 2;
        if (arr[mid] < key) low = mid + 1;
        else high = mid;
    }
    return low;
}
```

Usage: These variants power functions like `std::lower_bound()` in C++ and binary search trees' lookup logic.

4. Comparison

Algorithm	Works On	Time	Space	Sorted Data Needed	Notes
Linear Search	Any	O(n)	O(1)	No	Best for small/unsorted
Binary Search	Sorted	O(log n)	O(1)	Yes	Fastest on ordered arrays

Binary search trades simplicity for power , once your data is sorted, you unlock sublinear search.

Tiny Code

Compare on array `[2, 4, 6, 8, 10]`, key = 8:

- Linear: 4 steps- Binary: 2 steps This gap grows huge with size , for $n = 10^6$, linear takes up to a million steps, binary about 20.

Why It Matters

These two searches form the foundation of retrieval. Linear search shows brute-force iteration; binary search shows how structure (sorted order) leads to exponential improvement.

From databases to compiler symbol tables to tree lookups, this principle , *divide to search faster* , is everywhere.

Try It Yourself

1. Implement linear and binary search.
2. Count comparisons for (n = 10, 100, 1000).
3. Modify binary search to return the first occurrence of a duplicate.
4. Try binary search on unsorted data , what happens?
5. Combine with sorting: sort array, then search.

Mastering these searches builds intuition for all lookup operations , they are the gateway to efficient data retrieval.

17. Interpolation and Exponential Search

Linear and binary search work well across many scenarios, but they don't take into account how data is distributed. When values are uniformly distributed, we can *estimate* where the target lies, instead of always splitting the range in half. This leads to Interpolation Search, which "jumps" close to where the value should be.

For unbounded or infinite lists, we can't even know the size of the array up front , that's where Exponential Search shines, by quickly expanding its search window before switching to binary search.

Let's dive into both.

1. Interpolation Search

Idea: If data is sorted and uniformly distributed, you can *predict* where a key might be using linear interpolation. Instead of splitting at the middle, estimate the position based on the value's proportion in the range.

Formula:

$$\text{pos} = \text{low} + \frac{(key - arr[low]) \times (high - low)}{arr[high] - arr[low]}$$

This "guesses" where the key lies. If (key = arr[pos]), we're done. Otherwise, adjust `low` or `high` and repeat.

Steps:

1. Compute estimated position `pos`
2. Compare `arr[pos]` with `key`
3. Narrow range accordingly
4. Repeat while `low <= high` and `key` within range

Code:

```
int interpolation_search(int arr[], int n, int key) {
    int low = 0, high = n - 1;

    while (low <= high && key >= arr[low] && key <= arr[high]) {
        if (low == high) {
            if (arr[low] == key) return low;
            return -1;
        }
        int pos = low + ((double)(key - arr[low]) * (high - low)) / (arr[high] - arr[low]);

        if (arr[pos] == key)
            return pos;
        if (arr[pos] < key)
            low = pos + 1;
        else
            high = pos - 1;
    }
    return -1;
}
```

Example: arr = [10, 20, 30, 40, 50], key = 40 pos = 0 + ((40 - 10) * (4 - 0)) / (50 - 10) = 3 → found at index 3

Complexity:

- Best: (O(1))- Average: (Olog log n) (uniform data)- Worst: (O(n)) (non-uniform or skewed data)- Space: (O(1)) When to Use:
- Data is sorted and nearly uniform- Numeric data where values grow steadily Note: Interpolation search is adaptive , faster when data is predictable, slower when data is irregular.

2. Exponential Search

Idea: When you don't know the array size (e.g., infinite streams, linked data, files), you can't just binary search from 0 to n-1. Exponential search finds a search range dynamically by doubling its step size until it overshoots the target, then does binary search within that range.

Steps:

1. If `arr[0] == key`, return 0
2. Find a range `[bound/2, bound]` such that `arr[bound] >= key`
3. Perform binary search in that range

Code:

```
int exponential_search(int arr[], int n, int key) {
    if (arr[0] == key) return 0;
    int bound = 1;
    while (bound < n && arr[bound] < key)
        bound *= 2;
    int low = bound / 2;
    int high = (bound < n) ? bound : n - 1;
    // Binary search in [low, high]
    while (low <= high) {
        int mid = (low + high) / 2;
        if (arr[mid] == key) return mid;
        else if (arr[mid] < key) low = mid + 1;
        else high = mid - 1;
    }
    return -1;
}
```

Example: arr = [2, 4, 6, 8, 10, 12, 14, 16], key = 10

- Step: bound = 1 (4), 2 (6), 4 (10 key)- Binary search [2,4] → found Complexity:

- Time: (O$\log i$), where (i) is index of the target- Space: (O(1))- Best: (O(1)) When to Use:
- Unbounded or streamed data- Unknown array size but sorted order

3. Comparison

Algorithm	Best Case	Average Case	Worst Case	Data Requirement	Notes
Linear Search	O(1)	O(n)	O(n)	Unsorted	Works everywhere
Binary Search	O(1)	O(log n)	O(log n)	Sorted	Predictable halving
Interpolation Search	O(1)	O(log log n)	O(n)	Sorted + Uniform	Adaptive, fast on uniform data
Exponential Search	O(1)	O(log n)	O(log n)	Sorted	Great for unknown size

Interpolation improves on binary *if* data is smooth. Exponential shines when size is unknown.

Tiny Code

Interpolation intuition: If your data is evenly spaced (10, 20, 30, 40, 50), the value 40 should be roughly 75% along. Instead of halving every time, we jump *right near it*. It's data-aware searching.

Exponential intuition: When size is unknown, "expand until you find the wall," then search within.

Why It Matters

These two searches show how context shapes algorithm design:

- *Distribution* (Interpolation Search)- *Boundaries* (Exponential Search) They teach that performance depends not only on structure (sortedness) but also metadata , how much you know about data spacing or limits.

These principles resurface in skip lists, search trees, and probabilistic indexing.

Try It Yourself

1. Test interpolation search on [10, 20, 30, 40, 50] , note how few steps it takes.
2. Try the same on [1, 2, 4, 8, 16, 32, 64] , note slowdown.
3. Implement exponential search and simulate an "infinite" array by stopping at `n`.
4. Compare binary vs interpolation search on random vs uniform data.
5. Extend exponential search to linked lists , how does complexity change?

Understanding these searches helps you tailor lookups to the shape of your data , a key skill in algorithmic thinking.

18. Selection Algorithms (Quickselect, Median of Medians)

Sometimes you don't need to sort an entire array , you just want the k-th smallest (or largest) element. Sorting everything is overkill when you only need one specific rank. Selection algorithms solve this problem efficiently, often in linear time.

They're the backbone of algorithms for median finding, percentiles, and order statistics, and they underpin operations like *pivot selection* in Quick Sort.

1. The Selection Problem

Given an unsorted array of (n) elements and a number (k), find the element that would be at position (k) if the array were sorted.

For example: arr = [7, 2, 9, 4, 6], (k = 3) → Sorted = [2, 4, 6, 7, 9] → 3rd smallest = 6

We can solve this without sorting everything.

2. Quickselect

Idea: Quickselect is a selection variant of Quick Sort. It partitions the array around a pivot, but recurses only on the side that contains the k-th element.

It has average-case O(n) time because each partition roughly halves the search space.

Steps:

1. Choose a pivot (random or last element)
2. Partition array into elements < pivot and > pivot
3. Let `pos` be the pivot's index after partition
4. If `pos == k-1` → done
5. If `pos > k-1` → recurse left
6. If `pos < k-1` → recurse right

Code:

```
int partition(int arr[], int low, int high) {
    int pivot = arr[high];
    int i = low;
    for (int j = low; j < high; j++) {
        if (arr[j] < pivot) {
            int temp = arr[i]; arr[i] = arr[j]; arr[j] = temp;
            i++;
        }
    }
    int temp = arr[i]; arr[i] = arr[high]; arr[high] = temp;
    return i;
}

int quickselect(int arr[], int low, int high, int k) {
    if (low == high) return arr[low];
    int pos = partition(arr, low, high);
    int rank = pos - low + 1;
    if (rank == k) return arr[pos];
    if (rank > k) return quickselect(arr, low, pos - 1, k);
    return quickselect(arr, pos + 1, high, k - rank);
}
```

Example: arr = [7, 2, 9, 4, 6], (k = 3)

- Pivot = 6- Partition → [2, 4, 6, 9, 7], pos = 2- rank = 3 → found (6) Complexity:
- Average: (O(n))- Worst: (On^2) (bad pivots)- Space: (O(1))- In-place When to Use:
- Fast average case- You don't need full sorting Quickselect is used in C++'s `nth_element()` and many median-finding implementations.

3. Median of Medians

Idea: Guarantee worst-case (O(n)) time by choosing a good pivot deterministically.

This method ensures the pivot divides the array into reasonably balanced parts every time.

Steps:

1. Divide array into groups of 5
2. Find the median of each group (using insertion sort)
3. Recursively find the median of these medians → pivot

4. Partition array around this pivot
5. Recurse into the side containing the k-th element

This guarantees at least 30% of elements are eliminated each step → linear time in worst case.

Code Sketch:

```
int select_pivot(int arr[], int low, int high) {
    int n = high - low + 1;
    if (n <= 5) {
        insertion_sort(arr + low, n);
        return low + n / 2;
    }

    int medians[(n + 4) / 5];
    int i;
    for (i = 0; i < n / 5; i++) {
        insertion_sort(arr + low + i * 5, 5);
        medians[i] = arr[low + i * 5 + 2];
    }
    if (i * 5 < n) {
        insertion_sort(arr + low + i * 5, n % 5);
        medians[i] = arr[low + i * 5 + (n % 5) / 2];
        i++;
    }
    return select_pivot(medians, 0, i - 1);
}
```

You'd then partition around `pivot` and recurse just like Quickselect.

Complexity:

- Worst: (O(n))- Space: (O(1)) (in-place version)- Stable: No (doesn't preserve order) Why It Matters: Median of Medians is slower in practice than Quickselect but provides theoretical guarantees , vital in real-time or critical systems.

4. Special Cases

- Min / Max: trivial , just scan once ((O(n)))- Median: $k = \lceil n/2 \rceil$, can use Quickselect or Median of Medians- Top-k Elements: use partial selection or heaps (k smallest/largest) Example: To get top 5 scores from a million entries, use Quickselect to find 5th largest, then filter threshold.

5. Comparison

Algorithm	Best	Average	Worst	Stable	In-Place	Notes
Quickselect	O(n)	O(n)	$O(n^2)$	No	Yes	Fast in practice
Median of Medians	O(n)	O(n)	O(n)	No	Yes	Deterministic
Sorting	O(n log n)	O(n log n)	O(n log n)	Depends	Depends	Overkill for single element

Quickselect is fast and simple; Median of Medians is safe and predictable.

Tiny Code

Find 4th smallest in [9, 7, 2, 5, 4, 3]:

- Pivot = 4 → partition [2,3,4,9,7,5]- 4 at position 2 → rank = 3 < 4 → recurse right- New range [9,7,5], (k = 1) → smallest = 5 Result: 5

Why It Matters

Selection algorithms reveal a key insight:

> Sometimes you don't need everything , just what matters.

They form the basis for:

- Median filters in signal processing- Partitioning steps in sorting- k-th order statistics- Robust statistics and quantile computation They embody a "partial work, full answer" philosophy , do exactly enough.

Try It Yourself

1. Implement Quickselect and find k-th smallest for various k.
2. Compare runtime vs full sorting.
3. Modify Quickselect to find k-th largest.
4. Implement Median of Medians pivot selection.
5. Use Quickselect to find median of 1,000 random elements.

Mastering selection algorithms helps you reason about efficiency , you'll learn when to stop sorting and start selecting.

19. Range Searching and Nearest Neighbor

Searching isn't always about finding a single key. Often, you need to find all elements within a given range , or the closest match to a query point.

These problems are central to databases, computational geometry, and machine learning (like k-NN classification). This section introduces algorithms for range queries (e.g. find all values between `L` and `R`) and nearest neighbor searches (e.g. find the point closest to query `q`).

1. Range Searching

Idea: Given a set of data points (1D or multidimensional), quickly report all points within a specified range.

In 1D (simple arrays), range queries can be handled by binary search and prefix sums. In higher dimensions, we need trees designed for efficient spatial querying.

A. 1D Range Query (Sorted Array)

Goal: Find all elements in `[L, R]`.

Steps:

1. Use lower bound to find first element L
2. Use upper bound to find first element $>$ R
3. Output all elements in between

Code (C++-style pseudo):

```
int l = lower_bound(arr, arr + n, L) - arr;
int r = upper_bound(arr, arr + n, R) - arr;
for (int i = l; i < r; i++)
    printf("%d ", arr[i]);
```

Time Complexity:

- Binary search bounds: (Olog n)- Reporting results: (O(k)) where (k) = number of elements in range $\rightarrow$ Total: (Olog $n + k$)

B. Prefix Sum Range Query (For sums)

If you just need the sum (not the actual elements), use prefix sums:

$$\text{prefix}[i] = a_0 + a_1 + ... + a_i$$

Then range sum:

$$\text{sum}(L, R) = \text{prefix}[R] - \text{prefix}[L-1]$$

Code:

```
int prefix[n];
prefix[0] = arr[0];
for (int i = 1; i < n; i++)
    prefix[i] = prefix[i - 1] + arr[i];

int range_sum(int L, int R) {
    return prefix[R] - (L > 0 ? prefix[L - 1] : 0);
}
```

Time: (O(1)) per query after (O(n)) preprocessing.

Used in:

- Databases for fast range aggregation- Fenwick trees, segment trees

C. 2D Range Queries (Rectangular Regions)

For points ((x, y)), queries like:

> "Find all points where $L_x \leq x \leq R_x$ and $L_y \leq y \leq R_y$"

Use specialized structures:

- Range Trees (balanced BSTs per dimension)- Fenwick Trees / Segment Trees (for 2D arrays)- KD-Trees (spatial decomposition) Time: $(O\log^2 n + k)$ typical for 2D Space: $(On \log n)$

2. Nearest Neighbor Search

Idea: Given a set of points, find the one closest to query (q). Distance is often Euclidean, but can be any metric.

Brute Force: Check all points → (O(n)) per query. Too slow for large datasets.

We need structures that let us prune far regions fast.

A. KD-Tree

KD-tree = K-dimensional binary tree. Each level splits points by one coordinate, alternating axes. Used for efficient nearest neighbor search in low dimensions (2D-10D).

Construction:

1. Choose axis = depth % k
2. Sort points by axis
3. Pick median → root
4. Recursively build left and right

Query (Nearest Neighbor):

1. Traverse down tree based on query position
2. Backtrack , check whether hypersphere crosses splitting plane
3. Keep track of best (closest) distance

Complexity:

- Build: $(On \log n)$- Query: $(O\log n)$ avg, (O(n)) worst Use Cases:
- Nearest city lookup- Image / feature vector matching- Game AI spatial queries Code Sketch (2D Example):

```
struct Point { double x, y; };

double dist(Point a, Point b) {
    return sqrt((a.x - b.x)*(a.x - b.x) + (a.y - b.y)*(a.y - b.y));
}
```

(Full KD-tree implementation omitted for brevity , idea is recursive partitioning.)

B. Ball Tree / VP-Tree

For high-dimensional data, KD-trees degrade. Alternatives like Ball Trees (split by hyperspheres) or VP-Trees (Vantage Point Trees) perform better.

They split based on distance metrics, not coordinate axes.

C. Approximate Nearest Neighbor (ANN)

For large-scale, high-dimensional data (e.g. embeddings, vectors):

- Locality Sensitive Hashing (LSH)- HNSW (Hierarchical Navigable Small World Graphs) These trade exactness for speed, common in:
- Vector databases- Recommendation systems- AI model retrieval

3. Summary

Problem	Brute Force	Optimized	Time (Query)	Notes
1D Range Query	Scan O(n)	Binary Search	O(log n + k)	Sorted data
Range Sum	O(n)	Prefix Sum	O(1)	Static data
2D Range Query	O(n)	Range Tree	$O(\log^2 n + k)$	Spatial filtering
Nearest Neighbor	O(n)	KD-Tree	O(log n) avg	Exact, low-dim
Nearest Neighbor (high-dim)	O(n)	HNSW / LSH	~O(1)	Approximate

Tiny Code

Simple 1D range query:

```
int arr[] = {1, 3, 5, 7, 9, 11};
int L = 4, R = 10;
int l = lower_bound(arr, arr + 6, L) - arr;
int r = upper_bound(arr, arr + 6, R) - arr;
for (int i = l; i < r; i++)
    printf("%d ", arr[i]); // 5 7 9
```

Output: `5 7 9`

Why It Matters

Range and nearest-neighbor queries power:

- Databases (SQL range filters, BETWEEN)- Search engines (spatial indexing)- ML (k-NN classifiers, vector similarity)- Graphics / Games (collision detection, spatial queries) These are not just searches , they're geometric lookups, linking algorithms to spatial reasoning.

Try It Yourself

1. Write a function to return all numbers in `[L, R]` using binary search.
2. Build a prefix sum array and answer 5 range-sum queries in O(1).
3. Implement a KD-tree for 2D points and query nearest neighbor.
4. Compare brute-force vs KD-tree search on 1,000 random points.
5. Explore Python's `scipy.spatial.KDTree` or `sklearn.neighbors`.

These algorithms bridge searching with geometry and analytics, forming the backbone of spatial computation.

20. Search Optimizations and Variants

We've explored the main search families , linear, binary, interpolation, exponential , each fitting a different data shape or constraint. Now let's move one step further: optimizing search for performance and adapting it to specialized scenarios.

This section introduces practical variants and enhancements used in real systems, databases, and competitive programming, including jump search, fibonacci search, ternary search, and exponential + binary combinations.

1. Jump Search

Idea: If data is sorted, we can "jump" ahead by fixed steps instead of scanning linearly. It's like hopping through the array in blocks , when you overshoot the target, you step back and linearly search that block.

It strikes a balance between linear and binary search , fewer comparisons without the recursion or halving of binary search.

Steps:

1. Choose jump size = $\sqrt{n}$
2. Jump by blocks until `arr[step] > key`
3. Linear search in previous block

Code:

```
int jump_search(int arr[], int n, int key) {
    int step = sqrt(n);
    int prev = 0;

    while (arr[min(step, n) - 1] < key) {
        prev = step;
        step += sqrt(n);
        if (prev >= n) return -1;
    }

    for (int i = prev; i < min(step, n); i++) {
        if (arr[i] == key) return i;
    }
    return -1;
}
```

Example: arr = [1, 3, 5, 7, 9, 11, 13, 15], key = 11

- step = 2- Jump 5, 7, 9, 11 → found Complexity:
- Time: ($O\sqrt{n}$)- Space: (O(1))- Works on sorted data When to Use: For moderately sized sorted lists when you want fewer comparisons but minimal overhead.

2. Fibonacci Search

Idea: Similar to binary search, but it splits the array based on Fibonacci numbers instead of midpoints. This allows using only addition and subtraction (no division), useful on hardware where division is costly.

Also, like binary search, it halves (roughly) the search space each iteration.

Steps:

1. Find the smallest Fibonacci number n
2. Use it to compute probe index
3. Compare and move interval accordingly

Code (Sketch):

```
int fibonacci_search(int arr[], int n, int key) {
    int fibMMm2 = 0; // (m-2)'th Fibonacci
    int fibMMm1 = 1; // (m-1)'th Fibonacci
    int fibM = fibMMm2 + fibMMm1; // m'th Fibonacci

    while (fibM < n) {
        fibMMm2 = fibMMm1;
        fibMMm1 = fibM;
        fibM = fibMMm2 + fibMMm1;
    }

    int offset = -1;
    while (fibM > 1) {
        int i = min(offset + fibMMm2, n - 1);
        if (arr[i] < key) {
            fibM = fibMMm1;
            fibMMm1 = fibMMm2;
            fibMMm2 = fibM - fibMMm1;
            offset = i;
        } else if (arr[i] > key) {
            fibM = fibMMm2;
            fibMMm1 = fibMMm1 - fibMMm2;
            fibMMm2 = fibM - fibMMm1;
        } else return i;
    }
    if (fibMMm1 && arr[offset + 1] == key)
        return offset + 1;
    return -1;
}
```

Complexity:

- Time: ($O\log n$)- Space: ($O(1)$)- Sorted input required Fun Fact: Fibonacci search was originally designed for tape drives , where random access is expensive, and predictable jumps matter.

3. Ternary Search

Idea: When the function or sequence is unimodal (strictly increasing then decreasing), you can locate a maximum or minimum by splitting the range into three parts instead of two.

Used not for discrete lookup but for optimization on sorted functions.

Steps:

1. Divide range into thirds
2. Evaluate at two midpoints `m1`, `m2`
3. Eliminate one-third based on comparison
4. Repeat until range is small

Code:

```
double ternary_search(double low, double high, double (*f)(double)) {
    for (int i = 0; i < 100; i++) {
        double m1 = low + (high - low) / 3;
        double m2 = high - (high - low) / 3;
        if (f(m1) < f(m2))
            low = m1;
        else
            high = m2;
    }
    return (low + high) / 2;
}
```

Example: Find minimum of (f(x) = (x-3)^2) between [0,10]. After iterations, converges to (x 3).

Complexity:

- Time: $O(\log \text{range})$
- Space: $O(1)$
- Works for unimodal functions

Used in:

- Mathematical optimization
- Search-based tuning
- Game AI decision models

4. Binary Search Variants (Review)

Binary search can be tailored to answer richer queries:

- Lower Bound: first index key- Upper Bound: first index > key- Equal Range: range of all equal elements- Rotated Arrays: find element in rotated sorted array- Infinite Arrays: use exponential expansion Rotated Example: arr = [6,7,9,1,3,4], key = 3 → Find pivot, then binary search correct side.

5. Combined Searches

Real systems often chain algorithms:

- Exponential + Binary Search → when bounds unknown- Interpolation + Linear Search → when near target- Jump + Linear Search → hybrid iteration These hybrids use context switching , pick a fast search, then fall back to simple scan in a narrowed window.

6. Summary

Algorithm	Time	Space	Data Requirement	Special Strength
Jump Search	O(√n)	O(1)	Sorted	Fewer comparisons
Fibonacci Search	O(log n)	O(1)	Sorted	Division-free
Ternary Search	O(log range)	O(1)	Unimodal	Optimization
Binary Variants	O(log n)	O(1)	Sorted	Bound finding
Combined Searches	Adaptive	O(1)	Mixed	Practical hybrids

Tiny Code

Jump Search intuition:

```
// Blocks of size sqrt(n)
[1, 3, 5, 7, 9, 11, 13, 15]
Step: 3 → 7 > 6 → search previous block
```

Jumps reduce comparisons dramatically vs linear scan.

Why It Matters

Search optimization is about adapting structure to context. You don't always need a fancy data structure , sometimes a tweak like fixed-step jumping or Fibonacci spacing yields massive gains.

These ideas influence:

- Indexing in databases- Compilers' symbol resolution- Embedded systems with low-level constraints They embody the principle: search smarter, not harder.

Try It Yourself

1. Implement Jump Search and test vs Binary Search on 1M elements.
2. Write a Fibonacci Search , compare steps taken.
3. Use Ternary Search to find min of a convex function.
4. Modify binary search to find element in rotated array.
5. Combine Jump + Linear , how does it behave for small n?

Understanding these variants arms you with flexibility , the heart of algorithmic mastery.

Chapter 3. Data Structures in Actions

21. Arrays, Linked Lists, Stacks, Queues

Every data structure is built on top of a few core foundations , the ones that teach you how data is stored, accessed, and moved. In this section, we'll revisit the essentials: arrays, linked lists, stacks, and queues.

They're simple, but they show you the most important design trade-offs in algorithms:

- Contiguity vs. flexibility- Speed vs. dynamic growth- Last-in-first-out vs. first-in-first-out access

1. Arrays

Idea: A contiguous block of memory storing elements of the same type. Access by index in O(1) time , that's their superpower.

Operations:

- Access `arr[i]`: (O(1))- Update `arr[i]`: (O(1))- Insert at end: (O(1)) (amortized for dynamic arrays)- Insert in middle: (O(n))- Delete: (O(n)) Example:

```
int arr[5] = {10, 20, 30, 40, 50};
printf("%d", arr[2]); // 30
```

Strengths:

- Fast random access- Cache-friendly (contiguous memory)- Simple, predictable Weaknesses:
- Fixed size (unless using dynamic array)- Costly inserts/deletes Dynamic Arrays: Languages provide resizable arrays (like `vector` in C++ or `ArrayList` in Java) using doubling strategy , when full, allocate new array twice as big and copy. This gives amortized (O(1)) insertion at end.

2. Linked Lists

Idea: A chain of nodes, where each node stores a value and a pointer to the next. No contiguous memory required.

Operations:

- Access: (O(n))- Insert/Delete at head: (O(1))- Search: (O(n)) Example:

```
typedef struct Node {
    int data;
    struct Node* next;
} Node;

Node* head = NULL;
```

Types:

- Singly Linked List: one pointer (next)- Doubly Linked List: two pointers (next, prev)- Circular Linked List: last node points back to first Strengths:
- Dynamic size- Fast insert/delete (no shifting) Weaknesses:
- Slow access- Extra memory for pointers- Poor cache locality Linked lists shine when memory is fragmented or frequent insertions/deletions are needed.

3. Stack

Idea: A Last-In-First-Out (LIFO) structure , the most recently added element is the first to be removed.

Used in:

- Function call stacks- Expression evaluation- Undo operations Operations:
- `push(x)`: add element on top- `pop()`: remove top element- `peek()`: view top element Example (Array-based Stack):

```
#define MAX 100
int stack[MAX], top = -1;

void push(int x) { stack[++top] = x; }
int pop() { return stack[top--]; }
int peek() { return stack[top]; }
```

Complexity: All (O(1)): push, pop, peek

Variants:

- Linked-list-based stack (no fixed size)- Min-stack (tracks minimums) Stacks also appear implicitly , in recursion and backtracking algorithms.

4. Queue

Idea: A First-In-First-Out (FIFO) structure , the first added element leaves first.

Used in:

- Task scheduling- BFS traversal- Producer-consumer pipelines Operations:
- `enqueue(x)`: add to rear- `dequeue()`: remove from front- `front()`: view front Example (Array-based Queue):

```
#define MAX 100
int queue[MAX], front = 0, rear = 0;

void enqueue(int x) { queue[rear++] = x; }
int dequeue() { return queue[front++]; }
```

This simple implementation can waste space. A circular queue fixes that by wrapping indices modulo `MAX`:

```
rear = (rear + 1) % MAX;
```

Complexity: All (O(1)): enqueue, dequeue

Variants:

- Deque (double-ended queue): push/pop from both ends- Priority Queue: dequeue highest priority (not strictly FIFO)

Structure	Access	Insert	Delete	Order	Memory	Notes

5. Comparison

Structure	Access	Insert	Delete	Order	Memory	Notes
Array	O(1)	O(n)	O(n)	Indexed	Contiguous	Fast access
Linked List	O(n)	O(1)*	O(1)*	Sequential	Pointers	Flexible size
Stack	O(1)	O(1)	O(1)	LIFO	Minimal	Call stack, parsing
Queue	O(1)	O(1)	O(1)	FIFO	Minimal	Scheduling, BFS

(* at head or tail with pointer)

Tiny Code

Simple stack example:

```
push(10);
push(20);
printf("%d", pop()); // 20
```

Simple queue example:

```
enqueue(5);
enqueue(8);
printf("%d", dequeue()); // 5
```

These short routines appear in almost every algorithm , from recursion stacks to graph traversals.

Why It Matters

These four structures form the spine of data structures:

- Arrays teach indexing and memory- Linked lists teach pointers and dynamic allocation- Stacks teach recursion and reversal- Queues teach scheduling and order maintenance Every complex structure (trees, heaps, graphs) builds on these.

Master them, and every algorithm will feel more natural.

Try It Yourself

1. Implement a linked list with `insert_front` and `delete_value`.
2. Build a stack and use it to reverse an array.
3. Implement a queue for a round-robin scheduler.
4. Convert infix expression to postfix using a stack.
5. Compare time taken to insert 1000 elements in array vs linked list.

Understanding these foundations gives you the vocabulary of structure , the way algorithms organize their thoughts in memory.

22. Hash Tables and Variants (Cuckoo, Robin Hood, Consistent)

When you need lightning-fast lookups, insertions, and deletions, few data structures match the raw efficiency of a hash table. They're everywhere , from symbol tables and caches to compilers and databases , powering average-case O(1) access.

In this section, we'll unpack how hash tables work, their collision strategies, and explore modern variants like Cuckoo Hashing, Robin Hood Hashing, and Consistent Hashing, each designed to handle different real-world needs.

1. The Core Idea

A hash table maps keys to values using a hash function that transforms the key into an index in an array.

$$\text{index} = h(\text{key}) \bmod \text{table\_size}$$

If no two keys hash to the same index, all operations are (O(1)). But in practice, collisions happen , two keys may map to the same slot , and we must handle them smartly.

2. Collision Resolution Strategies

A. Separate Chaining Each table slot holds a linked list (or dynamic array) of entries with the same hash.

Pros: Simple, handles load factor > 1 Cons: Extra pointers, memory overhead

Code Sketch:

```c
typedef struct Node {
    int key, value;
    struct Node* next;
} Node;

Node* table[SIZE];

int hash(int key) { return key % SIZE; }

void insert(int key, int value) {
    int idx = hash(key);
    Node* node = malloc(sizeof(Node));
    node->key = key; node->value = value;
    node->next = table[idx];
    table[idx] = node;
}
```

B. Open Addressing All keys live directly in the table. On collision, find another slot.

Three main strategies:

- Linear probing: try next slot (+1)- Quadratic probing: step size increases quadratically- Double hashing: second hash decides step size Example (Linear Probing):

```c
int hash(int key) { return key % SIZE; }
int insert(int key, int value) {
    int idx = hash(key);
    while (table[idx].used)
        idx = (idx + 1) % SIZE;
    table[idx] = (Entry){key, value, 1};
}
```

Load Factor $\alpha = \frac{n}{m}$ affects performance , when too high, rehash to larger size.

3. Modern Variants

Classic hash tables can degrade under heavy collisions. Modern variants reduce probe chains and balance load more evenly.

A. Cuckoo Hashing

Idea: Each key has two possible locations , if both full, evict one ("kick out the cuckoo") and reinsert. Ensures constant lookup , at most two probes.

Steps:

1. Compute two hashes (h_1(key)), (h_2(key))
2. If slot 1 empty → place
3. Else evict occupant, reinsert it using alternate hash
4. Repeat until placed or cycle detected (rehash if needed)

Code Sketch (Conceptual):

```
int h1(int key) { return key % SIZE; }
int h2(int key) { return (key / SIZE) % SIZE; }

void insert(int key) {
    int pos1 = h1(key);
    if (!table1[pos1]) { table1[pos1] = key; return; }
    int displaced = table1[pos1]; table1[pos1] = key;

    int pos2 = h2(displaced);
    if (!table2[pos2]) { table2[pos2] = displaced; return; }
    // continue evicting if needed
}
```

Pros:

- Worst-case O(1) lookup (constant probes)- Predictable latency Cons:
- Rehash needed on insertion failure- More complex logic Used in high-performance caches and real-time systems.

B. Robin Hood Hashing

Idea: Steal slots from richer (closer) keys to ensure fairness. When inserting, if you find someone with smaller probe distance, swap , "steal from the rich, give to the poor."

This balances probe lengths and improves variance and average lookup time.

Key Principle:

$$\text{If new\_probe\_distance} > \text{existing\_probe\_distance} \Rightarrow \text{swap}$$

Code Sketch:

```
int insert(int key) {
    int idx = hash(key);
    int dist = 0;
    while (table[idx].used) {
        if (table[idx].dist < dist) {
            // swap entries
            Entry tmp = table[idx];
            table[idx] = (Entry){key, dist, 1};
            key = tmp.key;
            dist = tmp.dist;
        }
        idx = (idx + 1) % SIZE;
        dist++;
    }
    table[idx] = (Entry){key, dist, 1};
}
```

Pros:

- Reduced variance- Better performance under high load Cons:
- Slightly slower insertion Used in modern languages like Rust (`hashbrown`) and Swift.

C. Consistent Hashing

Idea: When distributing keys across multiple nodes, you want minimal movement when adding/removing a node. Consistent hashing maps both keys and nodes onto a circular hash ring.

Steps:

1. Hash nodes into a ring
2. Hash keys into same ring
3. Each key belongs to the next node clockwise

When a node is added or removed, only nearby keys move.

Used in:

- Distributed caches (Memcached, DynamoDB)- Load balancing- Sharding in databases Code (Conceptual):

```
Ring: 0 ------------------------------- 2^32
Nodes: N1 at hash("A"), N2 at hash("B")
Key: hash("User42") → assign to next node clockwise
```

Pros:

- Minimal rebalancing- Scalable Cons:
- More complex setup- Requires virtual nodes for even distribution

4. Complexity Overview

Variant	Insert	Search	Delete	Memory	Notes
Chaining	O(1) avg	O(1) avg	O(1) avg	High	Simple, dynamic
Linear Probing	O(1) avg	O(1) avg	O(1) avg	Low	Clustering risk
Cuckoo	O(1)	O(1)	O(1)	Medium	Two tables, predictable
Robin Hood	O(1)	O(1)	O(1)	Low	Balanced probes
Consistent	O(log n)	O(log n)	O(log n)	Depends	Distributed keys

Tiny Code

Simple hash table with linear probing:

```c
#define SIZE 10
int keys[SIZE], values[SIZE], used[SIZE];

int hash(int key) { return key % SIZE; }

void insert(int key, int value) {
    int idx = hash(key);
    while (used[idx]) idx = (idx + 1) % SIZE;
    keys[idx] = key; values[idx] = value; used[idx] = 1;
}
```

Lookup:

```c
int get(int key) {
    int idx = hash(key);
    while (used[idx]) {
        if (keys[idx] == key) return values[idx];
        idx = (idx + 1) % SIZE;
    }
    return -1;
}
```

Why It Matters

Hash tables show how structure and randomness combine for speed. They embody the idea that a good hash function + smart collision handling = near-constant performance.

Variants like Cuckoo and Robin Hood are examples of modern engineering trade-offs , balancing performance, memory, and predictability. Consistent hashing extends these ideas to distributed systems.

Try It Yourself

1. Implement a hash table with chaining and test collision handling.
2. Modify it to use linear probing , measure probe lengths.
3. Simulate Cuckoo hashing with random inserts.
4. Implement Robin Hood swapping logic , observe fairness.
5. Draw a consistent hash ring with 3 nodes and 10 keys , track movement when adding one node.

Once you master these, you'll see hashing everywhere , from dictionaries to distributed databases.

23. Heaps (Binary, Fibonacci, Pairing)

Heaps are priority-driven data structures , they always give you fast access to the most important element, typically the minimum or maximum. They're essential for priority queues, scheduling, graph algorithms (like Dijkstra), and streaming analytics.

In this section, we'll start from the basic binary heap and then explore more advanced ones like Fibonacci and pairing heaps, which trade off simplicity, speed, and amortized guarantees.

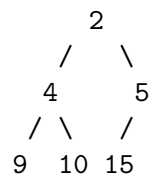
1. The Heap Property

A heap is a tree-based structure (often represented as an array) that satisfies:

- Min-Heap: Every node its children- Max-Heap: Every node its children This ensures the root always holds the smallest (or largest) element.

Complete Binary Tree: All levels filled except possibly the last, which is filled left to right.

Example (Min-Heap):



Here, the smallest element (2) is at the root.

2. Binary Heap

Storage: Stored compactly in an array. For index `i` (0-based):

- Parent = `(i - 1) / 2`- Left child = `2i + 1`- Right child = `2i + 2` Operations:

Operation	Description	Time
`push(x)`	Insert element	(Olog n)
`pop()`	Remove root	(Olog n)
`peek()`	Get root	(O(1))
`heapify()`	Build heap	(O(n))

A. Insertion (Push)

Insert at the end, then bubble up until heap property is restored.

Code:

```c
void push(int heap[], int *n, int x) {
    int i = (*n)++;
    heap[i] = x;
    while (i > 0 && heap[(i - 1)/2] > heap[i]) {
        int tmp = heap[i];
        heap[i] = heap[(i - 1)/2];
        heap[(i - 1)/2] = tmp;
        i = (i - 1) / 2;
    }
}
```

B. Removal (Pop)

Replace root with last element, then bubble down (heapify).

Code:

```c
void heapify(int heap[], int n, int i) {
    int smallest = i, l = 2*i + 1, r = 2*i + 2;
    if (l < n && heap[l] < heap[smallest]) smallest = l;
    if (r < n && heap[r] < heap[smallest]) smallest = r;
    if (smallest != i) {
        int tmp = heap[i]; heap[i] = heap[smallest]; heap[smallest] = tmp;
        heapify(heap, n, smallest);
    }
}
```

Pop:

```c
int pop(int heap[], int *n) {
    int root = heap[0];
    heap[0] = heap[--(*n)];
    heapify(heap, *n, 0);
    return root;
}
```

C. Building a Heap

Heapify bottom-up from last non-leaf: (O(n))

```
for (int i = n/2 - 1; i >= 0; i--)
    heapify(heap, n, i);
```

D. Applications

- Heapsort: Repeatedly pop min (O(n log n))- Priority Queue: Fast access to smallest/largest- Graph Algorithms: Dijkstra, Prim- Streaming: Median finding using two heaps

3. Fibonacci Heap

Idea: A heap optimized for algorithms that do many decrease-key operations (like Dijkstra's). It stores a collection of trees with lazy merging, giving amortized bounds:

Operation	Amortized Time
Insert	(O(1))
Find-Min	(O(1))
Extract-Min	(O$\log n$)
Decrease-Key	(O(1))
Merge	(O(1))

It achieves this by delaying structural fixes until absolutely necessary (using potential method in amortized analysis).

Structure:

- A circular linked list of roots- Each node can have multiple children- Consolidation on extract-min ensures minimal degree duplication Used in theoretical optimizations where asymptotic complexity matters (e.g. Dijkstra in (O$E + V\log V$) vs (O$E\log V$)).

4. Pairing Heap

Idea: A simpler, practical alternative to Fibonacci heaps. Self-adjusting structure using a tree with multiple children.

Operations:

- Insert: (O(1))- Extract-Min: (O$\log n$) amortized- Decrease-Key: (O$\log n$) amortized Steps:

- `merge` two heaps: attach one as child of the other- `extract-min`: remove root, merge children in pairs, then merge all results Why It's Popular:
- Easier to implement- Great real-world performance- Used in functional programming and priority schedulers

5. Comparison

Heap Type	Insert	Extract-Min	Decrease-Key	Merge	Simplicity	Use Case
Binary Heap	O(log n)	O(log n)	O(log n)	O(n)	Easy	General-purpose
Fibonacci Heap	O(1)	O(log n)	O(1)	O(1)	Complex	Theoretical optimality
Pairing Heap	O(1)	O(log n)	O(log n)	O(1)	Moderate	Practical alternative

Tiny Code

Binary Heap Demo:

```
int heap[100], n = 0;
push(heap, &n, 10);
push(heap, &n, 4);
push(heap, &n, 7);
printf("%d ", pop(heap, &n)); // 4
```

Output: `4`

Why It Matters

Heaps show how to prioritize elements dynamically. From sorting to scheduling, they're the backbone of many "choose the best next" algorithms. Variants like Fibonacci and Pairing Heaps demonstrate how amortized analysis can unlock deeper efficiency , crucial in graph theory and large-scale optimization.

Try It Yourself

1. Implement a binary min-heap with `push`, `pop`, and `peek`.
2. Use a heap to sort a list (Heapsort).
3. Build a priority queue for task scheduling.
4. Study how Dijkstra changes when replacing arrays with heaps.
5. Explore Fibonacci heap pseudo-code , trace `decrease-key`.

Mastering heaps gives you a deep sense of priority-driven design , how to keep "the best" element always within reach.

24. Balanced Trees (AVL, Red-Black, Splay, Treap)

Unbalanced trees can degrade into linear lists, turning your beautiful (Olog n) search into a sad (O(n)) crawl. Balanced trees solve this , they keep the height logarithmic, guaranteeing fast lookups, insertions, and deletions.

In this section, you'll learn how different balancing philosophies work , AVL (strict balance), Red-Black (relaxed balance), Splay (self-adjusting), and Treap (randomized balance).

1. The Idea of Balance

For a binary search tree (BST):

$$\text{height} = O(\log n)$$

only if it's balanced , meaning the number of nodes in left and right subtrees differ by a small factor.

Unbalanced BST (bad):

```
1
 \
  2
   \
    3
```

Balanced BST (good):

```
  2
 / \
1   3
```

Balance ensures efficient:

- `search(x)` $\rightarrow$ (Olog n)- `insert(x)` $\rightarrow$ (Olog n)- `delete(x)` $\rightarrow$ (Olog n)

2. AVL Tree (Adelson-Velsky & Landis)

Invented in 1962, AVL is the first self-balancing BST. It enforces strict balance:

$$|\text{height(left)} - \text{height(right)}| \leq 1$$

Whenever this condition breaks, rotations fix it.

Rotations:

- LL (Right Rotation): imbalance on left-left- RR (Left Rotation): imbalance on right-right- LR / RL: double rotation cases Code (Rotation Example):

```
Node* rotateRight(Node* y) {
    Node* x = y->left;
    Node* T = x->right;
    x->right = y;
    y->left = T;
    return x;
}
```

Height & Balance Factor:

```
int height(Node* n) { return n ? n->h : 0; }
int balance(Node* n) { return height(n->left) - height(n->right); }
```

Properties:

- Strict height bound: (Olog n)- More rotations (slower insertions)- Excellent lookup speed Used when lookups $>$ updates (databases, indexing).

3. Red-Black Tree

Idea: A slightly looser balance for faster insertions. Each node has a color (Red/Black) with these rules:

1. Root is black
2. Red node's children are black
3. Every path has same number of black nodes
4. Null nodes are black

Balance through color flips + rotations

Compared to AVL:

- Fewer rotations (faster insert/delete)- Slightly taller (slower lookup)- Simpler amortized balance Used in:
- C++ `std::map`, `std::set`- Java `TreeMap`, Linux scheduler Complexity: All major operations ($O\log n$)

4. Splay Tree

Idea: Bring recently accessed node to root via splaying (rotations). It adapts to access patterns , the more you access a key, the faster it becomes.

Splaying Steps:

- Zig: one rotation (root child)- Zig-Zig: two rotations (same side)- Zig-Zag: two rotations (different sides) Code (Conceptual):

```
Node* splay(Node* root, int key) {
    if (!root || root->key == key) return root;
    if (key < root->key) {
        if (!root->left) return root;
        // splay in left subtree
        if (key < root->left->key)
            root->left->left = splay(root->left->left, key),
            root = rotateRight(root);
        else if (key > root->left->key)
            root->left->right = splay(root->left->right, key),
            root->left = rotateLeft(root->left);
        return rotateRight(root);
    } else {
        if (!root->right) return root;
```

```
        // symmetric
    }
}
```

Why It's Cool: No strict balance, but amortized ($O \log n$). Frequently accessed elements stay near top.

Used in self-adjusting caches, rope data structures, memory allocators.

5. Treap (Tree + Heap)

Idea: Each node has two keys:

- BST key → order property- Priority → heap property Insertion = normal BST insert + heap fix via rotation.

Balance comes from randomization , random priorities ensure expected ($O \log n$) height.

Code Sketch:

```
typedef struct Node {
    int key, priority;
    struct Node *left, *right;
} Node;

Node* insert(Node* root, int key) {
    if (!root) return newNode(key, rand());
    if (key < root->key) root->left = insert(root->left, key);
    else root->right = insert(root->right, key);

    if (root->left && root->left->priority > root->priority)
        root = rotateRight(root);
    if (root->right && root->right->priority > root->priority)
        root = rotateLeft(root);
    return root;
}
```

Advantages:

- Simple logic- Random balancing- Expected ($O \log n$) Used in randomized algorithms and functional programming.

6. Comparison

Tree	Balance Type	Rotations	Height	Insert/Delete	Lookup	Notes
AVL	Strict	More	$(O \log n)$	Medium	Fast	Lookup-heavy
Red-Black	Relaxed	Fewer	$(O \log n)$	Fast	Medium	Library std
Splay	Adaptive	Variable	Amortized $(O \log n)$	Fast	Fast (amortized)	Access patterns
Treap	Randomized	Avg few	$(O \log n)$ expected	Simple	Simple	Probabilistic

Tiny Code

AVL Insert (Skeleton):

```
Node* insert(Node* root, int key) {
    if (!root) return newNode(key);
    if (key < root->key) root->left = insert(root->left, key);
    else root->right = insert(root->right, key);
    root->h = 1 + max(height(root->left), height(root->right));
    int b = balance(root);
    if (b > 1 && key < root->left->key) return rotateRight(root);
    if (b < -1 && key > root->right->key) return rotateLeft(root);
    // other cases...
    return root;
}
```

Why It Matters

Balanced trees guarantee predictable performance under dynamic updates. Each variant represents a philosophy:

- AVL: precision- Red-Black: practicality- Splay: adaptability- Treap: randomness Together, they teach one core idea , keep height in check, no matter the operations.

Try It Yourself

1. Implement an AVL tree and visualize rotations.
2. Insert keys [10, 20, 30, 40, 50] and trace Red-Black color changes.
3. Splay after each access , see which keys stay near top.
4. Build a Treap with random priorities , measure average height.
5. Compare performance of BST vs AVL on sorted input.

Balanced trees are the architects of order , always keeping chaos one rotation away.

25. Segment Trees and Fenwick Trees

When you need to answer range queries quickly (like sum, min, max) and support updates to individual elements, simple prefix sums won't cut it anymore.

You need something smarter , data structures that can divide and conquer over ranges, updating and combining results efficiently.

That's exactly what Segment Trees and Fenwick Trees (Binary Indexed Trees) do:

- Query over a range in (Olog n)- Update elements in (Olog n) They're the backbone of competitive programming, signal processing, and database analytics.

1. The Problem

Given an array `A[0..n-1]`, support:

1. `update(i, x)` → change `A[i]` to `x`
2. `query(L, R)` → compute sum (or min, max) of `A[L..R]`

Naive approach:

- Update: (O(1))- Query: (O(n)) Prefix sums fix one but not both. Segment and Fenwick trees fix both.

2. Segment Tree

Idea: Divide the array into segments (intervals) recursively. Each node stores an aggregate (sum, min, max) of its range. You can combine child nodes to get any range result.

Structure (Sum Example):

```
            [0,7] sum=36
          /              \
    [0,3]=10             [4,7]=26
    /     \              /      \
[0,1]=3 [2,3]=7   [4,5]=11   [6,7]=15
```

Each node represents a range [L,R]. Leaf nodes = single elements.

A. Build

Recursive Construction: Time: (O(n))

```
void build(int node, int L, int R) {
    if (L == R) tree[node] = arr[L];
    else {
        int mid = (L + R) / 2;
        build(2*node, L, mid);
        build(2*node+1, mid+1, R);
        tree[node] = tree[2*node] + tree[2*node+1];
    }
}
```

B. Query (Range Sum)

Query [l, r] recursively:

- If current range [L, R] fully inside [l, r], return node value- If disjoint, return 0- Else combine children

```
int query(int node, int L, int R, int l, int r) {
    if (r < L || R < l) return 0;
    if (l <= L && R <= r) return tree[node];
    int mid = (L + R) / 2;
    return query(2*node, L, mid, l, r)
         + query(2*node+1, mid+1, R, l, r);
}
```

C. Update

Change `arr[i] = x` and update tree nodes covering `i`.

```
void update(int node, int L, int R, int i, int x) {
    if (L == R) tree[node] = x;
    else {
        int mid = (L + R)/2;
        if (i <= mid) update(2*node, L, mid, i, x);
        else update(2*node+1, mid+1, R, i, x);
        tree[node] = tree[2*node] + tree[2*node+1];
    }
}
```

Complexities:

- Build: (O(n))- Query: (Olog n)- Update: (Olog n)- Space: (O(4n))

D. Variants

Segment trees are flexible:

- Range minimum/maximum- Range GCD- Lazy propagation → range updates- 2D segment tree for grids

3. Fenwick Tree (Binary Indexed Tree)

Idea: Stores cumulative frequencies using bit manipulation. Each node covers a range size = LSB(index).

Simpler, smaller, but supports only associative ops (sum, xor, etc.)

Indexing:

- Parent: `i + (i & -i)`- Child: `i - (i & -i)` Build: Initialize with zero, then add elements one by one.

Add / Update:

```
void add(int i, int x) {
    for (; i <= n; i += i & -i)
        bit[i] += x;
}
```

Prefix Sum:

```
int sum(int i) {
    int res = 0;
    for (; i > 0; i -= i & -i)
        res += bit[i];
    return res;
}
```

Range Sum [L, R]:

$$\text{sum}(R) - \text{sum}(L-1)$$

Complexities:

- Build: (O$n \log n$)- Query: (O$\log n$)- Update: (O$\log n$)- Space: (O(n))

4. Comparison

Feature	Segment Tree	Fenwick Tree
Space	O(4n)	O(n)
Build	O(n)	O(n log n)
Query	O(log n)	O(log n)
Update	O(log n)	O(log n)
Range Update	With Lazy	Tricky
Range Query	Flexible	Sum/XOR only
Implementation	Moderate	Simple

5. Applications

- Sum / Min / Max / XOR queries- Frequency counts- Inversions counting- Order statistics- Online problems where array updates over time Used in:
- Competitive programming- Databases (analytics on changing data)- Time series queries- Games (damage/range updates)

Tiny Code

Fenwick Tree Example:

```
int bit[1001], n;

void update(int i, int val) {
    for (; i <= n; i += i & -i)
        bit[i] += val;
}

int query(int i) {
    int res = 0;
    for (; i > 0; i -= i & -i)
        res += bit[i];
    return res;
}

// range sum
int range_sum(int L, int R) { return query(R) - query(L - 1); }
```

Why It Matters

Segment and Fenwick trees embody divide-and-conquer over data , balancing dynamic updates with range queries. They're how modern systems aggregate live data efficiently.

They teach a powerful mindset:

> "If you can split a problem, you can solve it fast."

Try It Yourself

1. Build a segment tree for sum queries.
2. Add range minimum queries (RMQ).
3. Implement a Fenwick tree , test with prefix sums.
4. Solve: number of inversions in array using Fenwick tree.
5. Add lazy propagation to segment tree for range updates.

Once you master these, range queries will never scare you again , you'll slice through them in logarithmic time.

26. Disjoint Set Union (Union-Find)

Many problems involve grouping elements into sets and efficiently checking whether two elements belong to the same group , like connected components in a graph, network connectivity, Kruskal's MST, or even social network clustering.

For these, the go-to structure is the Disjoint Set Union (DSU), also called Union-Find. It efficiently supports two operations:

1. `find(x)` → which set does `x` belong to?
2. `union(x, y)` → merge the sets containing `x` and `y`.

With path compression and union by rank, both operations run in near-constant time, specifically (O((n))), where α is the inverse Ackermann function (practically 4).

1. The Problem

Suppose you have (n) elements initially in separate sets. Over time, you want to:

- Merge two sets- Check if two elements share the same set Example:

```
Sets: {1}, {2}, {3}, {4}, {5}
Union(1,2) → {1,2}, {3}, {4}, {5}
Union(3,4) → {1,2}, {3,4}, {5}
Find(2) == Find(1)? Yes
Find(5) == Find(3)? No
```

2. Basic Implementation

Each element has a parent pointer. Initially, every node is its own parent.

Parent array representation:

```
int parent[N];

void make_set(int v) {
    parent[v] = v;
}

int find(int v) {
    if (v == parent[v]) return v;
    return find(parent[v]);
}
```

```
void union_sets(int a, int b) {
    a = find(a);
    b = find(b);
    if (a != b)
        parent[b] = a;
}
```

This works, but deep trees can form , making `find` slow. We fix that with path compression.

3. Path Compression

Every time we call `find(v)`, we make all nodes along the path point directly to the root. This flattens the tree dramatically.

Optimized Find:

```
int find(int v) {
    if (v == parent[v]) return v;
    return parent[v] = find(parent[v]);
}
```

So next time, lookups will be (O(1)) for those nodes.

4. Union by Rank / Size

When merging, always attach the smaller tree to the larger to keep depth small.

Union by Rank:

```
int parent[N], rank[N];

void make_set(int v) {
    parent[v] = v;
    rank[v] = 0;
}

void union_sets(int a, int b) {
    a = find(a);
    b = find(b);
    if (a != b) {
        if (rank[a] < rank[b])
```

```
            swap(a, b);
        parent[b] = a;
        if (rank[a] == rank[b])
            rank[a]++;
    }
}
```

Union by Size (Alternative): Track size of each set and attach smaller to larger.

```
int size[N];
void union_sets(int a, int b) {
    a = find(a);
    b = find(b);
    if (a != b) {
        if (size[a] < size[b]) swap(a, b);
        parent[b] = a;
        size[a] += size[b];
    }
}
```

5. Complexity

With both path compression and union by rank, all operations are effectively constant time:

$$O(\alpha(n)) \approx O(1)$$

For all practical (n), ((n) 4).

Operation	Time
Make set	O(1)
Find	O((n))
Union	O((n))

6. Applications

- Graph Connectivity: determine connected components- Kruskal's MST: add edges, avoid cycles- Dynamic connectivity- Image segmentation- Network clustering- Cycle detection in undirected graphs Example: Kruskal's Algorithm

```
sort(edges.begin(), edges.end());
for (edge e : edges)
    if (find(e.u) != find(e.v)) {
        union_sets(e.u, e.v);
        mst_weight += e.w;
    }
```

7. Example

```
int parent[6], rank[6];

void init() {
    for (int i = 1; i <= 5; i++) {
        parent[i] = i;
        rank[i] = 0;
    }
}

int main() {
    init();
    union_sets(1, 2);
    union_sets(3, 4);
    union_sets(2, 3);
    printf("%d\n", find(4)); // prints representative of {1,2,3,4}
}
```

Result: `{1,2,3,4}`, `{5}`

8. Visualization

```
Before compression:
1
 \
  2
   \
    3

After compression:
1
```

2
3

Every `find` call makes future queries faster.

9. Comparison

Variant	Find	Union	Notes
Basic	O(n)	O(n)	Deep trees
Path Compression	O((n))	O((n))	Very fast
+ Rank / Size	O((n))	O((n))	Balanced
Persistent DSU	O(log n)	O(log n)	Undo/rollback support

Tiny Code

Full DSU with path compression + rank:

```
int parent[1000], rank[1000];

void make_set(int v) {
    parent[v] = v;
    rank[v] = 0;
}

int find(int v) {
    if (v != parent[v])
        parent[v] = find(parent[v]);
    return parent[v];
}

void union_sets(int a, int b) {
    a = find(a);
    b = find(b);
    if (a != b) {
        if (rank[a] < rank[b]) swap(a, b);
        parent[b] = a;
        if (rank[a] == rank[b])
            rank[a]++;
    }
}
```

Why It Matters

Union-Find embodies structural sharing and lazy optimization , you don't balance eagerly, but just enough. It's one of the most elegant demonstrations of how constant-time algorithms are possible through clever organization.

It teaches a key algorithmic lesson:

> "Work only when necessary, and fix structure as you go."

Try It Yourself

1. Implement DSU and test `find`/`union`.
2. Build a program that counts connected components.
3. Solve Kruskal's MST using DSU.
4. Add `get_size(v)` to return component size.
5. Try rollback DSU (keep stack of changes).

Union-Find is the quiet powerhouse behind many graph and connectivity algorithms , simple, fast, and deeply elegant.

27. Probabilistic Data Structures (Bloom, Count-Min, HyperLogLog)

When you work with massive data streams , billions of elements, too big for memory , you can't store everything. But what if you don't need *perfect* answers, just *fast and tiny approximate ones*?

That's where probabilistic data structures shine. They trade a bit of accuracy for huge space savings and constant-time operations.

In this section, we'll explore three of the most famous:

- Bloom Filters → membership queries- Count-Min Sketch → frequency estimation- HyperLogLog → cardinality estimation Each of them answers "How likely is X?" or "How many?" efficiently , perfect for modern analytics, caching, and streaming systems.

1. Bloom Filter , "Is this element probably in the set?"

A Bloom filter answers:

> "Is `x` in the set?" with either maybe yes or definitely no.

No false negatives, but *some* false positives.

A. Idea

Use an array of bits (size `m`), all initialized to 0. Use k different hash functions.

To insert an element:

1. Compute k hashes: (h_1(x), h_2(x), ..., h_k(x))
2. Set each bit position $b_i = 1$

To query an element:

1. Compute same k hashes
2. If all bits are 1 $\rightarrow$ maybe yes
3. If any bit is 0 $\rightarrow$ definitely no

B. Example

Insert `dog`:

- (h_1(dog)=2, h_2(dog)=5, h_3(dog)=9) Set bits 2, 5, 9 $\rightarrow$ 1

Check `cat`:

- If any hash bit = 0 $\rightarrow$ not present

C. Complexity

Operation	Time	Space	Accuracy
Insert	O(k)	O(m)	Tunable
Query	O(k)	O(m)	False positives

False positive rate ($1 - e^{-kn/m}$^k)

Choose `m` and `k` based on expected `n` and acceptable error.

D. Code

```
#define M 1000
int bitset[M];

int hash1(int x) { return (x * 17) % M; }
int hash2(int x) { return (x * 31 + 7) % M; }

void add(int x) {
    bitset[hash1(x)] = 1;
    bitset[hash2(x)] = 1;
}

bool contains(int x) {
    return bitset[hash1(x)] && bitset[hash2(x)];
}
```

Used in:

- Caches (check before disk lookup)- Spam filters- Databases (join filtering)- Blockchain and peer-to-peer networks

2. Count-Min Sketch , "How often has this appeared?"

Tracks frequency counts in a stream, using sub-linear memory.

Instead of a full table, it uses a 2D array of counters, each row hashed with a different hash function.

A. Insert

For each row `i`:

- Compute hash (h_i(x))- Increment `count[i][h_i(x)]++` #### B. Query

For element `x`:

- Compute all (h_i(x))- Take `min(count[i][h_i(x)])` across rows → gives an upper-bounded estimate of true frequency

C. Code

```
#define W 1000
#define D 5
int count[D][W];

int hash(int i, int x) {
    return (x * (17*i + 3)) % W;
}

void add(int x) {
    for (int i = 0; i < D; i++)
        count[i][hash(i, x)]++;
}

int query(int x) {
    int res = INT_MAX;
    for (int i = 0; i < D; i++)
        res = min(res, count[i][hash(i, x)]);
    return res;
}
```

D. Complexity

Operation	Time	Space
Insert	O(D)	O(W×D)
Query	O(D)	O(W×D)

Error controlled by:

$$\varepsilon = \frac{1}{W}, \quad \delta = 1 - e^{-D}$$

Used in:

- Frequency counting in streams- Hot-key detection- Network flow analysis- Trending topics

3. HyperLogLog , "How many unique items?"

Estimates cardinality (number of distinct elements) with very small memory (~1.5 KB for millions).

A. Idea

Hash each element uniformly → 32-bit value. Split hash into:

- Prefix bits → bucket index- Suffix bits → count leading zeros Each bucket stores the max leading zero count seen. At the end, use harmonic mean of counts to estimate distinct values.

B. Formula

$$E = \alpha_m \cdot m^2 \cdot \Big(\sum_{i=1}^{m} 2^{-M[i]} \Big)^{-1}$$

where `M[i]` is the zero count in bucket `i`, and α_m is a correction constant.

Accuracy: ~1.04 / √m

C. Complexity

Operation	Time	Space	Error
Add	O(1)	O(m)	~1.04/√m
Merge	O(m)	O(m)	,

Used in:

- Web analytics (unique visitors)- Databases (`COUNT DISTINCT`)- Distributed systems (mergeable estimates)

4. Comparison

Structure	Purpose	Query	Memory	Error	Notes
Bloom	Membership	O(k)	Tiny	False positives	No deletions
Count-Min	Frequency	O(D)	Small	Overestimate	Streaming counts
Hyper-LogLog	Cardinality	O(1)	Very small	~1%	Mergeable

Tiny Code

Bloom Filter Demo:

```
add(42);
add(17);
printf("%d\n", contains(42)); // 1 (maybe yes)
printf("%d\n", contains(99)); // 0 (definitely no)
```

Why It Matters

Probabilistic data structures show how approximation beats impossibility when resources are tight. They make it feasible to process massive streams in real time, when storing everything is impossible.

They teach a deeper algorithmic truth:

> "A bit of uncertainty can buy you a world of scalability."

Try It Yourself

1. Implement a Bloom filter with 3 hash functions.
2. Measure false positive rate for 10K elements.
3. Build a Count-Min Sketch and test frequency estimation.
4. Approximate unique elements using HyperLogLog logic.
5. Explore real-world systems: Redis (Bloom/CM Sketch), PostgreSQL (HyperLogLog).

These tiny probabilistic tools are how big data becomes tractable.

28. Skip Lists and B-Trees

When you want fast search, insert, and delete but need a structure that's easier to code than trees or optimized for disk and memory blocks, two clever ideas step in:

- Skip Lists → randomized, layered linked lists that behave like balanced BSTs- B-Trees → multi-way trees that minimize disk I/O and organize large data blocks Both guarantee $(O \log n)$ operations, but they shine in very different environments , Skip Lists in-memory, B-Trees on disk.

1. Skip Lists

Invented by: William Pugh (1990) Goal: Simulate binary search using linked lists with probabilistic shortcuts.

A. Idea

A skip list is a stack of linked lists, each level skipping over more elements.

Example:

```
Level 3:             > 50
Level 2:     > 10    > 30    > 50
Level 1:  5  > 10  > 20  > 30  > 40  > 50
```

Higher levels are sparser and let you "skip" large chunks of the list.

You search top-down:

- Move right while next target- Drop down when you can't go further This mimics binary search , logarithmic layers, logarithmic hops.

B. Construction

Each inserted element is given a random height, with geometric distribution:

- Level 1 (base) always exists- Level 2 with probability ½- Level 3 with ¼, etc. Expected total nodes = 2n, Expected height = (Olog n)

C. Operations

Operation	Time	Space	Notes
Search	(Olog n)	O(n)	Randomized balance
Insert	(Olog n)	O(n)	Rebuild towers
Delete	(Olog n)	O(n)	Rewire pointers

Search Algorithm:

```
Node* search(SkipList* sl, int key) {
    Node* cur = sl->head;
    for (int lvl = sl->level; lvl >= 0; lvl--) {
        while (cur->forward[lvl] && cur->forward[lvl]->key < key)
            cur = cur->forward[lvl];
    }
    cur = cur->forward[0];
    if (cur && cur->key == key) return cur;
    return NULL;
}
```

Skip Lists are simple, fast, and probabilistically balanced , no rotations, no rebalancing.

D. Why Use Skip Lists?

- Easier to implement than balanced trees- Support concurrent access well- Randomized, not deterministic , but highly reliable Used in:
- Redis (sorted sets)- LevelDB / RocksDB internals- Concurrent maps

2. B-Trees

Invented by: Rudolf Bayer & Ed McCreight (1972) Goal: Reduce disk access by grouping data in blocks.

A B-Tree is a generalization of a BST:

- Each node holds multiple keys and children- Keys are kept sorted- Child subtrees span ranges between keys

A. Structure

A B-Tree of order `m`:

- Each node has `m` children- Each internal node has `k-1` keys if it has `k` children- All leaves at the same depth Example (order 3):

```
        [17 | 35]
       /    |     \
[5 10] [20 25 30] [40 45 50]
```

B. Operations

1. Search
    - Traverse from root - Binary search in each node's key array - Follow appropriate child $\rightarrow$ ($\text{Olog}_m\, n$)
2. Insert
    - Insert in leaf - If overflow $\rightarrow$ split node - Promote median key to parent
3. Delete
    - Borrow or merge if node underflows Each split or merge keeps height minimal.

C. Complexity

Operation	Time	Disk Accesses	Notes
Search	($\text{Olog}_m\, n$)	($\text{Olog}_m\, n$)	m = branching factor
Insert	($\text{Olog}_m\, n$)	(O(1)) splits	Balanced
Delete	($\text{Olog}_m\, n$)	(O(1)) merges	Balanced

Height $\log_m n \rightarrow$ very shallow when (m) large (e.g. 100).

D. B+ Tree Variant

In B+ Trees:

- All data in leaves (internal nodes = indexes)- Leaves linked $\rightarrow$ efficient range queries Used in:
- Databases (MySQL, PostgreSQL)- File systems (NTFS, HFS+)- Key-value stores

E. Example Flow

Insert 25:

```
[10 | 20 | 30] → overflow
Split → [10] [30]
Promote 20
Root: [20]
```

3. Comparison

Feature	Skip List	B-Tree
Balancing	Randomized	Deterministic
Fanout	2 (linked)	m-way
Environment	In-memory	Disk-based
Search	O(log n)	O$log_m n$
Insert/Delete	O(log n)	O$log_m n$
Concurrency	Easy	Complex
Range Queries	Sequential scan	Linked leaves (B+)

Tiny Code

Skip List Search (Conceptual):

```
Node* search(SkipList* list, int key) {
    Node* cur = list->head;
    for (int lvl = list->level; lvl >= 0; lvl--) {
        while (cur->next[lvl] && cur->next[lvl]->key < key)
            cur = cur->next[lvl];
    }
    cur = cur->next[0];
    return (cur && cur->key == key) ? cur : NULL;
}
```

B-Tree Node (Skeleton):

```
#define M 4
typedef struct {
    int keys[M-1];
    Node* child[M];
    int n;
} Node;
```

Why It Matters

Skip Lists and B-Trees show two paths to balance:

- Randomized simplicity (Skip List)- Block-based order (B-Tree) Both offer logarithmic guarantees, but one optimizes pointer chasing, the other I/O.

They're fundamental to:

- In-memory caches (Skip List)- On-disk indexes (B-Tree, B+ Tree)- Sorted data structures across systems

Try It Yourself

1. Build a basic skip list and insert random keys.
2. Trace a search path across levels.
3. Implement B-Tree insert and split logic.
4. Compare height of BST vs B-Tree for 1,000 keys.
5. Explore how Redis and MySQL use these internally.

Together, they form the bridge between linked lists and balanced trees, uniting speed, structure, and scalability.

29. Persistent and Functional Data Structures

Most data structures are ephemeral , when you update them, the old version disappears. But sometimes, you want to keep all past versions, so you can go back in time, undo operations, or run concurrent reads safely.

That's the magic of persistent data structures: every update creates a new version while sharing most of the old structure.

This section introduces the idea of persistence, explores how to make classic structures like arrays and trees persistent, and explains why functional programming loves them.

1. What Is Persistence?

A persistent data structure preserves previous versions after updates. You can access any version , past or present , without side effects.

Three levels:

Type	Description	Example
Partial	Can access past versions, but only modify the latest	Undo stack
Full	Can access and modify any version	Immutable map
Confluent	Can combine different versions	Git-like merges

This is essential in functional programming, undo systems, version control, persistent segment trees, and immutable databases.

2. Ephemeral vs Persistent

Ephemeral:

```
arr[2] = 7; // old value lost forever
```

Persistent:

```
new_arr = update(arr, 2, 7); // old_arr still exists
```

Persistent structures use structural sharing , unchanged parts are reused, not copied.

3. Persistent Linked List

Easiest example: each update creates a new head, reusing the tail.

```
struct Node { int val; Node* next; };

Node* push(Node* head, int x) {
    Node* newHead = malloc(sizeof(Node));
    newHead->val = x;
    newHead->next = head;
    return newHead;
}
```

Now both `old_head` and `new_head` coexist. Each version is immutable , you never change existing nodes.

Access: old and new lists share most of their structure:

```
v0: 1 → 2 → 3
v1: 0 → 1 → 2 → 3
```

Only one new node was created.

4. Persistent Binary Tree

For trees, updates create new paths from the root to the modified node, reusing the rest.

```
typedef struct Node {
    int key;
    struct Node *left, *right;
} Node;

Node* update(Node* root, int pos, int val) {
    if (!root) return newNode(val);
    Node* node = malloc(sizeof(Node));
    *node = *root; // copy
    if (pos < root->key) node->left = update(root->left, pos, val);
    else node->right = update(root->right, pos, val);
    return node;
}
```

Each `update` creates a new version , only $(\text{Olog}\, n)$ new nodes per change.

This is the core of persistent segment trees used in competitive programming.

5. Persistent Array (Functional Trick)

Arrays are trickier because of random access. Solutions:

- Use balanced binary trees as array replacements- Each update replaces one node- Persistent vector = tree of small arrays (used in Clojure, Scala) This gives:
- Access: $(\text{Olog}\, n)$- Update: $(\text{Olog}\, n)$- Space: $(\text{Olog}\, n)$ per update

6. Persistent Segment Tree

Used for versioned range queries:

- Each update = new root- Each version = snapshot of history Example: Track how array changes over time, query "sum in range [L,R] at version t".

Build:

```
Node* build(int L, int R) {
    if (L == R) return newNode(arr[L]);
    int mid = (L+R)/2;
    return newNode(
        build(L, mid),
        build(mid+1, R),
```

```
        sum
    );
}
```

Update: only (Olog n) new nodes

```
Node* update(Node* prev, int L, int R, int pos, int val) {
    if (L == R) return newNode(val);
    int mid = (L+R)/2;
    if (pos <= mid)
        return newNode(update(prev->left, L, mid, pos, val), prev->right);
    else
        return newNode(prev->left, update(prev->right, mid+1, R, pos, val));
}
```

Each version = new root; old ones still valid.

7. Functional Perspective

In functional programming, data is immutable by default. Instead of mutating, you create a new version.

This allows:

- Thread-safety (no races)- Time-travel debugging- Undo/redo systems- Concurrency without locks Languages like Haskell, Clojure, and Elm build everything this way.

For example, Clojure's `persistent vector` uses path copying and branching factor 32 for ($\text{Olog}_{32}\, n$) access.

8. Applications

- Undo / Redo stacks (text editors, IDEs)- Version control (Git trees)- Immutable databases (Datomic)- Segment trees over time (competitive programming)- Snapshots in memory allocators or games

9. Complexity

Structure	Update	Access	Space per Update	Notes
Persistent Linked List	O(1)	O(1)	O(1)	Simple sharing
Persistent Tree	O(log n)	O(log n)	O(log n)	Path copying
Persistent Array	O(log n)	O(log n)	O(log n)	Tree-backed
Persistent Segment Tree	O(log n)	O(log n)	O(log n)	Versioned queries

Tiny Code

Persistent Linked List Example:

```
Node* v0 = NULL;
v0 = push(v0, 3);
v0 = push(v0, 2);
Node* v1 = push(v0, 1);
// v0 = [2,3], v1 = [1,2,3]
```

Why It Matters

Persistence is about time as a first-class citizen. It lets you:

- Roll back- Compare versions- Work immutably and safely It's the algorithmic foundation behind functional programming, time-travel debugging, and immutable data systems.

It teaches this powerful idea:

> "Never destroy , always build upon what was."

Try It Yourself

1. Implement a persistent stack using linked lists.
2. Write a persistent segment tree for range sums.
3. Track array versions after each update and query old states.
4. Compare space/time with an ephemeral one.
5. Explore persistent structures in Clojure (`conj`, `assoc`) or Rust (`im` crate).

Persistence transforms data from fleeting state into a history you can navigate , a timeline of structure and meaning.

30. Advanced Trees and Range Queries

So far, you've seen balanced trees (AVL, Red-Black, Treap) and segment-based structures (Segment Trees, Fenwick Trees). Now it's time to combine those ideas and step into advanced trees , data structures that handle dynamic sets, order statistics, intervals, ranges, and geometry-like queries in logarithmic time.

This chapter is about trees that go beyond search , they store order, track ranges, and answer complex queries efficiently.

We'll explore:

- Order Statistic Trees (k-th element, rank queries)- Interval Trees (range overlaps)- Range Trees (multi-dimensional search)- KD-Trees (spatial partitioning)- Merge Sort Trees (offline range queries)

1. Order Statistic Tree

Goal: find the k-th smallest element, or the rank of an element, in $(O\log n)$.

Built on top of a balanced BST (e.g. Red-Black) by storing subtree sizes.

A. Augmented Tree Nodes

Each node keeps:

- `key`: element value- `left`, `right`: children- `size`: number of nodes in subtree

```
typedef struct Node {
    int key, size;
    struct Node *left, *right;
} Node;
```

Whenever you rotate or insert, update `size`:

```
int get_size(Node* n) { return n ? n->size : 0; }
void update_size(Node* n) {
    if (n) n->size = get_size(n->left) + get_size(n->right) + 1;
}
```

B. Find k-th Element

Recursively use subtree sizes:

```
Node* kth(Node* root, int k) {
    int left = get_size(root->left);
    if (k == left + 1) return root;
    else if (k <= left) return kth(root->left, k);
    else return kth(root->right, k - left - 1);
}
```

Time: $(\mathrm{O}\log n)$

C. Find Rank

Find position of a key (number of smaller elements):

```
int rank(Node* root, int key) {
    if (!root) return 0;
    if (key < root->key) return rank(root->left, key);
    if (key > root->key) return get_size(root->left) + 1 + rank(root->right, key);
    return get_size(root->left) + 1;
}
```

Used in:

- Databases (ORDER BY, pagination)- Quantile queries- Online median maintenance

2. Interval Tree

Goal: find all intervals overlapping with a given point or range.

Used in computational geometry, scheduling, and genomic data.

A. Structure

BST ordered by interval low endpoint. Each node stores:

- `low`, `high`: interval bounds- `max`: maximum `high` in its subtree

```
typedef struct {
    int low, high, max;
    struct Node *left, *right;
} Node;
```

B. Query Overlap

Check if `x` overlaps `node->interval`: If not, go left or right based on `max` values.

```
bool overlap(Interval a, Interval b) {
    return a.low <= b.high && b.low <= a.high;
}

Node* overlap_search(Node* root, Interval q) {
    if (!root) return NULL;
    if (overlap(root->interval, q)) return root;
    if (root->left && root->left->max >= q.low)
        return overlap_search(root->left, q);
    return overlap_search(root->right, q);
}
```

Time: $(\mathrm{O}\log n)$ average

C. Use Cases

- Calendar/schedule conflict detection- Collision detection- Genome region lookup- Segment intersection

3. Range Tree

Goal: multi-dimensional queries like

> "How many points fall inside rectangle [x1, x2] × [y1, y2]?"

Structure:

- Primary BST on x- Each node stores secondary BST on y Query time: $(\mathrm{O}\log^2 n)$ Space: $(\mathrm{O}n \log n)$

Used in:

- 2D search- Computational geometry- Databases (spatial joins)

4. KD-Tree

Goal: efficiently search points in k-dimensional space.

Alternate splitting dimensions at each level:

- Level 0 → split by x- Level 1 → split by y- Level 2 → split by z Each node stores:
- Point (vector)- Split axis Used for:
- Nearest neighbor search- Range queries- ML (k-NN classifiers) Time:
- Build: $(On \log n)$- Query: $(O\sqrt{n})$ average in 2D

5. Merge Sort Tree

Goal: query "number of elements k in range [L, R]"

Built like a segment tree, but each node stores a sorted list of its range.

Build: merge children lists Query: binary search in node lists

Time:

- Build: $(On \log n)$- Query: $(O\log^2 n)$ Used in offline queries and order-statistics over ranges.

6. Comparison

Tree Type	Use Case	Query	Update	Notes
Order Statistic	k-th, rank	O(log n)	O(log n)	Augmented BST
Interval	Overlaps	O(log n + k)	O(log n)	Store intervals
Range Tree	2D range	O(log² n + k)	O(log² n)	Multi-dim
KD-Tree	Spatial	O(√n) avg	O(log n)	Nearest neighbor
Merge Sort Tree	Offline rank	O(log² n)	Static	Built from sorted segments

Tiny Code

Order Statistic Example:

```
Node* root = NULL;
root = insert(root, 10);
root = insert(root, 20);
root = insert(root, 30);
printf("%d", kth(root, 2)->key); // 20
```

Interval Query:

```
Interval q = {15, 17};
Node* res = overlap_search(root, q);
if (res) printf("Overlap: [%d, %d]\n", res->low, res->high);
```

Why It Matters

These trees extend balance into dimensions and ranges. They let you query ordered data efficiently: "How many?", "Which overlaps?", "Where is k-th smallest?".

They teach a deeper design principle:

> "Augment structure with knowledge , balance plus metadata equals power."

Try It Yourself

1. Implement an order statistic tree , test rank/k-th queries.
2. Insert intervals and test overlap detection.
3. Build a simple KD-tree for 2D points.
4. Solve rectangle counting with a range tree.
5. Precompute a merge sort tree for offline queries.

These advanced trees form the final evolution of structured queries , blending geometry, order, and logarithmic precision.

Chapter 4. Graph Algorithms

31. Traversals (DFS, BFS, Iterative Deepening)

Graphs are everywhere , maps, networks, dependencies, state spaces. Before you can analyze them, you need a way to visit their vertices , systematically, without getting lost or looping forever.

That's where graph traversals come in. They're the foundation for everything that follows: connected components, shortest paths, spanning trees, topological sorts, and more.

This section walks through the three pillars:

- DFS (Depth-First Search) , explore deeply before backtracking- BFS (Breadth-First Search) , explore level by level- Iterative Deepening , a memory-friendly hybrid

1. Representing Graphs

Before traversal, you need a good structure.

Adjacency List (most common):

```
#define MAX 1000
vector<int> adj[MAX];
```

Add edges:

```
void add_edge(int u, int v) {
    adj[u].push_back(v);
    adj[v].push_back(u); // omit if directed
}
```

Track visited vertices:

```
bool visited[MAX];
```

2. Depth-First Search (DFS)

DFS dives deep, following one branch fully before exploring others. It's recursive, like exploring a maze by always turning left until you hit a wall.

A. Recursive Form

```
void dfs(int u) {
    visited[u] = true;
    for (int v : adj[u]) {
        if (!visited[v])
            dfs(v);
    }
}
```

Start it:

```
dfs(start_node);
```

B. Iterative Form (with Stack)

```
void dfs_iter(int start) {
    stack<int> s;
    s.push(start);
    while (!s.empty()) {
        int u = s.top(); s.pop();
        if (visited[u]) continue;
        visited[u] = true;
        for (int v : adj[u]) s.push(v);
    }
}
```

C. Complexity

Graph Type	Time	Space
Adjacency List	O(V + E)	O(V)

DFS is used in:

- Connected components- Cycle detection- Topological sort- Backtracking & search- Articulation points / bridges

3. Breadth-First Search (BFS)

BFS explores neighbors first , it's like expanding in waves. This guarantees shortest path in unweighted graphs.

A. BFS with Queue

```
void bfs(int start) {
    queue<int> q;
    q.push(start);
    visited[start] = true;
    while (!q.empty()) {
        int u = q.front(); q.pop();
        for (int v : adj[u]) {
            if (!visited[v]) {
                visited[v] = true;
                q.push(v);
            }
        }
    }
}
```

B. Track Distance

```
int dist[MAX];
void bfs_dist(int s) {
    fill(dist, dist + MAX, -1);
    dist[s] = 0;
    queue<int> q; q.push(s);
    while (!q.empty()) {
        int u = q.front(); q.pop();
        for (int v : adj[u]) {
            if (dist[v] == -1) {
                dist[v] = dist[u] + 1;
                q.push(v);
            }
        }
    }
}
```

Now `dist[v]` gives shortest distance from `s`.

C. Complexity

Same as DFS:

Time	Space
O(V + E)	O(V)

Used in:

- Shortest paths (unweighted)- Level-order traversal- Bipartite check- Connected components

4. Iterative Deepening Search (IDS)

DFS is memory-light but might go too deep. BFS is optimal but can use a lot of memory. Iterative Deepening Search (IDS) combines both.

It performs DFS with increasing depth limits:

```
bool dls(int u, int target, int depth) {
    if (u == target) return true;
    if (depth == 0) return false;
    for (int v : adj[u])
        if (dls(v, target, depth - 1)) return true;
    return false;
}

bool ids(int start, int target, int max_depth) {
    for (int d = 0; d <= max_depth; d++)
        if (dls(start, target, d)) return true;
    return false;
}
```

Used in:

- AI search problems (state spaces)- Game trees (chess, puzzles)

5. Traversal Order Examples

For a graph:

```
1 - 2 - 3
|   |
4 - 5
```

DFS (starting at 1): $1 \to 2 \to 3 \to 5 \to 4$ BFS (starting at 1): $1 \to 2 \to 4 \to 3 \to 5$

6. Directed vs Undirected

- Undirected: mark both directions- Directed: follow edge direction only DFS on directed graphs is core to:
- SCC (Strongly Connected Components)- Topological Sorting- Reachability analysis

7. Traversal Trees

Each traversal implicitly builds a spanning tree:

- DFS Tree: based on recursion- BFS Tree: based on levels Use them to:
- Detect cross edges, back edges- Classify edges (important for algorithms like Tarjan's)

8. Comparison

Aspect	DFS	BFS
Strategy	Deep first	Level-wise
Space	O(V) (stack)	O(V) (queue)
Path Optimality	Not guaranteed	Yes (unweighted)
Applications	Cycle detection, backtracking	Shortest path, level order

Tiny Code

DFS + BFS Combo:

```
void traverse(int n) {
    for (int i = 1; i <= n; i++) visited[i] = false;
    dfs(1);
    for (int i = 1; i <= n; i++) visited[i] = false;
    bfs(1);
}
```

Why It Matters

DFS and BFS are the roots of graph theory in practice. Every algorithm you'll meet later , shortest paths, flows, SCCs , builds upon them.

They teach you how to navigate structure, how to systematically explore unknowns, and how search lies at the heart of computation.

Try It Yourself

1. Build an adjacency list and run DFS/BFS from vertex 1.
2. Track discovery and finish times in DFS.
3. Use BFS to compute shortest paths in an unweighted graph.
4. Modify DFS to count connected components.
5. Implement IDS for a puzzle like the 8-puzzle.

Graph traversal is the art of exploration , once you master it, the rest of graph theory falls into place.

32. Strongly Connected Components (Tarjan, Kosaraju)

In directed graphs, edges have direction, so connectivity gets tricky. It's not enough for vertices to be reachable , you need mutual reachability.

That's the essence of a strongly connected component (SCC):

> A set of vertices where every vertex can reach every other vertex.

Think of SCCs as islands of mutual connectivity , inside, you can go anywhere; outside, you can't. They're the building blocks for simplifying directed graphs into condensation DAGs (no cycles).

We'll explore two classic algorithms:

- Kosaraju's Algorithm , clean, intuitive, two-pass- Tarjan's Algorithm , one-pass, stack-based elegance

1. Definition

A Strongly Connected Component (SCC) in a directed graph (G = (V, E)) is a maximal subset of vertices $C \subseteq V$ such that for every pair ((u, v) C): $u \to v$ and $v \to u$.

In other words, every node in (C) is reachable from every other node in (C).

Example:

```
1 → 2 → 3 → 1   forms an SCC
4 → 5           separate SCCs
```

2. Applications

- Condensation DAG: compress SCCs into single nodes , no cycles remain.- Component-based reasoning: topological sorting on DAG of SCCs.- Program analysis: detecting cycles, dependencies.- Web graphs: find clusters of mutually linked pages.- Control-flow: loops and strongly connected subroutines.

3. Kosaraju's Algorithm

A simple two-pass algorithm using DFS and graph reversal.

Steps:

1. Run DFS and push nodes onto a stack in finish-time order.
2. Reverse the graph (edges flipped).
3. Pop nodes from stack; DFS on reversed graph; each DFS = one SCC.

A. Implementation

```
vector<int> adj[MAX], rev[MAX];
bool visited[MAX];
stack<int> st;
vector<vector<int>> sccs;

void dfs1(int u) {
    visited[u] = true;
    for (int v : adj[u])
        if (!visited[v])
            dfs1(v);
```

```
    st.push(u);
}

void dfs2(int u, vector<int>& comp) {
    visited[u] = true;
    comp.push_back(u);
    for (int v : rev[u])
        if (!visited[v])
            dfs2(v, comp);
}

void kosaraju(int n) {
    // Pass 1: order by finish time
    for (int i = 1; i <= n; i++)
        if (!visited[i]) dfs1(i);

    // Reverse graph
    for (int u = 1; u <= n; u++)
        for (int v : adj[u])
            rev[v].push_back(u);

    // Pass 2: collect SCCs
    fill(visited, visited + n + 1, false);
    while (!st.empty()) {
        int u = st.top(); st.pop();
        if (!visited[u]) {
            vector<int> comp;
            dfs2(u, comp);
            sccs.push_back(comp);
        }
    }
}
```

Time Complexity: $(O(V + E))$, two DFS passes.

Space Complexity: $(O(V + E))$

B. Example

Graph:

```
1 → 2 → 3
↑   ↓   ↓
5 ← 4 ← 6
```

SCCs:

- {1,2,4,5}- {3,6}

4. Tarjan's Algorithm

More elegant: one DFS pass, no reversal, stack-based. It uses discovery times and low-link values to detect SCC roots.

A. Idea

- `disc[u]`: discovery time of node `u`- `low[u]`: smallest discovery time reachable from `u`- A node is root of an SCC if `disc[u] == low[u]` Maintain a stack of active nodes (in current DFS path).

B. Implementation

```
vector<int> adj[MAX];
int disc[MAX], low[MAX], timer;
bool inStack[MAX];
stack<int> st;
vector<vector<int>> sccs;

void dfs_tarjan(int u) {
    disc[u] = low[u] = ++timer;
    st.push(u);
    inStack[u] = true;

    for (int v : adj[u]) {
        if (!disc[v]) {
            dfs_tarjan(v);
            low[u] = min(low[u], low[v]);
        } else if (inStack[v]) {
            low[u] = min(low[u], disc[v]);
        }
```

```
    }

    if (disc[u] == low[u]) {
        vector<int> comp;
        while (true) {
            int v = st.top(); st.pop();
            inStack[v] = false;
            comp.push_back(v);
            if (v == u) break;
        }
        sccs.push_back(comp);
    }
}

void tarjan(int n) {
    for (int i = 1; i <= n; i++)
        if (!disc[i])
            dfs_tarjan(i);
}
```

Time Complexity: (O(V + E))

Space Complexity: (O(V))

C. Walkthrough

Graph:

```
1 → 2 → 3
↑   ↓   ↓
5 ← 4 ← 6
```

DFS visits nodes in order; when it finds a node whose `disc == low`, it pops from the stack to form an SCC.

Result:

```
SCC1: 1 2 4 5
SCC2: 3 6
```

5. Comparison

Feature	Kosaraju	Tarjan
DFS Passes	2	1
Reversal Needed	Yes	No
Stack	Yes (finish order)	Yes (active path)
Implementation	Simple conceptually	Compact, efficient
Time	O(V + E)	O(V + E)

6. Condensation Graph

Once SCCs are found, you can build a DAG: Each SCC becomes a node, edges represent cross-SCC connections. Topological sorting now applies.

Used in:

- Dependency analysis- Strong component compression- DAG dynamic programming

Tiny Code

Print SCCs (Tarjan):

```
tarjan(n);
for (auto &comp : sccs) {
    for (int x : comp) printf("%d ", x);
    printf("\n");
}
```

Why It Matters

SCC algorithms turn chaotic directed graphs into structured DAGs. They're the key to reasoning about cycles, dependencies, and modularity.

Understanding them reveals a powerful truth:

> "Every complex graph can be reduced to a simple hierarchy , once you find its strongly connected core."

Try It Yourself

1. Implement both Kosaraju and Tarjan , verify they match.
2. Build SCC DAG and run topological sort on it.
3. Detect cycles via SCC size > 1.
4. Use SCCs to solve 2-SAT (boolean satisfiability).
5. Visualize condensation of a graph with 6 nodes.

Once you can find SCCs, you can tame directionality , transforming messy networks into ordered systems.

33. Shortest Paths (Dijkstra, Bellman-Ford, A*, Johnson)

Once you can traverse a graph, the next natural question is:

> "What is the shortest path between two vertices?"

Shortest path algorithms are the heart of routing, navigation, planning, and optimization. They compute minimal cost paths , whether distance, time, or weight , and adapt to different edge conditions (non-negative, negative, heuristic).

This section covers the most essential algorithms:

- Dijkstra's Algorithm , efficient for non-negative weights- Bellman-Ford Algorithm , handles negative edges- A* , best-first with heuristics- Johnson's Algorithm , all-pairs shortest paths in sparse graphs

1. The Shortest Path Problem

Given a weighted graph (G = (V, E)) and a source (s), find dist[v], the minimum total weight to reach every vertex (v).

Variants:

- Single-source shortest path (SSSP) , one source to all- Single-pair , one source to one target- All-pairs shortest path (APSP) , every pair- Dynamic shortest path , with updates

2. Dijkstra's Algorithm

Best for non-negative weights. Idea: explore vertices in increasing distance order, like water spreading.

A. Steps

1. Initialize all distances to infinity.
2. Set source distance = 0.
3. Use a priority queue to always pick the node with smallest tentative distance.
4. Relax all outgoing edges.

B. Implementation (Adjacency List)

```cpp
#include <bits/stdc++.h>
using namespace std;

const int INF = 1e9;
vector<pair<int,int>> adj[1000]; // (neighbor, weight)
int dist[1000];

void dijkstra(int n, int s) {
    fill(dist, dist + n + 1, INF);
    dist[s] = 0;
    priority_queue<pair<int,int>, vector<pair<int,int>>, greater<>> pq;
    pq.push({0, s});

    while (!pq.empty()) {
        auto [d, u] = pq.top(); pq.pop();
        if (d != dist[u]) continue;
        for (auto [v, w] : adj[u]) {
            if (dist[v] > dist[u] + w) {
                dist[v] = dist[u] + w;
                pq.push({dist[v], v});
            }
        }
    }
}
```

Complexity:

- Using priority queue (binary heap): $O((V + E) \log V)$
- Space: $O(V + E)$

C. Example

Graph:

```
1 →(2) 2 →(3) 3
↓(4)       ↑(1)
4 →(2)
```

`dijkstra(1)` gives shortest distances:

```
dist[1] = 0
dist[2] = 2
dist[3] = 5
dist[4] = 4
```

D. Properties

- Works only if all edges $w \geq 0$- Can reconstruct path via `parent[v]`- Used in:
  - GPS and routing systems - Network optimization - Scheduling with positive costs

3. Bellman-Ford Algorithm

Handles negative edge weights, and detects negative cycles.

A. Idea

Relax all edges (V-1) times. If on (V)-th iteration you can still relax → negative cycle exists.

B. Implementation

```cpp
struct Edge { int u, v, w; };
vector<Edge> edges;
int dist[1000];

bool bellman_ford(int n, int s) {
    fill(dist, dist + n + 1, INF);
    dist[s] = 0;
```

```
    for (int i = 1; i <= n - 1; i++) {
        for (auto e : edges) {
            if (dist[e.u] + e.w < dist[e.v])
                dist[e.v] = dist[e.u] + e.w;
        }
    }
    // Check for negative cycle
    for (auto e : edges)
        if (dist[e.u] + e.w < dist[e.v])
            return false; // negative cycle
    return true;
}
```

Complexity: (O(VE)) Works even when (w $<$ 0).

C. Example

Graph:

```
1 →(2) 2 →(-5) 3 →(2) 4
```

Bellman-Ford finds path 1→2→3→4 with total cost (-1).

If a cycle reduces total weight indefinitely, algorithm detects it.

D. Use Cases

- Currency exchange arbitrage- Game graphs with penalties- Detecting impossible constraints

4. A* Search Algorithm

Heuristic-guided shortest path, perfect for pathfinding (AI, maps, games).

It combines actual cost and estimated cost:

$$f(v) = g(v) + h(v)$$

where

- (g(v)): known cost so far- (h(v)): heuristic estimate (must be admissible)

A. Pseudocode

```
priority_queue<pair<int,int>, vector<pair<int,int>>, greater<>> pq;
g[start] = 0;
pq.push({h[start], start});

while (!pq.empty()) {
    auto [f, u] = pq.top(); pq.pop();
    if (u == goal) break;
    for (auto [v, w] : adj[u]) {
        int new_g = g[u] + w;
        if (new_g < g[v]) {
            g[v] = new_g;
            pq.push({g[v] + h[v], v});
        }
    }
}
```

Heuristic Example:

- Euclidean distance (for grids)- Manhattan distance (for 4-direction movement)

B. Use Cases

- Game AI (pathfinding)- Robot motion planning- Map navigation Complexity: (O(E)) in best case, depends on heuristic quality.

5. Johnson's Algorithm

Goal: All-Pairs Shortest Path in sparse graphs with negative edges (no negative cycles).

Idea:

1. Add new vertex `q` connected to all others with edge weight 0
2. Run Bellman-Ford from `q` to get potential `h(v)`
3. Reweight edges: (w'(u, v) = w(u, v) + h(u) - h(v)) (now all weights 0)
4. Run Dijkstra from each vertex

Complexity: $(OVE + V^2 \log V)$

6. Summary

Algorithm	Handles Negative Weights	Detects Negative Cycle	Heuristic	Complexity	Use Case
Dijkstra	No	No	No	O((V+E) log V)	Non-negative weights
Bellman-Ford	Yes	Yes	No	O(VE)	Negative edges
A*	No (unless careful)	No	Yes	Depends	Pathfinding
Johnson	Yes (no neg. cycles)	Yes	No	O(VE + V log V)	All-pairs, sparse

Tiny Code

Dijkstra Example:

```
dijkstra(n, 1);
for (int i = 1; i <= n; i++)
    printf("dist[%d] = %d\n", i, dist[i]);
```

Why It Matters

Shortest paths are the essence of optimization , not just in graphs, but in reasoning: finding minimal cost, minimal distance, minimal risk.

These algorithms teach:

> "The path to a goal isn't random , it's guided by structure, weight, and knowledge."

Try It Yourself

1. Build a weighted graph and compare Dijkstra vs Bellman-Ford.
2. Introduce a negative edge and observe Bellman-Ford detecting it.
3. Implement A* on a grid with obstacles.
4. Use Dijkstra to plan routes in a city map dataset.
5. Try Johnson's algorithm for all-pairs shortest paths.

Master these, and you master direction + cost = intelligence in motion.

34. Shortest Path Variants (0-1 BFS, Bidirectional, Heuristic A*)

Sometimes the classic shortest path algorithms aren't enough. You might have special edge weights (only 0 or 1), a need for faster searches, or extra structure you can exploit.

That's where shortest path variants come in , they're optimized adaptations of the big three (BFS, Dijkstra, A*) for specific scenarios.

In this section, we'll explore:

- 0-1 BFS → when edge weights are only 0 or 1- Bidirectional Search → meet-in-the-middle for speed- Heuristic A* → smarter exploration guided by estimates Each shows how structure in your problem can yield speed-ups.

1. 0-1 BFS

If all edge weights are either 0 or 1, you don't need a priority queue. A deque (double-ended queue) is enough for (O(V + E)) time.

Why? Because edges with weight 0 should be processed immediately, while edges with weight 1 can wait one step longer.

A. Algorithm

Use a deque.

- When relaxing an edge with weight 0, push to front.- When relaxing an edge with weight 1, push to back.

```
const int INF = 1e9;
vector<pair<int,int>> adj[1000]; // (v, w)
int dist[1000];

void zero_one_bfs(int n, int s) {
    fill(dist, dist + n + 1, INF);
    deque<int> dq;
    dist[s] = 0;
    dq.push_front(s);

    while (!dq.empty()) {
        int u = dq.front(); dq.pop_front();
        for (auto [v, w] : adj[u]) {
            if (dist[v] > dist[u] + w) {
```

```
                dist[v] = dist[u] + w;
                if (w == 0) dq.push_front(v);
                else dq.push_back(v);
            }
        }
    }
}
```

B. Example

Graph:

```
1 -0-> 2 -1-> 3
|              ^
1              |
+--------------+
```

Shortest path from 1 to 3 = 1 (via edge 1-2-3). Deque ensures weight-0 edges don't get delayed.

C. Complexity

Time	Space	Notes
O(V + E)	O(V)	Optimal for binary weights

Used in:

- Layered BFS- Grid problems with binary costs- BFS with teleportation (weight 0 edges)

2. Bidirectional Search

Sometimes you just need one path , from source to target , in an unweighted graph. Instead of expanding from one side, expand from both ends and stop when they meet.

This reduces search depth from (Ob^d) to ($Ob^{d/2}$) (huge gain for large graphs).

A. Idea

Run BFS from both source and target simultaneously. When their frontiers intersect, you've found the shortest path.

B. Implementation

```
bool visited_from_s[MAX], visited_from_t[MAX];
queue<int> qs, qt;

int bidirectional_bfs(int s, int t) {
    qs.push(s); visited_from_s[s] = true;
    qt.push(t); visited_from_t[t] = true;

    while (!qs.empty() && !qt.empty()) {
        if (step(qs, visited_from_s, visited_from_t)) return 1;
        if (step(qt, visited_from_t, visited_from_s)) return 1;
    }
    return 0;
}

bool step(queue<int>& q, bool vis[], bool other[]) {
    int size = q.size();
    while (size--) {
        int u = q.front(); q.pop();
        if (other[u]) return true;
        for (int v : adj[u]) {
            if (!vis[v]) {
                vis[v] = true;
                q.push(v);
            }
        }
    }
    return false;
}
```

C. Complexity

Time	Space	Notes
$Ob^{d/2}$	$Ob^{d/2}$	Doubly fast in practice

Used in:

- Maze solvers- Shortest paths in large sparse graphs- Social network “degrees of separation”

3. Heuristic A* (Revisited)

A* generalizes Dijkstra with goal-directed search using heuristics. We revisit it here to show how heuristics change exploration order.

A. Cost Function

$$f(v) = g(v) + h(v)$$

- (g(v)): cost so far- (h(v)): estimated cost to goal- (h(v)) must be admissible ((h(v) true cost))

B. Implementation

```
struct Node {
    int v; int f, g;
    bool operator>(const Node& o) const { return f > o.f; }
};

priority_queue<Node, vector<Node>, greater<Node>> pq;

void astar(int start, int goal) {
    g[start] = 0;
    h[start] = heuristic(start, goal);
    pq.push({start, g[start] + h[start], g[start]});

    while (!pq.empty()) {
        auto [u, f_u, g_u] = pq.top(); pq.pop();
        if (u == goal) break;
        for (auto [v, w] : adj[u]) {
            int new_g = g[u] + w;
            if (new_g < g[v]) {
```

```
                g[v] = new_g;
                int f_v = new_g + heuristic(v, goal);
                pq.push({v, f_v, new_g});
            }
        }
    }
}
```

C. Example Heuristics

- Grid map: Manhattan distance (h(x, y) = |x - x_g| + |y - y_g|)
- Navigation: straight-line (Euclidean)- Game tree: evaluation function

D. Performance

Heuristic	Effect
Perfect (h = true cost)	Optimal, visits minimal nodes
Admissible but weak	Still correct, more nodes
Overestimate	May fail (non-admissible)

4. Comparison

Algorithm	Weight Type	Strategy	Time	Space	Notes
0-1 BFS	0 or 1	Deque-based	O(V+E)	O(V)	No heap
Bidirectional BFS	Unweighted	Two-way search	$Ob^{d/2}$	$Ob^{d/2}$	Meets in middle
A*	Non-negative	Heuristic search	Depends	O(V)	Guided

5. Example Scenario

Problem	Variant
Grid with teleport (cost 0)	0-1 BFS
Huge social graph (find shortest chain)	Bidirectional BFS
Game AI pathfinding	A* with Manhattan heuristic

Tiny Code

0-1 BFS Quick Demo:

```
add_edge(1, 2, 0);
add_edge(2, 3, 1);
zero_one_bfs(3, 1);
printf("%d\n", dist[3]); // shortest = 1
```

Why It Matters

Special cases deserve special tools. These variants show that understanding structure (like edge weights or symmetry) can yield huge gains.

They embody a principle:

> "Don't just run faster , run smarter, guided by what you know."

Try It Yourself

1. Implement 0-1 BFS for a grid with cost 0 teleports.
2. Compare BFS vs Bidirectional BFS on a large maze.
3. Write A* for an 8x8 chessboard knight's move puzzle.
4. Tune heuristics , see how overestimating breaks A*.
5. Combine A* and 0-1 BFS for hybrid search.

With these in hand, you can bend shortest path search to the shape of your problem , efficient, elegant, and exact.

35. Minimum Spanning Trees (Kruskal, Prim, Borůvka)

When a graph connects multiple points with weighted edges, sometimes you don't want the *shortest path*, but the *cheapest network* that connects everything.

That's the Minimum Spanning Tree (MST) problem:

> Given a connected, weighted, undirected graph, find a subset of edges that connects all vertices with minimum total weight and no cycles.

MSTs are everywhere , from building networks and designing circuits to clustering and approximation algorithms.

Three cornerstone algorithms solve it beautifully:

- Kruskal's , edge-based, union-find- Prim's , vertex-based, greedy expansion- Borůvka's , component merging in parallel

1. What Is a Spanning Tree?

A spanning tree connects all vertices with exactly (V-1) edges. Among all spanning trees, the one with minimum total weight is the MST.

Properties:

- Contains no cycles- Connects all vertices- Edge count = (V - 1)- Unique if all weights distinct

2. MST Applications

- Network design (roads, cables, pipelines)- Clustering (e.g., hierarchical clustering)- Image segmentation- Approximation (e.g., TSP $\sim 2 \times$ MST)- Graph simplification

3. Kruskal's Algorithm

Build the MST edge-by-edge, in order of increasing weight. Use Union-Find (Disjoint Set Union) to avoid cycles.

A. Steps

1. Sort all edges by weight.
2. Initialize each vertex as its own component.
3. For each edge (u, v):
    - If `u` and `v` are in different components $\rightarrow$ include edge - Union their sets Stop when (V-1) edges chosen.

B. Implementation

```cpp
struct Edge { int u, v, w; };
vector<Edge> edges;
int parent[MAX], rank_[MAX];

int find(int x) {
    return parent[x] == x ? x : parent[x] = find(parent[x]);
}
bool unite(int a, int b) {
    a = find(a); b = find(b);
    if (a == b) return false;
    if (rank_[a] < rank_[b]) swap(a, b);
    parent[b] = a;
    if (rank_[a] == rank_[b]) rank_[a]++;
    return true;
}

int kruskal(int n) {
    iota(parent, parent + n + 1, 0);
    sort(edges.begin(), edges.end(), [](Edge a, Edge b){ return a.w < b.w; });
    int total = 0;
    for (auto &e : edges)
        if (unite(e.u, e.v))
            total += e.w;
    return total;
}
```

Complexity:

- Sorting edges: ($OE \log E$)- Union-Find operations: (O((V))) (almost constant)- Total: ($OE \log E$)

C. Example

Graph:

```
1 -4- 2
|     |
2     3
 \-1-/
```

Edges sorted: (1-3,1), (1-2,4), (2-3,3)

Pick 1-3, 2-3 → MST weight = 1 + 3 = 4

4. Prim's Algorithm

Grow MST from a starting vertex, adding the smallest outgoing edge each step.

Similar to Dijkstra , but pick edges, not distances.

A. Steps

1. Start with one vertex, mark as visited.
2. Use priority queue for candidate edges.
3. Pick smallest edge that connects to an unvisited vertex.
4. Add vertex to MST, repeat until all visited.

B. Implementation

```
vector<pair<int,int>> adj[MAX]; // (v, w)
bool used[MAX];
int prim(int n, int start) {
    priority_queue<pair<int,int>, vector<pair<int,int>>, greater<>> pq;
    pq.push({0, start});
    int total = 0;

    while (!pq.empty()) {
        auto [w, u] = pq.top(); pq.pop();
        if (used[u]) continue;
        used[u] = true;
        total += w;
        for (auto [v, w2] : adj[u])
            if (!used[v]) pq.push({w2, v});
    }
    return total;
}
```

Complexity:

- $O((V + E) \log V)$ with binary heap

Used when:

- Graph is dense
- Easier to grow tree than sort all edges

C. Example

Graph:

```
1 -2- 2
|     |
4     1
 \-3-/
```

Start at 1 → choose (1-2), (1-3) → MST weight = 2 + 3 = 5

5. Borůvka's Algorithm

Less famous, but elegant , merges cheapest outgoing edge per component in parallel.

Each component picks one cheapest outgoing edge, adds it, merges components. Repeat until one component left.

Complexity: ($OE \log V$)

Used in parallel/distributed MST computations.

6. Comparison

Algorithm	Strategy	Time	Space	Best For
Kruskal	Edge-based, sort all edges	O(E log E)	O(E)	Sparse graphs
Prim	Vertex-based, grow tree	O(E log V)	O(V+E)	Dense graphs
Borůvka	Component merging	O(E log V)	O(E)	Parallel MST

7. MST Properties

- Cut Property: For any cut, smallest crossing edge MST.- Cycle Property: For any cycle, largest edge not MST.- MST may not be unique if equal weights.

8. Building the Tree

Store MST edges:

```
vector<Edge> mst_edges;
if (unite(e.u, e.v)) mst_edges.push_back(e);
```

Then use MST for:

- Path queries- Clustering (remove largest edge)- Approximation TSP (preorder traversal)

Tiny Code

Kruskal Example:

```
edges.push_back({1,2,4});
edges.push_back({1,3,1});
edges.push_back({2,3,3});
printf("MST = %d\n", kruskal(3)); // 4
```

Why It Matters

MSTs model connection without redundancy. They're about efficiency , connecting everything at minimal cost, a principle that appears in infrastructure, data, and even ideas.

They teach:

> "You can connect the whole with less , if you choose wisely."

Try It Yourself

1. Implement Kruskal's algorithm using union-find.
2. Run Prim's algorithm and compare output.
3. Build MST on random weighted graph , visualize tree.
4. Remove heaviest edge from MST to form two clusters.
5. Explore Borůvka for parallel execution.

MSTs are how you span complexity with minimal effort , a tree of balance, economy, and order.

36. Flows (Ford-Fulkerson, Edmonds-Karp, Dinic)

Some graphs don't just connect , they *carry* something. Imagine water flowing through pipes, traffic through roads, data through a network. Each edge has a capacity, and you want to know:

> "How much can I send from source to sink before the system clogs?"

That's the Maximum Flow problem , a cornerstone of combinatorial optimization, powering algorithms for matching, cuts, scheduling, and more.

This section covers the big three:

- Ford-Fulkerson , the primal idea- Edmonds-Karp , BFS-based implementation- Dinic's Algorithm , layered speed

1. Problem Definition

Given a directed graph (G = (V, E)), each edge ((u, v)) has a capacity (c(u, v) 0).

We have:

- Source (s)- Sink (t) We want the maximum flow from (s) to (t): a function (f(u, v)) that satisfies:

1. Capacity constraint: (0 f(u, v) c(u, v))
2. Flow conservation: For every vertex $v \neq s, t$: (f(u, v) = f(v, w))

Total flow = (f(s, v))

2. The Big Picture

Max Flow - Min Cut Theorem:

> The value of the maximum flow equals the capacity of the minimum cut.

So finding a max flow is equivalent to finding the bottleneck.

3. Ford-Fulkerson Method

The idea:

- While there exists a path from (s) to (t) with available capacity, push flow along it.

Each step:

1. Find augmenting path
2. Send flow = min residual capacity along it
3. Update residual capacities

Repeat until no augmenting path.

A. Residual Graph

Residual capacity:

$$r(u, v) = c(u, v) - f(u, v)$$

If (f(u, v) > 0), then add reverse edge ((v, u)) with capacity (f(u, v)).

This allows undoing flow if needed.

B. Implementation (DFS-style)

```
const int INF = 1e9;
vector<pair<int,int>> adj[MAX];
int cap[MAX][MAX];

int dfs(int u, int t, int flow, vector<int>& vis) {
    if (u == t) return flow;
    vis[u] = 1;
    for (auto [v, _] : adj[u]) {
        if (!vis[v] && cap[u][v] > 0) {
            int pushed = dfs(v, t, min(flow, cap[u][v]), vis);
            if (pushed > 0) {
                cap[u][v] -= pushed;
                cap[v][u] += pushed;
                return pushed;
            }
        }
    }
```

```
    return 0;
}

int ford_fulkerson(int s, int t, int n) {
    int flow = 0;
    while (true) {
        vector<int> vis(n + 1, 0);
        int pushed = dfs(s, t, INF, vis);
        if (pushed == 0) break;
        flow += pushed;
    }
    return flow;
}
```

Complexity: $(OE \cdot \text{max flow})$, depends on flow magnitude.

4. Edmonds-Karp Algorithm

A refinement:

> Always choose shortest augmenting path (by edges) using BFS.

Guarantees polynomial time.

A. Implementation (BFS + parent tracking)

```
int bfs(int s, int t, vector<int>& parent, int n) {
    fill(parent.begin(), parent.end(), -1);
    queue<pair<int,int>> q;
    q.push({s, INF});
    parent[s] = -2;
    while (!q.empty()) {
        auto [u, flow] = q.front(); q.pop();
        for (auto [v, _] : adj[u]) {
            if (parent[v] == -1 && cap[u][v] > 0) {
                int new_flow = min(flow, cap[u][v]);
                parent[v] = u;
                if (v == t) return new_flow;
                q.push({v, new_flow});
            }
```

```
        }
    }
    return 0;
}

int edmonds_karp(int s, int t, int n) {
    int flow = 0;
    vector<int> parent(n + 1);
    int new_flow;
    while ((new_flow = bfs(s, t, parent, n))) {
        flow += new_flow;
        int v = t;
        while (v != s) {
            int u = parent[v];
            cap[u][v] -= new_flow;
            cap[v][u] += new_flow;
            v = u;
        }
    }
    return flow;
}
```

Complexity: (OVE^2) Always terminates (no dependence on flow values).

5. Dinic's Algorithm

A modern classic , uses BFS to build level graph, and DFS to send blocking flow.

It works layer-by-layer, avoiding useless exploration.

A. Steps

1. Build level graph via BFS (assign levels to reachable nodes).
2. DFS sends flow along level-respecting paths.
3. Repeat until no path remains.

B. Implementation

```
vector<int> level, ptr;

bool bfs_level(int s, int t, int n) {
    fill(level.begin(), level.end(), -1);
    queue<int> q;
    q.push(s);
    level[s] = 0;
    while (!q.empty()) {
        int u = q.front(); q.pop();
        for (auto [v, _] : adj[u])
            if (level[v] == -1 && cap[u][v] > 0) {
                level[v] = level[u] + 1;
                q.push(v);
            }
    }
    return level[t] != -1;
}

int dfs_flow(int u, int t, int pushed) {
    if (u == t || pushed == 0) return pushed;
    for (int &cid = ptr[u]; cid < (int)adj[u].size(); cid++) {
        int v = adj[u][cid].first;
        if (level[v] == level[u] + 1 && cap[u][v] > 0) {
            int tr = dfs_flow(v, t, min(pushed, cap[u][v]));
            if (tr > 0) {
                cap[u][v] -= tr;
                cap[v][u] += tr;
                return tr;
            }
        }
    }
    return 0;
}

int dinic(int s, int t, int n) {
    int flow = 0;
    level.resize(n + 1);
    ptr.resize(n + 1);
    while (bfs_level(s, t, n)) {
        fill(ptr.begin(), ptr.end(), 0);
        while (int pushed = dfs_flow(s, t, INF))
            flow += pushed;
```

```
    }
    return flow;
}
```

Complexity: (OEV^2) worst case, $(OE\sqrt{V})$ in practice.

6. Comparison

Algorithm	Strategy	Handles	Time	Notes
Ford-Fulkerson	DFS augmenting paths	Integral capacities	$OE \times max_f low$	Simple, may loop on reals
Edmonds-Karp	BFS augmenting paths	All capacities	$O(VE^2)$	Always terminates
Dinic	Level graph + DFS	All capacities	$O(V^2E)$	Fast in practice

7. Applications

- Network routing- Bipartite matching- Task assignment (flows = people → jobs)- Image segmentation (min-cut)- Circulation with demands- Data pipelines, max throughput systems

Tiny Code

Ford-Fulkerson Example:

```
add_edge(1, 2, 3);
add_edge(1, 3, 2);
add_edge(2, 3, 5);
add_edge(2, 4, 2);
add_edge(3, 4, 3);
printf("Max flow = %d\n", ford_fulkerson(1, 4, 4)); // 5
```

Why It Matters

Flow algorithms transform capacity constraints into solvable systems. They reveal the deep unity between optimization and structure: every maximum flow defines a minimum bottleneck cut.

They embody a timeless truth:

> "To understand limits, follow the flow."

Try It Yourself

1. Implement Ford-Fulkerson using DFS.
2. Switch to Edmonds-Karp and observe performance gain.
3. Build Dinic's level graph and visualize layers.
4. Model job assignment as bipartite flow.
5. Verify Max Flow = Min Cut on small examples.

Once you master flows, you'll see them hidden in everything that moves , from data to decisions.

37. Cuts (Stoer-Wagner, Karger, Gomory-Hu)

Where flow problems ask *"How much can we send?"*, cut problems ask *"Where does it break?"*

A cut splits a graph into two disjoint sets. The minimum cut is the smallest set of edges whose removal disconnects the graph , the tightest "bottleneck" holding it together.

This chapter explores three major algorithms:

- Stoer-Wagner , deterministic min-cut for undirected graphs- Karger's Randomized Algorithm , fast, probabilistic- Gomory-Hu Tree , compress all-pairs min-cuts into one tree Cuts reveal hidden structure , clusters, vulnerabilities, boundaries , and form the dual to flows via the Max-Flow Min-Cut Theorem.

1. The Min-Cut Problem

Given a weighted undirected graph (G = (V, E)): Find the minimum total weight of edges whose removal disconnects the graph.

Equivalent to:

> The smallest sum of edge weights crossing any partition ($S, V \setminus S$).

For directed graphs, you use max-flow methods; For undirected graphs, specialized algorithms exist.

2. Applications

- Network reliability , weakest link detection- Clustering , partition graph by minimal interconnection- Circuit design , splitting components- Image segmentation , separating regions- Community detection , sparse connections between groups

3. Stoer-Wagner Algorithm (Deterministic)

A clean, deterministic method for global minimum cut in undirected graphs.

A. Idea

1. Start with the full vertex set (V).
2. Repeatedly run Maximum Adjacency Search:
    - Start from a vertex - Grow a set by adding the most tightly connected vertex - The last added vertex defines a cut3. Contract the last two added vertices into one.
3. Keep track of smallest cut seen.

Repeat until one vertex remains.

B. Implementation (Adjacency Matrix)

```
const int INF = 1e9;
int g[MAX][MAX], w[MAX];
bool added[MAX], exist[MAX];

int stoer_wagner(int n) {
    int best = INF;
    vector<int> v(n);
    iota(v.begin(), v.end(), 0);

    while (n > 1) {
        fill(w, w + n, 0);
        fill(added, added + n, false);
```

```
        int prev = 0;
        for (int i = 0; i < n; i++) {
            int sel = -1;
            for (int j = 0; j < n; j++)
                if (!added[j] && (sel == -1 || w[j] > w[sel])) sel = j;
            if (i == n - 1) {
                best = min(best, w[sel]);
                for (int j = 0; j < n; j++)
                    g[prev][j] = g[j][prev] += g[sel][j];
                v.erase(v.begin() + sel);
                n--;
                break;
            }
            added[sel] = true;
            for (int j = 0; j < n; j++) w[j] += g[sel][j];
            prev = sel;
        }
    }
    return best;
}
```

Complexity: (OV^3), or $(OVE + V^2 \log V)$ with heaps Input: weighted undirected graph Output: global min cut value

C. Example

Graph:

```
1 -3- 2
|     |
4     2
 \-5-/
```

Cuts:

- {1,2}|{3} → 7- {1,3}|{2} → 5 Min cut = 5

4. Karger's Algorithm (Randomized)

A simple, elegant probabilistic method. Repeatedly contract random edges until two vertices remain; the remaining crossing edges form a cut.

Run multiple times → high probability of finding min cut.

A. Algorithm

1. While ($|V| > 2$):
    - Choose random edge ((u, v)) - Contract (u, v) into one node - Remove self-loops2. Return number of edges between remaining nodes

Repeat ($On^2 \log n$) times for high confidence.

B. Implementation Sketch

```
struct Edge { int u, v; };
vector<Edge> edges;
int parent[MAX];

int find(int x) { return parent[x] == x ? x : parent[x] = find(parent[x]); }
void unite(int a, int b) { parent[find(b)] = find(a); }

int karger(int n) {
    int m = edges.size();
    iota(parent, parent + n, 0);
    int vertices = n;
    while (vertices > 2) {
        int i = rand() % m;
        int u = find(edges[i].u), v = find(edges[i].v);
        if (u == v) continue;
        unite(u, v);
        vertices--;
    }
    int cuts = 0;
    for (auto e : edges)
        if (find(e.u) != find(e.v)) cuts++;
    return cuts;
}
```

Expected Time: (On^2) per run Probability of success: (2 / (n(n-1))) per run Run multiple trials and take minimum.

C. Use Case

Great for large sparse graphs, or when approximate solutions are acceptable. Intuitive: the min cut survives random contractions if chosen carefully enough.

5. Gomory-Hu Tree

A compact way to store all-pairs min-cuts. It compresses (OV^2) flow computations into V-1 cuts.

A. Idea

- Build a tree where the min cut between any two vertices = the minimum edge weight on their path in the tree.

B. Algorithm

1. Pick vertex (s).
2. For each vertex $t \neq s$,
    - Run max flow to find min cut between (s, t). - Partition vertices accordingly.3. Connect partitions to form a tree.

Result: Gomory-Hu tree (V-1 edges).

Now any pair's min cut = smallest edge on path between them.

Complexity: (O(V)) max flow runs.

C. Uses

- Quickly answer all-pairs cut queries- Network reliability- Hierarchical clustering

6. Comparison

Algorithm	Type	Randomized	Graph	Complexity	Output
Stoer-Wagner	Deterministic	No	Undirected	$O(V^3)$	Global min cut
Karger	Randomized	Yes	Undirected	$O(n^2 \log n)$ (multi-run)	Probabilistic min cut
Gomory-Hu	Deterministic	No	Undirected	$O(V \times \text{MaxFlow})$	All-pairs min cuts

7. Relationship to Flows

By Max-Flow Min-Cut, min-cut capacity = max-flow value.

So you can find:

- s-t min cut = via max flow- global min cut = min over all (s, t) pairs Specialized algorithms just make it faster.

Tiny Code

Stoer-Wagner Example:

```
printf("Global Min Cut = %d\n", stoer_wagner(n));
```

Karger Multi-Run:

```
int ans = INF;
for (int i = 0; i < 100; i++)
    ans = min(ans, karger(n));
printf("Approx Min Cut = %d\n", ans);
```

Why It Matters

Cuts show you fragility , the weak seams of connection. While flows tell you *how much can pass*, cuts reveal *where it breaks first.*

They teach:

> "To understand strength, study what happens when you pull things apart."

Try It Yourself

1. Implement Stoer-Wagner and test on small graphs.
2. Run Karger 100 times and track success rate.
3. Build a Gomory-Hu tree and answer random pair queries.
4. Verify Max-Flow = Min-Cut equivalence on examples.
5. Use cuts for community detection in social graphs.

Mastering cuts gives you both grip and insight , where systems hold, and where they give way.

38. Matchings (Hopcroft-Karp, Hungarian, Blossom)

In many problems, we need to pair up elements efficiently: students to schools, jobs to workers, tasks to machines.

These are matching problems , find sets of edges with no shared endpoints that maximize cardinality or weight.

Depending on graph type, different algorithms apply:

- Hopcroft-Karp , fast matching in bipartite graphs- Hungarian Algorithm , optimal weighted assignment- Edmonds' Blossom Algorithm , general graphs (non-bipartite) Matching is a fundamental combinatorial structure, appearing in scheduling, flow networks, and resource allocation.

1. Terminology

- Matching: set of edges with no shared vertices- Maximum Matching: matching with largest number of edges- Perfect Matching: covers all vertices (each vertex matched once)- Maximum Weight Matching: matching with largest total edge weight Graph Types:
- Bipartite: vertices split into two sets (L, R); edges only between sets- General: arbitrary connections (may contain odd cycles)

2. Applications

- Job assignment- Network flows- Resource allocation- Student-project pairing- Stable marriages (with preferences)- Computer vision (feature correspondence)

3. Hopcroft-Karp Algorithm (Bipartite Matching)

A highly efficient algorithm for maximum cardinality matching in bipartite graphs.

It uses layered BFS + DFS to find multiple augmenting paths simultaneously.

A. Idea

1. Initialize matching empty.
2. While augmenting paths exist:
    - BFS builds layer graph (shortest augmenting paths). - DFS finds all augmenting paths along those layers. Each phase increases matching size significantly.

B. Complexity

$$O(E\sqrt{V})$$

Much faster than augmenting one path at a time (like Ford-Fulkerson).

C. Implementation

Let `pairU[u]` = matched vertex in R, or 0 if unmatched `pairV[v]` = matched vertex in L, or 0 if unmatched

```
vector<int> adjL[MAX];
int pairU[MAX], pairV[MAX], dist[MAX];
int nL, nR;

bool bfs() {
    queue<int> q;
    for (int u = 1; u <= nL; u++) {
        if (!pairU[u]) dist[u] = 0, q.push(u);
        else dist[u] = INF;
    }
    int found = INF;
    while (!q.empty()) {
        int u = q.front(); q.pop();
        if (dist[u] < found) {
            for (int v : adjL[u]) {
                if (!pairV[v]) found = dist[u] + 1;
```

```
                else if (dist[pairV[v]] == INF) {
                    dist[pairV[v]] = dist[u] + 1;
                    q.push(pairV[v]);
                }
            }
        }
    }
    return found != INF;
}

bool dfs(int u) {
    for (int v : adjL[u]) {
        if (!pairV[v] || (dist[pairV[v]] == dist[u] + 1 && dfs(pairV[v]))) {
            pairU[u] = v;
            pairV[v] = u;
            return true;
        }
    }
    dist[u] = INF;
    return false;
}

int hopcroft_karp() {
    int matching = 0;
    while (bfs()) {
        for (int u = 1; u <= nL; u++)
            if (!pairU[u] && dfs(u)) matching++;
    }
    return matching;
}
```

D. Example

Graph:

```
U = {1,2,3}, V = {a,b}
Edges: 1-a, 2-a, 3-b
```

Matching: {1-a, 3-b} (size 2)

4. Hungarian Algorithm (Weighted Bipartite Matching)

Solves assignment problem , given cost matrix c_{ij}, assign each (i) to one (j) minimizing total cost (or maximizing profit).

A. Idea

Subtract minimums row- and column-wise → expose zeros → find minimal zero-cover → adjust matrix → repeat.

Equivalent to solving min-cost perfect matching on a bipartite graph.

B. Complexity

$$O(V^3)$$

Works for dense graphs, moderate sizes.

C. Implementation Sketch (Matrix Form)

```
int hungarian(const vector<vector<int>>& cost) {
    int n = cost.size();
    vector<int> u(n+1), v(n+1), p(n+1), way(n+1);
    for (int i = 1; i <= n; i++) {
        p[0] = i; int j0 = 0;
        vector<int> minv(n+1, INF);
        vector<char> used(n+1, false);
        do {
            used[j0] = true;
            int i0 = p[j0], delta = INF, j1;
            for (int j = 1; j <= n; j++) if (!used[j]) {
                int cur = cost[i0-1][j-1] - u[i0] - v[j];
                if (cur < minv[j]) minv[j] = cur, way[j] = j0;
                if (minv[j] < delta) delta = minv[j], j1 = j;
            }
            for (int j = 0; j <= n; j++)
                if (used[j]) u[p[j]] += delta, v[j] -= delta;
                else minv[j] -= delta;
            j0 = j1;
        } while (p[j0]);
```

```
        do { int j1 = way[j0]; p[j0] = p[j1]; j0 = j1; } while (j0);
    }
    return -v[0]; // minimal cost
}
```

D. Example

Cost matrix:

```
  a  b  c
1 3  2  1
2 2  3  2
3 3  2  3
```

Optimal assignment = 1-c, 2-a, 3-b Cost = $1 + 2 + 2 = 5$

5. Edmonds' Blossom Algorithm (General Graphs)

For non-bipartite graphs, simple augmenting path logic breaks down (odd cycles). Blossom algorithm handles this via contraction of blossoms (odd cycles).

A. Idea

- Find augmenting paths- When odd cycle encountered (blossom), shrink it into one vertex- Continue search- Expand blossoms at end

B. Complexity

$$O(V^3)$$

Though complex to implement, it's the general-purpose solution for matchings.

C. Use Cases

- Non-bipartite job/task assignments- General pairing problems- Network design

6. Comparison

Algorithm	Graph Type	Weighted	Complexity	Output
Hopcroft-Karp	Bipartite	No	$O(E\sqrt{V})$	Max cardinality
Hungarian	Bipartite	Yes	$O(V^3)$	Min/Max cost matching
Blossom	General	Yes	$O(V^3)$	Max cardinality or weight

7. Relation to Flows

Bipartite matching = max flow on network:

- Left → Source edges (capacity 1)- Right → Sink edges (capacity 1)- Between sets → edges (capacity 1) Matching size = flow value

Tiny Code

Hopcroft-Karp Demo:

```
nL = 3; nR = 2;
adjL[1] = {1};
adjL[2] = {1};
adjL[3] = {2};
printf("Max Matching = %d\n", hopcroft_karp()); // 2
```

Why It Matters

Matchings are the language of pairing and assignment. They express cooperation without overlap , a structure of balance.

They reveal a deep duality:

> "Every match is a flow, every assignment an optimization."

Try It Yourself

1. Build a bipartite graph and run Hopcroft-Karp.
2. Solve an assignment problem with Hungarian algorithm.
3. Explore Blossom's contraction idea conceptually.
4. Compare max-flow vs matching approach.
5. Use matching to model scheduling (people tasks).

Matching teaches how to pair without conflict, a lesson both mathematical and universal.

39. Tree Algorithms (LCA, HLD, Centroid Decomposition)

Trees are the backbone of many algorithms , they are connected, acyclic, and wonderfully structured.

Because of their simplicity, they allow elegant divide-and-conquer, dynamic programming, and query techniques. This section covers three fundamental patterns:

- Lowest Common Ancestor (LCA) , answer ancestor queries fast- Heavy-Light Decomposition (HLD) , break trees into chains for segment trees / path queries- Centroid Decomposition , recursively split tree by balance for divide-and-conquer Each reveals a different way to reason about trees , by depth, by chains, or by balance.

1. Lowest Common Ancestor (LCA)

Given a tree, two nodes (u, v). The LCA is the lowest node (farthest from root) that is an ancestor of both.

Applications:

- Distance queries- Path decomposition- RMQ / binary lifting- Tree DP and rerooting

A. Naive Approach

Climb ancestors until they meet. But this is (O(n)) per query , too slow for many queries.

B. Binary Lifting

Precompute ancestors at powers of 2. Then jump up by powers to align depths.

Preprocessing:

1. DFS to record depth
2. `up[v][k]` = 2^k-th ancestor of v

Answering query:

1. Lift deeper node up to same depth
2. Lift both together while `up[u][k] != up[v][k]`
3. Return parent

Code:

```
const int LOG = 20;
vector<int> adj[MAX];
int up[MAX][LOG], depth[MAX];

void dfs(int u, int p) {
    up[u][0] = p;
    for (int k = 1; k < LOG; k++)
        up[u][k] = up[up[u][k-1]][k-1];
    for (int v : adj[u]) if (v != p) {
        depth[v] = depth[u] + 1;
        dfs(v, u);
    }
}

int lca(int u, int v) {
    if (depth[u] < depth[v]) swap(u, v);
    int diff = depth[u] - depth[v];
    for (int k = 0; k < LOG; k++)
        if (diff & (1 << k)) u = up[u][k];
    if (u == v) return u;
    for (int k = LOG-1; k >= 0; k--)
        if (up[u][k] != up[v][k])
            u = up[u][k], v = up[v][k];
    return up[u][0];
}
```

Complexity:

- Preprocess: $(O n \log n)$- Query: $(O \log n)$

C. Example

Tree:

```
    1
   / \
  2   3
 / \
4   5
```

- LCA(4,5) = 2- LCA(4,3) = 1

2. Heavy-Light Decomposition (HLD)

When you need to query paths (sum, max, min, etc.) on trees efficiently, you can use Heavy-Light Decomposition.

A. Idea

Decompose the tree into chains:

- Heavy edge = edge to child with largest subtree- Light edges = others Result: Every path from root to leaf crosses at most $(O \log n)$ light edges.

So, a path query can be broken into $(O \log^2 n)$ segment tree queries.

B. Steps

1. DFS to compute subtree sizes and identify heavy child
2. Decompose into chains
3. Assign IDs for segment tree
4. Use Segment Tree / BIT on linearized array

Key functions:

- `dfs_sz(u)` $\rightarrow$ compute subtree sizes- `decompose(u, head)` $\rightarrow$ assign chain heads Code (core):

```
int parent[MAX], depth[MAX], heavy[MAX], head[MAX], pos[MAX];
int cur_pos = 0;

int dfs_sz(int u) {
    int size = 1, max_sz = 0;
    for (int v : adj[u]) if (v != parent[u]) {
        parent[v] = u;
        depth[v] = depth[u] + 1;
        int sz = dfs_sz(v);
        if (sz > max_sz) max_sz = sz, heavy[u] = v;
        size += sz;
    }
    return size;
}

void decompose(int u, int h) {
    head[u] = h;
    pos[u] = cur_pos++;
    if (heavy[u] != -1) decompose(heavy[u], h);
    for (int v : adj[u])
        if (v != parent[u] && v != heavy[u])
            decompose(v, v);
}
```

Query path(u, v):

- While heads differ, move up chain by chain- Query segment tree in `[pos[head[u]], pos[u]]`- When in same chain, query segment `[pos[v], pos[u]]` Complexity:
- Build: (O(n))- Query/Update: (O$\log^2 n$)

C. Use Cases

- Path sums- Path maximums- Edge updates- Subtree queries

3. Centroid Decomposition

Centroid = node that splits tree into subtrees n/2 each. By removing centroids recursively, we form a centroid tree.

Used for divide-and-conquer on trees.

A. Steps

1. Find centroid
    - DFS to compute subtree sizes - Choose node where largest subtree n/22. Decompose:
    - Remove centroid - Recurse on subtrees Code (core):

```
int subtree[MAX];
bool removed[MAX];
vector<int> adj[MAX];

int dfs_size(int u, int p) {
    subtree[u] = 1;
    for (int v : adj[u])
        if (v != p && !removed[v])
            subtree[u] += dfs_size(v, u);
    return subtree[u];
}

int find_centroid(int u, int p, int n) {
    for (int v : adj[u])
        if (v != p && !removed[v])
            if (subtree[v] > n / 2)
                return find_centroid(v, u, n);
    return u;
}

void decompose(int u, int p) {
    int n = dfs_size(u, -1);
    int c = find_centroid(u, -1, n);
    removed[c] = true;
    // process centroid here
    for (int v : adj[c])
        if (!removed[v])
            decompose(v, c);
}
```

Complexity: $(On \log n)$

B. Applications

- Distance queries (decompose + store distance to centroid)- Tree problems solvable by divide-and-conquer- Dynamic queries (add/remove nodes)

4. Comparison

Algorithm	Purpose	Query	Preprocess	Complexity	Notes
LCA	Ancestor query	$(O\log n)$	$(On \log n)$	Fast ancestor lookup	
HLD	Path queries	$(O\log^2 n)$	(O(n))	Segment tree-friendly	
Centroid Decomposition	Divide tree	-	$(On \log n)$	Balanced splits	

5. Interconnections

- HLD often uses LCA internally.- Centroid decomposition may use distance to ancestor (via LCA).- All exploit tree structure to achieve sublinear queries.

Tiny Code

LCA(4,5):

```
dfs(1,1);
printf("%d\n", lca(4,5)); // 2
```

HLD Path Sum: Build segment tree on `pos[u]` order, query along chains.

Centroid: `decompose(1, -1);`

Why It Matters

Tree algorithms show how structure unlocks efficiency. They transform naive traversals into fast, layered, or recursive solutions.

To master data structures, you must learn to "climb" and "cut" trees intelligently.

> "Every rooted path hides a logarithm."

Try It Yourself

1. Implement binary lifting LCA and test queries.
2. Add segment tree over HLD and run path sums.
3. Decompose tree by centroid and count nodes at distance k.
4. Combine LCA + HLD for path min/max.
5. Draw centroid tree of a simple graph.

Master these, and trees will stop being "just graphs" , they'll become *tools*.

40. Advanced Graph Algorithms and Tricks

By now you've seen the big families , traversals, shortest paths, flows, matchings, cuts, and trees. But real-world graphs often bring extra constraints: dynamic updates, multiple sources, layered structures, or special properties (planar, DAG, sparse).

This section gathers powerful advanced graph techniques , tricks and patterns that appear across problems once you've mastered the basics.

We'll explore:

- Topological Sorting & DAG DP- Strongly Connected Components (Condensation Graphs)- Articulation Points & Bridges (2-Edge/Vertex Connectivity)- Eulerian & Hamiltonian Paths- Graph Coloring & Bipartiteness Tests- Cycle Detection & Directed Acyclic Reasoning- Small-to-Large Merging, DSU on Tree, Mo's Algorithm on Trees- Bitmask DP on Graphs- Dynamic Graphs (Incremental/Decremental BFS/DFS)- Special Graphs (Planar, Sparse, Dense) These aren't just algorithms , they're patterns that let you attack harder graph problems with insight.

1. Topological Sorting & DAG DP

In a DAG (Directed Acyclic Graph), edges always point forward. This makes it possible to order vertices linearly so all edges go from left to right , a topological order.

Use cases:

- Task scheduling- Dependency resolution- DP on DAG (longest/shortest path, counting paths) Algorithm (Kahn's):

```cpp
vector<int> topo_sort(int n) {
    vector<int> indeg(n+1), res;
    queue<int> q;
    for (int u = 1; u <= n; u++)
        for (int v : adj[u]) indeg[v]++;
    for (int u = 1; u <= n; u++)
        if (!indeg[u]) q.push(u);
    while (!q.empty()) {
        int u = q.front(); q.pop();
        res.push_back(u);
        for (int v : adj[u])
            if (--indeg[v] == 0) q.push(v);
    }
    return res;
}
```

DAG DP:

```cpp
vector<int> dp(n+1, 0);
for (int u : topo_order)
    for (int v : adj[u])
        dp[v] = max(dp[v], dp[u] + weight(u,v));
```

Complexity: O(V + E)

2. Strongly Connected Components (Condensation)

In directed graphs, vertices may form SCCs (mutually reachable components). Condensing SCCs yields a DAG, often easier to reason about.

Use:

- Component compression- Meta-graph reasoning- Cycle condensation Tarjan's Algorithm: DFS with low-link values, single pass.

Kosaraju's Algorithm: Two passes , DFS on graph and reversed graph.

Complexity: O(V + E)

Once SCCs are built, you can run DP or topological sort on the condensed DAG.

3. Articulation Points & Bridges

Find critical vertices/edges whose removal disconnects the graph.

- Articulation point: vertex whose removal increases component count- Bridge: edge whose removal increases component count Algorithm: Tarjan's DFS Track discovery time `tin[u]` and lowest reachable ancestor `low[u]`.

```
void dfs(int u, int p) {
    tin[u] = low[u] = ++timer;
    for (int v : adj[u]) {
        if (v == p) continue;
        if (!tin[v]) {
            dfs(v, u);
            low[u] = min(low[u], low[v]);
            if (low[v] > tin[u]) bridge(u, v);
            if (low[v] >= tin[u] && p != -1) cut_vertex(u);
        } else low[u] = min(low[u], tin[v]);
    }
}
```

Applications:

- Network reliability- Biconnected components- 2-edge/vertex connectivity tests

4. Eulerian & Hamiltonian Paths

- Eulerian Path: visits every edge exactly once
  - Exists if graph is connected and 0 or 2 vertices have odd degree- Hamiltonian Path: visits every vertex exactly once (NP-hard) Euler Tour Construction: Hierholzer's algorithm (O(E))

Applications:

- Route reconstruction (e.g., word chains)- Postman problems

5. Graph Coloring & Bipartiteness

Bipartite Check: DFS/ BFS alternating colors Fails if odd cycle found.

```cpp
bool bipartite(int n) {
    vector<int> color(n+1, -1);
    for (int i = 1; i <= n; i++) if (color[i] == -1) {
        queue<int> q; q.push(i); color[i] = 0;
        while (!q.empty()) {
            int u = q.front(); q.pop();
            for (int v : adj[u]) {
                if (color[v] == -1)
                    color[v] = color[u] ^ 1, q.push(v);
                else if (color[v] == color[u])
                    return false;
            }
        }
    }
    return true;
}
```

Applications:

- 2-SAT reduction- Planar graph coloring- Conflict-free assignment

6. Cycle Detection

- DFS + recursion stack for directed graphs- Union-Find for undirected graphs Used to test acyclicity, detect back edges, or find cycles for rollback or consistency checks.

7. DSU on Tree (Small-to-Large Merging)

For queries like "count distinct colors in subtree," merge results from smaller to larger subtrees to maintain O(n log n).

Pattern:

1. DFS through children
2. Keep large child's data structure
3. Merge small child's data in

Applications:

- Offline subtree queries- Heavy subproblem caching

8. Mo's Algorithm on Trees

Offline algorithm to answer path queries efficiently:

- Convert path queries to ranges via Euler Tour- Use Mo's ordering to process in O((N + Q)√N) Useful when online updates aren't required.

9. Bitmask DP on Graphs

For small graphs (n 20): State = subset of vertices e.g., Traveling Salesman Problem (TSP)

```
dp[mask][u] = min cost to visit mask, end at u
```

Transition:

```
dp[mask | (1<<v)][v] = min(dp[mask][u] + cost[u][v])
```

Complexity: $O(n^2\ 2\ )$

10. Dynamic Graphs

Graphs that change:

- Incremental BFS: maintain distances as edges added- Decremental connectivity: union-find rollback or dynamic trees Used in online queries, evolving networks, or real-time systems.

11. Special Graph Classes

- Planar graphs: 3V-6E; use face counting- Sparse graphs: adjacency lists best- Dense graphs: adjacency matrix / bitset Optimizations often hinge on density.

Tiny Code

Topological Order:

```
auto order = topo_sort(n);
for (int u : order) printf("%d ", u);
```

Bridge Check: `if (low[v] > tin[u])` edge is a bridge.

Euler Path Check: Count odd-degree nodes == 0 or 2.

Why It Matters

These advanced techniques complete your toolkit. They're not isolated , they combine to solve real-world puzzles: dependency graphs, robust networks, optimized paths, compressed states.

They teach a mindset:

> "Graphs are not obstacles , they're shapes of possibility."

Try It Yourself

1. Implement topological sort and DAG DP.
2. Find SCCs and build condensation graph.
3. Detect articulation points and bridges.
4. Check Euler path conditions on random graphs.
5. Try DSU on tree for subtree statistics.
6. Solve TSP via bitmask DP for n 15.

Once you can mix and match these tools, you're no longer just navigating graphs , you're shaping them.

Chapter 5. Dynamic Programming

41. DP Basics and State Transitions

Dynamic Programming (DP) is one of the most powerful ideas in algorithm design. It's about breaking a big problem into smaller overlapping subproblems, solving each once, and reusing their answers.

When brute force explodes exponentially, DP brings it back under control. This section introduces the mindset, the mechanics, and the math behind DP.

1. The Core Idea

Many problems have two key properties:

- Overlapping subproblems: The same smaller computations repeat many times.
- Optimal substructure: The optimal solution to a problem can be built from optimal solutions to its subproblems.

DP solves each subproblem once, stores the result, and reuses it. This saves exponential time , often reducing (O2^n) to (On^2) or (O(n)).

2. The Recipe

When approaching a DP problem, follow this pattern:

1. Define the state. Decide what subproblems you'll solve. Example: `dp[i] = best answer for first i elements`.
2. Write the recurrence. Express each state in terms of smaller ones. Example: `dp[i] = dp[i-1] + cost(i)`
3. Set the base cases. Where does the recursion start? Example: `dp[0] = 0`
4. Decide the order. Bottom-up (iterative) or top-down (recursive with memoization).
5. Return the final answer. Often `dp[n]` or `max(dp[i])`.

3. Example: Fibonacci Numbers

Let's begin with a classic , the nth Fibonacci number (F(n) = F(n-1) + F(n-2)).

Recursive (slow):

```
int fib(int n) {
    if (n <= 1) return n;
    return fib(n - 1) + fib(n - 2);
}
```

This recomputes the same values over and over , exponential time.

Top-Down DP (Memoization):

```
int dp[MAX];
int fib(int n) {
    if (n <= 1) return n;
    if (dp[n] != -1) return dp[n];
    return dp[n] = fib(n-1) + fib(n-2);
}
```

Bottom-Up DP (Tabulation):

```
int fib(int n) {
    int dp[n+1];
    dp[0] = 0; dp[1] = 1;
    for (int i = 2; i <= n; i++)
        dp[i] = dp[i-1] + dp[i-2];
    return dp[n];
}
```

Space Optimized:

```
int fib(int n) {
    int a = 0, b = 1, c;
    for (int i = 2; i <= n; i++) {
        c = a + b;
        a = b;
        b = c;
    }
    return b;
}
```

4. States, Transitions, and Dependencies

A DP table is a map from states to answers. Each state depends on others via a transition function.

Think of it like a graph , each edge represents a recurrence relation.

Example:

- State: `dp[i] = number of ways to reach step i`- Transition: `dp[i] = dp[i-1] + dp[i-2]` (like stairs)- Base: `dp[0] = 1`

5. Common DP Patterns

1. 1D Linear DP
    - Problems like Fibonacci, climbing stairs, LIS.
2. 2D DP
    - Grids, sequences, or combinations (LCS, knapsack).
3. Bitmask DP

- Subsets, TSP, combinatorial optimization.

4. DP on Trees
   - Subtree computations (sum, diameter).
5. Digit DP
   - Counting numbers with properties in a range.
6. Segment DP
   - Matrix chain multiplication, interval merges.

6. Top-Down vs Bottom-Up

Approach	Method	Pros	Cons
Top-Down	Recursion + Memoization	Easy to write, intuitive	Stack overhead, needs memo
Bottom-Up	Iteration	Fast, space-optimizable	Harder to derive order

When dependencies are simple and acyclic, bottom-up shines. When they're complex, top-down is easier.

7. Example 2: Climbing Stairs

You can climb 1 or 2 steps at a time. How many distinct ways to reach step (n)?

State: `dp[i] = ways to reach step i` Transition: `dp[i] = dp[i-1] + dp[i-2]` Base: `dp[0] = 1, dp[1] = 1`

Code:

```
int climb(int n) {
    int dp[n+1];
    dp[0] = dp[1] = 1;
    for (int i = 2; i <= n; i++)
        dp[i] = dp[i-1] + dp[i-2];
    return dp[n];
}
```

8. Debugging DP

To debug DP:

- Print intermediate states.- Visualize table (especially 2D).- Check base cases.- Trace one small example by hand.

9. Complexity

Most DP algorithms are linear or quadratic in number of states:

- Time = (#states) × (work per transition)- Space = (#states) Example: Fibonacci: (O(n)) time, (O(1)) space Knapsack: (O$n \times W$) LCS: (O$n \times m$)

Tiny Code

Fibonacci (tabulated):

```
int dp[100];
dp[0] = 0; dp[1] = 1;
for (int i = 2; i <= n; i++)
    dp[i] = dp[i-1] + dp[i-2];
printf("%d", dp[n]);
```

Why It Matters

DP is the art of remembering. It transforms recursion into iteration, chaos into order.

From optimization to counting, from paths to sequences , once you see substructure, DP becomes your hammer.

> "Every repetition hides a recurrence."

Try It Yourself

1. Write top-down and bottom-up Fibonacci.
2. Count ways to climb stairs with steps {1,2,3}.
3. Compute number of paths in an n×m grid.
4. Try to spot state, recurrence, base in each problem.
5. Draw dependency graphs to visualize transitions.

DP isn't a formula , it's a mindset: break problems into parts, remember the past, and build from it.

42. Classic Problems (Knapsack, Subset Sum, Coin Change)

Now that you know what dynamic programming *is*, let's dive into the classic trio , problems that every programmer meets early on:

- Knapsack (maximize value under weight constraint)- Subset Sum (can we form a given sum?)- Coin Change (how many ways or fewest coins to reach a total) These are the training grounds of DP: each shows how to define states, transitions, and base cases clearly.

1. 0/1 Knapsack Problem

Problem: You have `n` items, each with weight `w[i]` and value `v[i]`. A knapsack with capacity `W`. Pick items (each at most once) to maximize total value, without exceeding weight.

A. State

`dp[i][w]` = max value using first `i` items with capacity `w`

B. Recurrence

For item `i`:

- If we don't take it: `dp[i-1][w]`- If we take it (if `w[i]  w`): `dp[i-1][w - w[i]] + v[i]` So,

$$dp[i][w] = \max(dp[i-1][w], dp[i-1][w - w[i]] + v[i])$$

C. Base Case

`dp[0][w] = 0` for all w (no items = no value)

D. Implementation

```
int knapsack(int n, int W, int w[], int v[]) {
    int dp[n+1][W+1];
    for (int i = 0; i <= n; i++) {
        for (int j = 0; j <= W; j++) {
            if (i == 0 || j == 0) dp[i][j] = 0;
            else if (w[i-1] <= j)
                dp[i][j] = max(dp[i-1][j], dp[i-1][j - w[i-1]] + v[i-1]);
            else
                dp[i][j] = dp[i-1][j];
        }
    }
    return dp[n][W];
}
```

Complexity: Time: (O(nW)) Space: (O(nW)) (can be optimized to 1D (O(W)))

E. Space Optimization (1D DP)

```
int dp[W+1] = {0};
for (int i = 0; i < n; i++)
    for (int w = W; w >= weight[i]; w--)
        dp[w] = max(dp[w], dp[w - weight[i]] + value[i]);
```

F. Example

Items:

```
w = [2, 3, 4, 5]
v = [3, 4, 5, 6]
W = 5
```

Best: take items 1 + 2 → value 7

2. Subset Sum

Problem: Given a set `S` of integers, can we pick some to sum to `target`?

A. State

`dp[i][sum] = true` if we can form sum `sum` using first `i` elements.

B. Recurrence

- Don't take: `dp[i-1][sum]`- Take (if `a[i] sum`): `dp[i-1][sum - a[i]]` So,

$$dp[i][sum] = dp[i-1][sum]; ||; dp[i-1][sum - a[i]]$$

C. Base Case

`dp[0][0] = true` (sum 0 possible with no elements) `dp[0][sum] = false` for sum > 0

D. Implementation

```
bool subset_sum(int a[], int n, int target) {
    bool dp[n+1][target+1];
    for (int i = 0; i <= n; i++) dp[i][0] = true;
    for (int j = 1; j <= target; j++) dp[0][j] = false;

    for (int i = 1; i <= n; i++) {
        for (int j = 1; j <= target; j++) {
            if (a[i-1] > j) dp[i][j] = dp[i-1][j];
            else dp[i][j] = dp[i-1][j] || dp[i-1][j - a[i-1]];
        }
    }
    return dp[n][target];
}
```

Complexity: Time: $(\mathrm{O}n \cdot target)$

E. Example

S = [3, 34, 4, 12, 5, 2], target = 9 Yes $\rightarrow$ 4 + 5

3. Coin Change

Two variants:

(a) Count Ways (Unbounded Coins)

"How many ways to make total `T` with coins `c[]`?"

Order doesn't matter.

State: `dp[i][t] = ways using first i coins for total t`

Recurrence:

- Skip coin: `dp[i-1][t]`- Take coin (unlimited): `dp[i][t - c[i]]`

$$dp[i][t] = dp[i-1][t] + dp[i][t-c[i]]$$

Base: `dp[0][0] = 1`

1D Simplified:

```
int dp[T+1] = {0};
dp[0] = 1;
for (int coin : coins)
    for (int t = coin; t <= T; t++)
        dp[t] += dp[t - coin];
```

(b) Min Coins (Fewest Coins to Reach Total)

State: `dp[t] = min coins to reach t`

Recurrence:

$$dp[t] = \min_{c_i \leq t}(dp[t-c_i] + 1)$$

Base: `dp[0] = 0`, rest = INF

```
int dp[T+1];
fill(dp, dp+T+1, INF);
dp[0] = 0;
for (int t = 1; t <= T; t++)
    for (int c : coins)
        if (t >= c) dp[t] = min(dp[t], dp[t - c] + 1);
```

Example

Coins = [1,2,5], Total = 5

- Ways: 4 (5; 2+2+1; 2+1+1+1; 1+1+1+1+1)- Min Coins: 1 (5)

4. Summary

Problem	Type	State	Transition	Complexity
0/1 Knapsack	Max value	dp[i][w]	max(take, skip)	O(nW)
Subset Sum	Feasibility	dp[i][sum]	OR of include/exclude	O(n * sum)
Coin Change (ways)	Counting	dp[t]	dp[t] + dp[t - coin]	O(nT)
Coin Change (min)	Optimization	dp[t]	min(dp[t - coin] + 1)	O(nT)

Tiny Code

Min Coin Change (1D):

```
int dp[T+1];
fill(dp, dp+T+1, INF);
dp[0] = 0;
for (int c : coins)
    for (int t = c; t <= T; t++)
        dp[t] = min(dp[t], dp[t - c] + 1);
printf("%d\n", dp[T]);
```

Why It Matters

These three are archetypes:

- Knapsack: optimize under constraint- Subset Sum: choose feasibility- Coin Change: count or minimize Once you master them, you can spot their patterns in harder problems , from resource allocation to pathfinding.

  "Every constraint hides a choice; every choice hides a state."

Try It Yourself

1. Implement 0/1 Knapsack (2D and 1D).
2. Solve Subset Sum for target 30 with random list.
3. Count coin combinations for amount 10.
4. Compare "min coins" vs "ways to form."
5. Write down state-transition diagram for each.

These three form your DP foundation , the grammar for building more complex algorithms.

43. Sequence Problems (LIS, LCS, Edit Distance)

Sequence problems form the *heart* of dynamic programming. They appear in strings, arrays, genomes, text comparison, and version control. Their power comes from comparing prefixes , building large answers from aligned smaller ones.

This section explores three cornerstones:

- LIS (Longest Increasing Subsequence)- LCS (Longest Common Subsequence)- Edit Distance (Levenshtein Distance) Each teaches a new way to think about subproblems, transitions, and structure.

1. Longest Increasing Subsequence (LIS)

Problem: Given an array, find the length of the longest subsequence that is *strictly increasing*.

A subsequence isn't necessarily contiguous , you can skip elements.

Example: `[10, 9, 2, 5, 3, 7, 101, 18]` $\rightarrow$ LIS is `[2, 3, 7, 18]` $\rightarrow$ length 4

A. State

`dp[i]` = length of LIS ending at index `i`

B. Recurrence

$$dp[i] = 1 + \max_{j<i \wedge a[j]<a[i]} dp[j]$$

If no smaller `a[j]`, then `dp[i] = 1`.

C. Base

`dp[i] = 1` for all i (each element alone is an LIS)

D. Implementation

```cpp
int lis(int a[], int n) {
    int dp[n], best = 0;
    for (int i = 0; i < n; i++) {
        dp[i] = 1;
        for (int j = 0; j < i; j++)
            if (a[j] < a[i])
                dp[i] = max(dp[i], dp[j] + 1);
        best = max(best, dp[i]);
    }
    return best;
}
```

Complexity: $(\mathrm{O}n^2)$

E. Binary Search Optimization

Use a tail array:

- `tail[len] = min possible ending value of LIS of length len` For each `x`:
- Replace `tail[idx]` via lower_bound

```cpp
int lis_fast(vector<int>& a) {
    vector<int> tail;
    for (int x : a) {
        auto it = lower_bound(tail.begin(), tail.end(), x);
        if (it == tail.end()) tail.push_back(x);
        else *it = x;
    }
    return tail.size();
}
```

Complexity: $(\mathrm{O}n \log n)$

2. Longest Common Subsequence (LCS)

Problem: Given two strings, find the longest subsequence present in both.

Example: `s1 = "ABCBDAB"`, `s2 = "BDCABA"` LCS = "BCBA" → length 4

A. State

`dp[i][j]` = LCS length between `s1[0..i-1]` and `s2[0..j-1]`

B. Recurrence

$$dp[i][j] = \begin{cases} dp[i-1][j-1] + 1, & \text{if } s_1[i-1] = s_2[j-1], \\ \max(dp[i-1][j],\, dp[i][j-1]), & \text{otherwise.} \end{cases}$$

C. Base

`dp[0][*] = dp[*][0] = 0` (empty string)

D. Implementation

```
int lcs(string a, string b) {
    int n = a.size(), m = b.size();
    int dp[n+1][m+1];
    for (int i = 0; i <= n; i++)
        for (int j = 0; j <= m; j++)
            if (i == 0 || j == 0) dp[i][j] = 0;
            else if (a[i-1] == b[j-1])
                dp[i][j] = dp[i-1][j-1] + 1;
            else
                dp[i][j] = max(dp[i-1][j], dp[i][j-1]);
    return dp[n][m];
}
```

Complexity: (O(nm))

E. Reconstruct LCS

Trace back from `dp[n][m]`:

- If chars equal → take it and move diagonally- Else move toward larger neighbor

F. Example

a = “AGGTAB”, b = “GXTXAYB” LCS = “GTAB” → 4

3. Edit Distance (Levenshtein Distance)

Problem: Minimum operations (insert, delete, replace) to convert string `a` → `b`.

Example: `kitten → sitting` = 3 (replace k→s, insert i, insert g)

A. State

`dp[i][j]` = min edits to convert `a[0..i-1]` → `b[0..j-1]`

B. Recurrence

If `a[i-1] == b[j-1]`:

$$dp[i][j] = dp[i-1][j-1]$$

Else:

$$dp[i][j] = 1 + \min(dp[i-1][j], dp[i][j-1], dp[i-1][j-1])$$

(Delete, Insert, Replace)

C. Base

- `dp[0][j] = j` (insert all)- `dp[i][0] = i` (delete all)

D. Implementation

```
int edit_distance(string a, string b) {
    int n = a.size(), m = b.size();
    int dp[n+1][m+1];
    for (int i = 0; i <= n; i++)
        for (int j = 0; j <= m; j++) {
            if (i == 0) dp[i][j] = j;
            else if (j == 0) dp[i][j] = i;
            else if (a[i-1] == b[j-1])
                dp[i][j] = dp[i-1][j-1];
            else
                dp[i][j] = 1 + min({dp[i-1][j], dp[i][j-1], dp[i-1][j-1]});
        }
    return dp[n][m];
}
```

Complexity: (O(nm))

E. Example

a = "horse", b = "ros"

- replace h→r, delete r, delete e → 3

4. Summary

Problem	Type	State	Transition	Complexity
LIS	Single seq	dp[i]	1 + max(dp[j])	$O(n^2)$ / O(n log n)
LCS	Two seqs	dp[i][j]	if match +1 else max	O(nm)
Edit Distance	Two seqs	dp[i][j]	if match 0 else 1 + min	O(nm)

5. Common Insights

- LIS builds upward , from smaller sequences.- LCS aligns two sequences , compare prefixes.- Edit Distance quantifies *difference* , minimal edits. They're templates for bioinformatics, text diffing, version control, and more.

Tiny Code

LCS:

```
if (a[i-1] == b[j-1])
    dp[i][j] = dp[i-1][j-1] + 1;
else
    dp[i][j] = max(dp[i-1][j], dp[i][j-1]);
```

Why It Matters

Sequence DPs teach you how to compare progressions , how structure and similarity evolve over time.

They transform vague "compare these" tasks into crisp recurrence relations.

> "To align is to understand."

Try It Yourself

1. Implement LIS ($O(n^2)$ and O(n log n))
2. Find LCS of two given strings
3. Compute edit distance between "intention" and "execution"
4. Modify LCS to print one valid subsequence
5. Try to unify LCS and Edit Distance in a single table

Master these, and you can handle any DP on sequences , the DNA of algorithmic thinking.

44. Matrix and Chain Problems

Dynamic programming shines when a problem involves choices over intervals , which order, which split, which parenthesis. This chapter explores a class of problems built on chains and matrices, where order matters and substructure is defined by intervals.

We'll study:

- Matrix Chain Multiplication (MCM) - optimal parenthesization- Polygon Triangulation - divide shape into minimal-cost triangles- Optimal BST / Merge Patterns - weighted merging decisions These problems teach interval DP, where each state represents a segment ([i, j]).

1. Matrix Chain Multiplication (MCM)

Problem: Given matrices $A_1, A_2, ..., A_n$, find the parenthesization that minimizes total scalar multiplications.

Matrix A_i has dimensions $p[i-1] \times p[i]$. We can multiply $A_i \cdot A_{i+1}$ only if inner dimensions match.

Goal: Minimize operations:

$$\text{cost}(i, j) = \min_k \left(\text{cost}(i, k) + \text{cost}(k + 1, j) + p[i - 1] \cdot p[k] \cdot p[j]\right)$$

A. State

`dp[i][j]` = min multiplications to compute $A_i...A_j$

B. Base

`dp[i][i] = 0` (single matrix needs no multiplication)

C. Recurrence

$$dp[i][j] = \min_{i \le k < j} dp[i][k] + dp[k+1][j] + p[i-1] \times p[k] \times p[j]$$

D. Implementation

```
int matrix_chain(int p[], int n) {
    int dp[n][n];
    for (int i = 1; i < n; i++) dp[i][i] = 0;

    for (int len = 2; len < n; len++) {
        for (int i = 1; i + len - 1 < n; i++) {
            int j = i + len - 1;
            dp[i][j] = INT_MAX;
            for (int k = i; k < j; k++)
                dp[i][j] = min(dp[i][j],
                    dp[i][k] + dp[k+1][j] + p[i-1]*p[k]*p[j]);
        }
    }
    return dp[1][n-1];
}
```

Complexity: $(\mathrm{O}n^3)$ time, $(\mathrm{O}n^2)$ space

E. Example

p = [10, 20, 30, 40, 30] Optimal order: ((A1A2)A3)A4 → cost 30000

2. Polygon Triangulation

Given a convex polygon with `n` vertices, connect non-intersecting diagonals to minimize total cost. Cost of a triangle = perimeter or product of side weights.

This is the same structure as MCM , divide polygon by diagonals.

A. State

`dp[i][j]` = min triangulation cost for polygon vertices from i to j.

B. Recurrence

$$dp[i][j] = \min_{i<k<j}(dp[i][k] + dp[k][j] + cost(i, j, k))$$

Base: dp[i][i+1] = 0 (fewer than 3 points)

C. Implementation

```
double polygon_triangulation(vector<Point> &p) {
    int n = p.size();
    double dp[n][n];
    for (int i = 0; i < n; i++) for (int j = 0; j < n; j++) dp[i][j] = 0;
    for (int len = 2; len < n; len++) {
        for (int i = 0; i + len < n; i++) {
            int j = i + len;
            dp[i][j] = 1e18;
            for (int k = i+1; k < j; k++)
                dp[i][j] = min(dp[i][j],
                    dp[i][k] + dp[k][j] + dist(p[i],p[k])+dist(p[k],p[j])+dist(p[j],p[i]));
        }
    }
    return dp[0][n-1];
}
```

Complexity: (On^3)

3. Optimal Binary Search Tree (OBST)

Given sorted keys $k_1 < k_2 < \cdots < k_n$ with search frequencies (f[i]), construct a BST with minimal expected search cost.

The more frequently accessed nodes should be nearer the root.

A. State

`dp[i][j]` = min cost to build BST from keys `i..j` `sum[i][j]` = sum of frequencies from i to j (precomputed)

B. Recurrence

$$dp[i][j] = \min_{k=i}^{j}(dp[i][k-1] + dp[k+1][j] + sum[i][j])$$

Each root adds one to depth of its subtrees → extra cost = `sum[i][j]`

C. Implementation

```
int optimal_bst(int freq[], int n) {
    int dp[n][n], sum[n][n];
    for (int i = 0; i < n; i++) {
        dp[i][i] = freq[i];
        sum[i][i] = freq[i];
        for (int j = i+1; j < n; j++)
            sum[i][j] = sum[i][j-1] + freq[j];
    }
    for (int len = 2; len <= n; len++) {
        for (int i = 0; i+len-1 < n; i++) {
            int j = i + len - 1;
            dp[i][j] = INT_MAX;
            for (int r = i; r <= j; r++) {
                int left = (r > i) ? dp[i][r-1] : 0;
                int right = (r < j) ? dp[r+1][j] : 0;
                dp[i][j] = min(dp[i][j], left + right + sum[i][j]);
            }
        }
    }
    return dp[0][n-1];
}
```

Complexity: (On^3)

4. Merge Pattern Problems

Many problems , merging files, joining ropes, Huffman coding , involve repeatedly combining elements with minimal total cost.

All follow this template:

$$dp[i][j] = \min_{k}(dp[i][k] + dp[k+1][j] + \text{merge cost})$$

Same structure as MCM.

5. Key Pattern: Interval DP

State: `dp[i][j] = best answer for subarray [i..j]` Transition: Try all splits `k` between `i` and `j`

Template:

```
for (len = 2; len <= n; len++)
 for (i = 0; i + len - 1 < n; i++) {
    j = i + len - 1;
    dp[i][j] = INF;
    for (k = i; k < j; k++)
       dp[i][j] = min(dp[i][j], dp[i][k] + dp[k+1][j] + cost(i,j,k));
 }
```

6. Summary

Problem	State	Recurrence	Complexity
MCM	dp[i][j]	min(dp[i][k]+dp[k+1][j]+p[i-1]*p*[k]*p[j])	O(n³)
Polygon Triangulation	dp[i][j]	min(dp[i][k]+dp[k][j]+cost)	O(n³)
OBST	dp[i][j]	min(dp[i][k-1]+dp[k+1][j]+sum[i][j])	O(n³)
Merge Problems	dp[i][j]	min(dp[i][k]+dp[k+1][j]+merge cost)	O(n³)

Tiny Code

Matrix Chain (Compact):

```
for (len = 2; len < n; len++)
  for (i = 1; i + len - 1 < n; i++) {
    j = i + len - 1; dp[i][j] = INF;
    for (k = i; k < j; k++)
      dp[i][j] = min(dp[i][j], dp[i][k] + dp[k+1][j] + p[i-1]*p[k]*p[j]);
  }
```

Why It Matters

These problems are DP in 2D , reasoning over intervals and splits. They train your ability to "cut the problem" at every possible point.

> "Between every start and end lies a choice of where to divide."

Try It Yourself

1. Implement MCM and print parenthesization.
2. Solve polygon triangulation with edge weights.
3. Build OBST for frequencies [34, 8, 50].
4. Visualize DP table diagonally.
5. Generalize to merging `k` segments at a time.

Master these, and you'll see interval DP patterns hiding in parsing, merging, and even AI planning.

45. Bitmask DP and Traveling Salesman

Some dynamic programming problems require you to track which items have been used, or which subset of elements is active at a given point. This is where Bitmask DP shines. It encodes subsets as binary masks, allowing you to represent state space efficiently.

This technique is a must-know for:

- Traveling Salesman Problem (TSP)- Subset covering / visiting problems- Permutations and combinations of sets- Game states and toggles

1. The Idea of Bitmask DP

A bitmask is an integer whose binary representation encodes a subset.

For (n) elements:

- There are 2^n subsets.- A subset is represented by a mask from `0` to `(1 << n) - 1`. Example for `n = 4`:

Subset	Mask (binary)	Mask (decimal)
	0000	0
{0}	0001	1
{1}	0010	2
{0,1,3}	1011	11

We can check membership:

- `mask & (1 << i)` → whether element `i` is in subset We can add elements:
- `mask | (1 << i)` → add element `i` We can remove elements:
- `mask & ~(1 << i)` → remove element `i`

2. Example: Traveling Salesman Problem (TSP)

Problem: Given `n` cities and cost matrix `cost[i][j]`, find the minimum cost Hamiltonian cycle visiting all cities exactly once and returning to start.

A. State

`dp[mask][i]` = minimum cost to reach city `i` having visited subset `mask`

- `mask` → set of visited cities- `i` → current city

B. Base Case

`dp[1<<0][0] = 0` (start at city 0, only 0 visited)

C. Transition

For each subset `mask` and city `i` in `mask`, try moving from `i` to `j` not in `mask`:

$$dp[mask \cup (1 << j)][j] = \min\left(dp[mask \cup (1 << j)][j], dp[mask][i] + cost[i][j]\right)$$

D. Implementation

```
int tsp(int n, int cost[20][20]) {
    int N = 1 << n;
    const int INF = 1e9;
    int dp[N][n];
    for (int m = 0; m < N; m++)
        for (int i = 0; i < n; i++)
            dp[m][i] = INF;

    dp[1][0] = 0; // start at city 0

    for (int mask = 1; mask < N; mask++) {
        for (int i = 0; i < n; i++) {
            if (!(mask & (1 << i))) continue;
            for (int j = 0; j < n; j++) {
                if (mask & (1 << j)) continue;
                int next = mask | (1 << j);
```

```
                dp[next][j] = min(dp[next][j], dp[mask][i] + cost[i][j]);
            }
        }
    }

    int ans = INF;
    for (int i = 1; i < n; i++)
        ans = min(ans, dp[N-1][i] + cost[i][0]);
    return ans;
}
```

Complexity:

- States: ($On \cdot 2^n$)- Transitions: (O(n))- Total: ($On^2 \cdot 2^n$)

E. Example

```
n = 4
cost = {
 {0, 10, 15, 20},
 {10, 0, 35, 25},
 {15, 35, 0, 30},
 {20, 25, 30, 0}
}
```

Optimal path: $0 \to 1 \to 3 \to 2 \to 0$ Cost $= 80$

3. Other Common Bitmask DP Patterns

1. Subset Sum / Partition `dp[mask] = true if subset represented by mask satisfies property`
2. Counting Set Bits `__builtin_popcount(mask)` gives number of elements in subset.
3. Iterating Over Submasks

```
for (int sub = mask; sub; sub = (sub-1) & mask)
    // handle subset sub
```

4. Assigning Tasks (Assignment Problem)

- Each mask represents set of workers assigned.- State: `dp[mask] = min cost for assigned tasks`.

```
for (mask) for (task)
 if (!(mask & (1 << task)))
   dp[mask | (1 << task)] = min(dp[mask | (1 << task)],
        dp[mask] + cost[__builtin_popcount(mask)][task]);
```

4. Memory Tricks

- If only previous masks needed, use rolling arrays:

```
dp[next][j] = ...
swap(dp, next_dp)
```

- Compress dimensions: $(O2^n)$ memory for small `n`

5. Summary

Problem	State	Transition	Complexity
TSP	dp[mask][i]	min(dp[mask][i] + cost[i][j])	$O(n^2 \cdot 2$)
Assignment	dp[mask]	add one new element	$O(n^2 \cdot 2$)
Subset Sum	dp[mask]	union of valid subsets	$O(2$ $\cdot n)$

Tiny Code

Core Transition:

```
for (mask)
  for (i)
    if (mask & (1<<i))
      for (j)
        if (!(mask & (1<<j)))
          dp[mask|(1<<j)][j] = min(dp[mask|(1<<j)][j], dp[mask][i] + cost[i][j]);
```

Why It Matters

Bitmask DP is how you enumerate subsets efficiently. It bridges combinatorics and optimization, solving exponential problems with manageable constants.

> "Every subset is a story, and bits are its alphabet."

Try It Yourself

1. Solve TSP with 4 cities (hand-trace the table).
2. Implement Assignment Problem using bitmask DP.
3. Count subsets with even sum.
4. Use bitmask DP to find maximum compatible set of tasks.
5. Explore how to optimize memory with bit tricks.

Bitmask DP unlocks the world of subset-based reasoning , the foundation of combinatorial optimization.

46. Digit DP and SOS DP

In some problems, you don't iterate over indices or subsets , you iterate over digits or masks to count or optimize over structured states. Two major flavors stand out:

- Digit DP - counting numbers with certain properties (e.g. digit sum, constraints)- SOS DP (Sum Over Subsets) - efficiently computing functions over all subsets These are essential techniques when brute force would require enumerating every number or subset, which quickly becomes impossible.

1. Digit DP (Counting with Constraints)

Digit DP is used to count or sum over all numbers N that satisfy a condition, such as:

- The sum of digits equals a target.- The number doesn't contain a forbidden digit.- The number has certain parity or divisibility. Instead of iterating over all numbers (up to 10^1 !), we iterate digit-by-digit.

A. State Design

Typical DP state:

`dp[pos][sum][tight][leading_zero]`

- `pos`: current digit index (from most significant to least)- `sum`: property tracker (e.g. sum of digits, remainder)- `tight`: whether we're still restricted by N's prefix- `leading_zero`: whether we've started placing nonzero digits

B. Transition

At each digit position, we choose a digit `d`:

```
limit = tight ? (digit at pos in N) : 9
for (d = 0; d <= limit; d++) {
    new_tight = tight && (d == limit)
    new_sum = sum + d
    // or new_mod = (mod * 10 + d) % M
}
```

Transition accumulates results across valid choices.

C. Base Case

When `pos == len(N)` (end of digits):

- Return 1 if condition holds (e.g. `sum == target`), else 0

D. Example: Count numbers N with digit sum = S

```
long long dp[20][200][2];

long long solve(string s, int pos, int sum, bool tight) {
    if (pos == s.size()) return sum == 0;
    if (sum < 0) return 0;
    if (dp[pos][sum][tight] != -1) return dp[pos][sum][tight];

    int limit = tight ? (s[pos] - '0') : 9;
    long long res = 0;
```

```
    for (int d = 0; d <= limit; d++)
        res += solve(s, pos+1, sum-d, tight && (d==limit));

    return dp[pos][sum][tight] = res;
}
```

Usage:

```
string N = "12345";
int S = 9;
memset(dp, -1, sizeof dp);
cout << solve(N, 0, S, 1);
```

Complexity: O(number of digits × sum × 2) → typically O(20 × 200 × 2)

E. Example Variants

1. Count numbers divisible by 3 → track remainder: `new_rem = (rem*10 + d) % 3`
2. Count numbers without consecutive equal digits → add `last_digit` to state.
3. Count beautiful numbers (like palindromes, no repeated digits) → track bitmask of used digits.

F. Summary

Problem	State	Transition	Complexity
Sum of digits = S	dp[pos][sum][tight]	sum-d	O(len · S)
Divisible by k	dp[pos][rem][tight]	(rem*10+d)%k	O(len · k)
No repeated digits	dp[pos][mask][tight]	mask	O(len · 2^1)

Tiny Code

```
for (int d = 0; d <= limit; d++)
    res += solve(pos+1, sum-d, tight && (d==limit));
```

2. SOS DP (Sum Over Subsets)

When dealing with functions on subsets, we sometimes need to compute:

$$f(S) = \sum_{T \subseteq S} g(T)$$

Naively O(3). SOS DP reduces it to O(n · 2).

A. Setup

Let `f[mask] = g[mask]` initially. For each bit `i`:

```
for (mask = 0; mask < (1<<n); mask++)
    if (mask & (1<<i))
        f[mask] += f[mask^(1<<i)];
```

After this, `f[mask]` = sum of `g[sub]` for all `sub  mask`.

B. Example

Given array `a[mask]`, compute `sum[mask] = sum_{sub  mask} a[sub]`

```
int n = 3;
int N = 1 << n;
int f[N], a[N];
// initialize a[]
for (int mask = 0; mask < N; mask++) f[mask] = a[mask];
for (int i = 0; i < n; i++)
  for (int mask = 0; mask < N; mask++)
    if (mask & (1 << i))
        f[mask] += f[mask ^ (1 << i)];
```

C. Why It Works

Each iteration adds contributions from subsets differing by one bit. By processing all bits, every subset's contribution propagates upward.

D. Variants

- Sum over supersets: reverse direction.- Max instead of sum: replace `+=` with `max=`.- XOR convolution: combine values under XOR subset relation.

E. Applications

- Inclusion-exclusion acceleration- Precomputing subset statistics- DP over masks with subset transitions

F. Complexity

Problem	Naive	SOS DP
Subset sum	O(3)	O(n · 2)
Superset sum	O(3)	O(n · 2)

Why It Matters

Digit DP teaches counting under constraints , thinking digit by digit. SOS DP teaches subset propagation , spreading information efficiently.

Together, they show how to tame exponential state spaces with structure.

> "When the search space explodes, symmetry and structure are your compass."

Try It Yourself

1. Count numbers 10 whose digit sum = 10.
2. Count numbers 10 without repeated digits.
3. Compute f[mask] = sum_{sub mask} a[sub] for n=4.
4. Use SOS DP to find how many subsets of bits have even sum.
5. Modify Digit DP to handle leading zeros explicitly.

Master these, and you can handle structured exponential problems with elegance and speed.

47. DP Optimizations (Divide & Conquer, Convex Hull Trick, Knuth)

Dynamic Programming often starts with a simple recurrence, but naïve implementations can be too slow (e.g., (On^2) or worse). When the recurrence has special structure , such as monotonicity or convexity , we can exploit it to reduce time complexity drastically.

This chapter introduces three powerful optimization families:

1. Divide and Conquer DP
2. Convex Hull Trick (CHT)
3. Knuth Optimization

Each one is based on discovering order or geometry hidden inside transitions.

1. Divide and Conquer Optimization

If you have a recurrence like:

$$dp[i] = \min_{k<i} dp[k] + C(k, i)$$

and the optimal k for dp[i] optimal k for dp[i+1], you can use divide & conquer to compute dp in (O$n \log n$) or (O$n \log^2 n$).

This property is called monotonicity of argmin.

A. Conditions

Let (C(k, i)) be the cost to transition from (k) to (i). Divide and conquer optimization applies if:

$$opt(i) \leq opt(i + 1)$$

and (C) satisfies quadrangle inequality (or similar convex structure).

B. Template

```
void compute(int l, int r, int optL, int optR) {
    if (l > r) return;
    int mid = (l + r) / 2;
    pair<long long,int> best = {INF, -1};
    for (int k = optL; k <= min(mid, optR); k++) {
        long long val = dp_prev[k] + cost(k, mid);
        if (val < best.first) best = {val, k};
    }
    dp[mid] = best.first;
    int opt = best.second;
    compute(l, mid-1, optL, opt);
    compute(mid+1, r, opt, optR);
}
```

You call it as:

```
compute(1, n, 0, n-1);
```

C. Example: Divide Array into K Segments

Given array `a[1..n]`, divide into `k` parts to minimize

$$dp[i][k] = \min_{j<i} dp[j][k-1] + cost(j+1, i)$$

If cost satisfies quadrangle inequality, you can optimize each layer in ($On \log n$).

D. Complexity

Naive: (On^2) → Optimized: ($On \log n$)

2. Convex Hull Trick (CHT)

Applies when DP recurrence is linear in i and k:

$$dp[i] = \min_{k<i}(m_k \cdot x_i + b_k)$$

where:

- m_k is slope (depends on k)- (b_k = dp[k] + c(k))- x_i is known (monotonic) You can maintain lines $y = m_k x + b_k$ in a convex hull, and query min efficiently.

A. Conditions

- Slopes m_k are monotonic (either increasing or decreasing)- Query points x_i are sorted If both monotonic, we can use pointer walk in O(1) amortized per query. Otherwise, use Li Chao Tree (O(log n)).

B. Implementation (Monotonic Slopes)

```
struct Line { long long m, b; };
deque<Line> hull;

bool bad(Line l1, Line l2, Line l3) {
    return (l3.b - l1.b)*(l1.m - l2.m) <= (l2.b - l1.b)*(l1.m - l3.m);
}

void add(long long m, long long b) {
    Line l = {m, b};
    while (hull.size() >= 2 && bad(hull[hull.size()-2], hull.back(), l))
        hull.pop_back();
    hull.push_back(l);
}

long long query(long long x) {
    while (hull.size() >= 2 &&
          hull[0].m*x + hull[0].b >= hull[1].m*x + hull[1].b)
        hull.pop_front();
    return hull.front().m*x + hull.front().b;
}
```

C. Example: DP for Line-Based Recurrence

$$dp[i] = a_i^2 + \min_{j<i}(dp[j] + b_j \cdot a_i)$$

Here $m_j = b_j$, $x_i = a_i$, $b_j = dp[j]$

D. Complexity

- Naive: (On^2)- CHT: (O(n)) or (O$n \log n$)

3. Knuth Optimization

Used in interval DP problems (like Matrix Chain, Merging Stones).

If:

1. $dp[i][j] = \min_{k=i}^{j-1}(dp[i][k] + dp[k+1][j] + w(i,j))$
2. The cost $w(i,j)$ satisfies the quadrangle inequality:

$$w(a,c) + w(b,d) \leq w(a,d) + w(b,c)$$

3. And the monotonicity condition:

$$opt[i][j-1] \leq opt[i][j] \leq opt[i+1][j]$$

Then you can reduce the search space from (O(n)) to (O(1)) per cell, making total complexity (On^2) instead of (On^3).

A. Implementation

```
for (int len = 2; len <= n; len++) {
    for (int i = 1; i + len - 1 <= n; i++) {
        int j = i + len - 1;
        dp[i][j] = INF;
        for (int k = opt[i][j-1]; k <= opt[i+1][j]; k++) {
            long long val = dp[i][k] + dp[k+1][j] + cost(i,j);
            if (val < dp[i][j]) {
                dp[i][j] = val;
                opt[i][j] = k;
            }
        }
    }
}
```

B. Example

Optimal Binary Search Tree or Merging Stones (with additive cost). Typical improvement: ($On^3 \rightarrow On^2$)

4. Summary

Technique	Applies To	Key Property	Complexity
Divide & Conquer DP	1D transitions	Monotonic argmin	O(n log n)
Convex Hull Trick	Linear transitions	Monotonic slopes	O(n) / O(n log n)
Knuth Optimization	Interval DP	Quadrangle + Monotonicity	$O(n^2)$

Tiny Code

Divide & Conquer Template

```
void compute(int l, int r, int optL, int optR);
```

CHT Query

```
while (size>=2 && f[1](x) < f[0](x)) pop_front();
```

Why It Matters

These optimizations show that DP isn't just brute force with memory , it's mathematical reasoning on structure.

Once you spot monotonicity or linearity, you can shrink a quadratic solution into near-linear time.

> "Optimization is the art of seeing simplicity hiding in structure."

Try It Yourself

1. Optimize Matrix Chain DP using Knuth.
2. Apply Divide & Conquer on `dp[i] = min_{k<i}(dp[k]+(i-k)^2)`.
3. Solve Slope DP with CHT for convex cost functions.
4. Compare runtime vs naive DP on random data.
5. Derive conditions for opt monotonicity in your custom recurrence.

Master these techniques, and you'll turn your DPs from slow prototypes into lightning-fast solutions.

48. Tree DP and Rerooting

Dynamic Programming on trees is one of the most elegant and powerful patterns in algorithm design. Unlike linear arrays or grids, trees form hierarchical structures, where each node depends on its children or parent. Tree DP teaches you how to aggregate results up and down the tree, handling problems where subtrees interact.

In this section, we'll cover:

1. Basic Tree DP (rooted trees)
2. DP over children (bottom-up aggregation)
3. Rerooting technique (top-down propagation)
4. Common applications and examples

1. Basic Tree DP: The Idea

We define `dp[u]` to represent some property of the subtree rooted at `u`. Then we combine children's results to compute `dp[u]`.

This bottom-up approach is like postorder traversal.

Example structure:

```
function dfs(u, parent):
    dp[u] = base_value
    for v in adj[u]:
        if v == parent: continue
        dfs(v, u)
        dp[u] = combine(dp[u], dp[v])
```

Example 1: Size of Subtree

Let `dp[u] = number of nodes in subtree rooted at u`

```cpp
void dfs(int u, int p) {
    dp[u] = 1;
    for (int v : adj[u]) {
        if (v == p) continue;
        dfs(v, u);
        dp[u] += dp[v];
    }
}
```

Key idea: Combine children's sizes to get parent size. Complexity: (O(n))

Example 2: Height of Tree

Let `dp[u] = height of subtree rooted at u`

```
void dfs(int u, int p) {
    dp[u] = 0;
    for (int v : adj[u]) {
        if (v == p) continue;
        dfs(v, u);
        dp[u] = max(dp[u], 1 + dp[v]);
    }
}
```

This gives you the height when rooted at any node.

2. DP Over Children (Bottom-Up Aggregation)

Tree DP is all about merging children.

For example, if you want the number of ways to color or number of independent sets, you compute children's dp and merge results at parent.

Example 3: Counting Independent Sets

In a tree, an independent set is a set of nodes with no two adjacent.

State:

- `dp[u][0]` = ways if `u` is not selected- `dp[u][1]` = ways if `u` is selected Recurrence:

$$dp[u][0] = \prod_{v \in children(u)} (dp[v][0] + dp[v][1])$$

$$dp[u][1] = \prod_{v \in children(u)} dp[v][0]$$

Implementation:

```
void dfs(int u, int p) {
    dp[u][0] = dp[u][1] = 1;
    for (int v : adj[u]) {
        if (v == p) continue;
        dfs(v, u);
        dp[u][0] *= (dp[v][0] + dp[v][1]);
        dp[u][1] *= dp[v][0];
    }
}
```

Final answer = `dp[root][0] + dp[root][1]`

Example 4: Maximum Path Sum in Tree

Let `dp[u]` = max path sum starting at `u` and going down To find best path anywhere, store a global max over child pairs.

```
int ans = 0;
int dfs(int u, int p) {
    int best1 = 0, best2 = 0;
    for (int v : adj[u]) {
        if (v == p) continue;
        int val = dfs(v, u) + weight(u, v);
        if (val > best1) swap(best1, val);
        if (val > best2) best2 = val;
    }
    ans = max(ans, best1 + best2);
    return best1;
}
```

This gives tree diameter or max path sum.

3. Rerooting Technique

Rerooting DP allows you to compute answers for every node as root, without recomputing from scratch (On^2). It's also known as DP on trees with re-rooting.

Idea

1. First, compute `dp_down[u]` = answer for subtree when rooted at `u`.
2. Then, propagate info from parent to child (`dp_up[u]`), so each node gets info from outside its subtree.
3. Combine `dp_down` and `dp_up` to get `dp_all[u]`.

Example 5: Sum of Distances from Each Node

Let's find `ans[u]` = sum of distances from `u` to all nodes.

1. Root the tree at 0.
2. Compute subtree sizes and total distance from root.
3. Reroot to adjust distances using parent's info.

Step 1: Bottom-up:

```
void dfs1(int u, int p) {
    sz[u] = 1;
    for (int v : adj[u]) {
        if (v == p) continue;
        dfs1(v, u);
        sz[u] += sz[v];
        dp[u] += dp[v] + sz[v];
    }
}
```

Step 2: Top-down:

```
void dfs2(int u, int p) {
    for (int v : adj[u]) {
        if (v == p) continue;
        dp[v] = dp[u] - sz[v] + (n - sz[v]);
        dfs2(v, u);
    }
}
```

After `dfs2`, `dp[u]` = sum of distances from node `u`.

Complexity: (O(n))

4. General Rerooting Template

```
// 1. Postorder: compute dp_down[u] from children
void dfs_down(u, p):
    dp_down[u] = base
    for v in adj[u]:
        if v != p:
            dfs_down(v, u)
            dp_down[u] = merge(dp_down[u], dp_down[v])

// 2. Preorder: use parent's dp_up to compute dp_all[u]
void dfs_up(u, p, dp_up_parent):
    ans[u] = merge(dp_down[u], dp_up_parent)
    prefix, suffix = prefix products of children
    for each child v:
        dp_up_v = merge(prefix[v-1], suffix[v+1], dp_up_parent)
        dfs_up(v, u, dp_up_v)
```

This template generalizes rerooting to many problems:

- Maximum distance from each node- Number of ways to select subtrees- Sum of subtree sizes seen from each root

5. Summary

Pattern	Description	Complexity
Basic Tree DP	Combine child subresults	O(n)
DP Over Children	Each node depends on children	O(n)
Rerooting DP	Compute result for every root	O(n)
Multiple States	Track choices (e.g. include/exclude)	$O(n \cdot \text{state})$

Tiny Code

Subtree Size

```
void dfs(int u, int p) {
    dp[u] = 1;
    for (int v: adj[u]) if (v != p) {
```

```
        dfs(v,u);
        dp[u] += dp[v];
    }
}
```

Reroot Sum Distances

```
dp[v] = dp[u] - sz[v] + (n - sz[v]);
```

Why It Matters

Tree DP is how we think recursively over structure , each node's truth emerges from its children. Rerooting expands this idea globally, giving every node its own perspective.

> "In the forest of states, each root sees a different world , yet all follow the same law."

Try It Yourself

1. Count number of nodes in each subtree.
2. Compute sum of depths from each node.
3. Find tree diameter using DP.
4. Count number of independent sets modulo 1e9+7.
5. Implement rerooting to find max distance from each node.

Tree DP turns recursive patterns into universal strategies for hierarchical data.

49. DP Reconstruction and Traceback

So far, we've focused on computing optimal values (min cost, max score, count of ways). But in most real problems, we don't just want the number , we want to know how we got it.

That's where reconstruction comes in: once you've filled your DP table, you can trace back the decisions that led to the optimal answer.

This chapter shows you how to:

1. Record transitions during DP computation
2. Reconstruct paths, subsets, or sequences
3. Handle multiple reconstructions (paths, sets, parent links)
4. Understand traceback in 1D, 2D, and graph-based DPs

1. The Core Idea

Each DP state comes from a choice. If you store *which choice was best*, you can walk backward from the final state to rebuild the solution.

Think of it as:

```
dp[i] = best over options
choice[i] = argmin or argmax option
```

Then:

```
reconstruction_path = []
i = n
while i > 0:
    reconstruction_path.push(choice[i])
    i = choice[i].prev
```

You're not just solving , you're remembering the path.

2. Reconstruction in 1D DP

Example: Coin Change (Minimum Coins)

Problem: Find minimum number of coins to make value `n`.

Recurrence:

$$dp[x] = 1 + \min_{c \in coins, c \leq x} dp[x - c]$$

To reconstruct which coins were used:

```cpp
int dp[MAXN], prev_coin[MAXN];
dp[0] = 0;
for (int x = 1; x <= n; x++) {
    dp[x] = INF;
    for (int c : coins) {
        if (x >= c && dp[x-c] + 1 < dp[x]) {
            dp[x] = dp[x-c] + 1;
            prev_coin[x] = c;
        }
    }
}
```

Reconstruction:

```
vector<int> used;
int cur = n;
while (cur > 0) {
    used.push_back(prev_coin[cur]);
    cur -= prev_coin[cur];
}
```

Output: coins used in one optimal solution.

Example: LIS Reconstruction

You know how to find LIS length. Now reconstruct the sequence.

```
int dp[n], prev[n];
int best_end = 0;
for (int i = 0; i < n; i++) {
    dp[i] = 1; prev[i] = -1;
    for (int j = 0; j < i; j++)
        if (a[j] < a[i] && dp[j] + 1 > dp[i]) {
            dp[i] = dp[j] + 1;
            prev[i] = j;
        }
    if (dp[i] > dp[best_end]) best_end = i;
}
```

Rebuild LIS:

```
vector<int> lis;
for (int i = best_end; i != -1; i = prev[i])
    lis.push_back(a[i]);
reverse(lis.begin(), lis.end());
```

3. Reconstruction in 2D DP

Example: LCS (Longest Common Subsequence)

We have `dp[i][j]` filled using:

$$dp[i][j] = \begin{cases} dp[i-1][j-1] + 1, & \text{if } a[i-1] = b[j-1], \\ \max(dp[i-1][j], dp[i][j-1]), & \text{otherwise.} \end{cases}$$

To reconstruct LCS:

```
int i = n, j = m;
string lcs = "";
while (i > 0 && j > 0) {
    if (a[i-1] == b[j-1]) {
        lcs.push_back(a[i-1]);
        i--; j--;
    }
    else if (dp[i-1][j] > dp[i][j-1]) i--;
    else j--;
}
reverse(lcs.begin(), lcs.end());
```

Output: one valid LCS string.

Example: Edit Distance

Operations: insert, delete, replace.

You can store the operation:

```
if (a[i-1] == b[j-1]) op[i][j] = "match";
else if (dp[i][j] == dp[i-1][j-1] + 1) op[i][j] = "replace";
else if (dp[i][j] == dp[i-1][j] + 1) op[i][j] = "delete";
else op[i][j] = "insert";
```

Then backtrack to list operations:

```
while (i > 0 || j > 0) {
    if (op[i][j] == "match") i--, j--;
    else if (op[i][j] == "replace") { print("Replace"); i--; j--; }
    else if (op[i][j] == "delete") { print("Delete"); i--; }
    else { print("Insert"); j--; }
}
```

4. Reconstruction in Path Problems

When DP tracks shortest paths, you can keep parent pointers.

Example: Bellman-Ford Path Reconstruction

```
int dist[n], parent[n];
dist[src] = 0;
for (int k = 0; k < n-1; k++)
  for (auto [u,v,w] : edges)
    if (dist[u] + w < dist[v]) {
        dist[v] = dist[u] + w;
        parent[v] = u;
    }

vector<int> path;
for (int v = dest; v != src; v = parent[v])
    path.push_back(v);
path.push_back(src);
reverse(path.begin(), path.end());
```

You now have the actual shortest path.

5. Handling Multiple Solutions

Sometimes multiple optimal paths exist. You can:

- Store all predecessors instead of one- Backtrack recursively to enumerate all solutions- Tie-break deterministically (e.g., lexicographically smallest) Example:

```
if (new_val == dp[i]) parents[i].push_back(j);
```

Then recursively generate all possible paths.

6. Visualization

DP reconstruction often looks like following arrows in a grid or graph:

- LCS: diagonal ( ), up (↑), left (←)- Shortest path: parent edges- LIS: predecessor chain You're walking through decisions, not just numbers.

7. Summary

Type	State	Reconstruction
1D DP	`prev[i]`	Trace chain
2D DP	`op[i][j]`	Follow choices
Graph DP	`parent[v]`	Follow edges
Counting DP	optional	Recover counts / paths

Tiny Code

General pattern:

```
for (state)
  for (choice)
    if (better) {
        dp[state] = value;
        parent[state] = choice;
    }
```

Then:

```
while (state != base) {
    path.push_back(parent[state]);
    state = parent[state];
}
```

Why It Matters

Solving DP gets you the score , reconstructing shows you the story. It's the difference between knowing the answer and understanding the reasoning.

> "Numbers tell you the outcome; pointers tell you the path."

Try It Yourself

1. Reconstruct one LIS path.
2. Print all LCSs for small strings.
3. Show edit operations to transform "cat" → "cut".
4. Track subset used in Knapsack to reach exact weight.

5. Recover optimal merge order in Matrix Chain DP.

Reconstruction turns DP from a static table into a narrative of decisions , a map back through the maze of optimal choices.

50. Meta-DP and Optimization Templates

We've now explored many flavors of dynamic programming , on sequences, grids, trees, graphs, subsets, and digits. This final chapter in the DP arc zooms out to the *meta-level*: how to see DP patterns, generalize them, and turn them into reusable templates.

If classical DP is about solving one problem, meta-DP is about recognizing *families* of problems that share structure. You'll learn how to build your own DP frameworks, use common templates, and reason from first principles.

1. What Is Meta-DP?

A *Meta-DP* is a high-level abstraction of a dynamic programming pattern. It encodes:

- State definition pattern- Transition pattern- Optimization structure- Dimensional dependencies By learning these patterns, you can design DPs faster, reuse logic across problems, and spot optimizations early.

Think of Meta-DP as:

> "Instead of memorizing 100 DPs, master 10 DP blueprints."

2. The Four Building Blocks

Every DP has the same core ingredients:

1. State: what subproblem you're solving
    - Often `dp[i]`, `dp[i][j]`, or `dp[mask]` - Represents smallest unit of progress2. Transition: how to build larger subproblems from smaller ones
    - E.g. `dp[i] = min(dp[j] + cost(j, i))`3. Base Case: known trivial answers
    - E.g. `dp[0] = 0`4. Order: how to fill the states
    - E.g. increasing `i`, decreasing `i`, or topological order Once you can describe a problem in these four, it *is* a DP.

3. Meta-Templates for Common Structures

Below are generalized templates to use and adapt.

A. Line DP (1D Sequential)

Shape: linear progression Examples:

- Fibonacci- Knapsack (1D capacity)- LIS (sequential dependency)

```
for (int i = 1; i <= n; i++) {
    dp[i] = base;
    for (int j : transitions(i))
        dp[i] = min(dp[i], dp[j] + cost(j, i));
}
```

Visualization: $\rightarrow \rightarrow \rightarrow$ Each state depends on previous positions.

B. Grid DP (2D Spatial)

Shape: grid or matrix Examples:

- Paths in a grid- Edit Distance- Counting paths with obstacles

```
for (i = 0; i < n; i++)
  for (j = 0; j < m; j++)
    dp[i][j] = combine(dp[i-1][j], dp[i][j-1]);
```

Visualization: Moves from top-left to bottom-right.

C. Interval DP

Shape: segments or subarrays Examples:

- Matrix Chain Multiplication- Optimal BST- Merging Stones

```
for (len = 2; len <= n; len++)
  for (i = 0; i + len - 1 < n; i++) {
      j = i + len - 1;
      dp[i][j] = INF;
      for (k = i; k < j; k++)
          dp[i][j] = min(dp[i][j], dp[i][k] + dp[k+1][j] + cost(i,j));
  }
```

Key Insight: overlapping intervals, split points.

D. Subset DP

Shape: subsets of a set Examples:

- Traveling Salesman (TSP)- Assignment problem- SOS DP

```
for (mask = 0; mask < (1<<n); mask++)
  for (sub = mask; sub; sub = (sub-1)&mask)
      dp[mask] = combine(dp[mask], dp[sub]);
```

Key Insight: use bitmasks to represent subsets.

E. Tree DP

Shape: hierarchical dependencies Examples:

- Subtree sizes- Independent sets- Rerooting

```
void dfs(u, p):
  dp[u] = base
  for (v in children)
    if (v != p)
      dfs(v, u)
      dp[u] = merge(dp[u], dp[v])
```

F. Graph DP (Topological Order)

Shape: DAG structure Examples:

- Longest path in DAG- Counting paths- DAG shortest path

```
for (u in topo_order)
  for (v in adj[u])
    dp[v] = combine(dp[v], dp[u] + weight(u,v));
```

Key: process nodes in topological order.

G. Digit DP

Shape: positional digits, constrained transitions Examples:

- Count numbers satisfying digit conditions- Divisibility / digit sum problems

```
dp[pos][sum][tight] =   dp[next_pos][new_sum][new_tight];
```

H. Knuth / Divide & Conquer / Convex Hull Trick

Shape: optimization over monotone or convex transitions Examples:

- Cost-based splits- Line-based transitions

```
dp[i] = min_k (dp[k] + cost(k, i))
```

Key: structure in `opt[i]` or `slope`.

Question	Clue

4. Recognizing DP Type

Ask these diagnostic questions:

Question	Clue
"Does each step depend on smaller subproblems?"	DP
"Do I split a segment?"	Interval DP
"Do I choose subsets?"	Subset / Bitmask DP
"Do I move along positions?"	Line DP
"Do I merge children?"	Tree DP
"Do I process in a DAG?"	Graph DP
"Do I track digits or constraints?"	Digit DP

5. Optimization Layer

Once you have a working DP, ask:

- Can transitions be reduced (monotonicity)?- Can overlapping cost be cached (prefix sums)?- Can dimensions be compressed (rolling arrays)?- Can you reuse solutions for each segment (Divide & Conquer / Knuth)? This transforms your DP from conceptual to efficient.

6. Meta-DP: Transformations

- Compress dimensions: if only `dp[i-1]` needed, use 1D array.- Invert loops: bottom-up top-down.- Change base: prefix-sums for range queries.- State lifting: add dimension for new property (like remainder, parity, bitmask). > "When stuck, add a dimension. When slow, remove one."

7. Common Template Snippets

Rolling 1D Knapsack:

```
for (c = C; c >= w[i]; c--)
  dp[c] = max(dp[c], dp[c-w[i]] + val[i]);
```

Top-Down Memoization:

```
int solve(state):
  if (visited[state]) return dp[state];
  dp[state] = combine(solve(next_states));
```

Iterative DP:

```
for (state in order)
  dp[state] = merge(prev_states);
```

8. Building Your Own DP Framework

You can design a generic `DP(state, transition)` class:

```
struct DP {
    vector<long long> dp;
    function<long long(int,int)> cost;
    DP(int n, auto cost): dp(n, INF), cost(cost) {}
    void solve() { for (int i=1; i<n; i++) for (int j=0; j<i; j++)
         dp[i] = min(dp[i], dp[j] + cost(j, i)); }
};
```

Reusable, readable, flexible.

9. Summary

DP Type	Core State	Shape	Typical Complexity
Line DP	dp[i]	Linear	$O(n^2) \to O(n)$
Grid DP	dp[i][j]	Matrix	$O(n \cdot m)$
Interval DP	dp[i][j]	Triangular	$O(n^3)$
Subset DP	dp[mask]	Exponential	$O(n \cdot 2$)
Tree DP	dp[u]	Tree	O(n)
Digit DP	dp[pos][sum]	Recursive	$O(\text{len} \cdot \text{sum})$
Graph DP	dp[v]	DAG	O(V+E)

Tiny Code

```
for (state in order)
  dp[state] = combine(all_prev(state));
```

Why It Matters

Meta-DP turns your thinking from case-by-case to pattern-by-pattern. You stop memorizing formulas and start *seeing shapes*: lines, grids, intervals, trees, masks.

Once you can name the shape, you can write the DP.

> "DP is not about filling tables. It's about recognizing structure."

Try It Yourself

1. Classify each classic DP problem into a type.
2. Write one template per pattern (Line, Grid, Tree, etc.).
3. Create a `dp_solve(state, transitions)` function to generalize logic.
4. For each pattern, practice a small example.
5. Build your own "Little Book of DP Patterns" with code snippets.

This is your bridge from concrete solutions to algorithmic fluency , the foundation for mastering the next 950 algorithms ahead.

Chapter 6. Strings and Text Algorithms

51. Number Theory (GCD, Modular Arithmetic, CRT)

Number theory forms the mathematical backbone of many algorithms , from hashing and cryptography to modular combinatorics and primality testing. In algorithmic problem-solving, it's all about working with integers, divisibility, and modular systems efficiently.

This section covers the essential toolkit:

- GCD and Extended Euclidean Algorithm- Modular Arithmetic (addition, subtraction, multiplication, inverse)- Modular Exponentiation- Chinese Remainder Theorem (CRT)

1. The Greatest Common Divisor (GCD)

The GCD of two integers a and b, denoted $\gcd(a, b)$, is the largest integer that divides both. It's the cornerstone for fraction simplification, Diophantine equations, and modular inverses.

A. Euclidean Algorithm

Based on:

$$\gcd(a, b) = \gcd(b, a \bmod b)$$

```
int gcd(int a, int b) {
    return b == 0 ? a : gcd(b, a % b);
}
```

Time complexity: $O(\log \min(a, b))$

B. Extended Euclidean Algorithm

Finds integers (x, y) such that:

$$ax + by = \gcd(a, b)$$

This is critical for finding modular inverses.

```
int ext_gcd(int a, int b, int &x, int &y) {
    if (b == 0) {
        x = 1; y = 0;
        return a;
    }
    int x1, y1;
    int g = ext_gcd(b, a % b, x1, y1);
    x = y1;
    y = x1 - (a / b) * y1;
    return g;
}
```

C. Bezout's Identity

If $g = \gcd(a, b)$, then $ax + by = g$ has integer solutions. If $g = 1$, x is the modular inverse of $amodulob$.

2. Modular Arithmetic

A modular system "wraps around" after a certain value (m).

We write:

$$a \equiv b \pmod{m} \quad \text{if } m \mid (a - b)$$

It behaves like ordinary arithmetic, with the rule:

- $(a + b) \bmod m = ((a \bmod m) + (b \bmod m)) \bmod m$
- $(a \cdot b) \bmod m = ((a \bmod m) \cdot (b \bmod m)) \bmod m$
- $(a - b) \bmod m = ((a \bmod m) - (b \bmod m) + m) \bmod m$

A. Modular Exponentiation

Compute $a^b \bmod m$ efficiently using binary exponentiation.

```
long long modpow(long long a, long long b, long long m) {
    long long res = 1;
    a %= m;
    while (b > 0) {
        if (b & 1) res = (res * a) % m;
        a = (a * a) % m;
        b >>= 1;
    }
    return res;
}
```

Complexity: (O$\log b$)

B. Modular Inverse

Given (a), find a^{-1} such that:

$$a \cdot a^{-1} \equiv 1 \pmod{m}$$

Case 1: If (m) is prime, use Fermat's Little Theorem:

$$a^{-1} \equiv a^{m-2} \pmod{m}$$

```
int modinv(int a, int m) {
    return modpow(a, m-2, m);
}
```

Case 2: If (a) and (m) are coprime, use Extended GCD:

```
int inv(int a, int m) {
    int x, y;
    int g = ext_gcd(a, m, x, y);
    if (g != 1) return -1; // no inverse
    return (x % m + m) % m;
}
```

C. Modular Division

To divide $a/b \bmod m$:

$$a/b \equiv a \cdot b^{-1} \pmod{m}$$

So compute the inverse and multiply.

3. Chinese Remainder Theorem (CRT)

The CRT solves systems of congruences:

$$x \equiv a_1 \pmod{m_1}$$

$$x \equiv a_2 \pmod{m_2}$$

If moduli $m_1, m_2, \ldots, m_k$ are pairwise coprime, there exists a unique solution modulo $M = m_1 m_2 \ldots m_k$.

A. 2-Equation Example

Solve:

$$x \equiv a_1 \pmod{m_1}, \quad x \equiv a_2 \pmod{m_2}$$

Let:

- $M = m_1 m_2$- $M_1 = M/m_1$- $M_2 = M/m_2$ Find inverses $inv_1 = M_1^{-1} \bmod m_1$, $inv_2 = M_2^{-1} \bmod m_2$

Then:

$$x = (a_1 \cdot M_1 \cdot inv_1 + a_2 \cdot M_2 \cdot inv_2) \bmod M$$

B. Implementation

```
long long crt(vector<int> a, vector<int> m) {
    long long M = 1;
    for (int mod : m) M *= mod;
    long long res = 0;
    for (int i = 0; i < a.size(); i++) {
        long long Mi = M / m[i];
        long long inv = modinv(Mi % m[i], m[i]);
        res = (res + 1LL * a[i] * Mi % M * inv % M) % M;
    }
    return (res % M + M) % M;
}
```

C. Example

Solve:

```
x   2 (mod 3)
x   3 (mod 5)
x   2 (mod 7)
```

Solution: (x = 23) (mod 105)

Check:

- (23 % 3 = 2)- (23 % 5 = 3)- (23 % 7 = 2)

4. Tiny Code

GCD

```
int gcd(int a, int b) { return b ? gcd(b, a % b) : a; }
```

Modular Power

```
modpow(a, b, m)
```

Modular Inverse

```
modinv(a, m)
```

CRT

```
crt(a[], m[])
```

5. Summary

Concept	Formula	Purpose
GCD	$\gcd(a, b) = \gcd(b, a \bmod b)$	Simplify ratios
Extended GCD	$ax + by = \gcd(a, b)$	Find modular inverse
Modular Inverse	$a^{-1} \equiv a^{m-2} \pmod{m}$	Solve modular equations
Modular Exp	$a^b \bmod m$	Fast exponentiation
CRT	Combine congruences	Multi-mod system

Why It Matters

Number theory lets algorithms speak the language of integers , turning huge computations into modular games. From hashing to RSA, from combinatorics to cryptography, it's everywhere.

> "When numbers wrap around, math becomes modular , and algorithms become magical."

Try It Yourself

1. Compute gcd(48, 180).
2. Find inverse of 7 mod 13.
3. Solve $x \equiv 1 \pmod{2}, x \equiv 2 \pmod{3}, x \equiv 3 \pmod{5}$.
4. Implement modular division $a/b \bmod m$.
5. Use modpow to compute 3^{200} mod 13.

These basics unlock higher algorithms in cryptography, combinatorics, and beyond.

52. Primality and Factorization (Miller-Rabin, Pollard Rho)

Primality and factorization are core to number theory, cryptography, and competitive programming. Many modern systems (RSA, ECC) rely on the hardness of factoring large numbers. Here, we learn how to test if a number is prime and break it into factors efficiently.

We'll cover:

- Trial Division
- Sieve of Eratosthenes (for precomputation)
- Probabilistic Primality Test (Miller-Rabin)
- Integer Factorization (Pollard Rho)

1. Trial Division

The simplest way to test primality is by dividing by all integers up to $\sqrt{n}$.

```
bool is_prime(long long n) {
    if (n < 2) return false;
    if (n % 2 == 0) return n == 2;
    for (long long i = 3; i * i <= n; i += 2)
        if (n % i == 0) return false;
    return true;
}
```

Time Complexity: ($O\sqrt{n}$) Good for $n \leq 10^6$, impractical for large (n).

2. Sieve of Eratosthenes

For checking many numbers at once, use a sieve.

Idea: Mark all multiples of each prime starting from 2.

```
vector<bool> sieve(int n) {
    vector<bool> is_prime(n+1, true);
    is_prime[0] = is_prime[1] = false;
    for (int i = 2; i * i <= n; i++)
        if (is_prime[i])
            for (int j = i * i; j <= n; j += i)
                is_prime[j] = false;
    return is_prime;
}
```

Time Complexity: ($On \log \log n$)

Useful for generating primes up to 10^7.

3. Modular Multiplication

Before we do probabilistic tests or factorization, we need safe modular multiplication for large numbers.

```
long long modmul(long long a, long long b, long long m) {
    __int128 res = (__int128)a * b % m;
    return (long long)res;
}
```

Avoid overflow for $n \approx 10^{18}$.

4. Miller-Rabin Primality Test

A probabilistic test that can check if (n) is prime or composite in ($Ok \log^3 n$).

Idea: For a prime (n):

$$a^{n-1} \equiv 1 \pmod{n}$$

But for composites, most (a) fail this.

We write $n - 1 = 2^s \cdot d$, (d) odd.

For each base (a):

- Compute $x = a^d \bmod n$- If (x = 1) or (x = n - 1), pass- Else, square (s-1) times- If none equal (n - 1), composite

```
bool miller_rabin(long long n) {
    if (n < 2) return false;
    for (long long p : {2,3,5,7,11,13,17,19,23,29,31,37})
        if (n % p == 0) return n == p;
    long long d = n - 1, s = 0;
    while ((d & 1) == 0) d >>= 1, s++;
    auto modpow = [&](long long a, long long b) {
        long long r = 1;
        while (b) {
            if (b & 1) r = modmul(r, a, n);
            a = modmul(a, a, n);
            b >>= 1;
```

```
        }
        return r;
    };
    for (long long a : {2, 325, 9375, 28178, 450775, 9780504, 1795265022}) {
        if (a % n == 0) continue;
        long long x = modpow(a, d);
        if (x == 1 || x == n - 1) continue;
        bool composite = true;
        for (int r = 1; r < s; r++) {
            x = modmul(x, x, n);
            if (x == n - 1) {
                composite = false;
                break;
            }
        }
        if (composite) return false;
    }
    return true;
}
```

Deterministic for:

- $n < 2^{64}$ with bases above. Complexity: ($Ok \log^3 n$)

5. Pollard Rho Factorization

Efficient for finding nontrivial factors of large composites. Based on Floyd's cycle detection (Tortoise and Hare).

Idea: Define a pseudo-random function:

$$f(x) = (x^2 + c) \bmod n$$

Then find $\gcd(|x - y|, n)$ where x, y move at different speeds.

```
long long pollard_rho(long long n) {
    if (n % 2 == 0) return 2;
    auto f = [&](long long x, long long c) {
        return (modmul(x, x, n) + c) % n;
    };
    while (true) {
        long long x = rand() % (n - 2) + 2;
```

```
        long long y = x;
        long long c = rand() % (n - 1) + 1;
        long long d = 1;
        while (d == 1) {
            x = f(x, c);
            y = f(f(y, c), c);
            d = gcd(abs(x - y), n);
        }
        if (d != n) return d;
    }
}
```

Use:

1. Check if (n) is prime (Miller-Rabin)
2. If not, find a factor using Pollard Rho
3. Recurse on factors

Complexity: $\sim$ ($On^{1/4}$) average

6. Example

Factorize (n = 8051):

1. Miller-Rabin $\rightarrow$ composite
2. Pollard Rho $\rightarrow$ factor 83
3. (8051 / 83 = 97)
4. Both primes ($8051 = 83 \times 97$)

7. Tiny Code

```
void factor(long long n, vector<long long> &f) {
    if (n == 1) return;
    if (miller_rabin(n)) {
        f.push_back(n);
        return;
    }
    long long d = pollard_rho(n);
    factor(d, f);
    factor(n / d, f);
}
```

Call `factor(n, f)` to get prime factors.

8. Summary

Algorithm	Purpose	Complexity	Type
Trial Division	Small primes	($O\sqrt{n}$)	Deterministic
Sieve	Precompute primes	($On \log \log n$)	Deterministic
Miller-Rabin	Primality test	($Ok \log^3 n$)	Probabilistic
Pollard Rho	Factorization	($On^{1/4}$)	Probabilistic

Why It Matters

Modern security, number theory problems, and many algorithmic puzzles depend on knowing when a number is prime and factoring it quickly when it isn't. These tools are the entry point to RSA, modular combinatorics, and advanced cryptography.

Try It Yourself

1. Check if 97 is prime using trial division and Miller-Rabin.
2. Factorize 5959 (should yield 59×101).
3. Generate all primes 100 using a sieve.
4. Write a recursive factorizer using Pollard Rho + Miller-Rabin.
5. Measure performance difference between $\sqrt{n}$ trial and Pollard Rho for $n \approx 10^{12}$.

These techniques make huge numbers approachable , one factor at a time.

53. Combinatorics (Permutations, Combinations, Subsets)

Combinatorics is the art of counting structures , how many ways can we arrange, select, or group things? In algorithms, it's everywhere: DP transitions, counting paths, bitmask enumeration, and probabilistic reasoning. Here we'll build a toolkit for computing factorials, nCr, nPr, and subset counts, both exactly and under a modulus.

1. Factorials and Precomputation

Most combinatorial formulas rely on factorials:

$$n! = 1 \times 2 \times 3 \times \cdots \times n$$

We can precompute them modulo (m) (often $10^9 + 7$) for efficiency.

```
const int MOD = 1e9 + 7;
const int MAXN = 1e6;
long long fact[MAXN + 1], invfact[MAXN + 1];

long long modpow(long long a, long long b) {
    long long res = 1;
    while (b > 0) {
        if (b & 1) res = res * a % MOD;
        a = a * a % MOD;
        b >>= 1;
    }
    return res;
}

void init_factorials() {
    fact[0] = 1;
    for (int i = 1; i <= MAXN; i++)
        fact[i] = fact[i - 1] * i % MOD;
    invfact[MAXN] = modpow(fact[MAXN], MOD - 2);
    for (int i = MAXN - 1; i >= 0; i--)
        invfact[i] = invfact[i + 1] * (i + 1) % MOD;
}
```

Now you can compute (nCr) and (nPr) in (O(1)) time.

2. Combinations (nCr)

The number of ways to choose r items from (n) items:

$$C(n, r) = \frac{n!}{r!(n-r)!}$$

```
long long nCr(int n, int r) {
    if (r < 0 || r > n) return 0;
    return fact[n] * invfact[r] % MOD * invfact[n - r] % MOD;
}
```

Properties:

- $(C(n,0) = 1),\ (C(n,n) = 1)$
- $C(n,r) = C(n,n-r)$
- Pascal's Rule: $C(n,r) = C(n-1,r-1) + C(n-1,r)$

Example

(C(5, 2) = 10) There are 10 ways to pick 2 elements from a 5-element set.

3. Permutations (nPr)

Number of ways to arrange r elements chosen from (n):

$$P(n,r) = \frac{n!}{(n-r)!}$$

```
long long nPr(int n, int r) {
    if (r < 0 || r > n) return 0;
    return fact[n] * invfact[n - r] % MOD;
}
```

Example

(P(5, 2) = 20) Choosing 2 out of 5 elements and arranging them yields 20 orders.

4. Subsets and Power Set

Each element has 2 choices: include or exclude. Hence, number of subsets:

$$2^n$$

```
long long subsets_count(int n) {
    return modpow(2, n);
}
```

Enumerating subsets using bitmasks:

```
for (int mask = 0; mask < (1 << n); mask++) {
    for (int i = 0; i < n; i++)
        if (mask & (1 << i))
            ; // include element i
}
```

Total: 2^n subsets, (O$n2^n$) time to enumerate.

5. Multisets and Repetition

Number of ways to choose (r) items from (n) with repetition:

$$C(n + r - 1, r)$$

For example, number of ways to give 5 candies to 3 kids (each can get 0): (C(3+5-1, 5) = C(7,5) = 21)

6. Modular Combinatorics

When working modulo (p): - Use modular inverse for division. - $C(n, r) \bmod p = fact[n] \cdot invfact[r] \cdot invfact[n - r] \bmod p$

When $n \geq p$, use Lucas' Theorem:

$$C(n, r) \bmod p = C(n/p, r/p) \cdot C(n$$

7. Stirling and Bell Numbers (Advanced)

- Stirling Numbers of 2nd Kind: ways to partition (n) items into (k) non-empty subsets

$$S(n, k) = k \cdot S(n - 1, k) + S(n - 1, k - 1)$$

- Bell Numbers: total number of partitions

$$B(n) = \sum_{k=0}^{n} S(n, k)$$

Used in set partition and grouping problems.

8. Tiny Code

```
init_factorials();
printf("%lld\n", nCr(10, 3));  // 120
printf("%lld\n", nPr(10, 3));  // 720
printf("%lld\n", subsets_count(5)); // 32
```

9. Summary

Concept	Formula	Meaning	Example
Factorial	$n!$	All arrangements	$5! = 120$
Combination	$C(n,r) = \frac{n!}{r!(n-r)!}$	Choose	$C(5,2) = 10$
Permutation	$P(n,r) = \frac{n!}{(n-r)!}$	Arrange	$P(5,2) = 20$
Subsets	2^n	All combinations	$2^3 = 8$
Multisets	$C(n+r-1,r)$	Repetition allowed	$C(4,2) = 6$

Why It Matters

Combinatorics underlies probability, DP counting, and modular problems. You can't master competitive programming or algorithm design without counting possibilities correctly. It teaches how structure emerges from choice , and how to count it efficiently.

Try It Yourself

1. Compute $C(1000, 500) \bmod (10^9 + 7)$.
2. Count the number of 5-bit subsets with exactly 3 bits on, i.e. $C(5,3)$.
3. Write a loop to print all subsets of `{a, b, c, d}`.
4. Use Lucas' theorem for $C(10^6, 1000) \bmod 13$.
5. Implement Stirling recursion and print $S(5,2)$.

Every algorithmic counting trick , from Pascal's triangle to binomial theorem , starts right here.

54. Probability and Randomized Algorithms

Probability introduces controlled randomness into computation. Instead of deterministic steps, randomized algorithms use random choices to achieve speed, simplicity, or robustness. This section bridges probability theory and algorithm design , teaching how to model, analyze, and exploit randomness.

We'll cover:

- Probability Basics
- Expected Value
- Monte Carlo and Las Vegas Algorithms
- Randomized Data Structures and Algorithms

1. Probability Basics

Every event has a probability between 0 and 1.
If a sample space has n equally likely outcomes and k of them satisfy a condition, then

$$P(E) = \frac{k}{n}$$

Examples

- Rolling a fair die: $P(\text{even}) = \frac{3}{6} = \frac{1}{2}$
- Drawing an ace from a deck: $P(\text{ace}) = \frac{4}{52} = \frac{1}{13}$

Key Rules

- Complement: $P(\bar{E}) = 1 - P(E)$
- Addition: $P(A \cup B) = P(A) + P(B) - P(A \cap B)$
- Multiplication: $P(A \cap B) = P(A) \cdot P(B \mid A)$

2. Expected Value

The expected value is the weighted average of outcomes.

$$E[X] = \sum_i P(x_i) \cdot x_i$$

Example: Expected value of a die:

$$E[X] = \frac{1+2+3+4+5+6}{6} = 3.5$$

Properties:

- Linearity: $E[aX + bY] = aE[X] + bE[Y]$

- Useful for average-case analysis

In algorithms:

- Expected number of comparisons in QuickSort is $O(n \log n)$
- Expected time for hash table lookup is $O(1)$

3. Monte Carlo vs Las Vegas

Randomized algorithms are broadly two types:

Type	Output	Runtime	Example
Monte Carlo	May be wrong (probabilistically)	Fixed	Miller-Rabin Primality
Las Vegas	Always correct	Random runtime	Randomized QuickSort

Monte Carlo:

- Faster, approximate
- You can control error probability
- E.g. primality test returns "probably prime"

Las Vegas:

- Output guaranteed correct
- Runtime varies by luck
- E.g. QuickSort with random pivot

4. Randomization in Algorithms

Randomization helps break worst-case patterns.

A. Randomized QuickSort

Pick a random pivot instead of first element. Expected time becomes ($On \log n$) regardless of input order.

```
int partition(int a[], int l, int r) {
    int pivot = a[l + rand() % (r - l + 1)];
    // move pivot to end, then normal partition
}
```

This avoids adversarial inputs like sorted arrays.

B. Randomized Hashing

Hash collisions can be exploited by adversaries. Using random coefficients in hash functions makes attacks infeasible.

```
long long hash(long long x, long long a, long long b, long long p) {
    return (a * x + b) % p;
}
```

Pick random (a, b) for robustness.

C. Randomized Data Structures

1. Skip List: uses random levels for nodes Expected ($O \log n$) search/insert/delete
2. Treap: randomized heap priority + BST order Maintains balance in expectation

```
struct Node {
    int key, priority;
    Node *l, *r;
};
```

Randomized balancing gives good average performance without rotation logic.

D. Random Sampling

Pick random elements efficiently:

- Reservoir Sampling: sample (k) items from a stream of unknown size- Shuffle: Fisher-Yates Algorithm

```
for (int i = n - 1; i > 0; i--) {
    int j = rand() % (i + 1);
    swap(a[i], a[j]);
}
```

5. Probabilistic Guarantees

Randomized algorithms often use Chernoff bounds and Markov's inequality to bound errors:

- Markov: $P(X \geq kE[X]) \leq \frac{1}{k}$
- Chebyshev: $P(|X - E[X]| \geq c\sigma) \leq \frac{1}{c^2}$
- Chernoff: Exponentially small tail bounds

These ensure "with high probability" $(1 - \frac{1}{n^c})$ guarantees.

6. Tiny Code

Randomized QuickSort:

```
int partition(int arr[], int low, int high) {
    int pivotIdx = low + rand() % (high - low + 1);
    swap(arr[pivotIdx], arr[high]);
    int pivot = arr[high], i = low;
    for (int j = low; j < high; j++) {
        if (arr[j] < pivot) swap(arr[i++], arr[j]);
    }
    swap(arr[i], arr[high]);
    return i;
}

void quicksort(int arr[], int low, int high) {
    if (low < high) {
        int pi = partition(arr, low, high);
        quicksort(arr, low, pi - 1);
        quicksort(arr, pi + 1, high);
    }
}
```

7. Summary

Concept	Key Idea	Use Case
Expected Value	Weighted average outcome	Analyze average case
Monte Carlo	Probabilistic correctness	Primality test
Las Vegas	Probabilistic runtime	QuickSort
Random Pivot	Break worst-case	Sorting
Skip List / Treap	Random balancing	Data Structures

Concept	Key Idea	Use Case
Reservoir Sampling	Stream selection	Large data

Why It Matters

Randomization is not "luck" , it's a design principle. It transforms rigid algorithms into adaptive, robust systems. In complexity theory, randomness helps achieve bounds impossible deterministically.

> "A bit of randomness turns worst cases into best friends."

Try It Yourself

1. Simulate rolling two dice and compute expected sum.
2. Implement randomized QuickSort and measure average runtime.
3. Write a Monte Carlo primality checker.
4. Create a random hash function for integers.
5. Implement reservoir sampling for a large input stream.

These experiments show how uncertainty can become a powerful ally in algorithm design.

55. Sieve Methods and Modular Math

Sieve methods are essential tools in number theory for generating prime numbers, prime factors, and function values (,) efficiently. Combined with modular arithmetic, they form the backbone of algorithms in cryptography, combinatorics, and competitive programming.

This section introduces:

- Sieve of Eratosthenes- Optimized Linear Sieve- Sieve for Smallest Prime Factor (SPF)- Euler's Totient Function ( )- Modular Applications

1. The Sieve of Eratosthenes

The classic algorithm to find all primes (n).

Idea: Start from 2, mark all multiples as composite. Continue to $\sqrt{n}$.

```cpp
vector<int> sieve(int n) {
    vector<int> primes;
    vector<bool> is_prime(n + 1, true);
    is_prime[0] = is_prime[1] = false;
    for (int i = 2; i * i <= n; i++)
        if (is_prime[i])
            for (int j = i * i; j <= n; j += i)
                is_prime[j] = false;
    for (int i = 2; i <= n; i++)
        if (is_prime[i]) primes.push_back(i);
    return primes;
}
```

Time Complexity: (O$n \log \log n$)

Space: (O(n))

Example: Primes up to 20 $\rightarrow$ 2, 3, 5, 7, 11, 13, 17, 19

2. Linear Sieve (O(n))

Unlike the basic sieve, each number is marked exactly once by its smallest prime factor (SPF).

Idea:

- For each prime (p), mark $p \times i$ only once.- Use `spf[i]` to store smallest prime factor.

```cpp
const int N = 1e6;
int spf[N + 1];
vector<int> primes;

void linear_sieve() {
    for (int i = 2; i <= N; i++) {
        if (!spf[i]) {
            spf[i] = i;
            primes.push_back(i);
        }
        for (int p : primes) {
            if (p > spf[i] || 1LL * i * p > N) break;
            spf[i * p] = p;
        }
    }
}
```

Benefits:

- Get primes, SPF, and factorizations in (O(n)).- Ideal for problems needing many factorizations.

3. Smallest Prime Factor (SPF) Table

With `spf[]`, factorization becomes ($O \log n$).

```
vector<int> factorize(int x) {
    vector<int> f;
    while (x != 1) {
        f.push_back(spf[x]);
        x /= spf[x];
    }
    return f;
}
```

Example: spf[12] = 2 → factors = [2, 2, 3]

4. Euler's Totient Function ((n))

The number of integers (n) that are coprime with (n).

Formula:

$$\varphi(n) = n \prod_{p|n} \left(1 - \frac{1}{p}\right)$$

Properties:

- $\varphi(p) = p - 1$ if p is prime
- Multiplicative: if $\gcd(a, b) = 1$, then $\varphi(ab) = \varphi(a)\varphi(b)$

Implementation (Linear Sieve):

```
const int N = 1e6;
int phi[N + 1];
bool is_comp[N + 1];
vector<int> primes;

void phi_sieve() {
    phi[1] = 1;
```

```
    for (int i = 2; i <= N; i++) {
        if (!is_comp[i]) {
            primes.push_back(i);
            phi[i] = i - 1;
        }
        for (int p : primes) {
            if (1LL * i * p > N) break;
            is_comp[i * p] = true;
            if (i % p == 0) {
                phi[i * p] = phi[i] * p;
                break;
            } else {
                phi[i * p] = phi[i] * (p - 1);
            }
        }
    }
}
```

Example:

- $\varphi(6) = 6(1 - \frac{1}{2})(1 - \frac{1}{3}) = 2$
- Numbers coprime with 6: 1, 5

5. Modular Math Applications

Once we have primes and totients, we can do many modular computations.

A. Fermat's Little Theorem

If (p) is prime,

$$a^{p-1} \equiv 1 \pmod{p}$$

Hence,

$$a^{-1} \equiv a^{p-2} \pmod{p}$$

Used in: modular inverses, combinatorics.

B. Euler's Theorem

If $\gcd(a, n) = 1$, then

$$a^{\varphi(n)} \equiv 1 \pmod{n}$$

Generalizes Fermat's theorem to composite moduli.

C. Modular Exponentiation with Totient Reduction

For very large powers:

$$a^b \bmod n = a^{b \bmod \varphi(n)} \bmod n$$

(when a and n are coprime)

6. Tiny Code

Primes up to n:

```
auto primes = sieve(100);
```

Totients up to n:

```
phi_sieve();
cout << phi[10]; // 4
```

Factorization:

```
auto f = factorize(60); // [2, 2, 3, 5]
```

Concept	Description	Time	Use

7. Summary

Concept	Description	Time	Use
Eratosthenes	Mark multiples	(O$n \log \log n$)	Simple prime gen
Linear Sieve	Mark once	(O(n))	Prime + SPF
SPF Table	Smallest prime factor	(O(1)) query	Fast factorization
(n)	Coprime count	(O(n))	Modular exponent
Fermat / Euler	Inverses, reduction	(O$\log n$)	Modular arithmetic

Why It Matters

Sieve methods are the fastest way to preprocess arithmetic information. They unlock efficient solutions to problems involving primes, divisors, modular equations, and cryptography.

> "Before you can reason about numbers, you must first sieve them clean."

Try It Yourself

1. Generate all primes $\leq 10^6$ using a linear sieve.
2. Factorize 840 using the SPF array.
3. Compute $\varphi(n)$ for $n = 1..20$.
4. Verify $a^{\varphi(n)} \equiv 1 \pmod{n}$ for $a = 3$, $n = 10$.
5. Solve $a^b \bmod n$ with b very large using $\varphi(n)$.

Sieve once, and modular math becomes effortless forever after.

56. Linear Algebra (Gaussian Elimination, LU, SVD)

Linear algebra gives algorithms their mathematical backbone. From solving equations to powering ML models, it's the hidden engine behind optimization, geometry, and numerical computation.

In this section, we'll focus on the algorithmic toolkit:

- Gaussian Elimination (solve systems, invert matrices)
- LU Decomposition (efficient repeated solving)
- SVD (Singular Value Decomposition) overview

You'll see how algebra becomes code , step by step.

1. Systems of Linear Equations

We want to solve:

$$A \cdot x = b$$

where (A) is an $n \times n$ matrix, and (x, b) are vectors.

For example:

$$\begin{cases} 2x + 3y = 8 \\ x + 2y = 5 \end{cases}$$

The solution is the intersection of two lines. In general, $A^{-1}b$ gives (x), but we usually solve it more directly using Gaussian elimination.

2. Gaussian Elimination (Row Reduction)

Idea: Transform ([A|b]) (augmented matrix) into upper-triangular form, then back-substitute.

Steps:

1. For each row, select a pivot (non-zero leading element).
2. Eliminate below it using row operations.
3. After all pivots, back-substitute to get the solution.

A. Implementation (C)

```
const double EPS = 1e-9;

vector<double> gauss(vector<vector<double>> A, vector<double> b) {
    int n = A.size();
    for (int i = 0; i < n; i++) {
        // 1. Find pivot
        int pivot = i;
        for (int j = i + 1; j < n; j++)
            if (fabs(A[j][i]) > fabs(A[pivot][i]))
                pivot = j;
        swap(A[i], A[pivot]);
        swap(b[i], b[pivot]);
```

```
        // 2. Normalize pivot row
        double div = A[i][i];
        if (fabs(div) < EPS) continue;
        for (int k = i; k < n; k++) A[i][k] /= div;
        b[i] /= div;

        // 3. Eliminate below
        for (int j = i + 1; j < n; j++) {
            double factor = A[j][i];
            for (int k = i; k < n; k++) A[j][k] -= factor * A[i][k];
            b[j] -= factor * b[i];
        }
    }

    // 4. Back substitution
    vector<double> x(n);
    for (int i = n - 1; i >= 0; i--) {
        x[i] = b[i];
        for (int j = i + 1; j < n; j++)
            x[i] -= A[i][j] * x[j];
    }
    return x;
}
```

Time complexity: (On^3)

B. Example

Solve:

$$\{2x + 3y = 8 \; x + 2y = 5$$

Augmented matrix:

$$[2 \quad 3 \quad | \quad 8 \, 1 \quad 2 \quad | \quad 5]$$

Reduce:

- Row2 ← Row2 − ½ Row1 → $[1, 2|5]$ → $[0, 0.5|1]$- Back substitute → (y = 2, x = 1)

3. LU Decomposition

LU factorization expresses:

$$A = L \cdot U$$

where (L) is lower-triangular (1s on diagonal), (U) is upper-triangular.

This allows solving (A x = b) in two triangular solves:

1. Solve (L y = b)
2. Solve (U x = y)

Efficient when solving for multiple b's (same A).

A. Decomposition Algorithm

```
void lu_decompose(vector<vector<double>>& A, vector<vector<double>>& L, vector<vector<double>
    int n = A.size();
    L.assign(n, vector<double>(n, 0));
    U.assign(n, vector<double>(n, 0));

    for (int i = 0; i < n; i++) {
        // Upper
        for (int k = i; k < n; k++) {
            double sum = 0;
            for (int j = 0; j < i; j++)
                sum += L[i][j] * U[j][k];
            U[i][k] = A[i][k] - sum;
        }
        // Lower
        for (int k = i; k < n; k++) {
            if (i == k) L[i][i] = 1;
            else {
                double sum = 0;
                for (int j = 0; j < i; j++)
                    sum += L[k][j] * U[j][i];
                L[k][i] = (A[k][i] - sum) / U[i][i];
            }
        }
    }
}
```

Solve with forward + backward substitution.

4. Singular Value Decomposition (SVD)

SVD generalizes diagonalization for non-square matrices:

$$A = U\Sigma V^T$$

Where:

- (U): left singular vectors (orthogonal)- Σ: diagonal of singular values- V^T: right singular vectors Applications:
- Data compression (PCA)- Noise reduction- Rank estimation- Pseudoinverse $A^+ = V\Sigma^{-1}U^T$ In practice, use libraries (e.g. LAPACK, Eigen).

5. Numerical Stability and Pivoting

In floating-point math:

- Always pick largest pivot (partial pivoting)- Avoid dividing by small numbers- Use EPS = 1e-9 threshold Small numerical errors can amplify quickly , stability is key.

6. Tiny Code

```
vector<vector<double>> A = {{2, 3}, {1, 2}};
vector<double> b = {8, 5};
auto x = gauss(A, b);
// Output: x = [1, 2]
```

7. Summary

Algorithm	Purpose	Complexity	Notes
Gaussian Elimination	Solve Ax=b	(On^3)	Direct method
LU Decomposition	Repeated solves	(On^3)	Triangular factorization
SVD	General decomposition	(On^3)	Robust, versatile

Why It Matters

Linear algebra is the language of algorithms , it solves equations, optimizes functions, and projects data. Whether building solvers or neural networks, these methods are your foundation.

> "Every algorithm lives in a vector space , it just needs a basis to express itself."

Try It Yourself

1. Solve a 3×3 linear system with Gaussian elimination.
2. Implement LU decomposition and test $L \cdot U = A$.
3. Use LU to solve multiple (b) vectors.
4. Explore SVD using a math library; compute singular values of a 2×2 matrix.
5. Compare results between naive and pivoted elimination for unstable systems.

Start with row operations , and you'll see how geometry and algebra merge into code.

57. FFT and NTT (Fast Transforms)

The Fast Fourier Transform (FFT) is one of the most beautiful and practical algorithms ever invented. It converts data between time (or coefficient) domain and frequency (or point) domain efficiently. The Number Theoretic Transform (NTT) is its modular counterpart for integer arithmetic , ideal for polynomial multiplication under a modulus.

This section covers:

- Why we need transforms- Discrete Fourier Transform (DFT)- Cooley-Tukey FFT (complex numbers)- NTT (modular version)- Applications (polynomial multiplication, convolution)

1. Motivation

Suppose you want to multiply two polynomials:

$$A(x) = a_0 + a_1 x + a_2 x^2$$

$$B(x) = b_0 + b_1 x + b_2 x^2$$

Their product has coefficients:

$$c_k = \sum_{i+j=k} a_i \cdot b_j$$

This is convolution:

$$C = A * B$$

Naively, this takes (On^2). FFT reduces it to ($On \log n$).

2. Discrete Fourier Transform (DFT)

The DFT maps coefficients $a_0, a_1, \ldots, a_{n-1}$ to evaluations at (n)-th roots of unity:

$$A_k = \sum_{j=0}^{n-1} a_j \cdot e^{-2\pi i \cdot jk/n}$$

and the inverse transform recovers a_j from A_k.

3. Cooley-Tukey FFT

Key idea: recursively split the sum into even and odd parts:

$$A_k = A_{even}(w_n^2) + w_n^k \cdot A_{odd}(w_n^2)$$

Where $w_n = e^{-2\pi i/n}$ is an (n)-th root of unity.

Implementation (C++)

```cpp
#include <complex>
#include <vector>
#include <cmath>
using namespace std;

using cd = complex<double>;
const double PI = acos(-1);

void fft(vector<cd> &a, bool invert) {
    int n = a.size();
    for (int i = 1, j = 0; i < n; i++) {
        int bit = n >> 1;
        for (; j & bit; bit >>= 1) j ^= bit;
        j ^= bit;
        if (i < j) swap(a[i], a[j]);
```

```
    }

    for (int len = 2; len <= n; len <<= 1) {
        double ang = 2 * PI / len * (invert ? -1 : 1);
        cd wlen(cos(ang), sin(ang));
        for (int i = 0; i < n; i += len) {
            cd w(1);
            for (int j = 0; j < len / 2; j++) {
                cd u = a[i + j], v = a[i + j + len / 2] * w;
                a[i + j] = u + v;
                a[i + j + len / 2] = u - v;
                w *= wlen;
            }
        }
    }

    if (invert) {
        for (cd &x : a) x /= n;
    }
}
```

Polynomial Multiplication with FFT

```
vector<long long> multiply(vector<int> const& a, vector<int> const& b) {
    vector<cd> fa(a.begin(), a.end()), fb(b.begin(), b.end());
    int n = 1;
    while (n < (int)a.size() + (int)b.size()) n <<= 1;
    fa.resize(n);
    fb.resize(n);

    fft(fa, false);
    fft(fb, false);
    for (int i = 0; i < n; i++) fa[i] *= fb[i];
    fft(fa, true);

    vector<long long> result(n);
    for (int i = 0; i < n; i++)
        result[i] = llround(fa[i].real());
    return result;
}
```

Complexity: ($On \log n$)

4. Number Theoretic Transform (NTT)

FFT uses complex numbers , NTT uses modular arithmetic with roots of unity mod p. We need a prime (p) such that:

$$p = c \cdot 2^k + 1$$

so a primitive root (g) exists.

Popular choices:

- (p = 998244353, g = 3)- (p = 7340033, g = 3)

Implementation (NTT)

```
const int MOD = 998244353;
const int G = 3;

int modpow(int a, int b) {
    long long res = 1;
    while (b) {
        if (b & 1) res = res * a % MOD;
        a = 1LL * a * a % MOD;
        b >>= 1;
    }
    return res;
}

void ntt(vector<int> &a, bool invert) {
    int n = a.size();
    for (int i = 1, j = 0; i < n; i++) {
        int bit = n >> 1;
        for (; j & bit; bit >>= 1) j ^= bit;
        j ^= bit;
        if (i < j) swap(a[i], a[j]);
    }
    for (int len = 2; len <= n; len <<= 1) {
        int wlen = modpow(G, (MOD - 1) / len);
        if (invert) wlen = modpow(wlen, MOD - 2);
        for (int i = 0; i < n; i += len) {
            long long w = 1;
```

```
            for (int j = 0; j < len / 2; j++) {
                int u = a[i + j];
                int v = (int)(a[i + j + len / 2] * w % MOD);
                a[i + j] = u + v < MOD ? u + v : u + v - MOD;
                a[i + j + len / 2] = u - v >= 0 ? u - v : u - v + MOD;
                w = w * wlen % MOD;
            }
        }
    }
    if (invert) {
        int inv_n = modpow(n, MOD - 2);
        for (int &x : a) x = 1LL * x * inv_n % MOD;
    }
}
```

5. Applications

1. Polynomial Multiplication: $O(n \log n)$
2. Convolution: digital signal processing
3. Big Integer Multiplication (Karatsuba, FFT)
4. Subset Convolution and combinatorial transforms
5. Number-theoretic sums (NTT-friendly modulus)

6. Tiny Code

```
vector<int> A = {1, 2, 3};
vector<int> B = {4, 5, 6};
// Result = {4, 13, 28, 27, 18}
auto C = multiply(A, B);
```

7. Summary

Algorithm	Domain	Complexity	Type
DFT	Complex	$O(n^2)$	Naive
FFT	Complex	$O(n \log n)$	Recursive
NTT	Modular	$O(n \log n)$	Integer arithmetic

Why It Matters

FFT and NTT bring polynomial algebra to life. They turn slow convolutions into lightning-fast transforms. From multiplying huge integers to compressing signals, they're the ultimate divide-and-conquer on structure.

> "To multiply polynomials fast, you first turn them into music , then back again."

Try It Yourself

1. Multiply $(1 + 2x + 3x^2)$ and $(4 + 5x + 6x^2)$ using FFT.
2. Implement NTT over 998244353 and verify results mod p.
3. Compare (On^2) vs FFT performance for n = 1024.
4. Experiment with inverse FFT (invert = true).
5. Explore circular convolution for signal data.

Once you master FFT/NTT, you hold the power of speed in algebraic computation.

58. Numerical Methods (Newton, Simpson, Runge-Kutta)

Numerical methods let us approximate solutions when exact algebraic answers are hard or impossible. They are the foundation of scientific computing, simulation, and optimization , bridging the gap between continuous math and discrete computation.

In this section, we'll explore three classics:

- Newton-Raphson: root finding- Simpson's Rule: numerical integration- Runge-Kutta (RK4): solving differential equations These algorithms showcase how iteration, approximation, and convergence build powerful tools.

1. Newton-Raphson Method

Used to find a root of (f(x) = 0). Starting from a guess x_0, iteratively refine:

$$x_{n+1} = x_n - \frac{f(x_n)}{f'(x_n)}$$

Convergence is quadratic if (f) is smooth and x_0 is close enough.

A. Example

Solve (f(x) = x^2 - 2 = 0) We know root = $\sqrt{2}$

Start $x_0 = 1$

Iter	x_n	(fx_n)	(f'x_n)	x_{n+1}
0	1.000	-1.000	2.000	1.500
1	1.500	0.250	3.000	1.417
2	1.417	0.006	2.834	1.414

Converged: $1.414 \approx \sqrt{2}$

B. Implementation

```c
#include <math.h>
#include <stdio.h>

double f(double x) { return x * x - 2; }
double df(double x) { return 2 * x; }

double newton(double x0) {
    for (int i = 0; i < 20; i++) {
        double fx = f(x0);
        double dfx = df(x0);
        if (fabs(fx) < 1e-9) break;
        x0 = x0 - fx / dfx;
    }
    return x0;
}

int main() {
    printf("Root: %.6f\n", newton(1.0)); // 1.414214
}
```

Time Complexity: (O(k)) iterations, each (O(1))

2. Simpson's Rule (Numerical Integration)

When you can't integrate (f(x)) analytically, approximate the area under the curve.

Divide interval ([a, b]) into even (n) subintervals (width (h)).

$$I \approx \frac{h}{3}\Big(f(a) + 4\sum f(x_{odd}) + 2\sum f(x_{even}) + f(b)\Big)$$

A. Implementation

```c
#include <math.h>
#include <stdio.h>

double f(double x) { return x * x; } // integrate x^2

double simpson(double a, double b, int n) {
    double h = (b - a) / n;
    double s = f(a) + f(b);
    for (int i = 1; i < n; i++) {
        double x = a + i * h;
        s += f(x) * (i % 2 == 0 ? 2 : 4);
    }
    return s * h / 3;
}

int main() {
    printf(" ¹ x² dx   %.6f\n", simpson(0, 1, 100)); // ~0.333333
}
```

Accuracy: (Oh^4) Note: (n) must be even.

B. Example

$$\int_0^1 x^2 dx = \frac{1}{3}$$

With (n = 100), Simpson gives (0.333333).

3. Runge-Kutta (RK4)

Used to solve first-order ODEs:

$$y' = f(x, y), \quad y(x_0) = y_0$$

RK4 Formula:

$$k_1 = f(x_n, y_n)\ k_2 \quad = f(x_n + \frac{h}{2}, y_n + \frac{h}{2}k_1)\ k_3 = f(x_n + \frac{h}{2}, y_n + \frac{h}{2}k_2)\ k_4 \quad = f(x_n + h, y_n + hk_3)\ y_{n+1} = y_n + \frac{h}{6}$$

Accuracy: (Oh^4)

A. Example

Solve (y' = x + y), (y(0) = 1), step (h = 0.1).

Each iteration refines (y) with weighted slope average.

B. Implementation

```c
#include <stdio.h>

double f(double x, double y) {
    return x + y;
}

double runge_kutta(double x0, double y0, double h, double xn) {
    double x = x0, y = y0;
    while (x < xn) {
        double k1 = f(x, y);
        double k2 = f(x + h / 2, y + h * k1 / 2);
        double k3 = f(x + h / 2, y + h * k2 / 2);
        double k4 = f(x + h, y + h * k3);
        y += h * (k1 + 2*k2 + 2*k3 + k4) / 6;
        x += h;
    }
    return y;
}
```

```c
int main() {
    printf("y(0.1)   %.6f\n", runge_kutta(0, 1, 0.1, 0.1));
}
```

4. Tiny Code Summary

Method	Purpose	Formula	Accuracy	Type
Newton-Raphson	Root finding	$x_{n+1} = x_n - \frac{f}{f'}$	Quadratic	Iterative
Simpson's Rule	Integration	(h/3(…))	(Oh^4)	Deterministic
Runge-Kutta (RK4)	ODEs	Weighted slope avg	(Oh^4)	Iterative

5. Numerical Stability

- Small step (h): better accuracy, more cost- Large (h): faster, less stable- Always check convergence ($|x_{n+1} - x_n| < \varepsilon$)- Avoid division by small derivatives in Newton's method

Why It Matters

Numerical methods let computers simulate the continuous world. From physics to AI training, they solve what calculus cannot symbolically.

> "When equations won't talk, iterate , and they'll whisper their answers."

Try It Yourself

1. Use Newton's method for $\cos x - x = 0$.
2. Approximate $\int_0^{\pi/2} \sin x \, dx$ with Simpson's rule.
3. Solve $y' = y - x^2 + 1,\ y(0) = 0.5$ using RK4.
4. Compare RK4 with Euler's method for the same ODE.
5. Experiment with step sizes $h \in \{0.1, 0.01, 0.001\}$ and observe convergence.

Numerical thinking turns continuous problems into iterative algorithms , precise enough to power every simulation and solver you'll ever write.

59. Mathematical Optimization (Simplex, Gradient, Convex)

Mathematical optimization is about finding the best solution , smallest cost, largest profit, shortest path , under given constraints. It's the heart of machine learning, operations research, and engineering design.

In this section, we'll explore three pillars:

- Simplex Method , for linear programs
- Gradient Descent , for continuous optimization
- Convex Optimization , the theory ensuring global optima

1. What Is Optimization?

A general optimization problem looks like:

$$\min_x \ f(x)$$

subject to constraints:

$$g_i(x) \leq 0, \quad h_j(x) = 0$$

When (f) and g_i, h_j are linear, it's a Linear Program (LP). When (f) is differentiable, we can use gradients. When (f) is convex, every local minimum is global , the ideal world.

2. The Simplex Method (Linear Programming)

A linear program has the form:

$$\max \ c^T x$$

subject to

$$Ax \leq b, \quad x \geq 0$$

Geometrically, each constraint forms a half-space. The feasible region is a convex polytope, and the optimum lies at a vertex.

A. Example

Maximize (z = 3x + 2y) subject to

$$\Big\{ 2x + y \leq 18 \ 2x + 3y \leq 42 \ x, y \geq 0$$

Solution: (x=9, y=8), (z=43)

B. Algorithm (Sketch)

1. Convert inequalities to equalities by adding slack variables.
2. Initialize at a vertex (basic feasible solution).
3. At each step:
    - Choose entering variable (most negative coefficient in objective). - Choose leaving variable (min ratio test). - Pivot to new vertex.4. Repeat until optimal.

C. Implementation (Simplified Pseudocode)

```
// Basic simplex-like outline
while (exists negative coefficient in objective row) {
    choose entering column j;
    choose leaving row i (min b[i]/a[i][j]);
    pivot(i, j);
}
```

Libraries (like `GLPK` or `Eigen`) handle full implementations.

Time Complexity: worst ($O2^n$), but fast in practice.

3. Gradient Descent

For differentiable (f(x)), we move opposite the gradient:

$$x_{k+1} = x_k - \eta \nabla f(x_k)$$

where η is the learning rate.

Intuition: (f(x)) points uphill, so step opposite it.

A. Example

Minimize (f(x) = (x-3)^2)

$$f'(x) = 2(x-3)$$

Start $x_0 = 0$, $\eta = 0.1$

Iter	x_k	(fx_k)	Gradient	New (x)
0	0	9	-6	0.6
1	0.6	5.76	-4.8	1.08
2	1.08	3.69	-3.84	1.46
...	→3	→0	→0	→3

Converges to (x = 3)

B. Implementation

```c
#include <math.h>
#include <stdio.h>

double f(double x) { return (x - 3) * (x - 3); }
double df(double x) { return 2 * (x - 3); }

double gradient_descent(double x0, double lr) {
    for (int i = 0; i < 100; i++) {
        double g = df(x0);
        if (fabs(g) < 1e-6) break;
        x0 -= lr * g;
    }
    return x0;
}

int main() {
    printf("Min at x = %.6f\n", gradient_descent(0, 0.1));
}
```

C. Variants

- Momentum: (v = v + 1 − β f(x))- Adam: adaptive learning rates- Stochastic Gradient Descent (SGD): random subset of data All used heavily in machine learning.

4. Convex Optimization

A function (f) is convex if:

$$f(\lambda x + (1-\lambda)y) \leq \lambda f(x) + (1-\lambda)f(y)$$

This means any local minimum is global.

Examples:

- (f(x) = x^2) (convex)- (f(x) = x^3) (not convex) For convex functions with linear constraints, gradient-based methods always converge to the global optimum.

A. Checking Convexity

- 1D: (f''(x) 0)- Multivariate: Hessian (^2 f(x)) is positive semidefinite

5. Applications

- Linear Programming (Simplex): logistics, scheduling- Quadratic Programming: portfolio optimization- Gradient Methods: ML, curve fitting- Convex Programs: control systems, regularization

6. Tiny Code

Simple gradient descent to minimize (f(x,y)=x^{2+y}2):

```
double f(double x, double y) { return x*x + y*y; }
void grad(double x, double y, double *gx, double *gy) {
    *gx = 2*x; *gy = 2*y;
}

void optimize() {
    double x=5, y=3, lr=0.1;
    for(int i=0; i<100; i++){
        double gx, gy;
```

```
        grad(x, y, &gx, &gy);
        x -= lr * gx;
        y -= lr * gy;
    }
    printf("Min at (%.3f, %.3f)\n", x, y);
}
```

7. Summary

Algorithm	Domain	Complexity	Notes
Simplex	Linear	Polynomial (average case)	LP solver
Gradient Descent	Continuous	$O(k)$	Needs step size
Convex Methods	Convex	$O(k \log \frac{1}{\varepsilon})$	Global optima guaranteed

Why It Matters

Optimization turns math into decisions. From fitting curves to planning resources, it formalizes trade-offs and efficiency. It's where computation meets purpose , finding the best in all possible worlds.

> "Every algorithm is, at heart, an optimizer , searching for something better."

Try It Yourself

1. Solve a linear program with 2 constraints manually via Simplex.
2. Implement gradient descent for $f(x) = (x - 5)^2 + 2$.
3. Add momentum to your gradient descent loop.
4. Check convexity by plotting $f(x) = x^4 - 3x^2$.
5. Experiment with learning rates: too small leads to slow convergence; too large can diverge.

Mastering optimization means mastering how algorithms improve themselves , step by step, iteration by iteration.

60. Algebraic Tricks and Transform Techniques

In algorithm design, algebra isn't just theory , it's a toolbox for transforming problems. By expressing computations algebraically, we can simplify, accelerate, or generalize solutions. This section surveys common algebraic techniques that turn hard problems into manageable ones.

We'll explore:

- Algebraic identities and factorizations
- Generating functions and transforms
- Convolution tricks
- Polynomial methods and FFT applications
- Matrix and linear transforms for acceleration

1. Algebraic Identities

These let you rewrite or decompose expressions to reveal structure or reduce complexity.

Classic Forms:

- Difference of squares:
$$a^2 - b^2 = (a - b)(a + b)$$
- Sum of cubes:
$$a^3 + b^3 = (a + b)(a^2 - ab + b^2)$$
- Square of sum:
$$(a + b)^2 = a^2 + 2ab + b^2$$

Used in dynamic programming, geometry, and optimization when simplifying recurrence terms or constraints.

Example: Transforming $(x + y)^2$ lets you compute both $x^2 + y^2$ and cross terms efficiently.

2. Generating Functions

A generating function encodes a sequence $a_0, a_1, a_2, ...$ into a formal power series:

$$G(x) = a_0 + a_1 x + a_2 x^2 + ...$$

They turn recurrence relations and counting problems into algebraic equations.

Example: Fibonacci sequence

$$F(x) = F_0 + F_1 x + F_2 x^2 + ...$$

with recurrence $F_n = F_{n-1} + F_{n-2}$

Solve algebraically:

$$F(x) = \frac{x}{1 - x - x^2}$$

Applications: combinatorics, probability, counting partitions.

3. Convolution Tricks

Convolution arises in combining sequences:

$$(c_n) = (a * b) * n = \sum *i = 0^n a_i b_{n-i}$$

Naive computation: (On^2) Using Fast Fourier Transform (FFT): (O$n \log n$)

Example: Polynomial multiplication Let

$$A(x) = a_0 + a_1 x + a_2 x^2, \quad B(x) = b_0 + b_1 x + b_2 x^2$$

Then (C(x) = A(x)B(x)) gives coefficients by convolution.

This trick is used in:

- Large integer multiplication- Pattern matching (cross-correlation)- Subset sum acceleration

4. Polynomial Methods

Many algorithmic problems can be represented as polynomials, where coefficients encode combinatorial structure.

A. Polynomial Interpolation

Given (n+1) points, there's a unique degree-(n) polynomial passing through them.

Used in error correction, FFT-based reconstruction, and number-theoretic transforms.

Lagrange Interpolation:

$$P(x) = \sum_i y_i \prod_{j \neq i} \frac{x - x_j}{x_i - x_j}$$

B. Root Representation

Solve equations or check identities by working modulo a polynomial. Used in finite fields and coding theory (e.g., Reed-Solomon).

5. Transform Techniques

Transforms convert problems to simpler domains where operations become efficient.

Transform	Converts	Key Property	Used In
FFT / NTT	Time Frequency	Convolution → Multiplication	Signal, polynomial mult
Z-Transform	Sequence Function	Recurrence solving	DSP, control
Laplace Transform	Function Algebraic	Diff. eq. → Algebraic eq.	Continuous systems
Walsh-Hadamard Transform	Boolean vectors	XOR convolution	Subset sum, SOS DP

Example: Subset Convolution via FWT

For all subsets (S):

$$f'(S) = \sum_{T \subseteq S} f(T)$$

Use Fast Walsh-Hadamard Transform (FWHT) to compute in (O$n2^n$) instead of (O3^n).

6. Matrix Tricks

Matrix algebra enables transformations and compact formulations.

- Matrix exponentiation: solve recurrences in $O(\log n)$
- Diagonalization: $A = PDP^{-1}$, then $A^k = PD^kP^{-1}$
- Fast power: speeds up Fibonacci, linear recurrences, Markov chains

Example: Fibonacci

$$\begin{bmatrix} F_{n+1} \\ F_n \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ 1 & 0 \end{bmatrix}^n \begin{bmatrix} 1 \\ 0 \end{bmatrix}$$

7. Tiny Code

Polynomial Multiplication via FFT (Pseudo-C):

```
// Outline using complex FFT library
fft(A, false);
fft(B, false);
for (int i = 0; i < n; i++)
    C[i] = A[i] * B[i];
fft(C, true); // inverse
```

Matrix Power (Fibonacci):

```
void matmul(long long A[2][2], long long B[2][2]) {
    long long C[2][2] = {{0}};
    for (int i=0;i<2;i++)
        for (int j=0;j<2;j++)
            for (int k=0;k<2;k++)
                C[i][j] += A[i][k]*B[k][j];
    memcpy(A, C, sizeof(C));
}

void matpow(long long A[2][2], int n) {
    long long R[2][2] = {{1,0},{0,1}};
    while(n){
        if(n&1) matmul(R,A);
        matmul(A,A);
        n>>=1;
    }
    memcpy(A, R, sizeof(R));
}
```

8. Summary

Technique	Purpose	Speedup
Algebraic Identities	Simplify expressions	Constant factor
Generating Functions	Solve recurrences	Conceptual
FFT / Convolution	Combine sequences fast	$(\mathrm{O}n^2 \to \mathrm{O}n \log n)$
Polynomial Interpolation	Reconstruction	$(\mathrm{O}n^2 \to \mathrm{O}n \log^2 n)$
Matrix Tricks	Accelerate recurrences	$(\mathrm{O}(\mathrm{n}) \to \mathrm{O}\log n)$

Why It Matters

Algebra turns computation into structure. By rewriting problems in algebraic form, you reveal hidden symmetries, exploit fast transforms, and find elegant solutions. It's not magic , it's the math beneath performance.

> "The smartest code is often the one that solves itself on paper first."

Try It Yourself

1. Multiply two polynomials using FFT.
2. Represent Fibonacci as a matrix and compute F_{100}.
3. Use generating functions to count coin change ways.
4. Implement subset sum via Walsh-Hadamard transform.
5. Derive a recurrence and solve it algebraically.

Understanding algebraic tricks makes you not just a coder, but a mathematical engineer , bending structure to will.

Chapter 7. Strings and Text Algorithms

61. String Matching (KMP, Z, Rabin-Karp, Boyer-Moore)

String matching is one of the oldest and most fundamental problems in computer science: given a text (T) of length (n) and a pattern (P) of length (m), find all positions where (P) appears in (T).

This section walks you through both naive and efficient algorithms , from the straightforward brute-force method to elegant linear-time solutions like KMP and Z-algorithm, and clever heuristics like Boyer-Moore and Rabin-Karp.

1. Problem Setup

We're given:

- Text: $T = t_1 t_2 \ldots t_n$- Pattern: $P = p_1 p_2 \ldots p_m$ Goal: find all (i) such that

$$T[i \ldots i + m - 1] = P[1 \ldots m]$$

Naive solution: compare (P) with every substring of (T) Time complexity: (O(nm))

We'll now see how to reduce it to (O(n + m)) or close.

2. Knuth-Morris-Pratt (KMP)

KMP avoids rechecking characters by precomputing overlaps within the pattern.

It builds a prefix-function (also called failure function), which tells how much to shift when a mismatch happens.

A. Prefix Function

For each position (i), compute $\pi[i]$ = length of longest prefix that's also a suffix of (P[1..i]).

Example: Pattern `ababc`

i	P[i]	[i]
1	a	0
2	b	0
3	a	1
4	b	2
5	c	0

B. Search Phase

Use $\pi[]$ to skip mismatched prefixes in the text.

Time Complexity: (O(n + m)) Space: (O(m))

Tiny Code (C)

```c
void compute_pi(char *p, int m, int pi[]) {
    pi[0] = 0;
    for (int i = 1, k = 0; i < m; i++) {
        while (k > 0 && p[k] != p[i]) k = pi[k-1];
        if (p[k] == p[i]) k++;
        pi[i] = k;
    }
}

void kmp_search(char *t, char *p) {
    int n = strlen(t), m = strlen(p);
    int pi[m]; compute_pi(p, m, pi);
    for (int i = 0, k = 0; i < n; i++) {
```

```
        while (k > 0 && p[k] != t[i]) k = pi[k-1];
        if (p[k] == t[i]) k++;
        if (k == m) {
            printf("Found at %d\n", i - m + 1);
            k = pi[k-1];
        }
    }
}
```

3. Z-Algorithm

Z-algorithm computes the Z-array,
where $Z[i]$ = length of the longest substring starting at i that matches the prefix of P.

To match P in T, build the string:

$$S = P + \# + T$$

Then every i where $Z[i] = |P|$ corresponds to a match.

Time: $O(n + m)$
Simple and elegant.

Example:

```
P = "aba", T = "ababa"
S = "aba#ababa"
Z = [0,0,1,0,3,0,1,0]
Match at index 0, 2
```

4. Rabin-Karp (Rolling Hash)

Instead of comparing strings character-by-character, compute a hash for each window in (T), and compare hashes.

$$h(s_1 s_2 \ldots s_m) = (s_1 b^{m-1} + s_2 b^{m-2} + \ldots + s_m) \bmod M$$

Use a rolling hash to update in (O(1)) per shift.

Time: average (O(n + m)), worst (O(nm)) Good for multiple pattern search.

Tiny Code (Rolling Hash)

```c
#define B 256
#define M 101

void rabin_karp(char *t, char *p) {
    int n = strlen(t), m = strlen(p);
    int h = 1, pHash = 0, tHash = 0;
    for (int i = 0; i < m-1; i++) h = (h*B) % M;
    for (int i = 0; i < m; i++) {
        pHash = (B*pHash + p[i]) % M;
        tHash = (B*tHash + t[i]) % M;
    }
    for (int i = 0; i <= n-m; i++) {
        if (pHash == tHash && strncmp(&t[i], p, m) == 0)
            printf("Found at %d\n", i);
        if (i < n-m)
            tHash = (B*(tHash - t[i]*h) + t[i+m]) % M;
        if (tHash < 0) tHash += M;
    }
}
```

5. Boyer-Moore (Heuristic Skipping)

Boyer-Moore compares from right to left and uses two heuristics:

1. Bad Character Rule When mismatch at (j), shift pattern so next occurrence of (T[i]) in (P) aligns.
2. Good Suffix Rule Shift pattern so a suffix of matched portion aligns with another occurrence.

Time: (O(n/m)) on average Practical and fast, especially for English text.

6. Summary

Algorithm	Time	Space	Idea	Best For
Naive	(O(nm))	(O(1))	Direct compare	Simple cases
KMP	(O(n+m))	(O(m))	Prefix overlap	General use
Z	(O(n+m))	(O(n+m))	Prefix matching	Pattern prep
Rabin-Karp	(O(n+m)) avg	(O(1))	Hashing	Multi-pattern
Boyer-Moore	(O(n/m)) avg	($Om + \sigma$)	Right-to-left skip	Long texts

Why It Matters

String matching powers text editors, DNA search, spam filters, and search engines. These algorithms show how structure and clever preprocessing turn brute force into elegance.

> "To find is human, to match efficiently is divine."

Try It Yourself

1. Implement KMP and print all matches in a sentence.
2. Use Rabin-Karp to find multiple keywords.
3. Compare running times on large text files.
4. Modify KMP for case-insensitive matching.
5. Visualize prefix function computation step-by-step.

By mastering these, you'll wield the foundation of pattern discovery , the art of finding order in streams of symbols.

62. Multi-Pattern Search (Aho-Corasick)

So far, we've matched one pattern against a text. But what if we have many patterns , say, a dictionary of keywords , and we want to find all occurrences of all patterns in a single pass?

That's where the Aho-Corasick algorithm shines. It builds a trie with failure links, turning multiple patterns into one efficient automaton. Think of it as "KMP for many words at once."

1. Problem Setup

Given:

- A text (T) of length (n)- A set of patterns $P_1, P_2, \ldots, P_k$ with total length $m = \sum |P_i|$

Goal: find all occurrences of every P_i in (T).

Naive solution: Run KMP for each pattern , (O(kn))

Better idea: Merge all patterns into a trie, and use failure links to transition on mismatches.

Aho-Corasick achieves O(n + m + z), where (z) = number of matches reported.

2. Trie Construction

Each pattern is inserted into a trie node-by-node.

Example Patterns:

```
he, she, his, hers
```

Trie:

```
(root)
   h   e*
       r   s*
   s   h   e*
   h   i   s*
```

Each node may mark an output (end of pattern).

3. Failure Links

Failure link of a node points to the longest proper suffix that's also a prefix in the trie.

These links let us "fall back" like KMP.

When mismatch happens, follow failure link to find next possible match.

Building Failure Links (BFS)

1. Root's failure = null
2. Children of root → failure = root
3. BFS over nodes:
    - For each edge ((u, c) → v): follow failure links from (u) until you find (f) with edge (c) then v.fail = $f.c$

Example

For "he", "she", "his", "hers":

- `fail("he") = root- fail("hers") = "rs"` path invalid → fallback to `"s"` if exists So failure links connect partial suffixes.

4. Matching Phase

Now we can process the text in one pass:

```
state = root
for each character c in text:
    while state has no child c and state != root:
        state = state.fail
    if state has child c:
        state = state.child[c]
    else:
        state = root
    if state.output:
        report matches at this position
```

Each transition costs O(1) amortized. No backtracking , fully linear time.

5. Example Walkthrough

Patterns: `he`, `she`, `his`, `hers` Text: `ahishers`

At each character:

```
a → root (no match)
h → go to h
i → go to hi
s → go to his → output "his"
h → fallback → h
e → he → output "he"
r → her → continue
s → hers → output "hers"
```

Outputs: `"his"`, `"he"`, `"hers"`

6. Tiny Code (C Implementation Sketch)

```c
#define ALPHA 26

typedef struct Node {
    struct Node *next[ALPHA];
    struct Node *fail;
    int out;
} Node;

Node* newNode() {
    Node *n = calloc(1, sizeof(Node));
    return n;
}

void insert(Node *root, char *p) {
    for (int i = 0; p[i]; i++) {
        int c = p[i] - 'a';
        if (!root->next[c]) root->next[c] = newNode();
        root = root->next[c];
    }
    root->out = 1;
}

void build_failures(Node *root) {
    Node *q[10000];
    int front=0, back=0;
    root->fail = root;
    q[back++] = root;
    while (front < back) {
        Node *u = q[front++];
        for (int c=0; c<ALPHA; c++) {
            Node *v = u->next[c];
            if (!v) continue;
            Node *f = u->fail;
            while (f != root && !f->next[c]) f = f->fail;
            if (f->next[c] && f->next[c] != v) v->fail = f->next[c];
            else v->fail = root;
            if (v->fail->out) v->out = 1;
            q[back++] = v;
        }
    }
}
```

7. Complexity

Phase	Time	Space
Trie Build	(O(m))	(O(m))
Failure Links	(O(m))	(O(m))
Search	(O(n + z))	(O(1))

Total: O(n + m + z)

8. Summary

Step	Purpose
Trie	Merge patterns
Fail Links	Handle mismatches
Outputs	Collect matches
BFS	Build efficiently
One Pass	Match all patterns

Why It Matters

Aho-Corasick is the core of:

- Spam filters- Intrusion detection (e.g., Snort IDS)- Keyword search in compilers- DNA sequence scanners It's a masterclass in blending automata theory with practical efficiency.

  "Why search one word at a time when your algorithm can read the whole dictionary?"

Try It Yourself

1. Build an automaton for words {"he", "she", "hers"} and trace it manually.
2. Modify code for uppercase letters.
3. Extend to report overlapping matches.
4. Measure runtime vs. naive multi-search.
5. Visualize the failure links in a graph.

Once you grasp Aho-Corasick, you'll see pattern search not as a loop , but as a machine that reads and recognizes.

63. Suffix Structures (Suffix Array, Suffix Tree, LCP)

Suffix-based data structures are among the most powerful tools in string algorithms. They enable fast searching, substring queries, pattern matching, and lexicographic operations , all from one fundamental idea:

> Represent all suffixes of a string in a structured form.

In this section, we explore three key constructs:

- Suffix Array (SA) - lexicographically sorted suffix indices- Longest Common Prefix (LCP) array - shared prefix lengths between neighbors- Suffix Tree - compressed trie of all suffixes Together, they power many advanced algorithms in text processing, bioinformatics, and compression.

1. Suffix Array (SA)

A suffix array stores all suffixes of a string in lexicographic order, represented by their starting indices.

Example: String `banana$` All suffixes:

Index	Suffix
0	banana$
1	anana$
2	nana$
3	ana$
4	na$
5	a$
6	$

Sort them:

Sorted Order	Suffix	Index
0	`$`	6
1	`a$`	5
2	`ana$`	3
3	`anana$`	1
4	`banana$`	0
5	`na$`	4
6	`nana$`	2

Suffix Array: `[6, 5, 3, 1, 0, 4, 2]`

Construction (Prefix Doubling)

We iteratively sort suffixes by first 2 characters, using radix sort on pairs of ranks.

Steps:

1. Assign initial rank by character.
2. Sort by (rank[i], rank[i+k]).
3. Repeat doubling $k \leftarrow 2k$ until all ranks distinct.

Time Complexity: (O$n \log n$) Space: (O(n))

Tiny Code (C, Sketch)

```c
typedef struct { int idx, rank[2]; } Suffix;
int cmp(Suffix a, Suffix b) {
    return (a.rank[0]==b.rank[0]) ? (a.rank[1]-b.rank[1]) : (a.rank[0]-b.rank[0]);
}

void buildSA(char *s, int n, int sa[]) {
    Suffix suf[n];
    for (int i = 0; i < n; i++) {
        suf[i].idx = i;
        suf[i].rank[0] = s[i];
        suf[i].rank[1] = (i+1<n) ? s[i+1] : -1;
    }
    for (int k = 2; k < 2*n; k *= 2) {
        qsort(suf, n, sizeof(Suffix), cmp);
        int r = 0, rank[n]; rank[suf[0].idx]=0;
        for (int i=1;i<n;i++) {
            if (suf[i].rank[0]!=suf[i-1].rank[0] || suf[i].rank[1]!=suf[i-1].rank[1]) r++;
            rank[suf[i].idx]=r;
        }
        for (int i=0;i<n;i++){
            suf[i].rank[0] = rank[suf[i].idx];
            suf[i].rank[1] = (suf[i].idx+k/2<n)?rank[suf[i].idx+k/2]:-1;
        }
    }
    for (int i=0;i<n;i++) sa[i]=suf[i].idx;
}
```

2. Longest Common Prefix (LCP)

The LCP array stores the length of the longest common prefix between consecutive suffixes in SA order.

Example: `banana$`

SA	Suffix	LCP
6	$	0
5	a$	0
3	ana$	1
1	anana$	3
0	banana$	0
4	na$	0
2	nana$	2

So LCP = `[0,0,1,3,0,0,2]`

Kasai's Algorithm (Build in O(n))

We compute LCP in one pass using inverse SA:

```
void buildLCP(char *s, int n, int sa[], int lcp[]) {
    int rank[n];
    for (int i=0;i<n;i++) rank[sa[i]]=i;
    int k=0;
    for (int i=0;i<n;i++) {
        if (rank[i]==n-1) { k=0; continue; }
        int j = sa[rank[i]+1];
        while (i+k<n && j+k<n && s[i+k]==s[j+k]) k++;
        lcp[rank[i]]=k;
        if (k>0) k--;
    }
}
```

Time Complexity: (O(n))

3. Suffix Tree

A suffix tree is a compressed trie of all suffixes.

Each edge holds a substring interval, not individual characters. This gives:

- Construction in (O(n)) (Ukkonen's algorithm)- Pattern search in (O(m))- Many advanced uses (e.g., longest repeated substring) Example: String: `banana$` Suffix tree edges:

```
(root)
   b[0:0] → ...
   a[1:1] → ...
   n[2:2] → ...
```

Edges compress consecutive letters into intervals like `[start:end]`.

Comparison

Structure	Space	Build Time	Search
Suffix Array	(O(n))	($On \log n$)	($Om \log n$)
LCP Array	(O(n))	(O(n))	Range queries
Suffix Tree	(O(n))	(O(n))	(O(m))

Suffix Array + LCP compact Suffix Tree.

4. Applications

1. Substring search - binary search in SA
2. Longest repeated substring - max(LCP)
3. Lexicographic order - direct from SA
4. Distinct substrings count = (n(n+1)/2 - LCP[i])
5. Pattern frequency - range query in SA using LCP

5. Tiny Code (Search via SA)

```c
int searchSA(char *t, int n, char *p, int sa[]) {
    int l=0, r=n-1, m=strlen(p);
    while (l <= r) {
        int mid = (l+r)/2;
        int cmp = strncmp(t+sa[mid], p, m);
        if (cmp==0) return sa[mid];
        else if (cmp<0) l=mid+1;
        else r=mid-1;
    }
    return -1;
}
```

6. Summary

Concept	Purpose	Complexity
Suffix Array	Sorted suffix indices	(O$n \log n$)
LCP Array	Adjacent suffix overlap	(O(n))
Suffix Tree	Compressed trie of suffixes	(O(n))

Together they form the core of advanced string algorithms.

Why It Matters

Suffix structures reveal hidden order in strings. They turn raw text into searchable, analyzable data , ideal for compression, search engines, and DNA analysis.

> "All suffixes, perfectly sorted , the DNA of text."

Try It Yourself

1. Build suffix array for `banana$` by hand.
2. Write code to compute LCP and longest repeated substring.
3. Search multiple patterns using binary search on SA.
4. Count distinct substrings from SA + LCP.
5. Compare SA-based vs. tree-based search performance.

Mastering suffix structures equips you to tackle problems that were once "too big" for brute force , now solvable with elegance and order.

64. Palindromes and Periodicity (Manacher)

Palindromes are symmetric strings that read the same forwards and backwards , like “level”, “racecar”, or “madam”. They arise naturally in text analysis, bioinformatics, and even in data compression.

This section introduces efficient algorithms to detect and analyze palindromic structure and periodicity in strings, including the legendary Manacher’s Algorithm, which finds all palindromic substrings in linear time.

1. What Is a Palindrome?

A string (S) is a palindrome if:

$$S[i] = S[n - i + 1] \quad \text{for all } i$$

Examples:

- `"abba"` is even-length palindrome- `"aba"` is odd-length palindrome A string may contain many palindromic substrings , our goal is to find all centers efficiently.

2. Naive Approach

For each center (between characters or at characters), expand outward while characters match.

```
for each center c:
    expand left, right while S[l] == S[r]
```

Complexity: (On^2) , too slow for large strings.

We need something faster , that’s where Manacher’s Algorithm steps in.

3. Manacher’s Algorithm (O(n))

Manacher’s Algorithm finds the radius of the longest palindrome centered at each position in linear time.

It cleverly reuses previous computations using mirror symmetry and a current right boundary.

Step-by-Step

1. Preprocess string to handle even-length palindromes: Insert `#` between characters.

   Example:

   ```
   S = "abba"
   T = "^#a#b#b#a#$"
   ```

   (`^` and `$` are sentinels)

2. Maintain:

   - `C`: center of rightmost palindrome - `R`: right boundary - `P[i]`: palindrome radius at `i`

3. For each position `i`:

   - mirror position `mirror = 2*C - i` - initialize `P[i] = min(R - i, P[mirror])` - expand around `i` while characters match - if new palindrome extends past `R`, update `C` and `R`

4. The maximum value of `P[i]` gives the longest palindrome.

Example

```
S = "abba"
T = "^#a#b#b#a#$"
P = [0,0,1,0,3,0,3,0,1,0,0]
Longest radius = 3 → "abba"
```

Tiny Code (C Implementation)

```c
int manacher(char *s) {
    int n = strlen(s);
    char t[2*n + 3];
    int p[2*n + 3];
    int m = 0;
    t[m++] = '^';
    for (int i=0;i<n;i++) {
        t[m++] = '#';
        t[m++] = s[i];
    }
    t[m++] = '#'; t[m++] = '$';
    t[m] = '\0';
```

```
    int c = 0, r = 0, maxLen = 0;
    for (int i=1; i<m-1; i++) {
        int mirror = 2*c - i;
        if (i < r)
            p[i] = (r - i < p[mirror]) ? (r - i) : p[mirror];
        else p[i] = 0;
        while (t[i + 1 + p[i]] == t[i - 1 - p[i]])
            p[i]++;
        if (i + p[i] > r) {
            c = i;
            r = i + p[i];
        }
        if (p[i] > maxLen) maxLen = p[i];
    }
    return maxLen;
}
```

Time Complexity: (O(n)) Space: (O(n))

4. Periodicity and Repetition

A string (S) has a period (p) if:

$$S[i] = S[i + p] \text{ for all valid } i$$

Example: `abcabcabc` has period 3 (`abc`).

Checking Periodicity:

1. Build prefix function (as in KMP).
2. Let (n = |S|), $p = n - \pi[n-1]$.
3. If $n \mod p = 0$, period = (p).

Example:

```
S = "abababab"
  = [0,0,1,2,3,4]
p = 6 - 4 = 2
6 mod 2 = 0 → periodic
```

Tiny Code (Check Periodicity)

```
int period(char *s) {
    int n = strlen(s), pi[n];
    pi[0]=0;
    for(int i=1,k=0;i<n;i++){
        while(k>0 && s[k]!=s[i]) k=pi[k-1];
        if(s[k]==s[i]) k++;
        pi[i]=k;
    }
    int p = n - pi[n-1];
    return (n % p == 0) ? p : n;
}
```

5. Applications

- Palindrome Queries: is substring (S[l:r]) palindrome? → precompute radii- Longest Palindromic Substring- DNA Symmetry Analysis- Pattern Compression / Period Detection- String Regularity Tests

6. Summary

Concept	Purpose	Time
Naive Expand	Simple palindrome check	(On^2)
Manacher	Longest palindromic substring	(O(n))
KMP Prefix	Period detection	(O(n))

Why It Matters

Palindromes reveal hidden symmetries. Manacher's algorithm is a gem , a linear-time mirror-based solution to a quadratic problem.

> "In every word, there may hide a reflection."

Try It Yourself

1. Run Manacher's algorithm on `"abacdfgdcaba"`.
2. Modify code to print all palindromic substrings.
3. Use prefix function to find smallest period.

4. Combine both to find palindromic periodic substrings.
5. Compare runtime vs. naive expand method.

Understanding palindromes and periodicity teaches how structure emerges from repetition , a central theme in all of algorithmic design.

65. Edit Distance and Alignment

Edit distance measures how different two strings are , the minimal number of operations needed to turn one into the other. It's a cornerstone of spell checking, DNA sequence alignment, plagiarism detection, and fuzzy search.

The most common form is the Levenshtein distance, using:

- Insertion (add a character)- Deletion (remove a character)- Substitution (replace a character) We'll also touch on alignment, which generalizes this idea with custom scoring and penalties.

1. Problem Definition

Given two strings (A) and (B), find the minimum number of edits to convert $A \to B$.

If (A = "kitten") (B = "sitting")

One optimal sequence:

```
kitten → sitten (substitute 'k'→'s')
sitten → sittin (substitute 'e'→'i')
sittin → sitting (insert 'g')
```

So edit distance = 3.

2. Dynamic Programming Solution

Let $dp[i][j]$ be the minimum edits to convert $A[0..i-1] \to B[0..j-1]$.

Recurrence:

$$dp[i][j] = \begin{cases} dp[i-1][j-1], & \text{if } A[i-1] = B[j-1], \\ 1 + \min\left(dp[i-1][j],\, dp[i][j-1],\, dp[i-1][j-1]\right), & \text{otherwise} \end{cases}$$

Where: - $dp[i-1][j]$: delete from A - $dp[i][j-1]$: insert into A - $dp[i-1][j-1]$: substitute

Base cases:

$$dp[0][j] = j, \quad dp[i][0] = i$$

Time complexity: $O(|A||B|)$

Example

A = `kitten`, B = `sitting`

	“ ”	s	i	t	t	i	n	g
“ ”	0	1	2	3	4	5	6	7
k	1	1	2	3	4	5	6	7
i	2	2	1	2	3	4	5	6
t	3	3	2	1	2	3	4	5
t	4	4	3	2	1	2	3	4
e	5	5	4	3	2	2	3	4
n	6	6	5	4	3	3	2	3

Edit distance = 3

Tiny Code (C)

```c
#include <stdio.h>
#include <string.h>
#define MIN3(a,b,c) ((a<b)?((a<c)?a:c):((b<c)?b:c))

int edit_distance(char *A, char *B) {
    int n = strlen(A), m = strlen(B);
    int dp[n+1][m+1];
    for (int i=0;i<=n;i++) dp[i][0]=i;
    for (int j=0;j<=m;j++) dp[0][j]=j;
    for (int i=1;i<=n;i++)
        for (int j=1;j<=m;j++)
            if (A[i-1]==B[j-1])
                dp[i][j]=dp[i-1][j-1];
            else
                dp[i][j]=1+MIN3(dp[i-1][j], dp[i][j-1], dp[i-1][j-1]);
    return dp[n][m];
}

int main() {
```

```
    printf("%d\n", edit_distance("kitten","sitting")); // 3
}
```

3. Space Optimization

We only need the previous row to compute the current row.

So,
Space complexity: $O(\min(|A|, |B|))$

```
int edit_distance_opt(char *A, char *B) {
    int n=strlen(A), m=strlen(B);
    int prev[m+1], curr[m+1];
    for(int j=0;j<=m;j++) prev[j]=j;
    for(int i=1;i<=n;i++){
        curr[0]=i;
        for(int j=1;j<=m;j++){
            if(A[i-1]==B[j-1]) curr[j]=prev[j-1];
            else curr[j]=1+MIN3(prev[j], curr[j-1], prev[j-1]);
        }
        memcpy(prev,curr,sizeof(curr));
    }
    return prev[m];
}
```

4. Alignment

Alignment shows which characters correspond between two strings. Used in bioinformatics (e.g., DNA sequence alignment).

Each operation has a cost:

- Match: 0
- Mismatch: 1
- Gap (insert/delete): 1 We fill the DP table similarly, but track choices to trace back alignment.

Example Alignment

```
A: kitten-
B: sitt-ing
```

We can visualize the transformation path by backtracking dp table.

Scoring Alignment (General Form)

We can generalize:

$$dp[i][j] = \min \Big\{ dp[i-1][j-1] + cost(A_i, B_j) \; dp[i-1][j] + gap \; dp[i][j-1] + gap$$

Used in Needleman-Wunsch (global alignment) and Smith-Waterman (local alignment).

5. Variants

- Damerau-Levenshtein: adds transposition (swap adjacent chars)- Hamming Distance: only substitutions, equal-length strings- Weighted Distance: different operation costs- Local Alignment: only best matching substrings

6. Summary

Method	Operations	Time	Use
Levenshtein	insert, delete, replace	(O(nm))	Spell check, fuzzy search
Hamming	substitution only	(O(n))	DNA, binary strings
Alignment (Needleman-Wunsch)	with scoring	(O(nm))	Bioinformatics
Local Alignment (Smith-Waterman)	best substring	(O(nm))	DNA regions

Why It Matters

Edit distance transforms "difference" into data. It quantifies how far apart two strings are, enabling flexible, robust comparisons.

> "Similarity isn't perfection , it's the cost of becoming alike."

Try It Yourself

1. Compute edit distance between “intention” and “execution”.
2. Trace back operations to show alignment.
3. Modify costs (insertion=2, deletion=1, substitution=2) and compare results.
4. Implement Hamming distance for equal-length strings.
5. Explore Smith-Waterman for longest common substring.

Once you master edit distance, you can build tools that understand typos, align genomes, and search imperfectly , perfectly.

66. Compression (Huffman, Arithmetic, LZ77, BWT)

Compression algorithms let us encode information efficiently, reducing storage or transmission cost without losing meaning. They turn patterns and redundancy into shorter representations , the essence of data compression.

This section introduces the key families of lossless compression algorithms that form the backbone of formats like ZIP, PNG, and GZIP.

We'll explore:

- Huffman Coding (prefix-free variable-length codes)
- Arithmetic Coding (fractional interval encoding)
- LZ77 / LZ78 (dictionary-based methods)
- Burrows-Wheeler Transform (BWT) (reversible sorting transform)

1. Huffman Coding

Huffman coding assigns shorter codes to frequent symbols, and longer codes to rare ones , achieving optimal compression among prefix-free codes.

A. Algorithm

1. Count frequencies of all symbols.
2. Build a min-heap of nodes `(symbol, freq)`.
3. While heap size > 1:
    - Extract two smallest nodes `a`, `b`. - Create new node with `freq = a.freq + b.freq`. - Push back into heap.4. Assign `0` to left, `1` to right.
4. Traverse tree , collect codes.

Each symbol gets a unique prefix code (no code is prefix of another).

B. Example

Text: `ABRACADABRA`

Frequencies:

Symbol	Count
A	5
B	2
R	2
C	1
D	1

Building tree gives codes like:

```
A: 0
B: 101
R: 100
C: 1110
D: 1111
```

Encoded text: `0 101 100 0 1110 0 1111 0 101 100 0` Compression achieved!

Tiny Code (C, Sketch)

```c
typedef struct Node {
    char ch;
    int freq;
    struct Node *left, *right;
} Node;
```

Use a min-heap (priority queue) to build the tree. Traverse recursively to print codewords.

Complexity: $(On \log n)$

2. Arithmetic Coding

Instead of mapping symbols to bit strings, arithmetic coding maps the entire message to a single number in [0,1).

We start with interval ([0,1)), and iteratively narrow it based on symbol probabilities.

Example

Symbols: {A: 0.5, B: 0.3, C: 0.2} Message: `ABC`

Intervals:

```
Start: [0, 1)
A → [0, 0.5)
B → [0.25, 0.4)
C → [0.34, 0.37)
```

Final code = any number in [0.34, 0.37) (e.g. 0.35)

Decoding reverses this process.

Advantage: achieves near-optimal entropy compression. Used in: JPEG2000, H.264

Time Complexity: (O(n))

3. LZ77 (Sliding Window Compression)

LZ77 replaces repeated substrings with back-references `(offset, length, next_char)` pointing into a sliding window.

Example

Text: `abcabcabcx`

Window slides; when `abc` repeats:

```
(0,0,'a'), (0,0,'b'), (0,0,'c'),
(3,3,'x')  // "abc" repeats from 3 chars back
```

So sequence is compressed as references to earlier substrings.

Used in: DEFLATE (ZIP, GZIP), PNG

Time: (O(n)), Space: proportional to window size.

Tiny Code (Conceptual)

```
struct Token { int offset, length; char next; };
```

Search previous window for longest match before emitting token.

4. LZ78 (Dictionary-Based)

Instead of sliding window, LZ78 builds an explicit dictionary of substrings.

Algorithm:

- Start with empty dictionary.- Read input, find longest prefix in dictionary.- Output `(index, next_char)` and insert new entry. Example:

```
Input: ABAABABAABAB
Output: (0,A), (0,B), (1,B), (2,A), (4,A), (3,B)
```

Used in: LZW (GIF, TIFF)

5. Burrows-Wheeler Transform (BWT)

BWT is not compression itself , it permutes text to cluster similar characters, making it more compressible by run-length or Huffman coding.

Steps

1. Generate all rotations of string.
2. Sort them lexicographically.
3. Take last column as output.

Example: `banana$`

Rotations	Sorted
banana$	*banana*||*anana*b
a*banan*|*na*bana	
banana|*nana*ba	

Last column: `annb$aa` BWT(“banana") = "*annb*aa”

Reversible with index of original row.

Used in: bzip2, FM-index (bioinformatics)

6. Summary

Algorithm	Idea	Complexity	Use
Huffman	Variable-length prefix codes	(O$n \log n$)	General compression
Arithmetic	Interval encoding	(O(n))	Near-optimal entropy
LZ77	Sliding window matches	(O(n))	ZIP, PNG
LZ78	Dictionary building	(O(n))	GIF, TIFF
BWT	Permute for clustering	(O$n \log n$)	bzip2

Why It Matters

Compression algorithms reveal structure in data , they exploit patterns that humans can't see. They're also a window into information theory, showing how close we can get to the entropy limit.

> "To compress is to understand , every bit saved is a pattern found."

Try It Yourself

1. Build a Huffman tree for `MISSISSIPPI`.
2. Implement a simple LZ77 encoder for repeating patterns.
3. Apply BWT and observe clustering of symbols.
4. Compare Huffman and Arithmetic outputs on same input.
5. Explore DEFLATE format combining LZ77 + Huffman.

Understanding compression means learning to see redundancy , the key to efficient storage, transmission, and understanding itself.

67. Cryptographic Hashes and Checksums

In algorithms, hashing helps us map data to fixed-size values. But when used for security and verification, hashing becomes a cryptographic tool. This section explores cryptographic hashes and checksums , algorithms that verify integrity, detect corruption, and secure data.

We'll look at:

- Simple checksums (parity, CRC)- Cryptographic hash functions (MD5, SHA family, BLAKE3)- Properties like collision resistance and preimage resistance- Practical uses in verification, signing, and storage

1. Checksums

Checksums are lightweight methods to detect accidental errors in data (not secure against attackers). They're used in filesystems, networking, and storage to verify integrity.

A. Parity Bit

Adds one bit to make total 1s even or odd. Used in memory or communication to detect single-bit errors.

Example: Data = `1011` → has three 1s. Add parity bit `1` to make total 4 (even parity).

Limitation: Only detects odd number of bit errors.

B. Modular Sum (Simple Checksum)

Sum all bytes (mod 256 or 65536).

Tiny Code (C)

```c
uint8_t checksum(uint8_t *data, int n) {
    uint32_t sum = 0;
    for (int i = 0; i < n; i++) sum += data[i];
    return (uint8_t)(sum % 256);
}
```

Use: Simple file or packet validation.

C. CRC (Cyclic Redundancy Check)

CRCs treat bits as coefficients of a polynomial. Divide by a generator polynomial, remainder = CRC code.

Used in Ethernet, ZIP, and PNG.

Example: CRC-32, CRC-16.

Fast hardware and table-driven implementations available.

Key Property:

- Detects most burst errors- Not cryptographically secure

2. Cryptographic Hash Functions

A cryptographic hash function (h(x)) maps any input to a fixed-size output such that:

1. Deterministic: same input → same output
2. Fast computation
3. Preimage resistance: hard to find (x) given (h(x))
4. Second-preimage resistance: hard to find $x' \neq x$ with (h(x') = h(x))
5. Collision resistance: hard to find any two distinct inputs with same hash

Algorithm	Output (bits)	Notes
MD5	128	Broken (collisions found)
SHA-1	160	Deprecated
SHA-256	256	Standard (SHA-2 family)
SHA-3	256	Keccak-based sponge
BLAKE3	256	Fast, parallel, modern

Example

```
h("hello") = 2cf24dba5fb0a... (SHA-256)
```

Change one letter, hash changes completely (avalanche effect):

```
h("Hello") = 185f8db32271f...
```

Even small changes → big differences.

Tiny Code (C, using pseudo-interface)

```c
#include <openssl/sha.h>

unsigned char hash[SHA256_DIGEST_LENGTH];
SHA256((unsigned char*)"hello", 5, hash);
```

Print hash as hex string to verify.

3. Applications

- Data integrity: verify files (e.g., SHA256SUM)- Digital signatures: sign hashes, not raw data- Password storage: store hashes, not plaintext- Deduplication: detect identical files via hashes- Blockchain: link blocks with hash pointers- Git: stores objects via SHA-1 identifiers

4. Hash Collisions

A collision occurs when (h(x) = h(y)) for $x \neq y$. Good cryptographic hashes make this computationally infeasible.

By the birthday paradox, collisions appear after $2^{n/2}$ operations for an (n)-bit hash.

Hence, SHA-256 $\rightarrow \sim 2^{128}$ effort to collide.

5. Checksums vs Hashes

Feature	Checksum	Cryptographic Hash
Goal	Detect errors	Ensure integrity and authenticity
Resistance	Low	High
Output Size	Small	128-512 bits
Performance	Very fast	Fast but secure
Example	CRC32	SHA-256, BLAKE3

Why It Matters

Checksums catch accidental corruption, hashes protect against malicious tampering. Together, they guard the trustworthiness of data , the foundation of secure systems.

> "Integrity is invisible , until it's lost."

Try It Yourself

1. Compute CRC32 of a text file, flip one bit, and recompute.
2. Use `sha256sum` to verify file integrity.
3. Experiment: change one character in input, observe avalanche.
4. Compare performance of SHA-256 and BLAKE3.
5. Research how Git uses SHA-1 to track versions.

By learning hashes, you master one of the pillars of security , proof that something hasn't changed, even when everything else does.

68. Approximate and Streaming Matching

Exact string matching (like KMP or Boyer-Moore) demands perfect alignment between pattern and text. But what if errors, noise, or incomplete data exist?

That's where approximate matching and streaming matching come in. These algorithms let you search efficiently even when:

- The pattern might contain typos or mutations- The text arrives in a stream (too large to store entirely)- You want to match "close enough," not "exactly" They're crucial in search engines, spell checkers, bioinformatics, and real-time monitoring systems.

1. Approximate String Matching

Approximate string matching finds occurrences of a pattern in a text allowing mismatches, insertions, or deletions , often measured by edit distance.

A. Dynamic Programming (Levenshtein Distance)

Given two strings A and B, the edit distance is the minimum number of insertions, deletions, or substitutions to turn A into B.

We can build a DP table $dp[i][j]$:

- $dp[i][0] = i$ (delete all characters)
- $dp[0][j] = j$ (insert all characters)
- If $A[i] = B[j]$, then $dp[i][j] = dp[i-1][j-1]$
- Else $dp[i][j] = 1 + \min(dp[i-1][j], dp[i][j-1], dp[i-1][j-1])$

Tiny Code (C)

```c
int edit_distance(char *a, char *b) {
    int n = strlen(a), m = strlen(b);
    int dp[n+1][m+1];
    for (int i = 0; i <= n; i++) dp[i][0] = i;
    for (int j = 0; j <= m; j++) dp[0][j] = j;
```

```
    for (int i = 1; i <= n; i++)
        for (int j = 1; j <= m; j++)
            if (a[i-1] == b[j-1]) dp[i][j] = dp[i-1][j-1];
            else dp[i][j] = 1 + fmin(fmin(dp[i-1][j], dp[i][j-1]), dp[i-1][j-1]);
    return dp[n][m];
}
```

This computes Levenshtein distance in (O(nm)) time.

B. Bitap Algorithm (Shift-Or)

When pattern length is small, Bitap uses bitmasks to track mismatches. It efficiently supports up to k errors and runs in near linear time for small patterns.

Used in grep -E, ag, and fuzzy searching systems.

Idea: Maintain a bitmask where 1 = mismatch, 0 = match. Shift and OR masks as we scan text.

C. k-Approximate Matching

Find all positions where edit distance k. Efficient for small (k) (e.g., spell correction: edit distance 2).

Applications:

- Typo-tolerant search- DNA sequence matching- Autocomplete systems

2. Streaming Matching

In streaming, the text is too large or unbounded, so we must process input online. We can't store everything , only summaries or sketches.

A. Rolling Hash (Rabin-Karp style)

Maintains a moving hash of recent characters. When new character arrives, update hash in (O(1)). Compare with pattern's hash for possible match.

Good for sliding window matching.

Example:

```
hash = (base * (hash - old_char * base^(m-1)) + new_char) % mod;
```

B. Fingerprinting (Karp-Rabin Fingerprint)

A compact representation of a substring. If fingerprints match, do full verification (avoid false positives). Used in streaming algorithms and chunking.

C. Sketch-Based Matching

Algorithms like Count-Min Sketch or SimHash build summaries of large data. They help approximate similarity between streams.

Applications:

- Near-duplicate detection (SimHash in Google)- Network anomaly detection- Real-time log matching

3. Approximate Matching in Practice

Domain	Use Case	Algorithm
Spell Checking	"recieve" → "receive"	Edit Distance
DNA Alignment	Find similar sequences	Smith-Waterman
Autocomplete	Suggest close matches	Fuzzy Search
Logs & Streams	Online pattern alerts	Streaming Bitap, Karp-Rabin
Near-Duplicate	Detect similar text	SimHash, MinHash

Algorithm	Time	Space	Notes

4. Complexity

Algorithm	Time	Space	Notes
Levenshtein DP	(O(nm))	(O(nm))	Exact distance
Bitap	(O(n))	(O(1))	For small patterns
Rolling Hash	(O(n))	(O(1))	Probabilistic match
SimHash	(O(n))	(O(1))	Approximate similarity

Why It Matters

Real-world data is messy , typos, noise, loss, corruption. Approximate matching lets you build algorithms that forgive errors and adapt to streams. It powers everything from search engines to genomics, ensuring your algorithms stay practical in an imperfect world.

Try It Yourself

1. Compute edit distance between "kitten" and "sitting."
2. Implement fuzzy search that returns words with 1 typo.
3. Use rolling hash to detect repeated substrings in a stream.
4. Experiment with SimHash to compare document similarity.
5. Observe how small typos affect fuzzy vs exact search.

69. Bioinformatics Alignment (Needleman-Wunsch, Smith-Waterman)

In bioinformatics, comparing DNA, RNA, or protein sequences is like comparing strings , but with biological meaning. Each sequence is made of letters (A, C, G, T for DNA; amino acids for proteins). To analyze similarity, scientists use sequence alignment algorithms that handle insertions, deletions, and substitutions.

Two fundamental methods dominate:

- Needleman-Wunsch for global alignment- Smith-Waterman for local alignment

1. Sequence Alignment

Alignment means placing two sequences side by side to maximize matches and minimize gaps or mismatches.

For example:

```
A C G T G A
| | |   | |
A C G A G A
```

Here, mismatches and gaps may occur, but the alignment finds the best possible match under a scoring system.

Scoring System

Alignment uses scores instead of just counts. Typical scheme:

- Match: +1- Mismatch: -1- Gap (insertion or deletion): -2 You can adjust weights depending on the biological context.

2. Needleman-Wunsch (Global Alignment)

Used when you want to align entire sequences , from start to end.

It uses dynamic programming to build a score table (dp[i][j]), where each cell represents the best score for aligning prefixes (A[1..i]) and (B[1..j]).

Recurrence:

$$dp[i][j] = \max \Big\{ dp[i-1][j-1] + \text{score}(A_i, B_j) \; dp[i-1][j] + \text{gap penalty} \; dp[i][j-1] + \text{gap penalty}$$

Base cases:

$$dp[0][j] = j \times \text{gap penalty}, \quad dp[i][0] = i \times \text{gap penalty}$$

Tiny Code (C)

```c
int max3(int a, int b, int c) {
    return a > b ? (a > c ? a : c) : (b > c ? b : c);
}

int needleman_wunsch(char *A, char *B, int match, int mismatch, int gap) {
    int n = strlen(A), m = strlen(B);
    int dp[n+1][m+1];
    for (int i = 0; i <= n; i++) dp[i][0] = i * gap;
    for (int j = 0; j <= m; j++) dp[0][j] = j * gap;

    for (int i = 1; i <= n; i++) {
        for (int j = 1; j <= m; j++) {
            int s = (A[i-1] == B[j-1]) ? match : mismatch;
            dp[i][j] = max3(dp[i-1][j-1] + s, dp[i-1][j] + gap, dp[i][j-1] + gap);
        }
    }
    return dp[n][m];
}
```

Example:

```
A = "ACGT"
B = "AGT"
match = +1, mismatch = -1, gap = -2
```

Produces optimal alignment:

```
A C G T
A - G T
```

3. Smith-Waterman (Local Alignment)

Used when sequences may have similar segments, not full-length similarity. Perfect for finding motifs or conserved regions.

Recurrence is similar, but with local reset to zero:

$$dp[i][j] = \max\Big\{0,\ dp[i-1][j-1] + \text{score}(A_i, B_j),\ dp[i-1][j] + \text{gap penalty},\ dp[i][j-1] + \text{gap penalty}$$

Final answer = maximum value in the table (not necessarily at the end).

It finds the best substring alignment.

Example

```
A = "ACGTTG"
B = "CGT"
```

Smith-Waterman finds best local match:

```
A C G T
  | | |
  C G T
```

Unlike global alignment, extra prefixes or suffixes are ignored.

4. Variants and Extensions

Algorithm	Type	Notes
Needleman-Wunsch	Global	Aligns full sequences
Smith-Waterman	Local	Finds similar subsequences
Gotoh Algorithm	Global	Uses affine gap penalty (opening + extension)
BLAST	Heuristic	Speeds up search for large databases

BLAST (Basic Local Alignment Search Tool) uses word seeds and extension, trading exactness for speed , essential for large genome databases.

5. Complexity

Both Needleman-Wunsch and Smith-Waterman run in:

- Time: (O(nm))- Space: (O(nm)) But optimized versions use banded DP or Hirschberg's algorithm to cut memory to (O(n + m)).

Why It Matters

Sequence alignment bridges computer science and biology. It's how we:

- Compare species- Identify genes- Detect mutations- Trace ancestry- Build phylogenetic trees The idea of "minimum edit cost" echoes everywhere , from spell checkers to DNA analysis.

  "In biology, similarity is a story. Alignment is how we read it."

Try It Yourself

1. Implement Needleman-Wunsch for short DNA sequences.
2. Change gap penalties , see how alignment shifts.
3. Compare outputs from global and local alignment.
4. Use real sequences from GenBank to test.
5. Explore BLAST online and compare to exact alignment results.

70. Text Indexing and Search Structures

When text becomes large , think books, databases, or the entire web , searching naively for patterns (O(nm)) is far too slow. We need indexing structures that let us search fast, often in O(m) or O(log n) time.

This section covers the backbone of search engines and string processing:

- Suffix Arrays- Suffix Trees- Inverted Indexes- Tries and Prefix Trees- Compressed Indexes like FM-Index (Burrows-Wheeler)

1. Why Index?

A text index is like a table of contents , it doesn't store the book, but lets you jump straight to what you want.

If you have a text of length (n), and you'll run many queries, it's worth building an index (even if it costs (O$n \log n$) to build).

Without indexing: each query takes (O(nm)). With indexing: each query can take (O(m)) or less.

2. Suffix Array

A suffix array is a sorted array of all suffixes of a string.

For text `"banana"`, suffixes are:

```
0: banana
1: anana
2: nana
3: ana
4: na
5: a
```

Sorted lexicographically:

```
5: a
3: ana
1: anana
0: banana
4: na
2: nana
```

Suffix Array = `[5, 3, 1, 0, 4, 2]`

To search, binary search over the suffix array using your pattern , ($Om \log n$).

Tiny Code (C) (naive construction)

```c
int cmp(const void *a, const void *b, void *txt) {
    int i = *(int*)a, j = *(int*)b;
    return strcmp((char*)txt + i, (char*)txt + j);
}

void build_suffix_array(char *txt, int n, int sa[]) {
    for (int i = 0; i < n; i++) sa[i] = i;
    qsort_r(sa, n, sizeof(int), cmp, txt);
}
```

Modern methods like prefix doubling or radix sort build it in ($On \log n$).

Applications:

- Fast substring search- Longest common prefix (LCP) array- Pattern matching in DNA sequences- Plagiarism detection

3. Suffix Tree

A suffix tree is a compressed trie of all suffixes , each edge stores multiple characters.

For `"banana"`, you'd build a tree where each leaf corresponds to a suffix index.

Advantages:

- Pattern search in (O(m))- Space (O(n)) (with compression) Built using Ukkonen's algorithm in (O(n)).

Use Suffix Array + LCP as a space-efficient alternative.

4. FM-Index (Burrows-Wheeler Transform)

Used in compressed full-text search (e.g., Bowtie, BWA). Combines:

- Burrows-Wheeler Transform (BWT)- Rank/select bitvectors Supports pattern search in O(m) time with very low memory.

Idea: transform text so similar substrings cluster together, enabling compression and backward search.

Applications:

- DNA alignment- Large text archives- Memory-constrained search

5. Inverted Index

Used in search engines. Instead of suffixes, it indexes words.

For example, text corpus:

```
doc1: quick brown fox
doc2: quick red fox
```

Inverted index:

```
"quick" → [doc1, doc2]
"brown" → [doc1]
"red"   → [doc2]
"fox"   → [doc1, doc2]
```

Now searching "quick fox" becomes set intersection of lists.

Used with ranking functions (TF-IDF, BM25).

6. Tries and Prefix Trees

A trie stores strings character by character. Each node = prefix.

```
typedef struct Node {
    struct Node *child[26];
    int end;
} Node;
```

Perfect for:

- Autocomplete- Prefix search- Spell checkers Search: O(m), where m = pattern length.

Compressed tries (Patricia trees) reduce space.

7. Comparing Structures

Structure	Search Time	Build Time	Space	Notes
Trie	O(m)	O(n)	High	Prefix queries
Suffix Array	O(m log n)	O(n log n)	Medium	Sorted suffixes
Suffix Tree	O(m)	O(n)	High	Rich structure
FM-Index	O(m)	O(n)	Low	Compressed
Inverted Index	O(k)	O(N)	Medium	Word-based

Why It Matters

Text indexing is the backbone of search engines, DNA alignment, and autocomplete systems. Without it, Google searches, code lookups, or genome scans would take minutes, not milliseconds.

> "Indexing turns oceans of text into navigable maps."

Try It Yourself

1. Build a suffix array for "banana" and perform binary search for "ana."
2. Construct a trie for a dictionary and query prefixes.
3. Write a simple inverted index for a few documents.
4. Compare memory usage of suffix tree vs suffix array.
5. Experiment with FM-index using an online demo (like BWT explorer).

Chapter 8. Geometry, Graphics, and Spatial Algorithms

71. Convex Hull (Graham, Andrew, Chan)

In computational geometry, the convex hull of a set of points is the smallest convex polygon that contains all the points. Intuitively, imagine stretching a rubber band around a set of nails on a board , the shape the band takes is the convex hull.

Convex hulls are foundational for many geometric algorithms, like closest pair, Voronoi diagrams, and collision detection.

In this section, we'll explore three classical algorithms:

- Graham Scan - elegant and simple (O(n log n))- Andrew's Monotone Chain - robust and practical (O(n log n))- Chan's Algorithm - advanced and optimal (O(n log h), where h = number of hull points)

1. Definition

Given a set of points $P = p_1, p_2, ..., p_n$, the convex hull, (CH(P)), is the smallest convex polygon enclosing all points.

Formally:

$$\text{CH}(P) = \bigcap C \subseteq \mathbb{R}^2 \mid C \text{ is convex and } P \subseteq C$$

A polygon is convex if every line segment between two points of the polygon lies entirely inside it.

2. Orientation Test

All convex hull algorithms rely on an orientation test using cross product: Given three points (a, b, c):

$$\text{cross}(a, b, c) = (b_x - a_x)(c_y - a_y) - (b_y - a_y)(c_x - a_x)$$

- `> 0` → counter-clockwise turn- `< 0` → clockwise turn- `= 0` → collinear

3. Graham Scan

One of the earliest convex hull algorithms.

Idea:

1. Pick the lowest point (and leftmost if tie).
2. Sort all other points by polar angle with respect to it.
3. Traverse points and maintain a stack:
    - Add point - While last three points make a right turn, pop middle one4. Remaining points form convex hull in CCW order.

Tiny Code (C)

```c
typedef struct { double x, y; } Point;

double cross(Point a, Point b, Point c) {
    return (b.x - a.x)*(c.y - a.y) - (b.y - a.y)*(c.x - a.x);
}

int cmp(const void *p1, const void *p2) {
    Point *a = (Point*)p1, *b = (Point*)p2;
    // Compare by polar angle or distance
    return (a->y != b->y) ? (a->y - b->y) : (a->x - b->x);
}

int graham_scan(Point pts[], int n, Point hull[]) {
    qsort(pts, n, sizeof(Point), cmp);
    int top = 0;
    for (int i = 0; i < n; i++) {
        while (top >= 2 && cross(hull[top-2], hull[top-1], pts[i]) <= 0)
            top--;
        hull[top++] = pts[i];
    }
    return top; // number of hull points
}
```

Complexity:

- Sorting: ($O n \log n$)- Scanning: (O(n)) $\rightarrow$ Total: O(n log n)

Example

Input:

```
(0, 0), (1, 1), (2, 2), (2, 0), (0, 2)
```

Hull (CCW):

```
(0,0) → (2,0) → (2,2) → (0,2)
```

4. Andrew's Monotone Chain

Simpler and more robust for floating-point coordinates. Builds lower and upper hulls separately.

Steps:

1. Sort points lexicographically (x, then y).
2. Build lower hull (left-to-right)
3. Build upper hull (right-to-left)
4. Concatenate (excluding duplicates)

Tiny Code (C)

```c
int monotone_chain(Point pts[], int n, Point hull[]) {
    qsort(pts, n, sizeof(Point), cmp);
    int k = 0;
    // Lower hull
    for (int i = 0; i < n; i++) {
        while (k >= 2 && cross(hull[k-2], hull[k-1], pts[i]) <= 0) k--;
        hull[k++] = pts[i];
    }
    // Upper hull
    for (int i = n-2, t = k+1; i >= 0; i--) {
        while (k >= t && cross(hull[k-2], hull[k-1], pts[i]) <= 0) k--;
        hull[k++] = pts[i];
    }
    return k-1; // last point == first point
}
```

Time Complexity: ($O n \log n$)

5. Chan's Algorithm

When $h \ll n$, Chan's method achieves (O$n \log h$):

1. Partition points into groups of size (m).
2. Compute hulls for each group (Graham).
3. Merge hulls with Jarvis March (gift wrapping).
4. Choose (m) cleverly ($m = 2^k$) to ensure (O$n \log h$).

Used in: large-scale geometric processing.

6. Applications

Domain	Use
Computer Graphics	Shape boundary, hitboxes
GIS / Mapping	Region boundaries
Robotics	Obstacle envelopes
Clustering	Outlier detection
Data Analysis	Minimal bounding shape

7. Complexity Summary

Algorithm	Time	Space	Notes
Graham Scan	(O$n \log n$)	(O(n))	Simple, classic
Monotone Chain	(O$n \log n$)	(O(n))	Stable, robust
Chan's Algorithm	(O$n \log h$)	(O(n))	Best asymptotic

Why It Matters

Convex hulls are one of the cornerstones of computational geometry. They teach sorting, cross products, and geometric reasoning , and form the basis for many spatial algorithms.

> "Every scattered set hides a simple shape. The convex hull is that hidden simplicity."

Try It Yourself

1. Implement Graham Scan for 10 random points.
2. Plot the points and verify the hull.
3. Compare results with Andrew's Monotone Chain.
4. Test with collinear and duplicate points.
5. Explore 3D convex hulls (QuickHull, Gift Wrapping) next.

72. Closest Pair and Segment Intersection

Geometric problems often ask: *what's the shortest distance between two points?* or *do these segments cross?* These are classic building blocks in computational geometry , essential for collision detection, graphics, clustering, and path planning.

This section covers two foundational problems:

- Closest Pair of Points - find two points with minimum Euclidean distance- Segment Intersection - determine if (and where) two line segments intersect

1. Closest Pair of Points

Given (n) points in 2D, find a pair with the smallest distance. The brute force solution is (On^2), but using Divide and Conquer, we can solve it in O(n log n).

A. Divide and Conquer Algorithm

Idea:

1. Sort points by x-coordinate.
2. Split into left and right halves.
3. Recursively find closest pairs in each half (distance = (d)).
4. Merge step: check pairs across the split line within (d).

In merge step, we only need to check at most 6 neighbors per point (by geometric packing).

Tiny Code (C, Sketch)

```c
#include <math.h>
typedef struct { double x, y; } Point;

double dist(Point a, Point b) {
    double dx = a.x - b.x, dy = a.y - b.y;
```

```
    return sqrt(dx*dx + dy*dy);
}

double brute_force(Point pts[], int n) {
    double d = 1e9;
    for (int i = 0; i < n; i++)
        for (int j = i + 1; j < n; j++)
            d = fmin(d, dist(pts[i], pts[j]));
    return d;
}
```

Recursive divide and merge:

```
double closest_pair(Point pts[], int n) {
    if (n <= 3) return brute_force(pts, n);
    int mid = n / 2;
    double d = fmin(closest_pair(pts, mid),
                    closest_pair(pts + mid, n - mid));
    // merge step: check strip points within distance d
    // sort by y, check neighbors
    return d;
}
```

Time Complexity: ($O n \log n$)

Example:

Points:

```
(2,3), (12,30), (40,50), (5,1), (12,10), (3,4)
```

Closest pair: (2,3) and (3,4), distance = $\sqrt{2}$

B. Sweep Line Variant

Another method uses a line sweep and a balanced tree to keep active points. As you move from left to right, maintain a window of recent points within (d).

Used in large-scale spatial systems.

Applications

Domain	Use
Clustering	Find nearest neighbors
Robotics	Avoid collisions
GIS	Nearest city search
Networking	Sensor proximity

2. Segment Intersection

Given two segments (AB) and (CD), determine whether they intersect. It's the core of geometry engines and vector graphics systems.

A. Orientation Test

We use the cross product (orientation) test again. Two segments (AB) and (CD) intersect if and only if:

1. The segments straddle each other:

$$\text{orient}(A, B, C) \neq \text{orient}(A, B, D)$$

$$\text{orient}(C, D, A) \neq \text{orient}(C, D, B)$$

2. Special cases for collinear points (check bounding boxes).

Tiny Code (C)

```c
double cross(Point a, Point b, Point c) {
    return (b.x - a.x)*(c.y - a.y) - (b.y - a.y)*(c.x - a.x);
}

int on_segment(Point a, Point b, Point c) {
    return fmin(a.x, b.x) <= c.x && c.x <= fmax(a.x, b.x) &&
           fmin(a.y, b.y) <= c.y && c.y <= fmax(a.y, b.y);
}

int intersect(Point a, Point b, Point c, Point d) {
    double o1 = cross(a, b, c);
    double o2 = cross(a, b, d);
```

```
    double o3 = cross(c, d, a);
    double o4 = cross(c, d, b);
    if (o1*o2 < 0 && o3*o4 < 0) return 1; // general case
    if (o1 == 0 && on_segment(a,b,c)) return 1;
    if (o2 == 0 && on_segment(a,b,d)) return 1;
    if (o3 == 0 && on_segment(c,d,a)) return 1;
    if (o4 == 0 && on_segment(c,d,b)) return 1;
    return 0;
}
```

B. Line Sweep Algorithm (Bentley-Ottmann)

For multiple segments, check all intersections efficiently. Algorithm:

1. Sort all endpoints by x-coordinate.
2. Sweep from left to right.
3. Maintain active set (balanced BST).
4. Check neighboring segments for intersections.

Time complexity: $O((n + k) \log n)$, where k is the number of intersections.

Used in CAD, map rendering, and collision systems.

3. Complexity Summary

Problem	Naive	Optimal	Technique
Closest Pair	$O(n^2)$	$O(n \log n)$	Divide & Conquer
Segment Intersection	$O(n^2)$	$O((n + k) \log n)$	Sweep Line

Why It Matters

Geometric algorithms like these teach how to reason spatially , blending math, sorting, and logic. They power real-world systems where precision matters: from self-driving cars to game engines.

> "Every point has a neighbor; every path may cross another , geometry finds the truth in space."

Try It Yourself

1. Implement the closest pair algorithm using divide and conquer.
2. Visualize all pairwise distances , see which pairs are minimal.
3. Test segment intersection on random pairs.
4. Modify for 3D line segments using vector cross products.
5. Try building a line sweep visualizer to catch intersections step-by-step.

73. Line Sweep and Plane Sweep Algorithms

The sweep line (or plane sweep) technique is one of the most powerful paradigms in computational geometry. It transforms complex spatial problems into manageable one-dimensional events , by sweeping a line (or plane) across the input and maintaining a dynamic set of active elements.

This method underlies many geometric algorithms:

- Event sorting → handle things in order- Active set maintenance → track current structure- Updates and queries → respond as the sweep progresses Used for intersection detection, closest pair, rectangle union, computational geometry in graphics and GIS.

1. The Core Idea

Imagine a vertical line sweeping from left to right across the plane. At each "event" (like a point or segment endpoint), we update the set of objects the line currently touches , the active set.

Each event may trigger queries, insertions, or removals.

This approach works because geometry problems often depend only on local relationships between nearby elements as the sweep advances.

A. Sweep Line Template

A general structure looks like this:

```
struct Event { double x; int type; Object *obj; };
sort(events.begin(), events.end());

ActiveSet S;

for (Event e : events) {
```

```
    if (e.type == START) S.insert(e.obj);
    else if (e.type == END) S.erase(e.obj);
    else if (e.type == QUERY) handle_query(S, e.obj);
}
```

Sorting ensures events are processed in order of increasing x (or another dimension).

2. Classic Applications

Let's explore three foundational problems solvable by sweep techniques.

A. Segment Intersection (Bentley-Ottmann)

Goal: detect all intersections among (n) line segments.

Steps:

1. Sort endpoints by x-coordinate.
2. Sweep from left to right.
3. Maintain an ordered set of active segments (sorted by y).
4. When a new segment starts, check intersection with neighbors above and below.
5. When segments intersect, record intersection and insert a new event at the x-coordinate of intersection.

Complexity: $O((n + k) \log n)$, where k is the number of intersections.

B. Closest Pair of Points

Sweep line version sorts by x, then slides a vertical line while maintaining active points within a strip of width (d) (current minimum). Only need to check at most 6-8 nearby points in strip.

Complexity: (O$n \log n$)

C. Rectangle Union Area

Given axis-aligned rectangles, compute total area covered.

Idea:

- Treat vertical edges as events (entering/exiting rectangles).- Sweep line moves along x-axis.- Maintain y-intervals in active set (using a segment tree or interval tree).- At each step, multiply current width × height of union of active intervals. Complexity: (O$n \log n$)

Tiny Code Sketch (C)

```c
typedef struct { double x, y1, y2; int type; } Event;
Event events[MAX];
int n_events;

qsort(events, n_events, sizeof(Event), cmp_by_x);

double prev_x = events[0].x, area = 0;
SegmentTree T;

for (int i = 0; i < n_events; i++) {
    double dx = events[i].x - prev_x;
    area += dx * T.total_length(); // current union height
    if (events[i].type == START)
        T.insert(events[i].y1, events[i].y2);
    else
        T.remove(events[i].y1, events[i].y2);
    prev_x = events[i].x;
}
```

3. Other Applications

Problem	Description	Time
K-closest points	Maintain top k in active set	$O(n \log n)$
Union of rectangles	Compute covered area	$O(n \log n)$
Point location	Locate point in planar subdivision	$O(\log n)$
Visibility graph	Track visible edges	$O(n \log n)$

4. Plane Sweep Extensions

While line sweep moves in one dimension (x), plane sweep handles 2D or higher-dimensional spaces, where:

- Events are 2D cells or regions.- Sweep front is a plane instead of a line. Used in 3D collision detection, computational topology, and CAD systems.

Conceptual Visualization

1. Sort events by one axis (say, x).
2. Maintain structure (set, tree, or heap) of intersecting or active elements.
3. Update at each event and record desired output (intersection, union, coverage).

The key is the locality principle: only neighbors in the sweep structure can change outcomes.

5. Complexity

Phase	Complexity
Sorting events	$O(n \log n)$
Processing events	$O(n \log n)$
Total	$O(n \log n)$ (typical)

Why It Matters

The sweep line method transforms geometric chaos into order , turning spatial relationships into sorted sequences. It's the bridge between geometry and algorithms, blending structure with motion.

> "A sweep line sees everything , not all at once, but just in time."

Try It Yourself

1. Implement a sweep-line segment intersection finder.
2. Compute the union area of 3 rectangles with overlaps.
3. Animate the sweep line to visualize event processing.
4. Modify for circular or polygonal objects.
5. Explore how sweep-line logic applies to time-based events in scheduling.

74. Delaunay and Voronoi Diagrams

In geometry and spatial computing, Delaunay triangulations and Voronoi diagrams are duals , elegant structures that capture proximity, territory, and connectivity among points.

They're used everywhere: from mesh generation, pathfinding, geospatial analysis, to computational biology. This section introduces both, their relationship, and algorithms to construct them efficiently.

1. Voronoi Diagram

Given a set of sites (points) $P = p_1, p_2, \ldots, p_n$, the Voronoi diagram partitions the plane into regions , one per point , so that every location in a region is closer to its site than to any other.

Formally, the Voronoi cell for p_i is:

$$V(p_i) = x \in \mathbb{R}^2 \mid d(x, p_i) \leq d(x, p_j), \forall j \neq i$$

Each region is convex, and boundaries are formed by perpendicular bisectors.

Example

For points (A, B, C):

- Draw bisectors between each pair.- Intersection points define Voronoi vertices.- Resulting polygons cover the plane, one per site. Used to model nearest neighbor regions , "which tower serves which area?"

Properties

- Every cell is convex.- Neighboring cells share edges.- The diagram's vertices are centers of circumcircles through three sites.- Dual graph = Delaunay triangulation.

2. Delaunay Triangulation

The Delaunay triangulation (DT) connects points so that no point lies inside the circumcircle of any triangle.

Equivalently, it's the dual graph of the Voronoi diagram.

It tends to avoid skinny triangles , maximizing minimum angles, creating well-shaped meshes.

Formal Definition

A triangulation (T) of (P) is Delaunay if for every triangle $\triangle abc \in T$, no point $p \in P \setminus a, b, c$ lies inside the circumcircle of $\triangle abc$.

Why It Matters:

- Avoids sliver triangles.- Used in finite element meshes, terrain modeling, and path planning.- Leads to natural neighbor interpolation and smooth surfaces.

3. Relationship

Voronoi and Delaunay are geometric duals:

Voronoi	Delaunay
Regions = proximity zones	Triangles = neighbor connections
Edges = bisectors	Edges = neighbor pairs
Vertices = circumcenters	Faces = circumcircles

Connecting neighboring Voronoi cells gives Delaunay edges.

4. Algorithms

Several algorithms can build these diagrams efficiently.

A. Incremental Insertion

1. Start with a super-triangle enclosing all points.
2. Insert points one by one.
3. Remove triangles whose circumcircle contains the point.
4. Re-triangulate the resulting polygonal hole.

Time Complexity: (On^2), improved to (O$n \log n$) with randomization.

B. Divide and Conquer

1. Sort points by x.
2. Recursively build DT for left and right halves.
3. Merge by finding common tangents.

Time Complexity: (O$n \log n$) Elegant, structured, and deterministic.

C. Fortune's Sweep Line Algorithm

For Voronoi diagrams, Fortune's algorithm sweeps a line from top to bottom. Maintains a beach line of parabolic arcs and event queue.

Each event (site or circle) updates the structure , building Voronoi edges incrementally.

Time Complexity: ($O n \log n$)

D. Bowyer-Watson (Delaunay via Circumcircle Test)

A practical incremental version widely used in graphics and simulation.

Steps:

- Start with supertriangle- Insert point- Remove all triangles whose circumcircle contains point- Reconnect the resulting cavity

Tiny Code (Conceptual)

```
typedef struct { double x, y; } Point;

typedef struct { Point a, b, c; } Triangle;

bool in_circle(Point a, Point b, Point c, Point p) {
    double A[3][3] = {
        {a.x - p.x, a.y - p.y, (a.x*a.x + a.y*a.y) - (p.x*p.x + p.y*p.y)},
        {b.x - p.x, b.y - p.y, (b.x*b.x + b.y*b.y) - (p.x*p.x + p.y*p.y)},
        {c.x - p.x, c.y - p.y, (c.x*c.x + c.y*c.y) - (p.x*p.x + p.y*p.y)}
    };
    return determinant(A) > 0;
}
```

This test ensures Delaunay property.

5. Applications

Domain	Application
GIS	Nearest facility, region partition
Mesh Generation	Finite element methods
Robotics	Visibility graphs, navigation
Computer Graphics	Terrain triangulation

Domain	Application
Clustering	Spatial neighbor structure

6. Complexity Summary

Algorithm	Type	Time	Notes
Fortune	Voronoi	$O(n \log n)$	Sweep line
Bowyer-Watson	Delaunay	$O(n \log n)$	Incremental
Divide & Conquer	Delaunay	$O(n \log n)$	Recursive

Why It Matters

Voronoi and Delaunay diagrams reveal natural structure in point sets. They convert distance into geometry, showing how space is divided and connected. If geometry is the shape of space, these diagrams are its skeleton.

> "Every point claims its territory; every territory shapes its network."

Try It Yourself

1. Draw Voronoi regions for 5 random points by hand.
2. Build Delaunay triangles (connect neighboring sites).
3. Verify the empty circumcircle property.
4. Use a library (CGAL / SciPy) to visualize both structures.
5. Explore how adding new points reshapes the diagrams.

75. Point in Polygon and Polygon Triangulation

Geometry often asks two fundamental questions:

1. Is a point inside or outside a polygon?
2. How can a complex polygon be broken into triangles for computation?

These are the building blocks of spatial analysis, computer graphics, and computational geometry.

1. Point in Polygon (PIP)

Given a polygon defined by vertices (x_1, y_1, x_2, y_2, ..., x_n, y_n) and a test point ((x, y)), we want to determine if the point lies inside, on the boundary, or outside the polygon.

Methods

A. Ray Casting Algorithm

Shoot a ray horizontally to the right of the point. Count how many times it intersects polygon edges.

- Odd count → Inside- Even count → Outside This is based on the even-odd rule.

Tiny Code (Ray Casting in C)

```
bool point_in_polygon(Point p, Point poly[], int n) {
    bool inside = false;
    for (int i = 0, j = n - 1; i < n; j = i++) {
        if (((poly[i].y > p.y) != (poly[j].y > p.y)) &&
            (p.x < (poly[j].x - poly[i].x) *
                   (p.y - poly[i].y) /
                   (poly[j].y - poly[i].y) + poly[i].x))
            inside = !inside;
    }
    return inside;
}
```

This toggles `inside` every time a crossing is found.

B. Winding Number Algorithm

Counts how many times the polygon winds around the point.

- Nonzero winding number → Inside- Zero → Outside More robust for complex polygons with holes or self-intersections.

Method	Time Complexity	Robustness
Ray Casting	(O(n))	Simple, may fail on edge cases
Winding Number	(O(n))	More accurate for complex shapes

Edge Cases

Handle:

- Points on edges or vertices- Horizontal edges (special treatment to avoid double counting) Numerical precision is key.

Applications

- Hit testing in computer graphics- GIS spatial queries- Collision detection

2. Polygon Triangulation

A polygon triangulation divides a polygon into non-overlapping triangles whose union equals the polygon.

Why triangulate?

- Triangles are simple, stable, and efficient for rendering and computation.- Used in graphics pipelines, area computation, physics, and mesh generation.

A. Triangulation Basics

For a simple polygon with (n) vertices,

- Always possible- Always yields (n - 2) triangles Goal: Find a triangulation efficiently and stably.

B. Ear Clipping Algorithm

An intuitive and widely used method for triangulation.

Idea

1. Find an ear: a triangle formed by three consecutive vertices (v_{i-1}, v_i, v_{i+1}) such that:
   - It is convex - Contains no other vertex inside
2. Clip the ear (remove vertex v_i)
3. Repeat until only one triangle remains

Time Complexity: (On^2)

Tiny Code (Ear Clipping Sketch)

```
while (n > 3) {
    for (i = 0; i < n; i++) {
        if (is_ear(i)) {
            add_triangle(i-1, i, i+1);
            remove_vertex(i);
            break;
        }
    }
}
```

Helper `is_ear()` checks convexity and emptiness.

C. Dynamic Programming for Convex Polygons

If the polygon is convex, use DP triangulation:

$$dp[i][j] = \min_{k \in (i,j)} dp[i][k] + dp[k][j] + cost(i, j, k)$$

Cost: perimeter or area (for minimum-weight triangulation)

Time Complexity: (On^3) Space: (On^2)

D. Divide and Conquer

Recursively split polygon and triangulate sub-polygons. Useful for convex or near-convex shapes.

Algorithm	Time	Notes
Ear Clipping	(On^2)	Simple polygons
DP Triangulation	(On^3)	Weighted cost
Convex Polygon	(O(n))	Straightforward

3. Applications

Domain	Usage
Computer Graphics	Rendering, rasterization
Computational Geometry	Area computation, integration
Finite Element Analysis	Mesh subdivision
Robotics	Path planning, map decomposition

Why It Matters

Point-in-polygon answers where you are. Triangulation tells you how space is built. Together, they form the foundation of geometric reasoning.

> "From a single point to a thousand triangles, geometry turns space into structure."

Try It Yourself

1. Draw a non-convex polygon and test random points using the ray casting rule.
2. Implement the ear clipping algorithm for a simple polygon.
3. Visualize how each step removes an ear and simplifies the shape.
4. Compare triangulation results for convex vs concave shapes.

76. Spatial Data Structures (KD, R-tree)

When working with geometric data, points, rectangles, or polygons, efficient lookup and organization are crucial. Spatial data structures are designed to answer queries like:

- Which objects are near a given point?- Which shapes intersect a region?- What's the nearest neighbor? They form the backbone of computational geometry, computer graphics, GIS, and search systems.

1. Motivation

Brute force approaches that check every object have (O(n)) or worse performance. Spatial indexing structures, like KD-Trees and R-Trees, enable efficient range queries, nearest neighbor searches, and spatial joins.

2. KD-Tree (k-dimensional tree)

A KD-tree is a binary tree that recursively partitions space using axis-aligned hyperplanes.

Each node splits the data by one coordinate axis (x, y, z, …).

Structure

- Each node represents a point.- Each level splits by a different axis (x, y, x, y, …).- Left child contains points with smaller coordinate.- Right child contains larger coordinate.

Tiny Code (KD-tree Construction in 2D)

```
typedef struct {
    double x, y;
} Point;

int axis; // 0 for x, 1 for y

KDNode* build(Point points[], int n, int depth) {
    if (n == 0) return NULL;
    axis = depth % 2;
    int mid = n / 2;
    nth_element(points, points + mid, points + n, compare_by_axis);
    KDNode* node = new_node(points[mid]);
    node->left  = build(points, mid, depth + 1);
    node->right = build(points + mid + 1, n - mid - 1, depth + 1);
    return node;
}
```

Search Complexity:

- Average: (O$\log n$)- Worst-case: (O(n))

Queries

- Range query: Find points in a region.- Nearest neighbor: Search branches that might contain closer points.- K-nearest neighbors: Use priority queues.

Pros & Cons

Pros	Cons
Efficient for static data	Costly updates
Good for low dimensions	Degrades with high dimensions

Applications

- Nearest neighbor in ML- Collision detection- Clustering (e.g., k-means acceleration)

3. R-Tree (Rectangle Tree)

An R-tree is a height-balanced tree for rectangular bounding boxes. It's the spatial analog of a B-tree.

Idea

- Store objects or bounding boxes in leaf nodes.- Internal nodes store MBRs (Minimum Bounding Rectangles) that cover child boxes.- Query by traversing overlapping MBRs.

Tiny Code (R-Tree Node Sketch)

```
typedef struct {
    Rectangle mbr;
    Node* children[MAX_CHILDREN];
    int count;
} Node;
```

Insertion chooses the child whose MBR expands least to accommodate the new entry.

Operations

- Insert: Choose subtree → Insert → Adjust MBRs- Search: Descend into nodes whose MBR intersects query- Split: When full, use heuristics (linear, quadratic, R*-Tree) Complexity:
- Query: (Olog n)- Insert/Delete: (Olog n) average

Pros & Cons

Pros	Cons
Supports dynamic data	Overlaps can degrade performance
Ideal for rectangles	Complex split rules

Variants

- R*-Tree: Optimized reinsertion, better packing- R+ Tree: Non-overlapping partitions- Hilbert R-Tree: Uses space-filling curves

4. Comparison

Feature	KD-Tree	R-Tree
Data Type	Points	Rectangles / Regions
Dimensionality	Low (2-10)	Medium
Use Case	NN, range queries	Spatial joins, overlap queries
Updates	Expensive	Dynamic-friendly
Balance	Recursive median	B-tree-like

5. Other Spatial Structures

Structure	Description
Quadtree	Recursive 2D subdivision into 4 quadrants
Octree	3D analog of quadtree
BSP Tree	Binary partition using arbitrary planes
Grid Index	Divide space into uniform grid cells

6. Applications

Domain	Usage
GIS	Region queries, map intersections
Graphics	Ray tracing acceleration
Robotics	Collision and path planning
ML	Nearest neighbor search
Databases	Spatial indexing

Why It Matters

Spatial structures turn geometry into searchable data. They enable efficient algorithms for where and what's near, vital for real-time systems.

> "Divide space wisely, and queries become whispers instead of shouts."

Try It Yourself

1. Build a KD-tree for 10 random 2D points.
2. Implement nearest neighbor search.
3. Insert rectangles into a simple R-tree and query intersection with a bounding box.
4. Compare query time vs brute force.

77. Rasterization and Scanline Techniques

When you draw shapes on a screen, triangles, polygons, circles, they must be converted into pixels. This conversion is called rasterization. It's the bridge between geometric math and visible images.

Rasterization and scanline algorithms are foundational to computer graphics, game engines, and rendering pipelines.

1. What Is Rasterization?

Rasterization transforms vector shapes (continuous lines and surfaces) into discrete pixels on a grid.

For example, a triangle defined by vertices `(x1, y1), (x2, y2), (x3, y3)` must be filled pixel by pixel.

2. Core Idea

Each shape (line, polygon, circle) is sampled over a grid. The algorithm decides which pixels are inside, on, or outside the shape.

A rasterizer answers:

- Which pixels should be lit?- What color or depth should each pixel have?

3. Line Rasterization (Bresenham's Algorithm)

A classic method for drawing straight lines with integer arithmetic.

Key Idea: Move from one pixel to the next, choosing the pixel closest to the true line path.

```
void draw_line(int x0, int y0, int x1, int y1) {
    int dx = abs(x1 - x0), dy = abs(y1 - y0);
    int sx = (x0 < x1) ? 1 : -1;
    int sy = (y0 < y1) ? 1 : -1;
    int err = dx - dy;
    while (true) {
        plot(x0, y0); // draw pixel
        if (x0 == x1 && y0 == y1) break;
        int e2 = 2 * err;
        if (e2 > -dy) { err -= dy; x0 += sx; }
        if (e2 < dx) { err += dx; y0 += sy; }
    }
}
```

Why it works: Bresenham avoids floating-point math and keeps the line visually continuous.

4. Polygon Rasterization

To fill shapes, we need scanline algorithms, they sweep a horizontal line (y-axis) across the shape and fill pixels in between edges.

Scanline Fill Steps

1. Sort edges by their y-coordinates.
2. Scan each line (y).
3. Find intersections with polygon edges.
4. Fill between intersection pairs.

This guarantees correct filling for convex and concave polygons.

Example (Simple Triangle Rasterization)

```
for (int y = y_min; y <= y_max; y++) {
    find all x-intersections with polygon edges;
    sort x-intersections;
    for (int i = 0; i < count; i += 2)
        draw_line(x[i], y, x[i+1], y);
}
```

5. Circle Rasterization (Midpoint Algorithm)

Use symmetry, a circle is symmetric in 8 octants.

Each step calculates the error term to decide whether to move horizontally or diagonally.

```
void draw_circle(int xc, int yc, int r) {
    int x = 0, y = r, d = 3 - 2 * r;
    while (y >= x) {
        plot_circle_points(xc, yc, x, y);
        x++;
        if (d > 0) { y--; d += 4 * (x - y) + 10; }
        else d += 4 * x + 6;
    }
}
```

6. Depth and Shading

In 3D graphics, rasterization includes depth testing (Z-buffer) and color interpolation. Each pixel stores its depth; new pixels overwrite only if closer.

Interpolated shading (Gouraud, Phong) computes smooth color transitions across polygons.

7. Hardware Rasterization

Modern GPUs perform rasterization in parallel:

- Vertex Shader → Projection- Rasterizer → Pixel Grid- Fragment Shader → Color & Depth Each pixel is processed in fragment shaders for lighting, texture, and effects.

8. Optimizations

Technique	Purpose
Bounding Box Clipping	Skip off-screen regions
Early Z-Culling	Discard hidden pixels early
Edge Functions	Fast inside-test for triangles
Barycentric Coordinates	Interpolate depth/color smoothly

9. Why It Matters

Rasterization turns math into imagery. It's the foundation of all visual computing, renderers, CAD, games, and GUIs. Even with ray tracing rising, rasterization remains dominant for real-time rendering.

> "Every pixel you see began as math, it's just geometry painted by light."

10. Try It Yourself

1. Implement Bresenham's algorithm for lines.
2. Write a scanline polygon fill for triangles.
3. Extend it with color interpolation using barycentric coordinates.
4. Compare performance vs brute force (looping over all pixels).

78. Computer Vision (Canny, Hough, SIFT)

Computer vision is where algorithms learn to see, to extract structure, shape, and meaning from images. Behind every object detector, edge map, and keypoint matcher lies a handful of powerful geometric algorithms.

In this section, we explore four pillars of classical vision: Canny edge detection, Hough transform, and SIFT (Scale-Invariant Feature Transform).

1. The Vision Pipeline

Most vision algorithms follow a simple pattern:

1. Input: Raw pixels (grayscale or color)
2. Preprocess: Smoothing or filtering
3. Feature extraction: Edges, corners, blobs
4. Detection or matching: Shapes, keypoints
5. Interpretation: Object recognition, tracking

Canny, Hough, and SIFT live in the feature extraction and detection stages.

2. Canny Edge Detector

Edges mark places where intensity changes sharply, the outlines of objects. The Canny algorithm (1986) is one of the most robust and widely used edge detectors.

Steps

1. Smoothing: Apply Gaussian blur to reduce noise.
2. Gradient computation:
   - Compute G_x and G_y via Sobel filters
   - Gradient magnitude: $G = \sqrt{G_x^2 + G_y^2}$
   - Gradient direction: $\theta = \tan^{-1} \frac{G_y}{G_x}$
3. Non-maximum suppression:
   - Keep only local maxima along the gradient direction
4. Double thresholding:
   - Strong edges (high gradient)
   - Weak edges (connected to strong ones)
5. Edge tracking by hysteresis:
   - Connect weak edges linked to strong edges

Tiny Code (Pseudocode)

```
Image canny(Image input) {
    Image smoothed = gaussian_blur(input);
    Gradient grad = sobel(smoothed);
    Image suppressed = non_max_suppression(grad);
    Image edges = hysteresis_threshold(suppressed, low, high);
    return edges;
}
```

Why Canny Works

Canny maximizes three criteria:

1. Good detection (low false negatives)
2. Good localization (edges close to true edges)
3. Single response (no duplicates)

It's a careful balance between sensitivity and stability.

3. Hough Transform

Canny finds edge points, Hough connects them into shapes.

The Hough transform detects lines, circles, and other parametric shapes using voting in parameter space.

Line Detection

Equation of a line:

$$\rho = x \cos\theta + y \sin\theta$$

Each edge point votes for all (ρ, θ) combinations it could belong to. Peaks in the accumulator array correspond to strong lines.

Tiny Code (Hough Transform)

```
for each edge point (x, y):
  for theta in [0, 180):
    rho = x*cos(theta) + y*sin(theta);
    accumulator[rho, theta]++;
```

Then pick (ρ, θ) with highest votes.

Circle Detection

Use 3D accumulator $center_x, center_y, radius$. Each edge pixel votes for possible circle centers.

Applications

- Lane detection in self-driving- Shape recognition (circles, ellipses)- Document analysis (lines, grids)

4. SIFT (Scale-Invariant Feature Transform)

SIFT finds keypoints that remain stable under scale, rotation, and illumination changes.

It's widely used for image matching, panoramas, 3D reconstruction, and object recognition.

Steps

1. Scale-space extrema detection
    - Use Difference of Gaussians (DoG) across scales. - Detect maxima/minima in space-scale neighborhood.2. Keypoint localization
    - Refine keypoint position and discard unstable ones.3. Orientation assignment
    - Assign dominant gradient direction.4. Descriptor generation
    - Build a 128D histogram of gradient orientations in a local patch.

Tiny Code (Outline)

```
for each octave:
  build scale-space pyramid
  find DoG extrema
  localize keypoints
  assign orientations
  compute 128D descriptor
```

Properties

Property	Description
Scale Invariant	Detects features at multiple scales
Rotation Invariant	Uses local orientation
Robust	Handles lighting, noise, affine transforms

5. Comparison

Algorithm	Purpose	Output	Robustness
Canny	Edge detection	Binary edge map	Sensitive to thresholds
Hough	Shape detection	Lines, circles	Needs clean edges
SIFT	Feature detection	Keypoints, descriptors	Very robust

6. Applications

Domain	Use Case
Robotics	Visual SLAM, localization
AR / VR	Marker tracking
Search	Image matching
Medical	Edge segmentation
Industry	Quality inspection

7. Modern Successors

- ORB (FAST + BRIEF): Efficient for real-time- SURF: Faster SIFT alternative- Harris / FAST: Corner detectors- Deep features: CNN-based descriptors

Why It Matters

These algorithms gave machines their first eyes, before deep learning, they were how computers recognized structure. Even today, they're used in preprocessing, embedded systems, and hybrid pipelines.

> "Before neural nets could dream, vision began with gradients, geometry, and votes."

Try It Yourself

1. Implement Canny using Sobel and hysteresis.
2. Use Hough transform to detect lines in a synthetic image.
3. Try OpenCV SIFT to match keypoints between two rotated images.
4. Compare edge maps before and after Gaussian blur.

79. Pathfinding in Space (A*, RRT, PRM)

When navigating a maze, driving an autonomous car, or moving a robot arm, the question is the same: How do we find a path from start to goal efficiently and safely?

Pathfinding algorithms answer this question, balancing optimality, speed, and adaptability. In this section, we explore three foundational families:

- A*: Heuristic search in grids and graphs- RRT (Rapidly-Exploring Random Tree): Sampling-based exploration- PRM (Probabilistic Roadmap): Precomputed navigation networks

1. The Pathfinding Problem

Given:

- A space (grid, graph, or continuous)- A start node and goal node- A cost function (distance, time, energy)- Optional obstacles Find a collision-free, low-cost path.

2. A* (A-star) Search

A* combines Dijkstra's algorithm with a heuristic that estimates remaining cost. It's the most popular graph-based pathfinding algorithm.

Key Idea

Each node (n) has:

$$f(n) = g(n) + h(n)$$

- (g(n)): cost so far- (h(n)): estimated cost to goal- (f(n)): total estimated cost

Algorithm

1. Initialize priority queue with start node

2. While queue not empty:

   - Pop node with smallest (f(n)) - If goal reached → return path - For each neighbor:
     – Compute new (g), (f) - Update queue if better

Tiny Code (Grid A*)

```
typedef struct { int x, y; double g, f; } Node;

double heuristic(Node a, Node b) {
    return fabs(a.x - b.x) + fabs(a.y - b.y); // Manhattan
}

void a_star(Node start, Node goal) {
    PriorityQueue open;
    push(open, start);
    while (!empty(open)) {
        Node cur = pop_min(open);
        if (cur == goal) return reconstruct_path();
        for (Node n : neighbors(cur)) {
            double tentative_g = cur.g + dist(cur, n);
            if (tentative_g < n.g) {
                n.g = tentative_g;
                n.f = n.g + heuristic(n, goal);
                push(open, n);
            }
        }
    }
}
```

Complexity

- Time: ($OE \log V$)- Space: (O(V))- Optimal if (h(n)) is admissible (never overestimates)

Variants

Variant	Description
Dijkstra	A* with (h(n) = 0)
Greedy Best-First	Uses (h(n)) only
Weighted A*	Speeds up with tradeoff on optimality

Variant	Description
Jump Point Search	Optimized for uniform grids

3. RRT (Rapidly-Exploring Random Tree)

A* struggles in continuous or high-dimensional spaces (e.g. robot arms). RRT tackles this with randomized exploration.

Core Idea

- Grow a tree from the start by randomly sampling points.- Extend tree toward each sample (step size ϵ).- Stop when near the goal.

Tiny Code (RRT Sketch)

```
Tree T = {start};
for (int i = 0; i < MAX_ITERS; i++) {
    Point q_rand = random_point();
    Point q_near = nearest(T, q_rand);
    Point q_new = steer(q_near, q_rand, step_size);
    if (collision_free(q_near, q_new))
        add_edge(T, q_near, q_new);
    if (distance(q_new, goal) < eps)
        return path;
}
```

Pros & Cons

Pros	Cons
Works in continuous space	Paths are suboptimal
Handles high dimensions	Randomness may miss narrow passages
Simple and fast	Needs post-processing (smoothing)

Variants

Variant	Description
RRT*	Asymptotically optimal
Bi-RRT	Grow from both start and goal
Informed RRT*	Focus on promising regions

4. PRM (Probabilistic Roadmap)

PRM builds a graph of feasible configurations, a roadmap, then searches it.

Steps

1. Sample random points in free space
2. Connect nearby points with collision-free edges
3. Search roadmap (e.g., with A*)

Tiny Code (PRM Sketch)

```
Graph G = {};
for (int i = 0; i < N; i++) {
    Point p = random_free_point();
    G.add_vertex(p);
}
for each p in G:
    for each q near p:
        if (collision_free(p, q))
            G.add_edge(p, q);
path = a_star(G, start, goal);
```

Pros & Cons

Pros	Cons
Precomputes reusable roadmap	Needs many samples for coverage
Good for multiple queries	Poor for single-query planning
Works in high-dim spaces	May need post-smoothing

5. Comparison

Algorithm	Space	Nature	Optimal	Use Case
A*	Discrete	Deterministic	Yes	Grids, graphs
RRT	Continuous	Randomized	No (RRT* = Yes)	Robotics, motion planning
PRM	Continuous	Randomized	Approx.	Multi-query planning

6. Applications

Domain	Use Case
Robotics	Arm motion, mobile navigation
Games	NPC pathfinding, AI navigation mesh
Autonomous vehicles	Route planning
Aerospace	Drone and spacecraft trajectory
Logistics	Warehouse robot movement

Why It Matters

Pathfinding is decision-making in space, it gives agents the ability to move, explore, and act purposefully. From Pac-Man to Mars rovers, every journey starts with an algorithm.

> "To move with purpose, one must first see the paths that are possible."

Try It Yourself

1. Implement A* on a 2D grid with walls.
2. Generate an RRT in a 2D obstacle field.
3. Build a PRM for a continuous space and run A* on the roadmap.
4. Compare speed and path smoothness across methods.

80. Computational Geometry Variants and Applications

Computational geometry is the study of algorithms on geometric data, points, lines, polygons, circles, and higher-dimensional shapes. By now, you've seen core building blocks: convex hulls, intersections, nearest neighbors, triangulations, and spatial indexing.

This final section brings them together through variants, generalizations, and real-world applications, showing how geometry quietly powers modern computing.

1. Beyond the Plane

Most examples so far assumed 2D geometry. But real systems often live in 3D or N-D spaces.

Dimension	Example Problems	Typical Uses
2D	Convex hull, polygon area, line sweep	GIS, CAD, mapping
3D	Convex polyhedra, mesh intersection, visibility	Graphics, simulation
N-D	Voronoi in high-D, KD-trees, optimization	ML, robotics, data science

Higher dimensions add complexity (and sometimes impossibility):

- Exact geometry often replaced by approximations.- Volume, distance, and intersection tests become more expensive.

2. Approximate and Robust Geometry

Real-world geometry faces numerical errors (floating point) and degenerate cases (collinear, overlapping). To handle this, algorithms adopt robustness and approximation strategies.

- Epsilon comparisons: treat values within tolerance as equal- Orientation tests: robustly compute turn direction via cross product- Exact arithmetic: rational or symbolic computation- Grid snapping: quantize space for stability Approximate geometry accepts small error for large speed-up, essential in graphics and machine learning.

3. Geometric Duality

A powerful tool for reasoning about problems: map points to lines, lines to points. For example:

- A point ((a, b)) maps to line (y = ax - b).- A line (y = mx + c) maps to point ((m, -c)). Applications:
- Transforming line intersection problems into point location problems- Simplifying half-plane intersections- Enabling arrangement algorithms in computational geometry Duality is a common trick: turn geometry upside-down to make it simpler.

4. Geometric Data Structures

Recap of core spatial structures and what they're best at:

Structure	Stores	Queries	Use Case
KD-Tree	Points	NN, range	Low-D search
R-Tree	Rectangles	Overlaps	Spatial DB
Quad/Octree	Space partitions	Point lookup	Graphics, GIS
BSP Tree	Polygons	Visibility	Rendering
Delaunay Triangulation	Points	Neighbors	Mesh generation
Segment Tree	Intervals	Range	Sweep-line events

5. Randomized Geometry

Randomness simplifies deterministic geometry:

- Randomized incremental construction (Convex Hulls, Delaunay)- Random sampling for approximation (-nets, VC dimension)- Monte Carlo geometry for probabilistic intersection and coverage Example: randomized incremental convex hull builds expected ($On \log n$) structures with elegant proofs.

6. Computational Topology

Beyond geometry lies shape connectivity, studied by topology. Algorithms compute connected components, holes, homology, and Betti numbers.

Applications include:

- 3D printing (watertightness)- Data analysis (persistent homology)- Robotics (free space topology) Geometry meets topology in alpha-shapes, simplicial complexes, and manifold reconstruction.

7. Geometry Meets Machine Learning

Many ML methods are geometric at heart:

- Nearest neighbor $\rightarrow$ Voronoi diagram- SVM $\rightarrow$ hyperplane separation- K-means $\rightarrow$ Voronoi partitioning- Manifold learning $\rightarrow$ low-dim geometry- Convex optimization $\rightarrow$ geometric feasibility Visualization tools (t-SNE, UMAP) rely on spatial embedding and distance geometry.

8. Applications Across Fields

Field	Application	Geometric Core
Graphics	Rendering, collision	Triangulation, ray tracing
GIS	Maps, roads	Polygons, point-in-region
Robotics	Path planning	Obstacles, configuration space
Architecture	Modeling	Mesh operations
Vision	Object boundaries	Contours, convexity
AI	Clustering, similarity	Distance metrics
Physics	Simulation	Particle collision
Databases	Spatial joins	R-Trees, indexing

Geometry underpins structure, position, and relationship, the backbone of spatial reasoning.

9. Complexity and Open Problems

Some problems still challenge efficient solutions:

- Point location in dynamic settings- Visibility graphs in complex polygons- Motion planning in high dimensions- Geometric median / center problems- Approximation guarantees in robust settings These remain active areas in computational geometry research.

Tiny Code (Point-in-Polygon via Ray Casting)

```
bool inside(Point p, Polygon poly) {
    int cnt = 0;
    for (int i = 0; i < poly.n; i++) {
        Point a = poly[i], b = poly[(i + 1) % poly.n];
        if (intersect_ray(p, a, b)) cnt++;
    }
    return cnt % 2 == 1; // odd crossings = inside
}
```

This small routine appears everywhere, maps, games, GUIs, and physics engines.

10. Why It Matters

Computational geometry is more than shape, it's the mathematics of space, powering visual computing, spatial data, and intelligent systems. Everywhere something moves, collides, maps, or recognizes form, geometry is the invisible hand guiding it.

> "All computation lives somewhere, and geometry is how we understand the where."

Try It Yourself

1. Implement point-in-polygon and test on convex vs concave shapes.
2. Visualize a Delaunay triangulation and its Voronoi dual.
3. Experiment with KD-trees for nearest neighbor queries.
4. Write a small convex hull in 3D using incremental insertion.
5. Sketch an RRT path over a geometric map.

Chapter 9. Systems, Databases, and Distributed Algorithms

81. Concurrency Control (2PL, MVCC, OCC)

In multi-user or multi-threaded systems, many operations want to read or write shared data at the same time. Without discipline, this leads to chaos, lost updates, dirty reads, or even inconsistent states.

Concurrency control ensures correctness under parallelism, so that the result is as if each transaction ran alone (a property called serializability).

This section introduces three foundational techniques:

- 2PL - Two-Phase Locking- MVCC - Multi-Version Concurrency Control- OCC - Optimistic Concurrency Control

1. The Goal: Serializability

We want transactions to behave as if executed in some serial order, even though they're interleaved.

A schedule is *serializable* if it yields the same result as some serial order of transactions.

Concurrency control prevents problems like:

- Lost Update: Two writes overwrite each other.- Dirty Read: Read uncommitted data.- Non-repeatable Read: Data changes mid-transaction.- Phantom Read: New rows appear after a query.

2. Two-Phase Locking (2PL)

Idea: Use locks to coordinate access. Each transaction has two phases:

1. Growing phase: acquire locks (shared or exclusive)
2. Shrinking phase: release locks (no new locks allowed after release)

This ensures conflict-serializability.

Lock Types

Type	Operation	Shared?	Exclusive?
Shared (S)	Read	Yes	No
Exclusive (X)	Write	No	No

If a transaction needs to read: request S-lock. If it needs to write: request X-lock.

Tiny Code (Lock Manager Sketch)

```
void acquire_lock(Transaction *T, Item *X, LockType type) {
    while (conflict_exists(X, type))
        wait();
    add_lock(X, T, type);
}

void release_all(Transaction *T) {
    for (Lock *l in T->locks)
        unlock(l);
}
```

Example

```
T1: read(A); write(A)
T2: read(A); write(A)
```

Without locks → race condition. With 2PL → one must wait → consistent.

Variants

Variant	Description
Strict 2PL	Holds all locks until commit → avoids cascading aborts
Rigorous 2PL	Same as Strict, all locks released at end
Conservative 2PL	Acquires all locks before execution

Pros & Cons

Pros	Cons
Guarantees serializability	Can cause deadlocks
Simple concept	Blocking, contention under load

3. Multi-Version Concurrency Control (MVCC)

Idea: Readers don't block writers, and writers don't block readers. Each write creates a new version of data with a timestamp.

Transactions read from a consistent snapshot based on their start time.

Snapshot Isolation

- Readers see the latest committed version at transaction start.- Writers produce new versions; conflicts detected at commit time. Each record stores:
- `value`- `created_at`- `deleted_at` (if applicable)

Tiny Code (Version Chain)

```
struct Version {
    int value;
    Timestamp created;
    Timestamp deleted;
    Version *next;
};
```

Read finds version with `created <= tx.start && deleted > tx.start`.

Pros & Cons

Pros	Cons
No read locks	Higher memory (multiple versions)
Readers never block	Write conflicts at commit
Great for OLTP systems	GC of old versions needed

Used In

- PostgreSQL- Oracle- MySQL (InnoDB)- Spanner

4. Optimistic Concurrency Control (OCC)

Idea: Assume conflicts are rare. Let transactions run without locks. At commit time, validate, if conflicts exist, rollback.

Phases

1. Read phase - execute, read data, buffer writes.
2. Validation phase - check if conflicts occurred.
3. Write phase - apply changes if valid, else abort.

Tiny Code (OCC Validation)

```
bool validate(Transaction *T) {
    for (Transaction *U in committed_since(T.start))
        if (conflict(T, U))
            return false;
    return true;
}
```

Pros & Cons

Pros	Cons
No locks → no deadlocks	High abort rate under contention
Great for low-conflict workloads	Wasted work on abort

Used In

- In-memory DBs- Distributed systems- STM (Software Transactional Memory)

5. Choosing a Strategy

System Type	Preferred Control
OLTP (many reads/writes)	MVCC
OLAP (read-heavy)	MVCC or OCC
Real-time systems	2PL (predictable)
Low contention	OCC
High contention	2PL / MVCC

6. Why It Matters

Concurrency control is the backbone of consistency in databases, distributed systems, and even multi-threaded programs. It enforces correctness amid chaos, ensuring your data isn't silently corrupted.

> "Without order, parallelism is noise. Concurrency control is its conductor."

Try It Yourself

1. Simulate 2PL with two transactions updating shared data.
2. Implement a toy MVCC table with version chains.
3. Write an OCC validator for three concurrent transactions.
4. Experiment: under high conflict, which model performs best?

82. Logging, Recovery, and Commit Protocols

No matter how elegant your algorithms or how fast your storage, failures happen. Power cuts, crashes, and network splits are inevitable. What matters is recovery, restoring the system to a consistent state without losing committed work.

Logging, recovery, and commit protocols form the backbone of reliable transactional systems, ensuring durability and correctness in the face of crashes.

1. The Problem

We need to guarantee the ACID properties:

- Atomicity - all or nothing- Consistency - valid before and after- Isolation - no interference- Durability - once committed, always safe If a crash occurs mid-transaction, how do we roll back or redo correctly?

The answer: Log everything, then replay or undo after failure.

2. Write-Ahead Logging (WAL)

The golden rule:

> "Write log entries before modifying the database."

Every action is recorded in a sequential log on disk, ensuring the system can reconstruct the state.

Log Record Format

Each log entry typically includes:

- `LSN` (Log Sequence Number)- `Transaction ID`- `Operation` (update, insert, delete)- `Before image` (old value)- `After image` (new value)

```
struct LogEntry {
    int lsn;
    int tx_id;
    char op[10];
    Value before, after;
};
```

When a transaction commits, the system first flushes logs to disk (`fsync`). Only then is the commit acknowledged.

3. Recovery Actions

When the system restarts, it reads logs and applies a recovery algorithm.

Three Phases (ARIES Model)

1. Analysis - determine state at crash (active vs committed)
2. Redo - repeat all actions from last checkpoint
3. Undo - rollback incomplete transactions

ARIES (Algorithm for Recovery and Isolation Exploiting Semantics) is the most widely used approach (IBM DB2, PostgreSQL, SQL Server).

Redo Rule

If the system committed before crash → redo all updates so data is preserved.

Undo Rule

If the system didn't commit → undo to maintain atomicity.

Tiny Code (Simplified Recovery Sketch)

```
void recover(Log log) {
    for (Entry e : log) {
        if (e.committed)
            apply(e.after);
        else
            apply(e.before);
    }
}
```

4. Checkpointing

Instead of replaying the entire log, systems take checkpoints, periodic snapshots marking a safe state.

Type	Description
Sharp checkpoint	Stop all transactions briefly, flush data + log
Fuzzy checkpoint	Mark consistent LSN; continue running

Checkpoints reduce recovery time: only replay after the last checkpoint.

5. Commit Protocols

In distributed systems, multiple nodes must agree to commit or abort together. This is handled by atomic commit protocols.

Two-Phase Commit (2PC)

Goal: All participants either commit or abort in unison.

Steps:

1. Prepare phase (voting):
    - Coordinator asks all participants to "prepare" - Each replies yes/no2. Commit phase (decision):
    - If all say yes → commit - Else → abort

```
Coordinator: PREPARE
Participants: VOTE YES / NO
Coordinator: COMMIT / ABORT
```

If the coordinator crashes after prepare, participants must wait → blocking protocol.

Tiny Code (2PC Pseudocode)

```
bool two_phase_commit(Participants P) {
    for each p in P:
        if (!p.prepare()) return abort_all();
    for each p in P:
        p.commit();
    return true;
}
```

Three-Phase Commit (3PC)

Improves on 2PC by adding an intermediate phase to avoid indefinite blocking. More complex, used in systems with reliable failure detection.

6. Logging in Distributed Systems

Each participant maintains its own WAL. To recover globally:

- Use coordinated checkpoints- Maintain global commit logs- Consensus-based protocols (Paxos Commit, Raft) can replace 2PC for high availability

7. Example Timeline

Step	Action
T1 updates record A	WAL entry written
T1 updates record B	WAL entry written
T1 commits	WAL flush, commit record
Crash!	Disk may be inconsistent
Restart	Recovery scans log, redoes T1

8. Pros and Cons

Approach	Strength	Weakness
WAL	Simple, durable	Write overhead
Checkpointing	Faster recovery	I/O spikes
2PC	Global atomicity	Blocking
3PC / Consensus	Non-blocking	Complex, slower

9. Real Systems

System	Strategy
PostgreSQL	WAL + ARIES + Checkpoint
MySQL (InnoDB)	WAL + Fuzzy checkpoint
Spanner	WAL + 2PC + TrueTime
Kafka	WAL for durability
RocksDB	WAL + LSM checkpoints

10. Why It Matters

Logging and commit protocols make data survive crashes and stay consistent across machines. Without them, every failure risks corruption.

> "Persistence is not about never failing, it's about remembering how to stand back up."

Try It Yourself

1. Write a toy WAL system that logs before writes.
2. Simulate a crash mid-transaction and replay the log.
3. Implement a simple 2PC coordinator with two participants.

4. Compare recovery time with vs without checkpoints.

83. Scheduling (Round Robin, EDF, Rate-Monotonic)

In operating systems and real-time systems, scheduling determines the order in which tasks or processes run. Since resources like CPU time are limited, a good scheduler aims to balance fairness, efficiency, and responsiveness.

1. The Goal of Scheduling

Every system has tasks competing for the CPU. Scheduling decides:

- Which task runs next- How long it runs- When it yields or preempts Different goals apply in different domains:

Domain	Objective
General-purpose OS	Fairness, responsiveness
Real-time systems	Meeting deadlines
Embedded systems	Predictability
High-performance servers	Throughput, latency balance

A scheduler's policy can be preemptive (interrupts tasks) or non-preemptive (waits for voluntary yield).

2. Round Robin Scheduling

Round Robin (RR) is one of the simplest preemptive schedulers. Each process gets a fixed time slice (quantum) and runs in a circular queue.

If a process doesn't finish, it's put back at the end of the queue.

Tiny Code: Round Robin (Pseudocode)

```
queue processes;
while (!empty(processes)) {
    process = dequeue(processes);
    run_for_quantum(process);
    if (!process.finished)
```

```
        enqueue(processes, process);
}
```

Characteristics

- Fair: Every process gets CPU time.- Responsive: Short tasks don't starve.- Downside: Context switching overhead if quantum is too small. #### Example

Process	Burst Time
P1	4
P2	3
P3	2

Quantum = 1 Order: P1, P2, P3, P1, P2, P3, P1, P2 → all finish fairly.

3. Priority Scheduling

Each task has a priority. The scheduler always picks the highest-priority ready task.

- Preemptive: A higher-priority task can interrupt a lower one.- Non-preemptive: The CPU is released voluntarily. #### Problems
- Starvation: Low-priority tasks may never run.- Solution: Aging - gradually increase waiting task priority.

4. Earliest Deadline First (EDF)

EDF is a dynamic priority scheduler for real-time systems. Each task has a deadline, and the task with the earliest deadline runs first.

Rule

At any time, run the ready task with the closest deadline.

Example

Task	Execution Time	Deadline
T1	1	3
T2	2	5
T3	1	2

Order: T3 → T1 → T2

EDF is optimal for preemptive scheduling of independent tasks on a single processor.

5. Rate-Monotonic Scheduling (RMS)

In periodic real-time systems, tasks repeat at fixed intervals. RMS assigns higher priority to tasks with shorter periods.

Task	Period	Priority
T1	2 ms	High
T2	5 ms	Medium
T3	10 ms	Low

It's static (priorities don't change) and optimal among fixed-priority schedulers.

Utilization Bound

For n tasks, RMS is guaranteed schedulable if:

$$U = \sum_{i=1}^{n} \frac{C_i}{T_i} \leq n(2^{1/n} - 1)$$

For example, for 3 tasks, $U \leq 0.78$.

6. Shortest Job First (SJF)

Run the task with the shortest burst time first.

- Non-preemptive SJF: Once started, runs to completion.- Preemptive SJF (Shortest Remaining Time First): Preempts if a shorter job arrives. Advantage: Minimizes average waiting time. Disadvantage: Needs knowledge of future job lengths.

7. Multilevel Queue Scheduling

Divide processes into classes (interactive, batch, system). Each class has its own queue with own policy, e.g.:

- Queue 1: System → RR (quantum = 10ms)- Queue 2: Interactive → RR (quantum = 50ms)- Queue 3: Batch → FCFS (First-Come-First-Serve) CPU is assigned based on queue priority.

8. Multilevel Feedback Queue (MLFQ)

Processes move between queues based on behavior.

- CPU-bound → move down (lower priority)- I/O-bound → move up (higher priority) Goal: Adaptive scheduling that rewards interactive tasks.

Used in modern OS kernels (Linux, Windows).

9. Scheduling Metrics

Metric	Meaning
Turnaround Time	Completion − Arrival
Waiting Time	Time spent in ready queue
Response Time	Time from arrival to first execution
Throughput	Completed tasks per unit time
CPU Utilization	% of time CPU is busy

Schedulers balance these based on design goals.

10. Why It Matters

Schedulers shape how responsive, efficient, and fair a system feels. In operating systems, they govern multitasking. In real-time systems, they ensure deadlines are met. In servers, they keep latency low and throughput high.

> "Scheduling is not just about time. It's about fairness, foresight, and flow."

Try It Yourself

1. Simulate Round Robin with quantum = 2, compare average waiting time.
2. Implement EDF for a set of periodic tasks with deadlines.
3. Check schedulability under RMS for 3 periodic tasks.
4. Explore Linux CFS (Completely Fair Scheduler) source code.
5. Compare SJF and RR for CPU-bound vs I/O-bound workloads.

84. Caching and Replacement (LRU, LFU, CLOCK)

Caching is the art of remembering the past to speed up the future. In computing, caches store recently used or frequently accessed data to reduce latency and load on slower storage (like disks or networks). The challenge: caches have limited capacity, so when full, we must decide what to evict. That's where replacement policies come in.

1. The Need for Caching

Caches appear everywhere:

- CPU: L1, L2, L3 caches speed up memory access- Databases: query results or index pages- Web browsers / CDNs: recently fetched pages- Operating systems: page cache for disk blocks The principle guiding all caches is locality:
- Temporal locality: recently used items are likely used again soon- Spatial locality: nearby items are likely needed next

2. Cache Replacement Problem

When the cache is full, which item should we remove?

We want to minimize cache misses (requests not found in cache).

Formally:

> Given a sequence of accesses, find a replacement policy that minimizes misses.

Theoretical optimal policy (OPT): always evict the item used farthest in the future. But OPT requires future knowledge, so we rely on heuristics like LRU, LFU, CLOCK.

3. Least Recently Used (LRU)

LRU evicts the least recently accessed item. It assumes recently used = likely to be used again.

Implementation Approaches

- Stack (list): move item to top on access- Hash map + doubly linked list: `O(1)` insert, delete, lookup #### Tiny Code: LRU (Simplified)

```
typedef struct Node {
    int key;
    struct Node *prev, *next;
} Node;

HashMap cache;
List lru_list;

void access(int key) {
    if (in_cache(key)) move_to_front(key);
    else {
        if (cache_full()) remove_lru();
        insert_front(key);
    }
}
```

Pros

- Good for workloads with strong temporal locality #### Cons
- Costly in hardware or massive caches (metadata overhead)

4. Least Frequently Used (LFU)

LFU evicts the least frequently accessed item.

Tracks usage count for each item:

- Increment on each access- Evict lowest-count item #### Example

Item	Accesses	Frequency
A	3	3
B	1	1
C	2	2

Evict B.

Variants

- LFU with aging: gradually reduce counts to adapt to new trends- Approximate LFU: counters in ranges (for memory efficiency) #### Pros
- Great for stable, repetitive workloads #### Cons
- Poor for workloads with shifting popularity (slow adaptation)

5. FIFO (First In First Out)

Simple but naive:

- Evict the oldest item, ignoring usage Used in simple hardware caches. Good when access pattern is cyclic, bad otherwise.

6. Random Replacement (RR)

Evict a random entry.

Surprisingly competitive in some high-concurrency systems, and trivial to implement. Used in memcached (as an option).

7. CLOCK Algorithm

A practical approximation of LRU, widely used in OS page replacement.

Each page has a reference bit (R). Pages form a circular list.

Algorithm:

1. Clock hand sweeps over pages.
2. If `R = 0`, evict page.
3. If `R = 1`, set `R = 0` and skip.

This mimics LRU with O(1) cost and low overhead.

8. Second-Chance and Enhanced CLOCK

Second-Chance: give recently used pages a "second chance" before eviction. Enhanced CLOCK: also uses modify bit (M) to prefer clean pages.

Used in Linux's page replacement (with Active/Inactive lists).

9. Adaptive Algorithms

Modern systems use hybrid or adaptive policies:

- ARC (Adaptive Replacement Cache) - balances recency and frequency- CAR (Clock with Adaptive Replacement) - CLOCK-style adaptation- TinyLFU - frequency sketch + admission policy- Hyperbolic caching - popularity decay for large-scale systems These adapt dynamically to changing workloads.

10. Why It Matters

Caching is the backbone of system speed:

- OS uses it for paging- Databases for buffer pools- CPUs for memory hierarchies- CDNs for global acceleration Choosing the right eviction policy can mean orders of magnitude improvement in latency and throughput.

  "A good cache remembers what matters, and forgets what no longer does."

Try It Yourself

1. Simulate a cache of size 3 with sequence: A B C A B D A B C D Compare LRU, LFU, and FIFO miss counts.
2. Implement LRU with a doubly-linked list and hash map in C.
3. Try CLOCK with reference bits, simulate a sweep.
4. Experiment with ARC and TinyLFU for dynamic workloads.
5. Measure hit ratios for different access patterns (sequential, random, looping).

85. Networking (Routing, Congestion Control)

Networking algorithms make sure data finds its way through vast, connected systems, efficiently, reliably, and fairly. Two core pillars of network algorithms are routing (deciding *where* packets go) and congestion control (deciding *how fast* to send them).

Together, they ensure the internet functions under heavy load, dynamic topology, and unpredictable demand.

1. The Goals of Networking Algorithms

- Correctness: all destinations are reachable if paths exist- Efficiency: use minimal resources (bandwidth, latency, hops)- Scalability: support large, dynamic networks- Robustness: recover from failures- Fairness: avoid starving flows

2. Types of Routing

Routing decides paths packets should follow through a graph-like network.

Static vs Dynamic Routing

- Static: fixed routes, manual configuration (good for small networks)- Dynamic: routes adjust automatically as topology changes (internet-scale) #### Unicast, Multicast, Broadcast
- Unicast: one-to-one (most traffic)- Multicast: one-to-many (video streaming, gaming)- Broadcast: one-to-all (local networks)

3. Shortest Path Routing

Most routing relies on shortest path algorithms:

Dijkstra's Algorithm

- Builds shortest paths from one source- Complexity: `O(E log V)` with priority queue Used in:
- OSPF (Open Shortest Path First)- IS-IS (Intermediate System to Intermediate System) #### Bellman-Ford Algorithm
- Handles negative edges- Basis for Distance-Vector routing (RIP) #### Tiny Code: Dijkstra for Routing

```
#define INF 1e9
int dist[MAX], visited[MAX];
vector<pair<int,int>> adj[MAX];

void dijkstra(int s, int n) {
    for (int i = 0; i < n; i++) dist[i] = INF;
    dist[s] = 0;
    priority_queue<pair<int,int>> pq;
    pq.push({0, s});
    while (!pq.empty()) {
        int u = pq.top().second; pq.pop();
        if (visited[u]) continue;
        visited[u] = 1;
        for (auto [v, w]: adj[u]) {
```

```
            if (dist[v] > dist[u] + w) {
                dist[v] = dist[u] + w;
                pq.push({-dist[v], v});
            }
        }
    }
}
```

4. Distance-Vector vs Link-State

Feature	Distance-Vector (RIP)	Link-State (OSPF)
Info Shared	Distance to neighbors	Full topology map
Convergence	Slower (loops possible)	Fast (SPF computation)
Complexity	Lower	Higher
Examples	RIP, BGP (conceptually)	OSPF, IS-IS

RIP uses Bellman-Ford. OSPF floods link-state updates, runs Dijkstra at each node.

5. Hierarchical Routing

Large-scale networks (like the Internet) use hierarchical routing:

- Routers grouped into Autonomous Systems (AS)- Intra-AS routing: OSPF, IS-IS- Inter-AS routing: BGP (Border Gateway Protocol) BGP exchanges reachability info, not shortest paths, and prefers policy-based routing (e.g., cost, contracts, peering).

6. Congestion Control

Even with good routes, we can't flood links. Congestion control ensures fair and efficient use of bandwidth.

Implemented primarily at the transport layer (TCP).

TCP Congestion Control

Key components:

- Additive Increase, Multiplicative Decrease (AIMD)- Slow Start: probe capacity- Congestion Avoidance: grow cautiously- Fast Retransmit / Recovery Modern variants:
- TCP Reno: classic AIMD- TCP Cubic: non-linear growth for high-speed networks- BBR (Bottleneck Bandwidth + RTT): model-based control #### Algorithm Sketch (AIMD)

```
On ACK: cwnd += 1/cwnd  // increase slowly
On loss: cwnd /= 2      // halve window
```

7. Queue Management

Routers maintain queues. Too full? => Packet loss, latency spikes, tail drop.

Solutions:

- RED (Random Early Detection) - drop packets early- CoDel (Controlled Delay) - monitor queue delay, drop adaptively These prevent bufferbloat, improving latency for real-time traffic.

8. Flow Control vs Congestion Control

- Flow Control: prevent sender from overwhelming receiver- Congestion Control: prevent sender from overwhelming network TCP uses both: receive window (rwnd) and congestion window (cwnd). Actual sending rate = `min(rwnd, cwnd)`.

9. Data Plane vs Control Plane

- Control Plane: decides routes (OSPF, BGP)- Data Plane: forwards packets (fast path) Modern networking (e.g. SDN, Software Defined Networking) separates these:
- Controller computes routes- Switches act on flow rules

10. Why It Matters

Routing and congestion control shape the performance of:

- The Internet backbone- Data center networks (with load balancing)- Cloud services and microservice meshes- Content delivery networks (CDNs) Every packet's journey, from your laptop to a global data center, relies on these ideas.

"Networking is not magic. It's algorithms moving data through time and space."

Try It Yourself

1. Implement Dijkstra's algorithm for a small network graph.
2. Simulate RIP (Distance Vector): each node updates from neighbors.
3. Model TCP AIMD window growth; visualize with Python.
4. Try RED: drop packets when queue length $>$ threshold.
5. Compare TCP Reno, Cubic, BBR throughput in simulation.

86. Distributed Consensus (Paxos, Raft, PBFT)

In a distributed system, multiple nodes must agree on a single value, for example, the state of a log, a database entry, or a blockchain block. This agreement process is called consensus.

Consensus algorithms let distributed systems act as one reliable system, even when some nodes fail, crash, or lie (Byzantine faults).

1. Why Consensus?

Imagine a cluster managing a shared log (like in databases or Raft). Each node might:

- See different requests,- Fail and recover,- Communicate over unreliable links. We need all non-faulty nodes to agree on the same order of operations.

A valid consensus algorithm must satisfy:

- Agreement: all correct nodes choose the same value- Validity: the chosen value was proposed by a node- Termination: every correct node eventually decides- Fault Tolerance: works despite failures

2. The FLP Impossibility

The FLP theorem (Fischer, Lynch, Paterson, 1985) says:

> In an asynchronous system with even one faulty process, no deterministic algorithm can guarantee consensus.

So practical algorithms use:

- Randomization, or- Partial synchrony (timeouts, retries)

3. Paxos: The Classical Algorithm

Paxos, by Leslie Lamport, is the theoretical foundation for distributed consensus.

It revolves around three roles:

- Proposers: suggest values- Acceptors: vote on proposals- Learners: learn the final decision Consensus proceeds in two phases.

Phase 1 (Prepare)

1. Proposer picks a proposal number `n` and sends `(Prepare, n)` to acceptors.
2. Acceptors respond with their highest accepted proposal (if any).

Phase 2 (Accept)

1. If proposer receives a majority of responses, it sends `(Accept, n, v)` with value `v` (highest seen or new).
2. Acceptors accept if they haven't promised higher `n`.

When a majority accept, value `v` is chosen.

Guarantees

- Safety: no two different values chosen- Liveness: possible under stable leadership #### Drawbacks
- Complex to implement correctly- High messaging overhead > "Paxos is for theorists; Raft is for engineers."

4. Raft: Understandable Consensus

Raft was designed to be simpler and more practical than Paxos, focusing on replicated logs.

Roles

- Leader: coordinates all changes- Followers: replicate leader's log- Candidates: during elections #### Workflow

1. Leader Election

    - Timeout triggers candidate election. - Each follower votes; majority wins.2. Log Replication
    - Leader appends entries, sends `AppendEntries` RPCs. - Followers acknowledge; leader commits when majority ack.3. Safety
    - Logs are consistent across majority. - Followers accept only valid prefixes. Raft ensures:

- At most one leader per term- Committed entries never lost- Logs stay consistent #### Pseudocode Sketch

```
on timeout -> become_candidate()
send RequestVote(term, id)
if majority_votes -> become_leader()

on AppendEntries(term, entries):
    if term >= current_term:
        append(entries)
        reply success
```

5. PBFT: Byzantine Fault Tolerance

Paxos and Raft assume crash faults (nodes stop, not lie). For Byzantine faults (arbitrary behavior), we use PBFT (Practical Byzantine Fault Tolerance).

Tolerates up to `f` faulty nodes out of `3f + 1` total.

Phases

1. Pre-Prepare: Leader proposes value
2. Prepare: Nodes broadcast proposal hashes
3. Commit: Nodes confirm receipt by 2f+1 votes

Used in blockchains and critical systems (space, finance).

6. Quorum Concept

Consensus often relies on quorums (majorities):

- Two quorums always intersect, ensuring consistency.- Write quorum + read quorum total nodes. In Raft/Paxos:
- Majority = `N/2 + 1`- Guarantees overlap even if some nodes fail.

7. Log Replication and State Machines

Consensus underlies Replicated State Machines (RSM):

- Every node applies the same commands in the same order.- Guarantees deterministic, identical states. This model powers:
- Databases (etcd, Spanner, TiKV)- Coordination systems (ZooKeeper, Consul)- Kubernetes control planes

8. Leader Election

All practical consensus systems need leaders:

- Simplifies coordination- Reduces conflicts- Heartbeats detect failures- New elections restore progress Algorithms:
- Raft Election (random timeouts)- Bully Algorithm- Chang-Roberts Ring Election

9. Performance and Optimization

- Batching: amortize RPC overhead- Pipeline: parallelize appends- Read-only optimizations: serve from followers (stale reads)- Witness nodes: participate in quorum without full data Advanced:
- Multi-Paxos: reuse leader, fewer rounds- Fast Paxos: shortcut some phases- Viewstamped Replication: Paxos-like log replication

10. Why It Matters

Consensus is the backbone of reliability in modern distributed systems. Every consistent database, service registry, or blockchain depends on it.

Systems using consensus:

- etcd, Consul, ZooKeeper - cluster coordination- Raft in Kubernetes - leader election- PBFT in blockchains - fault-tolerant ledgers- Spanner, TiDB - consistent databases > "Consensus is how machines learn to agree, and trust."

Try It Yourself

1. Implement Raft leader election in C or Python.
2. Simulate Paxos on 5 nodes with message drops.
3. Explore PBFT: try failing nodes and Byzantine behavior.
4. Compare performance of Raft vs Paxos under load.
5. Build a replicated key-value store with Raft.

87. Load Balancing and Rate Limiting

When systems scale, no single server can handle all requests alone. Load balancing distributes incoming traffic across multiple servers to improve throughput, reduce latency, and prevent overload. Meanwhile, rate limiting protects systems by controlling how often requests are allowed, ensuring fairness, stability, and security.

These two ideas, spreading the load and controlling the flow, are cornerstones of modern distributed systems and APIs.

1. Why Load Balancing Matters

Imagine a web service receiving thousands of requests per second. If every request went to one machine, it would crash. A load balancer (LB) acts as a traffic director, spreading requests across many backends.

Goals:

- Efficiency - fully utilize servers- Reliability - no single point of failure- Scalability - handle growing workloads- Flexibility - add/remove servers dynamically

2. Types of Load Balancers

1. Layer 4 (Transport Layer)

Balances based on IP and port. Fast and protocol-agnostic (works for TCP/UDP).

Example: Linux IPVS, Envoy, HAProxy

2. Layer 7 (Application Layer)

Understands protocols like HTTP. Can route by URL path, headers, cookies.

Example: Nginx, Envoy, AWS ALB

3. Load Balancing Algorithms

Round Robin

Cycles through backends in order.

```
Req1 → ServerA
Req2 → ServerB
Req3 → ServerC
```

Simple, fair (if all nodes equal).

Weighted Round Robin

Assigns weights to reflect capacity. Example: ServerA(2x), ServerB(1x)

Least Connections

Send request to server with fewest active connections.

Least Response Time

Select backend with lowest latency (monitored dynamically).

Hash-Based (Consistent Hashing)

Deterministically route based on request key (like user ID).

- Keeps cache locality- Used in CDNs, distributed caches (e.g. memcached) #### Random

Pick a random backend, surprisingly effective under uniform load.

4. Consistent Hashing (In Depth)

Used for sharding and sticky sessions.

Key idea:

- Map servers to a hash ring- A request's key is hashed onto the ring- Assigned to next clockwise server When servers join/leave, only small fraction of keys move.

Used in:

- CDNs- Distributed caches (Redis Cluster, DynamoDB)- Load-aware systems

5. Health Checks and Failover

A smart LB monitors health of each server:

- Heartbeat pings (HTTP/TCP)- Auto-remove unhealthy servers- Rebalance traffic instantly Example: If ServerB fails, remove from rotation:

```
Healthy: [ServerA, ServerC]
```

Also supports active-passive failover: hot standby servers take over when active fails.

6. Global Load Balancing

Across regions or data centers:

- GeoDNS: route to nearest region- Anycast: advertise same IP globally; routing picks nearest- Latency-based routing: measure and pick lowest RTT Used by CDNs, cloud services, multi-region apps

7. Rate Limiting: The Other Side

If load balancing spreads the work, rate limiting keeps total work reasonable.

It prevents:

- Abuse (bots, DDoS)- Overload (too many requests)- Fairness issues (no user dominates resources) Policies:
- Per-user, per-IP, per-API-key- Global or per-endpoint

8. Rate Limiting Algorithms

Token Bucket

- Bucket holds tokens (capacity = burst limit)- Each request consumes 1 token- Tokens refill at constant rate (rate limit)- If empty → reject or delay Good for bursty traffic.

```
if (tokens > 0) {
    tokens--;
    allow();
} else reject();
```

Leaky Bucket

- Requests flow into a bucket, drain at fixed rate- Excess = overflow = dropped Smooths bursts; used for shaping.

Fixed Window Counter

- Count requests in fixed interval (e.g. 1s)- Reset every window- Simple but unfair around boundaries #### Sliding Window Log / Sliding Window Counter
- Maintain timestamps of requests- Remove old ones beyond time window- More accurate and fair

9. Combining Both

A full system might:

- Use rate limiting per user or service- Use load balancing across nodes- Apply circuit breakers when overload persists Together, they form resilient architectures that stay online even under spikes.

10. Why It Matters

These techniques make large-scale systems:

- Scalable - handle millions of users- Stable - prevent cascading failures- Fair - each client gets a fair share- Resilient - recover gracefully from spikes or node loss Used in:
- API Gateways (Kong, Envoy, Nginx)- Cloud Load Balancers (AWS ALB, GCP LB)- Kubernetes Ingress and Service Meshes- Distributed Caches and Databases > "Balance keeps systems alive. Limits keep them sane."

Try It Yourself

1. Simulate Round Robin and Least Connections balancing across 3 servers.
2. Implement a Token Bucket rate limiter in C or Python.
3. Test burst traffic, observe drops or delays.
4. Combine Consistent Hashing with Token Bucket for user-level control.
5. Visualize how load balancing + rate limiting keep system latency low.

88. Search and Indexing (Inverted, BM25, WAND)

Search engines, whether web-scale like Google or local like SQLite's FTS, rely on efficient indexing and ranking to answer queries fast. Instead of scanning all documents, they use indexes (structured lookup tables) to quickly find relevant matches.

This section explores inverted indexes, ranking algorithms (TF-IDF, BM25), and efficient retrieval techniques like WAND.

1. The Search Problem

Given:

- A corpus of documents- A query (e.g., "machine learning algorithms") We want to return:
- Relevant documents- Ranked by importance and similarity Naive search → O(N × M) comparisons Inverted indexes → O(K log N), where K = terms in query

2. Inverted Index: The Heart of Search

An inverted index maps terms → documents containing them.

Example

Term	Postings List
"data"	[1, 4, 5]
"algorithm"	[2, 3, 5]
"machine"	[1, 2]

Each posting may include:

- docID- term frequency (tf)- positions (for phrase search) #### Construction Steps

1. Tokenize documents → words
2. Normalize (lowercase, stemming, stopword removal)
3. Build postings: term → [docIDs, tf, positions]
4. Sort & compress for storage efficiency

Used by:

- Elasticsearch, Lucene, Whoosh, Solr

3. Boolean Retrieval

Simplest model:

- Query = Boolean expression e.g. `(machine AND learning) OR AI`

Use set operations on postings:

- AND → intersection- OR → union- NOT → difference Fast intersection uses merge algorithm on sorted lists.

```
void intersect(int A[], int B[], int n, int m) {
    int i = 0, j = 0;
    while (i < n && j < m) {
        if (A[i] == B[j]) { print(A[i]); i++; j++; }
        else if (A[i] < B[j]) i++;
        else j++;
    }
}
```

But Boolean search doesn't rank results, so we need scoring models.

4. Vector Space Model

Represent documents and queries as term vectors. Each dimension = term weight (tf-idf).

- tf: term frequency in document- idf: inverse document frequency $idf = \log \frac{N}{df_t}$

Cosine similarity measures relevance:

$$\text{score}(q, d) = \frac{q \cdot d}{|q||d|}$$

Simple, interpretable, forms basis of BM25 and modern embeddings.

5. BM25: The Classic Ranking Function

BM25 (Best Match 25) is the de facto standard in information retrieval.

$$\text{score}(q,d) = \sum_{t \in q} IDF(t) \cdot \frac{f(t,d) \cdot (k_1 + 1)}{f(t,d) + k_1 \cdot (1 - b + b \cdot \frac{|d|}{avgdl})}$$

Where:

- (f(t, d)): term frequency- (|d|): doc length- (avgdl): average doc length- k_1, b: tunable params (typ. 1.2-2.0, 0.75) #### Advantages
- Balances term frequency, document length, and rarity- Fast and effective baseline- Still used in Elasticsearch, Lucene, OpenSearch

6. Efficiency Tricks: WAND, Block-Max WAND

Ranking involves merging multiple postings. We can skip irrelevant documents early with WAND (Weak AND).

WAND Principle

- Each term has upper-bound score- Maintain pointers in each posting- Compute potential max score- If max < current threshold, skip doc Improves latency for top-k retrieval.

Variants:

- BMW (Block-Max WAND) - uses block-level score bounds- MaxScore - simpler thresholding- Dynamic pruning - skip unpromising candidates

7. Index Compression

Postings lists are long, compression is crucial.

Common schemes:

- Delta encoding: store gaps between docIDs- Variable-byte (VB) or Gamma coding- Frame of Reference (FOR) and SIMD-BP128 for vectorized decoding Goal: smaller storage + faster decompression

8. Advanced Retrieval

Proximity Search

Require words appear near each other. Use positional indexes.

Phrase Search

Match exact sequences using positions: “machine learning” “learning machine”

Fuzzy / Approximate Search

Allow typos: Use Levenshtein automata, n-grams, or k-approximate matching

Fielded Search

Score per field (title, body, tags) Weighted combination

9. Learning-to-Rank and Semantic Search

Modern search adds ML-based re-ranking:

- Learning to Rank (LTR): use features (tf, idf, BM25, clicks)- Neural re-ranking: BERT-style embeddings for semantic similarity- Hybrid retrieval: combine BM25 + dense vectors (e.g. ColBERT, RRF) Also: ANN (Approximate Nearest Neighbor) for vector-based search.

10. Why It Matters

Efficient search powers:

- Web search engines- IDE symbol lookup- Log search, code search- Database full-text search- AI retrieval pipelines (RAG) It’s where algorithms meet language and scale.

  “Search is how we connect meaning to memory.”

Try It Yourself

1. Build a tiny inverted index in C or Python.
2. Implement Boolean AND and OR queries.
3. Compute TF-IDF and BM25 scores for a toy dataset.
4. Add WAND pruning for top-k retrieval.
5. Compare BM25 vs semantic embeddings for relevance.

89. Compression and Encoding in Systems

Compression and encoding algorithms are the quiet workhorses of computing, shrinking data to save space, bandwidth, and time. They allow systems to store more, transmit faster, and process efficiently. From files and databases to networks and logs, compression shapes nearly every layer of system design.

1. Why Compression Matters

Compression is everywhere:

- Databases - column stores, indexes, logs- Networks - HTTP, TCP, QUIC payloads- File systems - ZFS, NTFS, btrfs compression- Streaming - video/audio codecs- Logs & telemetry - reduce I/O and storage cost Benefits:
- Smaller data = faster I/O- Less storage = lower cost- Less transfer = higher throughput Trade-offs:
- CPU overhead (compression/decompression)- Latency (especially for small data)- Suitability (depends on entropy and structure)

2. Key Concepts

Entropy

Minimum bits needed to represent data (Shannon). High entropy $\rightarrow$ less compressible.

Redundancy

Compression exploits repetition and patterns.

Lossless vs Lossy

- Lossless: reversible (ZIP, PNG, LZ4)- Lossy: approximate (JPEG, MP3, H.264) In system contexts, lossless dominates.

3. Common Lossless Compression Families

Huffman Coding

- Prefix-free variable-length codes- Frequent symbols = short codes- Optimal under symbol-level model Used in: DEFLATE, JPEG, MP3

Arithmetic Coding

- Encodes sequence as fractional interval- More efficient than Huffman for skewed distributions- Used in: H.264, bzip2, AV1 #### Dictionary-Based (LZ77, LZ78)
- Replace repeated substrings with references- Core of ZIP, gzip, zlib, LZMA, Snappy #### LZ77 Sketch

```
while (not EOF) {
    find longest match in sliding window;
    output (offset, length, next_char);
}
```

Variants:

- LZ4 - fast, lower ratio- Snappy - optimized for speed- Zstandard (Zstd) - tunable speed/ratio, dictionary support #### Burrows-Wheeler Transform (BWT)
- Reorders data to group similar symbols- Followed by Move-To-Front + Huffman- Used in bzip2, BWT-based compressors #### Run-Length Encoding (RLE)
- Replace consecutive repeats with (symbol, count)- Great for structured or sparse data Example: `AAAAABBBCC` → `(A,5)(B,3)(C,2)`

4. Specialized Compression in Systems

Columnar Databases

Compress per column:

- Dictionary encoding - map strings → ints- Run-length encoding - good for sorted columns- Delta encoding - store differences (time series)- Bit-packing - fixed-width integers in minimal bits Combine multiple for optimal ratio.

Example (time deltas):

```
[100, 102, 103, 107] → [100, +2, +1, +4]
```

Log and Telemetry Compression

- Structured formats → fieldwise encoding- Often Snappy or LZ4 for fast decode- Aggregators (Fluentd, Loki, Kafka) rely heavily on them #### Data Lakes and Files
- Parquet, ORC, Arrow → columnar + compressed- Choose codec per column: LZ4 for speed, Zstd for ratio

5. Streaming and Chunked Compression

Large data often processed in chunks:

- Enables random access and parallelism- Needed for network streams, distributed files Example: `zlib` block, `Zstd` frame, `gzip` chunk

Used in:

- HTTP chunked encoding- Kafka log segments- MapReduce shuffle

6. Encoding Schemes

Compression encoding. Encoding ensures safe transport.

Base64

- Maps 3 bytes → 4 chars- 33% overhead- Used for binary → text (emails, JSON APIs) #### URL Encoding
- Escape unsafe chars with `%xx` #### Delta Encoding
- Store differences, not full values #### Varint / Zigzag Encoding
- Compact integers (e.g. protobufs)- Smaller numbers → fewer bytes Example:

```
while (x >= 0x80) { emit((x & 0x7F) | 0x80); x >>= 7; }
emit(x);
```

7. Adaptive and Context Models

Modern compressors adapt to local patterns:

- PPM (Prediction by Partial Matching)- Context mixing (PAQ)- Zstd uses FSE (Finite State Entropy) coding Balance between speed, memory, and compression ratio.

8. Hardware Acceleration

Compression can be offloaded to:

- CPUs with SIMD (AVX2, SSE4.2)- GPUs (parallel encode/decode)- NICs / SmartNICs-ASICs (e.g., Intel QAT) Critical for high-throughput databases, network appliances, storage systems.

9. Design Trade-offs

Goal	Best Choice
Max speed	LZ4, Snappy
Max ratio	Zstd, LZMA
Balance	Zstd (tunable)
Column store	RLE, Delta, Dict
Logs / telemetry	Snappy, LZ4
Archival	bzip2, xz
Real-time	LZ4, Brotli (fast mode)

Choose based on CPU budget, I/O cost, latency tolerance.

10. Why It Matters

Compression is a first-class optimization:

- Saves petabytes in data centers- Boosts throughput across networks- Powers cloud storage (S3, BigQuery, Snowflake)- Enables efficient analytics and ML pipelines > "Every byte saved is time earned."

Try It Yourself

1. Compress text using Huffman coding (build frequency table).
2. Compare gzip, Snappy, and Zstd on a 1GB dataset.
3. Implement delta encoding and RLE for numeric data.
4. Try dictionary encoding on repetitive strings.
5. Measure compression ratio, speed, and CPU usage trade-offs.

90. Fault Tolerance and Replication

Modern systems must survive hardware crashes, network partitions, or data loss without stopping. Fault tolerance ensures that a system continues to function, even when parts fail. Replication underpins this resilience, duplicating data or computation across multiple nodes for redundancy, performance, and consistency.

Together, they form the backbone of reliability in distributed systems.

1. Why Fault Tolerance?

No system is perfect:

- Servers crash- Disks fail- Networks partition- Power goes out The question isn't *if* failure happens, but *when*. Fault-tolerant systems detect, contain, and recover from failure automatically.

Goals:

- Availability - keep serving requests- Durability - never lose data- Consistency - stay correct across replicas

2. Failure Models

Crash Faults

Node stops responding but doesn't misbehave. Handled by restarts or replication (Raft, Paxos).

Omission Faults

Lost messages or dropped updates. Handled with retries and acknowledgments.

Byzantine Faults

Arbitrary/malicious behavior. Handled by Byzantine Fault Tolerance (PBFT), expensive but robust.

3. Redundancy: The Core Strategy

Fault tolerance = redundancy + detection + recovery

Redundancy types:

- Hardware: multiple power supplies, disks (RAID)- Software: replicated services, retries- Data: multiple copies, erasure codes- Temporal: retry or checkpoint and replay

4. Replication Models

1. Active Replication

All replicas process requests in parallel (lockstep). Results must match. Used in real-time and Byzantine systems.

2. Passive (Primary-Backup)

One leader (primary) handles requests. Backups replicate log, take over on failure. Used in Raft, ZooKeeper, PostgreSQL streaming.

3. Quorum Replication

Writes and reads contact majority of replicas. Ensures overlap → consistency. Used in Cassandra, DynamoDB, Etcd.

5. Consistency Models

Replication introduces a trade-off between consistency and availability (CAP theorem).

Strong Consistency

All clients see the same value immediately. Example: Raft, Etcd, Spanner.

Eventual Consistency

Replicas converge over time. Example: DynamoDB, Cassandra.

Causal Consistency

Preserves causal order of events. Example: Vector clocks, CRDTs.

Choice depends on workload:

- Banking → strong- Social feeds → eventual- Collaborative editing → causal

6. Checkpointing and Recovery

To recover after crash:

- Periodically checkpoint state- On restart, replay log of missed events Example: Databases → Write-Ahead Log (WAL) Stream systems → Kafka checkpoints

```
1. Save state to disk
2. Record latest log position
3. On restart → reload + replay
```

7. Erasure Coding

Instead of full copies, store encoded fragments. With (k) data blocks, (m) parity blocks → tolerate (m) failures.

Example: Reed-Solomon (used in HDFS, Ceph)

k	m	Total	Fault Tolerance
4	2	6	2 failures

Better storage efficiency than 3× replication.

8. Failure Detection

Detecting failure is tricky in distributed systems (because of latency). Common techniques:

- Heartbeats - periodic "I'm alive" messages- Timeouts - suspect node if no heartbeat- Gossip protocols - share failure info among peers Used in Consul, Cassandra, Kubernetes health checks.

9. Self-Healing Systems

After failure:

1. Detect it
2. Isolate faulty component
3. Replace or restart
4. Rebalance load or re-replicate data

Patterns:

- Supervisor trees (Erlang/Elixir)- Self-healing clusters (Kubernetes)- Rebalancing (Cassandra ring repair) "Never trust a single machine, trust the system."

10. Why It Matters

Fault tolerance turns fragile infrastructure into reliable services.

Used in:

- Databases (replication + WAL)- Distributed storage (HDFS, Ceph, S3)- Orchestration (Kubernetes controllers)- Streaming systems (Kafka, Flink) Without replication and fault tolerance, large-scale systems would collapse under failure.

  "Resilience is built, not assumed."

Try It Yourself

1. Build a primary-backup key-value store: leader writes, follower replicates.
2. Add heartbeat + timeout detection to trigger failover.
3. Simulate partition: explore behavior under strong vs eventual consistency.
4. Implement checkpoint + replay recovery for a small app.
5. Compare 3× replication vs Reed-Solomon (4+2) for space and reliability.

Chapter 10. AI, ML and Optimization

91. Classical ML (k-means, Naive Bayes, SVM, Decision Trees)

Classical machine learning is built on interpretable mathematics and solid optimization foundations. Long before deep learning, these algorithms powered search engines, spam filters, and recommendation systems. They're still used today, fast, explainable, and easy to deploy.

This section covers the four pillars of classical ML:

- k-means - unsupervised clustering- Naive Bayes - probabilistic classification- SVM - margin-based classification- Decision Trees - rule-based learning

1. The Essence of Classical ML

Classical ML is about learning from data using statistical principles, often without huge compute. Given dataset (D = $\{x_i, y_i\}$), the task is to:

- Predict (y) from (x)- Generalize beyond seen data- Balance bias and variance

2. k-means Clustering

Goal: partition data into (k) groups (clusters) such that intra-cluster distance is minimized.

Objective

$$\min_{C} \sum_{i=1}^{k} \sum_{x \in C_i} |x - \mu_i|^2$$

Where μ_i = centroid of cluster (i).

Algorithm

1. Choose (k) random centroids
2. Assign each point to nearest centroid
3. Recompute centroids
4. Repeat until stable

Tiny Code (C-style)

```
for (iter = 0; iter < max_iter; iter++) {
    assign_points_to_clusters();
    recompute_centroids();
}
```

Pros

- Simple, fast ((O(nkd)))- Works well for spherical clusters #### Cons
- Requires (k)- Sensitive to initialization, outliers Variants:
- k-means++ (better initialization)- Mini-batch k-means (scalable)

3. Naive Bayes Classifier

A probabilistic model using Bayes' theorem under independence assumptions.

$$P(y|x) \propto P(y) \prod_{i=1}^{n} P(x_i|y)$$

Algorithm

1. Compute prior (P(y))
2. Compute likelihood (P$x_i|y$)
3. Predict class with max posterior

Types

- Multinomial NB - text (bag of words)- Gaussian NB - continuous features- Bernoulli NB - binary features #### Example (Spam Detection)

```
P(spam | "win money")  P(spam) * P("win"|spam) * P("money"|spam)
```

Pros

- Fast, works well for text- Needs little data- Probabilistic interpretation #### Cons
- Assumes feature independence- Poor for correlated features

4. Support Vector Machines (SVM)

SVM finds the max-margin hyperplane separating classes.

Objective

Maximize margin = distance between boundary and nearest points.

$$\min_{w,b} \frac{1}{2}|w|^2 \quad \text{s.t.} \quad y_i(w \cdot x_i + b) \geq 1$$

Can be solved via Quadratic Programming.

Intuition

- Each data point → vector- Hyperplane: $w \cdot x + b = 0$- Support vectors = boundary points #### Kernel Trick

Transform input via kernel (K$x_i, x_j = \ x_i \ \ x_j$):

- Linear: dot product- Polynomial: ($x_i \cdot x_j + c\hat{}$d)- RBF: $e^{-\gamma |x_i - x_j|^2}$ #### Pros
- Effective in high dimensions- Can model nonlinear boundaries- Few hyperparameters #### Cons
- Slow on large data- Harder to tune kernel parameters

5. Decision Trees

If-else structure for classification/regression.

At each node:

- Pick feature (f) and threshold (t)- Split to maximize information gain #### Metrics
- Entropy: $H = -\sum p_i \log p_i$- Gini: $G = 1 - \sum p_i^2$ #### Pseudocode

```
if (feature < threshold)
    go left;
else
    go right;
```

Build recursively until:

- Max depth- Min samples per leaf- Pure nodes #### Pros
- Interpretable- Handles mixed data- No scaling needed #### Cons
- Prone to overfitting- Unstable (small data changes) Fixes:
- Pruning (reduce depth)- Ensembles: Random Forests, Gradient Boosting

Algorithm	Bias	Variance

6. Bias-Variance Tradeoff

Algorithm	Bias	Variance
k-means	High	Low
Naive Bayes	High	Low
SVM	Low	Medium
Decision Tree	Low	High

Balancing both = good generalization.

7. Evaluation Metrics

For classification:

- Accuracy, Precision, Recall, F1-score- ROC-AUC, Confusion Matrix For clustering:
- Inertia, Silhouette Score Always use train/test split or cross-validation.

8. Scaling to Large Data

Techniques:

- Mini-batch training- Online updates (SGD)- Dimensionality reduction (PCA)- Approximation (Random Projections) Libraries:
- scikit-learn (Python)- liblinear, libsvm (C/C++)- MLlib (Spark)

9. When to Use What

Task	Recommended Algorithm
Text classification	Naive Bayes
Clustering	k-means
Nonlinear classification	SVM (RBF)
Tabular data	Decision Tree
Quick baseline	Logistic Regression / NB

10. Why It Matters

These algorithms are fast, interpretable, and theoretical foundations of modern ML. They remain the go-to choice for:

- Small to medium datasets- Real-time classification- Explainable AI > "Classical ML is the art of solving problems with math you can still write on a whiteboard."

Try It Yourself

1. Cluster 2D points with k-means, plot centroids.
2. Train Naive Bayes on a spam/ham dataset.
3. Classify linearly separable data with SVM.
4. Build a Decision Tree from scratch (entropy, Gini).
5. Compare models' accuracy and interpretability.

92. Ensemble Methods (Bagging, Boosting, Random Forests)

Ensemble methods combine multiple weak learners to build a strong predictor. Instead of relying on one model, ensembles vote, average, or boost multiple models, improving stability and accuracy.

They are the bridge between classical and modern ML , simple models, combined smartly, become powerful.

1. The Core Idea

> "Many weak learners, when combined, can outperform a single strong one."

Mathematically, if $f_1, f_2, \ldots, f_k$ are weak learners, an ensemble predictor is:

$$F(x) = \frac{1}{k} \sum_{i=1}^{k} f_i(x)$$

For classification, combine via majority vote. For regression, combine via average.

2. Bagging (Bootstrap Aggregating)

Bagging reduces variance by training models on different samples.

Steps

1. Draw (B) bootstrap samples from dataset (D).
2. Train one model per sample.
3. Aggregate predictions by averaging or voting.

$$\hat{f} * bag(x) = \frac{1}{B} \sum *b = 1^{B} f_b(x)$$

Each f_b is trained on a random subset (with replacement).

Example

- Base learner: Decision Tree- Ensemble: Bagged Trees- Famous instance: Random Forest #### Tiny Code (C-style Pseudocode)

```
for (int b = 0; b < B; b++) {
    D_b = bootstrap_sample(D);
    model[b] = train_tree(D_b);
}
prediction = average_predictions(model, x);
```

Pros

- Reduces variance- Works well with high-variance learners- Parallelizable #### Cons
- Increases computation- Doesn't reduce bias

3. Random Forest

A bagging-based ensemble of decision trees with feature randomness.

Key Ideas

- Each tree trained on bootstrap sample.- At each split, consider random subset of features.- Final prediction = majority vote or average. This decorrelates trees, improving generalization.

$$F(x) = \frac{1}{B} \sum_{b=1}^{B} T_b(x)$$

Pros

- Handles large feature sets- Low overfitting- Good default for tabular data #### Cons
- Less interpretable- Slower on huge datasets OOB (Out-of-Bag) error = internal validation from unused samples.

4. Boosting

Boosting focuses on reducing bias by sequentially training models , each one corrects errors from the previous.

Steps

1. Start with weak learner (f_1(x))
2. Train next learner (f_2(x)) on residuals/errors
3. Combine with weighted sum

$$F_m(x) = F_{m-1}(x) + \alpha_m f_m(x)$$

Weights α_m focus on difficult examples.

Tiny Code (Conceptual)

```
F = 0;
for (int m = 0; m < M; m++) {
    residual = y - predict(F, x);
    f_m = train_weak_learner(x, residual);
    F += alpha[m] * f_m;
}
```

5. AdaBoost (Adaptive Boosting)

AdaBoost adapts weights on samples after each iteration.

Algorithm

1. Initialize weights: $w_i = \frac{1}{n}$
2. Train weak classifier f_t
3. Compute error: ϵ_t
4. Update weights:

$$w_i \leftarrow w_i \cdot e^{\alpha_t \cdot I(y_i \neq f_t(x_i))}$$

   where $\alpha_t = \frac{1}{2} \ln\left(\frac{1-\epsilon_t}{\epsilon_t}\right)$
5. Normalize weights

Final classifier:

$$F(x) = \text{sign}\left(\sum_t \alpha_t f_t(x)\right)$$

Pros

- High accuracy on clean data- Simple and interpretable weights #### Cons
- Sensitive to outliers- Sequential $\rightarrow$ not easily parallelizable

6. Gradient Boosting

A modern version of boosting using gradient descent on loss.

At each step, fit new model to negative gradient of loss function.

Objective

$$F_m(x) = F_{m-1}(x) + \gamma_m h_m(x)$$

where $h_m(x) \approx -\frac{\partial L(y, F(x))}{\partial F(x)}$

Common Libraries

- XGBoost
- LightGBM
- CatBoost #### Pros
- High performance on tabular data- Flexible (custom loss)- Handles mixed feature types #### Cons
- Slower to train- Sensitive to hyperparameters

7. Stacking (Stacked Generalization)

Combine multiple models (base learners) via a meta-model.

Steps

1. Train base models (SVM, Tree, NB, etc.)
2. Collect their predictions
3. Train meta-model (e.g. Logistic Regression) on outputs

$$\hat{y} = f_{meta}(f_1(x), f_2(x), ..., f_k(x))$$

8. Bagging vs Boosting

Feature	Bagging	Boosting
Strategy	Parallel	Sequential
Goal	Reduce variance	Reduce bias
Weighting	Uniform	Adaptive
Example	Random Forest	AdaBoost, XGBoost

9. Bias-Variance Behavior

- Bagging: ↓ variance- Boosting: ↓ bias- Random Forest: balanced- Stacking: flexible but complex

10. Why It Matters

Ensemble methods are the workhorses of classical ML competitions and real-world tabular problems. They blend interpretability, flexibility, and predictive power.

> "One tree may fall, but a forest stands strong."

Try It Yourself

1. Train a Random Forest on the Iris dataset.
2. Implement AdaBoost from scratch using decision stumps.
3. Compare Bagging vs Boosting accuracy.
4. Try XGBoost with different learning rates.
5. Visualize feature importance across models.

93. Gradient Methods (SGD, Adam, RMSProp)

Gradient-based optimization is the heartbeat of machine learning. These methods update parameters iteratively by following the negative gradient of the loss function. They power everything from linear regression to deep neural networks.

1. The Core Idea

We want to minimize a loss function (Lθ). Starting from some initial parameters θ_0, we move in the opposite direction of the gradient:

$$\theta_{t+1} = \theta_t - \eta \cdot \nabla_\theta L(\theta_t)$$

where η is the learning rate (step size).

The gradient tells us which way the function increases fastest , we move the other way.

2. Batch Gradient Descent

Uses the entire dataset to compute the gradient.

$$\nabla_\theta L(\theta) = \frac{1}{N} \sum_{i=1}^{N} \nabla_\theta \ell_i(\theta)$$

- Accurate but slow for large (N)- Each update is expensive Tiny Code

```
for (int t = 0; t < T; t++) {
    grad = compute_full_gradient(data, theta);
    theta = theta - eta * grad;
}
```

Good for: small datasets or convex problems

3. Stochastic Gradient Descent (SGD)

Instead of full data, use one random sample per step.

$$\theta_{t+1} = \theta_t - \eta \cdot \nabla_\theta \ell_i(\theta_t)$$

- Noisy but faster updates- Can escape local minima- Great for online learning Tiny Code

```
for each sample (x_i, y_i):
    grad = grad_loss(theta, x_i, y_i);
    theta -= eta * grad;
```

Pros

- Fast convergence- Works on large datasets Cons
- Noisy updates- Requires learning rate tuning

4. Mini-Batch Gradient Descent

Compromise between batch and stochastic.

Use small subset (mini-batch) of samples:

$$\theta_{t+1} = \theta_t - \eta \cdot \frac{1}{m} \sum_{i=1}^{m} \nabla_\theta \ell_i(\theta_t)$$

Usually batch size = 32 or 64. Faster, more stable updates.

5. Momentum

Adds velocity to smooth oscillations.

$$v_t = \beta v_{t-1} + (1 - \beta)\nabla_\theta L(\theta_t)$$

$$\theta_{t+1} = \theta_t - \eta v_t$$

This accumulates past gradients to speed movement in consistent directions.

Think of it like a heavy ball rolling down a hill.

6. Nesterov Accelerated Gradient (NAG)

Improves momentum by looking ahead:

$$v_t = \beta v_{t-1} + \eta \nabla_\theta L(\theta_t - \beta v_{t-1})$$

It anticipates the future position before computing the gradient.

Faster convergence in convex settings.

7. RMSProp

Adjusts learning rate per parameter using exponential average of squared gradients:

$$E[g^2] * t = \rho E[g^2] * t - 1 + (1 - \rho) g_t^2$$

$$\theta_{t+1} = \theta_t - \frac{\eta}{\sqrt{E[g^2]_t + \epsilon}} g_t$$

This helps when gradients vary in magnitude.

Good for: non-stationary objectives, deep networks

8. Adam (Adaptive Moment Estimation)

Combines momentum + RMSProp:

$$m_t = \beta_1 m_{t-1} + (1 - \beta_1) g_t$$

$$v_t = \beta_2 v_{t-1} + (1 - \beta_2) g_t^2$$

Bias-corrected estimates:

$$\hat{m}_t = \frac{m_t}{1 - \beta_1^t}, \quad \hat{v}_t = \frac{v_t}{1 - \beta_2^t}$$

Update rule:

$$\theta_{t+1} = \theta_t - \frac{\eta \cdot \hat{m}_t}{\sqrt{\hat{v}_t} + \epsilon}$$

Tiny Code (Conceptual)

```
m = 0; v = 0;
for (int t = 1; t <= T; t++) {
    g = grad(theta);
    m = beta1 * m + (1 - beta1) * g;
    v = beta2 * v + (1 - beta2) * g * g;
    m_hat = m / (1 - pow(beta1, t));
    v_hat = v / (1 - pow(beta2, t));
    theta -= eta * m_hat / (sqrt(v_hat) + eps);
}
```

Pros

- Works well out of the box- Adapts learning rate- Great for deep learning Cons
- May not converge exactly- Needs decay schedule for stability

9. Learning Rate Schedules

Control η over time:

- Step decay: $\eta_t = \eta_0 \cdot \gamma^{\lfloor t/s \rfloor}$- Exponential decay: $\eta_t = \eta_0 e^{-\lambda t}$- Cosine annealing: smooth periodic decay- Warm restarts: reset learning rate periodically

10. Why It Matters

All modern deep learning is built on gradients. Choosing the right optimizer can mean faster training and better accuracy.

Optimizer	Adaptive	Momentum	Common Use
SGD	No	Optional	Simple tasks
SGD + Momentum	No	Yes	ConvNets
RMSProp	Yes	No	RNNs
Adam	Yes	Yes	Transformers, DNNs

> "Optimization is the art of taking small steps in the right direction , many times over."

Try It Yourself

1. Implement SGD and Adam on a linear regression task.
2. Compare training curves for SGD, Momentum, RMSProp, and Adam.
3. Experiment with learning rate schedules.
4. Visualize optimization paths on a 2D contour plot.

94. Deep Learning (Backpropagation, Dropout, Normalization)

Deep learning is about stacking layers of computation so that the network can learn hierarchical representations. From raw pixels to abstract features, deep nets build meaning through composition of functions.

At the core of this process are three ideas: backpropagation, regularization (dropout), and normalization.

1. The Essence of Deep Learning

A neural network is a chain of functions:

$$f(x;\theta) = f_L(f_{L-1}(\cdots f_1(x)))$$

Each layer transforms its input and passes it on.

Training involves finding parameters θ that minimize a loss (L(f$x;\theta$, y)).

2. Backpropagation

Backpropagation is the algorithm that teaches neural networks.

It uses the chain rule of calculus to efficiently compute gradients layer by layer.

For each layer (i):

$$\frac{\partial L}{\partial \theta_i} = \frac{\partial L}{\partial a_i} \cdot \frac{\partial a_i}{\partial \theta_i}$$

and propagate backward:

$$\frac{\partial L}{\partial a_{i-1}} = \frac{\partial L}{\partial a_i} \cdot \frac{\partial a_i}{\partial a_{i-1}}$$

So every neuron learns how much it contributed to the error.

Tiny Code

```
// Pseudocode for 2-layer network
forward:
    z1 = W1*x + b1;
    a1 = relu(z1);
    z2 = W2*a1 + b2;
    y_hat = softmax(z2);
    loss = cross_entropy(y_hat, y);

backward:
    dz2 = y_hat - y;
    dW2 = dz2 * a1.T;
    db2 = sum(dz2);
    da1 = W2.T * dz2;
    dz1 = da1 * relu_grad(z1);
    dW1 = dz1 * x.T;
    db1 = sum(dz1);
```

Each gradient is computed by local differentiation and multiplied back.

3. Activation Functions

Nonlinear activations let networks approximate nonlinear functions.

Function	Formula	Use
ReLU	$\max(0, x)$	Default, fast
Sigmoid	$\frac{1}{1+e^{-x}}$	Probabilities
Tanh	$\tanh(x)$	Centered activations
GELU	$x\,\Phi(x)$	Modern transformers

Without nonlinearity, stacking layers is just one big linear transformation.

4. Dropout

Dropout is a regularization technique that prevents overfitting. During training, randomly turn off neurons:

$$\tilde{a}_i = a_i \cdot m_i, \quad m_i \sim \text{Bernoulli}(p)$$

At inference, scale activations by (p) (keep probability).

It forces the network to not rely on any single path.

Tiny Code

```
for (int i = 0; i < n; i++) {
    if (rand_uniform() < p) a[i] = 0;
    else a[i] /= p; // scaling
}
```

5. Normalization

Normalization stabilizes and speeds up training by reducing internal covariate shift.

Batch Normalization

Normalize activations per batch:

$$\hat{x} = \frac{x - \mu_B}{\sqrt{\sigma_B^2 + \epsilon}}$$

$$y = \gamma \hat{x} + \beta$$

Learnable parameters γ, β restore flexibility.

Benefits:

- Smooth gradients- Allows higher learning rates- Acts as regularizer #### Layer Normalization

Used in transformers (normalizes across features, not batch).

6. Initialization

Proper initialization helps gradients flow.

Scheme	Formula	Use
Xavier	$\text{Var}(W) = \frac{1}{n_{in}}$	Tanh
He	$\text{Var}(W) = \frac{2}{n_{in}}$	ReLU

Poor initialization can lead to vanishing or exploding gradients.

7. Training Pipeline

1. Initialize weights
2. Forward pass
3. Compute loss
4. Backward pass (backprop)
5. Update weights (e.g. with Adam)

Repeat until convergence.

8. Deep Architectures

Model	Key Idea	Typical Use
MLP	Fully connected	Tabular data
CNN	Convolutions	Images
RNN	Sequential recurrence	Time series, text
Transformer	Self-attention	Language, vision

Each architecture stacks linear operations and nonlinearities in different ways.

9. Overfitting and Regularization

Common fixes:

- Dropout- Weight decay (L_2 regularization)- Data augmentation- Early stopping The key is to improve generalization, not just minimize training loss.

10. Why It Matters

Backpropagation turned neural networks from theory to practice. Normalization made them train faster. Dropout made them generalize better.

Together, they unlocked the deep learning revolution.

> "Depth gives power, but gradients give life."

Try It Yourself

1. Implement a 2-layer network with ReLU and softmax.
2. Add dropout and batch normalization.
3. Visualize training with and without dropout.
4. Compare performance on MNIST with and without normalization.

95. Sequence Models (Viterbi, Beam Search, CTC)

Sequence models process data where order matters, text, speech, DNA, time series. They capture dependencies across positions, predicting the next step from context.

This section explores three fundamental tools: Viterbi, Beam Search, and CTC (Connectionist Temporal Classification).

1. The Nature of Sequential Data

Sequential data has temporal or structural order. Each element x_t depends on past inputs $x_{1:t-1}$.

Common sequence tasks:

- Tagging (POS tagging, named entity recognition)- Transcription (speech $\rightarrow$ text)- Decoding (translation, path reconstruction) To handle such problems, we need models that remember.

2. Hidden Markov Models (HMMs)

A Hidden Markov Model assumes:

- A sequence of hidden states $z_1, z_2, \ldots, z_T$- Each state emits an observation x_t- Transition and emission probabilities govern the process

$$P(z_t|z_{t-1}) = A_{z_{t-1},z_t}, \quad P(x_t|z_t) = B_{z_t}(x_t)$$

Goal: find the most likely sequence of hidden states given observations.

3. The Viterbi Algorithm

Viterbi is a dynamic programming algorithm to decode the most probable path:

$$\delta_t(i) = \max_{z_{1:t-1}} P(z_{1:t-1}, z_t = i, x_{1:t})$$

Recurrence:

$$\delta_t(i) = \max_j \left(\delta_{t-1}(j) \cdot A_{j,i}\right) \cdot B_i(x_t)$$

Track backpointers to reconstruct the best sequence.

Time complexity: $O(T \cdot N^2)$,
where $N =$ number of states, $T =$ sequence length.

Tiny Code

```
for (t = 1; t < T; t++) {
    for (i = 0; i < N; i++) {
        double best = -INF;
        int argmax = -1;
        for (j = 0; j < N; j++) {
            double score = delta[t-1][j] * A[j][i];
            if (score > best) { best = score; argmax = j; }
        }
        delta[t][i] = best * B[i][x[t]];
        backptr[t][i] = argmax;
    }
}
```

Use `backptr` to trace back the optimal path.

4. Beam Search

For many sequence models (e.g. neural machine translation), exhaustive search is impossible. Beam search keeps only the top-k best hypotheses at each step.

Algorithm:

1. Start with an empty sequence and score 0
2. At each step, expand each candidate with all possible next tokens
3. Keep only k best sequences (beam size)
4. Stop when all sequences end or reach max length

Beam size controls trade-off:

- Larger beam → better accuracy, slower- Smaller beam → faster, riskier

Tiny Code

```
for (step = 0; step < max_len; step++) {
    vector<Candidate> new_beam;
    for (c in beam) {
        probs = model_next(c.seq);
        for (token, p in probs)
            new_beam.push({c.seq + token, c.score + log(p)});
    }
    beam = top_k(new_beam, k);
}
```

Use log probabilities to avoid underflow.

5. Connectionist Temporal Classification (CTC)

Used in speech recognition and handwriting recognition where input and output lengths differ.

CTC learns to align input frames with output symbols without explicit alignment.

Add a special blank symbol ( ) to allow flexible alignment.

Example (CTC decoding):

Frame	Output	After Collapse
A A A H H	A A H H	A A H

Loss:

$$P(y|x) = \sum_{\pi \in \text{Align}(x,y)} P(\pi|x)$$

where π are all alignments that reduce to (y).

CTC uses dynamic programming to compute forward-backward probabilities.

6. Comparing Methods

Method	Used In	Key Idea	Handles Alignment?
Viterbi	HMMs	Most probable state path	Yes
Beam Search	Neural decoders	Approximate search	Implicit
CTC	Speech / seq2seq	Sum over alignments	Yes

7. Use Cases

- Viterbi: POS tagging, speech decoding- Beam Search: translation, text generation- CTC: ASR, OCR, gesture recognition

8. Implementation Tips

- Use log-space for probabilities- In beam search, apply length normalization- In CTC, use dynamic programming tables- Combine CTC + beam search for speech decoding

9. Common Pitfalls

- Viterbi assumes Markov property (limited memory)- Beam Search can miss global optimum- CTC can confuse repeated characters without blanks

10. Why It Matters

Sequence models are the bridge between structure and time. They show how to decode hidden meaning in ordered data.

From decoding Morse code to transcribing speech, these algorithms give machines the gift of sequence understanding.

Try It Yourself

1. Implement Viterbi for a 3-state HMM.
2. Compare greedy decoding vs beam search on a toy language model.
3. Build a CTC loss table for a short sequence (like "HELLO").

96. Metaheuristics (GA, SA, PSO, ACO)

Metaheuristics are general-purpose optimization strategies that search through vast, complex spaces when exact methods are too slow or infeasible. They don't guarantee the perfect answer but often find good-enough solutions fast.

This section covers four classics:

- GA (Genetic Algorithm)- SA (Simulated Annealing)- PSO (Particle Swarm Optimization)- ACO (Ant Colony Optimization)

1. The Metaheuristic Philosophy

Metaheuristics draw inspiration from nature and physics. They combine exploration (searching widely) and exploitation (refining promising spots).

They're ideal for:

- NP-hard problems (TSP, scheduling)- Continuous optimization (parameter tuning)- Black-box functions (no gradients) They trade mathematical guarantees for practical power.

2. Genetic Algorithm (GA)

Inspired by natural selection, GAs evolve a population of solutions.

Core Steps

1. Initialize population randomly
2. Evaluate fitness of each
3. Select parents
4. Crossover to produce offspring
5. Mutate to add variation
6. Replace worst with new candidates

Repeat until convergence.

Tiny Code

```
for (gen = 0; gen < max_gen; gen++) {
    evaluate(pop);
    parents = select_best(pop);
    offspring = crossover(parents);
    mutate(offspring);
    pop = select_survivors(pop, offspring);
}
```

Operators

- Selection: tournament, roulette-wheel- Crossover: one-point, uniform- Mutation: bit-flip, Gaussian Strengths: global search, diverse exploration Weakness: may converge slowly

3. Simulated Annealing (SA)

Mimics cooling of metals, start hot (high randomness), slowly cool.

At each step:

1. Propose random neighbor
2. Accept if better
3. If worse, accept with probability
$$P = e^{-\frac{\Delta E}{T}}$$
4. Gradually lower (T)

Tiny Code

```
T = T_init;
state = random_state();
while (T > T_min) {
    next = neighbor(state);
    dE = cost(next) - cost(state);
    if (dE < 0 || exp(-dE/T) > rand_uniform())
        state = next;
    T *= alpha; // cooling rate
}
```

Strengths: escapes local minima Weakness: sensitive to cooling schedule

4. Particle Swarm Optimization (PSO)

Inspired by bird flocking. Each particle adjusts velocity based on:

- Its own best position- The global best found

$$v_i \leftarrow wv_i + c_1 r_1 (p_i - x_i) + c_2 r_2 (g - x_i)$$

$$x_i \leftarrow x_i + v_i$$

Tiny Code

```
for each particle i:
    v[i] = w*v[i] + c1*r1*(pbest[i]-x[i]) + c2*r2*(gbest-x[i]);
    x[i] += v[i];
    update_best(i);
```

Strengths: continuous domains, easy Weakness: premature convergence

5. Ant Colony Optimization (ACO)

Inspired by ant foraging, ants deposit pheromones on paths. The stronger the trail, the more likely others follow.

Steps:

1. Initialize pheromone on all edges
2. Each ant builds a solution (prob. pheromone)
3. Evaluate paths
4. Evaporate pheromone
5. Reinforce good paths

$$\tau_{ij} \leftarrow (1 - \rho)\tau_{ij} + \sum_k \Delta \tau_{ij}^k$$

Tiny Code

```
for each iteration:
    for each ant:
        path = build_solution(pheromone);
        score = evaluate(path);
    evaporate(pheromone);
    deposit(pheromone, best_paths);
```

Strengths: combinatorial problems (TSP) Weakness: parameter tuning, slower convergence

6. Comparing the Four

Method	Inspiration	Best For	Key Idea
GA	Evolution	Discrete search	Selection, crossover, mutation
SA	Thermodynamics	Local optima escape	Cooling + randomness
PSO	Swarm behavior	Continuous search	Local + global attraction
ACO	Ant foraging	Graph paths	Pheromone reinforcement

7. Design Patterns

Common metaheuristic pattern:

- Represent solution- Define fitness / cost function- Define neighbor / mutation operators- Balance randomness and greediness Tuning parameters often matters more than equations.

8. Hybrid Metaheuristics

Combine strengths:

- GA + SA: evolve population, fine-tune locally- PSO + DE: use swarm + differential evolution- ACO + Local Search: reinforce with hill-climbing These hybrids often outperform single methods.

9. Common Pitfalls

- Poor representation $\rightarrow$ weak search- Over-exploitation $\rightarrow$ stuck in local optima- Bad parameters $\rightarrow$ chaotic or stagnant behavior Always visualize progress (fitness over time).

10. Why It Matters

Metaheuristics give us adaptive intelligence, searching without gradients, equations, or complete knowledge. They reflect nature's way of solving complex puzzles: iterate, adapt, survive.

> "Optimization is not about perfection. It's about progress guided by curiosity."

Try It Yourself

1. Implement Simulated Annealing for the Traveling Salesman Problem.
2. Create a Genetic Algorithm for knapsack optimization.
3. Tune PSO parameters to fit a function $f(x) = x^2 + 10\sin x$.
4. Compare ACO paths for TSP at different evaporation rates.

97. Reinforcement Learning (Q-learning, Policy Gradients)

Reinforcement Learning (RL) is about learning through interaction , an agent explores an environment, takes actions, and learns from rewards. Unlike supervised learning (where correct labels are given), RL learns what to do by trial and error.

This section introduces two core approaches:

- Q-learning (value-based)- Policy Gradient (policy-based)

1. The Reinforcement Learning Setting

An RL problem is modeled as a Markov Decision Process (MDP):

- States S
- Actions A
- Transition $P(s' \mid s, a)$
- Reward $R(s, a)$
- Discount factor γ

The agent's goal is to find a policy $\pi(a \mid s)$ that maximizes expected return:

$$G_t = \sum_{k=0}^{\infty} \gamma^k R_{t+k+1}$$

2. Value Functions

The value function measures how good a state (or state-action pair) is.

- State-value:
$$V^\pi(s) = \mathbb{E}_\pi[G_t | S_t = s]$$
- Action-value (Q-function):
$$Q^\pi(s, a) = \mathbb{E}_\pi[G_t | S_t = s, A_t = a]$$

3. Bellman Equation

The Bellman equation relates a state's value to its neighbors:

$$Q^*(s,a) = R(s,a) + \gamma \max_{a'} Q^*(s',a')$$

This recursive definition drives value iteration and Q-learning.

4. Q-Learning

Q-learning learns the optimal action-value function off-policy (independent of behavior policy):

Update Rule:

$$Q(s,a) \leftarrow Q(s,a) + \alpha[r + \gamma \max_{a'} Q(s',a') - Q(s,a)]$$

Tiny Code

```
Q[s][a] += alpha * (r + gamma * max(Q[s_next]) - Q[s][a]);
s = s_next;
```

Repeat while exploring (e.g., ε-greedy):

- With probability ε, choose a random action
- With probability $1 - \varepsilon$, choose the best action

Over time, Q converges to Q^*.

5. Exploration vs Exploitation

RL is a balancing act:

- Exploration: try new actions to gather knowledge- Exploitation: use current best knowledge to maximize reward Strategies:
- -greedy- Softmax action selection- Upper Confidence Bound (UCB)

6. Policy Gradient Methods

Instead of learning Q-values, learn the policy directly. Represent policy with parameters θ:

$$\pi_\theta(a|s) = P(a|s;\theta)$$

Goal: maximize expected return

$$J(\theta) = \mathbb{E} * \pi * \theta[G_t]$$

Gradient ascent update:

$$\theta \leftarrow \theta + \alpha \nabla_\theta J(\theta)$$

REINFORCE Algorithm:

$$\nabla_\theta J(\theta) = \mathbb{E}\big[G_t \nabla_\theta \log \pi_\theta(a_t|s_t)\big]$$

Tiny Code

```
theta += alpha * G_t * grad_logpi(a_t, s_t);
```

7. Actor-Critic Architecture

Combines policy gradient (actor) + value estimation (critic).

- Actor: updates policy- Critic: estimates value (baseline) Update:

$$\theta \leftarrow \theta + \alpha_\theta \delta_t \nabla_\theta \log \pi_\theta(a_t|s_t)$$

$$w \leftarrow w + \alpha_w \delta_t \nabla_w V_w(s_t)$$

with TD error:

$$\delta_t = r + \gamma V(s') - V(s)$$

8. Comparing Methods

Method	Type	Learns	On/Off Policy	Continuous?	
Q-learning	Value-based	Q(s, a)	Off-policy	No	
Policy Gradient	Policy-based	(a	s)	On-policy	Yes
Actor-Critic	Hybrid	Both	On-policy	Yes	

9. Extensions

- Deep Q-Networks (DQN): use neural nets for Q(s, a)- PPO / A3C: advanced actor-critic methods- TD( ): tradeoff between MC and TD learning- Double Q-learning: reduce overestimation- Entropy regularization: encourage exploration

10. Why It Matters

Reinforcement learning powers autonomous agents, game AIs, and control systems. It's the foundation of AlphaGo, robotics control, and adaptive decision systems.

> "An agent learns not from instruction but from experience."

Try It Yourself

1. Implement Q-learning for a grid-world maze.
2. Add -greedy exploration.
3. Visualize the learned policy.
4. Try REINFORCE with a simple policy (e.g. softmax over actions).
5. Compare convergence of Q-learning vs Policy Gradient.

98. Approximation and Online Algorithms

In the real world, we often can't wait for a perfect solution , data arrives on the fly, or the problem is too hard to solve exactly. That's where approximation and online algorithms shine. They aim for good-enough results, fast and adaptively, under uncertainty.

1. The Big Picture

- Approximation algorithms: Solve NP-hard problems with provable bounds.- Online algorithms: Make immediate decisions without knowing the future. Both trade optimality for efficiency or adaptability.

2. Approximation Algorithms

An approximation algorithm finds a solution within a factor ρ of the optimal.

If (C) is cost of the algorithm, and C^* is optimal cost:

$$\rho = \max\left(\frac{C}{C^*}, \frac{C^*}{C}\right)$$

Example: $\rho = 2 \rightarrow$ solution at most twice worse than optimal.

3. Example: Vertex Cover

Problem: Given graph (G(V,E)), choose smallest set of vertices covering all edges.

Algorithm (2-approximation):

1. Initialize cover =
2. While edges remain:
    - Pick any edge (u, v) - Add both u, v to cover - Remove all edges incident on u or v Guarantee: At most 2× optimal size.

Tiny Code

```
cover = {};
while (!edges.empty()) {
    (u, v) = edges.pop();
    cover.add(u);
    cover.add(v);
    remove_incident_edges(u, v);
}
```

4. Example: Metric TSP (Triangle Inequality)

Algorithm (Christofides):

1. Find MST
2. Find odd-degree vertices
3. Find min perfect matching
4. Combine + shortcut to get tour

Guarantee: 1.5 × optimal.

5. Greedy Approximation: Set Cover

Goal: Cover universe (U) with minimum sets S_i.

Greedy Algorithm: Pick set covering most uncovered elements each time. Guarantee: $H_n \approx \ln n$ factor approximation.

6. Online Algorithms

Online algorithms must decide now, before future input is known.

Goal: Minimize competitive ratio:

$$\text{CR} = \max_{\text{input}} \frac{\text{Cost} * \text{online}}{\text{Cost} * \text{optimal offline}}$$

Lower CR $\rightarrow$ better adaptability.

7. Classic Example: Online Paging

You have k pages in cache, sequence of page requests.

- If page in cache $\rightarrow$ hit- Else $\rightarrow$ miss, must evict one page Strategies:
- LRU (Least Recently Used): evict oldest- FIFO: evict first loaded- Random: pick randomly Competitive Ratio:
- LRU: (k)- Random: (2k-1)

Tiny Code

```
cache = LRUCache(k);
for (page in requests) {
    if (!cache.contains(page))
        cache.evict_oldest();
    cache.add(page);
}
```

8. Online Bipartite Matching (Karp-Vazirani-Vazirani)

Given offline set U and online set V (arrives one by one), match greedily. Competitive ratio: $1 - \frac{1}{e}$

Used in ad allocation and resource assignment.

9. Approximation + Online Together

Modern algorithms blend both:

- Streaming algorithms: One pass, small memory (Count-Min, reservoir sampling)- Online learning: Update models incrementally (SGD, perceptron)- Approximate dynamic programming: RL and heuristic search These are approximate online solvers , both quick and adaptive.

10. Why It Matters

Approximation algorithms give us provable near-optimal answers. Online algorithms give us real-time adaptivity. Together, they model intelligence under limits , when time and information are scarce.

> "Sometimes, good and on time beats perfect and late."

Try It Yourself

1. Implement 2-approx vertex cover on a small graph.
2. Simulate online paging with LRU vs Random.
3. Build a greedy set cover solver.
4. Measure competitive ratio on test sequences.
5. Combine ideas: streaming + approximation for big data filtering.

99. Fairness, Causal Inference, and Robust Optimization

As algorithms increasingly shape decisions , from hiring to lending to healthcare , we must ensure they're fair, causally sound, and robust to uncertainty. This section blends ideas from ethics, statistics, and optimization to make algorithms not just efficient, but responsible and reliable.

1. Why Fairness Matters

Machine learning systems often inherit biases from data. Without intervention, they can amplify inequality or discrimination.

Fairness-aware algorithms explicitly measure and correct these effects.

Common sources of bias:

- Historical bias (biased data)- Measurement bias (imprecise features)- Selection bias (skewed samples) The goal: equitable treatment across sensitive groups (gender, race, region, etc.)

2. Formal Fairness Criteria

Several fairness notions exist, often conflicting:

Criterion	Description	Example
Demographic Parity	($\mathrm{P}\hat{Y} = 1 \mid A = a = \mathrm{P}\hat{Y} = 1 \mid A = b$)	Equal positive rate
Equal Opportunity	Equal true positive rates	Same recall for all groups
Equalized Odds	Equal TPR & FPR	Balanced errors
Calibration	Same predicted probability meaning	If model says 70%, all groups should achieve 70%

No single measure fits all , fairness depends on context and trade-offs.

3. Algorithmic Fairness Techniques

1. Pre-processing Rebalance or reweight data before training. Example: reweighing, sampling.
2. In-processing Add fairness constraints to loss function. Example: adversarial debiasing.
3. Post-processing Adjust predictions after training. Example: threshold shifting.

Tiny Code (Adversarial Debiasing Skeleton)

```
for x, a, y in data:
    y_pred = model(x)
    loss_main = loss_fn(y_pred, y)
    loss_adv = adv_fn(y_pred, a)
    loss_total = loss_main -   * loss_adv
    update(loss_total)
```

Here, the adversary tries to predict sensitive attribute, encouraging invariance.

4. Causal Inference Basics

Correlation causation. To reason about fairness and robustness, we need causal understanding , what *would* happen if we changed something.

Causal inference models relationships via Directed Acyclic Graphs (DAGs):

- Nodes: variables- Edges: causal influence

5. Counterfactual Reasoning

A counterfactual asks:

> "What would the outcome be if we intervened differently?"

Formally:

$$P(Y_{do(X=x)})$$

Used in:

- Fairness (counterfactual fairness)- Policy evaluation- Robust decision making

6. Counterfactual Fairness

An algorithm is counterfactually fair if prediction stays the same under hypothetical changes to sensitive attributes.

$$\widehat{Y} * A \leftarrow a(U) = \widehat{Y} * A \leftarrow a'(U)$$

This requires causal models , not just data.

7. Robust Optimization

In uncertain environments, we want solutions that hold up under worst-case conditions.

Formulation:

$$\min_{x} \max_{\xi \in \Xi} f(x, \xi)$$

where Ξ is the uncertainty set.

Example: Design a portfolio that performs well under varying market conditions.

Tiny Code

```
double robust_objective(double x[], Scenario Xi[], int N) {
    double worst = -INF;
    for (i=0; i<N; i++)
        worst = max(worst, f(x, Xi[i]));
    return worst;
}
```

This searches for a solution minimizing worst-case loss.

8. Distributional Robustness

Instead of worst-case instances, protect against worst-case distributions:

$$\min_{\theta} \sup_{Q \in \mathcal{B}(P)} \mathbb{E}_{x \sim Q}[L(\theta, x)]$$

Used in adversarial training and domain adaptation.

Example: Add noise or perturbations to improve resilience:

```
x_adv = x +   * sign(grad(loss, x))
```

9. Balancing Fairness, Causality, and Robustness

Goal	Method	Challenge
Fairness	Parity, Adversarial, Counterfactual	Competing definitions
Causality	DAGs, do-calculus, SCMs	Identifying true structure
Robustness	Min-max, DRO, Adversarial Training	Trade-off with accuracy

Real-world design involves balancing trade-offs.

Sometimes improving fairness reduces accuracy, or robustness increases conservatism.

10. Why It Matters

Algorithms don't exist in isolation , they affect people. Embedding fairness, causality, and robustness ensures systems are trustworthy, interpretable, and just.

> "The goal is not just intelligent algorithms , but responsible ones."

Try It Yourself

1. Train a simple classifier on biased data.
2. Apply reweighing or adversarial debiasing.
3. Draw a causal DAG of your data features.
4. Compute counterfactual fairness for a sample.
5. Implement a robust loss using adversarial perturbations.

100. AI Planning, Search, and Learning Systems

AI systems are not just pattern recognizers , they are decision makers. They plan, search, and learn in structured environments, choosing actions that lead to long-term goals. This section explores how modern AI combines planning, search, and learning to solve complex tasks.

1. What Is AI Planning?

AI planning is about finding a sequence of actions that transforms an initial state into a goal state.

Formally, a planning problem consists of:

- States (S)- Actions (A)- Transition function (T(s, a) $\rightarrow$s')- Goal condition $G \subseteq S$- Cost function (c(a)) The objective: Find a plan $\pi = [a_1, a_2, \ldots, a_n]$ minimizing total cost or maximizing reward.

2. Search-Based Planning

At the heart of planning lies search. Search explores possible action sequences, guided by heuristics.

Algorithm	Type	Description
DFS	Uninformed	Deep exploration, no guarantee
BFS	Uninformed	Finds shortest path
Dijkstra	Weighted	Optimal if costs 0
A*	Heuristic	Combines cost + heuristic

A* Search Formula:

$$f(n) = g(n) + h(n)$$

where:

- (g(n)): cost so far- (h(n)): heuristic estimate to goal If (h) is admissible, A* is optimal.

Tiny Code (A* Skeleton)

```
priority_queue<Node> open;
g[start] = 0;
open.push({start, h(start)});

while (!open.empty()) {
    n = open.pop_min();
    if (goal(n)) break;
    for (a in actions(n)) {
        s = step(n, a);
        cost = g[n] + c(n, a);
        if (cost < g[s]) {
            g[s] = cost;
            f[s] = g[s] + h(s);
            open.push({s, f[s]});
        }
    }
}
```

3. Heuristics and Admissibility

A heuristic (h(s)) estimates distance to the goal.

- Admissible: never overestimates- Consistent: satisfies triangle inequality Examples:
- Manhattan distance (grids)- Euclidean distance (geometry)- Pattern databases (puzzles) Good heuristics = faster convergence.

4. Classical Planning (STRIPS)

In symbolic AI, states are represented by facts (predicates), and actions have preconditions and effects.

Example:

```
Action: Move(x, y)
Precondition: At(x), Clear(y)
Effect: ¬At(x), At(y)
```

Search happens in logical state space.

Planners:

- Forward search (progression)- Backward search (regression)- Heuristic planners (FF, HSP)

5. Hierarchical Planning

Break complex goals into subgoals.

- HTN (Hierarchical Task Networks): Define high-level tasks broken into subtasks.

Example: "Make dinner" → [Cook rice, Stir-fry vegetables, Set table]

Hierarchy makes planning modular and interpretable.

6. Probabilistic Planning

When actions are uncertain:

- MDPs: full observability, stochastic transitions- POMDPs: partial observability Use value iteration, policy iteration, or Monte Carlo planning.

7. Learning to Plan

Combine learning with search:

- Learned heuristics: neural networks approximate (h(s))- AlphaZero-style planning: learn value + policy, guide tree search- Imitation learning: mimic expert demonstrations This bridges classical AI and modern ML.

Tiny Code (Learning-Guided A*)

```
f = g + alpha * learned_heuristic(s)
```

Neural net learns (h_ (s)) from solved examples.

8. Integrated Systems

Modern AI stacks combine:

- Search (planning backbone)- Learning (policy, heuristic, model)- Simulation (data generation) Examples:
- AlphaZero: self-play + MCTS + neural nets- MuZero: learns model + value + policy jointly- Large Language Agents: use reasoning + memory + search

9. Real-World Applications

- Robotics: motion planning, pathfinding- Games: Go, Chess, strategy games- Logistics: route optimization- Autonomy: drones, vehicles, AI assistants- Synthesis: program and query generation Each blends symbolic reasoning and statistical learning.

10. Why It Matters

Planning, search, and learning form the triad of intelligence:

- Search explores possibilities- Planning sequences actions toward goals- Learning adapts heuristics from experience Together, they power systems that think, adapt, and act.

  "Intelligence is not just knowing , it is choosing wisely under constraints."

Try It Yourself

1. Implement A* search on a grid maze.
2. Add a Manhattan heuristic.
3. Extend to probabilistic transitions (simulate noise).
4. Build a simple planner with preconditions and effects.
5. Train a neural heuristic to guide search on puzzles.

Chapter 1. Foundatmemtions of Algorithms

Section 1. What is an algorithms?

1 Euclid's GCD

Euclid's algorithm is one of the oldest and most elegant procedures in mathematics. It computes the greatest common divisor (GCD) of two integers by repeatedly applying a simple rule: replace the larger number with its remainder when divided by the smaller. When the remainder becomes zero, the smaller number at that step is the GCD.

What Problem Are We Solving?

We want the greatest common divisor of two integers a and b: the largest number that divides both without a remainder.

A naive way would be to check all numbers from $\min(a, b)$ down to 1. That's $O(\min(a, b))$ steps, which is too slow for large inputs. Euclid's insight gives a much faster recursive method using division:

$$\gcd(a, b) = \begin{cases} a, & \text{if } b = 0, \\ \gcd(b, a \bmod b), & \text{otherwise.} \end{cases}$$

How It Works (Plain Language)

Imagine two sticks of lengths a and b. You can keep cutting the longer stick by the shorter one until one divides evenly. The length of the last nonzero remainder is the GCD.

Steps:

1. Take a, b with $a \geq b$.
2. Replace a by b, and b by $a \bmod b$.
3. Repeat until $b = 0$.
4. Return a.

This process always terminates, since b strictly decreases each step.

Example Step by Step

Find $\gcd(48, 18)$:

Step	a	b	$a \bmod b$
1	48	18	12
2	18	12	6
3	12	6	0

When $b = 0$, $a = 6$. So $\gcd(48, 18) = 6$.

Tiny Code (Python)

```
def gcd(a, b):
    while b != 0:
        a, b = b, a % b
    return a

print(gcd(48, 18))  # Output: 6
```

Why It Matters

- Foundational example of algorithmic thinking
- Core building block in modular arithmetic, number theory, and cryptography
- Efficient: runs in $O(\log \min(a, b))$ steps
- Easy to implement iteratively or recursively

A Gentle Proof (Why It Works)

If $a = bq + r$, any common divisor of a and b also divides r, since $r = a - bq$. Thus, the set of common divisors of (a, b) and (b, r) is the same, and their greatest element (the GCD) is unchanged.

Repeatedly applying this property leads to $b = 0$, where $\gcd(a, 0) = a$.

Try It Yourself

1. Compute $\gcd(270, 192)$ step by step.
2. Implement the recursive version:

$$\gcd(a, b) = \gcd(b, , a \bmod b)$$

3. Extend to find $\gcd(a, b, c)$ using $\gcd(\gcd(a, b), c)$.

Test Cases

Input (a, b)	Expected Output
(48, 18)	6
(270, 192)	6
(7, 3)	1
(10, 0)	10

Complexity

Operation	Time	Space
GCD	$O(\log \min(a, b))$	$O(1)$

Euclid's GCD algorithm is where algorithmic elegance begins, a timeless loop of division that turns mathematics into motion.

2 Sieve of Eratosthenes

The Sieve of Eratosthenes is a classic ancient algorithm for finding all prime numbers up to a given limit. It works by iteratively marking the multiples of each prime, starting from 2. The numbers that remain unmarked at the end are primes.

What Problem Are We Solving?

We want to find all prime numbers less than or equal to n. A naive method checks each number k by testing divisibility from 2 to $\sqrt{k}$, which is too slow for large n. The sieve improves this by using elimination instead of repeated checking.

We aim for an algorithm with time complexity close to $O(n \log \log n)$.

How It Works (Plain Language)

1. Create a list `is_prime[0..n]` and mark all as true.
2. Mark 0 and 1 as non-prime.
3. Starting from $p = 2$, if p is still marked prime:
   - Mark all multiples of p (from p^2 to n) as non-prime.
4. Increment p and repeat until $p^2 > n$.
5. All indices still marked true are primes.

This process "filters out" composite numbers step by step, just like passing sand through finer and finer sieves.

Example Step by Step

Find all primes up to 30:

Start: $[2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30]$

- $p = 2$: cross out multiples of 2
- $p = 3$: cross out multiples of 3
- $p = 5$: cross out multiples of 5

Remaining numbers: $2, 3, 5, 7, 11, 13, 17, 19, 23, 29$

Tiny Code (Python)

```
def sieve(n):
    is_prime = [True] * (n + 1)
    is_prime[0] = is_prime[1] = False

    p = 2
    while p * p <= n:
        if is_prime[p]:
            for i in range(p * p, n + 1, p):
                is_prime[i] = False
        p += 1

    return [i for i in range(2, n + 1) if is_prime[i]]
```

```
print(sieve(30))  # [2, 3, 5, 7, 11, 13, 17, 19, 23, 29]
```

Why It Matters

- One of the earliest and most efficient ways to generate primes
- Forms the basis for number-theoretic algorithms and cryptographic systems
- Conceptually simple yet mathematically deep
- Demonstrates elimination instead of brute force

A Gentle Proof (Why It Works)

Every composite number n has a smallest prime divisor $p \leq \sqrt{n}$. Thus, when we mark multiples of primes up to $\sqrt{n}$, every composite number is crossed out by its smallest prime factor. Numbers that remain unmarked are prime by definition.

Try It Yourself

1. Run the sieve for $n = 50$ and list primes.
2. Modify to count primes instead of listing them.
3. Compare runtime with naive primality tests for large n.
4. Extend to a segmented sieve for $n > 10^7$.

Test Cases

Input n	Expected Primes
10	[2, 3, 5, 7]
20	[2, 3, 5, 7, 11, 13, 17, 19]
30	[2, 3, 5, 7, 11, 13, 17, 19, 23, 29]

Complexity

Operation	Time	Space
Sieve	$O(n \log \log n)$	$O(n)$

The Sieve of Eratosthenes turns the search for primes into a graceful pattern of elimination, simple loops revealing the hidden order of numbers.

3 Linear Step Trace

A Linear Step Trace is a simple yet powerful visualization tool for understanding how an algorithm progresses line by line. It records each step of execution, showing how variables change over time, helping beginners see the *flow* of computation.

What Problem Are We Solving?

When learning algorithms, it's easy to lose track of what's happening after each instruction. A Linear Step Trace helps us *see* execution in motion, one step, one update at a time.

Instead of abstract reasoning alone, we follow the exact state changes that occur during the run, making debugging and reasoning far easier.

How It Works (Plain Language)

1. Write down your pseudocode or code.
2. Create a table with columns for step number, current line, and variable values.
3. Each time a line executes, record the line number and updated variables.
4. Continue until the program finishes.

This method is algorithm-agnostic, it works for loops, recursion, conditionals, and all flow patterns.

Example Step by Step

Let's trace a simple loop:

```
sum = 0
for i in 1..4:
    sum = sum + i
```

Step	Line	i	sum	Note
1	1	-	0	Initialize sum
2	2	1	0	Loop start
3	3	1	1	sum = 0 + 1
4	2	2	1	Next iteration
5	3	2	3	sum = 1 + 2
6	2	3	3	Next iteration
7	3	3	6	sum = 3 + 3

Step	Line	i	sum	Note
8	2	4	6	Next iteration
9	3	4	10	sum = 6 + 4
10	-	-	10	End

Final result: $sum = 10$.

Tiny Code (Python)

```
sum = 0
trace = []

for i in range(1, 5):
    trace.append((i, sum))
    sum += i

trace.append(("final", sum))
print(trace)
# [(1, 0), (2, 1), (3, 3), (4, 6), ('final', 10)]
```

Why It Matters

- Builds *step-by-step literacy* in algorithm reading
- Great for teaching loops, conditions, and recursion
- Reveals hidden assumptions and logic errors
- Ideal for debugging and analysis

A Gentle Proof (Why It Works)

Every algorithm can be expressed as a sequence of state transitions. If each transition is recorded, we obtain a complete trace of computation. Thus, correctness can be verified by comparing expected vs. actual state sequences. This is equivalent to an inductive proof: each step matches the specification.

Try It Yourself

1. Trace a recursive factorial function step by step.
2. Add a "call stack" column to visualize recursion depth.
3. Trace an array-sorting loop and mark swaps.
4. Compare traces before and after optimization.

Test Cases

Program	Expected Final State
sum of 1..4	sum = 10
sum of 1..10	sum = 55
factorial(5)	result = 120

Complexity

Operation	Time	Space
Trace Recording	$O(n)$	$O(n)$

A Linear Step Trace transforms invisible logic into a visible path, a story of each line's journey, one state at a time.

4 Algorithm Flow Diagram Builder

An Algorithm Flow Diagram Builder turns abstract pseudocode into a visual map, a diagram of control flow that shows where decisions branch, where loops repeat, and where computations end. It's the bridge between code and comprehension.

What Problem Are We Solving?

When an algorithm becomes complex, it's easy to lose track of its structure. We may know what each line does, but not *how control moves* through the program.

A flow diagram lays out that control structure explicitly, revealing loops, branches, merges, and exits at a glance.

How It Works (Plain Language)

1. Identify actions and decisions
    - Actions: assignments, computations
    - Decisions: if, while, for, switch
2. Represent them with symbols
    - Rectangle → action
    - Diamond → decision
    - Arrow → flow of control
3. Connect nodes based on what happens next
4. Loop back arrows for iterations, and mark exit points

This yields a graph of control, a shape you can follow from start to finish.

Example Step by Step

Let's draw the flow for finding the sum of numbers 1 to n:

Pseudocode:

```
sum = 0
i = 1
while i   n:
    sum = sum + i
    i = i + 1
print(sum)
```

Flow Outline:

1. Start
2. Initialize `sum = 0`, `i = 1`
3. Decision: `i   n?`
    - Yes → Update `sum`, Increment `i` → Loop back
    - No → Print sum → End

Textual Diagram:

```
  [Start]
     |
[sum=0, i=1]
     |
  (i   n?) ----No----> [Print sum] -> [End]
     |
    Yes
     |
 [sum = sum + i]
     |
 [i = i + 1]
     |
   (Back to i   n?)
```

Tiny Code (Python)

```python
def sum_to_n(n):
    sum = 0
    i = 1
    while i <= n:
        sum += i
        i += 1
    return sum
```

Use this code to generate flow diagrams automatically with libraries like `graphviz` or `pyflowchart`.

Why It Matters

- Reveals structure at a glance
- Makes debugging easier by visualizing possible paths
- Helps design before coding
- Universal representation (language-agnostic)

A Gentle Proof (Why It Works)

Each algorithm's execution path can be modeled as a directed graph:

- Vertices = program states or actions
- Edges = transitions (next step)

A flow diagram is simply this control graph rendered visually. It preserves correctness since each edge corresponds to a valid jump in control flow.

Try It Yourself

1. Draw a flowchart for binary search.
2. Mark all possible comparison outcomes.
3. Add loopbacks for mid-point updates.
4. Compare with recursive version, note structural difference.

Test Cases

Algorithm	Key Decision Node	Expected Paths
Sum loop	$i \leq n$	2 (continue, exit)
Binary search	$key == mid?$	3 (left, right, found)

Complexity

Operation	Time	Space
Diagram Construction	$O(n)$ nodes	$O(n)$ edges

An Algorithm Flow Diagram is a lens, it turns invisible execution paths into a map you can walk, from "Start" to "End."

5 Long Division

Long Division is a step-by-step algorithm for dividing one integer by another. It's one of the earliest examples of a systematic computational procedure, showing how large problems can be solved through a sequence of local, repeatable steps.

What Problem Are We Solving?

We want to compute the quotient and remainder when dividing two integers a (dividend) and b (divisor).

Naively, repeated subtraction would take $O(a/b)$ steps, far too many for large numbers. Long Division improves this by grouping subtractions by powers of 10, performing digit-wise computation efficiently.

How It Works (Plain Language)

1. Align digits of a (the dividend).
2. Compare current portion of a to b.
3. Find the largest multiple of b that fits in the current portion.
4. Subtract, write the quotient digit, and bring down the next digit.
5. Repeat until all digits have been processed.
6. The digits written form the quotient; what's left is the remainder.

This method extends naturally to decimals, just continue bringing down zeros.

Example Step by Step

Compute $153 \div 7$:

Step	Portion	Quotient Digit	Remainder	Action
1	15	2	1	$7 \times 2 = 14$, subtract $15 - 14 = 1$
2	Bring down 3 → 13	1	6	$7 \times 1 = 7$, subtract $13 - 7 = 6$
3	No more digits	,	6	Done

Result: Quotient $= 21$, Remainder $= 6$ Check: $7 \times 21 + 6 = 153$

Tiny Code (Python)

```
def long_division(a, b):
    quotient = 0
    remainder = 0
    for digit in str(a):
        remainder = remainder * 10 + int(digit)
        q = remainder // b
        remainder = remainder % b
        quotient = quotient * 10 + q
    return quotient, remainder

print(long_division(153, 7))  # (21, 6)
```

Why It Matters

- Introduces loop invariants and digit-by-digit reasoning
- Foundation for division in arbitrary-precision arithmetic
- Core to implementing division in CPUs and big integer libraries
- Demonstrates decomposing a large task into simple, local operations

A Gentle Proof (Why It Works)

At each step:

- The current remainder r_i satisfies $0 \leq r_i < b$.
- The algorithm maintains the invariant:

  $$a = b \times Q_i + r_i$$

  where Q_i is the partial quotient so far.
- Each step reduces the unprocessed part of a, ensuring termination with correct Q and r.

Try It Yourself

1. Perform $2345 \div 13$ by hand.
2. Verify with Python's `divmod(2345, 13)`.
3. Extend your code to produce decimal expansions.
4. Compare digit-wise trace with manual process.

Test Cases

Dividend a	Divisor b	Expected Output (Q, R)
153	7	(21, 6)
100	8	(12, 4)
99	9	(11, 0)
23	5	(4, 3)

Complexity

Operation	Time	Space
Long Division	$O(d)$	$O(1)$

where d is the number of digits in a.

Long Division is more than arithmetic, it's the first encounter with algorithmic thinking: state, iteration, and correctness unfolding one digit at a time.

6 Modular Addition

Modular addition is arithmetic on a clock, we add numbers, then wrap around when reaching a fixed limit. It's the simplest example of modular arithmetic, a system that underlies cryptography, hashing, and cyclic data structures.

What Problem Are We Solving?

We want to add two integers a and b, but keep the result within a fixed modulus m. That means we compute the remainder after dividing the sum by m.

Formally, we want:

$$(a + b) \bmod m$$

This ensures results always lie in the range $[0, m - 1]$, regardless of how large a or b become.

How It Works (Plain Language)

1. Compute the sum $s = a + b$.
2. Divide s by m to find the remainder.
3. The remainder is the modular sum.

If $s \geq m$, we "wrap around" by subtracting m until it fits in the modular range.

This idea is like hours on a clock: $10 + 5$ hours on a 12-hour clock $\rightarrow 3$.

Example Step by Step

Let $a = 10$, $b = 7$, $m = 12$.

1. Compute $s = 10 + 7 = 17$.
2. $17 \bmod 12 = 5$.
3. So $(10 + 7) \bmod 12 = 5$.

Check: $17 - 12 = 5$, fits in $[0, 11]$.

Tiny Code (Python)

```
def mod_add(a, b, m):
    return (a + b) % m

print(mod_add(10, 7, 12))  # 5
```

Why It Matters

- Foundation of modular arithmetic
- Used in hashing, cyclic buffers, and number theory
- Crucial for secure encryption (RSA, ECC)
- Demonstrates wrap-around logic in bounded systems

A Gentle Proof (Why It Works)

By definition of modulus:

$$x \bmod m = r \quad \text{such that } x = q \times m + r,\ 0 \le r < m$$

Thus, for $a + b = q \times m + r$, we have $(a + b) \bmod m = r$. All equivalent sums differ by a multiple of m, so modular addition preserves congruence:

$$(a + b) \bmod m \equiv (a \bmod m + b \bmod m) \bmod m$$

Try It Yourself

1. Compute $(15 + 8) \bmod 10$.
2. Verify $(a + b) \bmod m = ((a \bmod m) + (b \bmod m)) \bmod m$.
3. Test with negative values: $(-3 + 5) \bmod 7$.
4. Apply to time arithmetic: what is $11 + 5$ on a 12-hour clock?

Test Cases

a	b	m	Result
10	7	12	5
5	5	10	0
8	15	10	3
11	5	12	4

Complexity

Operation	Time	Space
Modular Addition	$O(1)$	$O(1)$

Modular addition teaches the rhythm of modular arithmetic, every sum wraps back into harmony, always staying within its finite world.

7 Base Conversion

Base conversion is the algorithmic process of expressing a number in a different numeral system. It's how we translate between decimal, binary, octal, hexadecimal, or any base, the language of computers and mathematics alike.

What Problem Are We Solving?

We want to represent an integer n in base b. In base 10, digits go from 0 to 9. In base 2, only 0 and 1. In base 16, digits are $0 \ldots 9$ and $A \ldots F$.

The goal is to find a sequence of digits $d_k d_{k-1} \ldots d_0$ such that:

$$n = \sum_{i=0}^{k} d_i \cdot b^i$$

where $0 \leq d_i < b$.

How It Works (Plain Language)

1. Start with the integer n.
2. Repeatedly divide n by b.
3. Record the remainder each time (these are the digits).
4. Stop when $n = 0$.
5. The base-b representation is the remainders read in reverse order.

This works because division extracts digits starting from the least significant position.

Example Step by Step

Convert 45 to binary ($b = 2$):

Step	n	$n \div 2$	Remainder
1	45	22	1
2	22	11	0
3	11	5	1
4	5	2	1
5	2	1	0
6	1	0	1

Read remainders upward: 101101

So $45_{10} = 101101_2$.

Check: $1 \cdot 2^5 + 0 \cdot 2^4 + 1 \cdot 2^3 + 1 \cdot 2^2 + 0 \cdot 2^1 + 1 \cdot 2^0 = 32 + 0 + 8 + 4 + 0 + 1 = 45$

Tiny Code (Python)

```
def to_base(n, b):
    digits = []
    while n > 0:
        digits.append(n % b)
        n //= b
    return digits[::-1] or [0]

print(to_base(45, 2))  # [1, 0, 1, 1, 0, 1]
```

Why It Matters

- Converts numbers between human and machine representations
- Core in encoding, compression, and cryptography
- Builds intuition for positional number systems
- Used in parsing, serialization, and digital circuits

A Gentle Proof (Why It Works)

Each division step produces one digit $r_i = n_i \bmod b$. We have:

$$n_i = b \cdot n_{i+1} + r_i$$

Unfolding the recurrence gives:

$$n = \sum_{i=0}^{k} r_i b^i$$

So collecting remainders in reverse order reconstructs n exactly.

Try It Yourself

1. Convert 100_{10} to base 8.
2. Convert 255_{10} to base 16.
3. Verify by recombining digits via $\sum d_i b^i$.
4. Write a reverse converter: base-b to decimal.

Test Cases

Decimal n	Base b	Representation
45	2	101101
100	8	144
255	16	FF
31	5	111

Complexity

Operation	Time	Space
Base Conversion	$O(\log_b n)$	$O(\log_b n)$

Base conversion is arithmetic storytelling, peeling away remainders until only digits remain, revealing the same number through a different lens.

8 Factorial Computation

Factorial computation is the algorithmic act of multiplying a sequence of consecutive integers, a simple rule that grows explosively. It lies at the foundation of combinatorics, probability, and mathematical analysis.

What Problem Are We Solving?

We want to compute the factorial of a non-negative integer n, written $n!$, defined as:

$$n! = n \times (n-1) \times (n-2) \times \cdots \times 1$$

with the base case:

$$0! = 1$$

Factorial counts the number of ways to arrange n distinct objects, the building block of permutations and combinations.

How It Works (Plain Language)

There are two main ways:

Iterative:

- Start with `result = 1`
- Multiply by each i from 1 to n
- Return result

Recursive:

- $n! = n \times (n-1)!$
- Stop when $n = 0$

Both methods produce the same result; recursion mirrors the mathematical definition, iteration avoids call overhead.

Example Step by Step

Compute 5!:

Step	n	Product
1	1	1
2	2	2
3	3	6
4	4	24
5	5	120

So $5! = 120$

Tiny Code (Python)

Iterative Version

```python
def factorial_iter(n):
    result = 1
    for i in range(1, n + 1):
        result *= i
    return result

print(factorial_iter(5))  # 120
```

Recursive Version

```
def factorial_rec(n):
    if n == 0:
        return 1
    return n * factorial_rec(n - 1)

print(factorial_rec(5))  # 120
```

Why It Matters

- Core operation in combinatorics, calculus, and probability
- Demonstrates recursion, iteration, and induction
- Grows rapidly, useful for testing overflow and asymptotics
- Appears in binomial coefficients, Taylor series, and permutations

A Gentle Proof (Why It Works)

By definition, $n! = n \times (n-1)!$. Assume $(n-1)!$ is correctly computed. Then multiplying by n yields $n!$.

By induction:

- Base case: $0! = 1$
- Step: if $(n-1)!$ is correct, so is $n!$

Thus, the recursive and iterative definitions are equivalent and correct.

Try It Yourself

1. Compute 6! both iteratively and recursively.
2. Print intermediate products to trace the growth.
3. Compare runtime for $n = 1000$ using both methods.
4. Explore factorial in floating point (`math.gamma`) for non-integers.

Input n	Expected Output $n!$

Test Cases

Input n	Expected Output $n!$
0	1
1	1
3	6
5	120
6	720

Complexity

Operation	Time	Space
Iterative	$O(n)$	$O(1)$
Recursive	$O(n)$	$O(n)$ (stack)

Factorial computation is where simplicity meets infinity, a single rule that scales from 1 to astronomical numbers with graceful inevitability.

9 Iterative Process Tracer

An Iterative Process Tracer is a diagnostic algorithm that follows each iteration of a loop, recording variable states, conditions, and updates. It helps visualize the evolution of a program's internal state, turning looping logic into a clear timeline.

What Problem Are We Solving?

When writing iterative algorithms, it's easy to lose sight of what happens at each step. Are variables updating correctly? Are loop conditions behaving as expected? A tracer captures this process, step by step, so we can verify correctness, find bugs, and teach iteration with clarity.

How It Works (Plain Language)

1. Identify the loop (for or while).
2. Before or after each iteration, record:
    - The iteration number
    - Key variable values
    - Condition evaluations
3. Store these snapshots in a trace table.
4. After execution, review how values evolve over time.

Think of it as an "execution diary", every iteration gets a journal entry.

Example Step by Step

Let's trace a simple accumulation:

```
sum = 0
for i in 1..5:
    sum = sum + i
```

Step	i	sum	Description
1	1	1	Add first number
2	2	3	Add second number
3	3	6	Add third number
4	4	10	Add fourth number
5	5	15	Add fifth number

Final result: $sum = 15$

Tiny Code (Python)

```python
def trace_sum(n):
    sum = 0
    trace = []
    for i in range(1, n + 1):
        sum += i
        trace.append((i, sum))
    return trace

print(trace_sum(5))
# [(1, 1), (2, 3), (3, 6), (4, 10), (5, 15)]
```

Why It Matters

- Turns hidden state changes into visible data
- Ideal for debugging loops and verifying invariants
- Supports algorithm teaching and step-by-step reasoning
- Useful in profiling, logging, and unit testing

A Gentle Proof (Why It Works)

An iterative algorithm is a sequence of deterministic transitions:

$$S_{i+1} = f(S_i)$$

Recording S_i at each iteration yields the complete trajectory of execution. The trace table captures all intermediate states, ensuring reproducibility and clarity, a form of operational proof.

Try It Yourself

1. Trace variable updates in a multiplication loop.
2. Add condition checks (e.g. early exits).
3. Record both pre- and post-update states.
4. Compare traces of iterative vs recursive versions.

Test Cases

Input n	Expected Trace
3	[(1, 1), (2, 3), (3, 6)]
4	[(1, 1), (2, 3), (3, 6), (4, 10)]
5	[(1, 1), (2, 3), (3, 6), (4, 10), (5, 15)]

Complexity

Operation	Time	Space
Tracing	$O(n)$	$O(n)$

An Iterative Process Tracer makes thinking visible, a loop's internal rhythm laid out, step by step, until the final note resolves.

10 Tower of Hanoi

The Tower of Hanoi is a legendary recursive puzzle that beautifully illustrates how complex problems can be solved through simple repeated structure. It's a timeless example of *divide and conquer* thinking in its purest form.

What Problem Are We Solving?

We want to move n disks from a source peg to a target peg, using one auxiliary peg. Rules:

1. Move only one disk at a time.
2. Never place a larger disk on top of a smaller one.

The challenge is to find the minimal sequence of moves that achieves this.

How It Works (Plain Language)

The key insight: To move n disks, first move $n-1$ disks aside, move the largest one, then bring the smaller ones back.

Steps:

1. Move $n-1$ disks from source $\rightarrow$ auxiliary
2. Move the largest disk from source $\rightarrow$ target
3. Move $n-1$ disks from auxiliary $\rightarrow$ target

This recursive structure repeats until the smallest disk moves directly.

Example Step by Step

For $n = 3$, pegs: A (source), B (auxiliary), C (target)

Step	Move
1	A → C
2	A → B
3	C → B
4	A → C
5	B → A
6	B → C
7	A → C

Total moves: $2^3 - 1 = 7$

Tiny Code (Python)

```
def hanoi(n, source, target, aux):
    if n == 1:
        print(f"{source} → {target}")
        return
    hanoi(n - 1, source, aux, target)
    print(f"{source} → {target}")
    hanoi(n - 1, aux, target, source)

hanoi(3, 'A', 'C', 'B')
```

Why It Matters

- Classic recursive pattern: break → solve → combine
- Demonstrates exponential growth ($2^n - 1$ moves)
- Trains recursive reasoning and stack visualization
- Appears in algorithm analysis, recursion trees, and combinatorics

A Gentle Proof (Why It Works)

Let $T(n)$ be the number of moves for n disks. We must move $n-1$ disks twice and one largest disk once:

$$T(n) = 2T(n-1) + 1, \quad T(1) = 1$$

Solving the recurrence:

$$T(n) = 2^n - 1$$

Each recursive step preserves rules and reduces the problem size, ensuring correctness by structural induction.

Try It Yourself

1. Trace $n = 2$ and $n = 3$ by hand.
2. Count recursive calls.
3. Modify code to record moves in a list.
4. Extend to display peg states after each move.

Test Cases

n	Expected Moves
1	1
2	3
3	7
4	15

Complexity

Operation	Time	Space
Moves	$O(2^n)$	$O(n)$ (recursion stack)

The Tower of Hanoi turns recursion into art, every move guided by symmetry, every step revealing how simplicity builds complexity one disk at a time.

Section 2. Measuring time and space

11 Counting Operations

Counting operations is the first step toward understanding time complexity. It's the art of translating code into math by measuring how many *basic steps* an algorithm performs, helping us predict performance before running it.

What Problem Are We Solving?

We want to estimate how long an algorithm takes, not by clock time, but by how many fundamental operations it executes. Instead of relying on hardware speed, we count abstract steps, comparisons, assignments, additions, each treated as one unit of work.

This turns algorithms into analyzable formulas.

How It Works (Plain Language)

1. Identify the unit step (like one comparison or addition).
2. Break the algorithm into lines or loops.
3. Count repetitions for each operation.
4. Sum all counts to get a total step function $T(n)$.
5. Simplify to dominant terms for asymptotic analysis.

We're not measuring *seconds*, we're measuring *structure*.

Example Step by Step

Count operations for:

```
sum = 0
for i in range(1, n + 1):
    sum += i
```

Breakdown:

Line	Operation	Count
1	Initialization	1
2	Loop comparison	$n + 1$
3	Addition + assignment	n

Total:

$$T(n) = 1 + (n+1) + n = 2n + 2$$

Asymptotically:

$$T(n) = O(n)$$

Tiny Code (Python)

```
def count_sum_ops(n):
    ops = 0
    ops += 1  # init sum
    for i in range(1, n + 1):
        ops += 1  # loop check
        ops += 1  # sum += i
    ops += 1  # final loop check
    return ops
```

Test: `count_sum_ops(5)` → `13`

Why It Matters

- Builds intuition for algorithm growth
- Reveals hidden costs (nested loops, recursion)
- Foundation for Big-O and runtime proofs
- Language-agnostic: works for any pseudocode

A Gentle Proof (Why It Works)

Every program can be modeled as a finite sequence of operations parameterized by input size n. If $f(n)$ counts these operations exactly, then for large n, growth rate $\Theta(f(n))$ matches actual performance up to constant factors. Counting operations therefore predicts asymptotic runtime behavior.

Try It Yourself

1. Count operations in a nested loop:

```
for i in range(n):
    for j in range(n):
        x += 1
```

2. Derive $T(n) = n^2 + 2n + 1$.
3. Simplify to $O(n^2)$.
4. Compare iterative vs recursive counting.

Test Cases

Algorithm	Step Function	Big-O
Linear Loop	$2n + 2$	$O(n)$
Nested Loop	$n^2 + 2n + 1$	$O(n^2)$
Constant Work	c	$O(1)$

Complexity

Operation	Time	Space
Counting Steps	$O(1)$ (analysis)	$O(1)$

Counting operations transforms code into mathematics, a microscope for understanding how loops, branches, and recursion scale with input size.

12 Loop Analysis

Loop analysis is the key to unlocking how algorithms grow, it tells us how many times a loop runs and, therefore, how many operations are performed. Every time you see a loop, you're looking at a formula in disguise.

What Problem Are We Solving?

We want to determine how many iterations a loop executes as a function of input size n. This helps us estimate total runtime before measuring it empirically.

Whether a loop is linear, nested, logarithmic, or mixed, understanding its iteration count reveals the algorithm's true complexity.

How It Works (Plain Language)

1. Identify the loop variable (like `i` in `for i in range(...)`).
2. Find its update rule, additive (`i += 1`) or multiplicative (`i *= 2`).
3. Solve for how many times the condition holds true.
4. Multiply by inner loop work if nested.
5. Sum all contributions from independent loops.

This transforms loops into algebraic expressions you can reason about.

Example Step by Step

Example 1: Linear Loop

```
for i in range(1, n + 1):
    work()
```

i runs from 1 to n, incrementing by 1. Iterations: n Work: $O(n)$

Example 2: Logarithmic Loop

```
i = 1
while i <= n:
    work()
    i *= 2
```

i doubles each step: $1, 2, 4, 8, \ldots, n$ Iterations: $\log_2 n + 1$ Work: $O(\log n)$

Example 3: Nested Loop

```
for i in range(n):
    for j in range(n):
        work()
```

Outer loop: n Inner loop: n Total work: $n \times n = n^2$

Tiny Code (Python)

```
def linear_loop(n):
    count = 0
    for i in range(n):
        count += 1
    return count  # n

def log_loop(n):
    count = 0
    i = 1
    while i <= n:
        count += 1
        i *= 2
    return count  #  log2(n)
```

Why It Matters

- Reveals complexity hidden inside loops
- Core tool for deriving $O(n)$, $O(\log n)$, and $O(n^2)$
- Makes asymptotic behavior predictable and measurable
- Works for for-loops, while-loops, and nested structures

A Gentle Proof (Why It Works)

Each loop iteration corresponds to a true condition in its guard. If the loop variable i evolves monotonically (by addition or multiplication), the total number of iterations is the smallest k satisfying the exit condition.

For additive updates:

$$i_0 + k \cdot \Delta \geq n \implies k = \frac{n - i_0}{\Delta}$$

For multiplicative updates:

$$i_0 \cdot r^k \geq n \implies k = \log_r \frac{n}{i_0}$$

Try It Yourself

1. Analyze loop:

```
i = n
while i > 0:
    i //= 2
```

   $\rightarrow O(\log n)$

2. Analyze double loop:

```
for i in range(n):
    for j in range(i):
        work()
```

   $\rightarrow \frac{n(n-1)}{2} = O(n^2)$

3. Combine additive + multiplicative loops.

Test Cases

Code Pattern	Iterations	Complexity
`for i in range(n)`	n	$O(n)$
`while i < n: i *= 2`	$\log_2 n$	$O(\log n)$
`for i in range(n): for j in range(n)`	n^2	$O(n^2)$
`for i in range(n): for j in range(i)`	$\frac{n(n-1)}{2}$	$O(n^2)$

Complexity

Operation	Time	Space
Loop Analysis	$O(1)$ (per loop)	$O(1)$

Loop analysis turns repetition into arithmetic, every iteration becomes a term, every loop a story in the language of growth.

13 Recurrence Expansion

Recurrence expansion is how we *unfold* recursive definitions to see their true cost. Many recursive algorithms (like Merge Sort or Quick Sort) define runtime in terms of smaller copies of themselves. By expanding the recurrence, we reveal the total work step by step.

What Problem Are We Solving?

Recursive algorithms often express their runtime as:

$$T(n) = a \cdot T!\left(\frac{n}{b}\right) + f(n)$$

Here:

- a = number of recursive calls
- b = factor by which input size is reduced
- $f(n)$ = work done outside recursion (splitting, merging, etc.)

We want to estimate $T(n)$ by expanding this relation until the base case.

How It Works (Plain Language)

Think of recurrence expansion as peeling an onion. Each recursive layer contributes some cost, and we add all layers until the base.

Steps:

1. Write the recurrence.
2. Expand one level: replace $T(\cdot)$ with its formula.
3. Repeat until the argument becomes the base case.
4. Sum the work done at each level.
5. Simplify the sum to get asymptotic form.

Example Step by Step

Take Merge Sort:

$$T(n) = 2T!\left(\frac{n}{2}\right) + n$$

Expand:

- Level 0: $T(n) = 2T(n/2) + n$
- Level 1: $T(n/2) = 2T(n/4) + n/2 \rightarrow$ Substitute $T(n) = 4T(n/4) + 2n$
- Level 2: $T(n) = 8T(n/8) + 3n$
- ...
- Level $\log_2 n$: $T(1) = c$

Sum work across levels:

$$T(n) = n \log_2 n + n = O(n \log n)$$

Tiny Code (Python)

```
def recurrence_expand(a, b, f, n, base=1):
    level = 0
    total = 0
    size = n
    while size >= base:
        cost = (a  level) * f(size)
        total += cost
        size //= b
        level += 1
    return total
```

Use `f = lambda x: x` for Merge Sort.

Why It Matters

- Core tool for analyzing recursive algorithms
- Builds intuition before applying the Master Theorem
- Turns abstract recurrence into tangible pattern
- Helps visualize total work per recursion level

A Gentle Proof (Why It Works)

At level i:

- There are a^i subproblems.
- Each subproblem has size $\frac{n}{b^i}$.
- Work per level: $a^i \cdot f!\left(\frac{n}{b^i}\right)$

Total cost:

$$T(n) = \sum_{i=0}^{\log_b n} a^i f!\left(\frac{n}{b^i}\right)$$

Depending on how $f(n)$ compares to $n^{\log_b a}$, either top, bottom, or middle levels dominate.

Try It Yourself

1. Expand $T(n) = 3T(n/2) + n^2$.
2. Expand $T(n) = T(n/2) + 1$.
3. Visualize total work per level.
4. Check your result with Master Theorem.

Test Cases

Recurrence	Expansion Result	Complexity
$T(n) = 2T(n/2) + n$	$n \log n$	$O(n \log n)$
$T(n) = T(n/2) + 1$	$\log n$	$O(\log n)$
$T(n) = 4T(n/2) + n$	n^2	$O(n^2)$

Complexity

Operation	Time	Space
Expansion	$O(\log n)$ levels	$O(\log n)$ tree depth

Recurrence expansion turns recursion into rhythm, each level adding its verse, the sum revealing the melody of the algorithm's growth.

14 Amortized Analysis

Amortized analysis looks beyond the worst case of individual operations to capture the *average cost per operation* over a long sequence. It tells us when "expensive" actions even out, revealing algorithms that are faster than they first appear.

What Problem Are We Solving?

Some operations occasionally take a long time (like resizing an array), but most are cheap. A naive worst-case analysis exaggerates total cost. Amortized analysis finds the true average cost across a sequence.

We're not averaging across *inputs*, but across *operations in one run*.

How It Works (Plain Language)

Suppose an operation is usually $O(1)$, but sometimes $O(n)$. If that expensive case happens rarely enough, the *average per operation* is still small.

Three main methods:

1. Aggregate method, total cost ÷ number of operations
2. Accounting method, charge extra for cheap ops, save credit for costly ones
3. Potential method, define potential energy (stored work) and track change

Example Step by Step

Dynamic Array Resizing

When an array is full, double its size and copy elements.

Operation	Cost	Comment
Insert #1–#1	1	insert directly
Insert #2	2	resize to 2, copy 1
Insert #3	3	resize to 4, copy 2
Insert #5	5	resize to 8, copy 4
…	…	…

Total cost after n inserts $2n$ Average cost $= 2n/n = O(1)$ So each insert is amortized $O(1)$, not $O(n)$.

Tiny Code (Python)

```
def dynamic_array(n):
    arr = []
    capacity = 1
    cost = 0
    for i in range(n):
        if len(arr) == capacity:
            capacity *= 2
            cost += len(arr)  # copying cost
        arr.append(i)
        cost += 1  # insert cost
    return cost, cost / n  # total, amortized average
```

Try `dynamic_array(10)` → roughly total cost 20, average 2.

Why It Matters

- Shows average efficiency over sequences
- Key to analyzing stacks, queues, hash tables, and dynamic arrays
- Explains why "occasionally expensive" operations are still efficient overall
- Separates perception (worst-case) from reality (aggregate behavior)

A Gentle Proof (Why It Works)

Let C_i = cost of ith operation, and n = total operations.

Aggregate Method:

$$\text{Amortized cost} = \frac{\sum_{i=1}^{n} C_i}{n}$$

If $\sum C_i = O(n)$, each operation's average = $O(1)$.

Potential Method:

Define potential Φ_i representing saved work. Amortized cost = $C_i + \Phi_i - \Phi_{i-1}$ Summing over all operations telescopes potential away, leaving total cost bounded by initial + final potential.

Try It Yourself

1. Analyze amortized cost for stack with occasional full pop.
2. Use accounting method to assign "credits" to inserts.
3. Show $O(1)$ amortized insert in hash table with resizing.
4. Compare amortized vs worst-case time.

Test Cases

Operation Type	Worst Case	Amortized
Array Insert (Doubling)	$O(n)$	$O(1)$
Stack Push	$O(1)$	$O(1)$
Queue Dequeue (2-stack)	$O(n)$	$O(1)$
Union-Find (Path Compression)	$O(\log n)$	$O(\alpha(n))$

Complexity

Analysis Type	Formula	Goal
Aggregate	$\frac{\text{Total Cost}}{n}$	Simplicity
Accounting	Assign credits	Intuition
Potential	$\Delta\Phi$	Formal rigor

Amortized analysis reveals the calm beneath chaos — a few storms don't define the weather, and one $O(n)$ moment doesn't ruin $O(1)$ harmony.

15 Space Counting

Space counting is the spatial twin of operation counting, instead of measuring time, we measure how much *memory* an algorithm consumes. Every variable, array, stack frame, or temporary buffer adds to the footprint. Understanding it helps us write programs that fit in memory and scale gracefully.

What Problem Are We Solving?

We want to estimate the space complexity of an algorithm — how much memory it needs as input size n grows.

This includes:

- Static space (fixed variables)
- Dynamic space (arrays, recursion, data structures)
- Auxiliary space (extra working memory beyond input)

Our goal: express total memory as a function $S(n)$.

How It Works (Plain Language)

1. Count primitive variables (constants, counters, pointers). $\rightarrow$ constant space $O(1)$
2. Add data structure sizes (arrays, lists, matrices). $\rightarrow$ often proportional to n, n^2, etc.
3. Add recursion stack depth, if applicable.
4. Ignore constants for asymptotic space, focus on growth.

In the end,

$$S(n) = S_{\text{static}} + S_{\text{dynamic}} + S_{\text{recursive}}$$

Example Step by Step

Example 1: Linear Array

```
arr = [0] * n
```

- n integers $\rightarrow O(n)$ space

Example 2: 2D Matrix

```
matrix = [[0] * n for _ in range(n)]
```

- $n \times n$ elements $\rightarrow O(n^2)$ space

Example 3: Recursive Factorial

```
def fact(n):
    if n == 0:
        return 1
    return n * fact(n - 1)
```

- Depth $= n \rightarrow$ Stack $= O(n)$
- No extra data structures $\rightarrow S(n) = O(n)$

Tiny Code (Python)

```
def space_counter(n):
    const = 1             # O(1)
    arr = [0] * n         # O(n)
    matrix = [[0]*n for _ in range(n)]  # O(n^2)
    return const + len(arr) + len(matrix)
```

This simple example illustrates additive contributions.

Why It Matters

- Memory is a first-class constraint in large systems
- Critical for embedded, streaming, and real-time algorithms
- Reveals tradeoffs between time and space
- Guides design of in-place vs out-of-place solutions

A Gentle Proof (Why It Works)

Each algorithm manipulates a finite set of data elements. If s_i is the space allocated for structure i, total space is:

$$S(n) = \sum_i s_i(n)$$

Asymptotic space is dominated by the largest term, so $S(n) = \Theta(\max_i s_i(n))$.

This ensures our analysis scales with data growth.

Try It Yourself

1. Count space for Merge Sort (temporary arrays).
2. Compare with Quick Sort (in-place).
3. Add recursion cost explicitly.
4. Analyze time–space tradeoff for dynamic programming.

Test Cases

Algorithm	Space	Reason
Linear Search	$O(1)$	Constant extra memory
Merge Sort	$O(n)$	Extra array for merging
Quick Sort	$O(\log n)$	Stack depth
DP Table (2D)	$O(n^2)$	Full grid of states

Complexity

Component	Example	Cost
Variables	a, b, c	$O(1)$
Arrays	`arr[n]`	$O(n)$
Matrices	`matrix[n][n]`	$O(n^2)$
Recursion Stack	Depth n	$O(n)$

Space counting turns memory into a measurable quantity, every variable a footprint, every structure a surface, every stack frame a layer in the architecture of an algorithm.

16 Memory Footprint Estimator

A Memory Footprint Estimator calculates how much memory an algorithm or data structure truly consumes, not just asymptotically, but in *real bytes*. It bridges the gap between theoretical space complexity and practical implementation.

What Problem Are We Solving?

Knowing an algorithm is $O(n)$ in space isn't enough when working close to memory limits. We need actual estimates: how many bytes per element, how much total allocation, and what overheads exist.

A footprint estimator converts theoretical counts into quantitative estimates for real-world scaling.

How It Works (Plain Language)

1. Identify data types used: `int`, `float`, `pointer`, `struct`, etc.
2. Estimate size per element (language dependent, e.g. `int = 4 bytes`).
3. Multiply by count to find total memory usage.
4. Include overheads from:
    - Object headers or metadata
    - Padding or alignment
    - Pointers or references

Final footprint:

$$\text{Memory} = \sum_i (\text{count}_i \times \text{size}_i) + \text{overhead}$$

Example Step by Step

Suppose we have a list of $n = 1{,}000{,}000$ integers in Python.

Component	Size (Bytes)	Count	Total
List object	64	1	64
Pointers	8	1,000,000	8,000,000
Integer objects	28	1,000,000	28,000,000

Total 36 MB (plus interpreter overhead).

If using a fixed `array('i')` (C-style ints): 4 bytes $\times 10^6 = 4$ MB, far more memory-efficient.

Tiny Code (Python)

```
import sys

n = 1_000_000
arr_list = list(range(n))
arr_array = bytearray(n * 4)

print(sys.getsizeof(arr_list))   # list object
print(sys.getsizeof(arr_array))  # raw byte array
```

Compare memory cost using `sys.getsizeof()`.

Why It Matters

- Reveals true memory requirements
- Critical for large datasets, embedded systems, and databases
- Explains performance tradeoffs in languages with object overhead
- Supports system design and capacity planning

A Gentle Proof (Why It Works)

Each variable or element consumes a fixed number of bytes depending on type. If n_i elements of type t_i are allocated, total memory is:

$$M(n) = \sum_i n_i \cdot s(t_i)$$

Since $s(t_i)$ is constant, growth rate follows counts: $M(n) = O(\max_i n_i)$, matching asymptotic analysis while giving concrete magnitudes.

Try It Yourself

1. Estimate memory for a matrix of 1000×1000 floats (8 bytes each).
2. Compare Python list of lists vs NumPy array.
3. Add overheads for pointers and headers.
4. Repeat for custom `struct` or class with multiple fields.

Test Cases

Structure	Formula	Approx Memory
List of n ints	$n \times 28$ B	28 MB (1M items)
Array of n ints	$n \times 4$ B	4 MB
Matrix $n \times n$ floats	$8n^2$ B	8 MB for $n = 1000$
Hash Table n entries	$O(n)$	Depends on load factor

Complexity

Metric	Growth	Unit
Space	$O(n)$	Bytes
Overhead	$O(1)$	Metadata

A Memory Footprint Estimator turns abstract "$O(n)$ space" into tangible bytes, letting you *see* how close you are to the edge before your program runs out of room.

17 Time Complexity Table

A Time Complexity Table summarizes how different algorithms grow as input size increases, it's a map from formula to feeling, showing which complexities are fast, which are dangerous, and how they compare in scale.

What Problem Are We Solving?

We want a quick reference that links mathematical growth rates to practical performance. Knowing that an algorithm is $O(n \log n)$ is good; understanding what that *means* for $n = 10^6$ is better.

The table helps estimate feasibility: Can this algorithm handle a million inputs? A billion?

How It Works (Plain Language)

1. List common complexity classes: constant, logarithmic, linear, etc.
2. Write their formulas and interpretations.
3. Estimate operations for various n.
4. Highlight tipping points, where performance becomes infeasible.

This creates an *intuition grid* for algorithmic growth.

Example Step by Step

Let $n = 10^6$ (1 million). Estimate operations per complexity class (approximate scale):

Complexity	Formula	Operations (n=10)	Intuition
$O(1)$	constant	1	instant
$O(\log n)$	$\log_2 10^6 \approx 20$	20	lightning fast
$O(n)$	10^6	1,000,000	manageable
$O(n \log n)$	$10^6 \cdot 20$	20M	still OK
$O(n^2)$	$(10^6)^2$	10^{12}	too slow
$O(2^n)$	$2^{20} \approx 10^6$	impossible beyond $n = 30$	
$O(n!)$	factorial	$10^6!$	absurdly huge

The table makes complexity feel *real*.

Tiny Code (Python)

```
import math

def ops_estimate(n):
    return {
        "O(1)": 1,
        "O(log n)": math.log2(n),
        "O(n)": n,
        "O(n log n)": n * math.log2(n),
        "O(n^2)": n2
    }

print(ops_estimate(106))
```

Why It Matters

- Builds *numerical intuition* for asymptotics
- Helps choose the right algorithm for large n
- Explains why $O(n^2)$ might work for $n = 1000$ but not $n = 10^6$
- Connects abstract math to real-world feasibility

A Gentle Proof (Why It Works)

Each complexity class describes a function $f(n)$ bounding operations. Comparing $f(n)$ for common n values illustrates relative growth rates. Because asymptotic notation suppresses constants, differences in growth dominate as n grows.

Thus, numerical examples are faithful approximations of asymptotic behavior.

Try It Yourself

1. Fill the table for $n = 10^3, 10^4, 10^6$.
2. Plot growth curves for each $f(n)$.
3. Compare runtime if each operation = 1 microsecond.
4. Identify feasible vs infeasible complexities for your hardware.

Test Cases

n	$O(1)$	$O(\log n)$	$O(n)$	$O(n^2)$
10^3	1	10	1,000	1,000,000
10^6	1	20	1,000,000	10^{12}
10^9	1	30	1,000,000,000	10^{18}

Complexity

Operation	Type	Insight
Table Generation	$O(1)$	Static reference
Evaluation	$O(1)$	Analytical

A Time Complexity Table turns abstract Big-O notation into a living chart, where $O(\log n)$ feels tiny, $O(n^2)$ feels heavy, and $O(2^n)$ feels impossible.

18 Space–Time Tradeoff Explorer

A Space–Time Tradeoff Explorer helps us understand one of the most fundamental balances in algorithm design: using more memory to gain speed, or saving memory at the cost of time. It's the art of finding equilibrium between storage and computation.

What Problem Are We Solving?

We often face a choice:

- Precompute and store results for instant access (more space, less time)
- Compute on demand to save memory (less space, more time)

The goal is to analyze both sides and choose the best fit for the problem's constraints.

How It Works (Plain Language)

1. Identify repeated computations that can be stored.
2. Estimate memory cost of storing precomputed data.
3. Estimate time saved per query or reuse.
4. Compare tradeoffs using total cost models:

$$\text{Total Cost} = \text{Time Cost} + \lambda \cdot \text{Space Cost}$$

   where λ reflects system priorities.
5. Decide whether caching, tabulation, or recomputation is preferable.

You're tuning performance with two dials, one for memory, one for time.

Example Step by Step

Example 1: Fibonacci Numbers

- Recursive (no memory): $O(2^n)$ time, $O(1)$ space
- Memoized: $O(n)$ time, $O(n)$ space
- Iterative (tabulated): $O(n)$ time, $O(1)$ space (store only last two)

Different tradeoffs for the same problem.

Example 2: Lookup Tables

Suppose you need $\sin(x)$ for many x values:

- Compute each time $\rightarrow O(n)$ per query
- Store all results $\rightarrow O(n)$ memory, $O(1)$ lookup
- Hybrid: store sampled points, interpolate $\rightarrow$ balance

Tiny Code (Python)

```
def fib_naive(n):
    if n <= 1: return n
    return fib_naive(n-1) + fib_naive(n-2)

def fib_memo(n, memo={}):
    if n in memo: return memo[n]
    if n <= 1: return n
    memo[n] = fib_memo(n-1, memo) + fib_memo(n-2, memo)
    return memo[n]
```

Compare time vs memory for each version.

Why It Matters

- Helps design algorithms under memory limits or real-time constraints
- Essential in databases, graphics, compilers, and AI caching
- Connects theory (asymptotics) to engineering (resources)
- Promotes thinking in trade curves, not absolutes

A Gentle Proof (Why It Works)

Let $T(n) =$ time, $S(n) =$ space. If we precompute k results,

$$T'(n) = T(n) - \Delta T, \quad S'(n) = S(n) + \Delta S$$

Since ΔT and ΔS are usually monotonic, minimizing one increases the other. Thus, the optimal configuration lies where

$$\frac{dT}{dS} = -\lambda$$

reflecting the system's valuation of time vs memory.

Try It Yourself

1. Compare naive vs memoized vs iterative Fibonacci.
2. Build a lookup table for factorials modulo M.
3. Explore DP tabulation (space-heavy) vs rolling array (space-light).
4. Evaluate caching in a recursive tree traversal.

Test Cases

Problem	Space	Time	Strategy
Fibonacci	$O(1)$	$O(2^n)$	Naive recursion
Fibonacci	$O(n)$	$O(n)$	Memoization
Fibonacci	$O(1)$	$O(n)$	Iterative
Lookup Table	$O(n)$	$O(1)$	Precompute
Recompute	$O(1)$	$O(n)$	On-demand

Complexity

Operation	Dimension	Note
Space–Time Analysis	$O(1)$	Conceptual
Optimization	$O(1)$	Tradeoff curve

A Space–Time Tradeoff Explorer turns resource limits into creative levers, helping you choose when to remember, when to recompute, and when to balance both in harmony.

19 Profiling Algorithm

Profiling an algorithm means measuring how it *actually behaves*, how long it runs, how much memory it uses, how often loops iterate, and where time is really spent. It turns theoretical complexity into real performance data.

What Problem Are We Solving?

Big-O tells us how an algorithm scales, but not how it *performs in practice*. Constant factors, system load, compiler optimizations, and cache effects all matter.

Profiling answers:

- Where is the time going?
- Which function dominates?
- Are we bound by CPU, memory, or I/O?

It's the microscope for runtime behavior.

How It Works (Plain Language)

1. Instrument your code, insert timers, counters, or use built-in profilers.
2. Run with representative inputs.
3. Record runtime, call counts, and memory allocations.
4. Analyze hotspots, the 10% of code causing 90% of cost.
5. Optimize only where it matters.

Profiling doesn't guess, it measures.

Example Step by Step

Example 1: Timing a Function

```
import time

start = time.perf_counter()
result = algorithm(n)
end = time.perf_counter()

print("Elapsed:", end - start)
```

Measure total runtime for a given input size.

Example 2: Line-Level Profiling

```
import cProfile, pstats

cProfile.run('algorithm(1000)', 'stats')
p = pstats.Stats('stats')
p.sort_stats('cumtime').print_stats(10)
```

Shows the 10 most time-consuming functions.

Tiny Code (Python)

```
def slow_sum(n):
    s = 0
    for i in range(n):
        for j in range(i):
            s += j
    return s

import cProfile
cProfile.run('slow_sum(500)')
```

Output lists functions, calls, total time, and cumulative time.

Why It Matters

- Bridges theory (Big-O) and practice (runtime)
- Identifies bottlenecks for optimization
- Validates expected scaling across inputs
- Prevents premature optimization, measure first, fix later

A Gentle Proof (Why It Works)

Every algorithm execution is a trace of operations. Profiling samples or counts these operations in real time.

If t_i is time spent in component i, then total runtime $T = \sum_i t_i$. Ranking t_i reveals the dominant terms empirically, confirming or refuting theoretical assumptions.

Try It Yourself

1. Profile a recursive function (like Fibonacci).
2. Compare iterative vs recursive runtimes.
3. Plot n vs runtime to visualize empirical complexity.
4. Use `memory_profiler` to capture space usage.

Algorithm	Expected	Observed (example)	Notes

Test Cases

Algorithm	Expected	Observed (example)	Notes
Linear Search	$O(n)$	runtime n	scales linearly
Merge Sort	$O(n \log n)$	runtime grows slightly faster than n	merge overhead
Naive Fibonacci	$O(2^n)$	explodes at $n > 30$	confirms exponential cost

Complexity

Operation	Time	Space
Profiling Run	$O(n)$ (per trial)	$O(1)$
Report Generation	$O(f)$ (per function)	$O(f)$

Profiling is where math meets the stopwatch, transforming asymptotic guesses into concrete numbers and revealing the true heartbeat of your algorithm.

20 Benchmarking Framework

A Benchmarking Framework provides a structured way to compare algorithms under identical conditions. It measures performance across input sizes, multiple trials, and varying hardware, revealing which implementation truly performs best in practice.

What Problem Are We Solving?

You've got several algorithms solving the same problem — which one is *actually faster*? Which scales better? Which uses less memory?

Benchmarking answers these questions with fair, repeatable experiments instead of intuition or isolated timing tests.

How It Works (Plain Language)

1. Define test cases (input sizes, data patterns).
2. Run all candidate algorithms under the same conditions.
3. Repeat trials to reduce noise.
4. Record metrics:
    - Runtime
    - Memory usage
    - Throughput or latency
5. Aggregate results and visualize trends.

Think of it as a "tournament" where each algorithm plays by the same rules.

Example Step by Step

Suppose we want to benchmark sorting methods:

1. Inputs: random arrays of sizes 10^3, 10^4, 10^5
2. Algorithms: `bubble_sort`, `merge_sort`, `timsort`
3. Metric: average runtime over 5 runs
4. Result: table or plot

Size	Bubble Sort	Merge Sort	Timsort
10^3	0.05s	0.001s	0.0008s
10^4	5.4s	0.02s	0.012s
10^5	–	0.25s	0.15s

Timsort wins across all sizes, data confirms theory.

Tiny Code (Python)

```
import timeit
import random

def bench(func, n, trials=5):
    data = [random.randint(0, n) for _ in range(n)]
```

```
    return min(timeit.repeat(lambda: func(data.copy()), number=1, repeat=trials))

def bubble_sort(arr):
    for i in range(len(arr)):
        for j in range(len(arr)-1):
            if arr[j] > arr[j+1]:
                arr[j], arr[j+1] = arr[j+1], arr[j]

def merge_sort(arr):
    if len(arr) <= 1: return arr
    mid = len(arr)//2
    return merge(merge_sort(arr[:mid]), merge_sort(arr[mid:]))

def merge(left, right):
    result = []
    while left and right:
        result.append(left.pop(0) if left[0] < right[0] else right.pop(0))
    return result + left + right

print("Bubble:", bench(bubble_sort, 1000))
print("Merge:", bench(merge_sort, 1000))
```

Why It Matters

- Converts abstract complexity into empirical performance
- Supports evidence-based optimization
- Detects constant factor effects Big-O hides
- Ensures fair comparisons across algorithms

A Gentle Proof (Why It Works)

Let $t_{i,j}$ be time of algorithm i on trial j. Benchmarking reports min, max, or mean$(t_{i,*})$.

By controlling conditions (hardware, input distribution), we treat $t_{i,j}$ as samples of the same distribution, allowing valid comparisons of $E[t_i]$ (expected runtime). Hence, results reflect true relative performance.

Try It Yourself

1. Benchmark linear vs binary search on sorted arrays.

2. Test dynamic array insertion vs linked list insertion.
3. Run across input sizes 10^3, 10^4, 10^5.
4. Plot results: n (x-axis) vs time (y-axis).

Test Cases

Comparison	Expectation
Bubble vs Merge	Merge faster after small n
Linear vs Binary Search	Binary faster for $n > 100$
List vs Dict lookup	Dict $O(1)$ outperforms List $O(n)$

Complexity

Step	Time	Space
Run Each Trial	$O(n)$	$O(1)$
Aggregate Results	$O(k)$	$O(k)$
Total Benchmark	$O(nk)$	$O(1)$

(k = number of trials)

A Benchmarking Framework transforms comparison into science, fair tests, real data, and performance truths grounded in experiment, not hunch.

Section 3. Big-O, Big-Theta, Big-Omega

21 Growth Rate Comparator

A Growth Rate Comparator helps us *see* how functions grow relative to each other, the backbone of asymptotic reasoning. It lets us answer questions like: does n^2 outgrow $n \log n$? How fast is 2^n compared to $n!$?

What Problem Are We Solving?

We need a clear way to compare how fast two functions increase as n becomes large. When analyzing algorithms, runtime functions like n, $n \log n$, and n^2 all seem similar at small scales, but their growth rates diverge quickly.

A comparator gives us a mathematical and visual way to rank them.

How It Works (Plain Language)

1. Write the two functions $f(n)$ and $g(n)$.
2. Compute the ratio $\frac{f(n)}{g(n)}$ as $n \to \infty$.
3. Interpret the result:
   - If $\frac{f(n)}{g(n)} \to 0 \to f(n) = o(g(n))$ (grows slower)
   - If $\frac{f(n)}{g(n)} \to c > 0 \to f(n) = \Theta(g(n))$ (same growth)
   - If $\frac{f(n)}{g(n)} \to \infty \to f(n) = \omega(g(n))$ (grows faster)

This ratio test tells us which function dominates for large n.

Example Step by Step

Example 1: Compare $n \log n$ vs n^2

$$\frac{n \log n}{n^2} = \frac{\log n}{n}$$

As $n \to \infty$, $\frac{\log n}{n} \to 0 \to n \log n = o(n^2)$

Example 2: Compare 2^n vs $n!$

$$\frac{2^n}{n!} \to 0$$

since $n!$ grows faster than 2^n. $\to 2^n = o(n!)$

Tiny Code (Python)

```
import math

def compare_growth(f, g, ns):
    for n in ns:
        ratio = f(n)/g(n)
        print(f"n={n:6}, ratio={ratio:.6e}")
```

```
compare_growth(lambda n: n*math.log2(n),
               lambda n: n2,
               [10, 100, 1000, 10000])
```

Output shows ratio shrinking → confirms slower growth.

Why It Matters

- Builds intuition for asymptotic dominance
- Essential for Big-O, Big-Theta, Big-Omega proofs
- Clarifies why some algorithms scale better
- Translates math into visual and numerical comparisons

A Gentle Proof (Why It Works)

By definition of asymptotic notation:

If $\lim_{n\to\infty} \frac{f(n)}{g(n)} = 0$, then for any $\varepsilon > 0$, $f(n) < \varepsilon g(n)$ for large n.

Thus, $f(n)$ grows slower than $g(n)$.

This formal limit test underlies Big-O reasoning.

Try It Yourself

1. Compare n^3 vs 2^n
2. Compare $\sqrt{n}$ vs $\log n$
3. Compare $n!$ vs n^n
4. Plot both functions and see where one overtakes the other

Test Cases

$f(n)$	$g(n)$	Result	Relation
$\log n$	$\sqrt{n}$	0	$o(\sqrt{n})$
n	$n \log n$	0	$o(n \log n)$
n^2	2^n	0	$o(2^n)$
2^n	$n!$	0	$o(n!)$

Complexity

Operation	Time	Space
Comparison	$O(1)$ per pair	$O(1)$

A Growth Rate Comparator turns asymptotic theory into a conversation, showing, with numbers and limits, who really grows faster as n climbs toward infinity.

22 Dominant Term Extractor

A Dominant Term Extractor simplifies complexity expressions by identifying which term matters most as n grows large. It's how we turn messy runtime formulas into clean Big-O notation, by keeping only what truly drives growth.

What Problem Are We Solving?

Algorithms often produce composite cost formulas like

$$T(n) = 3n^2 + 10n + 25$$

Not all terms grow equally. The dominant term determines long-run behavior, so we want to isolate it and discard the rest.

This step bridges detailed operation counting and asymptotic notation.

How It Works (Plain Language)

1. Write the runtime function $T(n)$ (from counting steps).
2. List all terms by their growth type (n^3, n^2, n, $\log n$, constants).
3. Find the fastest-growing term as $n \to \infty$.
4. Drop coefficients and lower-order terms.
5. The result is the Big-O class.

Think of it as zooming out on a curve, smaller waves vanish at infinity.

Example Step by Step

Example 1:

$$T(n) = 5n^3 + 2n^2 + 7n + 12$$

For large n, n^3 dominates.

So:

$$T(n) = O(n^3)$$

Example 2:

$$T(n) = n^2 + n \log n + 10n$$

Compare term by term:

$$n^2 > n \log n > n$$

So dominant term is n^2. $\Rightarrow T(n) = O(n^2)$

Tiny Code (Python)

```
def dominant_term(terms):
    growth_order = {'1': 0, 'logn': 1, 'n': 2, 'nlogn': 3, 'n^2': 4, 'n^3': 5, '2^n': 6}
    return max(terms, key=lambda t: growth_order[t])

print(dominant_term(['n^2', 'nlogn', 'n']))  # n^2
```

You can extend this with symbolic simplification using SymPy.

Why It Matters

- Simplifies detailed formulas into clean asymptotics
- Focuses attention on scaling behavior, not constants
- Makes performance comparison straightforward
- Core step in deriving Big-O from raw step counts

A Gentle Proof (Why It Works)

Let

$$T(n) = a_k n^k + a_{k-1} n^{k-1} + \cdots + a_0$$

As $n \to \infty$,

$$\frac{a_{k-1} n^{k-1}}{a_k n^k} = \frac{a_{k-1}}{a_k n} \to 0$$

All lower-order terms vanish relative to the largest exponent. So $T(n) = \Theta(n^k)$.

This generalizes beyond polynomials to any family of functions with strict growth ordering.

Try It Yourself

1. Simplify $T(n) = 4n \log n + 10n + 100$.
2. Simplify $T(n) = 2n^3 + 50n^2 + 1000$.
3. Simplify $T(n) = 5n + 10 \log n + 100$.
4. Verify using ratio test: $\frac{\text{lower term}}{\text{dominant term}} \to 0$.

Test Cases

Expression	Dominant Term	Big-O
$3n^2 + 4n + 10$	n^2	$O(n^2)$
$5n + 8 \log n + 7$	n	$O(n)$
$n \log n + 100n$	$n \log n$	$O(n \log n)$
$4n^3 + n^2 + 2n$	n^3	$O(n^3)$

Complexity

Operation	Time	Space
Extraction	$O(k)$	$O(1)$

(k = number of terms)

A Dominant Term Extractor is like a spotlight, it shines on the one term that decides the pace, letting you see the true asymptotic character of your algorithm.

23 Limit-Based Complexity Test

The Limit-Based Complexity Test is a precise way to compare how fast two functions grow by using limits. It's a mathematical tool that turns intuition ("this one feels faster") into proof ("this one *is* faster").

What Problem Are We Solving?

When analyzing algorithms, we often ask: Does $f(n)$ grow slower, equal, or faster than $g(n)$? Instead of guessing, we use limits to determine the exact relationship and classify them using Big-O, Θ, or Ω.

This method gives a formal and reliable comparison of growth rates.

How It Works (Plain Language)

1. Start with two positive functions $f(n)$ and $g(n)$.
2. Compute the ratio:
$$L = \lim_{n \to \infty} \frac{f(n)}{g(n)}$$
3. Interpret the limit:
   - If $L = 0$, then $f(n) = o(g(n)) \to f$ grows slower.
   - If $0 < L < \infty$, then $f(n) = \Theta(g(n)) \to$ same growth rate.
   - If $L = \infty$, then $f(n) = \omega(g(n)) \to f$ grows faster.

The ratio tells us how one function "scales" relative to another.

Example Step by Step

Example 1:

Compare $f(n) = n \log n$ and $g(n) = n^2$.

$$\frac{f(n)}{g(n)} = \frac{n \log n}{n^2} = \frac{\log n}{n}$$

As $n \to \infty$, $\frac{\log n}{n} \to 0$. So $n \log n = o(n^2) \to$ grows slower.

Example 2:

Compare $f(n) = 3n^2 + 4n$ and $g(n) = n^2$.

$$\frac{f(n)}{g(n)} = \frac{3n^2 + 4n}{n^2} = 3 + \frac{4}{n}$$

As $n \to \infty$, $\frac{4}{n} \to 0$. So $\lim = 3$, constant and positive. Therefore, $f(n) = \Theta(g(n))$.

Tiny Code (Python)

```
import sympy as sp

n = sp.symbols('n', positive=True)
f = n * sp.log(n)
g = n2
L = sp.limit(f/g, n, sp.oo)
print("Limit:", L)
```

Outputs `0`, confirming $n \log n = o(n^2)$.

Why It Matters

- Provides formal proof of asymptotic relationships
- Eliminates guesswork in comparing growth rates
- Core step in Big-O proofs and recurrence analysis
- Helps verify if approximations are valid

A Gentle Proof (Why It Works)

The definition of asymptotic comparison uses limits:

If $\lim_{n\to\infty} \frac{f(n)}{g(n)} = 0$, then for any $\varepsilon > 0$, $\exists N$ such that $\forall n > N$, $f(n) \leq \varepsilon g(n)$.

This satisfies the formal condition for $f(n) = o(g(n))$. Similarly, constant or infinite limits define Θ and ω.

Try It Yourself

1. Compare n^3 vs 2^n.
2. Compare $\sqrt{n}$ vs $\log n$.
3. Compare $n!$ vs n^n.
4. Check ratio for $n^2 + n$ vs n^2.

Test Cases

$f(n)$	$g(n)$	Limit	Relationship
n	$n \log n$	0	$o(g(n))$
$n^2 + n$	n^2	1	$\Theta(g(n))$
2^n	n^3	∞	$\omega(g(n))$
$\log n$	$\sqrt{n}$	0	$o(g(n))$

Complexity

Operation	Time	Space
Limit Evaluation	$O(1)$ symbolic	$O(1)$

The Limit-Based Complexity Test is your mathematical magnifying glass, a clean, rigorous way to compare algorithmic growth and turn asymptotic intuition into certainty.

24 Summation Simplifier

A Summation Simplifier converts loops and recursive cost expressions into closed-form formulas using algebra and known summation rules. It bridges the gap between raw iteration counts and Big-O notation.

What Problem Are We Solving?

When analyzing loops, we often get total work expressed as a sum:

$$T(n) = \sum_{i=1}^{n} i \quad \text{or} \quad T(n) = \sum_{i=1}^{n} \log i$$

But Big-O requires us to simplify these sums into familiar functions of n. Summation simplification transforms iteration patterns into asymptotic form.

How It Works (Plain Language)

1. Write down the summation from your loop or recurrence.
2. Apply standard formulas or approximations:
   - $\sum_{i=1}^{n} 1 = n$
   - $\sum_{i=1}^{n} i = \frac{n(n+1)}{2}$
   - $\sum_{i=1}^{n} i^2 = \frac{n(n+1)(2n+1)}{6}$
   - $\sum_{i=1}^{n} \log i = O(n \log n)$
3. Drop constants and lower-order terms.
4. Return simplified function $f(n) \to$ then apply Big-O.

It's like algebraic compression for iteration counts.

Example Step by Step

Example 1:

$$T(n) = \sum_{i=1}^{n} i$$

Use formula:

$$T(n) = \frac{n(n+1)}{2}$$

Simplify:

$$T(n) = O(n^2)$$

Example 2:

$$T(n) = \sum_{i=1}^{n} \log i$$

Approximate by integral:

$$\int_{1}^{n} \log x, dx = n \log n - n + 1$$

So $T(n) = O(n \log n)$

Example 3:

$$T(n) = \sum_{i=1}^{n} \frac{1}{i}$$

$\log n$ (Harmonic series)

Tiny Code (Python)

```
import sympy as sp

i, n = sp.symbols('i n', positive=True)
expr = sp.summation(i, (i, 1, n))
print(sp.simplify(expr))  # n*(n+1)/2
```

Or use `sp.summation(sp.log(i), (i,1,n))` for logarithmic sums.

Why It Matters

- Converts nested loops into analyzable formulas
- Core tool in time complexity derivation
- Helps visualize how cumulative work builds up
- Connects discrete steps with continuous approximations

A Gentle Proof (Why It Works)

If $f(i)$ is positive and increasing, then by the integral test:

$$\int_1^n f(x), dx \leq \sum_{i=1}^{n} f(i) \leq f(n) + \int_1^n f(x), dx$$

So for asymptotic purposes, $\sum f(i)$ and $\int f(x)$ grow at the same rate.

This equivalence justifies approximations like $\sum \log i = O(n \log n)$.

Try It Yourself

1. Simplify $\sum_{i=1}^{n} i^3$.
2. Simplify $\sum_{i=1}^{n} \sqrt{i}$.
3. Simplify $\sum_{i=1}^{n} \frac{1}{i^2}$.
4. Approximate $\sum_{i=1}^{n/2} i$ using integrals.

Test Cases

Summation	Formula	Big-O
$\sum 1$	n	$O(n)$
$\sum i$	$\frac{n(n+1)}{2}$	$O(n^2)$
$\sum i^2$	$\frac{n(n+1)(2n+1)}{6}$	$O(n^3)$
$\sum \log i$	$n \log n$	$O(n \log n)$
$\sum \frac{1}{i}$	$\log n$	$O(\log n)$

Complexity

Operation	Time	Space
Simplification	$O(1)$ (formula lookup)	$O(1)$

A Summation Simplifier turns looping arithmetic into elegant formulas, the difference between counting steps and *seeing* the shape of growth.

25 Recurrence Tree Method

The Recurrence Tree Method is a visual technique for solving divide-and-conquer recurrences. It expands the recursive formula into a tree of subproblems, sums the work done at each level, and reveals the total cost.

What Problem Are We Solving?

Many recursive algorithms (like Merge Sort or Quick Sort) define their running time as

$$T(n) = a, T! \left(\frac{n}{b}\right) + f(n)$$

where:

- a = number of subproblems,
- b = size reduction factor,
- $f(n)$ = non-recursive work per call.

The recurrence tree lets us see the full cost by summing over levels instead of applying a closed-form theorem immediately.

How It Works (Plain Language)

1. Draw the recursion tree
   - Root: problem of size n, cost $f(n)$.
   - Each node: subproblem of size $\frac{n}{b}$ with cost $f(\frac{n}{b})$.
2. Expand levels until base case ($n = 1$).
3. Sum work per level:
   - Level i has a^i nodes, each size $\frac{n}{b^i}$.
   - Total work at level i:
   $$W_i = a^i \cdot f!\left(\frac{n}{b^i}\right)$$
4. Add all levels:
   $$T(n) = \sum_{i=0}^{\log_b n} W_i$$
5. Identify the dominant level (top, middle, or bottom).
6. Simplify to Big-O form.

Example Step by Step

Take Merge Sort:

$$T(n) = 2T!\left(\frac{n}{2}\right) + n$$

Level 0: $1 \times n = n$ Level 1: $2 \times \frac{n}{2} = n$ Level 2: $4 \times \frac{n}{4} = n$ Depth: $\log_2 n$ levels

Total work:

$$T(n) = n \log_2 n + n = O(n \log n)$$

Every level costs n, total $= n \times \log n$.

Tiny Code (Python)

```
import math

def recurrence_tree(a, b, f, n):
    total = 0
    level = 0
    while n >= 1:
        work = (alevel) * f(n/(blevel))
        total += work
        level += 1
        n /= b
    return total
```

Use `f = lambda x: x` for $f(n) = n$.

Why It Matters

- Makes recurrence structure visible and intuitive
- Explains why Master Theorem results hold
- Highlights dominant levels (top-heavy vs bottom-heavy)
- Great teaching and reasoning tool for recursive cost breakdown

A Gentle Proof (Why It Works)

Each recursive call contributes $f(n)$ work plus child subcalls. Because each level's subproblems have equal size, total cost is additive:

$$T(n) = \sum_{i=0}^{\log_b n} a^i f!\left(\frac{n}{b^i}\right)$$

Dominant level dictates asymptotic order:

- Top-heavy: $f(n)$ dominates $\to O(f(n))$
- Balanced: all levels equal $\to O(f(n) \log n)$
- Bottom-heavy: leaves dominate $\to O(n^{\log_b a})$

This reasoning leads directly to the Master Theorem.

Try It Yourself

1. Build tree for $T(n) = 3T(n/2) + n$.
2. Sum each level's work.
3. Compare with Master Theorem result.
4. Try $T(n) = T(n/2) + 1$ (logarithmic tree).

Test Cases

Recurrence	Level Work	Levels	Total	Big-O
$2T(n/2) + n$	n	$\log n$	$n \log n$	$O(n \log n)$
$T(n/2) + 1$	1	$\log n$	$\log n$	$O(\log n)$
$4T(n/2) + n$	$a^i = 4^i$, work $= n \cdot 2^i$	bottom dominates	$O(n^2)$	

Complexity

Step	Time	Space
Tree Construction	$O(\log n)$ levels	$O(\log n)$

The Recurrence Tree Method turns abstract formulas into living diagrams, showing each layer's effort, revealing which level truly drives the algorithm's cost.

26 Master Theorem Evaluator

The Master Theorem Evaluator gives a quick, formula-based way to solve divide-and-conquer recurrences of the form

$$T(n) = a, T!\left(\frac{n}{b}\right) + f(n)$$

It tells you the asymptotic behavior of $T(n)$ without full expansion or summation, a shortcut born from the recurrence tree.

What Problem Are We Solving?

We want to find the Big-O complexity of divide-and-conquer algorithms quickly. Manually expanding recursions (via recurrence trees) works, but is tedious. The Master Theorem classifies solutions by comparing the recursive work $(a, T(n/b))$ and non-recursive work $(f(n))$.

How It Works (Plain Language)

Given

$$T(n) = a, T!\left(\frac{n}{b}\right) + f(n)$$

- a = number of subproblems
- b = shrink factor
- $f(n)$ = work done outside recursion

Compute critical exponent:

$$n^{\log_b a}$$

Compare $f(n)$ to $n^{\log_b a}$:

1. Case 1 (Top-heavy): If $f(n) = O(n^{\log_b a - \varepsilon})$,

   $$T(n) = \Theta(n^{\log_b a})$$

   Recursive part dominates.

2. Case 2 (Balanced): If $f(n) = \Theta(n^{\log_b a} \log^k n)$,

   $$T(n) = \Theta(n^{\log_b a} \log^{k+1} n)$$

   Both contribute equally.

3. Case 3 (Bottom-heavy): If $f(n) = \Omega(n^{\log_b a + \varepsilon})$ and regularity condition holds:

   $$af(n/b) \leq cf(n)$$

   for some $c < 1$, then

   $$T(n) = \Theta(f(n))$$

   Non-recursive part dominates.

Example Step by Step

Example 1:

$$T(n) = 2T(n/2) + n$$

- $a = 2$, $b = 2$, $f(n) = n$
- $n^{\log_2 2} = n$ So $f(n) = \Theta(n^{\log_2 2}) \rightarrow$ Case 2

$$T(n) = \Theta(n \log n)$$

Example 2:

$$T(n) = 4T(n/2) + n$$

- $a = 4$, $b = 2 \to n^{\log_2 4} = n^2$
- $f(n) = n = O(n^{2-\varepsilon}) \to$ Case 1

$$T(n) = \Theta(n^2)$$

Example 3:

$$T(n) = T(n/2) + n$$

- $a = 1$, $b = 2$, $n^{\log_2 1} = 1$
- $f(n) = n = \Omega(n^{0+\varepsilon}) \to$ Case 3

$$T(n) = \Theta(n)$$

Tiny Code (Python)

```
import math

def master_theorem(a, b, f_exp):
    critical = math.log(a, b)
    if f_exp < critical:
        return f"O(n^{critical:.2f})"
    elif f_exp == critical:
        return f"O(n^{critical:.2f} log n)"
    else:
        return f"O(n^{f_exp})"
```

For $T(n) = 2T(n/2) + n$, call `master_theorem(2,2,1)` $\to$ `O(n log n)`

Why It Matters

- Solves recurrences in seconds
- Foundation for analyzing divide-and-conquer algorithms
- Validates intuition from recurrence trees
- Used widely in sorting, searching, matrix multiplication, FFT

A Gentle Proof (Why It Works)

Each recursion level costs:

$$a^i, f!\left(\frac{n}{b^i}\right)$$

Total cost:

$$T(n) = \sum_{i=0}^{\log_b n} a^i f!\left(\frac{n}{b^i}\right)$$

The relative growth of $f(n)$ to $n^{\log_b a}$ determines which level dominates, top, middle, or bottom, yielding the three canonical cases.

Try It Yourself

1. $T(n) = 3T(n/2) + n$
2. $T(n) = 2T(n/2) + n^2$
3. $T(n) = 8T(n/2) + n^3$
4. Identify $a, b, f(n)$ and apply theorem.

Test Cases

Recurrence	Case	Result
$2T(n/2) + n$	2	$O(n \log n)$
$4T(n/2) + n$	1	$O(n^2)$
$T(n/2) + n$	3	$O(n)$
$3T(n/3) + n \log n$	2	$O(n \log^2 n)$

Complexity

Step	Time	Space
Evaluation	$O(1)$	$O(1)$

The Master Theorem Evaluator is your formulaic compass, it points instantly to the asymptotic truth hidden in recursive equations, no tree-drawing required.

27 Big-Theta Proof Builder

A Big-Theta Proof Builder helps you formally prove that a function grows at the same rate as another. It's the precise way to show that $f(n)$ and $g(n)$ are asymptotically equivalent, growing neither faster nor slower beyond constant factors.

What Problem Are We Solving?

We often say an algorithm is $T(n) = \Theta(n \log n)$, but how do we prove it? A Big-Theta proof uses inequalities to pin $T(n)$ between two scaled versions of a simpler function $g(n)$, confirming tight asymptotic bounds.

This transforms intuition into rigorous evidence.

How It Works (Plain Language)

We say

$$f(n) = \Theta(g(n))$$

if there exist constants $c_1, c_2 > 0$ and n_0 such that for all $n \geq n_0$:

$$c_1 g(n) \leq f(n) \leq c_2 g(n)$$

So $f(n)$ is sandwiched between two constant multiples of $g(n)$.

Steps:

1. Identify $f(n)$ and candidate $g(n)$.
2. Find constants c_1, c_2, and threshold n_0.
3. Verify inequality for all $n \geq n_0$.
4. Conclude $f(n) = \Theta(g(n))$.

Example Step by Step

Example 1:

$$f(n) = 3n^2 + 10n + 5$$

Candidate: $g(n) = n^2$

For large n, $10n + 5$ is small compared to $3n^2$.

We can show:

$$3n^2 \leq 3n^2 + 10n + 5 \leq 4n^2, \quad \text{for } n \geq 10$$

Thus, $f(n) = \Theta(n^2)$ with $c_1 = 3$, $c_2 = 4$, $n_0 = 10$.

Example 2:

$$f(n) = n \log n + 100n$$

Candidate: $g(n) = n \log n$

For $n \geq 2$, $\log n \geq 1$, so $100n \leq 100n \log n$. Hence,

$$n \log n \leq f(n) \leq 101n \log n$$

$\rightarrow f(n) = \Theta(n \log n)$

Tiny Code (Python)

```
def big_theta_proof(f, g, n0, c1, c2):
    for n in range(n0, n0 + 5):
        if not (c1*g(n) <= f(n) <= c2*g(n)):
            return False
    return True

f = lambda n: 3*n2 + 10*n + 5
g = lambda n: n2
print(big_theta_proof(f, g, 10, 3, 4))  # True
```

Why It Matters

- Converts informal claims ("it's n^2-ish") into formal proofs
- Builds rigor in asymptotic reasoning
- Essential for algorithm analysis, recurrence proofs, and coursework
- Reinforces understanding of constants and thresholds

A Gentle Proof (Why It Works)

By definition,

$$f(n) = \Theta(g(n)) \iff \exists c_1, c_2, n_0 : c_1 g(n) \leq f(n) \leq c_2 g(n)$$

This mirrors how Big-O and Big-Omega combine:

- $f(n) = O(g(n))$ gives upper bound,
- $f(n) = \Omega(g(n))$ gives lower bound. Together, they form a tight bound, hence Θ.

Try It Yourself

1. Prove $5n^3 + n^2 + 100 = \Theta(n^3)$.
2. Prove $4n + 10 = \Theta(n)$.
3. Show $n \log n + 100n = \Theta(n \log n)$.
4. Fail a proof: $n^2 + 3n = \Theta(n)$ (not true).

Test Cases

$f(n)$	$g(n)$	c_1, c_2, n_0	Result
$3n^2 + 10n + 5$	n^2	$3, 4, 10$	$\Theta(n^2)$
$n \log n + 100n$	$n \log n$	$1, 101, 2$	$\Theta(n \log n)$
$10n + 50$	n	$10, 11, 5$	$\Theta(n)$

Complexity

Step	Time	Space
Verification	$O(1)$ (symbolic)	$O(1)$

The Big-Theta Proof Builder is your asymptotic courtroom, you bring evidence, constants, and inequalities, and the proof delivers a verdict: $\Theta(g(n))$, beyond reasonable doubt.

28 Big-Omega Case Finder

A Big-Omega Case Finder helps you identify lower bounds on an algorithm's growth, the *guaranteed minimum* cost, even in the best-case scenario. It's the mirror image of Big-O, showing what an algorithm must at least do.

What Problem Are We Solving?

Big-O gives us an upper bound ("it won't be slower than this"), but sometimes we need to know the floor, a complexity it can never beat.

Big-Omega helps us state:

- The fastest possible asymptotic behavior, or
- The minimal cost inherent to the problem itself.

This is key when analyzing best-case performance or complexity limits (like comparison sorting's $\Omega(n \log n)$ lower bound).

How It Works (Plain Language)

We say

$$f(n) = \Omega(g(n))$$

if $\exists c > 0, n_0$ such that

$$f(n) \geq c \cdot g(n) \quad \text{for all } n \geq n_0$$

Steps:

1. Identify candidate lower-bound function $g(n)$.
2. Show $f(n)$ eventually stays above a constant multiple of $g(n)$.
3. Find constants c and n_0.
4. Conclude $f(n) = \Omega(g(n))$.

Example Step by Step

Example 1:

$$f(n) = 3n^2 + 5n + 10$$

Candidate: $g(n) = n^2$

For $n \geq 1$,

$$f(n) \geq 3n^2 \geq 3 \cdot n^2$$

So $f(n) = \Omega(n^2)$ with $c = 3$, $n_0 = 1$.

Example 2:

$$f(n) = n \log n + 100n$$

Candidate: $g(n) = n$

Since $\log n \geq 1$ for $n \geq 2$,

$$f(n) = n \log n + 100n \geq n + 100n = 101n$$

$\rightarrow f(n) = \Omega(n)$ with $c = 101$, $n_0 = 2$

Tiny Code (Python)

```
def big_omega_proof(f, g, n0, c):
    for n in range(n0, n0 + 5):
        if f(n) < c * g(n):
            return False
    return True

f = lambda n: 3*n2 + 5*n + 10
g = lambda n: n2
print(big_omega_proof(f, g, 1, 3))  # True
```

Why It Matters

- Defines best-case performance
- Provides theoretical lower limits (impossible to beat)
- Complements Big-O (upper bound) and Theta (tight bound)
- Key in proving problem hardness or optimality

A Gentle Proof (Why It Works)

If

$$\lim_{n \to \infty} \frac{f(n)}{g(n)} = L > 0,$$

then for any $c \leq L$, $f(n) \geq c \cdot g(n)$ for large n. Thus $f(n) = \Omega(g(n))$. This mirrors the formal definition of Ω and follows directly from asymptotic ratio reasoning.

Try It Yourself

1. Show $4n^3 + n^2 = \Omega(n^3)$
2. Show $n \log n + n = \Omega(n)$
3. Show $2^n + n^5 = \Omega(2^n)$
4. Compare with their Big-O forms for contrast.

Test Cases

$f(n)$	$g(n)$	Constants	Result
$3n^2 + 10n$	n^2	$c = 3$, $n_0 = 1$	$\Omega(n^2)$
$n \log n + 100n$	n	$c = 101$, $n_0 = 2$	$\Omega(n)$
$n^3 + n^2$	n^3	$c = 1$, $n_0 = 1$	$\Omega(n^3)$

Complexity

Step	Time	Space
Verification	$O(1)$	$O(1)$

The Big-Omega Case Finder shows the *floor beneath the curve*, ensuring every algorithm stands on a solid lower bound, no matter how fast it tries to run.

29 Empirical Complexity Estimator

An Empirical Complexity Estimator bridges theory and experiment, it measures actual runtimes for various input sizes and fits them to known growth models like $O(n)$, $O(n \log n)$, or $O(n^2)$. It's how we *discover* complexity when the math is unclear or the code is complex.

What Problem Are We Solving?

Sometimes the exact formula for $T(n)$ is too messy, or the implementation details are opaque. We can still estimate complexity empirically by observing how runtime changes as n grows.

This approach is especially useful for:

- Black-box code (unknown implementation)
- Experimental validation of asymptotic claims
- Comparing real-world scaling with theoretical predictions

How It Works (Plain Language)

1. Choose representative input sizes $n_1, n_2, \ldots, n_k$.
2. Measure runtime $T(n_i)$ for each size.
3. Normalize or compare ratios:
   - $T(2n)/T(n) \approx 2 \to O(n)$
   - $T(2n)/T(n) \approx 4 \to O(n^2)$
   - $T(2n)/T(n) \approx \log 2 \to O(\log n)$
4. Fit data to candidate models using regression or ratio tests.
5. Visualize trends (e.g., log–log plot) to identify slope = exponent.

Example Step by Step

Suppose we test input sizes: $n = 1000, 2000, 4000, 8000$

n	$T(n)$ (ms)	Ratio $T(2n)/T(n)$
1000	5	–
2000	10	2.0
4000	20	2.0
8000	40	2.0

Ratio $\approx 2 \rightarrow$ linear growth $\rightarrow T(n) = O(n)$

Now suppose:

n	$T(n)$	Ratio
1000	5	–
2000	20	4
4000	80	4
8000	320	4

Ratio $\approx 4 \rightarrow$ quadratic growth $\rightarrow O(n^2)$

Tiny Code (Python)

```
import time, math

def empirical_estimate(f, ns):
    times = []
    for n in ns:
        start = time.perf_counter()
        f(n)
        end = time.perf_counter()
        times.append(end - start)
    for i in range(1, len(ns)):
        ratio = times[i] / times[i-1]
        print(f"n={ns[i]:6}, ratio={ratio:.2f}")
```

Test with different algorithms to see scaling.

Why It Matters

- Converts runtime data into Big-O form
- Detects bottlenecks or unexpected scaling
- Useful when theoretical analysis is hard
- Helps validate optimizations or refactors

A Gentle Proof (Why It Works)

If $T(n) \approx c \cdot f(n)$, then the ratio test

$$\frac{T(kn)}{T(n)} \approx \frac{f(kn)}{f(n)}$$

reveals the exponent p if $f(n) = n^p$:

$$\frac{f(kn)}{f(n)} = k^p \implies p = \log_k \frac{T(kn)}{T(n)}$$

Repeated over multiple n, this converges to the true growth exponent.

Try It Yourself

1. Measure runtime of sorting for increasing n.
2. Estimate p using ratio test.
3. Plot $\log n$ vs $\log T(n)$, slope exponent.
4. Compare p to theoretical value.

Test Cases

Algorithm	Observed Ratio	Estimated Complexity
Bubble Sort	4	$O(n^2)$
Merge Sort	2.2	$O(n \log n)$
Linear Search	2	$O(n)$
Binary Search	1.1	$O(\log n)$

Complexity

Step	Time	Space
Measurement	$O(k \cdot T(n))$	$O(k)$
Estimation	$O(k)$	$O(1)$

(k = number of sample points)

An Empirical Complexity Estimator transforms stopwatches into science, turning performance data into curves, curves into equations, and equations into Big-O intuition.

30 Complexity Class Identifier

A Complexity Class Identifier helps you categorize problems and algorithms into broad complexity classes like constant, logarithmic, linear, quadratic, exponential, or polynomial time. It's a way to understand *where your algorithm lives* in the vast map of computational growth.

What Problem Are We Solving?

When analyzing an algorithm, we often want to know how big its time cost gets as input grows. Instead of exact formulas, we classify algorithms into families based on their asymptotic growth.

This tells us what is *feasible* (polynomial) and what is *explosive* (exponential), guiding both design choices and theoretical limits.

How It Works (Plain Language)

We map the growth rate of $T(n)$ to a known complexity class:

Class	Example	Description
$O(1)$	Hash lookup	Constant time, no scaling
$O(\log n)$	Binary search	Sublinear, halves each step
$O(n)$	Linear scan	Work grows with input size
$O(n \log n)$	Merge sort	Near-linear with log factor
$O(n^2)$	Nested loops	Quadratic growth
$O(n^3)$	Matrix multiplication	Cubic growth
$O(2^n)$	Backtracking	Exponential explosion
$O(n!)$	Brute-force permutations	Factorial blowup

Steps to Identify:

1. Analyze loops and recursion structure.
2. Count dominant operations.
3. Match pattern to table above.
4. Verify with recurrence or ratio test.
5. Assign class: constant → logarithmic → polynomial → exponential.

Example Step by Step

Example 1: Single loop:

```
for i in range(n):
    work()
```

$\rightarrow O(n) \rightarrow$ Linear

Example 2: Nested loops:

```
for i in range(n):
    for j in range(n):
        work()
```

$\rightarrow O(n^2) \rightarrow$ Quadratic

Example 3: Divide and conquer:

$$T(n) = 2T(n/2) + n$$

$\rightarrow O(n \log n) \rightarrow$ Log-linear

Example 4: Brute force subsets:

$$2^n \text{ possibilities}$$

$\rightarrow O(2^n) \rightarrow$ Exponential

Tiny Code (Python)

```
def classify_complexity(code_structure):
    if "nested n" in code_structure:
        return "O(n^2)"
    if "divide and conquer" in code_structure:
        return "O(n log n)"
    if "constant" in code_structure:
        return "O(1)"
    return "O(n)"
```

You can extend this to pattern-match pseudocode shapes.

Why It Matters

- Gives instant intuition about scalability
- Guides design trade-offs (speed vs. simplicity)
- Connects practical code to theoretical limits
- Helps compare algorithms solving the same problem

A Gentle Proof (Why It Works)

If an algorithm performs $f(n)$ fundamental operations for input size n, and $f(n)$ is asymptotically similar to a known class $g(n)$:

$$f(n) = \Theta(g(n))$$

then it belongs to the same class. Classes form equivalence groups under Θ notation, simplifying infinite functions into a finite taxonomy.

Try It Yourself

Classify each:

1. $T(n) = 5n + 10$
2. $T(n) = n \log n + 100$
3. $T(n) = n^3 + 4n^2$
4. $T(n) = 2^n$

Identify their Big-O class and interpret feasibility.

Test Cases

$T(n)$	Class	Description
$7n + 3$	$O(n)$	Linear
$3n^2 + 10n$	$O(n^2)$	Quadratic
$n \log n$	$O(n \log n)$	Log-linear
2^n	$O(2^n)$	Exponential
100	$O(1)$	Constant

Complexity

Step	Time	Space
Classification	$O(1)$	$O(1)$

The Complexity Class Identifier is your map of the algorithmic universe, helping you locate where your code stands, from calm constant time to the roaring infinity of factorial growth.

Section 4. Algorithm Paradigms

31 Greedy Coin Example

The Greedy Coin Example introduces the greedy algorithm paradigm, solving problems by always taking the best immediate option, hoping it leads to a globally optimal solution. In coin change, we repeatedly pick the largest denomination not exceeding the remaining amount.

What Problem Are We Solving?

We want to make change for a target amount using the fewest coins possible. A greedy algorithm always chooses the locally optimal coin, the largest denomination remaining total, and repeats until the target is reached.

This method works for canonical coin systems (like U.S. currency) but fails for some arbitrary denominations.

How It Works (Plain Language)

1. Sort available coin denominations in descending order.
2. For each coin:
    - Take as many as possible without exceeding the total.
    - Subtract their value from the remaining amount.
3. Continue with smaller coins until the remainder is 0.

Greedy assumes: local optimum $\rightarrow$ global optimum.

Step	Coin	Count	Remaining

Example Step by Step

Let coins = {25, 10, 5, 1}, target = 63

Step	Coin	Count	Remaining
1	25	2	13
2	10	1	3
3	5	0	3
4	1	3	0

Total = $2\times25 + 1\times10 + 3\times1 = 63$ Coins used = 6

Greedy solution = optimal (U.S. system is canonical).

Counterexample:

Coins = {4, 3, 1}, target = 6

- Greedy: $4 + 1 + 1 = 3$ coins
- Optimal: $3 + 3 = 2$ coins

So greedy may fail for non-canonical systems.

Tiny Code (Python)

```
def greedy_change(coins, amount):
    coins.sort(reverse=True)
    result = []
    for coin in coins:
        while amount >= coin:
            amount -= coin
            result.append(coin)
    return result

print(greedy_change([25,10,5,1], 63))  # [25, 25, 10, 1, 1, 1]
```

Why It Matters

- Demonstrates local decision-making
- Fast and simple: $O(n)$ over denominations
- Foundation for greedy design in spanning trees, scheduling, compression
- Highlights where greedy works and where it fails

A Gentle Proof (Why It Works)

For canonical systems, greedy satisfies the optimal substructure and greedy-choice property:

- Greedy-choice property: Locally best $\rightarrow$ part of a global optimum.
- Optimal substructure: Remaining subproblem has optimal greedy solution.

Inductively, greedy yields minimal coin count.

Try It Yourself

1. Try greedy change with {25, 10, 5, 1} for 68.
2. Try {9, 6, 1} for 11, compare with brute force.
3. Identify when greedy fails, test {4, 3, 1}.
4. Extend algorithm to return both coins and count.

Test Cases

Coins	Amount	Result	Optimal?
{25,10,5,1}	63	[25,25,10,1,1,1]	
{9,6,1}	11	[9,1,1]	
{4,3,1}	6	[4,1,1]	(3+3 better)

Complexity

Step	Time	Space
Sorting	$O(k \log k)$	$O(1)$
Selection	$O(k)$	$O(k)$

(k = number of denominations)

The Greedy Coin Example is the first mirror of the greedy philosophy, simple, intuitive, and fast, a lens into problems where choosing *best now* means *best overall*.

32 Greedy Template Simulator

The Greedy Template Simulator shows how every greedy algorithm follows the same pattern, repeatedly choosing the best local option, updating the state, and moving toward the goal. It's a reusable mental and coding framework for designing greedy solutions.

What Problem Are We Solving?

Many optimization problems can be solved by making local choices without revisiting earlier decisions. Instead of searching all paths (like backtracking) or building tables (like DP), greedy algorithms follow a deterministic path of best-next choices.

We want a general template to simulate this structure, useful for scheduling, coin change, and spanning tree problems.

How It Works (Plain Language)

1. Initialize the problem state (remaining value, capacity, etc.).
2. While goal not reached:
    - Evaluate all local choices.
    - Pick the best immediate option (by some criterion).
    - Update the state accordingly.
3. End when no more valid moves exist.

Greedy depends on a selection rule (which local choice is best) and a feasibility check (is the choice valid?).

Example Step by Step

Problem: Job Scheduling by Deadline (Maximize Profit)

Job	Deadline	Profit
A	2	60
B	1	100
C	3	20

Job	Deadline	Profit
D	2	40

Steps:

1. Sort jobs by profit (desc): B(100), A(60), D(40), C(20)
2. Take each job if slot deadline available
3. Fill slots:
    - Day 1: B
    - Day 2: A
    - Day 3: C → Total Profit = 180

Greedy rule: "Pick highest profit first if deadline allows."

Tiny Code (Python)

```
def greedy_template(items, is_valid, select_best, update_state):
    state = initialize(items)
    while not goal_reached(state):
        best = select_best(items, state)
        if is_valid(best, state):
            update_state(best, state)
        else:
            break
    return state
```

Concrete greedy solutions just plug in:

- `select_best`: define local criterion
- `is_valid`: define feasibility condition
- `update_state`: modify problem state

Why It Matters

- Reveals shared skeleton behind all greedy algorithms
- Simplifies learning, "different bodies, same bones"
- Encourages reusable code via template-based design
- Helps debug logic: if it fails, test greedy-choice property

A Gentle Proof (Why It Works)

If a problem has:

- Greedy-choice property: local best is part of global best
- Optimal substructure: subproblem solutions are optimal

Then any algorithm following this template produces a global optimum. Formally proved via induction on input size.

Try It Yourself

1. Implement template for:
    - Coin change
    - Fractional knapsack
    - Interval scheduling
2. Compare with brute-force or DP to confirm optimality.
3. Identify when greedy fails (e.g., non-canonical coin sets).

Test Cases

Problem	Local Rule	Works?	Note
Fractional Knapsack	Max value/weight		Continuous
Interval Scheduling	Earliest finish		Non-overlapping
Coin Change (25,10,5,1)	Largest coin remaining		Canonical only
Job Scheduling	Highest profit first		Sorted by profit

Complexity

Step	Time	Space
Selection	$O(n \log n)$ (sort)	$O(n)$
Iteration	$O(n)$	$O(1)$

The Greedy Template Simulator is the skeleton key of greedy design, once you learn its shape, every greedy algorithm looks like a familiar face.

33 Divide & Conquer Skeleton

The Divide & Conquer Skeleton captures the universal structure of algorithms that solve big problems by splitting them into smaller, independent pieces, solving each recursively, then combining their results. It's the framework behind mergesort, quicksort, binary search, and more.

What Problem Are We Solving?

Some problems are too large or complex to handle at once. Divide & Conquer (D&C) solves them by splitting into smaller subproblems of the same type, solving recursively, and combining the results into a whole.

We want a reusable template that reveals this recursive rhythm.

How It Works (Plain Language)

Every D&C algorithm follows this triplet:

1. Divide: Break the problem into smaller subproblems.
2. Conquer: Solve each subproblem (often recursively).
3. Combine: Merge or assemble partial solutions.

This recursion continues until a base case (small enough to solve directly).

General Recurrence:

$$T(n) = aT!\left(\frac{n}{b}\right) + f(n)$$

- a: number of subproblems
- b: factor by which size is reduced
- $f(n)$: cost to divide/combine

Example Step by Step

Example: Merge Sort

1. Divide: Split array into two halves
2. Conquer: Recursively sort each half
3. Combine: Merge two sorted halves into one

For $n = 8$:

- Level 0: size 8

- Level 1: size $4 + 4$
- Level 2: size $2 + 2 + 2 + 2$
- Level 3: size 1 (base case)

Each level costs $O(n) \rightarrow$ total $O(n \log n)$.

Tiny Code (Python)

```
def divide_and_conquer(problem, base_case, divide, combine):
    if base_case(problem):
        return solve_directly(problem)
    subproblems = divide(problem)
    solutions = [divide_and_conquer(p, base_case, divide, combine) for p in subproblems]
    return combine(solutions)
```

Plug in custom `divide`, `combine`, and base-case logic for different problems.

Why It Matters

- Models recursive structure of many core algorithms
- Reveals asymptotic pattern via recurrence
- Enables parallelization (subproblems solved independently)
- Balances simplicity (small subproblems) with power (reduction)

A Gentle Proof (Why It Works)

If each recursive level divides the work evenly and recombines in finite time, then total cost is sum of all level costs:

$$T(n) = \sum_{i=0}^{\log_b n} a^i \cdot f!\left(\frac{n}{b^i}\right)$$

Master Theorem or tree expansion shows convergence to $O(n^{\log_b a})$ or $O(n \log n)$, depending on $f(n)$.

Correctness follows by induction: each subproblem solved optimally combined result optimal.

Try It Yourself

1. Write a D&C template for:
   - Binary Search
   - Merge Sort
   - Karatsuba Multiplication
2. Identify a, b, $f(n)$ for each.
3. Solve their recurrences with Master Theorem.

Test Cases

Algorithm	a	b	$f(n)$	Complexity
Binary Search	1	2	1	$O(\log n)$
Merge Sort	2	2	n	$O(n \log n)$
Quick Sort	2	2	n (expected)	$O(n \log n)$
Karatsuba	3	2	n	$O(n^{\log_2 3})$

Complexity

Step	Time	Space
Recursive calls	$O(n)$ to $O(n \log n)$	$O(\log n)$ (stack)
Combine	$O(f(n))$	depends on merging

The Divide & Conquer Skeleton is the heartbeat of recursion, a rhythm of divide, solve, combine, pulsing through the core of algorithmic design.

34 Backtracking Maze Solver

The Backtracking Maze Solver illustrates the backtracking paradigm, exploring all possible paths through a search space, stepping forward when valid, and undoing moves when a dead end is reached. It's the classic model for recursive search and constraint satisfaction.

What Problem Are We Solving?

We want to find a path from start to goal in a maze or search space filled with constraints. Brute force would try every path blindly; backtracking improves on this by pruning paths as soon as they become invalid.

This approach powers solvers for mazes, Sudoku, N-Queens, and combinatorial search problems.

How It Works (Plain Language)

1. Start at the initial position.
2. Try a move (north, south, east, west).
3. If move is valid, mark position and recurse from there.
4. If stuck, backtrack: undo last move and try a new one.
5. Stop when goal is reached or all paths are explored.

The algorithm is depth-first in nature, it explores one branch fully before returning.

Example Step by Step

Maze (Grid Example)

```
S . . #
# . # .
. . . G
```

- Start at S (0,0), Goal at G (2,3)
- Move right, down, or around obstacles (#)
- Mark visited cells
- When trapped, step back and try another path

Path Found: S $\rightarrow$ (0,1) $\rightarrow$ (1,1) $\rightarrow$ (2,1) $\rightarrow$ (2,2) $\rightarrow$ G

Tiny Code (Python)

```
def solve_maze(maze, x, y, goal):
    if (x, y) == goal:
        return True
    if not valid_move(maze, x, y):
        return False
    maze[x][y] = 'V'  # Mark visited
    for dx, dy in [(0,1), (1,0), (0,-1), (-1,0)]:
        if solve_maze(maze, x+dx, y+dy, goal):
            return True
    maze[x][y] = '.'  # Backtrack
    return False
```

The recursion explores all paths, marking and unmarking as it goes.

Why It Matters

- Demonstrates search with undoing
- Foundational for DFS, constraint satisfaction, puzzle solving
- Illustrates state exploration and recursive pruning
- Framework for N-Queens, Sudoku, graph coloring

A Gentle Proof (Why It Works)

By exploring all valid moves recursively:

- Every feasible path is eventually checked.
- Infeasible branches terminate early due to validity checks.
- Backtracking guarantees all combinations are explored once.

Thus, completeness is ensured, and if a path exists, it will be found.

Try It Yourself

1. Draw a 4×4 maze with one solution.
2. Run backtracking manually, marking path and undoing wrong turns.
3. Modify rules (e.g., diagonal moves allowed).
4. Compare runtime with BFS (which finds shortest path).

Test Cases

Maze	Solution Found	Notes
Open grid	Yes	Path straight to goal
Maze with block	Yes	Backs up and reroutes
No path	No	Exhausts all options

Complexity

Step	Time	Space
Search	O(4) worst-case	O(n) recursion stack

(n = number of cells)

Pruning and constraints reduce practical cost.

The Backtracking Maze Solver is a journey of trial and error, a guided wanderer exploring paths, retreating gracefully, and finding solutions hidden in the labyrinth.

35 Karatsuba Multiplication

The Karatsuba Multiplication algorithm is a divide-and-conquer technique that multiplies two large numbers faster than the classical grade-school method. It reduces the multiplication count from 4 to 3 per recursive step, improving complexity from $O(n^2)$ to approximately $O(n^{1} \cdot \quad)$.

What Problem Are We Solving?

When multiplying large numbers (or polynomials), the standard approach performs every pairwise digit multiplication, $O(n^2)$ work for n-digit numbers. Karatsuba observed that some of this work is redundant. By reusing partial results cleverly, we can cut down the number of multiplications and gain speed.

This is the foundation of many fast arithmetic algorithms and symbolic computation libraries.

How It Works (Plain Language)

Given two n-digit numbers:

$$x = 10^m \cdot a + b \; y = 10^m \cdot c + d$$

where (a, b, c, d) are roughly n/2-digit halves of x and y.

1. Compute three products:
   - (p_1 = a c)
   - (p_2 = b d)
   - (p_3 = (a + b)(c + d))
2. Combine results using:

$$x \cdot y = 10^{2m} \cdot p_1 + 10^m \cdot (p_3 - p_1 - p_2) + p_2$$

This reduces recursive multiplications from 4 to 3.

Example Step by Step

Multiply 12×34.

Split:

- a = 1, b = 2
- c = 3, d = 4

Compute:

- (p_1 = 1 ×3 = 3)
- (p_2 = 2 ×4 = 8)
- (p_3 = (1 + 2)(3 + 4) = 3 ×7 = 21)

Combine:

$$(10^2) \cdot 3 + 10 \cdot (21 - 3 - 8) + 8 = 300 + 100 + 8 = 408$$

So $12 \times 34 = 408$ (correct).

Tiny Code (Python)

```
def karatsuba(x, y):
    if x < 10 or y < 10:
        return x * y
    n = max(len(str(x)), len(str(y)))
    m = n // 2
    a, b = divmod(x, 10m)
    c, d = divmod(y, 10m)
    p1 = karatsuba(a, c)
    p2 = karatsuba(b, d)
    p3 = karatsuba(a + b, c + d)
    return p1 * 10(2*m) + (p3 - p1 - p2) * 10m + p2
```

Why It Matters

- First sub-quadratic multiplication algorithm
- Basis for advanced methods (Toom–Cook, FFT-based)
- Applies to integers, polynomials, big-number arithmetic
- Showcases power of divide and conquer

A Gentle Proof (Why It Works)

The product expansion is:

$$(a \cdot 10^m + b)(c \cdot 10^m + d) = ac \cdot 10^{2m} + (ad + bc)10^m + bd$$

Observe:

$$(a + b)(c + d) = ac + ad + bc + bd$$

Thus:

$$ad + bc = (a + b)(c + d) - ac - bd$$

Karatsuba leverages this identity to compute (ad + bc) without a separate multiplication.

Recurrence:

$$T(n) = 3T(n/2) + O(n)$$

Solution: $T(n) = O(n^{\log_2 3}) \approx O(n^{1.585})$

Try It Yourself

1. Multiply 1234×5678 using Karatsuba steps.
2. Compare with grade-school multiplication count.
3. Visualize recursive calls as a tree.
4. Derive recurrence and verify complexity.

Test Cases

x	y	Result	Method
12	34	408	Works
123	456	56088	Works
9999	9999	99980001	Works

Complexity

Step	Time	Space
Multiplication	$O(n^{1} \cdot \quad)$	O(n)
Base case	O(1)	O(1)

Karatsuba Multiplication reveals the magic of algebraic rearrangement, using one clever identity to turn brute-force arithmetic into an elegant, faster divide-and-conquer dance.

36 DP State Diagram Example

The DP State Diagram Example introduces the idea of representing dynamic programming (DP) problems as graphs of states connected by transitions. It's a visual and structural way to reason about overlapping subproblems, dependencies, and recurrence relations.

What Problem Are We Solving?

Dynamic programming problems often involve a set of subproblems that depend on one another. Without a clear mental model, it's easy to lose track of which states rely on which others.

A state diagram helps us:

- Visualize states as nodes
- Show transitions as directed edges

- Understand dependency order for iteration or recursion

This builds intuition for state definition, transition logic, and evaluation order.

How It Works (Plain Language)

1. Define the state, what parameters represent a subproblem (e.g., index, capacity, sum).
2. Draw each state as a node.
3. Add edges to show transitions between states.
4. Assign recurrence along edges:

$$dp[\text{state}] = \text{combine}(dp[\text{previous states}])$$

5. Solve by topological order (bottom-up) or memoized recursion (top-down).

Example Step by Step

Example: Fibonacci Sequence

$$F(n) = F(n-1) + F(n-2)$$

State diagram:

```
F(5)

F(4) F(3)

F(3)F(2)F(2)F(1)
```

Each node = state `F(k)` Edges = dependencies on `F(k-1)` and `F(k-2)`

Observation: Many states repeat, shared subproblems suggest memoization or bottom-up DP.

Another Example: 0/1 Knapsack

State: `dp[i][w]` = max value using first i items, capacity w. Transitions:

- Include item i: `dp[i-1][w-weight[i]] + value[i]`
- Exclude item i: `dp[i-1][w]`

Diagram: a grid of states, each cell connected from previous row and shifted left.

Tiny Code (Python)

```
def fib_dp(n):
    dp = [0, 1]
    for i in range(2, n + 1):
        dp.append(dp[i-1] + dp[i-2])
    return dp[n]
```

Each entry `dp[i]` represents a state, filled based on prior dependencies.

Why It Matters

- Makes DP visual and tangible
- Clarifies dependency direction (acyclic structure)
- Ensures correct order of computation
- Serves as blueprint for bottom-up or memoized implementation

A Gentle Proof (Why It Works)

If a problem's structure can be represented as a DAG of states, and:

- Every state's value depends only on earlier states
- Base states are known

Then by evaluating nodes in topological order, we guarantee correctness, each subproblem is solved after its dependencies.

This matches mathematical induction over recurrence depth.

Try It Yourself

1. Draw state diagram for Fibonacci.
2. Draw grid for 0/1 Knapsack (rows = items, cols = capacity).
3. Visualize transitions for Coin Change (ways to make sum).
4. Trace evaluation order bottom-up.

Test Cases

Problem	State	Transition	Diagram Shape
Fibonacci	dp[i]	dp[i-1]+dp[i-2]	Chain
Knapsack	dp[i][w]	max(include, exclude)	Grid
Coin Change	dp[i][s]	dp[i-1][s]+dp[i][s-coin]	Lattice

Complexity

Step	Time	Space
Diagram construction	$O(n^2)$ (visual)	$O(n^2)$
DP evaluation	$O(n \cdot m)$ typical	$O(n \cdot m)$

The DP State Diagram turns abstract recurrences into maps of reasoning, every arrow a dependency, every node a solved step, guiding you from base cases to the final solution.

37 DP Table Visualization

The DP Table Visualization is a way to make dynamic programming tangible, turning states and transitions into a clear table you can fill, row by row or column by column. Each cell represents a subproblem, and the process of filling it shows the algorithm's structure.

What Problem Are We Solving?

Dynamic programming can feel abstract when written as recurrences. A table transforms that abstraction into something concrete:

- Rows and columns correspond to subproblem parameters
- Cell values show computed solutions
- Filling order reveals dependencies

This approach is especially powerful for tabulation (bottom-up DP).

How It Works (Plain Language)

1. Define your DP state (e.g., `dp[i][j]` = best value up to item i and capacity j).
2. Initialize base cases (first row/column).
3. Iterate through the table in dependency order.

4. Apply recurrence at each cell:

$$dp[i][j] = \text{combine}(dp[i-1][j], dp[i-1][j-w_i] + v_i)$$

5. Final cell gives the answer (often bottom-right).

Example Step by Step

Example: 0/1 Knapsack

Items:

Item	Weight	Value
1	1	15
2	3	20
3	4	30

Capacity = 4

State: `dp[i][w]` = max value with first i items, capacity w.

Recurrence:

$$dp[i][w] = \max(dp[i-1][w], dp[i-1][w-w_i] + v_i)$$

DP Table:

i/w	0	1	2	3	4
0	0	0	0	0	0
1	0	15	15	15	15
2	0	15	15	20	35
3	0	15	15	20	35

Final answer: 35 (items 1 and 2)

Tiny Code (Python)

```
def knapsack(weights, values, W):
    n = len(weights)
    dp = [[0]*(W+1) for _ in range(n+1)]
    for i in range(1, n+1):
        for w in range(W+1):
            if weights[i-1] <= w:
                dp[i][w] = max(dp[i-1][w],
                               dp[i-1][w-weights[i-1]] + values[i-1])
            else:
                dp[i][w] = dp[i-1][w]
    return dp
```

Each `dp[i][w]` is one table cell, filled in increasing order of i and w.

Why It Matters

- Turns recurrence into geometry
- Makes dependencies visible and traceable
- Clarifies filling order (row-wise, diagonal, etc.)
- Serves as debugging tool and teaching aid

A Gentle Proof (Why It Works)

The table order ensures every subproblem is solved after its dependencies. By induction:

- Base row/column initialized correctly
- Each cell built from valid earlier states
- Final cell accumulates optimal solution

This is equivalent to a topological sort on the DP dependency graph.

Try It Yourself

1. Draw the DP table for Coin Change (number of ways).
2. Fill row by row.
3. Trace dependencies with arrows.
4. Mark the path that contributes to the final answer.

Test Cases

Problem	State	Fill Order	Output
Knapsack	dp[i][w]	Row-wise	Max value
LCS	dp[i][j]	Diagonal	LCS length
Edit Distance	dp[i][j]	Row/col	Min ops

Complexity

Step	Time	Space
Filling table	$O(n \cdot m)$	$O(n \cdot m)$
Traceback (optional)	O(n+m)	O(1)

The DP Table Visualization is the grid view of recursion, a landscape of subproblems, each solved once, all leading toward the final cell that encodes the complete solution.

38 Recursive Subproblem Tree Demo

The Recursive Subproblem Tree Demo shows how a dynamic programming problem expands into a tree of subproblems. It visualizes recursion structure, repeated calls, and where memoization or tabulation can save redundant work.

What Problem Are We Solving?

When writing a recursive solution, the same subproblems are often solved multiple times. Without visualizing this, we may not realize how much overlap occurs.

By drawing the recursion as a subproblem tree, we can:

- Identify repeated nodes (duplicate work)
- Understand recursion depth
- Decide between memoization (top-down) or tabulation (bottom-up)

How It Works (Plain Language)

1. Start from the root: the full problem (e.g., `F(n)`).
2. Expand recursively into smaller subproblems (children).
3. Continue until base cases (leaves).
4. Observe repeated nodes (same subproblem appearing multiple times).
5. Replace repeated computations with a lookup in a table.

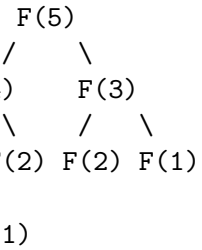
The resulting structure is a tree that becomes a DAG after memoization.

Example Step by Step

Example: Fibonacci (Naive Recursive)

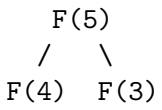
$$F(n) = F(n-1) + F(n-2)$$

For $n = 5$:



Repeated nodes: `F(3)`, `F(2)` Memoization would store these results and reuse them.

With Memoization (Tree Collapsed):



Each node computed once, repeated calls replaced by cache lookups.

Tiny Code (Python)

```
def fib(n, memo=None):
    if memo is None:
        memo = {}
    if n in memo:
        return memo[n]
    if n <= 1:
        return n
    memo[n] = fib(n-1, memo) + fib(n-2, memo)
    return memo[n]
```

The memo dictionary turns the recursion tree into a DAG.

Why It Matters

- Exposes hidden redundancy in recursive algorithms
- Motivates memoization (cache results)
- Shows connection between recursion and iteration
- Visual tool for understanding time complexity

A Gentle Proof (Why It Works)

Let $T(n)$ be the recursion tree size.

Naive recursion for Fibonacci:

$$T(n) = T(n-1) + T(n-2) + 1$$

$O(2^n)$ calls

With memoization, each subproblem computed once:

$$T(n) = O(n)$$

Proof by induction:

- Base case $n = 1$: trivial
- Inductive step: if all smaller values memoized, reuse ensures constant-time lookups per state

Try It Yourself

1. Draw the recursion tree for Fibonacci(6).
2. Count repeated nodes.
3. Add a memo table and redraw as DAG.
4. Apply same technique to factorial or grid path problems.

Test Cases

Function	Naive Calls	Memoized Calls	Time
fib(5)	15	6	O(2) → O(n)
fib(10)	177	11	O(2) → O(n)
fib(20)	21891	21	O(2) → O(n)

Complexity

Step	Time	Space
Naive recursion	O(2)	O(n)
With memoization	O(n)	O(n)

The Recursive Subproblem Tree Demo turns hidden recursion into a picture, every branch a computation, every repeated node a chance to save time, and every cache entry a step toward efficiency.

39 Greedy Choice Visualization

The Greedy Choice Visualization helps you see how greedy algorithms make decisions step by step, choosing the locally optimal option at each point and committing to it. By tracing choices visually, you can verify whether the greedy strategy truly leads to a global optimum.

What Problem Are We Solving?

A greedy algorithm always chooses the best immediate option. But not every problem supports this approach, some require backtracking or DP. To know when greediness works, we need to see the chain of choices and their effects.

A greedy choice diagram reveals:

- What each local decision looks like
- How each choice affects remaining subproblems
- Whether local optima accumulate into a global optimum

How It Works (Plain Language)

1. Start with the full problem (e.g., a set of intervals, coins, or items).
2. Sort or prioritize by a greedy criterion (e.g., largest value, earliest finish).
3. Pick the best option currently available.
4. Eliminate incompatible elements (conflicts, overlaps).
5. Repeat until no valid choices remain.
6. Visualize each step as a growing path or sequence.

The resulting picture shows a selection frontier, how choices narrow possibilities.

Example Step by Step

Example 1: Interval Scheduling

Goal: select max non-overlapping intervals.

Interval	Start	End
A	1	4
B	3	5
C	0	6
D	5	7
E	8	9

Greedy Rule: Choose earliest finish time.

Steps:

1. Sort by finish → A(1–4), B(3–5), C(0–6), D(5–7), E(8–9)
2. Pick A → remove overlaps (B, C)
3. Next pick D (5–7)
4. Next pick E (8–9)

Visualization:

```
Timeline: 0---1---3---4---5---7---8---9
           [A]     [D]      [E]
```

Total = 3 intervals → optimal.

Example 2: Fractional Knapsack

Item	Value	Weight	Ratio
1	60	10	6
2	100	20	5
3	120	30	4

Greedy Rule: Max value/weight ratio Visualization: pick items in decreasing ratio order → 1, 2, part of 3.

Tiny Code (Python)

```
def greedy_choice(items, key):
    items = sorted(items, key=key, reverse=True)
    chosen = []
    for it in items:
        if valid(it, chosen):
            chosen.append(it)
    return chosen
```

By logging or plotting at each iteration, you can visualize how the solution grows.

Why It Matters

- Shows local vs global tradeoffs visually
- Confirms greedy-choice property (local best = globally best)
- Helps diagnose greedy failures (where path deviates from optimum)
- Strengthens understanding of problem structure

A Gentle Proof (Why It Works)

A greedy algorithm works if:

1. Greedy-choice property: local best can lead to global best.
2. Optimal substructure: optimal solution of whole contains optimal solutions of parts.

Visualization helps verify these conditions, if each chosen step leaves a smaller problem that is still optimally solvable by the same rule, the algorithm is correct.

Try It Yourself

1. Draw intervals and apply earliest-finish greedy rule.
2. Visualize coin selections for greedy coin change.
3. Try a counterexample where greedy fails (e.g., coin set {4,3,1}).
4. Plot selection order to see divergence from optimum.

Test Cases

Problem	Greedy Rule	Works?	Note
Interval Scheduling	Earliest finish	Yes	Optimal
Fractional Knapsack	Max ratio	Yes	Continuous fractions
Coin Change (25,10,5,1)	Largest coin remaining	Yes	Canonical
Coin Change (4,3,1)	Largest coin remaining	No	Not canonical

Complexity

Step	Time	Space
Sort elements	O(n log n)	O(n)
Selection loop	O(n)	O(1)

The Greedy Choice Visualization transforms abstract decision logic into a picture, a timeline or path that shows exactly how local choices unfold into (or away from) the global goal.

40 Amortized Merge Demo

The Amortized Merge Demo illustrates how expensive operations can appear cheap when averaged over a long sequence. By analyzing total cost across all steps, we reveal why some algorithms with occasional heavy work still run efficiently overall.

What Problem Are We Solving?

Some data structures or algorithms perform occasional costly operations (like merging arrays, resizing tables, or rebuilding heaps). If we only look at worst-case time per step, they seem inefficient, but amortized analysis shows that, over many operations, the *average* cost per operation stays low.

This method explains why dynamic arrays, union-find, and incremental merges remain efficient.

How It Works (Plain Language)

1. Perform a sequence of operations (O_1, O_2, ..., O_n).
2. Some are cheap (constant time), some are expensive (linear or log).
3. Compute total cost over all (n) operations.
4. Divide total by (n) → amortized cost per operation.

Amortized analysis tells us:

$$\text{Amortized cost} = \frac{\text{Total cost over sequence}}{n}$$

Even if a few operations are expensive, their cost is "spread out" across many cheap ones.

Example Step by Step

Example: Dynamic Array Doubling

Suppose we double the array each time it's full.

Operation	Capacity	Actual Cost	Total Elements	Cumulative Cost
Insert 1–1	1	1	1	1
Insert 2–2	2	2	2	3
Insert 3–4	4	3	3	6
Insert 4–4	4	1	4	7
Insert 5–8	8	5	5	12
Insert 6–8	8	1	6	13
Insert 7–8	8	1	7	14
Insert 8–8	8	1	8	15
Insert 9–16	16	9	9	24

Total cost (for 9 inserts) = 24 Amortized cost = 24 / 9 2.67 O(1)

So although some inserts cost O(n), the average cost per insert = O(1).

Example: Amortized Merge in Union-Find

When combining sets, always attach the smaller tree to the larger one. Each element's depth increases at most O(log n) times → total cost O(n log n).

Tiny Code (Python)

```
def dynamic_array_append(arr, x, capacity):
    if len(arr) == capacity:
        capacity *= 2  # double size
        arr.extend([None]*(capacity - len(arr)))  # copy cost = len(arr)
    arr[len(arr)//2] = x
    return arr, capacity
```

This simulates doubling capacity, where copy cost = current array size.

Why It Matters

- Explains hidden efficiency behind resizing structures
- Shows why occasional spikes don't ruin performance
- Foundation for analyzing stacks, queues, hash tables
- Builds intuition for amortized O(1) operations

A Gentle Proof (Why It Works)

Consider dynamic array resizing:

- Every element gets moved at most once per doubling.
- Over n insertions, total copies 2n.

Thus,

$$\text{Total cost} = O(n) \implies \text{Amortized cost} = O(1)$$

This uses the aggregate method of amortized analysis:

$$\text{Amortized cost per operation} = \frac{\text{total work}}{\#\text{ operations}}$$

Try It Yourself

1. Simulate 10 inserts into a doubling array.
2. Track total copy cost.
3. Plot actual vs amortized cost.
4. Repeat with tripling growth factor, compare average cost.

Test Cases

Operation Type	Cost Model	Amortized Cost	Notes
Array Doubling	Copy + Insert	O(1)	Spread cost
Union-Find Merge	Attach smaller to larger	O((n))	= inverse Ackermann
Stack Push	Resize occasionally	O(1)	Average constant
Queue Enqueue	Circular buffer	O(1)	Rotational reuse

Complexity

Step	Worst Case	Amortized	Space
Single Insert	O(n)	O(1)	O(n)
n Inserts	O(n)	O(n)	O(n)

The Amortized Merge Demo reveals the calm beneath algorithmic chaos, even when some steps are costly, the long-run rhythm stays smooth, predictable, and efficient.

Section 5. Recurrence Relations

41 Linear Recurrence Solver

A Linear Recurrence Solver finds closed-form or iterative solutions for sequences defined in terms of previous values. It transforms recursive definitions like $T(n) = aT(n-1) + b$ into explicit formulas, helping us understand algorithmic growth.

What Problem Are We Solving?

Many algorithms, especially recursive ones, define running time through a recurrence relation, for example:

$$T(n) = a, T(n-1) + b$$

To reason about complexity or compute exact values, we want to solve the recurrence, converting it from a self-referential definition into a direct expression in n.

This solver provides a methodical way to do that.

How It Works (Plain Language)

A linear recurrence has the general form:

$$T(n) = a_1 T(n-1) + a_2 T(n-2) + \cdots + a_k T(n-k) + f(n)$$

1. Identify coefficients $(a_1, a_2, ...)$.
2. Write the characteristic equation for the homogeneous part.
3. Solve for roots $(r_1, r_2, ...)$.
4. Form the homogeneous solution using those roots.
5. Add a particular solution if $f(n)$ is non-zero.
6. Apply initial conditions to fix constants.

Example Step by Step

Example 1:

$$T(n) = 2T(n-1) + 3, \quad T(0) = 1$$

1. Homogeneous part: $T(n) - 2T(n-1) = 0 \rightarrow$ Characteristic root: $r = 2 \rightarrow$ Homogeneous solution: $T_h(n) = C \cdot 2^n$
2. Particular solution: constant p Plug in: $p = 2p + 3 \implies p = -3$
3. General solution:
$$T(n) = C \cdot 2^n - 3$$
4. Apply $T(0) = 1$: $1 = C - 3 \implies C = 4$

Final:

$$T(n) = 4 \cdot 2^n - 3$$

Example 2 (Fibonacci):

$$F(n) = F(n-1) + F(n-2), \quad F(0) = 0, F(1) = 1$$

Characteristic equation:

$$r^2 - r - 1 = 0$$

Roots:

$$r_1 = \frac{1+\sqrt{5}}{2}, \quad r_2 = \frac{1-\sqrt{5}}{2}$$

General solution:

$$F(n) = Ar_1^n + Br_2^n$$

Solving constants yields Binet's Formula:

$$F(n) = \frac{1}{\sqrt{5}} \left[\left(\frac{1+\sqrt{5}}{2} \right)^n - \left(\frac{1-\sqrt{5}}{2} \right)^n \right]$$

Tiny Code (Python)

```
def linear_recurrence(a, b, n, t0):
    T = [t0]
    for i in range(1, n + 1):
        T.append(a * T[i - 1] + b)
    return T
```

This simulates a simple first-order recurrence like $T(n) = aT(n-1) + b$.

Why It Matters

- Converts recursive definitions into explicit formulas
- Helps analyze time complexity for recursive algorithms
- Bridges math and algorithm design
- Used in DP transitions, counting problems, and algorithm analysis

A Gentle Proof (Why It Works)

Unroll $T(n) = aT(n-1) + b$:

$$T(n) = a^n T(0) + b(a^{n-1} + a^{n-2} + \cdots + 1)$$

Sum is geometric:

$$T(n) = a^n T(0) + b\frac{a^n - 1}{a - 1}$$

Hence the closed form is:

$$T(n) = a^n T(0) + \frac{b(a^n - 1)}{a - 1}$$

This matches the method of characteristic equations for constant coefficients.

Try It Yourself

1. Solve $T(n) = 3T(n-1) + 2, , T(0) = 1$
2. Solve $T(n) = 2T(n-1) - T(n-2)$
3. Compare numeric results with iterative simulation
4. Draw recursion tree to confirm growth trend

Test Cases

Recurrence	Initial	Solution	Growth
$T(n) = 2T(n-1) + 3$	$T(0) = 1$	$4 \cdot 2^n - 3$	$O(2^n)$
$T(n) = T(n-1) + 1$	$T(0) = 0$	n	$O(n)$
$T(n) = 3T(n-1)$	$T(0) = 1$	3^n	$O(3^n)$

Complexity

Method	Time	Space
Recursive (unrolled)	O(n)	O(n)
Closed-form	O(1)	O(1)

A Linear Recurrence Solver turns repeated dependence into explicit growth, revealing the hidden pattern behind each recursive step.

42 Master Theorem

The Master Theorem provides a direct method to analyze divide-and-conquer recurrences, allowing you to find asymptotic bounds without expanding or guessing. It is a cornerstone tool for understanding recursive algorithms such as merge sort, binary search, and Strassen's multiplication.

What Problem Are We Solving?

Many recursive algorithms can be expressed as:

$$T(n) = a, T!\left(\frac{n}{b}\right) + f(n)$$

where:

- a: number of subproblems
- b: shrink factor (problem size per subproblem)
- $f(n)$: additional work outside recursion (combine, partition, etc.)

We want to find an asymptotic expression for $T(n)$ by comparing recursive cost ($n^{\log_b a}$) with non-recursive cost ($f(n)$).

How It Works (Plain Language)

1. Write the recurrence in standard form:

$$T(n) = a, T(n/b) + f(n)$$

2. Compute the critical exponent $\log_b a$.
3. Compare $f(n)$ with $n^{\log_b a}$:
    - If $f(n)$ is smaller, recursion dominates.
    - If they are equal, both contribute equally.
    - If $f(n)$ is larger, the outside work dominates.

The theorem gives three standard cases depending on which term grows faster.

The Three Cases

Case 1 (Recursive Work Dominates):

If

$$f(n) = O(n^{\log_b a - \varepsilon})$$

for some $\varepsilon > 0$, then

$$T(n) = \Theta(n^{\log_b a})$$

Case 2 (Balanced Work):

If

$$f(n) = \Theta(n^{\log_b a})$$

then

$$T(n) = \Theta(n^{\log_b a} \log n)$$

Case 3 (Non-Recursive Work Dominates):

If

$$f(n) = \Omega(n^{\log_b a + \varepsilon})$$

and

$$a, f(n/b) \leq c, f(n)$$

for some constant $c < 1$, then

$$T(n) = \Theta(f(n))$$

Example Step by Step

Example 1: Merge Sort

$$T(n) = 2T(n/2) + O(n)$$

- $a = 2$, $b = 2$, so $\log_b a = 1$
- $f(n) = O(n)$
- $f(n) = \Theta(n^{\log_b a}) \to$ Case 2

Result:

$$T(n) = \Theta(n \log n)$$

Example 2: Binary Search

$$T(n) = T(n/2) + O(1)$$

- $a = 1$, $b = 2$, so $\log_b a = 0$
- $f(n) = O(1) = \Theta(n^0) \to$ Case 2

Result:

$$T(n) = \Theta(\log n)$$

Example 3: Strassen's Matrix Multiplication

$$T(n) = 7T(n/2) + O(n^2)$$

- $a = 7$, $b = 2$, so $\log_2 7 \approx 2.81$
- $f(n) = O(n^2) = O(n^{2.81-\varepsilon}) \to$ Case 1

Result:

$$T(n) = \Theta(n^{\log_2 7})$$

Tiny Code (Python)

```
import math

def master_theorem(a, b, f_exp):
    log_term = math.log(a, b)
    if f_exp < log_term:
        return f"Theta(n^{round(log_term, 2)})"
```

```
    elif abs(f_exp - log_term) < 1e-9:
        return f"Theta(n^{round(log_term, 2)} * log n)"
    else:
        return f"Theta(n^{f_exp})"
```

This helper approximates the result by comparing exponents.

Why It Matters

- Converts recursive definitions into asymptotic forms
- Avoids repeated substitution or tree expansion
- Applies to most divide-and-conquer algorithms
- Clarifies when combining work dominates or not

A Gentle Proof (Why It Works)

Expand the recurrence:

$$T(n) = aT(n/b) + f(n)$$

After k levels:

$$T(n) = a^k T(n/b^k) + \sum_{i=0}^{k-1} a^i f(n/b^i)$$

Recursion depth: $k = \log_b n$

Now compare total cost per level to $n^{\log_b a}$:

- If $f(n)$ grows slower, top levels dominate → Case 1
- If equal, all levels contribute → Case 2
- If faster, bottom level dominates → Case 3

The asymptotic result depends on which component dominates the sum.

Try It Yourself

1. Solve $T(n) = 3T(n/2) + n$
2. Solve $T(n) = 4T(n/2) + n^2$
3. Sketch recursion trees and check which term dominates

Test Cases

Recurrence	Case	Solution
$T(n) = 2T(n/2) + n$	Case 2	$\Theta(n \log n)$
$T(n) = T(n/2) + 1$	Case 2	$\Theta(\log n)$
$T(n) = 7T(n/2) + n^2$	Case 1	$\Theta(n^{\log_2 7})$
$T(n) = 2T(n/2) + n^2$	Case 3	$\Theta(n^2)$

Complexity Summary

Component	Expression	Interpretation
Recursive work	$n^{\log_b a}$	Work across recursive calls
Combine work	$f(n)$	Work per level
Total cost	$\max(n^{\log_b a}, f(n))$	Dominant term decides growth

The Master Theorem serves as a blueprint for analyzing recursive algorithms, once the recurrence is in standard form, its complexity follows by simple comparison.

43 Substitution Method

The Substitution Method is a systematic way to prove the asymptotic bound of a recurrence by guessing a solution and then proving it by induction. It's one of the most flexible techniques for verifying time complexity.

What Problem Are We Solving?

Many algorithms are defined recursively, for example:

$$T(n) = 2T(n/2) + n$$

We often want to show that $T(n) = O(n \log n)$ or $T(n) = \Theta(n^2)$. But before we can apply a theorem, we must confirm that our guess fits.

The substitution method provides a proof framework:

1. Guess the asymptotic bound.
2. Prove it by induction.
3. Adjust constants if necessary.

How It Works (Plain Language)

1. Make a guess for $T(n)$, typically inspired by known patterns. For example, for $T(n) = 2T(n/2) + n$, guess $T(n) = O(n \log n)$.
2. Write the inductive hypothesis: Assume $T(k) \leq c, k \log k$ for all $k < n$.
3. Substitute into the recurrence: Replace recursive terms with the hypothesis.
4. Simplify and verify: Show the inequality holds for n, adjusting constants if needed.
5. Conclude that the guess is valid.

Example Step by Step

Example 1:

$$T(n) = 2T(n/2) + n$$

Goal: Show $T(n) = O(n \log n)$

1. Hypothesis: $T(k) \leq c, k \log k$ for all $k < n$
2. Substitute: $T(n) \leq 2[c(n/2) \log(n/2)] + n$
3. Simplify: $= cn \log(n/2) + n = cn(\log n - 1) + n = cn \log n - cn + n$
4. Adjust constant: If $c \geq 1$, then $-cn + n \leq 0$, so $T(n) \leq cn \log n$

Therefore, $T(n) = O(n \log n)$.

Example 2:

$$T(n) = 3T(n/2) + n$$

Guess: $T(n) = O(n^{\log_2 3})$

1. Hypothesis: $T(k) \leq c, k^{\log_2 3}$
2. Substitute: $T(n) \leq 3c(n/2)^{\log_2 3} + n = 3c \cdot n^{\log_2 3}/3 + n = cn^{\log_2 3} + n$
3. Dominant term: $n^{\log_2 3} \quad T(n) = O(n^{\log_2 3})$

Tiny Code (Python)

```
def substitution_check(a, b, f_exp, guess_exp):
    from math import log
    lhs = a * (1 / b)  guess_exp
    rhs = 1
    if lhs < 1:
        return f"Guess n^{guess_exp} holds (Case 1)"
    elif abs(lhs - 1) < 1e-9:
        return f"Guess n^{guess_exp} log n (Case 2)"
    else:
        return f"Guess n^{guess_exp} fails (try larger exponent)"
```

Helps verify whether a guessed exponent fits the recurrence.

Why It Matters

- Builds proof-based understanding of complexity
- Confirms asymptotic bounds from intuition or Master Theorem
- Works even when Master Theorem fails (irregular forms)
- Reinforces connection between recursion and growth rate

A Gentle Proof (Why It Works)

Let $T(n) = aT(n/b) + f(n)$ Guess $T(n) = O(n^{\log_b a})$.

Inductive step:

$$T(n) = aT(n/b) + f(n) \leq a(c(n/b)^{\log_b a}) + f(n)$$
$$= cn^{\log_b a} + f(n)$$

If $f(n)$ grows slower, $T(n)$ remains $O(n^{\log_b a})$ by choosing c large enough.

Try It Yourself

1. Prove $T(n) = 2T(n/2) + n^2 = O(n^2)$
2. Prove $T(n) = T(n-1) + 1 = O(n)$
3. Adjust constants to make the induction hold

Test Cases

Recurrence	Guess	Result
$T(n) = 2T(n/2) + n$	$O(n \log n)$	Correct
$T(n) = T(n-1) + 1$	$O(n)$	Correct
$T(n) = 3T(n/2) + n$	$O(n^{\log_2 3})$	Correct

Complexity Summary

Method	Effort	When to Use
Master Theorem	Quick	Standard divide-and-conquer
Substitution	Moderate	Custom or irregular recurrences
Iteration	Detailed	Step-by-step expansion

The Substitution Method blends intuition with rigor, you make a good guess, and algebra does the rest.

44 Iteration Method

The Iteration Method (also called the Recursion Expansion Method) solves recurrences by repeatedly substituting the recursive term until the pattern becomes clear. It is a constructive way to derive closed-form or asymptotic solutions.

What Problem Are We Solving?

Recursive algorithms often define their running time in terms of smaller instances:

$$T(n) = a, T(n/b) + f(n)$$

Instead of guessing or applying a theorem, the iteration method unfolds the recurrence layer by layer, showing exactly how cost accumulates across recursion levels.

This method is especially helpful when $f(n)$ follows a recognizable pattern, like linear, quadratic, or logarithmic functions.

How It Works (Plain Language)

1. Write down the recurrence:

$$T(n) = a, T(n/b) + f(n)$$

2. Expand one level at a time:

$$T(n) = a[a, T(n/b^2) + f(n/b)] + f(n)$$

$$= a^2 T(n/b^2) + af(n/b) + f(n)$$

3. Continue expanding k levels until the subproblem size becomes 1:

$$T(n) = a^k T(n/b^k) + \sum_{i=0}^{k-1} a^i f(n/b^i)$$

4. When $n/b^k = 1$, we have $k = \log_b n$.
5. Substitute $k = \log_b n$ to find the closed form or asymptotic bound.

Example Step by Step

Example 1: Merge Sort

$$T(n) = 2T(n/2) + n$$

Step 1: Expand

[ ]

Step 2: Base Case

When $n/2^k = 1 \implies k = \log_2 n$

So:

$$T(n) = n \cdot T(1) + n \log_2 n = O(n \log n)$$

$T(n) = \Theta(n \log n)$

Example 2: Binary Search

$$T(n) = T(n/2) + 1$$

Expand:

[ ]

$T(n) = O(\log n)$

Example 3: Linear Recurrence

$$T(n) = T(n-1) + 1$$

Expand:

$$T(n) = T(n-1) + 1 = T(n-2) + 2 = \cdots = T(1) + (n-1)$$

$T(n) = O(n)$

Tiny Code (Python)

```
def iterate_recurrence(a, b, f, n):
    total = 0
    level = 0
    while n > 1:
        total += (a  level) * f(n / (b  level))
        n /= b
        level += 1
    return total
```

This illustrates the summation process level by level.

Why It Matters

- Makes recursion visually transparent
- Works for irregular $f(n)$ (when Master Theorem doesn't apply)
- Derives exact sums, not just asymptotic bounds
- Builds intuition for recursion trees and logarithmic depth

A Gentle Proof (Why It Works)

Each level i of the recursion contributes:

$$a^i \cdot f(n/b^i)$$

Total number of levels:

$$\log_b n$$

So total cost:

$$T(n) = \sum_{i=0}^{\log_b n - 1} a^i f(n/b^i)$$

This sum can be approximated or bounded using standard summation techniques, depending on $f(n)$'s growth rate.

Try It Yourself

1. Solve $T(n) = 3T(n/2) + n^2$
2. Solve $T(n) = 2T(n/2) + n \log n$
3. Solve $T(n) = T(n/2) + n/2$
4. Compare with Master Theorem results

Test Cases

Recurrence	Solution	Growth
$T(n) = 2T(n/2) + n$	$n \log n$	$O(n \log n)$
$T(n) = T(n/2) + 1$	$\log n$	$O(\log n)$
$T(n) = T(n-1) + 1$	n	$O(n)$
$T(n) = 3T(n/2) + n^2$	n^2	$O(n^2)$

Complexity Summary

Step	Time	Space
Expansion	$O(\log n)$ levels	Stack depth $O(\log n)$
Summation	Depends on $f(n)$	Often geometric or arithmetic

The Iteration Method unpacks recursion into layers of work, turning a recurrence into a concrete sum, and a sum into a clear complexity bound.

45 Generating Function Method

The Generating Function Method transforms a recurrence relation into an algebraic equation by encoding the sequence into a power series. Once transformed, algebraic manipulation yields a closed-form expression or asymptotic approximation.

What Problem Are We Solving?

A recurrence defines a sequence $T(n)$ recursively:

$$T(n) = a_1 T(n-1) + a_2 T(n-2) + \cdots + f(n)$$

We want to find a closed-form formula instead of computing step by step. By representing $T(n)$ as coefficients in a power series, we can use algebraic tools to solve recurrences cleanly, especially linear recurrences with constant coefficients.

How It Works (Plain Language)

1. Define the generating function Let

$$G(x) = \sum_{n=0}^{\infty} T(n) x^n$$

2. Multiply the recurrence by x^n and sum over all n.
3. Use properties of sums (shifting indices, factoring constants) to rewrite in terms of $G(x)$.
4. Solve the algebraic equation for $G(x)$.
5. Expand $G(x)$ back into a series (using partial fractions or known expansions).
6. Extract $T(n)$ as the coefficient of x^n.

Example Step by Step

Example 1: Fibonacci Sequence

$$T(n) = T(n-1) + T(n-2), \quad T(0) = 0, ; T(1) = 1$$

Step 1: Define generating function

$$G(x) = \sum_{n=0}^{\infty} T(n)x^n$$

Step 2: Multiply recurrence by x^n and sum over $n \geq 2$:

$$\sum_{n=2}^{\infty} T(n)x^n = \sum_{n=2}^{\infty} T(n-1)x^n + \sum_{n=2}^{\infty} T(n-2)x^n$$

Step 3: Rewrite using shifts:

$$G(x) - T(0) - T(1)x = x(G(x) - T(0)) + x^2 G(x)$$

Plug in initial values $T(0) = 0, T(1) = 1$:

$$G(x) - x = xG(x) + x^2 G(x)$$

Step 4: Solve for $G(x)$:

$$G(x)(1 - x - x^2) = x$$

So:

$$G(x) = \frac{x}{1 - x - x^2}$$

Step 5: Expand using partial fractions to get coefficients:

$$T(n) = \frac{1}{\sqrt{5}} \left[\left(\frac{1+\sqrt{5}}{2} \right)^n - \left(\frac{1-\sqrt{5}}{2} \right)^n \right]$$

Binet's Formula derived directly.

Example 2: $T(n) = 2T(n-1) + 3$, $T(0) = 1$

Let $G(x) = \sum_{n=0}^{\infty} T(n)x^n$

Multiply by x^n and sum over $n \geq 1$:

$$G(x) - T(0) = 2xG(x) + 3x \cdot \frac{1}{1-x}$$

Simplify:

$$G(x)(1-2x) = 1 + \frac{3x}{1-x}$$

Solve and expand using partial fractions → recover closed-form:

$$T(n) = 4 \cdot 2^n - 3$$

Tiny Code (Python)

```
from sympy import symbols, Function, Eq, rsolve

n = symbols('n', integer=True)
T = Function('T')
recurrence = Eq(T(n), 2*T(n-1) + 3)
solution = rsolve(recurrence, T(n), {T(0): 1})
print(solution)  # 4*2n - 3
```

Use `sympy.rsolve` to compute closed forms symbolically.

Why It Matters

- Converts recurrence relations into algebraic equations
- Reveals exact closed forms, not just asymptotics
- Works for non-homogeneous and constant-coefficient recurrences
- Bridges combinatorics, discrete math, and algorithm analysis

A Gentle Proof (Why It Works)

Given a linear recurrence:

$$T(n) - a_1 T(n-1) - \cdots - a_k T(n-k) = f(n)$$

Multiply by x^n and sum from $n = k$ to ∞:

$$\sum_{n=k}^{\infty} T(n)x^n = a_1 x \sum_{n=k}^{\infty} T(n-1)x^{n-1} + \cdots + f(x)$$

Using index shifts, each term can be written in terms of $G(x)$, leading to:

$$P(x)G(x) = Q(x)$$

where $P(x)$ and $Q(x)$ are polynomials. Solving for $G(x)$ gives the sequence structure.

Try It Yourself

1. Solve $T(n) = 3T(n-1) - 2T(n-2)$ with $T(0) = 2, T(1) = 3$.
2. Find $T(n)$ if $T(n) = T(n-1) + 1$, $T(0) = 0$.
3. Compare your generating function with unrolled expansion.

Test Cases

Recurrence	Closed Form	Growth
$T(n) = 2T(n-1) + 3$	$4 \cdot 2^n - 3$	$O(2^n)$
$T(n) = T(n-1) + 1$	n	$O(n)$
$T(n) = T(n-1) + T(n-2)$	Binet's Formula	$O(\phi^n)$

Complexity Summary

Step	Type	Complexity
Transformation	Algebraic	O(k) terms
Solution	Symbolic (via roots)	O(k^3)
Evaluation	Closed form	O(1)

The Generating Function Method turns recurrences into algebra, summations become equations, and equations yield exact formulas.

46 Matrix Exponentiation

The Matrix Exponentiation Method transforms linear recurrences into matrix form, allowing efficient computation of terms in $O(\log n)$ time using fast exponentiation. It's ideal for sequences like Fibonacci, Tribonacci, and many dynamic programming transitions.

What Problem Are We Solving?

Many recurrences follow a linear relation among previous terms, such as:

$$T(n) = a_1 T(n-1) + a_2 T(n-2) + \cdots + a_k T(n-k)$$

Naively computing $T(n)$ takes $O(n)$ steps. By encoding this recurrence in a matrix, we can compute $T(n)$ efficiently via exponentiation, reducing runtime to $O(k^3 \log n)$.

How It Works (Plain Language)

1. Express the recurrence as a matrix multiplication.
2. Construct the transition matrix M that moves the state from $n-1$ to n.
3. Compute M^n using fast exponentiation (divide and conquer).
4. Multiply M^n by the initial vector to obtain $T(n)$.

This approach generalizes well to any linear homogeneous recurrence with constant coefficients.

Example Step by Step

Example 1: Fibonacci Sequence

$$F(n) = F(n-1) + F(n-2)$$

Define state vector:

$$\begin{bmatrix} F(n) \\ F(n-1) \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} F(n-1) \\ F(n-2) \end{bmatrix}$$

So:

$$M = \begin{bmatrix} 1 & 1[6pt]1 & 0 \end{bmatrix}$$

Therefore:

$$\begin{bmatrix} F(n) & F(n-1) \end{bmatrix} = M^{n-1} \begin{bmatrix} F(1) & F(0) \end{bmatrix}$$

Given $F(1) = 1, F(0) = 0$,

$$F(n) = (M^{n-1})_{0,0}$$

Example 2: Second-Order Recurrence

$$T(n) = 2T(n-1) + 3T(n-2)$$

Matrix form:

$$\begin{bmatrix} T(n) \\ T(n-1) \end{bmatrix} = \begin{bmatrix} 2 & 3 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} T(n-1) \\ T(n-2) \end{bmatrix}$$

So:

$$\vec{T}(n) = M^{n-2}\vec{T}(2)$$

Tiny Code (Python)

```
def mat_mult(A, B):
    return [[sum(A[i][k] * B[k][j] for k in range(len(A)))
             for j in range(len(B[0]))] for i in range(len(A))]

def mat_pow(M, n):
    if n == 1:
        return M
    if n % 2 == 0:
        half = mat_pow(M, n // 2)
        return mat_mult(half, half)
    else:
        return mat_mult(M, mat_pow(M, n - 1))

def fib_matrix(n):
    if n == 0:
        return 0
    M = [[1, 1], [1, 0]]
    Mn = mat_pow(M, n - 1)
    return Mn[0][0]
```

`fib_matrix(n)` computes $F(n)$ in $O(\log n)$.

Why It Matters

- Converts recursive computation into linear algebra
- Enables $O(\log n)$ computation for $T(n)$
- Generalizes to higher-order recurrences
- Common in DP transitions, Fibonacci-like sequences, and combinatorial counting

A Gentle Proof (Why It Works)

The recurrence:

$$T(n) = a_1 T(n-1) + a_2 T(n-2) + \cdots + a_k T(n-k)$$

can be expressed as:

$$\vec{T}(n) = M \cdot \vec{T}(n-1)$$

where M is the companion matrix:

$$M = \begin{bmatrix} a_1 & a_2 & \cdots & a_k \\ 1 & 0 & \cdots & 0 \\ 0 & 1 & \cdots & 0 \\ \vdots & & \ddots & 0 \end{bmatrix}$$

Repeatedly multiplying gives:

$$\vec{T}(n) = M^{n-k}\vec{T}(k)$$

Hence, $T(n)$ is computed by raising M to a power, exponential recursion becomes logarithmic multiplication.

Try It Yourself

1. Write matrix form for $T(n) = 3T(n-1) - 2T(n-2)$
2. Compute $T(10)$ with $T(0) = 2$, $T(1) = 3$
3. Implement matrix exponentiation for 3×3 matrices (Tribonacci)
4. Compare with iterative solution runtime

Test Cases

Recurrence	Matrix	$T(n)$ / Symbol	Complexity
$F(n) = F(n-1) + F(n-2)$	$\begin{bmatrix} 1 & 1 \\ 1 & 0 \end{bmatrix}$	$F(n)$	$O(\log n)$
$T(n) = 2T(n-1) + 3T(n-2)$	$\begin{bmatrix} 2 & 3 \\ 1 & 0 \end{bmatrix}$	$T(n)$	$O(\log n)$
$T(n) = T(n-1) + T(n-2) + T(n-3)$	$\begin{bmatrix} 1 & 1 & 1 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{bmatrix}$	Tribonacci	$O(\log n)$

Complexity Summary

Step	Time	Space
Matrix exponentiation	$O(k^3 \log n)$	$O(k^2)$
Iterative recurrence	$O(n)$	$O(k)$

Matrix Exponentiation turns recurrence solving into matrix powering, a bridge between recursion and linear algebra, giving exponential speed-up with mathematical elegance.

47 Recurrence to DP Table

The Recurrence to DP Table method converts a recursive relation into an iterative table-based approach, removing redundant computation and improving efficiency from exponential to polynomial time. It's a cornerstone of Dynamic Programming.

What Problem Are We Solving?

Recursive formulas often recompute overlapping subproblems. For example:

$$T(n) = T(n-1) + T(n-2)$$

A naive recursive call tree grows exponentially because it recomputes $T(k)$ many times. By converting this recurrence into a DP table, we compute each subproblem once and store results, achieving linear or polynomial time.

How It Works (Plain Language)

1. Identify the recurrence and base cases.
2. Create a table (array or matrix) to store subproblem results.
3. Iteratively fill the table using the recurrence formula.
4. Read off the final answer from the last cell.

This technique is called tabulation, a bottom-up form of dynamic programming.

Example Step by Step

Example 1: Fibonacci Numbers

Recursive formula:

$$F(n) = F(n-1) + F(n-2), \quad F(0) = 0, , F(1) = 1$$

DP version:

n	0	1	2	3	4	5
F(n)	0	1	1	2	3	5

Algorithm:

1. Initialize base cases: `F[0]=0`, `F[1]=1`
2. Loop from 2 to n: `F[i] = F[i-1] + F[i-2]`
3. Return `F[n]`

Example 2: Coin Change (Count Ways)

Recurrence:

$$\text{ways}(n, c) = \text{ways}(n, c-1) + \text{ways}(n - \text{coin}[c], c)$$

Convert to 2D DP table indexed by (n, c).

Example 3: Grid Paths

Recurrence:

$$P(i, j) = P(i-1, j) + P(i, j-1)$$

DP table:

ij	0	1	2
0	1	1	1
1	1	2	3
2	1	3	6

Each cell = sum of top and left.

Tiny Code (Python)

```
def fib_dp(n):
    if n == 0:
        return 0
    dp = [0] * (n + 1)
    dp[1] = 1
    for i in range(2, n + 1):
        dp[i] = dp[i - 1] + dp[i - 2]
    return dp[n]
```

Why It Matters

- Converts exponential recursion to polynomial iteration
- Avoids repeated subproblem computations
- Enables space and time optimization
- Forms the foundation of bottom-up dynamic programming

A Gentle Proof (Why It Works)

Given recurrence:

$$T(n) = a_1 T(n-1) + a_2 T(n-2) + \cdots + a_k T(n-k)$$

Each term depends only on previously computed subproblems. So by filling the table in increasing order, we ensure all dependencies are ready.

By induction, if base cases are correct, each computed cell is correct.

Try It Yourself

1. Convert $F(n) = F(n-1) + F(n-2)$ to a 1D DP array
2. Build a 2D table for grid paths $P(i, j) = P(i-1, j) + P(i, j-1)$
3. Write a DP table for factorial $n! = n \times (n-1)!$
4. Optimize space (keep only last k terms)

Test Cases

Input	Recurrence	Expected
$F(5)$	$F(n) = F(n-1) + F(n-2)$	5
Grid(2,2)	$P(i,j) = P(i-1,j) + P(i,j-1)$	6
$n = 3, coins = [1,2]$	$\text{ways}(n,c) = \text{ways}(n,c-1) + \text{ways}(n - \text{coin}[c], c)$	2

Complexity Summary

Method	Time	Space
Recursive	$O(2^n)$	$O(n)$
DP Table	$O(n)$	$O(n)$
Space-Optimized DP	$O(n)$	$O(1)$

Transforming a recurrence into a DP table captures the essence of dynamic programming, structure, reuse, and clarity over brute repetition.

48 Divide & Combine Template

The Divide & Combine Template is a structural guide for solving problems by breaking them into smaller, similar subproblems, solving each independently, and combining their results. It's the core skeleton behind divide-and-conquer algorithms like Merge Sort, Quick Sort, and Karatsuba Multiplication.

What Problem Are We Solving?

Many complex problems can be decomposed into smaller copies of themselves. Instead of solving the full instance at once, we divide it into subproblems, solve each recursively, and combine their results.

This approach reduces complexity, promotes parallelism, and yields recurrence relations like:

$$T(n) = aT\left(\frac{n}{b}\right) + f(n)$$

How It Works (Plain Language)

1. Divide: Split the problem into a subproblems, each of size $\frac{n}{b}$.
2. Conquer: Recursively solve the subproblems.
3. Combine: Merge their results into a full solution.
4. Base Case: Stop dividing when the subproblem becomes trivially small.

This recursive structure underpins most efficient algorithms for sorting, searching, and multiplication.

Example Step by Step

Example 1: Merge Sort

- Divide: Split array into two halves
- Conquer: Recursively sort each half
- Combine: Merge two sorted halves

Recurrence:

$$T(n) = 2T\left(\frac{n}{2}\right) + O(n)$$

Example 2: Karatsuba Multiplication

- Divide numbers into halves
- Conquer with 3 recursive multiplications
- Combine using linear combinations

Recurrence:

$$T(n) = 3T\left(\frac{n}{2}\right) + O(n)$$

Example 3: Binary Search

- Divide the array by midpoint
- Conquer on one half
- Combine trivially (return result)

Recurrence:

$$T(n) = T\left(\frac{n}{2}\right) + O(1)$$

Generic Template (Pseudocode)

```
def divide_and_combine(problem):
    if is_small(problem):
        return solve_directly(problem)
    subproblems = divide(problem)
    results = [divide_and_combine(p) for p in subproblems]
    return combine(results)
```

This general template can adapt to many problem domains, arrays, trees, graphs, geometry, and algebra.

Why It Matters

- Clarifies recursion structure and base case reasoning
- Enables asymptotic analysis via recurrence
- Lays foundation for parallel and cache-efficient algorithms
- Promotes clean decomposition and reusability

A Gentle Proof (Why It Works)

If a problem can be decomposed into independent subproblems whose results can be merged deterministically, recursive decomposition is valid. By induction:

- Base case: small input solved directly.
- Inductive step: if each subproblem is solved correctly, and the combine step correctly merges, the final solution is correct.

Thus correctness follows from structural decomposition.

Try It Yourself

1. Implement divide-and-conquer sum over an array.
2. Write recursive structure for Maximum Subarray (Kadane's divide form).
3. Express recurrence $T(n) = 2T(n/2) + n$ and solve via the Master Theorem.
4. Modify template for parallel processing (e.g., thread pool).

Test Cases

Problem	Divide	Combine	Complexity
Merge Sort	Halve array	Merge sorted halves	$O(n \log n)$
Binary Search	Halve search space	Return result	$O(\log n)$
Karatsuba	Split numbers	Combine linear parts	$O(n^{1.585})$
Closest Pair (2D)	Split points	Merge cross-boundary pairs	$O(n \log n)$

Complexity Summary

Given:

$$T(n) = aT\left(\frac{n}{b}\right) + f(n)$$

By the Master Theorem:

- If $f(n) = O(n^{\log_b a - \epsilon})$, then $T(n) = \Theta(n^{\log_b a})$
- If $f(n) = \Theta(n^{\log_b a})$, then $T(n) = \Theta(n^{\log_b a} \log n)$
- If $f(n) = \Omega(n^{\log_b a + \epsilon})$, then $T(n) = \Theta(f(n))$

The Divide & Combine Template provides the blueprint for recursive problem solving, simple, elegant, and foundational across all algorithmic domains.

49 Memoized Recursive Solver

A Memoized Recursive Solver transforms a plain recursive solution into an efficient one by caching intermediate results. It's the top-down version of dynamic programming, retaining recursion's clarity while avoiding redundant work.

What Problem Are We Solving?

Recursive algorithms often recompute the same subproblems multiple times. Example:

$$F(n) = F(n-1) + F(n-2)$$

A naive recursive call tree repeats $F(3)$, $F(2)$, etc., exponentially many times. By memoizing (storing) results after the first computation, we reuse them in $O(1)$ time later.

How It Works (Plain Language)

1. Define the recurrence clearly.
2. Add a cache (dictionary or array) to store computed results.
3. Before each recursive call, check the cache.
4. If present, return cached value.
5. Otherwise, compute, store, and return.

This approach preserves recursive elegance while matching iterative DP performance.

Example Step by Step

Example 1: Fibonacci Numbers

Naive recursion:

$$F(n) = F(n-1) + F(n-2)$$

Memoized version:

n	F(n)	Cached?
0	0	Base
1	1	Base
2	1	Computed
3	2	Computed
4	3	Cached lookups

Time drops from $O(2^n)$ to $O(n)$.

Example 2: Binomial Coefficient

Recurrence:

$$C(n,k) = C(n-1,k-1) + C(n-1,k)$$

Without memoization: exponential With memoization: $O(nk)$

Example 3: Coin Change

$$\text{ways}(n) = \text{ways}(n - \text{coin}) + \text{ways}(n, \text{next})$$

Memoize by (n, index) to avoid recomputing states.

Tiny Code (Python)

```
def fib_memo(n, memo={}):
    if n in memo:
        return memo[n]
    if n <= 1:
        return n
    memo[n] = fib_memo(n-1, memo) + fib_memo(n-2, memo)
    return memo[n]
```

Or explicitly pass cache:

```
def fib_memo(n):
    memo = {}
    def helper(k):
        if k in memo:
            return memo[k]
        if k <= 1:
            return k
        memo[k] = helper(k-1) + helper(k-2)
        return memo[k]
    return helper(n)
```

Why It Matters

- Retains intuitive recursive structure
- Cuts time complexity drastically
- Natural stepping stone to tabulation (bottom-up DP)
- Enables solving overlapping subproblem recurrences efficiently

A Gentle Proof (Why It Works)

Let S be the set of all distinct subproblems. Without memoization, each is recomputed exponentially many times. With memoization, each $s \in S$ is computed exactly once. Thus, total time $= O(|S|)$.

Try It Yourself

1. Add memoization to naive Fibonacci.
2. Memoize binomial coefficients $C(n, k)$.
3. Apply memoization to knapsack recursion.
4. Count total recursive calls with and without memoization.

Test Cases

Problem	Naive Time	Memoized Time
Fibonacci(40)	$O(2^{40})$	$O(40)$
Binomial(20,10)	$O(2^{20})$	$O(200)$
Coin Change(100)	$O(2^n)$	$O(n \cdot k)$

Complexity Summary

Method	Time	Space
Recursive	Exponential	$O(n)$ stack
Memoized	Polynomial (distinct subproblems)	Cache + stack

Memoization blends clarity and efficiency, recursion that remembers. It turns naive exponential algorithms into elegant linear or polynomial solutions with a single insight: never solve the same problem twice.

50 Characteristic Polynomial Solver

The Characteristic Polynomial Solver is a powerful algebraic technique for solving linear homogeneous recurrence relations with constant coefficients. It expresses the recurrence in terms of polynomial roots, giving closed-form solutions.

What Problem Are We Solving?

When faced with recurrences like:

$$T(n) = a_1 T(n-1) + a_2 T(n-2) + \cdots + a_k T(n-k)$$

we want a closed-form expression for $T(n)$ instead of step-by-step computation. The characteristic polynomial captures the recurrence's structure, its roots determine the general form of the solution.

How It Works (Plain Language)

1. Write the recurrence in standard form:

$$T(n) - a_1 T(n-1) - a_2 T(n-2) - \cdots - a_k T(n-k) = 0$$

2. Replace $T(n-i)$ with r^{n-i} to form a polynomial equation:

$$r^k - a_1 r^{k-1} - a_2 r^{k-2} - \cdots - a_k = 0$$

3. Solve for roots $r_1, r_2, \ldots, r_k$.
4. The general solution is:

$$T(n) = c_1 r_1^n + c_2 r_2^n + \cdots + c_k r_k^n$$

5. Use initial conditions to solve for constants c_i.

If there are repeated roots, multiply by n^p for multiplicity p.

Example Step by Step

Example 1: Fibonacci

Recurrence:

$$F(n) = F(n-1) + F(n-2)$$

Characteristic polynomial:

$$r^2 - r - 1 = 0$$

Roots:

$$r_1 = \frac{1+\sqrt{5}}{2}, \quad r_2 = \frac{1-\sqrt{5}}{2}$$

General solution:

$$F(n) = c_1 r_1^n + c_2 r_2^n$$

Using $F(0) = 0$, $F(1) = 1$:

$$c_1 = \frac{1}{\sqrt{5}}, \quad c_2 = -\frac{1}{\sqrt{5}}$$

So:

$$F(n) = \frac{1}{\sqrt{5}} \left(\left(\frac{1+\sqrt{5}}{2} \right)^n - \left(\frac{1-\sqrt{5}}{2} \right)^n \right)$$

This is Binet's Formula.

Example 2: $T(n) = 3T(n-1) - 2T(n-2)$

Characteristic polynomial:

$$r^2 - 3r + 2 = 0 \implies (r-1)(r-2) = 0$$

Roots: $r_1 = 1, , r_2 = 2$

Solution:

$$T(n) = c_1(1)^n + c_2(2)^n = c_1 + c_2 2^n$$

Use base cases to find c_1, c_2.

Example 3: Repeated Roots

$$T(n) = 2T(n-1) - T(n-2)$$

Characteristic:

$$r^2 - 2r + 1 = 0 \implies (r-1)^2 = 0$$

Solution:

$$T(n) = (c_1 + c_2 n) \cdot 1^n = c_1 + c_2 n$$

Tiny Code (Python)

```
import sympy as sp

def solve_recurrence(coeffs, initials):
    n = len(coeffs)
    r = sp.symbols('r')
    poly = rn - sum(coeffs[i]*r(n-i-1) for i in range(n))
    roots = sp.roots(poly, r)
    r_syms = list(roots.keys())
    c = sp.symbols(' '.join([f'c{i+1}' for i in range(n)]))
    Tn = sum(c[i]*r_syms[i]sp.symbols('n') for i in range(n))
    equations = []
```

```
    for i, val in enumerate(initials):
        equations.append(Tn.subs(sp.symbols('n'), i) - val)
    sol = sp.solve(equations, c)
    return Tn.subs(sol)
```

Call `solve_recurrence([1, 1], [0, 1])` → Binet's formula.

Why It Matters

- Gives closed-form solutions for linear recurrences
- Eliminates need for iteration or recursion
- Connects algorithm analysis to algebra and eigenvalues
- Used in runtime analysis, combinatorics, and discrete modeling

A Gentle Proof (Why It Works)

Suppose recurrence:

$$T(n) = a_1 T(n-1) + \cdots + a_k T(n-k)$$

Assume $T(n) = r^n$:

$$r^n = a_1 r^{n-1} + \cdots + a_k r^{n-k}$$

Divide by r^{n-k}:

$$r^k = a_1 r^{k-1} + \cdots + a_k$$

Solve polynomial for roots. Each root corresponds to an independent solution. By linearity, the sum of independent solutions is also a solution.

Try It Yourself

1. Solve $T(n) = 2T(n-1) + T(n-2)$ with $T(0) = 0, T(1) = 1$.
2. Solve $T(n) = T(n-1) + 2T(n-2)$ with $T(0) = 2, T(1) = 3$.
3. Solve with repeated root $r = 1$.
4. Verify results numerically for $n = 0 \ldots 5$.

Test Cases

Recurrence	Polynomial	Roots	Closed Form
$F(n) = F(n-1)+F(n-2)$	$r^2 - r - 1 = 0$	$\frac{1\pm\sqrt{5}}{2}$	Binet
$T(n) =$ $3T(n-1) - 2T(n-2)$	$r^2 - 3r + 2 = 0$	1, 2	$c_1 + c_2 2^n$
$T(n) = 2T(n-1) - T(n-2)$	$(r-1)^2 = 0$	1 (double)	$c_1 + c_2 n$

Complexity Summary

Step	Time	Space
Solve polynomial	$O(k^3)$	$O(k)$
Evaluate closed form	$O(1)$	$O(1)$

The Characteristic Polynomial Solver is the algebraic heart of recurrence solving, turning repeated patterns into exact formulas through the power of roots and symmetry.

Section 6. Searching basics

51 Search Space Visualizer

A Search Space Visualizer is a conceptual tool to map and understand the entire landscape of possibilities an algorithm explores. By modeling the search process as a tree or graph, you gain intuition about completeness, optimality, and complexity before diving into code.

What Problem Are We Solving?

When tackling problems like optimization, constraint satisfaction, or pathfinding, the solution isn't immediate, we must explore a space of possibilities. Understanding how large that space is, how it grows, and how it can be pruned is crucial for algorithmic design.

Visualizing the search space helps answer questions like:

- How many states are reachable?
- How deep or wide is the search?
- What's the branching factor?
- Where does the goal lie?

How It Works (Plain Language)

1. Model states as nodes. Each represents a partial or complete solution.
2. Model transitions as edges. Each move or decision takes you to a new state.
3. Define start and goal nodes. Typically, the root (start) expands toward one or more goals.
4. Trace the exploration. Breadth-first explores level by level; depth-first dives deep.
5. Label nodes with cost or heuristic values if applicable (for A*, branch-and-bound, etc.).

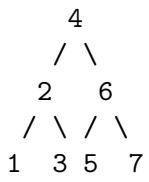
This structure reveals not just correctness but also efficiency and complexity.

Example Step by Step

Example 1: Binary Search Tree Traversal

For array `[1, 2, 3, 4, 5, 6, 7]` and target = 6:

Search space (comparisons):



Path explored: $4 \to 6$ (found)

Search space depth: $\log_2 7 \approx 3$

Example 2: 8-Queens Problem

Each level represents placing a queen in a new row. Branching factor shrinks as constraints reduce possibilities.

Visualization shows 8! total paths, but pruning cuts most.

Example 3: Maze Solver

States = grid cells; edges = possible moves.

Visualization helps you see BFS's wavefront vs DFS's depth-first path.

Tiny Code (Python)

```
from collections import deque

def visualize_bfs(graph, start):
    visited = set()
    queue = deque([(start, [start])])
    while queue:
        node, path = queue.popleft()
        print(f"Visiting: {node}, Path: {path}")
        visited.add(node)
        for neighbor in graph[node]:
            if neighbor not in visited:
                queue.append((neighbor, path + [neighbor]))
```

Use on a small adjacency list to see BFS layers unfold.

Why It Matters

- Builds intuition about algorithm behavior
- Shows breadth vs depth tradeoffs
- Reveals redundant paths and pruning opportunities
- Useful for teaching, debugging, and complexity estimation

A Gentle Proof (Why It Works)

Let each state $s \in S$ be connected by transitions E. Search algorithms define an ordering of node expansion (DFS, BFS, heuristic-based). Visualizing S as a graph preserves:

- Completeness: BFS explores all finite paths
- Optimality: with uniform cost, shortest path = first found
- Complexity: proportional to nodes generated (often $O(b^d)$)

Try It Yourself

1. Draw search tree for binary search on 7 elements.
2. Visualize DFS vs BFS on a maze.
3. Build search space for placing 4 queens on a 4×4 board.
4. Compare path counts with and without pruning.

Test Cases

Problem	Search Space Size	Visualization Insight
Binary Search	$\log_2 n$	Narrow, balanced
8-Queens	8!	Heavy pruning needed
Maze (10x10)	100 nodes	BFS = wave, DFS = path
Sudoku	9^{81}	Prune with constraints

Algorithm	Nodes Explored	Memory	Visualization

Complexity Summary

Algorithm	Nodes Explored	Memory	Visualization
BFS	$O(b^d)$	$O(b^d)$	Tree layers
DFS	$O(bd)$	$O(d)$	Deep path
A*	$O(b^d)$	$O(b^d)$	Cost-guided frontier

A Search Space Visualizer turns abstract computation into geometry, making invisible exploration visible, and helping you reason about complexity before coding.

52 Decision Tree Depth Estimator

A Decision Tree Depth Estimator helps you reason about how many questions, comparisons, or branching choices an algorithm must make in the worst, best, or average case. It models decision-making as a tree, where each node is a test and each leaf is an outcome.

What Problem Are We Solving?

Any algorithm that proceeds by comparisons or conditional branches (like sorting, searching, or classification) can be represented as a decision tree. Analyzing its depth gives insight into:

- Worst-case time complexity (longest path)
- Best-case time complexity (shortest path)
- Average-case complexity (weighted path length)

By studying depth, we understand the minimum information needed to solve the problem.

How It Works (Plain Language)

1. Represent each comparison or condition as a branching node.
2. Follow each branch based on true/false or less/greater outcomes.
3. Each leaf represents a solved instance (e.g. sorted array, found key).
4. The depth = number of decisions on a path.
5. Maximum depth $\rightarrow$ worst-case cost.

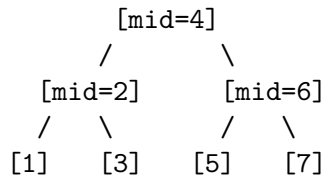
This model abstracts away details and focuses purely on information flow.

Example Step by Step

Example 1: Binary Search

- Each comparison halves the search space.
- Decision tree has depth $\log_2 n$.
- Minimum comparisons in worst case: $\lceil \log_2 n \rceil$.

Tree for $n = 8$ elements:



Depth: $3 = \log_2 8$

Example 2: Comparison Sort

Each leaf represents a possible ordering. A valid sorting tree must distinguish all $n!$ orderings.

So:

$$2^h \geq n! \implies h \geq \log_2(n!)$$

Thus, any comparison sort has lower bound:

$$\Omega(n \log n)$$

Example 3: Decision-Making Algorithm

If solving a yes/no classification with b possible outcomes, minimum number of comparisons required $= \lceil \log_2 b \rceil$.

Tiny Code (Python)

```python
import math

def decision_tree_depth(outcomes):
    # Minimum comparisons to distinguish outcomes
    return math.ceil(math.log2(outcomes))

print(decision_tree_depth(8))  # 3
print(decision_tree_depth(120))  # ~7 (for 5!)
```

Why It Matters

- Reveals theoretical limits (no sort faster than $O(n \log n)$ by comparison)
- Models decision complexity in search and optimization
- Bridges information theory and algorithm design
- Helps compare branching strategies

A Gentle Proof (Why It Works)

Each comparison splits the search space in two. To distinguish N possible outcomes, need at least h comparisons such that:

$$2^h \geq N$$

Thus:

$$h \geq \lceil \log_2 N \rceil$$

For sorting:

$$N = n! \implies h \geq \log_2(n!) = \Omega(n \log n)$$

This bound holds independent of implementation, it's a lower bound on information required.

Try It Yourself

1. Build decision tree for 3-element sorting.
2. Count comparisons for binary search on $n = 16$.
3. Estimate lower bound for 4-element comparison sort.
4. Visualize tree for classification with 8 classes.

Test Cases

Problem	Outcomes	Depth Bound
Binary Search (n=8)	8	3
Sort 3 elements	$3! = 6$	≥ 3
Sort 5 elements	$5! = 120$	≥ 7
Classify 8 outcomes	8	3

Complexity Summary

Algorithm	Search Space	Depth	Meaning
Binary Search	n	$\log_2 n$	Worst-case comparisons
Comparison Sort	$n!$	$\log_2 n!$	Info-theoretic limit
Classifier	b	$\log_2 b$	Min tests for b classes

A Decision Tree Depth Estimator helps uncover the invisible "question complexity" behind every algorithm, how many decisions must be made, no matter how clever your code is.

53 Comparison Counter

A Comparison Counter measures how many times an algorithm compares elements or conditions, a direct way to understand its time complexity, efficiency, and practical performance. Counting comparisons gives insight into what really drives runtime, especially in comparison-based algorithms.

What Problem Are We Solving?

Many algorithms, sorting, searching, selection, optimization, revolve around comparisons. Every `if`, `<`, or `==` is a decision that costs time.

By counting comparisons, we can:

- Estimate exact step counts for small inputs
- Verify asymptotic bounds ($O(n^2)$, $O(n \log n)$, etc.)
- Compare different algorithms empirically
- Identify hot spots in implementation

This turns performance from a vague idea into measurable data.

How It Works (Plain Language)

1. Instrument the algorithm: wrap every comparison in a counter.
2. Increment the counter each time a comparison occurs.
3. Run the algorithm with sample inputs.
4. Observe patterns as input size grows.
5. Fit results to complexity functions (n, $n \log n$, n^2, etc.).

This gives both empirical evidence and analytic insight.

Example Step by Step

Example 1: Linear Search

Search through an array of size n. Each comparison checks one element.

Case	Comparisons
Best	1
Worst	n
Average	$\frac{n+1}{2}$

So:

$$T(n) = O(n)$$

Example 2: Binary Search

Each step halves the search space.

Case	Comparisons
Best	1
Worst	$\lceil \log_2 n \rceil$
Average	$\approx \log_2 n - 1$

So:

$$T(n) = O(\log n)$$

Example 3: Bubble Sort

For array of length n, each pass compares adjacent elements.

Pass	Comparisons
1	$n-1$
2	$n-2$
...	...
n-1	1

Total:

$$C(n) = (n-1) + (n-2) + \cdots + 1 = \frac{n(n-1)}{2}$$

So:

$$T(n) = O(n^2)$$

Tiny Code (Python)

```
class Counter:
    def __init__(self):
        self.count = 0
    def compare(self, a, b, op):
        self.count += 1
        if op == '<': return a < b
        if op == '>': return a > b
        if op == '==': return a == b

# Example: Bubble Sort
def bubble_sort(arr):
    c = Counter()
    n = len(arr)
    for i in range(n):
        for j in range(n - i - 1):
            if c.compare(arr[j], arr[j + 1], '>'):
                arr[j], arr[j + 1] = arr[j + 1], arr[j]
    return arr, c.count
```

Run on small arrays to record exact comparison counts.

Why It Matters

- Converts abstract complexity into measurable data
- Reveals hidden constants and practical performance
- Useful for algorithm profiling and pedagogy
- Helps confirm theoretical analysis

A Gentle Proof (Why It Works)

Each comparison corresponds to one node in the algorithm's decision tree. The number of comparisons = number of nodes visited. Counting comparisons thus measures path length, which correlates to runtime for comparison-based algorithms.

By summing over all paths, we recover the exact cost function $C(n)$.

Try It Yourself

1. Count comparisons in bubble sort vs insertion sort for $n = 5$.
2. Measure binary search comparisons for $n = 16$.
3. Compare selection sort and merge sort.
4. Fit measured values to theoretical $O(n^2)$ or $O(n \log n)$.

Test Cases

Algorithm	Input Size	Comparisons	Pattern
Linear Search	10	10	$O(n)$
Binary Search	16	4	$O(\log n)$
Bubble Sort	5	10	$\frac{n(n-1)}{2}$
Merge Sort	8	17	$\approx n \log n$

Complexity Summary

Algorithm	Best Case	Worst Case	Average Case
Linear Search	1	n	$\frac{n+1}{2}$
Binary Search	1	$\log_2 n$	$\log_2 n - 1$
Bubble Sort	$n - 1$	$\frac{n(n-1)}{2}$	$\frac{n(n-1)}{2}$

A Comparison Counter brings complexity theory to life, every `if` becomes a data point, and every loop reveals its true cost.

54 Early Termination Heuristic

An Early Termination Heuristic is a strategy to stop an algorithm before full completion when the desired result is already guaranteed or further work won't change the outcome. It's a simple yet powerful optimization that saves time in best and average cases.

What Problem Are We Solving?

Many algorithms perform redundant work after the solution is effectively found or when additional steps no longer improve results. By detecting these conditions early, we can cut off unnecessary computation, reducing runtime without affecting correctness.

Key question: *"Can we stop now without changing the answer?"*

How It Works (Plain Language)

1. Identify a stopping condition beyond the usual loop limit.
2. Check at each step if the result is already determined.
3. Exit early when the condition is satisfied.
4. Return partial result if it's guaranteed to be final.

This optimization is common in search, sorting, simulation, and iterative convergence algorithms.

Example Step by Step

Example 1: Bubble Sort

Normally runs $n-1$ passes, even if array sorted early. Add a flag to track swaps; if none occur, terminate.

```
def bubble_sort(arr):
    n = len(arr)
    for i in range(n):
        swapped = False
        for j in range(n - i - 1):
            if arr[j] > arr[j + 1]:
                arr[j], arr[j + 1] = arr[j + 1], arr[j]
```

```
                swapped = True
        if not swapped:
            break  # early termination
    return arr
```

Best case: already sorted → 1 pass only

$$T(n) = O(n)$$

Worst case: reversed → still $O(n^2)$

Example 2: Linear Search

Searching for key k in array `A`:

- Stop when found (don't scan full array).
- Average case improves from $O(n)$ to $\frac{n}{2}$ comparisons.

Example 3: Convergence Algorithms

In iterative solvers:

- Stop when error $<$ (tolerance threshold).
- Avoids unnecessary extra iterations.

Example 4: Constraint Search

In backtracking or branch-and-bound:

- Stop exploring when solution cannot improve current best.
- Reduces search space dramatically.

Why It Matters

- Improves average-case performance
- Reduces energy and time in real-world systems
- Maintains correctness (never stops too early)
- Enables graceful degradation for approximate algorithms

A Gentle Proof (Why It Works)

Let $f(i)$ represent progress measure after i iterations. If $f(i)$ satisfies a stopping invariant P, then continuing further does not alter the final answer. Thus:

$$\exists i < n; |; P(f(i)) = \text{True} \implies T(n) = i$$

reducing total operations from n to i in favorable cases.

Try It Yourself

1. Add early stop to selection sort (when prefix sorted).
2. Apply tolerance check to Newton's method.
3. Implement linear search with immediate exit.
4. Compare runtime with and without early termination.

Test Cases

Algorithm	Condition	Best Case	Worst Case		
Bubble Sort	No swaps in pass	$O(n)$	$O(n^2)$		
Linear Search	Found early	$O(1)$	$O(n)$		
Newton's Method	$	x_{i+1}-x_i	$< $	$O(\log n)$	$O(n)$
DFS	Goal found early	$O(d)$	$O(b^d)$		

Complexity Summary

Case	Description	Time
Best	Early stop triggered	Reduced from n to k
Average	Depends on data order	Often sublinear
Worst	Condition never met	Same as original

An Early Termination Heuristic adds a simple yet profound optimization, teaching algorithms when to quit, not just how to run.

55 Sentinel Technique

The Sentinel Technique is a simple but elegant optimization that eliminates redundant boundary checks in loops by placing a *special marker* (the sentinel) at the end of a data structure. It's a subtle trick that makes code faster, cleaner, and safer.

What Problem Are We Solving?

In many algorithms, especially search and scanning loops, we repeatedly check for two things:

1. Whether the element matches a target
2. Whether we've reached the end of the structure

This double condition costs extra comparisons every iteration. By adding a sentinel value, we can guarantee termination and remove one check.

How It Works (Plain Language)

1. Append a sentinel value (e.g. target or infinity) to the end of the array.
2. Loop until match found, without checking bounds.
3. Stop automatically when you hit the sentinel.
4. Check afterward if the match was real or sentinel-triggered.

This replaces:

```
while i < n and A[i] != key:
    i += 1
```

with a simpler loop:

```
A[n] = key
while A[i] != key:
    i += 1
```

No more bound check inside the loop.

Example Step by Step

Example 1: Linear Search with Sentinel

Without sentinel:

```
def linear_search(A, key):
    for i in range(len(A)):
        if A[i] == key:
            return i
    return -1
```

Every step checks both conditions.

With sentinel:

```python
def linear_search_sentinel(A, key):
    n = len(A)
    A.append(key)  # add sentinel
    i = 0
    while A[i] != key:
        i += 1
    return i if i < n else -1
```

- Only one condition inside loop
- Works for both found and not-found cases

Cost Reduction: from `2n+1` comparisons to `n+1`

Example 2: Merging Sorted Lists

Add infinity sentinel at the end of each list:

- Prevents repeated end-of-array checks
- Simplifies inner loop logic

E.g. in Merge Sort, use sentinel values to avoid `if i < n` checks.

Example 3: String Parsing

Append `'\0'` (null terminator) so loops can stop automatically on sentinel. Used widely in C strings.

Why It Matters

- Removes redundant checks
- Simplifies loop logic
- Improves efficiency and readability
- Common in systems programming, parsing, searching

A Gentle Proof (Why It Works)

Let n be array length. Normally, each iteration does:

- 1 comparison with bound
- 1 comparison with key

So total $\approx 2n + 1$ comparisons.

With sentinel:

- 1 comparison per element
- 1 final check after loop

So total $\approx n + 1$

Improvement factor $2\times$ speedup for long lists.

Try It Yourself

1. Implement sentinel linear search and count comparisons.
2. Add infinity sentinel in merge routine.
3. Write a parser that stops on sentinel `'\0'`.
4. Compare runtime vs standard implementation.

Test Cases

Input	Key	Output	Comparisons
[1,2,3,4], 3	3	2	3
[1,2,3,4], 5	-1	4	5
[] , 1	-1	0	1

Complexity Summary

Case	Time	Space	Notes
Best	$O(1)$	$O(1)$	Found immediately
Worst	$O(n)$	$O(1)$	Found at end / not found
Improvement	~2× fewer comparisons	+1 sentinel	Always safe

The Sentinel Technique is a quiet masterpiece of algorithmic design, proving that sometimes, one tiny marker can make a big difference.

56 Binary Predicate Tester

A Binary Predicate Tester is a simple yet fundamental tool for checking whether a condition involving two operands holds true, a building block for comparisons, ordering, filtering, and search logic across algorithms. It clarifies logic and promotes reuse by abstracting condition checks.

What Problem Are We Solving?

Every algorithm depends on decisions, "Is this element smaller?", "Are these two equal?", "Does this satisfy the constraint?". These yes/no questions are binary predicates: functions that return either `True` or `False`.

By formalizing them as reusable testers, we gain:

- Clarity, separate logic from control flow
- Reusability, pass as arguments to algorithms
- Flexibility, easily switch from `<` to `>` or `==`

This underlies sorting, searching, and functional-style algorithms.

How It Works (Plain Language)

1. Define a predicate function that takes two arguments.
2. Returns `True` if condition satisfied, `False` otherwise.
3. Use the predicate inside loops, filters, or algorithmic decisions.
4. Swap out predicates to change algorithm behavior dynamically.

Predicates serve as the comparison layer, they don't control flow, but inform it.

Example Step by Step

Example 1: Sorting by Predicate

Define different predicates:

```
def less(a, b): return a < b
def greater(a, b): return a > b
def equal(a, b): return a == b
```

Pass to sorting routine:

```
def compare_sort(arr, predicate):
    n = len(arr)
    for i in range(n):
        for j in range(0, n - i - 1):
            if predicate(arr[j + 1], arr[j]):
                arr[j], arr[j + 1] = arr[j + 1], arr[j]
    return arr
```

Now you can sort ascending or descending just by changing the predicate.

Example 2: Binary Search Condition

Binary search relies on predicate `is_less(mid_value, key)` to decide direction:

```
def is_less(a, b): return a < b
```

So the decision step becomes:

```
if is_less(arr[mid], key):
    left = mid + 1
else:
    right = mid - 1
```

This makes the comparison logic explicit, not buried inside control.

Example 3: Filtering or Matching

```
def between(a, b): return a < b
filtered = [x for x in data if between(x, 10)]
```

Easily swap predicates for greater-than or equality checks.

Why It Matters

- Encapsulates decision logic cleanly
- Enables higher-order algorithms (pass functions as arguments)
- Simplifies testing and customization
- Core to generic programming and templates (C++, Python `key` functions)

A Gentle Proof (Why It Works)

Predicates abstract the notion of ordering or relation. If a predicate satisfies:

- Reflexivity ($P(x, x) =$ False or True, as defined)
- Antisymmetry ($P(a, b) \Rightarrow \neg P(b, a)$)
- Transitivity ($P(a, b) \wedge P(b, c) \Rightarrow P(a, c)$)

then it defines a strict weak ordering, sufficient for sorting and searching algorithms.

Thus, correctness of algorithms depends on predicate consistency.

Try It Yourself

1. Write predicates for `<`, `>`, `==`, and `divisible(a,b)`.
2. Use them in a selection algorithm.
3. Test sorting ascending and descending using same code.
4. Verify predicate correctness (antisymmetry, transitivity).

Test Cases

Predicate	a	b	Result	Meaning
less	3	5	True	$3 < 5$
greater	7	2	True	$7 > 2$
equal	4	4	True	$4 == 4$
divisible	6	3	True	$6 \% 3 == 0$

Complexity Summary

Operation	Time	Space	Notes
Predicate call	$O(1)$	$O(1)$	Constant per check
Algorithm using predicate	Depends on structure	,	e.g. sort: $O(n^2)$

A Binary Predicate Tester turns hidden conditions into visible design, clarifying logic, encouraging reuse, and laying the foundation for generic algorithms that *think in relationships*, not instructions.

57 Range Test Function

A Range Test Function checks whether a given value lies within specified bounds, a universal operation in algorithms that handle intervals, array indices, numeric domains, or search constraints. It's small but powerful, providing correctness and safety across countless applications.

What Problem Are We Solving?

Many algorithms operate on ranges, whether scanning arrays, iterating loops, searching intervals, or enforcing constraints. Repeatedly checking `if low <= x <= high` can clutter code and lead to subtle off-by-one errors.

By defining a reusable range test, we make such checks:

- Centralized (one definition, consistent semantics)
- Readable (intent clear at call site)
- Safe (avoid inconsistent inequalities)

How It Works (Plain Language)

1. Encapsulate the boundary logic into a single function.
2. Input: a value `x` and bounds `(low, high)`.
3. Return: `True` if `x` satisfies range condition, else `False`.
4. Can handle open, closed, or half-open intervals.

Variants:

- Closed: `[low, high]` → `low  x  high`
- Half-open: `[low, high)` → `low  x < high`
- Open: `(low, high)` → `low < x < high`

Example Step by Step

Example 1: Array Index Bounds

Prevent out-of-bounds access:

```
def in_bounds(i, n):
    return 0 <= i < n

if in_bounds(idx, len(arr)):
    value = arr[idx]
```

No more manual range logic.

Example 2: Range Filtering

Filter values inside range `[a, b]`:

```
def in_range(x, low, high):
    return low <= x <= high

data = [1, 3, 5, 7, 9]
filtered = [x for x in data if in_range(x, 3, 7)]
# → [3, 5, 7]
```

Example 3: Constraint Checking

Used in search or optimization algorithms:

```
if not in_range(candidate, min_val, max_val):
    continue  # skip invalid candidate
```

Keeps loops clean and avoids boundary bugs.

Example 4: Geometry / Interval Problems

Check interval overlap:

```
def overlap(a1, a2, b1, b2):
    return in_range(a1, b1, b2) or in_range(b1, a1, a2)
```

Why It Matters

- Prevents off-by-one errors
- Improves code clarity and consistency
- Essential in loop guards, search boundaries, and validity checks
- Enables parameter validation and defensive programming

A Gentle Proof (Why It Works)

Range test expresses a logical conjunction:

$$P(x) = (x \geq \text{low}) \wedge (x \leq \text{high})$$

For closed intervals, the predicate is reflexive and transitive within the set $[\text{low}, \text{high}]$. By encoding this predicate as a function, correctness follows from elementary properties of inequalities.

Half-open variants preserve well-defined iteration bounds (important for array indices).

Try It Yourself

1. Implement `in_open_range(x, low, high)` for $(low, high)$.
2. Write `in_half_open_range(i, 0, n)` for loops.
3. Use range test in binary search termination condition.
4. Check index validity in matrix traversal.

Test Cases

Input	Range	Type	Result
5	[1, 10]	Closed	True
10	[1, 10)	Half-open	False
0	(0, 5)	Open	False
3	[0, 3]	Closed	True

Complexity Summary

Operation	Time	Space	Notes
Range check	$O(1)$	$O(1)$	Constant-time comparison
Used per loop	$O(n)$	$O(1)$	Linear overall

A Range Test Function is a tiny guardrail with big impact, protecting correctness at every boundary and making algorithms easier to reason about.

58 Search Invariant Checker

A Search Invariant Checker ensures that key conditions (invariants) hold throughout a search algorithm's execution. By maintaining these invariants, we guarantee correctness, prevent subtle bugs, and provide a foundation for proofs and reasoning.

What Problem Are We Solving?

When performing iterative searches (like binary search or interpolation search), we maintain certain truths that must always hold, such as:

- The target, if it exists, is always within the current bounds.
- The search interval shrinks every step.
- Indices remain valid and ordered.

Losing these invariants can lead to infinite loops, incorrect results, or index errors. By explicitly checking invariants, we make correctness visible and testable.

How It Works (Plain Language)

1. Define invariants, conditions that must stay true during every iteration.
2. After each update step, verify these conditions.
3. If an invariant fails, assert or log an error.
4. Use invariants both for debugging and proofs.

Common search invariants:

- $ low high $
- $ target [low, high] $
- Interval size decreases: $ (high - low) $ shrinks each step

Example Step by Step

Example: Binary Search Invariants

Goal: Maintain correct search window in [low, high].

1. Initialization: $ low = 0 $, $ high = n - 1 $
2. Invariant 1: $ target [low, high] $
3. Invariant 2: $ low high $
4. Step: Compute mid, narrow range
5. Check: Each iteration, assert these invariants

Tiny Code (Python)

```
def binary_search(arr, target):
    low, high = 0, len(arr) - 1
    while low <= high:
        assert 0 <= low <= high < len(arr), "Invariant broken!"
        mid = (low + high) // 2

        if arr[mid] == target:
            return mid
        elif arr[mid] < target:
            low = mid + 1
        else:
            high = mid - 1
    return -1
```

If the invariant fails, we catch logic errors early.

Why It Matters

- Proof of correctness: Each iteration preserves truth
- Debugging aid: Detect logic flaws immediately
- Safety guarantee: Prevent invalid access or infinite loops
- Documentation: Clarifies algorithm intent

A Gentle Proof (Why It Works)

Suppose invariant P holds before iteration. The update step transforms state $(\text{low}, \text{high})$ to $(\text{low}', \text{high}')$.

We prove:

1. Base Case: P holds before first iteration (initialization)
2. Inductive Step: If P holds before iteration, and update rules maintain P, then P holds afterward

Hence, by induction, P always holds. This ensures algorithm correctness.

Try It Yourself

1. Add invariants to ternary search
2. Prove binary search correctness using invariant preservation
3. Test boundary cases (empty array, one element)
4. Visualize shrinking interval and check invariant truth at each step

Test Cases

Input Array	Target	Invariants Hold	Result
[1, 3, 5, 7, 9]	5	Yes	Index 2
[2, 4, 6]	3	Yes	Not found
[1]	1	Yes	Index 0
[]	10	Yes	Not found

Complexity

Operation	Time	Space	Notes
Check invariant	$O(1)$	$O(1)$	Constant-time check
Total search	$O(\log n)$	$O(1)$	Preserves correctness

The Search Invariant Checker turns implicit assumptions into explicit guarantees, making your search algorithms not only fast but provably correct.

59 Probe Counter

A Probe Counter tracks how many probes or lookup attempts a search algorithm performs. It's a diagnostic tool to understand efficiency and compare performance between different search strategies or data structures.

What Problem Are We Solving?

In searching (especially in hash tables, linear probing, or open addressing), performance depends not just on complexity but on how many probes are required to find or miss an element.

By counting probes, we:

- Reveal the cost of each search
- Compare performance under different load factors
- Diagnose clustering or inefficient probing patterns

How It Works (Plain Language)

1. Initialize a counter `probes = 0`.
2. Each time the algorithm checks a position or node, increment `probes`.
3. When the search ends, record or return the probe count.
4. Use statistics (mean, max, variance) to measure performance.

Example Step by Step

Example: Linear Probing in a Hash Table

1. Compute hash: $h = \text{key} \bmod m$
2. Start at h, check slot
3. If collision, move to next slot
4. Increment `probes` each time
5. Stop when slot is empty or key is found

If the table is nearly full, probe count increases, revealing efficiency loss.

Tiny Code (Python)

```
def linear_probe_search(table, key):
    m = len(table)
    h = key % m
    probes = 0
    i = 0

    while table[(h + i) % m] is not None:
        probes += 1
        if table[(h + i) % m] == key:
            return (h + i) % m, probes
        i += 1
        if i == m:
            break  # table full
    return None, probes
```

Example run:

```
table = [10, 21, 32, None, None]
index, probes = linear_probe_search(table, 21)
# probes = 1
```

Why It Matters

- Performance insight: Understand search cost beyond asymptotics
- Clustering detection: Reveal poor distribution or collisions
- Load factor tuning: Find thresholds before degradation
- Algorithm comparison: Evaluate quadratic vs linear probing

A Gentle Proof (Why It Works)

Let L be the load factor (fraction of table filled). Expected probes for a successful search in linear probing:

$$E[P_{\text{success}}] = \frac{1}{2}\left(1 + \frac{1}{1-L}\right)$$

Expected probes for unsuccessful search:

$$E[P_{\text{fail}}] = \frac{1}{2}\left(1 + \frac{1}{(1-L)^2}\right)$$

As $L \to 1$, probe counts grow rapidly, performance decays.

Try It Yourself

1. Create a hash table with linear probing
2. Insert keys at different load factors
3. Measure probe counts for hits and misses
4. Compare linear vs quadratic probing

Test Cases

Table (size 7)	Key	Load Factor	Expected Probes	Notes
[10, 21, 32, None…]	21	0.4	1	Direct hit
[10, 21, 32, 43, 54]	43	0.7	3	Clustered region
[10, 21, 32, 43, 54]	99	0.7	5	Miss after probing

Complexity

Operation	Time (Expected)	Time (Worst)	Space
Probe count	$O(1)$ per step	$O(n)$	$O(1)$
Total search	$O(1)$ average	$O(n)$	$O(1)$

By counting probes, we move from theory to measured understanding, a simple metric that reveals the hidden costs behind collisions, load factors, and search efficiency.

60 Cost Curve Plotter

A Cost Curve Plotter visualizes how an algorithm's running cost grows as the input size increases. It turns abstract complexity into a tangible curve, helping you compare theoretical and empirical performance side by side.

What Problem Are We Solving?

Big-O notation tells us how cost scales, but not how much or where performance starts to break down. A cost curve lets you:

- See real growth vs theoretical models
- Identify crossover points between algorithms
- Detect anomalies or overhead
- Build intuition about efficiency and scaling

How It Works (Plain Language)

1. Choose an algorithm and a range of input sizes.
2. For each n, run the algorithm and record:
    - Time cost (runtime)
    - Space cost (memory usage)
    - Operation count
3. Plot $(n, \text{cost}(n))$ points
4. Overlay theoretical curves ($O(n)$, $O(n \log n)$, $O(n^2)$) for comparison

This creates a visual map of performance over scale.

Example Step by Step

Let's measure sorting cost for different input sizes:

n	Time (ms)
100	0.3
500	2.5
1000	5.2
2000	11.3
4000	23.7

Plot these points. The curve shape suggests $O(n \log n)$ behavior.

Tiny Code (Python + Matplotlib)

```
import time, random, matplotlib.pyplot as plt

def measure_cost(algorithm, sizes):
    results = []
    for n in sizes:
        arr = [random.randint(0, 100000) for _ in range(n)]
        start = time.time()
        algorithm(arr)
        end = time.time()
        results.append((n, end - start))
    return results

def plot_cost_curve(results):
    xs, ys = zip(*results)
    plt.plot(xs, ys, marker='o')
    plt.xlabel("Input size (n)")
    plt.ylabel("Time (seconds)")
    plt.title("Algorithm Cost Curve")
    plt.grid(True)
    plt.show()
```

Why It Matters

- Brings Big-O to life
- Visual debugging, detect unexpected spikes
- Compare algorithms empirically
- Tune thresholds, know when to switch strategies

A Gentle Proof (Why It Works)

If theoretical cost is $f(n)$ and empirical cost is $g(n)$, then we expect:

$$\lim_{n \to \infty} \frac{g(n)}{f(n)} = c$$

where c is a constant scaling factor.

The plotted curve visually approximates $g(n)$; comparing its shape to $f(n)$ reveals whether the complexity class matches expectations.

Try It Yourself

1. Compare bubble sort vs merge sort vs quicksort.
2. Overlay n, $n \log n$, and n^2 reference curves.
3. Experiment with different data distributions (sorted, reversed).
4. Plot both time and memory cost curves.

Test Cases

Algorithm	Input Size	Time (ms)	Shape	Match
Bubble Sort	1000	80	Quadratic	$O(n^2)$
Merge Sort	1000	5	Linearithmic	$O(n \log n)$
Quick Sort	1000	3	Linearithmic	$O(n \log n)$

Complexity

Aspect	Cost	Notes
Measurement	$O(k \cdot T(n))$	k sample sizes measured
Plotting	$O(k)$	Draw curve from k points
Space	$O(k)$	Store measurement data

The Cost Curve Plotter turns theory into shape, a simple graph that makes scaling behavior and trade-offs instantly clear.

Section 7. Sorting basics

61 Swap Counter

A Swap Counter tracks the number of element swaps performed during a sorting process. It helps us understand how much rearrangement an algorithm performs and serves as a diagnostic for efficiency, stability, and input sensitivity.

What Problem Are We Solving?

Many sorting algorithms (like Bubble Sort, Selection Sort, or Quick Sort) rearrange elements through swaps. Counting swaps shows how "active" the algorithm is:

- Bubble Sort → high swap count
- Insertion Sort → fewer swaps on nearly sorted input
- Selection Sort → fixed number of swaps

By tracking swaps, we compare algorithms on data movement cost, not just comparisons.

How It Works (Plain Language)

1. Initialize a `swap_count = 0`.
2. Each time two elements exchange positions, increment the counter.
3. At the end, report `swap_count` to measure rearrangement effort.
4. Use results to compare sorting strategies or analyze input patterns.

Example Step by Step

Example: Bubble Sort on [3, 2, 1]

1. Compare 3 and 2 → swap → count = 1 → [2, 3, 1]
2. Compare 3 and 1 → swap → count = 2 → [2, 1, 3]
3. Compare 2 and 1 → swap → count = 3 → [1, 2, 3]

Total swaps: 3

If input is [1, 2, 3], no swaps occur, cost reflects sortedness.

Tiny Code (Python)

```
def bubble_sort_with_swaps(arr):
    n = len(arr)
    swaps = 0
    for i in range(n):
        for j in range(0, n - i - 1):
            if arr[j] > arr[j + 1]:
                arr[j], arr[j + 1] = arr[j + 1], arr[j]
                swaps += 1
    return arr, swaps
```

Example:

```
arr, swaps = bubble_sort_with_swaps([3, 2, 1])
# swaps = 3
```

Why It Matters

- Quantifies data movement cost
- Measures input disorder (zero swaps → already sorted)
- Compares algorithms on swap efficiency
- Reveals adaptive behavior in real data

A Gentle Proof (Why It Works)

Every swap reduces the inversion count by one. An inversion is a pair (i, j) such that $i < j$ and $a_i > a_j$.

If initial inversion count $= I$, and each swap fixes one inversion:

$$\text{Total Swaps} = I_{\text{initial}}$$

Thus, swap count directly equals disorder measure, a meaningful cost metric.

Try It Yourself

1. Count swaps for Bubble Sort, Insertion Sort, and Selection Sort.
2. Run on sorted, reversed, and random lists.
3. Compare counts, which adapts best to nearly sorted data?
4. Plot swap count vs input size.

Test Cases

Input	Algorithm	Swaps	Observation
[3, 2, 1]	Bubble Sort	3	Full reversal
[1, 2, 3]	Bubble Sort	0	Already sorted
[2, 3, 1]	Insertion Sort	2	Moves minimal elements
[3, 1, 2]	Selection Sort	2	Swaps once per position

Complexity

Metric	Cost	Notes
Time (Tracking)	$O(1)$	Increment counter per swap
Total Swaps	$O(n^2)$	Worst case for Bubble Sort
Space	$O(1)$	Constant extra memory

A Swap Counter offers a clear window into sorting dynamics, revealing how "hard" the algorithm works and how far the input is from order.

62 Inversion Counter

An Inversion Counter measures how far a sequence is from being sorted by counting all pairs that are out of order. It's a numerical measure of disorder, zero for a sorted list, maximum for a fully reversed one.

What Problem Are We Solving?

Sorting algorithms fix *inversions*. Each inversion is a pair (i, j) such that $i < j$ and $a_i > a_j$. Counting inversions gives us:

- A quantitative measure of unsortedness

- A way to analyze algorithm progress
- Insight into best-case vs worst-case behavior

This metric is also used in Kendall tau distance, ranking comparisons, and adaptive sorting research.

How It Works (Plain Language)

1. Take an array $A = [a_1, a_2, \ldots, a_n]$.
2. For each pair (i, j) where $i < j$, check if $a_i > a_j$.
3. Increment count for each inversion found.
4. A sorted array has 0 inversions; a reversed one has $\frac{n(n-1)}{2}$.

Example Step by Step

Array: [3, 1, 2]

- (3, 1): inversion
- (3, 2): inversion
- (1, 2): no inversion

Total inversions: 2

A perfect diagnostic: small count → nearly sorted.

Tiny Code (Brute Force)

```
def count_inversions_bruteforce(arr):
    count = 0
    n = len(arr)
    for i in range(n):
        for j in range(i + 1, n):
            if arr[i] > arr[j]:
                count += 1
    return count
```

Output: `count_inversions_bruteforce([3, 1, 2])` → `2`

Optimized Approach (Merge Sort)

Counting inversions can be done in $O(n \log n)$ by modifying merge sort.

```
def count_inversions_merge(arr):
    def merge_count(left, right):
        i = j = inv = 0
        merged = []
        while i < len(left) and j < len(right):
            if left[i] <= right[j]:
                merged.append(left[i])
                i += 1
            else:
                merged.append(right[j])
                inv += len(left) - i
                j += 1
        merged += left[i:]
        merged += right[j:]
        return merged, inv

    def sort_count(sub):
        if len(sub) <= 1:
            return sub, 0
        mid = len(sub) // 2
        left, invL = sort_count(sub[:mid])
        right, invR = sort_count(sub[mid:])
        merged, invM = merge_count(left, right)
        return merged, invL + invR + invM

    _, total = sort_count(arr)
    return total
```

Result: $O(n \log n)$ instead of $O(n^2)$.

Why It Matters

- Quantifies disorder precisely
- Used in sorting network analysis
- Predicts best-case improvements for adaptive sorts
- Connects to ranking correlation metrics

A Gentle Proof (Why It Works)

Every swap in a stable sort fixes exactly one inversion. If we let I denote total inversions:

$$I_{\text{sorted}} = 0, \quad I_{\text{reverse}} = \frac{n(n-1)}{2}$$

Hence, inversion count measures *distance to sorted order*, a lower bound on swaps needed by any comparison sort.

Try It Yourself

1. Count inversions for sorted, reversed, and random arrays.
2. Plot inversion count vs swap count.
3. Test merge sort counter vs brute force counter.
4. Measure how inversion count affects adaptive algorithms.

Test Cases

Input	Inversions	Interpretation
[1, 2, 3]	0	Already sorted
[3, 2, 1]	3	Fully reversed
[2, 3, 1]	2	Two pairs out of order
[1, 3, 2]	1	Slightly unsorted

Complexity

Method	Time	Space	Notes
Brute Force	$O(n^2)$	$O(1)$	Simple but slow
Merge Sort Based	$O(n \log n)$	$O(n)$	Efficient for large arrays

An Inversion Counter transforms "how sorted is this list?" into a precise number, perfect for analysis, comparison, and designing smarter sorting algorithms.

63 Stability Checker

A Stability Checker verifies whether a sorting algorithm preserves the relative order of equal elements. Stability is essential when sorting complex records with multiple keys, ensuring secondary attributes remain in order after sorting by a primary one.

What Problem Are We Solving?

When sorting, sometimes values tie, they're equal under the primary key. A stable sort keeps these tied elements in their original order. For example, sorting students by grade while preserving the order of names entered earlier.

Without stability, sorting by multiple keys becomes error-prone, and chained sorts may lose meaning.

How It Works (Plain Language)

1. Label each element with its original position.
2. Perform the sort.
3. After sorting, for all pairs with equal keys, check if the original indices remain in ascending order.
4. If yes, the algorithm is stable. Otherwise, it's not.

Example Step by Step

Array with labels: `[(A, 3), (B, 1), (C, 3)]` Sort by value → `[ (B, 1), (A, 3), (C, 3) ]`

Check ties:

- Elements with value `3`: A before C, and A's original index < C's original index → stable.

If result was `[ (B, 1), (C, 3), (A, 3) ]`, order of equals reversed → unstable.

Tiny Code (Python)

```
def is_stable_sort(original, sorted_arr, key=lambda x: x):
    positions = {}
    for idx, val in enumerate(original):
        positions.setdefault(key(val), []).append(idx)

    last_seen = {}
    for val in sorted_arr:
        k = key(val)
        pos = positions[k].pop(0)
        if k in last_seen and last_seen[k] > pos:
            return False
        last_seen[k] = pos
    return True
```

Usage:

```
data = [('A', 3), ('B', 1), ('C', 3)]
sorted_data = sorted(data, key=lambda x: x[1])
is_stable_sort(data, sorted_data, key=lambda x: x[1])  # True
```

Why It Matters

- Preserves secondary order: essential for multi-key sorts
- Chaining safety: sort by multiple fields step-by-step
- Predictable results: avoids random reorder of equals
- Common property: Merge Sort, Insertion Sort stable; Quick Sort not (by default)

A Gentle Proof (Why It Works)

Let a_i and a_j be elements with equal keys k. If $i < j$ in the input and positions of a_i and a_j after sorting are p_i and p_j, then the algorithm is stable if and only if:

$$i < j \implies p_i < p_j \text{ whenever } k_i = k_j$$

Checking this property across all tied keys confirms stability.

Try It Yourself

1. Compare stable sort (Merge Sort) vs unstable sort (Selection Sort).
2. Sort list of tuples by one key, check tie preservation.
3. Chain sorts (first by last name, then by first name).
4. Run checker to confirm final stability.

Test Cases

Input	Sorted Result	Stable?	Explanation
[(A,3),(B,1),(C,3)]	[(B,1),(A,3),(C,3)]	Yes	A before C preserved
[(A,3),(B,1),(C,3)]	[(B,1),(C,3),(A,3)]	No	A and C order reversed
[(1,10),(2,10),(3,10)]	[(1,10),(2,10),(3,10)]	Yes	All tied, all preserved

Complexity

Operation	Time	Space	Notes
Checking	$O(n)$	$O(n)$	One pass over sorted array
Sorting	Depends	,	Checker independent of sort

The Stability Checker ensures your sorts respect order among equals, a small step that safeguards multi-key sorting correctness and interpretability.

64 Comparison Network Visualizer

A Comparison Network Visualizer shows how fixed sequences of comparisons sort elements, revealing the structure of sorting networks. These diagrams help us see how parallel sorting works, step by step, independent of input data.

What Problem Are We Solving?

Sorting networks are data-oblivious, their comparison sequence is fixed, not driven by data. To understand or design them, we need a clear visual of which elements compare and when. The visualizer turns an abstract sequence of comparisons into a layered network diagram.

This is key for:

- Analyzing parallel sorting

- Designing hardware-based sorters
- Studying bitonic or odd-even merges

How It Works (Plain Language)

1. Represent each element as a horizontal wire.
2. Draw a vertical comparator line connecting the two wires being compared.
3. Group comparators into layers that can run in parallel.
4. The network executes layer by layer, swapping elements if out of order.

Result: a visual map of sorting logic.

Example Step by Step

Sorting 4 elements with Bitonic Sort network:

```
Layer 1: Compare (0,1), (2,3)
Layer 2: Compare (0,2), (1,3)
Layer 3: Compare (1,2)
```

Visual:

```
0
1
2
3
```

Each dot pair = comparator. The structure is static, independent of values.

Tiny Code (Python)

```python
def visualize_network(n, layers):
    wires = [[' '] * (len(layers) + 1) for _ in range(n)]

    for layer_idx, layer in enumerate(layers):
        for (i, j) in layer:
            wires[i][layer_idx] = ' '
            wires[j][layer_idx] = ' '
```

```
    for i in range(n):
        print(f"{i}: " + " ".join(wires[i]))

layers = [[(0,1), (2,3)], [(0,2), (1,3)], [(1,2)]]
visualize_network(4, layers)
```

This prints a symbolic visualization of comparator layers.

Why It Matters

- Reveals parallelism in sorting logic
- Helps debug data-oblivious algorithms
- Useful for hardware and GPU design
- Foundation for Bitonic, Odd-Even Merge, and Batcher networks

A Gentle Proof (Why It Works)

A sorting network guarantees correctness if it sorts all binary sequences of length n.

By the Zero-One Principle:

> If a comparison network correctly sorts all sequences of 0s and 1s, it correctly sorts all sequences of arbitrary numbers.

So visualizing comparators ensures completeness and layer correctness.

Try It Yourself

1. Draw a 4-input bitonic sorting network.
2. Visualize how comparators "flow" through layers.
3. Check how many layers can run in parallel.
4. Test sorting 0/1 sequences manually through the network.

Test Cases

Inputs	Network Type	Layers	Sorted Output
[3,1,4,2]	Bitonic Sort	3	[1,2,3,4]
[1,0,1,0]	Odd-Even Merge	3	[0,0,1,1]

Complexity

Metric	Value	Notes
Comparators	$O(n \log^2 n)$	Batcher's network complexity
Depth	$O(\log^2 n)$	Layers executed in parallel
Space	$O(n)$	One wire per input

A Comparison Network Visualizer makes parallel sorting tangible, every comparator and layer visible, transforming abstract hardware logic into a clear, educational blueprint.

65 Adaptive Sort Detector

An Adaptive Sort Detector measures how "sorted" an input sequence already is and predicts whether an algorithm can take advantage of it. It's a diagnostic tool that estimates presortedness and guides the choice of an adaptive sorting algorithm.

What Problem Are We Solving?

Not all inputs are random, many are partially sorted. Some algorithms (like Insertion Sort or Timsort) perform much faster on nearly sorted data. We need a way to detect sortedness before choosing the right strategy.

An adaptive detector quantifies how close an input is to sorted order.

How It Works (Plain Language)

1. Define a measure of disorder (e.g., number of inversions, runs, or local misplacements).
2. Traverse the array, counting indicators of unsortedness.
3. Return a metric (e.g., 0 = fully sorted, 1 = fully reversed).
4. Use this score to decide whether to apply:
    - Simple insertion-like sort (for nearly sorted data)
    - General-purpose sort (for random data)

Example Step by Step

Array: [1, 2, 4, 3, 5, 6]

1. Compare adjacent pairs:
   - 1 ≤ 2 (ok)
   - 2 ≤ 4 (ok)
   - 4 > 3 (disorder)
   - 3 ≤ 5 (ok)
   - 5 ≤ 6 (ok)
2. Count = 1 local inversion

Sortedness score:

$$s = 1 - \frac{\text{disorder}}{n-1} = 1 - \frac{1}{5} = 0.8$$

80% sorted, good candidate for adaptive sort.

Tiny Code (Python)

```
def adaptive_sort_detector(arr):
    disorder = 0
    for i in range(len(arr) - 1):
        if arr[i] > arr[i + 1]:
            disorder += 1
    return 1 - disorder / max(1, len(arr) - 1)

arr = [1, 2, 4, 3, 5, 6]
score = adaptive_sort_detector(arr)
# score = 0.8
```

You can use this score to select algorithms dynamically.

Why It Matters

- Detects near-sorted input efficiently
- Enables algorithm selection at runtime
- Saves time on real-world data (logs, streams, merges)
- Core idea behind Timsort's run detection

A Gentle Proof (Why It Works)

If an algorithm's time complexity depends on disorder d, e.g. $O(n+d)$, and $d = O(1)$ for nearly sorted arrays, then the adaptive algorithm approaches linear time.

The detector approximates d, helping us decide when $O(n+d)$ beats $O(n \log n)$.

Try It Yourself

1. Test arrays with 0, 10%, 50%, and 100% disorder.
2. Compare runtime of Insertion Sort vs Merge Sort.
3. Use inversion counting for more precise detection.
4. Integrate detector into a hybrid sorting routine.

Test Cases

Input	Disorder	Score	Recommendation
[1,2,3,4,5]	0	1.0	Insertion Sort
[1,3,2,4,5]	1	0.8	Adaptive Sort
[3,2,1]	2	0.0	Merge / Quick Sort
[2,1,3,5,4]	2	0.6	Adaptive Sort

Complexity

Operation	Time	Space	Notes
Disorder check	$O(n)$	$O(1)$	Single scan
Sorting (chosen)	Adaptive	,	Depends on algorithm selected

The Adaptive Sort Detector bridges theory and pragmatism, quantifying how ordered your data is and guiding smarter algorithm choices for real-world performance.

66 Sorting Invariant Checker

A Sorting Invariant Checker verifies that key ordering conditions hold throughout a sorting algorithm's execution. It's used to reason about correctness step by step, ensuring that each iteration preserves progress toward a fully sorted array.

What Problem Are We Solving?

When debugging or proving correctness of sorting algorithms, we need to ensure that certain invariants (conditions that must always hold) remain true. If any invariant breaks, the algorithm may produce incorrect output, even if it "looks" right at a glance.

A sorting invariant formalizes what "partial progress" means. Examples:

- "All elements before index `i` are in sorted order."
- "All elements beyond pivot are greater or equal to it."
- "Heap property holds at every node."

How It Works (Plain Language)

1. Define one or more invariants that describe correctness.
2. After each iteration or recursion step, check that these invariants still hold.
3. If any fail, stop and debug, the algorithm logic is wrong.
4. Once sorting finishes, the global invariant (sorted array) must hold.

This approach is key for formal verification and debuggable code.

Example Step by Step

Insertion Sort invariant:

> Before processing element `i`, the subarray `arr[:i]` is sorted.

- Initially `i = 1`: subarray `[arr[0]]` is sorted.
- After inserting `arr[1]`, subarray `[arr[0:2]]` is sorted.
- By induction, full array sorted at end.

Check after every insertion: `assert arr[:i] == sorted(arr[:i])`

Tiny Code (Python)

```
def insertion_sort_with_invariant(arr):
    for i in range(1, len(arr)):
        key = arr[i]
        j = i - 1
        while j >= 0 and arr[j] > key:
            arr[j + 1] = arr[j]
```

```
            j -= 1
        arr[j + 1] = key
        # Check invariant
        assert arr[:i+1] == sorted(arr[:i+1]), f"Invariant broken at i={i}"
    return arr
```

If invariant fails, an assertion error reveals the exact iteration.

Why It Matters

- Builds correctness proofs via induction
- Early bug detection, pinpoints iteration errors
- Clarifies algorithm intent
- Teaches structured reasoning about program logic

Used in:

- Formal proofs (loop invariants)
- Algorithm verification
- Education and analysis

A Gentle Proof (Why It Works)

Let $P(i)$ denote the invariant "prefix of length i is sorted."

- Base case: $P(1)$ holds trivially.
- Inductive step: If $P(i)$ holds, inserting next element keeps $P(i+1)$ true.

By induction, $P(n)$ holds, full array is sorted.

Thus, the invariant framework guarantees correctness if each step preserves truth.

Try It Yourself

1. Add invariants to Selection Sort ("min element placed at index i").
2. Add heap property invariant to Heap Sort.
3. Run assertions in test suite.
4. Use `try/except` to log rather than stop when invariants fail.

Test Cases

Algorithm	Invariant	Holds?	Notes
Insertion Sort	Prefix sorted at each step	Yes	Classic inductive invariant
Selection Sort	Min placed at position i	Yes	Verified iteratively
Quick Sort	Pivot partitions left pivot right	Yes	Must hold after partition
Bubble Sort	Largest element bubbles to correct position	Yes	After each full pass

Complexity

Check Type	Time	Space	Notes
Assertion	$O(k)$	$O(1)$	For prefix length k
Total cost	$O(n^2)$ worst	For nested invariant checks	

A Sorting Invariant Checker transforms correctness from intuition into logic, enforcing order, proving validity, and illuminating the structure of sorting algorithms one invariant at a time.

67 Distribution Histogram Sort Demo

A Distribution Histogram Sort Demo visualizes how elements spread across buckets or bins during distribution-based sorting. It helps learners see *why* and *how* counting, radix, or bucket sort achieve linear-time behavior by organizing values before final ordering.

What Problem Are We Solving?

Distribution-based sorts (Counting, Bucket, Radix) don't rely on pairwise comparisons. Instead, they classify elements into bins based on keys or digits. Understanding these algorithms requires visualizing how data is distributed across categories, a histogram captures that process.

The demo shows:

- How counts are collected
- How prefix sums turn counts into positions
- How items are rebuilt in sorted order

How It Works (Plain Language)

1. Initialize buckets, one for each key or range.
2. Traverse input and increment count in the right bucket.
3. Visualize the resulting histogram of frequencies.
4. (Optional) Apply prefix sums to show cumulative positions.
5. Reconstruct output by reading bins in order.

This visualization connects counting logic to the final sorted array.

Example Step by Step

Example: Counting sort on `[2, 1, 2, 0, 1]`

Value	Count
0	1
1	2
2	2

Prefix sums → `[1, 3, 5]` Rebuild array → `[0, 1, 1, 2, 2]`

The histogram clearly shows where each group of values will end up.

Tiny Code (Python)

```
import matplotlib.pyplot as plt

def histogram_sort_demo(arr, max_value):
    counts = [0] * (max_value + 1)
    for x in arr:
        counts[x] += 1

    plt.bar(range(len(counts)), counts)
    plt.xlabel("Value")
    plt.ylabel("Frequency")
    plt.title("Distribution Histogram for Counting Sort")
    plt.show()

    # Optional reconstruction
    sorted_arr = []
```

```
    for val, freq in enumerate(counts):
        sorted_arr.extend([val] * freq)
    return sorted_arr
```

Example:

```
histogram_sort_demo([2, 1, 2, 0, 1], 2)
```

Why It Matters

- Makes non-comparison sorting intuitive
- Shows data frequency patterns
- Bridges between counting and position assignment
- Helps explain $O(n + k)$ complexity visually

A Gentle Proof (Why It Works)

Each value's frequency f_i determines exactly how many times it appears. By prefix-summing counts:

$$p_i = \sum_{j<i} f_j$$

we assign unique output positions for each value, ensuring stable, correct ordering in linear time.

Thus, sorting becomes position mapping, not comparison.

Try It Yourself

1. Plot histograms for random, sorted, and uniform arrays.
2. Compare bucket sizes in Bucket Sort vs digit positions in Radix Sort.
3. Add prefix-sum labels to histogram bars.
4. Animate step-by-step rebuild of output.

Test Cases

Input	Max	Histogram	Sorted Output
[2,1,2,0,1]	2	[1,2,2]	[0,1,1,2,2]
[3,3,3,3]	3	[0,0,0,4]	[3,3,3,3]
[0,1,2,3]	3	[1,1,1,1]	[0,1,2,3]

Complexity

Operation	Time	Space	Notes
Counting	$O(n)$	$O(k)$	k = number of buckets
Prefix summation	$O(k)$	$O(k)$	Single pass over counts
Reconstruction	$O(n+k)$	$O(n+k)$	Build sorted array

The Distribution Histogram Sort Demo transforms abstract counting logic into a concrete visual, showing how frequency shapes order and making linear-time sorting crystal clear.

68 Key Extraction Function

A Key Extraction Function isolates the specific feature or attribute from a data element that determines its position in sorting. It's a foundational tool for flexible, reusable sorting logic, enabling algorithms to handle complex records, tuples, or custom objects.

What Problem Are We Solving?

Sorting real-world data often involves structured elements, tuples, objects, or dictionaries, not just numbers. We rarely sort entire elements directly; instead, we sort by a key:

- Name alphabetically
- Age numerically
- Date chronologically

A key extractor defines *how to view* each item for comparison, decoupling *data* from *ordering*.

How It Works (Plain Language)

1. Define a key function: `key(x)` $\rightarrow$ extracts sortable attribute.
2. Apply key function during comparisons.
3. Algorithm sorts based on these extracted values.
4. The original elements remain intact, only their order changes.

Example Step by Step

Suppose you have:

```
students = [
    ("Alice", 22, 3.8),
    ("Bob", 20, 3.5),
    ("Clara", 21, 3.9)
]
```

To sort by age, use `key=lambda x: x[1]`. To sort by GPA (descending), use `key=lambda x: -x[2]`.

Results:

- By age → `[("Bob", 20, 3.5), ("Clara", 21, 3.9), ("Alice", 22, 3.8)]`
- By GPA → `[("Clara", 21, 3.9), ("Alice", 22, 3.8), ("Bob", 20, 3.5)]`

Tiny Code (Python)

```
def sort_by_key(data, key):
    return sorted(data, key=key)

students = [("Alice", 22, 3.8), ("Bob", 20, 3.5), ("Clara", 21, 3.9)]

# Sort by age
result = sort_by_key(students, key=lambda x: x[1])
# Sort by GPA descending
result2 = sort_by_key(students, key=lambda x: -x[2])
```

This abstraction allows clean, reusable sorting.

Why It Matters

- Separates logic: comparison mechanism vs data structure
- Reusability: one algorithm, many orderings
- Composability: multi-level sorting by chaining keys
- Stability synergy: stable sorts + key extraction = multi-key sorting

A Gentle Proof (Why It Works)

Let $f(x)$ be the key extractor. We sort based on $f(x)$, not x. If the comparator satisfies:

$$f(x_i) \leq f(x_j) \implies x_i \text{ precedes } x_j$$

then the resulting order respects the intended attribute. Because f is deterministic, sort correctness follows directly from comparator correctness.

Try It Yourself

1. Sort strings by length: `key=len`
2. Sort dictionary list by field: `key=lambda d: d['score']`
3. Compose keys: `key=lambda x: (x.grade, x.name)`
4. Combine with stability to simulate SQL "ORDER BY"

Test Cases

Input	Key	Result
[("A",3),("B",1),("C",2)]	`lambda x:x[1]`	[("B",1),("C",2),("A",3)]
["cat","a","bird"]	`len`	["a","cat","bird"]
[{"x":5},{"x":2},{"x":4}]	`lambda d:d["x"]`	[{"x":2},{"x":4},{"x":5}]

Complexity

Step	Time	Space	Notes
Key extraction	$O(n)$	$O(1)$	One call per element
Sorting	$O(n \log n)$	$O(n)$	Depends on algorithm used
Composition	$O(k \cdot n)$	$O(1)$	For multi-key chaining

The Key Extraction Function is the bridge between raw data and custom order, empowering algorithms to sort not just numbers, but meaning.

69 Partially Ordered Set Builder

A Partially Ordered Set (Poset) Builder constructs a visual and logical model of relationships that define *partial orderings* among elements, where some items can be compared, and others cannot. It's a conceptual tool for understanding sorting constraints, dependency graphs, and precedence structures.

What Problem Are We Solving?

Not all collections have a total order. Sometimes only partial comparisons make sense, such as:

- Task dependencies (A before B, C independent)
- Version control merges
- Topological ordering in DAGs

A poset captures these relationships:

- Reflexive: every element itself
- Antisymmetric: if A B and B A, then A = B
- Transitive: if A B and B C, then A C

Building a poset helps us visualize constraints before attempting to sort or schedule.

How It Works (Plain Language)

1. Define a relation ( ) among elements.
2. Build a graph where an edge A → B means "A B."
3. Ensure reflexivity, antisymmetry, and transitivity.
4. Visualize the result as a Hasse diagram (omit redundant edges).
5. Use this structure to find linear extensions (valid sorted orders).

Example Step by Step

Example: Suppose we have tasks with dependencies:

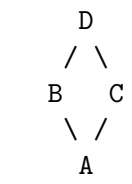
```
A  B, A  C, B  D, C  D
```

Construct the poset:

- Nodes: A, B, C, D

- Edges: A→B, A→C, B→D, C→D

Hasse diagram:



Possible total orders (linear extensions):

- A, B, C, D
- A, C, B, D

Tiny Code (Python)

```
from collections import defaultdict

def build_poset(relations):
    graph = defaultdict(list)
    for a, b in relations:
        graph[a].append(b)
    return graph

relations = [('A', 'B'), ('A', 'C'), ('B', 'D'), ('C', 'D')]
poset = build_poset(relations)
for k, v in poset.items():
    print(f"{k} → {v}")
```

Output:

```
A → ['B', 'C']
B → ['D']
C → ['D']
```

You can extend this to visualize with tools like `networkx`.

Why It Matters

- Models dependencies and precedence
- Foundation of topological sorting
- Explains why total order isn't always possible
- Clarifies constraint satisfaction in scheduling

Used in:

- Build systems (make, DAGs)
- Task planning
- Compiler dependency analysis

A Gentle Proof (Why It Works)

A poset $(P, \leq)$ satisfies three axioms:

1. Reflexivity: $\forall x, x \leq x$
2. Antisymmetry: $(x \leq y \land y \leq x) \implies x = y$
3. Transitivity: $(x \leq y \land y \leq z) \implies x \leq z$

These properties ensure consistent structure. Sorting a poset means finding a linear extension consistent with all $\leq$ relations, which a topological sort guarantees for DAGs.

Try It Yourself

1. Define tasks with prerequisites.
2. Draw a Hasse diagram.
3. Perform topological sort to list valid total orders.
4. Add extra relation, check if antisymmetry breaks.

Test Cases

Relations	Poset Edges	Linear Orders
A B, A C, B D, C D	A→B, A→C, B→D, C→D	[A,B,C,D], [A,C,B,D]
A B, B C, A C	A→B, B→C, A→C	[A,B,C]
A B, B A (invalid)	,	Violates antisymmetry

Complexity

Operation	Time	Space	Notes
Build relation graph	$O(E)$	$O(V)$	E = number of relations
Check antisymmetry	$O(E)$	$O(V)$	Detect cycles or bidirectional
Topological sort	$O(V + E)$	$O(V)$	For linear extensions

The Partially Ordered Set Builder turns abstract ordering constraints into structured insight, showing not just *what comes first*, but *what can coexist*.

70 Complexity Comparator

A Complexity Comparator helps us understand how different algorithms scale by comparing their time or space complexity functions directly. It's a tool for intuition: how does $O(n)$ stack up against $O(n \log n)$ or $O(2^n)$ as n grows large?

What Problem Are We Solving?

When faced with multiple algorithms solving the same problem, we must decide which is more efficient for large inputs. Rather than guess, we compare growth rates of their complexity functions.

Example: Is $O(n^2)$ slower than $O(n \log n)$? For small n, maybe not. But as $n \to \infty$, n^2 grows faster, so the $O(n \log n)$ algorithm is asymptotically better.

How It Works (Plain Language)

1. Define the two functions $f(n)$ and $g(n)$ representing their costs.
2. Compute the ratio $\frac{f(n)}{g(n)}$ as $n \to \infty$.
3. Interpret the limit:
   - If $\lim_{n\to\infty} \frac{f(n)}{g(n)} = 0$, then $f(n) = o(g(n))$ (grows slower).
   - If limit is ∞, then $f(n) = \omega(g(n))$ (grows faster).
   - If limit is constant, then $f(n) = \Theta(g(n))$ (same growth).
4. Visualize using plots or tables for small n to understand crossover points.

Example Step by Step

Compare $f(n) = n \log n$ and $g(n) = n^2$:

- Compute ratio: $\frac{f(n)}{g(n)} = \frac{n \log n}{n^2} = \frac{\log n}{n}$.
- As $n \to \infty$, $\frac{\log n}{n} \to 0$. Therefore, $f(n) = o(g(n))$.

Interpretation: $O(n \log n)$ grows slower than $O(n^2)$, so it's more scalable.

Tiny Code (Python)

```
import math

def compare_growth(f, g, n_values):
    for n in n_values:
        print(f"n={n:6d} f(n)={f(n):10.2f} g(n)={g(n):10.2f} ratio={f(n)/g(n):10.6f}")

compare_growth(lambda n: n * math.log2(n),
               lambda n: n2,
               [2, 4, 8, 16, 32, 64, 128])
```

Output shows how $\frac{f(n)}{g(n)}$ decreases with n.

Why It Matters

- Makes asymptotic comparison visual and numeric
- Reveals crossover points for real-world input sizes
- Helps choose between multiple implementations
- Deepens intuition about scaling laws

A Gentle Proof (Why It Works)

We rely on limit comparison:

If $\lim_{n \to \infty} \frac{f(n)}{g(n)} = c$:

- If $0 < c < \infty$, then $f(n) = \Theta(g(n))$
- If $c = 0$, then $f(n) = o(g(n))$
- If $c = \infty$, then $f(n) = \omega(g(n))$

This follows from formal definitions of asymptotic notation, ensuring consistency across comparisons.

Try It Yourself

1. Compare $O(n^2)$ vs $O(n^3)$
2. Compare $O(n \log n)$ vs $O(n^{1.5})$
3. Compare $O(2^n)$ vs $O(n!)$
4. Plot their growth using Python or Excel

Test Cases

$f(n)$	$g(n)$	Ratio as $n \to \infty$	Relationship
n	$n \log n$	0	$n = o(n \log n)$
$n \log n$	n^2	0	$n \log n = o(n^2)$
n^2	n^2	1	Θ
2^n	n^3	∞	$2^n = \omega(n^3)$

Complexity

Operation	Time	Space	Notes
Function ratio	$O(1)$	$O(1)$	Constant-time comparison
Empirical table	$O(k)$	$O(k)$	For k sampled points
Plot visualization	$O(k)$	$O(k)$	Helps understand crossover

The Complexity Comparator is your lens for asymptotic insight, showing not just which algorithm is faster, but *why* it scales better.

Section 8. Data Structure Overview

71 Stack Simulation

A Stack Simulation lets us watch the push and pop operations unfold step by step, revealing the LIFO (Last In, First Out) nature of this simple yet powerful data structure.

What Problem Are We Solving?

Stacks are everywhere: in recursion, expression evaluation, backtracking, and function calls. But for beginners, their dynamic behavior can feel abstract. A simulation makes it concrete, every push adds a layer, every pop removes one.

Goal: Understand how and when elements enter and leave the stack, and why order matters.

How It Works (Plain Language)

1. Start with an empty stack.
2. Push(x): Add element `x` to the top.
3. Pop(): Remove the top element.
4. Peek() (optional): Look at the top without removing it.
5. The most recently pushed element is always the first removed.

Think of a stack of plates: you can only take from the top.

Example Step by Step

Operations:

```
Push(10)
Push(20)
Push(30)
Pop()
Push(40)
```

Stack evolution:

Step	Operation	Stack State (Top → Bottom)
1	Push(10)	10
2	Push(20)	20, 10
3	Push(30)	30, 20, 10
4	Pop()	20, 10
5	Push(40)	40, 20, 10

Tiny Code (Python)

```
class Stack:
    def __init__(self):
        self.data = []

    def push(self, x):
        self.data.append(x)
        print(f"Pushed {x}: {self.data[::-1]}")

    def pop(self):
        if self.data:
            x = self.data.pop()
            print(f"Popped {x}: {self.data[::-1]}")
            return x

# Demo
s = Stack()
s.push(10)
s.push(20)
s.push(30)
s.pop()
s.push(40)
```

Each action prints the current state, simulating stack behavior.

Why It Matters

- Models function calls and recursion
- Essential for undo operations and backtracking

- Underpins expression parsing and evaluation
- Builds intuition for control flow and memory frames

A Gentle Proof (Why It Works)

A stack enforces LIFO ordering: If you push elements in order $a_1, a_2, \ldots, a_n$, you must pop them in reverse: $a_n, \ldots, a_2, a_1$.

Formally, each push increases size by 1, each pop decreases it by 1, ensuring $|S| = \text{pushes} - \text{pops}$ and order reverses naturally.

Try It Yourself

1. Simulate postfix expression evaluation (`3 4 + 5 *`)
2. Trace recursive function calls (factorial or Fibonacci)
3. Implement browser backtracking with a stack
4. Push strings and pop them to reverse order

Test Cases

Operation Sequence	Final Stack (Top → Bottom)
Push(1), Push(2), Pop()	1
Push('A'), Push('B'), Push('C')	C, B, A
Push(5), Pop(), Pop()	(empty)
Push(7), Push(9), Push(11), Pop()	9, 7

Complexity

Operation	Time	Space	Note
Push(x)	O(1)	O(n)	Append to list
Pop()	O(1)	O(n)	Remove last item
Peek()	O(1)	O(n)	Access last item

A Stack Simulation makes abstract order tangible, every push and pop tells a story of control, memory, and flow.

72 Queue Simulation

A Queue Simulation shows how elements move through a first-in, first-out structure, perfect for modeling waiting lines, job scheduling, or data streams.

What Problem Are We Solving?

Queues capture fairness and order. They're essential in task scheduling, buffering, and resource management, but their behavior can seem opaque without visualization.

Simulating operations reveals how enqueue and dequeue actions shape the system over time.

Goal: Understand FIFO (First-In, First-Out) order and how it ensures fairness in processing.

How It Works (Plain Language)

1. Start with an empty queue.
2. Enqueue(x): Add element `x` to the rear.
3. Dequeue(): Remove the front element.
4. Peek() (optional): See the next item to be processed.

Like a line at a ticket counter, first person in is first to leave.

Example Step by Step

Operations:

```
Enqueue(10)
Enqueue(20)
Enqueue(30)
Dequeue()
Enqueue(40)
```

Queue evolution:

Step	Operation	Queue State (Front → Rear)
1	Enqueue(10)	10
2	Enqueue(20)	10, 20
3	Enqueue(30)	10, 20, 30
4	Dequeue()	20, 30
5	Enqueue(40)	20, 30, 40

Step	Operation	Queue State (Front → Rear)

Tiny Code (Python)

```
from collections import deque

class Queue:
    def __init__(self):
        self.data = deque()

    def enqueue(self, x):
        self.data.append(x)
        print(f"Enqueued {x}: {list(self.data)}")

    def dequeue(self):
        if self.data:
            x = self.data.popleft()
            print(f"Dequeued {x}: {list(self.data)}")
            return x

# Demo
q = Queue()
q.enqueue(10)
q.enqueue(20)
q.enqueue(30)
q.dequeue()
q.enqueue(40)
```

Each step prints the queue's current state, helping you trace order evolution.

Why It Matters

- Models real-world waiting lines
- Used in schedulers, network buffers, and BFS traversals
- Ensures fair access to limited resources
- Builds intuition for stream processing

A Gentle Proof (Why It Works)

A queue preserves arrival order. If elements arrive in order $a_1, a_2, \ldots, a_n$, they exit in the same order, $a_1, a_2, \ldots, a_n$.

Each enqueue appends to the rear, each dequeue removes from the front. Thus, insertion and removal sequences match, enforcing FIFO.

Try It Yourself

1. Simulate a print queue, jobs enter and complete in order.
2. Implement BFS on a small graph using a queue.
3. Model ticket line arrivals and departures.
4. Track packet flow through a network buffer.

Test Cases

Operation Sequence	Final Queue (Front → Rear)
Enqueue(1), Enqueue(2), Dequeue()	2
Enqueue('A'), Enqueue('B'), Enqueue('C')	A, B, C
Enqueue(5), Dequeue(), Dequeue()	(empty)
Enqueue(7), Enqueue(9), Enqueue(11), Dequeue()	9, 11

Complexity

Operation	Time	Space	Note
Enqueue(x)	O(1)	O(n)	Append to rear
Dequeue()	O(1)	O(n)	Remove from front
Peek()	O(1)	O(n)	Access front item

A Queue Simulation clarifies the rhythm of fairness, each arrival patiently waits its turn, no one cutting in line.

73 Linked List Builder

A Linked List Builder shows how elements connect through pointers, the foundation for dynamic memory structures where data grows or shrinks on demand.

What Problem Are We Solving?

Arrays have fixed size and require contiguous memory. Linked lists solve this by linking scattered nodes dynamically, one pointer at a time.

By simulating node creation and linkage, we build intuition for pointer manipulation and traversal, essential for mastering lists, stacks, queues, and graphs.

Goal: Understand how nodes link together and how to maintain references during insertion or deletion.

How It Works (Plain Language)

A singly linked list is a sequence of nodes, each holding:

- A value
- A pointer to the next node

Basic operations:

1. Create node(value) → allocate new node.
2. Insert after → link new node between existing ones.
3. Delete → redirect pointers to skip a node.
4. Traverse → follow next pointers until `None`.

Like a chain, each link knows only the next one.

Example Step by Step

Build a list:

```
Insert(10)
Insert(20)
Insert(30)
```

Process:

1. Create node(10): head → 10 → None
2. Create node(20): head → 10 → 20 → None
3. Create node(30): head → 10 → 20 → 30 → None

Traversal from `head` prints: `10 → 20 → 30 → None`

Tiny Code (Python)

```
class Node:
    def __init__(self, value):
        self.value = value
        self.next = None

class LinkedList:
    def __init__(self):
        self.head = None

    def insert(self, value):
        new_node = Node(value)
        if not self.head:
            self.head = new_node
        else:
            cur = self.head
            while cur.next:
                cur = cur.next
            cur.next = new_node
        self.display()

    def display(self):
        cur = self.head
        elems = []
        while cur:
            elems.append(str(cur.value))
            cur = cur.next
        print(" → ".join(elems) + " → None")

# Demo
ll = LinkedList()
ll.insert(10)
ll.insert(20)
ll.insert(30)
```

Why It Matters

- Enables dynamic memory allocation
- No need for contiguous storage
- Powers stacks, queues, hash chains, adjacency lists

- Builds foundation for advanced pointer-based structures

A Gentle Proof (Why It Works)

Let n be the number of nodes. Each node has exactly one outgoing pointer (to `next`) or `None`. Traversing once visits every node exactly once.

Therefore, insertion or traversal takes $O(n)$ time, and storage is $O(n)$ (one node per element).

Try It Yourself

1. Insert values `{5, 15, 25, 35}`
2. Delete the second node and reconnect links
3. Reverse the list manually by reassigning pointers
4. Visualize how each `next` changes during reversal

Test Cases

Operation Sequence	Expected Output
Insert(10), Insert(20)	$10 \to 20 \to$ None
Insert(5), Insert(15), Insert(25)	$5 \to 15 \to 25 \to$ None
Empty List	None
Single Node	$42 \to$ None

Complexity

Operation	Time	Space	Note
Insert End	O(n)	O(n)	Traverse to tail
Delete Node	O(n)	O(n)	Find predecessor
Search	O(n)	O(n)	Sequential traversal
Traverse	O(n)	O(n)	Visit each node once

A Linked List Builder is your first dance with pointers, where structure emerges from simple connections, and memory becomes fluid, flexible, and free.

74 Array Index Visualizer

An Array Index Visualizer helps you see how arrays organize data in contiguous memory and how indexing gives $O(1)$ access to any element.

What Problem Are We Solving?

Arrays are the simplest data structure, but beginners often struggle to grasp how indexing truly works under the hood. By visualizing index positions and memory offsets, you can see why arrays allow direct access yet require fixed size and contiguous space.

Goal: Understand the relationship between index, address, and element access.

How It Works (Plain Language)

An array stores n elements consecutively in memory. If the base address is A_0, and each element takes s bytes, then:

$$A_i = A_0 + i \times s$$

So accessing index i is constant-time:

- Compute address
- Jump directly there
- Retrieve value

This visualization ties logical indices (0, 1, 2, …) to physical locations.

Example Step by Step

Suppose we have an integer array:

```
arr = [10, 20, 30, 40]
```

Base address: `1000`, element size: `4 bytes`

Index	Address	Value
0	1000	10
1	1004	20
2	1008	30

Index	Address	Value
3	1012	40

Access `arr[2]`:

- Compute $A_0 + 2 \times 4 = 1008$
- Retrieve `30`

Tiny Code (Python)

```
def visualize_array(arr, base=1000, size=4):
    print(f"{'Index':<8}{'Address':<10}{'Value':<8}")
    for i, val in enumerate(arr):
        address = base + i * size
        print(f"{i:<8}{address:<10}{val:<8}")

arr = [10, 20, 30, 40]
visualize_array(arr)
```

Output:

```
Index   Address   Value
0       1000      10
1       1004      20
2       1008      30
3       1012      40
```

Why It Matters

- Instant access via address computation
- Contiguity ensures cache locality
- Fixed size and type consistency
- Core of higher-level structures (strings, matrices, tensors)

A Gentle Proof (Why It Works)

Let A_0 be the base address. Each element occupies s bytes. To access element i:

$$A_i = A_0 + i \times s$$

This is a simple arithmetic operation, so access is $O(1)$, independent of n.

Try It Yourself

1. Visualize array `[5, 10, 15, 20, 25]` with base `5000` and size `8`.
2. Access `arr[4]` manually using formula.
3. Compare array vs. linked list access time.
4. Modify size and re-run visualization.

Test Cases

Array	Base	Size	Access	Expected Address	Value
[10, 20, 30]	1000	4	arr[1]	1004	20
[7, 14, 21, 28]	500	2	arr[3]	506	28

Complexity

Operation	Time	Space	Note
Access	O(1)	O(n)	Direct via formula
Update	O(1)	O(n)	Single write
Traverse	O(n)	O(n)	Visit all
Insert/Delete	O(n)	O(n)	Requires shifting

An Array Index Visualizer reveals how logic meets hardware, every index a direct pointer, every element a predictable step from the base.

75 Hash Function Mapper

A Hash Function Mapper shows how keys are transformed into array indices, turning arbitrary data into fast-access positions.

What Problem Are We Solving?

We often need to store and retrieve data by key (like "Alice" or "user123"), not by numeric index. But arrays only understand numbers. A hash function bridges this gap, mapping keys into integer indices so we can use array-like speed for key-based lookup.

Goal: Understand how keys become indices and how hash collisions occur.

How It Works (Plain Language)

A hash function takes a key and computes an index:

$$\text{index} = h(\text{key}) \bmod m$$

where:

- $h(\text{key})$ is a numeric hash value,
- m is the table size.

For example:

```
key = "cat"
h(key) = 493728
m = 10
index = 493728 % 10 = 8
```

Now `"cat"` is mapped to slot 8.

If another key maps to the same index, a collision occurs, handled by chaining or probing.

Example Step by Step

Suppose a table of size 5.

Keys: `"red"`, `"blue"`, `"green"`

Key	Hash Value	Index (`% 5`)
red	432	2
blue	107	2 (collision)
green	205	0

We see `"red"` and `"blue"` collide at index 2.

Tiny Code (Python)

```
def simple_hash(key):
    return sum(ord(c) for c in key)

def map_keys(keys, size=5):
    table = [[] for _ in range(size)]
    for k in keys:
        idx = simple_hash(k) % size
        table[idx].append(k)
        print(f"Key: {k:6} -> Index: {idx}")
    return table

keys = ["red", "blue", "green"]
table = map_keys(keys)
```

Output:

```
Key: red    -> Index: 2
Key: blue   -> Index: 2
Key: green  -> Index: 0
```

Why It Matters

- Enables constant-time average lookup and insertion
- Forms the backbone of hash tables, dictionaries, caches
- Shows tradeoffs between hash quality and collision handling

A Gentle Proof (Why It Works)

If a hash function distributes keys uniformly, expected number of keys per slot is $\frac{n}{m}$.

Thus, expected lookup time:

$$E[T] = O(1 + \frac{n}{m})$$

For well-chosen m and good h, $E[T] \approx O(1)$.

Try It Yourself

1. Map `["cat", "dog", "bat", "rat"]` to a table of size 7.
2. Observe collisions and try a larger table.
3. Replace `sum(ord(c))` with a polynomial hash:

$$h(\text{key}) = \sum c_i \times 31^i$$

4. Compare distribution quality.

Test Cases

Keys	Table Size	Result (Indices)
[“a”, “b”, “c”]	3	1, 2, 0
[“hi”, “ih”]	5	collision (same sum)

Complexity

Operation	Time (Expected)	Space	Note
Insert	O(1)	O(n)	Average, good hash
Search	O(1)	O(n)	With uniform hashing
Delete	O(1)	O(n)	Same cost as lookup

A Hash Function Mapper makes hashing tangible, you watch strings become slots, collisions emerge, and order dissolve into probability and math.

76 Binary Tree Builder

A Binary Tree Builder illustrates how hierarchical data structures are constructed by linking nodes with left and right children.

What Problem Are We Solving?

Linear structures like arrays and lists can't efficiently represent hierarchical relationships. When you need ordering, searching, and hierarchical grouping, a binary tree provides the foundation.

Goal: Understand how nodes are connected to form a tree and how recursive structure emerges naturally.

How It Works (Plain Language)

A binary tree is made of nodes. Each node has:

- a value
- a left child
- a right child

To build a tree:

1. Start with a root node
2. Recursively insert new nodes:
    - If value $<$ current $\rightarrow$ go left
    - Else $\rightarrow$ go right
3. Repeat until you find a null link

This produces a Binary Search Tree (BST), maintaining order property.

Example Step by Step

Insert values: `[10, 5, 15, 3, 7, 12, 18]`

Process:

```
10
  5
     3
     7
  15
      12
      18
```

Traversal orders:

- Inorder: 3, 5, 7, 10, 12, 15, 18
- Preorder: 10, 5, 3, 7, 15, 12, 18
- Postorder: 3, 7, 5, 12, 18, 15, 10

Tiny Code (Python)

```
class Node:
    def __init__(self, value):
        self.value = value
        self.left = None
        self.right = None

class BST:
    def __init__(self):
        self.root = None

    def insert(self, value):
        self.root = self._insert(self.root, value)

    def _insert(self, node, value):
        if node is None:
            return Node(value)
        if value < node.value:
            node.left = self._insert(node.left, value)
        else:
            node.right = self._insert(node.right, value)
        return node

    def inorder(self, node):
        if node:
            self.inorder(node.left)
            print(node.value, end=" ")
            self.inorder(node.right)

# Demo
tree = BST()
for val in [10, 5, 15, 3, 7, 12, 18]:
    tree.insert(val)
tree.inorder(tree.root)
```

Output: `3 5 7 10 12 15 18`

Why It Matters

- Core structure for search trees, heaps, and expression trees

- Forms basis for balanced trees (AVL, Red-Black)
- Enables divide-and-conquer recursion naturally

A Gentle Proof (Why It Works)

A binary search tree maintains the invariant:

$$\forall \text{node},\ v : \Big\{ v_{\text{left}} < v_{\text{root}} < v_{\text{right}}$$

Insertion preserves this by recursive placement. Each insertion follows a single path of height h, so time is $O(h)$. For balanced trees, $h = O(\log n)$.

Try It Yourself

1. Insert `[8, 3, 10, 1, 6, 14, 4, 7, 13]`.
2. Draw the tree structure.
3. Perform inorder traversal (should print sorted order).
4. Compare with unbalanced insertion order.

Test Cases

Input Sequence	Inorder Traversal
[10, 5, 15, 3, 7]	3, 5, 7, 10, 15
[2, 1, 3]	1, 2, 3
[5]	5

Complexity

Operation	Time (Avg)	Time (Worst)	Space
Insert	O(log n)	O(n)	O(n)
Search	O(log n)	O(n)	O(1)
Delete	O(log n)	O(n)	O(1)
Traverse	O(n)	O(n)	O(n)

A Binary Tree Builder reveals order within hierarchy, each node a decision, each branch a story of lesser and greater.

77 Heap Structure Demo

A Heap Structure Demo helps you visualize how binary heaps organize data to always keep the smallest or largest element at the top, enabling fast priority access.

What Problem Are We Solving?

We often need a structure that quickly retrieves the minimum or maximum element, like in priority queues or scheduling. Sorting every time is wasteful. A heap maintains partial order so the root is always extreme, and rearrangement happens locally.

Goal: Understand how insertion and removal maintain the heap property.

How It Works (Plain Language)

A binary heap is a complete binary tree stored as an array. Each node satisfies:

- Min-heap: parent children
- Max-heap: parent children

Insertion and deletion are handled with *sift up* and *sift down* operations.

Insert (Heapify Up)

1. Add new element at the end
2. Compare with parent
3. Swap if violates heap property
4. Repeat until heap property holds

Remove Root (Heapify Down)

1. Replace root with last element
2. Compare with children
3. Swap with smaller (min-heap) or larger (max-heap) child
4. Repeat until property restored

Example Step by Step (Min-Heap)

Insert `[10, 4, 15, 2]`

1. `[10]`
2. `[10, 4]` → swap(4, 10) → `[4, 10]`
3. `[4, 10, 15]` (no swap)
4. `[4, 10, 15, 2]` → swap(2, 10) → swap(2, 4) → `[2, 4, 15, 10]`

Final heap (array): `[2, 4, 15, 10]` Tree view:

```
    2
   / \
  4   15
 /
10
```

Tiny Code (Python)

```python
import heapq

def heap_demo():
    heap = []
    for x in [10, 4, 15, 2]:
        heapq.heappush(heap, x)
        print("Insert", x, "→", heap)
    while heap:
        print("Pop:", heapq.heappop(heap), "→", heap)

heap_demo()
```

Output:

```
Insert 10 → [10]
Insert 4 → [4, 10]
Insert 15 → [4, 10, 15]
Insert 2 → [2, 4, 15, 10]
Pop: 2 → [4, 10, 15]
Pop: 4 → [10, 15]
Pop: 10 → [15]
Pop: 15 → []
```

Why It Matters

- Enables priority queues (task schedulers, Dijkstra)
- Supports O(1) access to min/max
- Keeps O(log n) insertion/removal cost
- Basis for Heapsort

A Gentle Proof (Why It Works)

Let $h = \lfloor \log_2 n \rfloor$ be heap height. Each insert and delete moves along one path of height h. Thus:

$$T_{\text{insert}} = T_{\text{delete}} = O(\log n)$$
$$T_{\text{find-min}} = O(1)$$

Try It Yourself

1. Insert `[7, 2, 9, 1, 5]` into a min-heap
2. Trace swaps on paper
3. Remove min repeatedly and record order (should be sorted ascending)
4. Repeat for max-heap version

Test Cases

Operation	Input	Output (Heap)
Insert	[5, 3, 8]	[3, 5, 8]
Pop	[3, 5, 8]	Pop 3 → [5, 8]
Insert	[10, 2, 4]	[2, 10, 4]

Complexity

Operation	Time	Space	Note
Insert	O(log n)	O(n)	Percolate up
Delete	O(log n)	O(n)	Percolate down
Find Min/Max	O(1)	O(1)	Root access
Build Heap	O(n)	O(n)	Bottom-up heapify

A Heap Structure Demo shows order through shape, every parent above its children, every insertion a climb toward balance.

78 Union-Find Concept

A Union-Find Concept (also called Disjoint Set Union, DSU) demonstrates how to efficiently manage dynamic grouping, deciding whether elements belong to the same set and merging sets when needed.

What Problem Are We Solving?

In many problems, we need to track connected components, e.g. in graphs, social networks, or Kruskal's MST. We want to answer two operations efficiently:

- Find(x): which group is x in?
- Union(x, y): merge the groups of x and y

Naive approaches (like scanning arrays) cost too much. Union-Find structures solve this in *almost constant time* using parent pointers and path compression.

How It Works (Plain Language)

Each element points to a parent. The root is the representative of its set. If two elements share the same root, they're in the same group.

Operations:

1. Find(x): Follow parent pointers until reaching a root (node where `parent[x] == x`) Use path compression to flatten paths for next time
2. Union(x, y): Find roots of x and y If different, attach one root to the other (merge sets) Optionally, use union by rank/size to keep tree shallow

Example Step by Step

Start with `{1}, {2}, {3}, {4}`

Perform:

```
Union(1, 2) → {1,2}, {3}, {4}
Union(3, 4) → {1,2}, {3,4}
Union(2, 3) → {1,2,3,4}
```

All now connected under one root.

If `Find(4)` → returns `1` (root of its set)

Tiny Code (Python)

```
class UnionFind:
    def __init__(self, n):
        self.parent = [i for i in range(n)]
        self.rank = [0] * n

    def find(self, x):
        if self.parent[x] != x:
            self.parent[x] = self.find(self.parent[x])  # Path compression
        return self.parent[x]

    def union(self, x, y):
        rx, ry = self.find(x), self.find(y)
        if rx == ry:
            return
        if self.rank[rx] < self.rank[ry]:
            self.parent[rx] = ry
        elif self.rank[rx] > self.rank[ry]:
            self.parent[ry] = rx
        else:
            self.parent[ry] = rx
            self.rank[rx] += 1

# Demo
uf = UnionFind(5)
uf.union(0, 1)
uf.union(2, 3)
uf.union(1, 2)
print([uf.find(i) for i in range(5)])
```

Output: `[0, 0, 0, 0, 4]`

Why It Matters

- Foundation for Kruskal's Minimum Spanning Tree

- Detects cycles in undirected graphs
- Efficient for connectivity queries in dynamic graphs
- Used in percolation, image segmentation, clustering

A Gentle Proof (Why It Works)

Each operation has amortized cost given by the inverse Ackermann function $\alpha(n)$, practically constant.

$$T_{\text{find}}(n), T_{\text{union}}(n) = O(\alpha(n))$$

Because path compression ensures every node points closer to root each time, flattening structure to near-constant depth.

Try It Yourself

1. Start with `{0}, {1}, {2}, {3}, {4}`
2. Apply: `Union(0,1), Union(2,3), Union(1,2)`
3. Query `Find(3)` $\rightarrow$ should match root of `0`
4. Print parent array after each operation

Test Cases

Operation Sequence	Resulting Sets
Union(1, 2), Union(3, 4)	{1,2}, {3,4}, {0}
Union(2, 3)	{0}, {1,2,3,4}
Find(4)	Root = 1 (or 0)

Complexity

Operation	Amortized Time	Space	Notes
Find	$O(\alpha(n))$	$O(n)$	Path compression
Union	$O(\alpha(n))$	$O(n)$	With rank heuristic
Connected(x, y)	$O(\alpha(n))$	$O(1)$	Via root comparison

A Union-Find Concept turns disjoint sets into a living network, connections formed and flattened, unity discovered through structure.

79 Graph Representation Demo

A Graph Representation Demo reveals how graphs can be encoded in data structures, showing the tradeoffs between adjacency lists, matrices, and edge lists.

What Problem Are We Solving?

Graphs describe relationships, roads between cities, links between websites, friendships in a network. But before we can run algorithms (like BFS, Dijkstra, or DFS), we need a representation that matches the graph's density, size, and operations.

Goal: Understand how different representations encode edges and how to choose the right one.

How It Works (Plain Language)

A graph is defined as:

$$G = (V, E)$$

where:

- $V =$ set of vertices
- $E =$ set of edges (pairs of vertices)

We can represent G in three main ways:

1. Adjacency Matrix
    - 2D array of size $|V| \times |V|$
    - Entry $(i, j) = 1$ if edge (i, j) exists, else 0
2. Adjacency List
    - For each vertex, a list of its neighbors
    - Compact for sparse graphs
3. Edge List
    - Simple list of all edges
    - Easy to iterate, hard for quick lookup

Example Step by Step

Consider an undirected graph:

```
Vertices: {A, B, C, D}
Edges: {(A, B), (A, C), (B, D)}
```

Adjacency Matrix

	A	B	C	D
A	0	1	1	0
B	1	0	0	1
C	1	0	0	0
D	0	1	0	0

Adjacency List

```
A: [B, C]
B: [A, D]
C: [A]
D: [B]
```

Edge List

```
[(A, B), (A, C), (B, D)]
```

Tiny Code (Python)

```python
from collections import defaultdict

# Adjacency List
graph = defaultdict(list)
edges = [("A", "B"), ("A", "C"), ("B", "D")]

for u, v in edges:
    graph[u].append(v)
    graph[v].append(u)  # undirected
```

```
print("Adjacency List:")
for node, neighbors in graph.items():
    print(f"{node}: {neighbors}")

# Adjacency Matrix
vertices = ["A", "B", "C", "D"]
n = len(vertices)
matrix = [[0]*n for _ in range(n)]
index = {v: i for i, v in enumerate(vertices)}

for u, v in edges:
    i, j = index[u], index[v]
    matrix[i][j] = matrix[j][i] = 1

print("\nAdjacency Matrix:")
for row in matrix:
    print(row)
```

Output:

```
Adjacency List:
A: ['B', 'C']
B: ['A', 'D']
C: ['A']
D: ['B']

Adjacency Matrix:
[0, 1, 1, 0]
[1, 0, 0, 1]
[1, 0, 0, 0]
[0, 1, 0, 0]
```

Why It Matters

- Adjacency matrix → fast lookup ($O(1)$), high space ($O(V^2)$)
- Adjacency list → efficient for sparse graphs ($O(V + E)$)
- Edge list → simple to iterate, ideal for algorithms like Kruskal

Choosing wisely impacts performance of every algorithm on the graph.

A Gentle Proof (Why It Works)

Let V be number of vertices, E edges.

Representation	Storage	Edge Check	Iteration
Adjacency Matrix	$O(V^2)$	$O(1)$	$O(V^2)$
Adjacency List	$O(V+E)$	$O(\deg(v))$	$O(V+E)$
Edge List	$O(E)$	$O(E)$	$O(E)$

Sparse graphs ($E \ll V^2$) $\rightarrow$ adjacency list preferred. Dense graphs ($E \approx V^2$) $\rightarrow$ adjacency matrix is fine.

Try It Yourself

1. Draw a graph with 5 nodes, 6 edges
2. Write all three representations
3. Compute storage cost
4. Pick best format for BFS vs Kruskal's MST

Test Cases

Graph Type	Representation	Benefit
Sparse	List	Space efficient
Dense	Matrix	Constant lookup
Weighted	Edge List	Easy sorting

Complexity

Operation	Matrix	List	Edge List
Space	$O(V^2)$	$O(V+E)$	$O(E)$
Add Edge	$O(1)$	$O(1)$	$O(1)$
Check Edge	$O(1)$	$O(\deg(v))$	$O(E)$
Iterate	$O(V^2)$	$O(V+E)$	$O(E)$

A Graph Representation Demo shows the blueprint of connection, the same network, three different lenses: matrix, list, or edge table.

80 Trie Structure Visualizer

A Trie Structure Visualizer helps you see how strings and prefixes are stored efficiently, one character per edge, building shared paths for common prefixes.

What Problem Are We Solving?

When you need to store and search many strings, especially by prefix, linear scans or hash tables aren't ideal. We want something that makes prefix queries fast and memory use efficient through shared structure.

A trie (prefix tree) does exactly that, storing strings as paths, reusing common prefixes.

Goal: Understand how each character extends a path and how search and insert work along edges.

How It Works (Plain Language)

A trie starts with an empty root node. Each edge represents a character. Each node may have multiple children, one for each possible next character.

To insert a word:

1. Start at root
2. For each character:
    - If it doesn't exist, create a new child
    - Move to that child
3. Mark last node as "end of word"

To search:

1. Start at root
2. Follow edges by each character
3. If path exists and end is marked, word found

Example Step by Step

Insert `cat`, `car`, `dog`

```
(root)
    c
        a
            t*
            r*
    d
         o
             g*
```

Asterisk `*` marks word end. Common prefix `ca` is shared.

Search `"car"`:

- `c`
- `a`
- `r`
- End marked → found

Search `"cap"`:

- `c`
- `a`
- `p` → not found

Tiny Code (Python)

```
class TrieNode:
    def __init__(self):
        self.children = {}
        self.is_end = False

class Trie:
    def __init__(self):
        self.root = TrieNode()

    def insert(self, word):
        node = self.root
```

```
        for ch in word:
            if ch not in node.children:
                node.children[ch] = TrieNode()
            node = node.children[ch]
        node.is_end = True

    def search(self, word):
        node = self.root
        for ch in word:
            if ch not in node.children:
                return False
            node = node.children[ch]
        return node.is_end

# Demo
trie = Trie()
for w in ["cat", "car", "dog"]:
    trie.insert(w)
print(trie.search("car"))  # True
print(trie.search("cap"))  # False
```

Why It Matters

- Enables prefix search, autocomplete, dictionary lookup
- Avoids recomputing prefixes
- Efficient for string-intensive applications
- Foundation for compressed tries, DAWGs, and suffix trees

A Gentle Proof (Why It Works)

Each character in word w follows one path in trie. Insert cost $= O(|w|)$, Search cost $= O(|w|)$.

For n words of average length L, total nodes $O(nL)$.

Prefix query cost $= O(p)$, where $p =$ prefix length.

Try It Yourself

1. Insert `["cat", "cap", "can", "dog"]`
2. Draw tree paths
3. Query prefixes `"ca"` and `"do"`

4. Count total nodes created

Test Cases

Operation	Input	Output
Insert	“cat”, “car”	Shared path “ca”
Search	“car”	True
Search	“cap”	False
Prefix	“ca”	Exists

Complexity

Operation	Time	Space	Note
Insert	O(L)	O(L)	L = length of word
Search	O(L)	O(1)	Follow path
Prefix Query	O(p)	O(1)	Shared traversal

A Trie Structure Visualizer shows structure born from language, every word a path, every prefix a meeting point, every branch a shared memory.

Section 9. Graphs and Trees overview

81 Graph Model Constructor

A Graph Model Constructor is how we formally build graphs, sets of vertices connected by edges, to represent relationships, networks, or structures in the world.

What Problem Are We Solving?

We often face problems where elements are connected, roads between cities, friendships in a network, dependencies in a project. To reason about these, we need a way to model entities (vertices) and connections (edges).

The Graph Model Constructor provides the blueprint for turning real-world relationships into graph data structures we can analyze.

How It Works (Plain Language)

A graph is defined as:

$$G = (V, E)$$

where

- V = set of vertices (nodes)
- E = set of edges (connections) between vertices

Each edge can be:

- Undirected: (u, v) means u and v are connected both ways
- Directed: (u, v) means a one-way connection from u to v

You can build graphs in multiple ways:

1. Edge List – list of pairs (u, v)
2. Adjacency List – dictionary of node $\rightarrow$ neighbor list
3. Adjacency Matrix – 2D table of connections (1 = edge, 0 = none)

Example

Input relationships

```
A connected to B
A connected to C
B connected to C
C connected to D
```

Vertices

```
V = {A, B, C, D}
```

Edges

```
E = {(A, B), (A, C), (B, C), (C, D)}
```

Edge List

```
[(A, B), (A, C), (B, C), (C, D)]
```

Adjacency List

```
A: [B, C]
B: [A, C]
C: [A, B, D]
D: [C]
```

Adjacency Matrix

	A	B	C	D
A	0	1	1	0
B	1	0	1	0
C	1	1	0	1
D	0	0	1	0

Tiny Code (Python)

```
def build_graph(edge_list):
    graph = {}
    for u, v in edge_list:
        graph.setdefault(u, []).append(v)
        graph.setdefault(v, []).append(u)  # undirected
    return graph

edges = [("A","B"),("A","C"),("B","C"),("C","D")]
graph = build_graph(edges)
for node, neighbors in graph.items():
    print(node, ":", neighbors)
```

Output

```
A : ['B', 'C']
B : ['A', 'C']
C : ['A', 'B', 'D']
D : ['C']
```

Why It Matters

- Graphs let us model relationships in any domain: roads, social networks, dependencies, knowledge.
- Once constructed, you can apply graph algorithms, BFS, DFS, shortest paths, spanning trees, connectivity, to solve real problems.
- The constructor phase defines how efficiently later algorithms run.

A Gentle Proof (Why It Works)

Given n vertices and m edges, we represent each edge (u, v) by linking u and v. Construction time $= O(n + m)$, since each vertex and edge is processed once.

Adjacency list size $= O(n + m)$ Adjacency matrix size $= O(n^2)$

Thus, adjacency lists are more space-efficient for sparse graphs, while matrices offer constant-time edge lookups for dense graphs.

Try It Yourself

1. Build a graph of 5 cities and their direct flights.
2. Represent it as both edge list and adjacency list.
3. Count number of edges and neighbors per vertex.
4. Draw the resulting graph on paper.

Test Cases

Input	Representation	Key Property
`[(1,2), (2,3)]`	Adjacency List	3 vertices, 2 edges
Directed edges	Adjacency List	One-way links only
Fully connected 3 nodes	Adjacency Matrix	All 1s except diagonal

Complexity

Representation	Space	Lookup	Iteration
Edge List	O(m)	O(m)	O(m)
Adjacency List	O(n + m)	O(deg(v))	O(m)
Adjacency Matrix	$O(n^2)$	O(1)	$O(n^2)$

A Graph Model Constructor builds the world of connections, from abstract relations to concrete data structures, forming the backbone of every graph algorithm that follows.

82 Adjacency Matrix Builder

An Adjacency Matrix Builder constructs a 2D grid representation of a graph, showing whether pairs of vertices are connected. It's a simple and powerful way to capture all edges in a compact mathematical form.

What Problem Are We Solving?

We need a fast, systematic way to test if two vertices are connected. While adjacency lists are space-efficient, adjacency matrices make edge lookup $O(1)$, perfect when connections are dense or frequent checks are needed.

The Adjacency Matrix Builder gives us a table-like structure to store edge information clearly.

How It Works (Plain Language)

An adjacency matrix is an $n \times n$ table for a graph with n vertices:

$$A[i][j] = \begin{cases} 1, & \text{if there is an edge from } i \text{ to } j, \\ 0, & \text{otherwise.} \end{cases}$$

- For undirected graphs, the matrix is symmetric: $A[i][j] = A[j][i]$
- For directed graphs, symmetry may not hold
- For weighted graphs, store weights instead of 1s

Example

Vertices: $V = A, B, C, D$ Edges: $(A, B), (A, C), (B, C), (C, D)$

Adjacency Matrix (Undirected)

	A	B	C	D
A	0	1	1	0
B	1	0	1	0
C	1	1	0	1
D	0	0	1	0

To check if A and C are connected, test $A[A][C] = 1$

Tiny Code (Python)

```
def adjacency_matrix(vertices, edges, directed=False):
    n = len(vertices)
    index = {v: i for i, v in enumerate(vertices)}
    A = [[0] * n for _ in range(n)]

    for u, v in edges:
        i, j = index[u], index[v]
        A[i][j] = 1
        if not directed:
            A[j][i] = 1
    return A
```

```
vertices = ["A", "B", "C", "D"]
edges = [("A", "B"), ("A", "C"), ("B", "C"), ("C", "D")]
A = adjacency_matrix(vertices, edges)
for row in A:
    print(row)
```

Output

```
[0, 1, 1, 0]
[1, 0, 1, 0]
[1, 1, 0, 1]
[0, 0, 1, 0]
```

Why It Matters

- Constant-time check for edge existence
- Simple mathematical representation for graph algorithms and proofs
- Foundation for matrix-based graph algorithms like:
  - Floyd–Warshall (all-pairs shortest path)
  - Adjacency matrix powers (reachability)
  - Spectral graph theory (Laplacian, eigenvalues)

A Gentle Proof (Why It Works)

Each vertex pair (u, v) corresponds to one matrix cell $A[i][j]$. We visit each edge once to set two symmetric entries (undirected) or one (directed). Thus:

- Time complexity: $O(n^2)$ to initialize, $O(m)$ to fill
- Space complexity: $O(n^2)$

This tradeoff is worth it when $m \approx n^2$ (dense graphs).

Try It Yourself

1. Build an adjacency matrix for a directed triangle (A→B, B→C, C→A)
2. Modify it to add a self-loop on B
3. Check if $A[B][B] = 1$
4. Compare the symmetry of directed vs undirected graphs

Test Cases

Graph Type	Edges	Symmetry	Value
Undirected	(A,B)	Symmetric	A[B][A] = 1
Directed	(A,B)	Not symmetric	A[B][A] = 0
Weighted	(A,B,w=5)	Value stored	A[A][B] = 5

Complexity

Operation	Time	Space
Build Matrix	$O(n^2)$	$O(n^2)$
Edge Check	$O(1)$	-
Iterate Neighbors	$O(n)$	-

An Adjacency Matrix Builder turns a graph into a table, a universal structure for analysis, efficient queries, and algorithmic transformation.

83 Adjacency List Builder

An Adjacency List Builder constructs a flexible representation of a graph, storing each vertex's neighbors in a list. It's memory-efficient for sparse graphs and intuitive for traversal-based algorithms.

What Problem Are We Solving?

We need a way to represent graphs compactly while still supporting quick traversal of connected vertices. When graphs are sparse (few edges compared to n^2), an adjacency matrix wastes space. An adjacency list focuses only on existing edges, making it both lean and intuitive.

How It Works (Plain Language)

Each vertex keeps a list of all vertices it connects to. In a directed graph, edges point one way; in an undirected graph, each edge appears twice.

For a graph with vertices V and edges E, the adjacency list is:

$$\text{Adj}[u] = v \mid (u, v) \in E$$

You can think of it as a dictionary (or map) where each key is a vertex, and its value is a list of neighbors.

Example

Vertices: $V = A, B, C, D$ Edges: $(A, B), (A, C), (B, C), (C, D)$

Adjacency List (Undirected)

```
A: [B, C]
B: [A, C]
C: [A, B, D]
D: [C]
```

Tiny Code (Python)

```python
def adjacency_list(vertices, edges, directed=False):
    adj = {v: [] for v in vertices}
    for u, v in edges:
        adj[u].append(v)
        if not directed:
            adj[v].append(u)
    return adj

vertices = ["A", "B", "C", "D"]
edges = [("A", "B"), ("A", "C"), ("B", "C"), ("C", "D")]

graph = adjacency_list(vertices, edges)
for node, nbrs in graph.items():
    print(f"{node}: {nbrs}")
```

Output

```
A: ['B', 'C']
B: ['A', 'C']
C: ['A', 'B', 'D']
D: ['C']
```

Why It Matters

- Space-efficient for sparse graphs ($O(n + m)$)
- Natural fit for DFS, BFS, and pathfinding
- Easy to modify and extend (weighted edges, labels)
- Forms the basis for graph traversal algorithms and network models

A Gentle Proof (Why It Works)

Each edge is stored exactly once (directed) or twice (undirected). If n is the number of vertices and m is the number of edges:

- Initialization: $O(n)$
- Insertion: $O(m)$
- Total Space: $O(n + m)$

No wasted space for missing edges, each list grows only with actual neighbors.

Try It Yourself

1. Build an adjacency list for a directed graph with edges (A→B, A→C, C→A)
2. Add a new vertex E with no edges; confirm it still appears as `E: []`
3. Count how many total neighbors there are, it should match the edge count

Test Cases

Graph Type	Input Edges	Representation
Undirected	(A,B)	A: [B], B: [A]
Directed	(A,B)	A: [B], B: []
Weighted	(A,B,5)	A: [(B,5)]

Complexity

Operation	Time	Space
Build List	$O(n + m)$	$O(n + m)$
Check Neighbors	$O(\deg(v))$	-
Add Edge	$O(1)$	-
Remove Edge	$O(\deg(v))$	-

An Adjacency List Builder keeps your graph representation clean and scalable, perfect for algorithms that walk, explore, and connect the dots across large networks.

84 Degree Counter

A Degree Counter computes how many edges touch each vertex in a graph. For undirected graphs, the degree is the number of neighbors. For directed graphs, we distinguish between in-degree and out-degree.

What Problem Are We Solving?

We want to know how connected each vertex is. Degree counts help answer structural questions:

- Is the graph regular (all vertices same degree)?
- Are there sources (zero in-degree) or sinks (zero out-degree)?
- Which node is a hub in a network?

These insights are foundational for traversal, centrality, and optimization.

How It Works (Plain Language)

For each edge (u, v):

- Undirected: increment `degree[u]` and `degree[v]`
- Directed: increment `out_degree[u]` and `in_degree[v]`

When done, every vertex has its connection count.

Example

Undirected graph:

$$V = A, B, C, D, \quad E = (A, B), (A, C), (B, C), (C, D)$$

Vertex	Degree
A	2
B	2
C	3
D	1

Directed version:

- In-degree(A)=1 (from C), Out-degree(A)=2 (to B,C)

Tiny Code (Python)

```
def degree_counter(vertices, edges, directed=False):
    if directed:
        indeg = {v: 0 for v in vertices}
        outdeg = {v: 0 for v in vertices}
        for u, v in edges:
            outdeg[u] += 1
            indeg[v] += 1
        return indeg, outdeg
    else:
        deg = {v: 0 for v in vertices}
        for u, v in edges:
            deg[u] += 1
            deg[v] += 1
        return deg

vertices = ["A", "B", "C", "D"]
edges = [("A","B"), ("A","C"), ("B","C"), ("C","D")]
print(degree_counter(vertices, edges))
```

Output

```
{'A': 2, 'B': 2, 'C': 3, 'D': 1}
```

Why It Matters

- Reveals connectivity patterns
- Identifies isolated nodes
- Enables graph classification (regular, sparse, dense)
- Essential for graph algorithms (topological sort, PageRank, BFS pruning)

A Gentle Proof (Why It Works)

In any undirected graph, the sum of all degrees equals twice the number of edges:

$$\sum_{v \in V} \deg(v) = 2|E|$$

In directed graphs:

$$\sum_{v \in V} \text{in}(v) = \sum_{v \in V} \text{out}(v) = |E|$$

These equalities guarantee correctness, every edge contributes exactly once (or twice if undirected).

Try It Yourself

1. Create an undirected graph with edges (A,B), (B,C), (C,A)
    - Verify all vertices have degree 2
2. Add an isolated vertex D
    - Check that its degree is 0
3. Convert to directed edges and count in/out separately

Test Cases

Graph	Input Edges	Output
Undirected	(A,B), (A,C)	A:2, B:1, C:1
Directed	(A,B), (B,C)	in(A)=0, out(A)=1; in(C)=1, out(C)=0
Isolated Node	(A,B), V={A,B,C}	C:0

Complexity

Operation	Time	Space
Count Degrees	$O(m)$	$O(n)$
Lookup Degree	$O(1)$	-

A Degree Counter exposes the heartbeat of a graph, showing which nodes are busy, which are lonely, and how the network's structure unfolds.

85 Path Existence Tester

A Path Existence Tester checks whether there is a route between two vertices in a graph, whether you can travel from a source to a destination by following edges.

What Problem Are We Solving?

In many scenarios, navigation, dependency resolution, communication, the essential question is: "Can we get from A to B?"

This is not about finding the *shortest* path, but simply checking if a path *exists* at all.

Examples:

- Is a file accessible from the root directory?
- Can data flow between two nodes in a network?
- Does a dependency graph contain a reachable edge?

How It Works (Plain Language)

We use graph traversal to explore from the source node. If the destination is reached, a path exists.

Steps:

1. Choose a traversal (DFS or BFS)
2. Start from source node `s`
3. Mark visited nodes
4. Traverse neighbors recursively (DFS) or level by level (BFS)
5. If destination `t` is visited, a path exists

Example

Graph:

$$V = A, B, C, D, \quad E = (A, B), (B, C), (C, D)$$

Query: Is there a path from A to D?

Traversal (DFS or BFS):

- Start at A → B → C → D
- D is reached → Path exists

Query: Is there a path from D to A?

- Start at D → no outgoing edges → No path

Tiny Code (Python)

```
from collections import deque

def path_exists(graph, source, target):
    visited = set()
    queue = deque([source])

    while queue:
        node = queue.popleft()
        if node == target:
            return True
        if node in visited:
            continue
        visited.add(node)
        queue.extend(graph.get(node, []))
    return False

graph = {
    "A": ["B"],
    "B": ["C"],
    "C": ["D"],
    "D": []
}
print(path_exists(graph, "A", "D"))  # True
print(path_exists(graph, "D", "A"))  # False
```

Why It Matters

- Core to graph connectivity
- Used in cycle detection, topological sorting, and reachability queries
- Foundational in AI search, routing, compilers, and network analysis

A Gentle Proof (Why It Works)

Let the graph be $G = (V, E)$ and traversal be BFS or DFS. Every edge (u, v) is explored once. If a path exists, traversal will eventually reach all nodes in the connected component of `s`. Thus, if `t` lies in that component, it will be discovered.

Traversal completeness ensures correctness.

Try It Yourself

1. Build a directed graph $A \to B \to C$, and check $A \to C$ and $C \to A$.
2. Add an extra edge $C \to A$.
    - Now the graph is strongly connected.
    - Every node should reach every other node.
3. Visualize traversal using a queue or recursion trace.

Test Cases

Graph	Source	Target	Result
A→B→C	A	C	True
A→B→C	C	A	False
A B	A	B	True
Disconnected	A	D	False

Complexity

Operation	Time	Space
BFS / DFS	$O(n+m)$	$O(n)$

n = vertices, m = edges.

A Path Existence Tester is the simplest yet most powerful diagnostic for graph connectivity, revealing whether two points belong to the same connected world.

86 Tree Validator

A Tree Validator checks whether a given graph satisfies the defining properties of a tree: it is connected and acyclic.

What Problem Are We Solving?

We often encounter structures that *look* like trees, but we must confirm they truly are. For example:

- Can this dependency graph be represented as a tree?
- Is the given parent–child relation a valid hierarchy?
- Does this undirected graph contain cycles or disconnected parts?

A Tree Validator formalizes that check.

A tree must satisfy:

1. Connectivity: every vertex reachable from any other.
2. Acyclicity: no cycles exist.
3. (Equivalently for undirected graphs)

$$|E| = |V| - 1$$

How It Works (Plain Language)

We can validate using traversal and counting:

Method 1: DFS + Parent Check

1. Start DFS from any node.
2. Track visited nodes.
3. If a neighbor is visited *and not parent*, a cycle exists.
4. After traversal, check all nodes visited (connectedness).

Method 2: Edge–Vertex Property

1. Check if graph has exactly $|V| - 1$ edges.
2. Run DFS/BFS to ensure graph is connected.

Example

Graph 1:

$$V = A, B, C, D, \quad E = (A, B), (A, C), (B, D)$$

- $|V| = 4$, $|E| = 3$
- Connected, no cycle $\rightarrow$ Tree

Graph 2:

$$V = A, B, C, \quad E = (A, B), (B, C), (C, A)$$

- $|V| = 3$, $|E| = 3$
- Cycle present $\rightarrow$ Not a tree

Tiny Code (Python)

```
def is_tree(graph):
    n = len(graph)
    visited = set()
    parent = {}

    def dfs(node, par):
        visited.add(node)
        for nbr in graph[node]:
            if nbr == par:
                continue
```

```
            if nbr in visited:
                return False  # cycle detected
            if not dfs(nbr, node):
                return False
        return True

    # Start from first node
    start = next(iter(graph))
    if not dfs(start, None):
        return False

    # Check connectivity
    return len(visited) == n
```

Example:

```
graph = {
    "A": ["B", "C"],
    "B": ["A", "D"],
    "C": ["A"],
    "D": ["B"]
}
print(is_tree(graph))  # True
```

Why It Matters

Tree validation ensures:

- Hierarchies are acyclic
- Data structures (like ASTs, tries) are well-formed
- Network topologies avoid redundant links
- Algorithms relying on tree properties (DFS order, LCA, spanning tree) are safe

A Gentle Proof (Why It Works)

A connected graph without cycles is a tree. Inductive reasoning:

- Base: single node, zero edges, trivially a tree.
- Induction: adding one edge that connects a new node preserves acyclicity. If a cycle forms, it violates tree property.

Also, for undirected graph:

$$\text{Tree} \iff \text{Connected} \wedge |E| = |V| - 1$$

Try It Yourself

1. Draw a small graph with 4 nodes.
2. Add edges one by one.
    - After each addition, test if graph is still a tree.
3. Introduce a cycle and rerun validator.
4. Remove an edge and check connectivity failure.

Test Cases

Graph	Connected	Cycle	Tree
A–B–C			
A–B, B–C, C–A			
A–B, C			
Single Node			

Complexity

Operation	Time	Space
DFS	$O(n+m)$	$O(n)$

A Tree Validator ensures structure, order, and simplicity, the quiet geometry behind every hierarchy.

86 Tree Validator

A Tree Validator checks whether a given graph satisfies the defining properties of a tree: it is connected and acyclic.

What Problem Are We Solving?

We often encounter structures that *look* like trees, but we must confirm they truly are. For example:

- Can this dependency graph be represented as a tree?
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- Does this undirected graph contain cycles or disconnected parts?

A Tree Validator formalizes that check.

A tree must satisfy:

1. Connectivity: every vertex reachable from any other.
2. Acyclicity: no cycles exist.
3. (Equivalently for undirected graphs)

$$|E| = |V| - 1$$

How It Works (Plain Language)

We can validate using traversal and counting.

Method 1: DFS + Parent Check

1. Start DFS from any node.
2. Track visited nodes.
3. If a neighbor is visited *and not parent*, a cycle exists.
4. After traversal, check all nodes visited (connectedness).

Method 2: Edge–Vertex Property

1. Check if graph has exactly $|V| - 1$ edges.
2. Run DFS or BFS to ensure graph is connected.

Example

Graph 1:

$$V = A, B, C, D, \quad E = (A, B), (A, C), (B, D)$$

- $|V| = 4$, $|E| = 3$
- Connected, no cycle $\rightarrow$ Tree

Graph 2:

$$V = A, B, C, \quad E = (A, B), (B, C), (C, A)$$

- $|V| = 3$, $|E| = 3$
- Cycle present → Not a tree

Tiny Code (Python)

```
def is_tree(graph):
    n = len(graph)
    visited = set()
    parent = {}

    def dfs(node, par):
        visited.add(node)
        for nbr in graph[node]:
            if nbr == par:
                continue
            if nbr in visited:
                return False  # cycle detected
            if not dfs(nbr, node):
                return False
        return True

    # Start from first node
    start = next(iter(graph))
    if not dfs(start, None):
        return False

    # Check connectivity
    return len(visited) == n
```

Example:

```
graph = {
    "A": ["B", "C"],
    "B": ["A", "D"],
    "C": ["A"],
    "D": ["B"]
}
print(is_tree(graph))  # True
```

Why It Matters

Tree validation ensures:

- Hierarchies are acyclic
- Data structures (like ASTs, tries) are well-formed
- Network topologies avoid redundant links
- Algorithms relying on tree properties (DFS order, LCA, spanning tree) are safe

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A connected graph without cycles is a tree. Inductive reasoning:

- Base: single node, zero edges, trivially a tree.
- Induction: adding one edge that connects a new node preserves acyclicity. If a cycle forms, it violates the tree property.

Also, for an undirected graph:

$$\text{Tree} \iff \text{Connected} \land |E| = |V| - 1$$

Try It Yourself

1. Draw a small graph with 4 nodes.
2. Add edges one by one.
    - After each addition, test if the graph is still a tree.
3. Introduce a cycle and rerun the validator.
4. Remove an edge and check for connectivity failure.

Test Cases

Graph	Connected	Cycle	Tree
A–B–C	Yes	No	Yes
A–B, B–C, C–A	Yes	Yes	No
A–B, C	No	No	No
Single Node	Yes	No	Yes

Complexity

Operation	Time	Space
DFS	$O(n+m)$	$O(n)$

A Tree Validator ensures structure, order, and simplicity, the quiet geometry behind every hierarchy.

87 Rooted Tree Builder

A Rooted Tree Builder constructs a tree from a given parent array or edge list, designating one node as the root and connecting all others accordingly.

What Problem Are We Solving?

Often we receive data in *flat* form—like a list of parent indices, database references, or parent–child pairs—and we need to reconstruct the actual tree structure.

For example:

- A parent array `[ -1, 0, 0, 1, 1, 2 ]` represents which node is parent of each.
- In file systems, each directory knows its parent; we need to rebuild the hierarchy.

The Rooted Tree Builder formalizes this reconstruction.

How It Works (Plain Language)

A parent array encodes each node's parent:

- `parent[i] = j` means node `j` is the parent of `i`.
- If `parent[i] = -1`, then `i` is the root.

Steps:

1. Find the root (the node with parent `-1`).
2. Initialize an adjacency list `children` for each node.
3. For each node `i`:
    - If `parent[i] != -1`, append `i` to `children[parent[i]]`.

4. Output the adjacency structure.

This gives a tree with parent–child relationships.

Example

Parent array:

```
Index:  0  1  2  3  4  5
Parent: -1  0  0  1  1  2
```

Interpretation:

- 0 is root.
- 1 and 2 are children of 0.
- 3 and 4 are children of 1.
- 5 is child of 2.

Tree:

```
0
  1
     3
     4
  2
      5
```

Tiny Code (Python)

```
def build_tree(parent):
    n = len(parent)
    children = [[] for _ in range(n)]
    root = None

    for i in range(n):
        if parent[i] == -1:
            root = i
        else:
            children[parent[i]].append(i)

    return root, children
```

Example:

```
parent = [-1, 0, 0, 1, 1, 2]
root, children = build_tree(parent)

print("Root:", root)
for i, c in enumerate(children):
    print(f"{i}: {c}")
```

Output:

```
Root: 0
0: [1, 2]
1: [3, 4]
2: [5]
3: []
4: []
5: []
```

Why It Matters

Tree reconstruction is foundational in:

- Compilers: abstract syntax tree (AST) reconstruction
- Databases: reconstructing hierarchical relationships
- Operating systems: file directory trees
- Organization charts: building hierarchies from parent–child data

It connects linear storage to hierarchical structure.

A Gentle Proof (Why It Works)

If the parent array satisfies:

- Exactly one root: one entry with `-1`
- All other nodes have exactly one parent
- The resulting structure is connected and acyclic

Then the output is a valid rooted tree:

$$|E| = |V| - 1, \text{ and exactly one node has no parent.}$$

Each child is linked once, forming a tree rooted at the unique node with `-1`.

Try It Yourself

1. Write your own parent array (e.g., `[ -1, 0, 0, 1, 2 ]`).
2. Convert it into a tree.
3. Draw the hierarchy manually.
4. Verify connectivity and acyclicity.

Test Cases

Parent Array	Root	Children Structure
[-1, 0, 0, 1, 1, 2]	0	0:[1,2], 1:[3,4], 2:[5]
[-1, 0, 1, 2]	0	0:[1], 1:[2], 2:[3]
[-1]	0	0:[]

Complexity

Operation	Time	Space
Build	$O(n)$	$O(n)$

The Rooted Tree Builder bridges the gap between flat data and hierarchical form, turning arrays into living structures.

88 Traversal Order Visualizer

A Traversal Order Visualizer shows how different tree traversals (preorder, inorder, postorder, level order) explore nodes, revealing the logic behind recursive and iterative visits.

What Problem Are We Solving?

When working with trees, the order of visiting nodes matters. Different traversals serve different goals:

- Preorder: process parent before children
- Inorder: process left child, then parent, then right child
- Postorder: process children before parent
- Level order: visit nodes breadth-first

Understanding these traversals helps in:

- Expression parsing
- File system navigation
- Tree printing and evaluation

A visualizer clarifies *when* and *why* each node is visited.

How It Works (Plain Language)

Consider a binary tree:

```
      A
     / \
    B   C
   / \
  D   E
```

Each traversal orders nodes differently:

Traversal	Order
Preorder	A, B, D, E, C
Inorder	D, B, E, A, C
Postorder	D, E, B, C, A
Level order	A, B, C, D, E

Visualization strategy:

- Start at the root.
- Use recursion (depth-first) or queue (breadth-first).
- Record each visit step.
- Output sequence in order visited.

Example Step by Step

Tree:

```
A
  B
     D
     E
  C
```

Preorder

1. Visit A
2. Visit B
3. Visit D
4. Visit E
5. Visit C

Sequence: A B D E C

Inorder

1. Traverse left subtree of A (B)
2. Traverse left of B (D) → visit D
3. Visit B
4. Traverse right of B (E) → visit E
5. Visit A
6. Visit right subtree (C)

Sequence: D B E A C

Tiny Code (Python)

```
class Node:
    def __init__(self, val):
        self.val = val
        self.left = None
        self.right = None

def preorder(root):
    if not root:
        return []
    return [root.val] + preorder(root.left) + preorder(root.right)

def inorder(root):
    if not root:
        return []
    return inorder(root.left) + [root.val] + inorder(root.right)

def postorder(root):
    if not root:
        return []
```

```
    return postorder(root.left) + postorder(root.right) + [root.val]

def level_order(root):
    if not root:
        return []
    queue = [root]
    result = []
    while queue:
        node = queue.pop(0)
        result.append(node.val)
        if node.left:
            queue.append(node.left)
        if node.right:
            queue.append(node.right)
    return result
```

Why It Matters

Traversal order determines:

- Computation sequence (evaluation, deletion, printing)
- Expression tree evaluation (postorder)
- Serialization/deserialization (preorder + inorder)
- Breadth-first exploration (level order)

Understanding traversal = understanding how algorithms move through structure.

A Gentle Proof (Why It Works)

Each traversal is a systematic walk:

- Preorder ensures root-first visitation.
- Inorder ensures sorted order in binary search trees.
- Postorder ensures children processed before parent.
- Level order ensures minimal depth-first layering.

Since each node is visited exactly once, correctness follows from recursion and induction.

Try It Yourself

1. Build a binary tree with 5 nodes.
2. Write out all four traversals by hand.
3. Trace recursive calls step by step.
4. Observe how order changes per traversal.

Test Cases

Traversal	Example Tree	Expected Order
Preorder	A-B-C	A B C
Inorder	A-B-C	B A C
Postorder	A-B-C	B C A
Level order	A-B-C	A B C

Complexity

Operation	Time	Space
DFS (Pre/In/Post)	$O(n)$	$O(h)$ (stack)
BFS (Level)	$O(n)$	$O(n)$ (queue)

The Traversal Order Visualizer turns abstract definitions into motion, showing how structure guides computation.

89 Edge Classifier

An Edge Classifier determines the type of each edge encountered during a graph traversal, whether it is a tree edge, back edge, forward edge, or cross edge. This classification helps us understand the structure and flow of a directed or undirected graph.

What Problem Are We Solving?

In graph algorithms, not all edges play the same role. When we traverse using DFS, we can interpret the relationship between vertices based on discovery times.

Edge classification helps answer questions like:

- Is there a cycle? (Look for back edges)

- How is the graph structured? (Tree vs forward edges)
- Is this DAG (Directed Acyclic Graph)? (No back edges)
- What's the hierarchical relation between nodes?

By tagging edges, we gain structural insight into traversal behavior.

How It Works (Plain Language)

During DFS, we assign each vertex:

- Discovery time when first visited.
- Finish time when exploration completes.

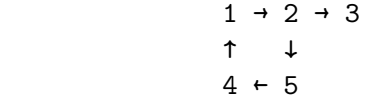
Each edge (u, v) is then classified as:

Type	Condition
Tree edge	v is first discovered by (u, v)
Back edge	v is ancestor of u (cycle indicator)
Forward edge	v is descendant of u, but already visited
Cross edge	v is neither ancestor nor descendant of u

In undirected graphs, only tree and back edges occur.

Example

Graph (directed):



During DFS starting at 1:

- (1,2): tree edge
- (2,3): tree edge
- (3,4): back edge (cycle 1–2–3–4–1)
- (2,5): tree edge
- (5,4): tree edge
- (4,1): back edge

So we detect cycles due to back edges.

Tiny Code (Python)

```
def classify_edges(graph):
    time = 0
    discovered = {}
    finished = {}
    classification = []

    def dfs(u):
        nonlocal time
        time += 1
        discovered[u] = time
        for v in graph[u]:
            if v not in discovered:
                classification.append(((u, v), "Tree"))
                dfs(v)
            elif v not in finished:
                classification.append(((u, v), "Back"))
            elif discovered[u] < discovered[v]:
                classification.append(((u, v), "Forward"))
            else:
                classification.append(((u, v), "Cross"))
        time += 1
        finished[u] = time

    for node in graph:
        if node not in discovered:
            dfs(node)
    return classification
```

Why It Matters

Edge classification underpins:

- Cycle detection (look for back edges)
- Topological sorting (DAGs have no back edges)
- DFS tree structure analysis
- Strongly connected component detection

It converts traversal into structural insight.

A Gentle Proof (Why It Works)

DFS imposes a temporal order on discovery and finish times. An edge (u, v) can only fall into one of the four categories because:

$$\text{Each vertex has a distinct discovery and finish time interval.}$$

By comparing intervals $(d[u], f[u])$ and $(d[v], f[v])$, we deduce whether v lies inside, before, or after u's traversal window.

Try It Yourself

1. Draw a small directed graph.
2. Assign discovery/finish times using DFS.
3. Compare intervals for each edge.
4. Label each edge as Tree, Back, Forward, or Cross.
5. Verify that DAGs have no back edges.

Test Cases

Edge	Type
(A, B)	Tree
(B, C)	Tree
(C, A)	Back
(B, D)	Tree
(D, E)	Tree
(E, B)	Back

Complexity

Operation	Time	Space
DFS Traversal	$O(n + m)$	$O(n)$
Classification	$O(m)$	$O(m)$

The Edge Classifier transforms traversal into topology, making invisible structures like cycles, hierarchies, and cross-links explicit.

90 Connectivity Checker

A Connectivity Checker determines whether a graph is connected, that is, whether every vertex can be reached from any other vertex. It's a fundamental diagnostic tool in graph theory and network analysis.

What Problem Are We Solving?

Connectivity tells us whether the graph forms a single whole or multiple isolated parts.

We often ask:

- Can all nodes communicate in this network?
- Is this maze solvable from start to end?
- Does this undirected graph form one component or many?
- For directed graphs: can we reach every vertex from every other vertex?

The Connectivity Checker gives a yes/no answer, and can also enumerate connected components.

How It Works (Plain Language)

Undirected Graph:

1. Pick a starting node.
2. Perform DFS or BFS, marking all reachable nodes.
3. After traversal, if all nodes are marked, the graph is connected.

Directed Graph:

- Use two traversals:

    1. Run DFS from any node. If not all nodes are visited, not strongly connected.
    2. Reverse all edges and run DFS again. If still not all nodes are visited, not strongly connected.

Alternatively, detect strongly connected components (SCCs) via Kosaraju's or Tarjan's algorithm.

Example (Undirected)

Graph 1:

```
1, 2, 3
|       |
4, 5, 6
```

All nodes reachable → Connected.

Graph 2:

```
1, 2    3, 4
```

Two separate parts → Not connected.

Example (Directed)

Graph:

```
1 → 2 → 3
↑       ↓
```

Every node reachable from every other → Strongly connected

Graph:

```
1 → 2 → 3
```

No path from 3 → 1 → Not strongly connected

Tiny Code (Python)

```
from collections import deque

def is_connected(graph):
    n = len(graph)
    visited = set()

    # BFS from first node
    start = next(iter(graph))
    queue = deque([start])
    while queue:
        u = queue.popleft()
        if u in visited:
            continue
        visited.add(u)
        for v in graph[u]:
            if v not in visited:
                queue.append(v)

    return len(visited) == n
```

Example:

```
graph = {
    1: [2, 4],
    2: [1, 3],
    3: [2, 6],
    4: [1, 5],
    5: [4, 6],
    6: [3, 5]
}
print(is_connected(graph))  # True
```

Why It Matters

Connectivity is central in:

- Network reliability, ensure all nodes communicate
- Graph algorithms, many assume connected graphs
- Clustering, find connected components
- Pathfinding, unreachable nodes signal barriers

It's often the *first diagnostic check* before deeper analysis.

A Gentle Proof (Why It Works)

For undirected graphs, connectivity is equivalence relation:

- Reflexive: node connects to itself
- Symmetric: if A connects to B, B connects to A
- Transitive: if A connects to B and B connects to C, A connects to C

Therefore, DFS/BFS reachability partitioning defines connected components uniquely.

Try It Yourself

1. Draw a graph with 6 nodes.
2. Run BFS or DFS from node 1.
3. Mark all reachable nodes.
4. If some remain unvisited, you've found multiple components.
5. For directed graphs, try reversing edges and retesting.

Test Cases

Graph	Type	Result
1–2–3	Undirected	Connected
1–2, 3–4	Undirected	Not Connected
1→2→3, 3→1	Directed	Strongly Connected
1→2→3	Directed	Not Strongly Connected

Complexity

Operation	Time	Space
DFS/BFS	$O(n + m)$	$O(n)$

A Connectivity Checker ensures your graph is a single story, not a collection of isolated tales, a foundation before every journey through the graph.

Section 10. Algorithm Design Patterns

91 Brute Force Pattern

The Brute Force Pattern is the simplest and most universal approach to problem-solving: try every possible option, evaluate them all, and pick the best. It trades computational efficiency for conceptual clarity and correctness.

What Problem Are We Solving?

Sometimes, before clever optimizations or heuristics, we need a baseline solution, a way to ensure correctness. The brute force approach guarantees finding the right answer by exploring all possible configurations, even if it's slow.

Common use cases:

- Exhaustive search (e.g., generating all permutations or subsets)
- Baseline testing before implementing heuristics
- Proving optimality by comparison

How It Works (Plain Language)

A brute force algorithm generally follows this structure:

1. Enumerate all candidate solutions.
2. Evaluate each candidate for validity or cost.
3. Select the best (or first valid) solution.

This is conceptually simple, though often expensive in time.

Example: Traveling Salesman Problem (TSP)

Given n cities and distances between them, find the shortest tour visiting all.

Brute force solution:

1. Generate all $n!$ possible tours.
2. Compute the total distance for each.
3. Return the shortest tour.

This ensures correctness but grows factorially in complexity.

Tiny Code (Python)

```
from itertools import permutations

def tsp_bruteforce(dist):
    n = len(dist)
    cities = list(range(n))
    best = float('inf')
    best_path = None

    for perm in permutations(cities[1:]):  # fix city 0 as start
        path = [0] + list(perm) + [0]
        cost = sum(dist[path[i]][path[i+1]] for i in range(n))
        if cost < best:
            best = cost
            best_path = path
    return best, best_path

# Example distance matrix
dist = [
    [0, 10, 15, 20],
    [10, 0, 35, 25],
    [15, 35, 0, 30],
    [20, 25, 30, 0]
]

print(tsp_bruteforce(dist))  # (80, [0, 1, 3, 2, 0])
```

Why It Matters

Brute force is valuable for:

- Correctness: guarantees the right answer.
- Benchmarking: provides a ground truth for optimization.
- Small inputs: often feasible when n is small.
- Teaching: clarifies the structure of search and evaluation.

It is the seed from which more refined algorithms (like DP, backtracking, and heuristics) evolve.

A Gentle Proof (Why It Works)

Let S be the finite set of all possible solutions. If the algorithm evaluates every $s \in S$ and correctly computes its quality, and selects the minimum (or maximum), the chosen s^* is provably optimal:

$$s^* = \arg\min_{s \in S} f(s)$$

Completeness and correctness are inherent, though efficiency is not.

Try It Yourself

1. Enumerate all subsets of $1, 2, 3$.
2. Check which subsets sum to 4.
3. Confirm all possibilities are considered.
4. Reflect on the time cost: 2^n subsets for n elements.

Test Cases

Problem	Input Size	Feasible?	Notes
TSP	n = 4		$4! = 24$ paths
TSP	n = 10		$10! \approx 3.6 \times 10^6$
Subset Sum	n = 10		$2^{10} = 1024$ subsets
Subset Sum	n = 30		$2^{30} \approx 10^9$ subsets

Complexity

Operation	Time	Space
Enumeration	$O(k^n)$ (varies)	$O(n)$

The Brute Force Pattern is the blank canvas of algorithmic design: simple, exhaustive, and pure, a way to guarantee truth before seeking elegance.

92 Greedy Pattern

The Greedy Pattern builds a solution step by step, choosing at each stage the locally optimal move, the one that seems best right now, with the hope (and often the proof) that this path leads to a globally optimal result.

What Problem Are We Solving?

Greedy algorithms are used when problems exhibit two key properties:

1. Greedy-choice property – a global optimum can be reached by choosing local optima.
2. Optimal substructure – an optimal solution contains optimal solutions to subproblems.

You'll meet greedy reasoning everywhere: scheduling, pathfinding, compression, and resource allocation.

How It Works (Plain Language)

Greedy thinking is "take the best bite each time." There's no looking back, no exploring alternatives, just a sequence of decisive moves.

General shape:

1. Start with an empty or initial solution.
2. Repeatedly choose the best local move (by some rule).
3. Stop when no more moves are possible or desired.

Example: Coin Change (Canonical Coins)

Given coins $25, 10, 5, 1$, make change for 63 cents.

Greedy approach:

- Take largest coin $\leq$ remaining value.
- Subtract and repeat. Result: $25 + 25 + 10 + 1 + 1 + 1 = 63$ (6 coins total)

Works for canonical systems, not all, a nice teaching point.

Tiny Code (Python)

```
def greedy_coin_change(coins, amount):
    result = []
    for c in sorted(coins, reverse=True):
        while amount >= c:
            amount -= c
            result.append(c)
    return result

print(greedy_coin_change([25, 10, 5, 1], 63))
# [25, 25, 10, 1, 1, 1]
```

Why It Matters

The greedy pattern is a core design paradigm:

- Simple and fast – often linear or $O(n \log n)$.
- Provably optimal when conditions hold.
- Intuitive – builds insight into structure of problems.
- Foundation – many approximation and heuristic algorithms are "greedy at heart."

A Gentle Proof (Why It Works)

For problems with optimal substructure, we can often prove by induction:

If a greedy choice g leaves a subproblem P', and

$$\text{OPT}(P) = g + \text{OPT}(P')$$

then solving P' optimally ensures global optimality.

For coin change with canonical coins, this holds since choosing a larger coin never prevents an optimal total.

Try It Yourself

1. Apply the greedy method to Activity Selection: Sort activities by finishing time, pick earliest finishing one, and skip overlapping.
2. Compare against brute force enumeration.
3. Check if the greedy result is optimal, why or why not?

Test Cases

Problem	Greedy Works?	Note
Activity Selection		Local earliest-finish leads to global max
Coin Change (1, 3, 4) for 6		3+3 better than 4+1+1
Huffman Coding		Greedy merging yields optimal tree
Kruskal's MST		Greedy edge selection builds MST

Complexity

Operation	Time	Space
Selection	$O(n \log n)$ (sorting)	$O(1)$
Step Choice	$O(n)$	$O(1)$

The Greedy Pattern is the art of decisive reasoning, choosing what seems best now, and trusting the problem's structure to reward confidence.

93 Divide and Conquer Pattern

The Divide and Conquer Pattern breaks a big problem into smaller, similar subproblems, solves each one (often recursively), and then combines their results into the final answer.

It's the pattern behind merge sort, quicksort, binary search, and fast algorithms across mathematics and computation.

What Problem Are We Solving?

We use divide and conquer when:

1. The problem can be split into smaller subproblems of the same type.
2. Those subproblems are independent and easier to solve.
3. Their solutions can be merged efficiently.

It's the algorithmic mirror of mathematical induction, reduce, solve, combine.

How It Works (Plain Language)

Think of divide and conquer as a recursive three-step dance:

1. Divide – split the problem into smaller parts.
2. Conquer – solve each part recursively.
3. Combine – merge the sub-results into a final answer.

Each recursive call tackles a fraction of the work until reaching a base case.

Example: Merge Sort

Sort an array $A[1..n]$.

1. Divide: split A into two halves.
2. Conquer: recursively sort each half.
3. Combine: merge the two sorted halves.

Recurrence:

$$T(n) = 2T\left(\frac{n}{2}\right) + O(n)$$

Solution:

$$T(n) = O(n \log n)$$

Tiny Code (Python)

```
def merge_sort(arr):
    if len(arr) <= 1:
        return arr
    mid = len(arr) // 2
    left = merge_sort(arr[:mid])
```

```
    right = merge_sort(arr[mid:])
    return merge(left, right)

def merge(left, right):
    result = []
    i = j = 0
    while i < len(left) and j < len(right):
        if left[i] <= right[j]:
            result.append(left[i]); i += 1
        else:
            result.append(right[j]); j += 1
    result.extend(left[i:]); result.extend(right[j:])
    return result
```

Why It Matters

Divide and conquer turns recursion into efficiency. It's a framework for:

- Sorting (Merge Sort, Quick Sort)
- Searching (Binary Search)
- Matrix Multiplication (Strassen's Algorithm)
- FFT (Fast Fourier Transform)
- Geometry (Closest Pair, Convex Hull)
- Data Science (Divide-and-Conquer Regression, Decision Trees)

It captures the principle: *solve big problems by shrinking them.*

A Gentle Proof (Why It Works)

Assume each subproblem of size $\frac{n}{2}$ is solved optimally.

If we combine k subresults with cost $f(n)$, the total cost follows the recurrence

$$T(n) = aT\left(\frac{n}{b}\right) + f(n)$$

Using the Master Theorem, we compare $f(n)$ with $n^{\log_b a}$ to find $T(n)$.

For merge sort: $a = 2, b = 2, f(n) = n \quad T(n) = O(n \log n)$.

Try It Yourself

1. Apply divide and conquer to maximum subarray sum (Kadane's alternative).
2. Write a binary search with clear divide/conquer steps.
3. Visualize recursion tree and total cost at each level.

Test Cases

Problem	Divide	Combine	Works Well?
Merge Sort	Split array	Merge halves	
Quick Sort	Partition array	Concatenate	(average)
Binary Search	Split range	Return match	
Closest Pair	Divide plane	Compare boundary	

Complexity

Step	Cost
Divide	$O(1)$ or $O(n)$
Conquer	$aT(n/b)$
Combine	$O(n)$ (typical)

Overall: $O(n \log n)$ in many classic cases.

Divide and conquer is the essence of recursive decomposition, see the whole by mastering the parts.

94 Dynamic Programming Pattern

The Dynamic Programming (DP) Pattern solves complex problems by breaking them into overlapping subproblems, solving each once, and storing results to avoid recomputation.

It transforms exponential recursive solutions into efficient polynomial ones through memoization or tabulation.

What Problem Are We Solving?

When a problem has:

1. Overlapping subproblems – the same subtask appears multiple times.
2. Optimal substructure – an optimal solution can be built from optimal subsolutions.

Naive recursion repeats work. DP ensures each subproblem is solved once.

How It Works (Plain Language)

Think of DP as smart recursion:

- Define a state that captures progress.
- Define a recurrence that relates larger states to smaller ones.
- Store results to reuse later.

Two main flavors:

1. Top-down (Memoization) – recursion with caching.
2. Bottom-up (Tabulation) – fill a table iteratively.

Example: Fibonacci Numbers

Naive recursion:

$$F(n) = F(n-1) + F(n-2)$$

This recomputes many values.

DP solution:

1. Base: $F(0) = 0, F(1) = 1$
2. Build up table:

$$F[i] = F[i-1] + F[i-2]$$

Result: $O(n)$ time, $O(n)$ space (or $O(1)$ optimized).

Tiny Code (Python)

```
def fib(n):
    dp = [0, 1] + [0]*(n-1)
    for i in range(2, n+1):
        dp[i] = dp[i-1] + dp[i-2]
    return dp[n]
```

Or memoized recursion:

```
from functools import lru_cache

@lru_cache(None)
def fib(n):
    if n < 2:
        return n
    return fib(n-1) + fib(n-2)
```

Why It Matters

DP is the core of algorithmic problem solving:

- Optimization: shortest paths, knapsack, edit distance
- Counting: number of ways to climb stairs, partitions
- Sequence analysis: LIS, LCS
- Resource allocation: scheduling, investment problems

It's how we bring structure to recursion.

A Gentle Proof (Why It Works)

Let $T(n)$ be the cost to solve all distinct subproblems. Since each is solved once and combined in constant time:

$$T(n) = O(\text{number of states}) \times O(\text{transition cost})$$

For Fibonacci:

- States $= n$
- Transition cost $= O(1)$ $\quad T(n) = O(n)$

Memoization ensures every subproblem is visited at most once.

Try It Yourself

1. Write DP for coin change (ways to form a sum).
2. Trace longest common subsequence (LCS) table.
3. Compare top-down vs bottom-up performance.

Test Cases

Problem	State	Transition	Time
Fibonacci	n	$dp[n] = dp[n-1] + dp[n-2]$	$O(n)$
Knapsack	(i, w)	$\max(\text{take}, \text{skip})$	$O(nW)$
Edit Distance	(i, j)	Compare chars	$O(nm)$

Complexity

Type	Time	Space
Top-down Memoization	$O(\#\text{states})$	$O(\#\text{states})$
Bottom-up Tabulation	$O(\#\text{states})$	$O(\#\text{states})$

Dynamic Programming is divide and conquer with memory, think recursively, compute once, reuse forever.

95 Backtracking Pattern

The Backtracking Pattern explores all possible solutions by building them step by step and abandoning a path as soon as it becomes invalid.

It's a systematic search strategy for problems where we need to generate combinations, permutations, or subsets, and prune impossible or suboptimal branches early.

What Problem Are We Solving?

We face problems where:

- The solution space is large, but structured.
- We can detect invalid partial solutions early.

Examples:

- N-Queens (place queens safely)
- Sudoku (fill grid with constraints)
- Subset Sum (choose elements summing to target)

Brute force explores everything blindly. Backtracking cuts off dead ends as soon as they appear.

How It Works (Plain Language)

Imagine exploring a maze:

1. Take a step (make a choice).
2. If it leads to a valid partial solution, continue.
3. If it fails, backtrack, undo and try another path.

Each level of recursion corresponds to a decision point.

Example: N-Queens Problem

We need to place n queens on an $n \times n$ board so no two attack each other.

At each row, choose a column that is safe. If none works, backtrack to previous row.

Tiny Code (Python)

```
def solve_n_queens(n):
    res, board = [], [-1]*n

    def is_safe(row, col):
        for r in range(row):
            c = board[r]
            if c == col or abs(c - col) == abs(r - row):
                return False
        return True

    def backtrack(row=0):
        if row == n:
            res.append(board[:])
            return
        for col in range(n):
            if is_safe(row, col):
```

```
                board[row] = col
                backtrack(row + 1)
                board[row] = -1  # undo

    backtrack()
    return res
```

Why It Matters

Backtracking is a universal solver for:

- Combinatorial search: subsets, permutations, partitions
- Constraint satisfaction: Sudoku, graph coloring, N-Queens
- Optimization with pruning (branch and bound builds on it)

It's not just brute force, it's guided exploration.

A Gentle Proof (Why It Works)

Let S be the total number of possible states. Backtracking prunes all invalid paths early, so actual visited nodes $\leq S$.

If each state takes $O(1)$ time to check and recurse, total complexity is proportional to the number of valid partial states, often far smaller than full enumeration.

Try It Yourself

1. Solve Subset Sum using backtracking.
2. Generate all permutations of `[1,2,3]`.
3. Implement Sudoku Solver (9×9 constraint satisfaction).

Trace calls, each recursive call represents a partial decision.

Test Cases

Problem	Decision	Constraint	Output
N-Queens	Choose column	Non-attacking queens	Placements
Subset Sum	Include/Exclude	Sum target	Valid subsets
Sudoku	Fill cell	Row/Col/Subgrid unique	Completed grid

Complexity

Problem	Time	Space
N-Queens	$O(n!)$ worst	$O(n)$
Subset Sum	$O(2^n)$	$O(n)$
Sudoku	Exponential	Grid size

Backtracking is the art of searching by undoing, try, test, and retreat until you find a valid path.

96 Branch and Bound

The Branch and Bound pattern is an optimization framework that systematically explores the search space while pruning paths that cannot yield better solutions than the best one found so far.

It extends backtracking with bounds that let us skip unpromising branches early.

What Problem Are We Solving?

We want to solve optimization problems where:

- The search space is combinatorial (e.g., permutations, subsets).
- Each partial solution can be evaluated or bounded.
- We seek the best solution under some cost function.

Examples:

- Knapsack Problem: maximize value under capacity.
- Traveling Salesman Problem (TSP): find shortest tour.
- Job Scheduling: minimize total completion time.

Brute-force search is exponential. Branch and Bound cuts branches that cannot improve the best known answer.

How It Works (Plain Language)

Think of exploring a tree:

1. Branch: expand possible choices.
2. Bound: compute a limit on achievable value from this branch.
3. If bound best found so far, prune (stop exploring).
4. Otherwise, explore deeper.

We use:

- Upper bound: best possible value from this path.
- Lower bound: best value found so far.

Prune when upper bound lower bound.

Example: 0/1 Knapsack

Given items with weights and values, choose subset with max value capacity.

We recursively include/exclude each item, but prune branches that cannot beat current best (e.g., exceeding weight or potential value too low).

Tiny Code (Python)

```
def knapsack_branch_bound(items, capacity):
    best_value = 0

    def bound(i, curr_w, curr_v):
        # Simple bound: add remaining items greedily
        if i >= len(items):
            return curr_v
        w, v = curr_w, curr_v
        for j in range(i, len(items)):
            if w + items[j][0] <= capacity:
                w += items[j][0]
                v += items[j][1]
        return v

    def dfs(i, curr_w, curr_v):
        nonlocal best_value
        if curr_w > capacity:
```

```
            return
        if curr_v > best_value:
            best_value = curr_v
        if i == len(items):
            return
        if bound(i, curr_w, curr_v) <= best_value:
            return
        # Include item
        dfs(i+1, curr_w + items[i][0], curr_v + items[i][1])
        # Exclude item
        dfs(i+1, curr_w, curr_v)

    dfs(0, 0, 0)
    return best_value
```

Why It Matters

Branch and Bound:

- Generalizes backtracking with mathematical pruning.
- Turns exponential search into practical algorithms.
- Provides exact solutions when heuristics might fail.

Used in:

- Integer programming
- Route optimization
- Scheduling and assignment problems

A Gentle Proof (Why It Works)

Let $U(n)$ be an upper bound of a subtree. If $U(n) \leq V^*$ (best known value), no solution below can exceed V^*.

By monotonic bounding, pruning preserves correctness — no optimal solution is ever discarded.

The algorithm is complete (explores all promising branches) and optimal (finds global best).

Try It Yourself

1. Solve 0/1 Knapsack with branch and bound.
2. Implement TSP with cost matrix and prune by lower bounds.
3. Compare nodes explored vs brute-force enumeration.

Test Cases

Items (w,v)	Capacity	Best Value	Branches Explored
[(2,3),(3,4),(4,5)]	5	7	Reduced
[(1,1),(2,2),(3,5),(4,6)]	6	8	Reduced

Complexity

Problem	Time (Worst)	Time (Typical)	Space
Knapsack	$O(2^n)$	Much less (pruning)	$O(n)$
TSP	$O(n!)$	Pruned significantly	$O(n)$

Branch and Bound is search with insight, it trims the impossible and focuses only where the optimum can hide.

97 Randomized Pattern

The Randomized Pattern introduces chance into algorithm design. Instead of following a fixed path, the algorithm makes random choices that, on average, lead to efficient performance or simplicity.

Randomization can help break symmetry, avoid worst-case traps, and simplify complex logic.

What Problem Are We Solving?

We want algorithms that:

- Avoid pathological worst-case inputs.
- Simplify decisions that are hard deterministically.
- Achieve good expected performance.

Common examples:

- Randomized QuickSort: pivot chosen at random.
- Randomized Search / Sampling: estimate quantities via random trials.
- Monte Carlo and Las Vegas Algorithms: trade accuracy for speed or vice versa.

How It Works (Plain Language)

Randomization can appear in two forms:

1. Las Vegas Algorithm
    - Always produces the correct result.
    - Runtime is random (e.g., Randomized QuickSort).
2. Monte Carlo Algorithm
    - Runs in fixed time.
    - May have a small probability of error (e.g., primality tests).

By picking random paths or samples, we smooth out bad cases and often simplify logic.

Example: Randomized QuickSort

Choose a pivot randomly to avoid worst-case splits.

At each step:

1. Pick random pivot p from array.
2. Partition array into smaller ($< \mathrm{p}$) and larger ($> \mathrm{p}$).
3. Recursively sort halves.

Expected runtime is $O(n \log n)$ even if input is adversarial.

Tiny Code (Python)

```
import random

def randomized_quicksort(arr):
    if len(arr) <= 1:
        return arr
    pivot = random.choice(arr)
    left = [x for x in arr if x < pivot]
    mid = [x for x in arr if x == pivot]
```

```
    right = [x for x in arr if x > pivot]
    return randomized_quicksort(left) + mid + randomized_quicksort(right)
```

Why It Matters

Randomized algorithms are:

- Simple: randomization replaces complex logic.
- Efficient: often faster in expectation.
- Robust: resistant to adversarial input.

They appear in:

- Sorting, searching, and hashing.
- Approximation algorithms.
- Cryptography and sampling.
- Machine learning (e.g., SGD, bagging).

A Gentle Proof (Why It Works)

Let $T(n)$ be expected time of Randomized QuickSort:

$$T(n) = n - 1 + \frac{2}{n} \sum_{k=0}^{n-1} T(k)$$

Solving yields $T(n) = O(n \log n)$. Random pivot ensures each element has equal probability to split array, making balanced partitions likely on average.

Expected cost avoids $O(n^2)$ worst-case of fixed-pivot QuickSort.

Try It Yourself

1. Implement Randomized QuickSort, run on sorted input.
2. Compare average time to standard QuickSort.
3. Try a random primality test (e.g., Miller–Rabin).
4. Use random sampling to approximate π via Monte Carlo.

Test Cases

Input	Expected Result	Notes
[1,2,3,4,5]	[1,2,3,4,5]	Random pivot avoids worst-case
[5,4,3,2,1]	[1,2,3,4,5]	Still fast due to random splits

Complexity

Algorithm	Expected Time	Worst Time	Space
Randomized QuickSort	$O(n \log n)$	$O(n^2)$ (rare)	$O(\log n)$
Randomized Search	$O(1)$ expected	$O(n)$ worst	$O(1)$

Randomization turns rigid logic into flexible, average-case excellence, a practical ally in uncertain or adversarial worlds.

98 Approximation Pattern

The Approximation Pattern is used when finding the exact solution is too expensive or impossible. Instead of striving for perfection, we design algorithms that produce results *close enough* to optimal, fast, predictable, and often guaranteed within a factor.

This pattern shines in NP-hard problems, where exact methods scale poorly.

What Problem Are We Solving?

Some problems, like Traveling Salesman, Vertex Cover, or Knapsack, have no known polynomial-time exact solutions. We need algorithms that give good-enough answers quickly, especially for large inputs.

Approximation algorithms ensure:

- Predictable performance.
- Measurable accuracy.
- Polynomial runtime.

How It Works (Plain Language)

An approximation algorithm outputs a solution within a known ratio of the optimal value:

If the optimal cost is OPT, and our algorithm returns ALG, then for a minimization problem:

$$\frac{\text{ALG}}{\text{OPT}} \leq \alpha$$

where α is the approximation factor (e.g., 2, 1.5, or $(1 + \epsilon)$).

Example: Vertex Cover (2-Approximation)

Problem: find smallest set of vertices touching all edges.

Algorithm:

1. Start with an empty set C.
2. While edges remain:
   - Pick any uncovered edge (u, v).
   - Add both u and v to C.
   - Remove all edges incident to u or v.
3. Return C.

This guarantees $|C| \leq 2 \cdot |C^*|$, where C^* is the optimal vertex cover.

Tiny Code (Python)

```
def vertex_cover(edges):
    cover = set()
    while edges:
        (u, v) = edges.pop()
        cover.add(u)
        cover.add(v)
        edges = [(x, y) for (x, y) in edges if x not in (u, v) and y not in (u, v)]
    return cover
```

Why It Matters

Approximation algorithms:

- Provide provable guarantees.
- Scale to large problems.
- Offer predictable trade-offs between time and accuracy.

Widely used in:

- Combinatorial optimization.
- Scheduling, routing, resource allocation.
- AI planning, clustering, and compression.

A Gentle Proof (Why It Works)

Let C^* be optimal cover. Every edge must be covered by C^*. We select 2 vertices per edge, so:

$$|C| = 2 \cdot (\text{number of edges selected}) \leq 2 \cdot |C^*|$$

Thus, the approximation factor is 2.

Try It Yourself

1. Implement the 2-approx Vertex Cover algorithm.
2. Compare result size with brute-force solution for small graphs.
3. Explore $(1 + \epsilon)$-approximation using greedy selection.
4. Apply same idea to Set Cover or Knapsack.

Test Cases

Graph	Optimal	Algorithm	Ratio
Triangle	2	2	1.0
Square	2	4	2.0

Complexity

Algorithm	Time	Space	Guarantee
Vertex Cover (Greedy)	$O(E)$	$O(V)$	2-Approx
Knapsack (FPTAS)	$O(n^3/\epsilon)$	$O(n^2)$	$(1+\epsilon)$

Approximation is the art of being *nearly perfect, swiftly*, a pragmatic bridge between theory and the real world.

99 Online Algorithm Pattern

The Online Algorithm Pattern is used when input arrives sequentially, and decisions must be made immediately without knowledge of future data. There's no rewinding or re-optimizing later, you commit as you go.

This pattern models real-time decision-making, from caching to task scheduling and resource allocation.

What Problem Are We Solving?

In many systems, data doesn't come all at once. You must decide now, not after seeing the full picture.

Typical scenarios:

- Cache replacement (decide which page to evict next).
- Task assignment (jobs arrive in real time).
- Dynamic routing (packets arrive continuously).

Offline algorithms know everything upfront; online algorithms don't, yet must perform competitively.

How It Works (Plain Language)

An online algorithm processes inputs one by one. Each step:

1. Receive input item x_t at time t.
2. Make a decision d_t using current state only.
3. Cannot change d_t later.

Performance is measured by the competitive ratio:

$$\text{Competitive Ratio} = \max_{\text{inputs}} \frac{\text{Cost} * \text{ALG}}{\text{Cost} * \text{OPT}}$$

If ALG's cost is at most k times optimal, the algorithm is k-competitive.

Example: Paging / Cache Replacement

You have cache of size k. Sequence of page requests arrives. If requested page is not in cache → page fault → load it (evict one if full).

Algorithms:

- FIFO (First In First Out): Evict oldest.
- LRU (Least Recently Used): Evict least recently accessed.
- Random: Evict randomly.

LRU is k-competitive, meaning it performs within factor k of optimal.

Tiny Code (Python)

```
def lru_cache(pages, capacity):
    cache = []
    faults = 0
    for p in pages:
        if p not in cache:
            faults += 1
            if len(cache) == capacity:
                cache.pop(0)
            cache.append(p)
        else:
            cache.remove(p)
            cache.append(p)
    return faults
```

Why It Matters

Online algorithms:

- Reflect real-world constraints (no foresight).
- Enable adaptive systems in streaming, caching, and scheduling.
- Provide competitive guarantees even under worst-case input.

Used in:

- Operating systems (page replacement).
- Networking (packet routing).
- Finance (online pricing, bidding).
- Machine learning (online gradient descent).

A Gentle Proof (Why It Works)

For LRU Cache: Every cache miss means a unique page not seen in last k requests. The optimal offline algorithm (OPT) can avoid some faults but at most k times fewer. Thus:

$$\text{Faults(LRU)} \leq k \cdot \text{Faults(OPT)}$$

So LRU is k-competitive.

Try It Yourself

1. Simulate LRU, FIFO, Random cache on same request sequence.
2. Count page faults.
3. Compare with offline OPT (Belady's Algorithm).
4. Experiment with $k = 2, 3, 4$.

Test Cases

Pages	Cache Size	Algorithm	Faults	Ratio (vs OPT)
[1,2,3,1,2,3]	2	LRU	6	3.0
[1,2,3,4,1,2,3,4]	3	LRU	8	2.7

Complexity

Algorithm	Time	Space	Competitive Ratio
FIFO	$O(nk)$	$O(k)$	k
LRU	$O(nk)$	$O(k)$	k
OPT (offline)	$O(nk)$	$O(k)$	1

Online algorithms embrace uncertainty, they act wisely *now*, trusting analysis to prove they won't regret it later.

100 Hybrid Strategy Pattern

The Hybrid Strategy Pattern combines multiple algorithmic paradigms, such as divide and conquer, greedy, and dynamic programming, to balance their strengths and overcome individual weaknesses. Instead of sticking to one design philosophy, hybrid algorithms adapt to the structure of the problem and the size of the input.

What Problem Are We Solving?

No single paradigm fits all problems. Some inputs are small and benefit from brute force; others require recursive structure; still others need heuristics.

We need a meta-strategy that blends paradigms, switching between them based on conditions like:

- Input size (e.g., small vs large)
- Structure (e.g., sorted vs unsorted)
- Precision requirements (e.g., exact vs approximate)

Hybrid strategies offer practical performance beyond theoretical asymptotics.

How It Works (Plain Language)

A hybrid algorithm uses *decision logic* to pick the best method for each situation.

Common patterns:

1. Small-case base switch: Use brute force when n is small (e.g., Insertion Sort inside QuickSort).
2. Stage combination: Use one algorithm for setup, another for refinement (e.g., Greedy for initial solution, DP for optimization).

3. Conditional strategy: Choose algorithm based on data distribution (e.g., QuickSort vs HeapSort).

Example: Introsort

Introsort starts like QuickSort for average speed, but if recursion depth grows too large (bad pivot splits), it switches to HeapSort to guarantee $O(n \log n)$ worst-case time.

Steps:

1. Partition using QuickSort.
2. Track recursion depth.
3. If depth $>$ threshold $(2 \log n)$, switch to HeapSort.

This ensures best of both worlds: average speed + worst-case safety.

Tiny Code (Python)

```
def introsort(arr, depth_limit):
    if len(arr) <= 1:
        return arr
    if depth_limit == 0:
        return heapsort(arr)
    pivot = arr[len(arr)//2]
    left = [x for x in arr if x < pivot]
    mid = [x for x in arr if x == pivot]
    right = [x for x in arr if x > pivot]
    return introsort(left, depth_limit - 1) + mid + introsort(right, depth_limit - 1)
```

(Uses heapsort when depth limit is reached)

Why It Matters

Hybrid strategies give real-world efficiency, predictable performance, and robust fallback behavior. They mirror how expert developers build systems, not one-size-fits-all, but layered and conditional.

Common hybrids:

- Timsort = MergeSort + InsertionSort
- Introsort = QuickSort + HeapSort

- Branch-and-Bound + Greedy = Search with pruning and heuristics
- Neural + Symbolic = Learning + Logical reasoning

A Gentle Proof (Why It Works)

Let $A_1, A_2, \ldots, A_k$ be candidate algorithms with cost functions $T_i(n)$. Hybrid strategy H chooses A_i when condition $C_i(n)$ holds.

If decision logic ensures

$$T_H(n) = \min_i T_i(n) \mid C_i(n)$$

then H performs at least as well as the best applicable algorithm.

Thus $T_H(n) = O(\min_i T_i(n))$.

Try It Yourself

1. Implement QuickSort + InsertionSort hybrid.
2. Set threshold $n_0 = 10$ for switching.
3. Compare performance vs pure QuickSort.
4. Experiment with different thresholds.

Test Cases

Input Size	Algorithm	Time	Notes
10	Insertion Sort	Fastest	Simplicity wins
1000	QuickSort	Optimal	Low overhead
1e6	Introsort	Stable	No worst-case blowup

Complexity

Component	Best	Average	Worst	Space
QuickSort	$O(n \log n)$	$O(n \log n)$	$O(n^2)$	$O(\log n)$
HeapSort	$O(n \log n)$	$O(n \log n)$	$O(n \log n)$	$O(1)$
Introsort	$O(n \log n)$	$O(n \log n)$	$O(n \log n)$	$O(\log n)$

A hybrid strategy is not just an algorithmic trick, it's a mindset: combine precision, adaptability, and pragmatism to build algorithms that thrive in the wild.

Chapter 2. Sorting and searching

11. Elementary sorting

101 Bubble Sort

Bubble Sort is like washing dishes one by one, you keep moving the biggest plate to the bottom until everything is clean and sorted. It is simple, visual, and perfect for building your sorting intuition before diving into more advanced methods.

What Problem Are We Solving?

We want to arrange a list of elements in order (ascending or descending) by repeatedly comparing and swapping adjacent items that are out of order.

Formally: Given an array `A[0…n-1]`, repeat passes until no swaps occur. Each pass bubbles up the largest remaining element to its final position.

Example

Step	Array State	Description
0	[5, 3, 4, 1]	Initial array
1	[3, 4, 1, 5]	5 bubbled to the end
2	[3, 1, 4, 5]	4 bubbled to position 3
3	[1, 3, 4, 5]	Array fully sorted

How Does It Work (Plain Language)?

Imagine bubbles rising to the surface, the biggest one reaches the top first. In Bubble Sort, each sweep through the list compares neighboring pairs, swapping them if they are in the wrong order. After each full pass, one more element settles into place.

We repeat until a pass finishes with no swaps, meaning the array is sorted.

Step-by-Step Process

Step	Action	Resulting Array
1	Compare A[0] and A[1]	Swap if needed
2	Compare A[1] and A[2]	Swap if needed
3	Continue through A[n-2]	Repeat comparisons
4	Repeat passes until sorted	Early stop if sorted

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdbool.h>

void bubble_sort(int a[], int n) {
    bool swapped;
    for (int pass = 0; pass < n - 1; pass++) {
        swapped = false;
        for (int i = 0; i < n - pass - 1; i++) {
            if (a[i] > a[i + 1]) {
                int temp = a[i];
                a[i] = a[i + 1];
                a[i + 1] = temp;
                swapped = true;
            }
        }
        if (!swapped) break; // early exit if already sorted
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    bubble_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def bubble_sort(a):
    n = len(a)
    for pass_num in range(n - 1):
        swapped = False
        for i in range(n - pass_num - 1):
            if a[i] > a[i + 1]:
                a[i], a[i + 1] = a[i + 1], a[i]
                swapped = True
        if not swapped:
            break

arr = [5, 3, 4, 1, 2]
bubble_sort(arr)
print(arr)
```

Why It Matters

- Teaches comparison-based sorting through intuition
- Builds understanding of adjacent swaps and pass-based progress
- Introduces stability (equal elements keep their relative order)
- Sets the stage for improved versions (Improved Bubble Sort, Cocktail Shaker Sort, Comb Sort)

A Gentle Proof (Why It Works)

After the first pass, the largest element moves to the last position. After the second pass, the second largest is in position n-2.

So after k passes, the last k elements are sorted.

If we track comparisons: 1st pass: (n−1) comparisons 2nd pass: (n−2) comparisons … (n−1)th pass: 1 comparison

Pass	Comparisons	Elements Sorted at End
1	n−1	Largest element
2	n−2	Next largest
…	…	…
n−1	1	Fully sorted array

Total comparisons = (n−1) + (n−2) + … + 1 = n(n−1)/2

So time = $O(n^2)$ in the worst case. If already sorted, early exit makes it O(n).

Try It Yourself

Task	Description
1	Sort [3, 2, 1] step by step
2	Count how many swaps occur
3	Add a flag to detect early termination
4	Compare with Insertion Sort on the same data
5	Modify to sort descending

Test Cases

Input	Output	Passes	Swaps
[3, 2, 1]	[1, 2, 3]	3	3
[1, 2, 3]	[1, 2, 3]	1	0
[5, 1, 4, 2, 8]	[1, 2, 4, 5, 8]	4	5

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	O(n)
Space	O(1) (in-place)
Stable	Yes
Adaptive	Yes (stops early if sorted)

Bubble Sort is your first step into the sorting world, simple enough to code by hand, visual enough to animate, and powerful enough to spark intuition for more advanced sorts.

102 Improved Bubble Sort

Improved Bubble Sort builds on the basic version by recognizing that once part of the array is sorted, there's no need to revisit it. It introduces small optimizations like early termination and tracking the last swap position to reduce unnecessary comparisons.

What Problem Are We Solving?

Basic Bubble Sort keeps scanning the whole array every pass, even when the tail is already sorted. Improved Bubble Sort fixes this by remembering where the last swap happened. Elements beyond that index are already in place, so the next pass can stop earlier.

This optimization is especially effective for arrays that are nearly sorted.

Example

Step	Array State	Last Swap Index	Range Checked
0	[5, 3, 4, 1, 2]	-	0 to 4
1	[3, 4, 1, 2, 5]	3	0 to 3
2	[3, 1, 2, 4, 5]	2	0 to 2
3	[1, 2, 3, 4, 5]	1	0 to 1
4	[1, 2, 3, 4, 5]	0	Stop early

How Does It Work (Plain Language)?

We improve efficiency by narrowing each pass to only the unsorted part. We also stop early when no swaps occur, signaling the array is already sorted.

Step by step:

1. Track index of the last swap in each pass
2. Next pass ends at that index
3. Stop when no swaps occur (fully sorted)

This reduces unnecessary comparisons in nearly sorted arrays.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void improved_bubble_sort(int a[], int n) {
    int new_n;
    while (n > 1) {
        new_n = 0;
```

```
        for (int i = 1; i < n; i++) {
            if (a[i - 1] > a[i]) {
                int temp = a[i - 1];
                a[i - 1] = a[i];
                a[i] = temp;
                new_n = i;
            }
        }
        n = new_n;
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    improved_bubble_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def improved_bubble_sort(a):
    n = len(a)
    while n > 1:
        new_n = 0
        for i in range(1, n):
            if a[i - 1] > a[i]:
                a[i - 1], a[i] = a[i], a[i - 1]
                new_n = i
        n = new_n

arr = [5, 3, 4, 1, 2]
improved_bubble_sort(arr)
print(arr)
```

Why It Matters

- Reduces redundant comparisons

- Automatically adapts to partially sorted data
- Stops as soon as the array is sorted
- Retains stability and simplicity

A Gentle Proof (Why It Works)

If the last swap occurs at index `k`, all elements after `k` are already in order. Next pass only needs to scan up to `k`. If no swaps occur (`k = 0`), the array is sorted.

Pass	Comparisons	Last Swap	Range Next Pass
1	n−1	k	0..k
2	k −1	k	0..k
…	…	…	…

In the best case (already sorted), only one pass occurs: O(n) Worst case remains $O(n^2)$

Try It Yourself

Task	Description
1	Sort [1, 2, 3, 4, 5] and observe early stop
2	Sort [5, 4, 3, 2, 1] and track last swap index
3	Modify to print last swap index each pass
4	Compare with standard Bubble Sort pass count
5	Try arrays with repeated values to verify stability

Test Cases

Input	Output	Passes	Improvement
[1, 2, 3, 4, 5]	[1, 2, 3, 4, 5]	1	Early stop
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	4	Fewer checks each pass
[2, 1, 3, 4, 5]	[1, 2, 3, 4, 5]	1	Detects sorted tail

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	O(n)
Space	O(1)
Stable	Yes
Adaptive	Yes

Improved Bubble Sort shows how a small observation can make a classic algorithm smarter. By tracking the last swap, it skips already-sorted tails and gives a glimpse of how adaptive sorting works in practice.

103 Cocktail Shaker Sort

Cocktail Shaker Sort, also known as Bidirectional Bubble Sort, improves on Bubble Sort by sorting in both directions during each pass. It moves the largest element to the end and the smallest to the beginning, reducing the number of passes required.

What Problem Are We Solving?

Standard Bubble Sort only bubbles up in one direction, pushing the largest element to the end each pass. If small elements start near the end, they take many passes to reach their position.

Cocktail Shaker Sort fixes this by sweeping back and forth, bubbling both ends at once.

Example

Step	Direction	Array State	Description
0	–	[5, 3, 4, 1, 2]	Initial array
1	Left → Right	[3, 4, 1, 2, 5]	5 bubbled to end
2	Right → Left	[1, 3, 4, 2, 5]	1 bubbled to start
3	Left → Right	[1, 3, 2, 4, 5]	4 bubbled to position 4
4	Right → Left	[1, 2, 3, 4, 5]	2 bubbled to position 2

Sorted after 4 directional passes.

How Does It Work (Plain Language)?

Cocktail Shaker Sort is like stirring from both sides of the array. Each forward pass moves the largest unsorted element to the end. Each backward pass moves the smallest unsorted element to the start.

The unsorted region shrinks from both ends with each full cycle.

Step-by-Step Process

Step	Action	Result
1	Sweep left to right, bubble largest to end	
2	Sweep right to left, bubble smallest to start	
3	Narrow bounds, repeat until sorted	

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdbool.h>

void cocktail_shaker_sort(int a[], int n) {
    bool swapped = true;
    int start = 0, end = n - 1;

    while (swapped) {
        swapped = false;

        // Forward pass
        for (int i = start; i < end; i++) {
            if (a[i] > a[i + 1]) {
                int temp = a[i];
                a[i] = a[i + 1];
                a[i + 1] = temp;
                swapped = true;
            }
        }
        if (!swapped) break;
```

```
        swapped = false;
        end--;

        // Backward pass
        for (int i = end - 1; i >= start; i--) {
            if (a[i] > a[i + 1]) {
                int temp = a[i];
                a[i] = a[i + 1];
                a[i + 1] = temp;
                swapped = true;
            }
        }
        start++;
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    cocktail_shaker_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def cocktail_shaker_sort(a):
    n = len(a)
    start, end = 0, n - 1
    swapped = True

    while swapped:
        swapped = False
        for i in range(start, end):
            if a[i] > a[i + 1]:
                a[i], a[i + 1] = a[i + 1], a[i]
                swapped = True
        if not swapped:
            break
        swapped = False
```

```
        end -= 1
        for i in range(end - 1, start - 1, -1):
            if a[i] > a[i + 1]:
                a[i], a[i + 1] = a[i + 1], a[i]
                swapped = True
        start += 1

arr = [5, 3, 4, 1, 2]
cocktail_shaker_sort(arr)
print(arr)
```

Why It Matters

- Sorts in both directions, reducing unnecessary passes
- Performs better than Bubble Sort on many practical inputs
- Stable and easy to visualize
- Demonstrates bidirectional improvement, a foundation for adaptive sorting

A Gentle Proof (Why It Works)

Each forward pass moves the maximum element of the unsorted range to the end. Each backward pass moves the minimum element of the unsorted range to the start. Thus, the unsorted range shrinks from both sides, guaranteeing progress each cycle.

Cycle	Forward Pass	Backward Pass	Sorted Range
1	Largest to end	Smallest to start	[0], [n-1]
2	Next largest	Next smallest	[0,1], [n-2,n-1]
…	…	…	…

Worst case still $O(n^2)$, best case $O(n)$ if already sorted.

Try It Yourself

Task	Description
1	Sort [5, 3, 4, 1, 2] and track forward/backward passes
2	Visualize the shrinking unsorted range
3	Compare with standard Bubble Sort on reverse array
4	Modify code to print array after each pass

Task	Description
5	Test stability with duplicate values

Test Cases

Input	Output	Passes	Notes
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	4	Fewer passes than bubble sort
[1, 2, 3, 4, 5]	[1, 2, 3, 4, 5]	1	Early termination
[2, 1, 3, 5, 4]	[1, 2, 3, 4, 5]	2	Moves smallest quickly

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	O(n)
Space	O(1)
Stable	Yes
Adaptive	Yes

Cocktail Shaker Sort takes the simplicity of Bubble Sort and doubles its efficiency for certain inputs. By sorting in both directions, it highlights the power of symmetry and small algorithmic tweaks.

104 Selection Sort

Selection Sort is like organizing a deck of cards by repeatedly picking the smallest card and placing it in order. It is simple, predictable, and useful for understanding how selection-based sorting works.

What Problem Are We Solving?

We want to sort an array by repeatedly selecting the smallest (or largest) element from the unsorted part and swapping it into the correct position.

Selection Sort separates the array into two parts:

- A sorted prefix (built one element at a time)
- An unsorted suffix (from which we select the next minimum)

Example

Step	Array State	Action	Sorted Part	Unsorted Part
0	[5, 3, 4, 1, 2]	Start	[]	[5,3,4,1,2]
1	[1, 3, 4, 5, 2]	Place 1 at index 0	[1]	[3,4,5,2]
2	[1, 2, 4, 5, 3]	Place 2 at index 1	[1,2]	[4,5,3]
3	[1, 2, 3, 5, 4]	Place 3 at index 2	[1,2,3]	[5,4]
4	[1, 2, 3, 4, 5]	Place 4 at index 3	[1,2,3,4]	[5]
5	[1, 2, 3, 4, 5]	Done	[1,2,3,4,5]	[]

How Does It Work (Plain Language)?

Selection Sort looks through the unsorted portion, finds the smallest element, and moves it to the front. It does not care about intermediate order until each selection is done.

Each pass fixes one position permanently.

Step-by-Step Process

Step	Action	Effect
1	Find smallest in unsorted part	Move it to front
2	Repeat for next unsorted index	Grow sorted prefix
3	Stop when entire array sorted	

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void selection_sort(int a[], int n) {
    for (int i = 0; i < n - 1; i++) {
        int min_idx = i;
        for (int j = i + 1; j < n; j++) {
            if (a[j] < a[min_idx]) {
                min_idx = j;
            }
```

```
        }
        int temp = a[i];
        a[i] = a[min_idx];
        a[min_idx] = temp;
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    selection_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def selection_sort(a):
    n = len(a)
    for i in range(n - 1):
        min_idx = i
        for j in range(i + 1, n):
            if a[j] < a[min_idx]:
                min_idx = j
        a[i], a[min_idx] = a[min_idx], a[i]

arr = [5, 3, 4, 1, 2]
selection_sort(arr)
print(arr)
```

Why It Matters

- Simple, deterministic sorting algorithm
- Demonstrates selection rather than swapping neighbors
- Good for small lists and teaching purposes
- Useful when minimizing number of swaps matters

A Gentle Proof (Why It Works)

At each iteration, the smallest remaining element is placed at its correct position. Once placed, it never moves again.

The algorithm performs n−1 selections and at most n−1 swaps. Each selection requires scanning the unsorted part: O(n) comparisons.

Pass	Search Range	Comparisons	Swap
1	n elements	n−1	1
2	n−1 elements	n−2	1
…	…	…	…
n−1	2 elements	1	1

Total comparisons = $n(n-1)/2 = O(n^2)$

Try It Yourself

Task	Description
1	Trace sorting of [5, 3, 4, 1, 2] step by step
2	Count total swaps and comparisons
3	Modify to find maximum each pass (descending order)
4	Add print statements to see progress
5	Compare with Bubble Sort efficiency

Test Cases

Input	Output	Passes	Swaps
[3, 2, 1]	[1, 2, 3]	2	2
[1, 2, 3]	[1, 2, 3]	2	0
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	4	4

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$

Aspect	Value
Time (Best)	$O(n^2)$
Space	O(1)
Stable	No (swap may break order)
Adaptive	No

Selection Sort is a calm, methodical sorter. It does not adapt, but it does not waste swaps either. It is the simplest demonstration of the idea: find the smallest, place it, repeat.

105 Double Selection Sort

Double Selection Sort is a refined version of Selection Sort. Instead of finding just the smallest element each pass, it finds both the smallest and the largest, placing them at the beginning and end simultaneously. This halves the number of passes needed.

What Problem Are We Solving?

Standard Selection Sort finds one element per pass. Double Selection Sort improves efficiency by selecting two elements per pass, one from each end, reducing total iterations by about half.

It is useful when both extremes can be found in a single scan, improving constant factors while keeping overall simplicity.

Example

Step	Array State	Min	Max	Action	Sorted Part
0	[5, 3, 4, 1, 2]	1	5	Swap 1 → front, 5 → back	[1, …, 5]
1	[1, 3, 4, 2, 5]	2	4	Swap 2 → index 1, 4 → index 3	[1,2, …,4,5]
2	[1, 2, 3, 4, 5]	3	3	Middle element sorted	[1,2,3,4,5]

Sorted in 3 passes instead of 5.

How Does It Work (Plain Language)?

Double Selection Sort narrows the unsorted range from both sides. Each pass:

1. Scans the unsorted section once.
2. Finds both the smallest and largest elements.
3. Swaps them to their correct positions at the front and back.

Then it shrinks the bounds and repeats.

Step-by-Step Process

Step	Action	Effect
1	Find smallest and largest in unsorted	Move smallest left, largest right
2	Shrink unsorted range	Repeat search
3	Stop when range collapses	Array sorted

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void double_selection_sort(int a[], int n) {
    int left = 0, right = n - 1;

    while (left < right) {
        int min_idx = left, max_idx = left;

        for (int i = left; i <= right; i++) {
            if (a[i] < a[min_idx]) min_idx = i;
            if (a[i] > a[max_idx]) max_idx = i;
        }

        // Move smallest to front
        int temp = a[left];
        a[left] = a[min_idx];
        a[min_idx] = temp;
```

```c
        // If max element was swapped into min_idx
        if (max_idx == left) max_idx = min_idx;

        // Move largest to back
        temp = a[right];
        a[right] = a[max_idx];
        a[max_idx] = temp;

        left++;
        right--;
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    double_selection_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def double_selection_sort(a):
    left, right = 0, len(a) - 1
    while left < right:
        min_idx, max_idx = left, left
        for i in range(left, right + 1):
            if a[i] < a[min_idx]:
                min_idx = i
            if a[i] > a[max_idx]:
                max_idx = i

        a[left], a[min_idx] = a[min_idx], a[left]
        if max_idx == left:
            max_idx = min_idx
        a[right], a[max_idx] = a[max_idx], a[right]

        left += 1
        right -= 1
```

```
arr = [5, 3, 4, 1, 2]
double_selection_sort(arr)
print(arr)
```

Why It Matters

- Improves Selection Sort by reducing passes
- Selects two extremes in one scan
- Fewer total swaps and comparisons
- Demonstrates bidirectional selection

A Gentle Proof (Why It Works)

Each pass moves two elements to their correct final positions. Thus, after k passes, the first k and last k positions are sorted. The unsorted range shrinks by 2 each pass.

Pass	Range Checked	Elements Fixed	Remaining Unsorted
1	[0..n−1]	2	n−2
2	[1..n−2]	2	n−4
…	…	…	…

Total passes = n/2, each O(n) scan O(n^2) overall.

Try It Yourself

Task	Description
1	Sort [5, 3, 4, 1, 2] manually
2	Count passes and swaps
3	Print range boundaries each pass
4	Compare to Selection Sort passes
5	Modify for descending order

Test Cases

Input	Output	Passes	Swaps
[3, 2, 1]	[1, 2, 3]	2	2
[1, 2, 3, 4, 5]	[1, 2, 3, 4, 5]	2	0
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	3	6

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	$O(n^2)$
Space	O(1)
Stable	No
Adaptive	No

Double Selection Sort keeps Selection Sort's simplicity but doubles its reach. By grabbing both ends each pass, it highlights how symmetry can bring efficiency without new data structures.

106 Insertion Sort

Insertion Sort builds the sorted array one element at a time, like sorting playing cards in your hand. It takes each new element and inserts it into the correct position among those already sorted.

What Problem Are We Solving?

We want a simple, stable way to sort elements by inserting each into place within the growing sorted section. This works especially well for small arrays or nearly sorted data.

Insertion Sort splits the array into two parts:

- Sorted prefix: elements that are already in order
- Unsorted suffix: remaining elements yet to be inserted

Example

Step	Array State	Element Inserted	Action	Sorted Prefix
0	[5, 3, 4, 1, 2]	-	Start with first element sorted	[5]
1	[3, 5, 4, 1, 2]	3	Insert 3 before 5	[3, 5]
2	[3, 4, 5, 1, 2]	4	Insert 4 before 5	[3, 4, 5]
3	[1, 3, 4, 5, 2]	1	Insert 1 at front	[1, 3, 4, 5]
4	[1, 2, 3, 4, 5]	2	Insert 2 after 1	[1, 2, 3, 4, 5]

How Does It Work (Plain Language)?

Imagine picking cards one by one and placing each into the correct spot among those already held. Insertion Sort repeats this logic for arrays:

1. Start with the first element (already sorted)
2. Take the next element
3. Compare backward through the sorted section
4. Shift elements to make space and insert it

Step-by-Step Process

Step	Action	Result
1	Take next unsorted element	
2	Move through sorted part to find position	
3	Shift larger elements right	
4	Insert element in correct position	

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void insertion_sort(int a[], int n) {
    for (int i = 1; i < n; i++) {
        int key = a[i];
        int j = i - 1;
        while (j >= 0 && a[j] > key) {
```

```
            a[j + 1] = a[j];
            j--;
        }
        a[j + 1] = key;
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    insertion_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def insertion_sort(a):
    for i in range(1, len(a)):
        key = a[i]
        j = i - 1
        while j >= 0 and a[j] > key:
            a[j + 1] = a[j]
            j -= 1
        a[j + 1] = key

arr = [5, 3, 4, 1, 2]
insertion_sort(arr)
print(arr)
```

Why It Matters

- Simple, intuitive, and stable
- Works well for small or nearly sorted arrays
- Commonly used as a subroutine in advanced algorithms (like Timsort)
- Demonstrates concept of incremental insertion

A Gentle Proof (Why It Works)

At step `i`, the first `i` elements are sorted. Inserting element `a[i]` keeps the prefix sorted. Each insertion shifts elements greater than `key` to the right, ensuring correct position.

Pass	Sorted Portion	Comparisons (Worst)	Shifts (Worst)
1	[a ,a]	1	1
2	[a ,a ,a]	2	2
…	…	…	…
n-1	[a …a]	n-1	n-1

Total $(n^2)/2$ operations in the worst case.

If already sorted, only one comparison per element $\rightarrow$ O(n).

Try It Yourself

Task	Description
1	Sort [5, 3, 4, 1, 2] step by step
2	Count shifts and comparisons
3	Modify to sort descending
4	Compare runtime with Bubble Sort
5	Insert print statements to trace insertions

Test Cases

Input	Output	Passes	Swaps/Shifts
[3, 2, 1]	[1, 2, 3]	2	3
[1, 2, 3]	[1, 2, 3]	2	0
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	4	8

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	O(n)

Aspect	Value
Space	O(1)
Stable	Yes
Adaptive	Yes

Insertion Sort captures the logic of careful, incremental organization. It is slow for large random lists, but elegant, stable, and highly efficient when the data is already close to sorted.

107 Binary Insertion Sort

Binary Insertion Sort improves on traditional Insertion Sort by using binary search to find the correct insertion point instead of linear scanning. This reduces the number of comparisons from linear to logarithmic per insertion, while keeping the same stable, adaptive behavior.

What Problem Are We Solving?

Standard Insertion Sort searches linearly through the sorted part to find where to insert the new element. If the sorted prefix is long, this costs O(n) comparisons per element.

Binary Insertion Sort replaces that with binary search, which finds the position in O(log n) time, while still performing O(n) shifts.

This makes it a good choice when comparisons are expensive but shifting is cheap.

Example

Step	Sorted Portion	Element to Insert	Insertion Index (Binary Search)	Resulting Array
0	[5]	3	0	[3, 5, 4, 1, 2]
1	[3, 5]	4	1	[3, 4, 5, 1, 2]
2	[3, 4, 5]	1	0	[1, 3, 4, 5, 2]
3	[1, 3, 4, 5]	2	1	[1, 2, 3, 4, 5]

How Does It Work (Plain Language)?

Just like Insertion Sort, we build a sorted prefix one element at a time. But instead of scanning backwards linearly, we use binary search to locate the correct position to insert the next element.

We still need to shift larger elements to the right, but we now know exactly where to stop.

Step-by-Step Process

Step	Action	Effect
1	Perform binary search in sorted prefix	Find insertion point
2	Shift larger elements right	Create space
3	Insert element at found index	Maintain order
4	Repeat until sorted	Fully sorted array

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

int binary_search(int a[], int item, int low, int high) {
    while (low <= high) {
        int mid = (low + high) / 2;
        if (item == a[mid]) return mid + 1;
        else if (item > a[mid]) low = mid + 1;
        else high = mid - 1;
    }
    return low;
}

void binary_insertion_sort(int a[], int n) {
    for (int i = 1; i < n; i++) {
        int key = a[i];
        int j = i - 1;
        int pos = binary_search(a, key, 0, j);

        while (j >= pos) {
```

```
            a[j + 1] = a[j];
            j--;
        }
        a[pos] = key;
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    binary_insertion_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def binary_search(a, item, low, high):
    while low <= high:
        mid = (low + high) // 2
        if item == a[mid]:
            return mid + 1
        elif item > a[mid]:
            low = mid + 1
        else:
            high = mid - 1
    return low

def binary_insertion_sort(a):
    for i in range(1, len(a)):
        key = a[i]
        pos = binary_search(a, key, 0, i - 1)
        a[pos + 1 : i + 1] = a[pos : i]
        a[pos] = key

arr = [5, 3, 4, 1, 2]
binary_insertion_sort(arr)
print(arr)
```

Why It Matters

- Fewer comparisons than standard Insertion Sort
- Retains stability and adaptiveness
- Great when comparisons dominate runtime (e.g., complex objects)
- Demonstrates combining search and insertion ideas

A Gentle Proof (Why It Works)

Binary search always finds the correct index in O(log i) comparisons for the i-th element. Shifting elements still takes O(i) time. So total cost:

$$T(n) = \sum_{i=1}^{n-1} (\log i + i) = O(n^2)$$

but with fewer comparisons than standard Insertion Sort.

Step	Comparisons	Shifts	Total Cost
1	log 1 = 0	1	1
2	log 2 = 1	2	3
3	log 3 2	3	5
…	…	…	…

Try It Yourself

Task	Description
1	Sort [5, 3, 4, 1, 2] step by step
2	Print insertion index each pass
3	Compare comparisons vs normal Insertion Sort
4	Modify to sort descending
5	Try with already sorted list

Test Cases

Input	Output	Comparisons	Shifts
[3, 2, 1]	[1, 2, 3]	~3	3
[1, 2, 3]	[1, 2, 3]	~2	0

Input	Output	Comparisons	Shifts
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	~7	8

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	O(n log n) comparisons, O(n) shifts
Space	O(1)
Stable	Yes
Adaptive	Yes

Binary Insertion Sort is a thoughtful balance, smarter searches, same simple structure. It reminds us that even small changes (like using binary search) can bring real efficiency when precision matters.

108 Gnome Sort

Gnome Sort is a simple sorting algorithm that works by swapping adjacent elements, similar to Bubble Sort, but with a twist, it moves backward whenever a swap is made. Imagine a gnome tidying flower pots: each time it finds two out of order, it swaps them and steps back to recheck the previous pair.

What Problem Are We Solving?

We want a simple, intuitive, and in-place sorting method that uses local swaps to restore order. Gnome Sort is particularly easy to implement and works like an insertion sort with adjacent swaps instead of shifting elements.

It's not the fastest, but it's charmingly simple, perfect for understanding local correction logic.

Step	Position	Array State	Action

Example

Step	Position	Array State	Action
0	1	[5, 3, 4, 1, 2]	Compare $5 > 3 \rightarrow$ Swap, move back
1	0	[3, 5, 4, 1, 2]	At start $\rightarrow$ move forward
2	1	[3, 5, 4, 1, 2]	Compare $5 > 4 \rightarrow$ Swap, move back
3	0	[3, 4, 5, 1, 2]	At start $\rightarrow$ move forward
4	1	[3, 4, 5, 1, 2]	Compare $4 < 5 \rightarrow$ OK $\rightarrow$ move forward
5	3	[3, 4, 5, 1, 2]	Compare $5 > 1 \rightarrow$ Swap, move back
6	2	[3, 4, 1, 5, 2]	Compare $4 > 1 \rightarrow$ Swap, move back
7	1	[3, 1, 4, 5, 2]	Compare $3 > 1 \rightarrow$ Swap, move back
8	0	[1, 3, 4, 5, 2]	At start $\rightarrow$ move forward
9	...	...	Continue until sorted [1,2,3,4,5]

How Does It Work (Plain Language)?

The algorithm "walks" through the list:

1. If the current element is greater or equal to the previous one, move forward.
2. If not, swap them and move one step back.
3. Repeat until the end is reached.

If you reach the start of the array, step forward.

It's like Insertion Sort, but instead of shifting, it walks and swaps.

Step-by-Step Process

Step	Condition	Action
If A[i] A[i−1]	Move forward (i++)	
If A[i] < A[i−1]	Swap, move backward (i−−)	
If i == 0	Move forward (i++)	

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void gnome_sort(int a[], int n) {
    int i = 1;
    while (i < n) {
        if (i == 0 || a[i] >= a[i - 1]) {
            i++;
        } else {
            int temp = a[i];
            a[i] = a[i - 1];
            a[i - 1] = temp;
            i--;
        }
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    gnome_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def gnome_sort(a):
    i = 1
    n = len(a)
    while i < n:
        if i == 0 or a[i] >= a[i - 1]:
            i += 1
        else:
            a[i], a[i - 1] = a[i - 1], a[i]
            i -= 1
```

```
arr = [5, 3, 4, 1, 2]
gnome_sort(arr)
print(arr)
```

Why It Matters

- Demonstrates sorting through local correction
- Visually intuitive (good for animation)
- Requires no additional memory
- Stable and adaptive on partially sorted data

A Gentle Proof (Why It Works)

Each time we swap out-of-order elements, we step back to verify order with the previous one. Thus, by the time we move forward again, all prior elements are guaranteed to be sorted.

Gnome Sort effectively performs Insertion Sort via adjacent swaps.

Pass	Swaps	Movement	Sorted Portion
1	Few	Backward	Expands gradually
n	Many	Oscillating	Fully sorted

Worst-case swaps: $O(n^2)$ Best-case (already sorted): $O(n)$

Try It Yourself

Task	Description
1	Sort [5, 3, 4, 1, 2] step by step
2	Trace `i` pointer movement
3	Compare with Insertion Sort shifts
4	Animate using console output
5	Try reversed input to see maximum swaps

Test Cases

Input	Output	Swaps	Notes
[3, 2, 1]	[1, 2, 3]	3	Many backtracks
[1, 2, 3]	[1, 2, 3]	0	Already sorted
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	8	Moderate swaps

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	O(n)
Space	O(1)
Stable	Yes
Adaptive	Yes

Gnome Sort is a whimsical algorithm that teaches persistence: every time something's out of order, step back, fix it, and keep going. It's inefficient for large data but delightful for learning and visualization.

109 Odd-Even Sort

Odd-Even Sort, also known as Brick Sort, is a parallel-friendly variant of Bubble Sort. It alternates between comparing odd-even and even-odd indexed pairs to gradually sort the array. It's especially useful in parallel processing where pairs can be compared simultaneously.

What Problem Are We Solving?

Bubble Sort compares every adjacent pair in one sweep. Odd-Even Sort breaks this into two alternating phases:

- Odd phase: compare (1,2), (3,4), (5,6), …
- Even phase: compare (0,1), (2,3), (4,5), …

Repeating these two passes ensures all adjacent pairs eventually become sorted.

It's ideal for parallel systems or hardware implementations since comparisons in each phase are independent.

Example

Phase	Type	Array State	Action
0	Init	[5, 3, 4, 1, 2]	Start
1	Even	[3, 5, 1, 4, 2]	Compare (0,1), (2,3), (4,5)
2	Odd	[3, 1, 5, 2, 4]	Compare (1,2), (3,4)
3	Even	[1, 3, 2, 4, 5]	Compare (0,1), (2,3), (4,5)
4	Odd	[1, 2, 3, 4, 5]	Compare (1,2), (3,4) → Sorted

How Does It Work (Plain Language)?

Odd-Even Sort moves elements closer to their correct position with every alternating phase. It works like a traffic system: cars at even intersections move, then cars at odd intersections move. Over time, all cars (elements) line up in order.

Step-by-Step Process

Step	Action	Result
1	Compare all even-odd pairs	Swap if out of order
2	Compare all odd-even pairs	Swap if out of order
3	Repeat until no swaps occur	Sorted array

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdbool.h>

void odd_even_sort(int a[], int n) {
    bool sorted = false;
    while (!sorted) {
        sorted = true;

        // Even phase
        for (int i = 0; i < n - 1; i += 2) {
            if (a[i] > a[i + 1]) {
```

```
                int temp = a[i];
                a[i] = a[i + 1];
                a[i + 1] = temp;
                sorted = false;
            }
        }

        // Odd phase
        for (int i = 1; i < n - 1; i += 2) {
            if (a[i] > a[i + 1]) {
                int temp = a[i];
                a[i] = a[i + 1];
                a[i + 1] = temp;
                sorted = false;
            }
        }
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    odd_even_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def odd_even_sort(a):
    n = len(a)
    sorted = False
    while not sorted:
        sorted = True

        # Even phase
        for i in range(0, n - 1, 2):
            if a[i] > a[i + 1]:
                a[i], a[i + 1] = a[i + 1], a[i]
                sorted = False
```

```
        # Odd phase
        for i in range(1, n - 1, 2):
            if a[i] > a[i + 1]:
                a[i], a[i + 1] = a[i + 1], a[i]
                sorted = False

arr = [5, 3, 4, 1, 2]
odd_even_sort(arr)
print(arr)
```

Why It Matters

- Demonstrates parallel sorting principles
- Conceptually simple, easy to visualize
- Can be implemented on parallel processors (SIMD, GPU)
- Stable and in-place

A Gentle Proof (Why It Works)

Odd-Even Sort systematically removes all inversions by alternating comparisons:

- Even phase fixes pairs (0,1), (2,3), (4,5), …
- Odd phase fixes pairs (1,2), (3,4), (5,6), …

After n iterations, every element "bubbles" to its position. It behaves like Bubble Sort but is more structured and phase-based.

Phase	Comparisons	Independent?	Swaps
Even	n/2	Yes	Some
Odd	n/2	Yes	Some

Total complexity remains $O(n^2)$, but parallelizable phases reduce wall-clock time.

Try It Yourself

Task	Description
1	Trace [5, 3, 4, 1, 2] through phases
2	Count number of phases to sort

Task	Description
3	Implement using threads (parallel version)
4	Compare with Bubble Sort
5	Animate even and odd passes

Test Cases

Input	Output	Phases	Notes
[3, 2, 1]	[1, 2, 3]	3	Alternating passes
[1, 2, 3]	[1, 2, 3]	1	Early stop
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	4	Moderate passes

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Best)	O(n)
Space	O(1)
Stable	Yes
Adaptive	Yes

Odd-Even Sort shows that structure matters. By alternating phases, it opens the door to parallel sorting, where independent comparisons can run at once, a neat step toward high-performance sorting.

110 Stooge Sort

Stooge Sort is one of the most unusual and quirky recursive sorting algorithms. It's not efficient, but it's fascinating because it sorts by recursively sorting overlapping sections of the array, a great way to study recursion and algorithmic curiosity.

What Problem Are We Solving?

Stooge Sort doesn't aim for speed. Instead, it provides an example of a recursive divide-and-conquer strategy that's neither efficient nor conventional. It divides the array into overlapping parts and recursively sorts them, twice on the first two-thirds, once on the last two-thirds.

This algorithm is often used for educational purposes to demonstrate how recursion can be applied in non-traditional ways.

Example

Step	Range	Action	Array State
0	[0..4]	Start sorting [5,3,4,1,2]	[5,3,4,1,2]
1	[0..3]	Sort first 2/3 (4 elements)	[3,4,1,5,2]
2	[1..4]	Sort last 2/3 (4 elements)	[3,1,4,2,5]
3	[0..3]	Sort first 2/3 again (4 elements)	[1,3,2,4,5]
4	Repeat	Until subarrays shrink to length 1	[1,2,3,4,5]

How Does It Work (Plain Language)?

If the first element is larger than the last, swap them. Then recursively:

1. Sort the first two-thirds of the array.
2. Sort the last two-thirds of the array.
3. Sort the first two-thirds again.

It's like checking the front, then the back, then rechecking the front, until everything settles in order.

Step-by-Step Process

Step	Action
1	Compare first and last elements; swap if needed
2	Recursively sort first 2/3 of array
3	Recursively sort last 2/3 of array
4	Recursively sort first 2/3 again
5	Stop when subarray length 1

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void stooge_sort(int a[], int l, int h) {
    if (a[l] > a[h]) {
        int temp = a[l];
        a[l] = a[h];
        a[h] = temp;
    }
    if (h - l + 1 > 2) {
        int t = (h - l + 1) / 3;
        stooge_sort(a, l, h - t);
        stooge_sort(a, l + t, h);
        stooge_sort(a, l, h - t);
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    stooge_sort(a, 0, n - 1);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def stooge_sort(a, l, h):
    if a[l] > a[h]:
        a[l], a[h] = a[h], a[l]
    if h - l + 1 > 2:
        t = (h - l + 1) // 3
        stooge_sort(a, l, h - t)
        stooge_sort(a, l + t, h)
        stooge_sort(a, l, h - t)

arr = [5, 3, 4, 1, 2]
stooge_sort(arr, 0, len(arr) - 1)
print(arr)
```

Why It Matters

- Demonstrates recursive divide-and-conquer logic
- A fun counterexample to "more recursion = more speed"
- Useful in theoretical discussions or algorithmic humor
- Helps build understanding of overlapping subproblems

A Gentle Proof (Why It Works)

At each step, Stooge Sort ensures:

- The smallest element moves toward the front,
- The largest element moves toward the back,
- The array converges to sorted order through overlapping recursive calls.

Each recursion operates on 2/3 of the range, repeated 3 times, giving recurrence:

$$T(n) = 3T(2n/3) + O(1)$$

Solving it (using Master Theorem):

$$T(n) = O(n^{\log_{1.5} 3}) \approx O(n^{2.7095})$$

Slower than Bubble Sort ($O(n^2)$)!

Step	Subarray Length	Recursive Calls	Work per Level
n	3	O(1)	Constant
n/2	3×3	O(3)	Larger
…	…	…	…

Try It Yourself

Task	Description
1	Sort [5, 3, 4, 1, 2] manually and trace recursive calls
2	Count total swaps
3	Print recursion depth
4	Compare with Merge Sort steps
5	Measure runtime for n=10, 100, 1000

Test Cases

Input	Output	Recursion Depth	Notes
[3, 2, 1]	[1, 2, 3]	3	Works recursively
[1, 2, 3]	[1, 2, 3]	1	Minimal swaps
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	6	Many overlaps

Complexity

Aspect	Value
Time (Worst)	$O(n^{2.7095})$
Time (Best)	$O(n^{2.7095})$
Space	O(log n) recursion stack
Stable	No
Adaptive	No

Stooge Sort is a delightful oddity, slow, redundant, but undeniably creative. It reminds us that not every recursive idea leads to efficiency, and that algorithm design is as much art as science.

Section 12. Divide and conquer sorting

111 Merge Sort

Merge Sort is one of the most famous divide-and-conquer sorting algorithms. It splits the array into halves, sorts each half recursively, and then merges the two sorted halves into a single sorted array. It guarantees O(n log n) performance, is stable, and serves as the backbone of many modern sorting libraries.

What Problem Are We Solving?

We want a sorting algorithm that is:

- Efficient on large datasets (O(n log n))
- Stable (preserves equal element order)
- Predictable (no worst-case degradation)

Merge Sort achieves this by dividing the problem into smaller, easily solved subproblems and combining their results.

It's ideal for:

- Sorting linked lists
- External sorting (on disk)
- Stable merges (for multi-key sorting)

Example

Step	Action	Result
0	Input	[5, 3, 4, 1, 2]
1	Split	[5, 3, 4] and [1, 2]
2	Split further	[5], [3, 4], [1], [2]
3	Sort subarrays	[3, 4, 5], [1, 2]
4	Merge sorted halves	[1, 2, 3, 4, 5]

How Does It Work (Plain Language)?

1. Divide: Split the array into two halves.
2. Conquer: Recursively sort both halves.
3. Combine: Merge the sorted halves into a single sorted array.

Think of it as sorting two smaller piles, then interleaving them in order, like merging two stacks of playing cards.

Step-by-Step Process

- If the array has 0 or 1 element, it's already sorted.
- Recursively sort left and right halves.
- Use a helper merge function to combine them.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void merge(int a[], int left, int mid, int right) {
    int n1 = mid - left + 1, n2 = right - mid;
    int L[n1], R[n2];

    for (int i = 0; i < n1; i++) L[i] = a[left + i];
    for (int j = 0; j < n2; j++) R[j] = a[mid + 1 + j];

    int i = 0, j = 0, k = left;
    while (i < n1 && j < n2) {
        if (L[i] <= R[j]) a[k++] = L[i++];
        else a[k++] = R[j++];
    }
    while (i < n1) a[k++] = L[i++];
    while (j < n2) a[k++] = R[j++];
}

void merge_sort(int a[], int left, int right) {
    if (left < right) {
        int mid = left + (right - left) / 2;
        merge_sort(a, left, mid);
        merge_sort(a, mid + 1, right);
        merge(a, left, mid, right);
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    merge_sort(a, 0, n - 1);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def merge_sort(a):
    if len(a) > 1:
        mid = len(a) // 2
```

```
        left = a[:mid]
        right = a[mid:]

        merge_sort(left)
        merge_sort(right)

        i = j = k = 0
        while i < len(left) and j < len(right):
            if left[i] <= right[j]:
                a[k] = left[i]
                i += 1
            else:
                a[k] = right[j]
                j += 1
            k += 1

        while i < len(left):
            a[k] = left[i]
            i += 1
            k += 1
        while j < len(right):
            a[k] = right[j]
            j += 1
            k += 1

arr = [5, 3, 4, 1, 2]
merge_sort(arr)
print(arr)
```

Why It Matters

- Stable: Keeps relative order of equal elements
- Deterministic O(n log n): Always efficient
- Parallelizable: Subarrays can be sorted independently
- Foundation: For hybrid algorithms like TimSort and External Merge Sort

A Gentle Proof (Why It Works)

Merge Sort divides the array into two halves at each level. There are log n levels of recursion, and each merge takes O(n) time.

So total time:

$$T(n) = O(n \log n)$$

Merging is linear because each element is copied once per level.

Step	Work	Subarrays	Total
1	O(n)	1	O(n)
2	O(n/2) × 2	2	O(n)
3	O(n/4) × 4	4	O(n)
...	...	...	O(n log n)

Try It Yourself

1. Split [5, 3, 4, 1, 2] into halves step by step.
2. Merge [3, 5] and [1, 4] manually.
3. Trace the recursive calls on paper.
4. Implement an iterative bottom-up version.
5. Modify to sort descending.
6. Print arrays at each merge step.
7. Compare the number of comparisons vs. Bubble Sort.
8. Try merging two pre-sorted arrays [1,3,5] and [2,4,6].
9. Sort a list of strings (alphabetically).
10. Visualize the recursion tree for n = 8.

Test Cases

Input	Output	Notes
[3, 2, 1]	[1, 2, 3]	Standard test
[1, 2, 3]	[1, 2, 3]	Already sorted
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	General case
[2, 2, 1, 1]	[1, 1, 2, 2]	Tests stability

Complexity

Aspect	Value
Time (Worst)	O(n log n)
Time (Best)	O(n log n)

Aspect	Value
Time (Average)	O(n log n)
Space	O(n)
Stable	Yes
Adaptive	No

Merge Sort is your first taste of divide and conquer sorting, calm, reliable, and elegant. It divides the problem cleanly, conquers recursively, and merges with precision.

112 Iterative Merge Sort

Iterative Merge Sort is a non-recursive version of Merge Sort that uses bottom-up merging. Instead of dividing recursively, it starts with subarrays of size 1 and iteratively merges them in pairs, doubling the size each round. This makes it ideal for environments where recursion is expensive or limited.

What Problem Are We Solving?

Recursive Merge Sort requires function calls and stack space. In some systems, recursion might be slow or infeasible (e.g. embedded systems, large arrays). Iterative Merge Sort avoids recursion by sorting iteratively, merging subarrays of increasing size until the entire array is sorted.

It's especially handy for:

- Iterative environments (no recursion)
- Large data sets (predictable memory)
- External sorting with iterative passes

Example

Step	Subarray Size	Action	Array State
0	1	Each element is trivially sorted	[5, 3, 4, 1, 2]
1	1	Merge pairs of 1-element subarrays	[3, 5, 1, 4, 2]
2	2	Merge pairs of 2-element subarrays	[1, 3, 4, 5, 2]
3	4	Merge 4-element sorted block with last	[1, 2, 3, 4, 5]
4	Done	Fully sorted	[1, 2, 3, 4, 5]

How Does It Work (Plain Language)?

Think of it as sorting small groups first and then merging those into bigger groups, no recursion required.

Process:

1. Start with subarrays of size 1 (already sorted).
2. Merge adjacent pairs of subarrays.
3. Double the subarray size and repeat.
4. Continue until subarray size n.

Step-by-Step Process

- Outer loop: size = 1, 2, 4, 8, … until n
- Inner loop: merge every two adjacent blocks of given size

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void merge(int a[], int left, int mid, int right) {
    int n1 = mid - left + 1, n2 = right - mid;
    int L[n1], R[n2];
    for (int i = 0; i < n1; i++) L[i] = a[left + i];
    for (int j = 0; j < n2; j++) R[j] = a[mid + 1 + j];

    int i = 0, j = 0, k = left;
    while (i < n1 && j < n2) {
        if (L[i] <= R[j]) a[k++] = L[i++];
        else a[k++] = R[j++];
    }
    while (i < n1) a[k++] = L[i++];
    while (j < n2) a[k++] = R[j++];
}

void iterative_merge_sort(int a[], int n) {
    for (int size = 1; size < n; size *= 2) {
        for (int left = 0; left < n - 1; left += 2 * size) {
```

```
            int mid = left + size - 1;
            int right = (left + 2 * size - 1 < n - 1) ? (left + 2 * size - 1) : (n - 1);
            if (mid < right)
                merge(a, left, mid, right);
        }
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    iterative_merge_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def merge(a, left, mid, right):
    left_arr = a[left:mid+1]
    right_arr = a[mid+1:right+1]
    i = j = 0
    k = left
    while i < len(left_arr) and j < len(right_arr):
        if left_arr[i] <= right_arr[j]:
            a[k] = left_arr[i]
            i += 1
        else:
            a[k] = right_arr[j]
            j += 1
        k += 1
    while i < len(left_arr):
        a[k] = left_arr[i]
        i += 1
        k += 1
    while j < len(right_arr):
        a[k] = right_arr[j]
        j += 1
        k += 1
```

```
def iterative_merge_sort(a):
    n = len(a)
    size = 1
    while size < n:
        for left in range(0, n, 2 * size):
            mid = min(left + size - 1, n - 1)
            right = min(left + 2 * size - 1, n - 1)
            if mid < right:
                merge(a, left, mid, right)
        size *= 2

arr = [5, 3, 4, 1, 2]
iterative_merge_sort(arr)
print(arr)
```

Why It Matters

- Eliminates recursion (more predictable memory usage)
- Still guarantees O(n log n) performance
- Useful for iterative, bottom-up, or external sorting
- Easier to parallelize since merge operations are independent

A Gentle Proof (Why It Works)

Each iteration doubles the sorted block size. Since each element participates in log n merge levels, and each level costs O(n) work, total cost:

$$T(n) = O(n \log n)$$

Like recursive Merge Sort, each merge step is linear, and merging subarrays is stable.

Iteration	Block Size	Merges	Work
1	1	n/2	O(n)
2	2	n/4	O(n)
3	4	n/8	O(n)
...	...	...	...

Total = O(n log n)

Try It Yourself

1. Sort [5, 3, 4, 1, 2] manually using bottom-up passes.
2. Trace each pass: subarray size = $1 \rightarrow 2 \rightarrow 4$.
3. Print intermediate arrays after each pass.
4. Compare recursion depth with recursive version.
5. Implement a space-efficient version (in-place merge).
6. Modify to sort descending.
7. Apply to linked list version.
8. Test performance on large array (n = 10).
9. Visualize merging passes as a tree.
10. Implement on external storage (file-based).

Test Cases

Input	Output	Notes
[3, 2, 1]	[1, 2, 3]	Small test
[1, 2, 3]	[1, 2, 3]	Already sorted
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	General test
[2, 2, 1, 1]	[1, 1, 2, 2]	Tests stability

Complexity

Aspect	Value
Time (Worst)	O(n log n)
Time (Best)	O(n log n)
Space	O(n)
Stable	Yes
Adaptive	No

Iterative Merge Sort is the non-recursive twin of classic Merge Sort, efficient, stable, and memory-predictable, making it perfect when stack space is at a premium.

113 Quick Sort

Quick Sort is one of the fastest and most widely used sorting algorithms. It works by partitioning an array into two halves around a pivot element and recursively sorting the two parts. With

average-case O(n log n) performance and in-place operation, it's the go-to choice in many libraries and real-world systems.

What Problem Are We Solving?

We need a sorting algorithm that's:

- Efficient in practice (fast average case)
- In-place (minimal memory use)
- Divide-and-conquer-based (parallelizable)

Quick Sort partitions the array so that:

- All elements smaller than the pivot go left
- All elements larger go right

Then it sorts each half recursively.

It's ideal for:

- Large datasets in memory
- Systems where memory allocation is limited
- Average-case performance optimization

Example

Step	Pivot	Action	Array State
0	5	Partition	[3, 4, 1, 2, 5]
1	3	Partition left	[1, 2, 3, 4, 5]
2	Done	Sorted	[1, 2, 3, 4, 5]

How Does It Work (Plain Language)?

1. Choose a pivot element.
2. Rearrange (partition) array so:
    - Elements smaller than pivot move to the left
    - Elements larger than pivot move to the right
3. Recursively apply the same logic to each half.

Think of the pivot as the "divider" that splits the unsorted array into two smaller problems.

Step-by-Step Process

Step	Action
1	Select a pivot (e.g., last element)
2	Partition array around pivot
3	Recursively sort left and right subarrays
4	Stop when subarray size 1

Tiny Code (Easy Versions)

C (Lomuto Partition Scheme)

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int temp = *a;
    *a = *b;
    *b = temp;
}

int partition(int a[], int low, int high) {
    int pivot = a[high];
    int i = low - 1;
    for (int j = low; j < high; j++) {
        if (a[j] < pivot) {
            i++;
            swap(&a[i], &a[j]);
        }
    }
    swap(&a[i + 1], &a[high]);
    return i + 1;
}

void quick_sort(int a[], int low, int high) {
    if (low < high) {
        int pi = partition(a, low, high);
        quick_sort(a, low, pi - 1);
        quick_sort(a, pi + 1, high);
    }
```

```
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    quick_sort(a, 0, n - 1);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def partition(a, low, high):
    pivot = a[high]
    i = low - 1
    for j in range(low, high):
        if a[j] < pivot:
            i += 1
            a[i], a[j] = a[j], a[i]
    a[i + 1], a[high] = a[high], a[i + 1]
    return i + 1

def quick_sort(a, low, high):
    if low < high:
        pi = partition(a, low, high)
        quick_sort(a, low, pi - 1)
        quick_sort(a, pi + 1, high)

arr = [5, 3, 4, 1, 2]
quick_sort(arr, 0, len(arr) - 1)
print(arr)
```

Why It Matters

- In-place and fast in most real-world cases
- Divide and conquer: naturally parallelizable
- Often used as the default sorting algorithm in libraries (C, Java, Python)
- Introduces partitioning, a key algorithmic pattern

A Gentle Proof (Why It Works)

Each partition divides the problem into smaller subarrays. Average partition splits are balanced, giving O(log n) depth and O(n) work per level:

$$T(n) = 2T(n/2) + O(n) = O(n \log n)$$

If the pivot is poor (e.g. smallest or largest), complexity degrades:

$$T(n) = T(n-1) + O(n) = O(n^2)$$

Case	Partition Quality	Complexity
Best	Perfect halves	O(n log n)
Average	Random	O(n log n)
Worst	Unbalanced	$O(n^2)$

Choosing pivots wisely (randomization, median-of-three) avoids worst-case splits.

Try It Yourself

1. Sort [5, 3, 4, 1, 2] and trace partitions.
2. Change pivot selection (first, middle, random).
3. Count comparisons and swaps for each case.
4. Implement using Hoare Partition scheme.
5. Modify to sort descending.
6. Visualize recursion tree for n = 8.
7. Compare runtime with Merge Sort.
8. Try sorted input [1, 2, 3, 4, 5] and note behavior.
9. Add a counter to count recursive calls.
10. Implement tail recursion optimization.

Test Cases

Input	Output	Notes
[3, 2, 1]	[1, 2, 3]	Basic
[1, 2, 3]	[1, 2, 3]	Worst case (sorted input)
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	General
[2, 2, 1, 1]	[1, 1, 2, 2]	Duplicates

Input	Output	Notes

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)
Time (Worst)	$O(n^2)$
Space	O(log n) (recursion)
Stable	No
Adaptive	No

Quick Sort is the practical workhorse of sorting, swift, elegant, and widely loved. It teaches how a single smart pivot can bring order to chaos.

114 Hoare Partition Scheme

The Hoare Partition Scheme is an early and elegant version of Quick Sort's partitioning method, designed by C.A.R. Hoare himself. It's more efficient than the Lomuto scheme in many cases because it does fewer swaps and uses two pointers moving inward from both ends.

What Problem Are We Solving?

In Quick Sort, we need a way to divide an array into two parts:

- Elements less than or equal to the pivot
- Elements greater than or equal to the pivot

Hoare's scheme achieves this using two indices that move toward each other, swapping elements that are out of place. It reduces the number of swaps compared to the Lomuto scheme and often performs better on real data.

It's especially useful for:

- Large arrays (fewer writes)
- Performance-critical systems
- In-place partitioning without extra space

Example

Step	Pivot	Left (i)	Right (j)	Array State	Action
0	5	i=0	j=4	[5, 3, 4, 1, 2]	pivot = 5
1	5	i→2	j→4	[5, 3, 4, 1, 2]	a[j]=2<5 swap(5,2) → [2,3,4,1,5]
2	5	i→2	j→3	[2,3,4,1,5]	a[i]=4>5? no swap
3	stop	-	-	[2,3,4,1,5]	partition done

The pivot ends up near its correct position, but not necessarily in the final index.

How Does It Work (Plain Language)?

The algorithm picks a pivot (commonly the first element), then moves two pointers:

- Left pointer (i): moves right, skipping small elements
- Right pointer (j): moves left, skipping large elements

When both pointers find misplaced elements, they are swapped. This continues until they cross, at that point, the array is partitioned.

Step-by-Step Process

1. Choose a pivot (e.g. first element).
2. Set two indices: `i = left - 1`, `j = right + 1`.
3. Increment `i` until `a[i] >= pivot`.
4. Decrement `j` until `a[j] <= pivot`.
5. If `i < j`, swap `a[i]` and `a[j]`. Otherwise, return `j` (partition index).

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int temp = *a;
    *a = *b;
    *b = temp;
```

```c
}

int hoare_partition(int a[], int low, int high) {
    int pivot = a[low];
    int i = low - 1;
    int j = high + 1;

    while (1) {
        do { i++; } while (a[i] < pivot);
        do { j--; } while (a[j] > pivot);
        if (i >= j) return j;
        swap(&a[i], &a[j]);
    }
}

void quick_sort_hoare(int a[], int low, int high) {
    if (low < high) {
        int p = hoare_partition(a, low, high);
        quick_sort_hoare(a, low, p);
        quick_sort_hoare(a, p + 1, high);
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    quick_sort_hoare(a, 0, n - 1);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def hoare_partition(a, low, high):
    pivot = a[low]
    i = low - 1
    j = high + 1
    while True:
        i += 1
        while a[i] < pivot:
```

```
            i += 1
        j -= 1
        while a[j] > pivot:
            j -= 1
        if i >= j:
            return j
        a[i], a[j] = a[j], a[i]

def quick_sort_hoare(a, low, high):
    if low < high:
        p = hoare_partition(a, low, high)
        quick_sort_hoare(a, low, p)
        quick_sort_hoare(a, p + 1, high)

arr = [5, 3, 4, 1, 2]
quick_sort_hoare(arr, 0, len(arr) - 1)
print(arr)
```

Why It Matters

- Fewer swaps than Lomuto partition
- More efficient in practice on most datasets
- Still in-place, divide-and-conquer, O(n log n) average
- Introduces the idea of two-pointer partitioning

A Gentle Proof (Why It Works)

The loop invariants ensure that:

- Left side: all elements pivot
- Right side: all elements pivot
- `i` and `j` move inward until they cross When they cross, all elements are partitioned correctly.

The pivot does not end in its final sorted position, but the subarrays can be recursively sorted independently.

$$T(n) = T(k) + T(n - k - 1) + O(n)$$

Average complexity O(n log n); worst-case $O(n^2)$ if pivot is poor.

Case	Pivot	Behavior	Complexity
Best	Median	Balanced halves	O(n log n)
Average	Random	Slight imbalance	O(n log n)
Worst	Min/Max	Unbalanced	$O(n^2)$

Try It Yourself

1. Sort [5, 3, 4, 1, 2] step by step using Hoare's scheme.
2. Print `i` and `j` at each iteration.
3. Compare with Lomuto's version on the same array.
4. Try different pivot positions (first, last, random).
5. Measure number of swaps vs. Lomuto.
6. Modify to sort descending.
7. Visualize partition boundaries.
8. Test on array with duplicates [3,3,2,1,4].
9. Implement hybrid pivot selection (median-of-three).
10. Compare runtime with Merge Sort.

Test Cases

Input	Output	Notes
[3, 2, 1]	[1, 2, 3]	Simple
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	General
[2, 2, 1, 1]	[1, 1, 2, 2]	Works with duplicates
[1, 2, 3, 4, 5]	[1, 2, 3, 4, 5]	Sorted input (worst case)

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)
Time (Worst)	$O(n^2)$
Space	O(log n) recursion
Stable	No
Adaptive	No

Hoare Partition Scheme is elegant and efficient, the original genius of Quick Sort. Its two-pointer dance is graceful and economical, a timeless classic in algorithm design.

115 Lomuto Partition Scheme

The Lomuto Partition Scheme is a simple and widely taught method for partitioning in Quick Sort. It's easier to understand and implement than Hoare's scheme, though it often performs slightly more swaps. It always selects a pivot (commonly the last element) and partitions the array in a single forward pass.

What Problem Are We Solving?

We need a clear and intuitive way to partition an array around a pivot, ensuring all smaller elements go to the left and all larger elements go to the right.

Lomuto's method uses one scanning pointer and one boundary pointer, making it easy for beginners and ideal for pedagogical purposes or small datasets.

Example

Step	Pivot	i (Boundary)	j (Scan)	Array State	Action
0	2	i=-1	j=0	[5, 3, 4, 1, 2]	pivot = 2
1	2	i=-1	j=0	a[0]=5>2 → no swap	
2	2	i=-1	j=1	a[1]=3>2 → no swap	
3	2	i=-1	j=2	a[2]=4>2 → no swap	
4	2	i=0	j=3	a[3]=1<2 → swap(5,1) → [1,3,4,5,2]	
5	2	i=0	j=4	end of scan; swap pivot with a[i+1]=a[1]	
6	Done	-	-	[1,2,4,5,3] partitioned	

Pivot 2 is placed in its final position at index 1. Elements left of 2 are smaller, right are larger.

How Does It Work (Plain Language)?

1. Choose a pivot (commonly last element).
2. Initialize boundary pointer `i` before start of array.
3. Iterate through array with pointer `j`:

- If `a[j] < pivot`, increment `i` and swap `a[i]` with `a[j]`.

4. After loop, swap `pivot` into position `i + 1`.
5. Return `i + 1` (pivot's final position).

It's like separating a deck of cards, you keep moving smaller cards to the front as you scan.

Step-by-Step Process

Step	Action
1	Choose pivot (usually last element)
2	Move smaller elements before pivot
3	Move larger elements after pivot
4	Place pivot in its correct position
5	Return pivot index for recursive sorting

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int temp = *a;
    *a = *b;
    *b = temp;
}

int lomuto_partition(int a[], int low, int high) {
    int pivot = a[high];
    int i = low - 1;
    for (int j = low; j < high; j++) {
        if (a[j] < pivot) {
            i++;
            swap(&a[i], &a[j]);
        }
    }
    swap(&a[i + 1], &a[high]);
    return i + 1;
```

```c
}

void quick_sort_lomuto(int a[], int low, int high) {
    if (low < high) {
        int pi = lomuto_partition(a, low, high);
        quick_sort_lomuto(a, low, pi - 1);
        quick_sort_lomuto(a, pi + 1, high);
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    quick_sort_lomuto(a, 0, n - 1);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def lomuto_partition(a, low, high):
    pivot = a[high]
    i = low - 1
    for j in range(low, high):
        if a[j] < pivot:
            i += 1
            a[i], a[j] = a[j], a[i]
    a[i + 1], a[high] = a[high], a[i + 1]
    return i + 1

def quick_sort_lomuto(a, low, high):
    if low < high:
        pi = lomuto_partition(a, low, high)
        quick_sort_lomuto(a, low, pi - 1)
        quick_sort_lomuto(a, pi + 1, high)

arr = [5, 3, 4, 1, 2]
quick_sort_lomuto(arr, 0, len(arr) - 1)
print(arr)
```

Why It Matters

- Simple and easy to implement
- Pivot ends in correct final position each step
- Useful for educational demonstration of Quick Sort
- Common in textbooks and basic Quick Sort examples

A Gentle Proof (Why It Works)

Invariant:

- Elements left of `i` are smaller than pivot.
- Elements between `i` and `j` are greater or not yet checked. At the end, swapping pivot with `a[i+1]` places it in its final position.

Time complexity:

$$T(n) = T(k) + T(n - k - 1) + O(n)$$

Average: O(n log n) Worst (already sorted): O(n^2)

Case	Partition	Complexity
Best	Balanced	O(n log n)
Average	Random	O(n log n)
Worst	Unbalanced	O(n^2)

Try It Yourself

1. Sort [5, 3, 4, 1, 2] using Lomuto step by step.
2. Trace `i` and `j` positions at each comparison.
3. Compare with Hoare partition's number of swaps.
4. Test with sorted input, see worst case.
5. Randomize pivot to avoid worst-case.
6. Modify to sort descending order.
7. Count total swaps and comparisons.
8. Combine with tail recursion optimization.
9. Visualize partition boundary after each pass.
10. Implement a hybrid Quick Sort using Lomuto for small arrays.

Test Cases

Input	Output	Notes
[3, 2, 1]	[1, 2, 3]	Simple
[1, 2, 3]	[1, 2, 3]	Worst-case
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	General
[2, 2, 1, 1]	[1, 1, 2, 2]	Handles duplicates

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)
Time (Worst)	$O(n^2)$
Space	O(log n) recursion
Stable	No
Adaptive	No

Lomuto's scheme is the friendly teacher of Quick Sort, easy to grasp, simple to code, and perfect for building intuition about partitioning and divide-and-conquer sorting.

116 Randomized Quick Sort

Randomized Quick Sort enhances the classic Quick Sort by choosing the pivot randomly. This small tweak eliminates the risk of hitting the worst-case $O(n^2)$ behavior on already sorted or adversarial inputs, making it one of the most robust and practical sorting strategies in real-world use.

What Problem Are We Solving?

Regular Quick Sort can degrade badly if the pivot is chosen poorly (for example, always picking the first or last element in a sorted array). Randomized Quick Sort fixes this by selecting a random pivot, ensuring that, on average, partitions are balanced, regardless of input distribution.

This makes it ideal for:

- Unpredictable or adversarial inputs

- Large datasets where worst-case avoidance matters
- Performance-critical systems requiring consistent behavior

Example

Step	Action	Array State	Pivot
0	Choose random pivot	[5, 3, 4, 1, 2]	4
1	Partition around 4	[3, 2, 1, 4, 5]	4 at index 3
2	Recurse on left [3, 2, 1]	[1, 2, 3]	2
3	Merge subarrays	[1, 2, 3, 4, 5]	Done

Randomization ensures the pivot is unlikely to create unbalanced partitions.

How Does It Work (Plain Language)?

It's the same Quick Sort, but before partitioning, we randomly pick one element and use it as the pivot. This random pivot is swapped into the last position, and the normal Lomuto or Hoare partitioning continues.

This small randomness makes it robust and efficient on average, even for worst-case inputs.

Step-by-Step Process

1. Pick a random pivot index between `low` and `high`.
2. Swap the random pivot with the last element.
3. Partition the array (e.g., Lomuto or Hoare).
4. Recursively sort left and right partitions.

Tiny Code (Easy Versions)

C (Lomuto + Random Pivot)

```c
#include <stdio.h>
#include <stdlib.h>
#include <time.h>

void swap(int *a, int *b) {
    int temp = *a;
```

```
    *a = *b;
    *b = temp;
}

int lomuto_partition(int a[], int low, int high) {
    int pivot = a[high];
    int i = low - 1;
    for (int j = low; j < high; j++) {
        if (a[j] < pivot) {
            i++;
            swap(&a[i], &a[j]);
        }
    }
    swap(&a[i + 1], &a[high]);
    return i + 1;
}

int randomized_partition(int a[], int low, int high) {
    int pivotIndex = low + rand() % (high - low + 1);
    swap(&a[pivotIndex], &a[high]);
    return lomuto_partition(a, low, high);
}

void randomized_quick_sort(int a[], int low, int high) {
    if (low < high) {
        int pi = randomized_partition(a, low, high);
        randomized_quick_sort(a, low, pi - 1);
        randomized_quick_sort(a, pi + 1, high);
    }
}

int main(void) {
    srand(time(NULL));
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    randomized_quick_sort(a, 0, n - 1);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
import random

def lomuto_partition(a, low, high):
    pivot = a[high]
    i = low - 1
    for j in range(low, high):
        if a[j] < pivot:
            i += 1
            a[i], a[j] = a[j], a[i]
    a[i + 1], a[high] = a[high], a[i + 1]
    return i + 1

def randomized_partition(a, low, high):
    pivot_index = random.randint(low, high)
    a[pivot_index], a[high] = a[high], a[pivot_index]
    return lomuto_partition(a, low, high)

def randomized_quick_sort(a, low, high):
    if low < high:
        pi = randomized_partition(a, low, high)
        randomized_quick_sort(a, low, pi - 1)
        randomized_quick_sort(a, pi + 1, high)

arr = [5, 3, 4, 1, 2]
randomized_quick_sort(arr, 0, len(arr) - 1)
print(arr)
```

Why It Matters

- Prevents worst-case $O(n^2)$ behavior
- Simple yet highly effective
- Ensures consistent average-case across all inputs
- Foundation for Randomized Select and Randomized Algorithms

A Gentle Proof (Why It Works)

Random pivot selection ensures the expected split size is balanced, independent of input order. Each pivot divides the array such that expected recursion depth is O(log n) and total

comparisons O(n log n).

Expected complexity:

$$E[T(n)] = O(n \log n)$$

Worst-case only occurs with extremely low probability (1/n!).

Case	Pivot Choice	Complexity
Best	Balanced	O(n log n)
Average	Random	O(n log n)
Worst	Unlucky (rare)	O(n^2)

Try It Yourself

1. Sort [5, 3, 4, 1, 2] multiple times, note pivot differences.
2. Print pivot each recursive call.
3. Compare against deterministic pivot (first, last).
4. Test on sorted input [1, 2, 3, 4, 5].
5. Test on reverse input [5, 4, 3, 2, 1].
6. Count recursive depth across runs.
7. Modify to use Hoare partition.
8. Implement `random.choice()` version.
9. Compare runtime vs. normal Quick Sort.
10. Seed RNG to reproduce same run.

Test Cases

Input	Output	Notes
[3, 2, 1]	[1, 2, 3]	Random pivot each run
[1, 2, 3]	[1, 2, 3]	Avoids O(n^2)
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	General
[2, 2, 1, 1]	[1, 1, 2, 2]	Handles duplicates

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)

Aspect	Value
Time (Worst)	$O(n^2)$ (rare)
Space	O(log n)
Stable	No
Adaptive	No

Randomized Quick Sort shows the power of randomness, a tiny change transforms a fragile algorithm into a reliably fast one, making it one of the most practical sorts in modern computing.

117 Heap Sort

Heap Sort is a classic comparison-based, in-place, O(n log n) sorting algorithm built upon the heap data structure. It first turns the array into a max-heap, then repeatedly removes the largest element (the heap root) and places it at the end, shrinking the heap as it goes. It's efficient and memory-friendly but not stable.

What Problem Are We Solving?

We want a sorting algorithm that:

- Has guaranteed O(n log n) time in all cases
- Uses constant extra space (O(1))
- Doesn't require recursion or extra arrays like Merge Sort

Heap Sort achieves this by using a binary heap to always extract the largest element efficiently, then placing it in its correct position at the end.

Perfect for:

- Memory-constrained systems
- Predictable performance needs
- Offline sorting when data fits in RAM

Example

Step	Action	Array State	Heap Size
0	Build max-heap	[5, 3, 4, 1, 2]	5
1	Swap root with last	[2, 3, 4, 1, 5]	4

Step	Action	Array State	Heap Size
2	Heapify root	[4, 3, 2, 1, 5]	4
3	Swap root with last	[1, 3, 2, 4, 5]	3
4	Heapify root	[3, 1, 2, 4, 5]	3
5	Repeat until heap shrinks	[1, 2, 3, 4, 5]	0

How Does It Work (Plain Language)?

Think of a heap like a tree stored in an array. The root (index 0) is the largest element. Heap Sort works in two main steps:

1. Build a max-heap (arranged so every parent its children)
2. Extract max repeatedly:
    - Swap root with last element
    - Reduce heap size
    - Heapify root to restore max-heap property

After each extraction, the sorted part grows at the end of the array.

Step-by-Step Process

Step	Description
1	Build a max-heap from the array
2	Swap the first (max) with the last element
3	Reduce heap size by one
4	Heapify the root
5	Repeat until heap is empty

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int temp = *a;
```

```
    *a = *b;
    *b = temp;
}

void heapify(int a[], int n, int i) {
    int largest = i;
    int left = 2 * i + 1;
    int right = 2 * i + 2;

    if (left < n && a[left] > a[largest]) largest = left;
    if (right < n && a[right] > a[largest]) largest = right;

    if (largest != i) {
        swap(&a[i], &a[largest]);
        heapify(a, n, largest);
    }
}

void heap_sort(int a[], int n) {
    // Build max heap
    for (int i = n / 2 - 1; i >= 0; i--)
        heapify(a, n, i);

    // Extract elements from heap
    for (int i = n - 1; i > 0; i--) {
        swap(&a[0], &a[i]);
        heapify(a, i, 0);
    }
}

int main(void) {
    int a[] = {5, 3, 4, 1, 2};
    int n = sizeof(a) / sizeof(a[0]);
    heap_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```
def heapify(a, n, i):
    largest = i
    left = 2 * i + 1
    right = 2 * i + 2
    if left < n and a[left] > a[largest]:
        largest = left
    if right < n and a[right] > a[largest]:
        largest = right
    if largest != i:
        a[i], a[largest] = a[largest], a[i]
        heapify(a, n, largest)

def heap_sort(a):
    n = len(a)
    # Build max heap
    for i in range(n // 2 - 1, -1, -1):
        heapify(a, n, i)
    # Extract max and heapify
    for i in range(n - 1, 0, -1):
        a[0], a[i] = a[i], a[0]
        heapify(a, i, 0)

arr = [5, 3, 4, 1, 2]
heap_sort(arr)
print(arr)
```

Why It Matters

- Predictable O(n log n) in all cases
- In-place, no extra memory needed
- Excellent when memory is tight or recursion is not preferred
- Demonstrates tree-based sorting logic

A Gentle Proof (Why It Works)

Building the heap: O(n) Extracting each element: O(log n) Total time:

$$T(n) = O(n) + n \times O(\log n) = O(n \log n)$$

Each element is "bubbled down" log n levels at most once.

Phase	Work	Total
Build heap	O(n)	Linear
Extract n elements	n × O(log n)	O(n log n)

Not stable, because swapping can break equal-element order.

Try It Yourself

1. Build max-heap from [5, 3, 4, 1, 2].
2. Draw heap tree for each step.
3. Trace heapify calls and swaps.
4. Implement min-heap version for descending sort.
5. Count comparisons per phase.
6. Compare with Merge Sort space usage.
7. Modify to stop early if already sorted.
8. Animate heap construction.
9. Test on reverse array [5,4,3,2,1].
10. Add debug prints showing heap after each step.

Test Cases

Input	Output	Notes
[3, 2, 1]	[1, 2, 3]	Small test
[1, 2, 3]	[1, 2, 3]	Already sorted
[5, 3, 4, 1, 2]	[1, 2, 3, 4, 5]	General case
[2, 2, 1, 1]	[1, 1, 2, 2]	Not stable but correct

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(1)
Stable	No

Aspect	Value
Adaptive	No

Heap Sort is the workhorse of guaranteed performance, steady, space-efficient, and built on elegant tree logic. It never surprises you with bad cases, a reliable friend when consistency matters.

118 3-Way Quick Sort

3-Way Quick Sort is a refined version of Quick Sort designed to handle arrays with many duplicate elements efficiently. Instead of dividing the array into two parts (less than and greater than pivot), it divides into three regions:

- `< pivot`
- `= pivot`
- `> pivot`

This avoids redundant work when many elements are equal to the pivot, making it especially effective for datasets with low entropy or repeated keys.

What Problem Are We Solving?

Standard Quick Sort can perform unnecessary work when duplicates are present. For example, if all elements are the same, standard Quick Sort still recurses O(n log n) times.

3-Way Quick Sort fixes this by:

- Skipping equal elements during partitioning
- Shrinking recursion depth dramatically

It's ideal for:

- Arrays with many duplicates
- Sorting strings with common prefixes
- Key-value pairs with repeated keys

Step	Pivot	Action	Array State	Partitions

Example

Step	Pivot	Action	Array State	Partitions
0	3	Start	[3, 2, 3, 1, 3]	l=0, i=0, g=4
1	3	a[i]=3 → equal	[3, 2, 3, 1, 3]	i=1
2	3	a[i]=2 < 3 → swap(a[l],a[i])	[2, 3, 3, 1, 3]	l=1, i=2
3	3	a[i]=3 → equal	[2, 3, 3, 1, 3]	i=3
4	3	a[i]=1 < 3 → swap(a[l],a[i])	[2, 1, 3, 3, 3]	l=2, i=4
5	3	a[i]=3 → equal	[2, 1, 3, 3, 3]	Done

Now recursively sort left `< pivot` region [2,1], skip the middle `=3` block, and sort right `> pivot` (empty).

How Does It Work (Plain Language)?

We track three zones using three pointers:

- `lt` (less than region)
- `i` (current element)
- `gt` (greater than region)

Each iteration compares `a[i]` with the pivot:

- If `< pivot`: swap with `lt`, expand both regions
- If `> pivot`: swap with `gt`, shrink right region
- If `= pivot`: move forward

Continue until `i > gt`. This single pass partitions array into three regions, no need to revisit equals.

Step-by-Step Process

Step	Condition	Action
1	`a[i] < pivot`	swap(a[i], a[lt]), i++, lt++
2	`a[i] > pivot`	swap(a[i], a[gt]), gt–
3	`a[i] == pivot`	i++

Step	Condition	Action
4	Stop when i > gt	

Then recursively sort `[low..lt-1]` and `[gt+1..high]`.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int temp = *a;
    *a = *b;
    *b = temp;
}

void quicksort_3way(int a[], int low, int high) {
    if (low >= high) return;

    int pivot = a[low];
    int lt = low, i = low, gt = high;

    while (i <= gt) {
        if (a[i] < pivot) {
            swap(&a[lt], &a[i]);
            lt++; i++;
        } else if (a[i] > pivot) {
            swap(&a[i], &a[gt]);
            gt--;
        } else {
            i++;
        }
    }

    quicksort_3way(a, low, lt - 1);
    quicksort_3way(a, gt + 1, high);
}
```

```c
int main(void) {
    int a[] = {3, 2, 3, 1, 3};
    int n = sizeof(a) / sizeof(a[0]);
    quicksort_3way(a, 0, n - 1);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def quicksort_3way(a, low, high):
    if low >= high:
        return
    pivot = a[low]
    lt, i, gt = low, low, high
    while i <= gt:
        if a[i] < pivot:
            a[lt], a[i] = a[i], a[lt]
            lt += 1
            i += 1
        elif a[i] > pivot:
            a[i], a[gt] = a[gt], a[i]
            gt -= 1
        else:
            i += 1
    quicksort_3way(a, low, lt - 1)
    quicksort_3way(a, gt + 1, high)

arr = [3, 2, 3, 1, 3]
quicksort_3way(arr, 0, len(arr) - 1)
print(arr)
```

Why It Matters

- Efficient for arrays with duplicates
- Reduces unnecessary recursion and comparisons
- Used in string sorting and key-heavy data
- Generalizes the idea of “partition” to multi-way splitting

A Gentle Proof (Why It Works)

Standard Quick Sort always divides into two regions, even if all elements equal the pivot, leading to $O(n^2)$ on identical elements.

3-Way Quick Sort partitions into three zones:

- `< pivot` (left)
- `= pivot` (middle)
- `> pivot` (right)

The middle zone is skipped from recursion, reducing work dramatically.

If all elements are equal → only one pass O(n).

Expected complexity:

$$T(n) = O(n \log n)$$

Worst-case (no duplicates): same as Quick Sort.

Case	Duplicates	Complexity
All equal	O(n)	One pass only
Many	O(n log n)	Efficient
None	O(n log n)	Normal behavior

Try It Yourself

1. Sort [3, 2, 3, 1, 3] step by step.
2. Print regions (`lt`, `i`, `gt`) after each iteration.
3. Compare recursion depth with normal Quick Sort.
4. Test input [1, 1, 1, 1].
5. Test input [5, 4, 3, 2, 1].
6. Sort [“apple”, “apple”, “banana”, “apple”].
7. Visualize partitions on paper.
8. Modify to count swaps and comparisons.
9. Implement descending order.
10. Apply to random integers with duplicates (e.g. [1,2,2,2,3,3,1]).

Input	Output	Notes

Test Cases

Input	Output	Notes
[3, 2, 3, 1, 3]	[1, 2, 3, 3, 3]	Duplicates
[5, 4, 3, 2, 1]	[1, 2, 3, 4, 5]	No duplicates
[2, 2, 2, 2]	[2, 2, 2, 2]	All equal (O(n))
[1, 3, 1, 3, 1]	[1, 1, 1, 3, 3]	Clustered duplicates

Complexity

Aspect	Value
Time (Best)	O(n) (all equal)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(log n) recursion
Stable	No
Adaptive	Yes (handles duplicates efficiently)

3-Way Quick Sort shows how a small change, three-way partitioning, can transform Quick Sort into a powerful tool for duplicate-heavy datasets, blending elegance with efficiency.

119 External Merge Sort

External Merge Sort is a specialized sorting algorithm designed for very large datasets that don't fit entirely into main memory (RAM). It works by sorting chunks of data in memory, writing them to disk, and then merging those sorted chunks. This makes it a key tool in databases, file systems, and big data processing.

What Problem Are We Solving?

When data exceeds RAM capacity, in-memory sorts like Quick Sort or Heap Sort fail, they need random access to all elements. External Merge Sort solves this by processing data in blocks:

- Sort manageable chunks in memory
- Write sorted chunks ("runs") to disk
- Merge runs sequentially using streaming I/O

This minimizes disk reads/writes, the main bottleneck in large-scale sorting.

It's ideal for:

- Large files (GBs to TBs)
- Database query engines
- Batch processing pipelines

Example

Let's say you have 1 GB of data and only 100 MB of RAM.

Step	Action	Description
1	Split	Divide file into 10 chunks of 100 MB
2	Sort	Load each chunk in memory, sort, write to disk
3	Merge	Use k-way merge (e.g. 10-way) to merge sorted runs
4	Output	Final sorted file written sequentially

How Does It Work (Plain Language)?

Think of it like sorting pages of a giant book:

1. Take a few pages at a time (fit in memory)
2. Sort them and place them in order piles
3. Combine the piles in order until the whole book is sorted

It's a multi-pass algorithm:

- Pass 1: Create sorted runs
- Pass 2+: Merge runs in multiple passes until one remains

Step	Description

Step-by-Step Process

Step	Description
1	Divide the large file into blocks fitting memory
2	Load a block, sort it using in-memory sort
3	Write each sorted block (run) to disk
4	Merge all runs using k-way merging
5	Repeat merges until a single sorted file remains

Tiny Code (Simplified Simulation)

Python (Simulated External Sort)

```
import heapq
import tempfile

def sort_chunk(chunk):
    chunk.sort()
    temp = tempfile.TemporaryFile(mode="w+t")
    temp.writelines(f"{x}\n" for x in chunk)
    temp.seek(0)
    return temp

def merge_files(files, output_file):
    iters = [map(int, f) for f in files]
    with open(output_file, "w") as out:
        for num in heapq.merge(*iters):
            out.write(f"{num}\n")

def external_merge_sort(input_data, chunk_size=5):
    chunks = []
    for i in range(0, len(input_data), chunk_size):
        chunk = input_data[i:i + chunk_size]
        chunks.append(sort_chunk(chunk))
    merge_files(chunks, "sorted_output.txt")
```

```
data = [42, 17, 93, 8, 23, 4, 16, 99, 55, 12, 71, 3]
external_merge_sort(data, chunk_size=4)
```

This example simulates external sorting in Python, splitting input into chunks, sorting each, and merging with `heapq.merge`.

Why It Matters

- Handles massive datasets beyond memory limits
- Sequential disk I/O (fast and predictable)
- Foundation of database sort-merge joins
- Works well with distributed systems (MapReduce, Spark)

A Gentle Proof (Why It Works)

Each pass performs O(n) work to read and write the entire dataset. If `r` is the number of runs, and `k` is merge fan-in (number of runs merged at once):

$$\text{Number of passes} = \lceil \log_k r \rceil$$

Total cost

$$O(n \log_k r)$$

dominated by I/O operations rather than comparisons.

For `r = n/M` (chunks of memory size `M`), performance is optimized by choosing `k  M`.

Phase	Work	Cost
Create Runs	O(n log M)	Sort chunks
Merge Runs	O(n log_k r)	Merge passes

Try It Yourself

1. Split [42, 17, 93, 8, 23, 4, 16, 99, 55, 12, 71, 3] into 4-element chunks.
2. Sort each chunk individually.
3. Simulate merging sorted runs.
4. Try merging 2-way vs 4-way, count passes.
5. Visualize merging tree (runs combining).
6. Test with random large arrays (simulate files).

7. Modify chunk size and observe performance.
8. Compare I/O counts with in-memory sort.
9. Use `heapq.merge` to merge sorted streams.
10. Extend to merge files on disk (not just lists).

Test Cases

Input	Memory Limit	Output	Notes
[9, 4, 7, 2, 5, 1, 8, 3, 6]	3 elements	[1,2,3,4,5,6,7,8,9]	3-way merge
1 GB integers	100 MB	Sorted file	10 sorted runs
[1,1,1,1,1]	small	[1,1,1,1,1]	Handles duplicates

Complexity

Aspect	Value
Time	O(n log_k (n/M))
Space	O(M) (memory buffer)
I/O Passes	O(log_k (n/M))
Stable	Yes
Adaptive	Yes (fewer runs if data partially sorted)

External Merge Sort is the unsung hero behind large-scale sorting, when memory ends, it steps in with disk-based precision, keeping order across terabytes with calm efficiency.

120 Parallel Merge Sort

Parallel Merge Sort takes the familiar divide-and-conquer structure of Merge Sort and spreads the work across multiple threads or processors, achieving faster sorting on multi-core CPUs or distributed systems. It's an ideal illustration of how parallelism can amplify a classic algorithm without changing its logic.

What Problem Are We Solving?

Traditional Merge Sort runs sequentially, so even though its complexity is O(n log n), it uses only one CPU core. On modern hardware with many cores, that's a waste.

Parallel Merge Sort tackles this by:

- Sorting subarrays in parallel
- Merging results concurrently
- Utilizing full CPU or cluster potential

It's essential for:

- High-performance computing
- Large-scale sorting
- Real-time analytics pipelines

Example

Sort [5, 3, 4, 1, 2] using 2 threads:

Step	Action	Threads	Result
1	Split array into halves	2 threads	[5, 3, 4], [1, 2]
2	Sort each half concurrently	T1: sort [5,3,4], T2: sort [1,2]	[3,4,5], [1,2]
3	Merge results	1 thread	[1,2,3,4,5]

Parallelism reduces total time roughly by 1 / number of threads (with overhead).

How Does It Work (Plain Language)?

It's still divide and conquer, just with teamwork:

1. Split array into two halves.
2. Sort each half in parallel.
3. Merge the two sorted halves.
4. Stop splitting when subarrays are small (then sort sequentially).

Each recursive level can launch new threads until you reach a threshold or maximum depth.

Step-by-Step Process

Step	Description
1	Divide the array into halves
2	Sort both halves concurrently
3	Wait for both to finish
4	Merge results sequentially

Step	Description
5	Repeat recursively for subparts

This pattern fits well with thread pools, task schedulers, or fork-join frameworks.

Tiny Code (Easy Versions)

C (POSIX Threads Example)

```c
#include <stdio.h>
#include <stdlib.h>
#include <pthread.h>

typedef struct {
    int *arr;
    int left;
    int right;
} Args;

void merge(int arr[], int l, int m, int r) {
    int n1 = m - l + 1, n2 = r - m;
    int L[n1], R[n2];
    for (int i = 0; i < n1; i++) L[i] = arr[l + i];
    for (int j = 0; j < n2; j++) R[j] = arr[m + 1 + j];

    int i = 0, j = 0, k = l;
    while (i < n1 && j < n2) {
        arr[k++] = (L[i] <= R[j]) ? L[i++] : R[j++];
    }
    while (i < n1) arr[k++] = L[i++];
    while (j < n2) arr[k++] = R[j++];
}

void *parallel_merge_sort(void *arg) {
    Args *args = (Args *)arg;
    int l = args->left, r = args->right;
    int *arr = args->arr;

    if (l < r) {
```

```
        int m = l + (r - l) / 2;

        Args leftArgs = {arr, l, m};
        Args rightArgs = {arr, m + 1, r};
        pthread_t leftThread, rightThread;

        pthread_create(&leftThread, NULL, parallel_merge_sort, &leftArgs);
        pthread_create(&rightThread, NULL, parallel_merge_sort, &rightArgs);

        pthread_join(leftThread, NULL);
        pthread_join(rightThread, NULL);

        merge(arr, l, m, r);
    }
    return NULL;
}

int main(void) {
    int arr[] = {5, 3, 4, 1, 2};
    int n = sizeof(arr) / sizeof(arr[0]);
    Args args = {arr, 0, n - 1};
    parallel_merge_sort(&args);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

(Note: This simple version may create too many threads; real implementations limit thread depth.)

Python (Using multiprocessing)

```
from multiprocessing import Pool

def merge(left, right):
    result = []
    i = j = 0
    while i < len(left) and j < len(right):
        if left[i] < right[j]:
            result.append(left[i])
            i += 1
```

```
        else:
            result.append(right[j])
            j += 1
    result.extend(left[i:])
    result.extend(right[j:])
    return result

def parallel_merge_sort(arr):
    if len(arr) <= 1:
        return arr
    if len(arr) < 1000:  # threshold
        return sorted(arr)
    mid = len(arr) // 2
    with Pool(2) as p:
        left, right = p.map(parallel_merge_sort, [arr[:mid], arr[mid:]])
    return merge(left, right)

arr = [5, 3, 4, 1, 2]
print(parallel_merge_sort(arr))
```

Why It Matters

- Exploits multi-core architectures
- Significantly reduces wall-clock time
- Maintains O(n log n) work
- Great showcase of parallel divide-and-conquer

Used in:

- HPC (High Performance Computing)
- Modern standard libraries (`std::execution::par`)
- Big data frameworks (Spark, Hadoop)

A Gentle Proof (Why It Works)

Each recursive call sorts n/2 elements, but now in parallel. Let P = number of processors.

Work (total operations):

$$T_{work}(n) = O(n \log n)$$

Span (critical path time):

$$T_{span}(n) = O(\log^2 n)$$

Total time

$$O\left(\frac{n \log n}{P} + \log^2 n\right)$$

Speedup P×, limited by synchronization and merge overhead.

Phase	Parallelizable	Work
Sort subarrays	Yes	O(n log n / P)
Merge	Partially	O(n log P)

Try It Yourself

1. Run with 1, 2, 4, 8 threads, compare speed.
2. Print thread IDs at each recursive call.
3. Implement threshold for small subarrays.
4. Merge using parallel merging.
5. Measure CPU utilization during sort.
6. Test with large random list (10 elements).
7. Compare with sequential Merge Sort.
8. Profile with timing tools.
9. Try OpenMP version in C.
10. Extend to distributed nodes (MPI).

Test Cases

Input	Threads	Output	Notes
[3,2,1]	2	[1,2,3]	Simple
[5,3,4,1,2]	2	[1,2,3,4,5]	Balanced work
1e6 random ints	8	sorted	Parallel boost
[1,1,1,1]	4	[1,1,1,1]	Stable behavior

Complexity

Aspect	Value
Work	O(n log n)
Span	O(log² n)
Parallel Time	O(n log n / P + log² n)
Space	O(n)

Aspect	Value
Stable	Yes
Adaptive	No

Parallel Merge Sort is Merge Sort reborn for the multi-core era, the same elegance, now with teamwork. It's how classic algorithms learn to scale with hardware.

Section 13. Counting and distribution sorts

121 Counting Sort

Counting Sort is a non-comparison sorting algorithm that sorts integers (or items mapped to integer keys) by counting occurrences of each value. Instead of comparing elements, it directly uses their values as indices in a counting array. It's fast (O(n + k)), stable, and perfect when the input range is limited and small.

What Problem Are We Solving?

When keys are integers within a known range, comparison-based sorts (O(n log n)) are overkill. Counting Sort leverages that limited range to sort in linear time, without any comparisons.

Perfect for:

- Sorting grades (0–100)
- Sorting digits or ASCII codes (0–255)
- Pre-step for Radix Sort or Bucket Sort
- Scenarios where key range n^2

Example

Sort array `[4, 2, 2, 8, 3, 3, 1]`

Step	Description	Result
1	Find max = 8	Range = 0–8
2	Initialize count[9] = [0,0,0,0,0,0,0,0,0]	
3	Count each number	count = [0,1,2,2,1,0,0,0,1]
4	Prefix sum (positions)	count = [0,1,3,5,6,6,6,6,7]
5	Place elements by count	[1,2,2,3,3,4,8]

The count array tracks the position boundaries for each key.

How Does It Work (Plain Language)?

Counting Sort doesn't compare elements. It counts how many times each value appears, then uses those counts to reconstruct the sorted list.

Think of it as filling labeled bins:

- One bin for each number
- Drop each element into its bin
- Then walk through bins in order and empty them

Step-by-Step Process

Step	Description
1	Find min and max (determine range `k`)
2	Create count array of size `k + 1`
3	Count occurrences of each value
4	Transform counts into prefix sums (for positions)
5	Traverse input in reverse (for stability), placing elements
6	Copy sorted output back

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <string.h>

void counting_sort(int arr[], int n) {
    int max = arr[0];
    for (int i = 1; i < n; i++)
        if (arr[i] > max) max = arr[i];

    int count[max + 1];
    memset(count, 0, sizeof(count));

    for (int i = 0; i < n; i++)
```

```
        count[arr[i]]++;

    for (int i = 1; i <= max; i++)
        count[i] += count[i - 1];

    int output[n];
    for (int i = n - 1; i >= 0; i--) {
        output[count[arr[i]] - 1] = arr[i];
        count[arr[i]]--;
    }

    for (int i = 0; i < n; i++)
        arr[i] = output[i];
}

int main(void) {
    int arr[] = {4, 2, 2, 8, 3, 3, 1};
    int n = sizeof(arr) / sizeof(arr[0]);
    counting_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Python

```
def counting_sort(arr):
    max_val = max(arr)
    count = [0] * (max_val + 1)

    for num in arr:
        count[num] += 1

    for i in range(1, len(count)):
        count[i] += count[i - 1]

    output = [0] * len(arr)
    for num in reversed(arr):
        count[num] -= 1
        output[count[num]] = num
```

```
    return output

arr = [4, 2, 2, 8, 3, 3, 1]
print(counting_sort(arr))
```

Why It Matters

- Linear time when range is small (`O(n + k)`)
- Stable, preserving input order
- Foundation for Radix Sort
- Great for integer, digit, or bucket sorting

A Gentle Proof (Why It Works)

Counting Sort replaces comparison by index-based placement.

If `n` is number of elements and `k` is key range:

- Counting occurrences: O(n)
- Prefix sums: O(k)
- Placement: O(n)

Total = O(n + k)

Stable because we traverse input in reverse while placing.

Phase	Work	Complexity
Count elements	O(n)	Scan once
Prefix sum	O(k)	Range pass
Place elements	O(n)	Stable write

Try It Yourself

1. Sort `[4, 2, 2, 8, 3, 3, 1]` step by step.
2. Show count array after counting.
3. Convert count to prefix sums.
4. Place elements in output (reverse scan).
5. Compare stable vs unstable version.
6. Change input to `[9, 9, 1, 2]`.
7. Try sorting `[5, 3, 5, 1, 0]`.
8. Handle input with min > 0 (offset counts).

9. Measure runtime vs Bubble Sort.
10. Use as subroutine in Radix Sort.

Test Cases

Input	Output	Notes
[4,2,2,8,3,3,1]	[1,2,2,3,3,4,8]	Example
[1,4,1,2,7,5,2]	[1,1,2,2,4,5,7]	Stable
[9,9,9,9]	[9,9,9,9]	Repeats
[0,1,2,3]	[0,1,2,3]	Already sorted

Complexity

Aspect	Value
Time	O(n + k)
Space	O(n + k)
Stable	Yes
Adaptive	No
Range-sensitive	Yes

Counting Sort is like sorting by bins, no comparisons, no stress, just clean counts and linear time. It's a powerhouse behind Radix Sort and data bucketing in performance-critical pipelines.

122 Stable Counting Sort

Stable Counting Sort refines the basic Counting Sort by ensuring equal elements preserve their original order. This property, called *stability*, is crucial when sorting multi-key data, for example, sorting people by age, then by name. Stable versions are also the building blocks for Radix Sort, where each digit's sort depends on stability.

What Problem Are We Solving?

Basic Counting Sort can break order among equal elements because it places them in arbitrary order. When sorting records or tuples where order matters (e.g., by secondary key), we need stability, if `a` and `b` have equal keys, their order in output must match input.

Stable Counting Sort ensures that:

If `arr[i]` and `arr[j]` have the same key and `i < j`, then `arr[i]` appears before `arr[j]` in the sorted output.

Perfect for:

- Radix Sort digits
- Multi-field records (e.g. sort by name, then by score)
- Databases and stable pipelines

Example

Sort `[4a, 2b, 2a, 8a, 3b, 3a, 1a]` (letters mark order)

Step	Description	Result
1	Count frequencies	count = [0,1,2,2,1,0,0,0,1]
2	Prefix sums (positions)	count = [0,1,3,5,6,6,6,6,7]
3	Traverse input in reverse	output = [1a, 2b, 2a, 3b, 3a, 4a, 8a]

See how `2b` (index 1) appears before `2a` (index 2), stable ordering preserved.

How Does It Work (Plain Language)?

It's Counting Sort with a twist: we fill the output from the end of the input, ensuring last-seen equal items go last. By traversing in reverse, earlier elements are placed later, preserving their original order.

This is the core idea behind stable sorting.

Step-by-Step Process

Step	Description
1	Determine key range (0..max)
2	Count frequency of each key
3	Compute prefix sums (to determine positions)
4	Traverse input right to left
5	Place elements in output using count as index
6	Decrement count[key] after placement

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <string.h>

typedef struct {
    int key;
    char tag; // to visualize stability
} Item;

void stable_counting_sort(Item arr[], int n) {
    int max = arr[0].key;
    for (int i = 1; i < n; i++)
        if (arr[i].key > max) max = arr[i].key;

    int count[max + 1];
    memset(count, 0, sizeof(count));

    // Count occurrences
    for (int i = 0; i < n; i++)
        count[arr[i].key]++;

    // Prefix sums
    for (int i = 1; i <= max; i++)
        count[i] += count[i - 1];

    Item output[n];

    // Traverse input in reverse for stability
    for (int i = n - 1; i >= 0; i--) {
        int k = arr[i].key;
        output[count[k] - 1] = arr[i];
        count[k]--;
    }

    for (int i = 0; i < n; i++)
        arr[i] = output[i];
}
```

```c
int main(void) {
    Item arr[] = {{4,'a'},{2,'b'},{2,'a'},{8,'a'},{3,'b'},{3,'a'},{1,'a'}};
    int n = sizeof(arr)/sizeof(arr[0]);
    stable_counting_sort(arr, n);
    for (int i = 0; i < n; i++) printf("(%d,%c) ", arr[i].key, arr[i].tag);
    printf("\n");
}
```

Python

```python
def stable_counting_sort(arr):
    max_val = max(arr)
    count = [0] * (max_val + 1)

    for num in arr:
        count[num] += 1

    for i in range(1, len(count)):
        count[i] += count[i - 1]

    output = [0] * len(arr)
    for num in reversed(arr):
        count[num] -= 1
        output[count[num]] = num

    return output

arr = [4, 2, 2, 8, 3, 3, 1]
print(stable_counting_sort(arr))
```

Why It Matters

- Stable sorting is essential for multi-key operations
- Required for Radix Sort correctness
- Guarantees consistent behavior for duplicates
- Used in databases, language sort libraries, pipelines

A Gentle Proof (Why It Works)

Each key is assigned a position range via prefix sums. Traversing input from right to left ensures that earlier items occupy smaller indices, preserving order.

If `a` appears before `b` in input and `key(a) = key(b)`, then `count[key(a)]` places `a` before `b`, stable.

Phase	Work	Complexity
Counting	O(n)	Pass once
Prefix sums	O(k)	Range pass
Placement	O(n)	Reverse traversal

Total = O(n + k), same as basic Counting Sort, but stable.

Try It Yourself

1. Sort `[(4,'a'), (2,'b'), (2,'a'), (3,'a')]`.
2. Show count and prefix arrays.
3. Traverse input from end, track output.
4. Compare with unstable version.
5. Try sorting `[5,3,5,1,0]`.
6. Visualize stability when equal keys appear.
7. Modify to handle offset keys (negative values).
8. Combine with Radix Sort (LSD).
9. Profile runtime vs normal Counting Sort.
10. Check stability by adding tags (letters).

Test Cases

Input	Output	Notes
[4,2,2,8,3,3,1]	[1,2,2,3,3,4,8]	Same as basic
[(2,'a'),(2,'b')]	[(2,'a'),(2,'b')]	Stable preserved
[1,1,1]	[1,1,1]	Idempotent
[0,1,2,3]	[0,1,2,3]	Already sorted

Complexity

Aspect	Value
Time	O(n + k)
Space	O(n + k)
Stable	Yes
Adaptive	No
Range-sensitive	Yes

Stable Counting Sort is Counting Sort with memory, it not only sorts fast but also remembers your order, making it indispensable for multi-pass algorithms like Radix Sort.

123 Radix Sort (LSD)

Radix Sort (Least Significant Digit first) is a non-comparison, stable sorting algorithm that processes integers (or strings) digit by digit, starting from the least significant digit (LSD). By repeatedly applying a stable sort (like Counting Sort) on each digit, it can sort numbers in linear time when digit count is small.

What Problem Are We Solving?

When sorting integers or fixed-length keys (like dates, IDs, or strings of digits), traditional comparison-based sorts spend unnecessary effort. Radix Sort (LSD) sidesteps comparisons by leveraging digit-wise order and stability to achieve O(d × (n + k)) performance.

Perfect for:

- Sorting numbers, dates, zip codes, or strings
- Datasets with bounded digit length
- Applications where deterministic performance matters

Example

Sort `[170, 45, 75, 90, 802, 24, 2, 66]`

Pass	Digit Place	Input	Output (Stable Sort)
1	Ones	[170,45,75,90,802,24,2,66]	[170,90,802,2,24,45,75,66]
2	Tens	[170,90,802,2,24,45,75,66]	[802,2,24,45,66,170,75,90]
3	Hundreds	[802,2,24,45,66,170,75,90]	[2,24,45,66,75,90,170,802]

Final sorted output: `[2, 24, 45, 66, 75, 90, 170, 802]`

Each pass uses Stable Counting Sort on the current digit.

How Does It Work (Plain Language)?

Think of sorting by digit positions:

1. Group by ones place (units)
2. Group by tens
3. Group by hundreds, etc.

Each pass reorders elements according to the digit at that place, while keeping earlier digit orders intact (thanks to stability).

It's like sorting by last name, then first name, one field at a time, stable each round.

Step-by-Step Process

Step	Description
1	Find the maximum number to know the number of digits `d`
2	For each digit place (1, 10, 100, …):
3	Use a stable counting sort based on that digit
4	After the last pass, the array is fully sorted

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

int get_max(int a[], int n) {
    int max = a[0];
    for (int i = 1; i < n; i++)
        if (a[i] > max) max = a[i];
    return max;
}

void counting_sort_digit(int a[], int n, int exp) {
    int output[n];
    int count[10] = {0};
```

```c
    for (int i = 0; i < n; i++)
        count[(a[i] / exp) % 10]++;

    for (int i = 1; i < 10; i++)
        count[i] += count[i - 1];

    for (int i = n - 1; i >= 0; i--) {
        int digit = (a[i] / exp) % 10;
        output[count[digit] - 1] = a[i];
        count[digit]--;
    }

    for (int i = 0; i < n; i++)
        a[i] = output[i];
}

void radix_sort(int a[], int n) {
    int max = get_max(a, n);
    for (int exp = 1; max / exp > 0; exp *= 10)
        counting_sort_digit(a, n, exp);
}

int main(void) {
    int a[] = {170, 45, 75, 90, 802, 24, 2, 66};
    int n = sizeof(a) / sizeof(a[0]);
    radix_sort(a, n);
    for (int i = 0; i < n; i++) printf("%d ", a[i]);
    printf("\n");
}
```

Python

```python
def counting_sort_digit(arr, exp):
    n = len(arr)
    output = [0] * n
    count = [0] * 10

    for num in arr:
        index = (num // exp) % 10
        count[index] += 1
```

```
    for i in range(1, 10):
        count[i] += count[i - 1]

    for num in reversed(arr):
        index = (num // exp) % 10
        count[index] -= 1
        output[count[index]] = num

    for i in range(n):
        arr[i] = output[i]

def radix_sort(arr):
    max_val = max(arr)
    exp = 1
    while max_val // exp > 0:
        counting_sort_digit(arr, exp)
        exp *= 10

arr = [170, 45, 75, 90, 802, 24, 2, 66]
radix_sort(arr)
print(arr)
```

Why It Matters

- Linear time (O(d × (n + k))) for fixed digits
- Stable, retains order for equal keys
- Great for large numeric datasets
- Foundation for efficient key-based sorting (strings, dates)

A Gentle Proof (Why It Works)

At each digit position:

- Stable Counting Sort reorders by that digit
- Earlier digits remain ordered (stability)
- After all digits, array is fully ordered

If each digit has range `k` and `d` total digits:

$$T(n) = O(d \times (n + k))$$

Phase	Work	Complexity
Per digit	O(n + k)	Counting sort
All digits	d × O(n + k)	Total

If `d` and `k` are constants → O(n) overall.

Try It Yourself

1. Sort `[170, 45, 75, 90, 802, 24, 2, 66]`.
2. Trace each pass (ones, tens, hundreds).
3. Show count table per digit.
4. Compare stable vs unstable sorting.
5. Add zeros: `[07, 70, 700]`.
6. Try `[3, 1, 2, 10, 11, 21]`.
7. Count digit comparisons.
8. Modify to handle negative numbers (offset).
9. Change base to 16 (hex).
10. Compare with Merge Sort performance on large input.

Test Cases

Input	Output	Notes
[170,45,75,90,802,24,2,66]	[2,24,45,66,75,90,170,802]	Classic
[9,8,7,6,5]	[5,6,7,8,9]	Reversed
[10,1,100,1000]	[1,10,100,1000]	Different lengths
[22,22,11,11]	[11,11,22,22]	Stable

Complexity

Aspect	Value
Time	O(d × (n + k))
Space	O(n + k)
Stable	Yes
Adaptive	No
Range-sensitive	Yes

Radix Sort (LSD) is the assembly line of sorting, each pass builds upon the last, producing perfectly ordered output from simple stable steps.

124 Radix Sort (MSD)

Radix Sort (Most Significant Digit first) is a recursive variant of Radix Sort that begins sorting from the most significant digit (MSD) and works downward. Unlike LSD Radix Sort, which is iterative and stable across all digits, MSD focuses on prefix-based grouping and recursively sorts subgroups. This makes it ideal for variable-length keys such as strings, IP addresses, or long integers.

What Problem Are We Solving?

LSD Radix Sort works best for fixed-length keys, where every element has the same number of digits. But when keys differ in length (e.g., strings "a", "ab", "abc"), we need to respect prefix order, "a" should come before "ab".

MSD Radix Sort handles this by grouping by prefix digits, then recursively sorting each group.

Perfect for:

- Strings, words, or variable-length keys
- Hierarchical data (prefix-sensitive)
- Lexicographic ordering (dictionary order)

Example

Sort: `["b", "ba", "abc", "ab", "ac"]`

Step	Digit	Groups
1	1st char	a → ["abc", "ab", "ac"], b → ["b", "ba"]
2	Group "a"	2nd char → b: ["abc", "ab"], c: ["ac"]
3	Group "ab"	3rd char → c: ["abc"], end: ["ab"]
4	Final merge	["ab", "abc", "ac", "b", "ba"]

Lexicographic order preserved, even with varying lengths.

How Does It Work (Plain Language)?

MSD Radix Sort organizes data by prefix trees (tries) conceptually:

- Partition elements by their most significant digit (or character)
- Recurse within each group for next digit
- Merge groups in order of digit values

If LSD is like bucket sorting digits from the back, MSD is tree-like sorting from the top.

Step-by-Step Process

Step	Description
1	Find highest digit place (or first character)
2	Partition array into groups by that digit
3	Recursively sort each group by next digit
4	Concatenate groups in order

For strings, if one string ends early, it's considered smaller.

Tiny Code (Easy Versions)

Python (String Example)

```
def msd_radix_sort(arr, pos=0):
    if len(arr) <= 1:
        return arr

    # Buckets for ASCII range (0-255) + 1 for end-of-string
    buckets = [[] for _ in range(257)]
    for word in arr:
        index = ord(word[pos]) + 1 if pos < len(word) else 0
        buckets[index].append(word)

    result = []
    for bucket in buckets:
        if bucket:
            # Only recurse if there's more than one element and not EOS
            if len(bucket) > 1 and (pos < max(len(w) for w in bucket)):
```

```
                bucket = msd_radix_sort(bucket, pos + 1)
            result.extend(bucket)
    return result

arr = ["b", "ba", "abc", "ab", "ac"]
print(msd_radix_sort(arr))
```

Output:

```
$$'ab', 'abc', 'ac', 'b', 'ba']
```

C (Numeric Example)

```c
#include <stdio.h>

int get_digit(int num, int exp, int base) {
    return (num / exp) % base;
}

void msd_radix_sort_rec(int arr[], int n, int exp, int base, int max) {
    if (exp == 0 || n <= 1) return;

    int buckets[base][n];
    int count[base];
    for (int i = 0; i < base; i++) count[i] = 0;

    // Distribute
    for (int i = 0; i < n; i++) {
        int d = get_digit(arr[i], exp, base);
        buckets[d][count[d]++] = arr[i];
    }

    // Recurse and collect
    int idx = 0;
    for (int i = 0; i < base; i++) {
        if (count[i] > 0) {
            msd_radix_sort_rec(buckets[i], count[i], exp / base, base, max);
            for (int j = 0; j < count[i]; j++)
                arr[idx++] = buckets[i][j];
        }
```

```
    }
}

void msd_radix_sort(int arr[], int n) {
    int max = arr[0];
    for (int i = 1; i < n; i++)
        if (arr[i] > max) max = arr[i];

    int exp = 1;
    while (max / exp >= 10) exp *= 10;

    msd_radix_sort_rec(arr, n, exp, 10, max);
}

int main(void) {
    int arr[] = {170, 45, 75, 90, 802, 24, 2, 66};
    int n = sizeof(arr) / sizeof(arr[0]);
    msd_radix_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Handles variable-length keys
- Natural for lexicographic ordering
- Used in string sorting, trie-based systems, suffix array construction
- Recursively partitions, often faster for large diverse keys

A Gentle Proof (Why It Works)

Each recursive call partitions the array by digit prefix. Since partitions are disjoint and ordered by digit, concatenating them yields a fully sorted sequence.

For `n` elements, `d` digits, and base `k`:

$$T(n) = O(n + k) \text{ per level, depth } \leq d$$
$$\Rightarrow O(d \times (n + k))$$

Stability preserved via ordered grouping.

Phase	Work	Description
Partition	O(n)	Place items in digit buckets
Recurse	O(d)	Each level processes subgroups
Total	O(d(n + k))	Linear in digits

Try It Yourself

1. Sort `["b", "ba", "abc", "ab", "ac"]`.
2. Draw recursion tree by character.
3. Compare order with lexicographic.
4. Test `["dog", "cat", "apple", "apricot"]`.
5. Sort integers `[170,45,75,90,802,24,2,66]`.
6. Change base (binary, hex).
7. Compare with LSD Radix Sort.
8. Add duplicates and test stability.
9. Visualize grouping buckets.
10. Implement with trie-like data structure.

Test Cases

Input	Output	Notes
[“b”,“ba”,“abc”,“ab”,“ac”]	[“ab”,“abc”,“ac”,“b”,“ba”]	Variable length
[170,45,75,90,802,24,2,66]	[2,24,45,66,75,90,170,802]	Numeric
[“a”,“aa”,“aaa”]	[“a”,“aa”,“aaa”]	Prefix order
[“z”,“y”,“x”]	[“x”,“y”,“z”]	Reverse input

Complexity

Aspect	Value
Time	O(d × (n + k))
Space	O(n + k)
Stable	Yes
Adaptive	No
Suitable for	Variable-length keys

Radix Sort (MSD) is lexicographic sorting by recursion, it builds order from the top down, treating prefixes as leaders and details as followers, much like how dictionaries arrange words.

125 Bucket Sort

Bucket Sort is a distribution-based sorting algorithm that divides the input into several buckets (bins), sorts each bucket individually (often with Insertion Sort), and then concatenates them. When input data is uniformly distributed, Bucket Sort achieves linear time performance (O(n)).

What Problem Are We Solving?

Comparison-based sorts take O(n log n) time in the general case. But if we know that data values are spread evenly across a range, we can exploit this structure to sort faster by grouping similar values together.

Bucket Sort works best when:

- Input is real numbers in [0, 1) or any known range
- Data is uniformly distributed
- Buckets are balanced, each with few elements

Used in:

- Probability distributions
- Histogram-based sorting
- Floating-point sorting

Example

Sort `[0.78, 0.17, 0.39, 0.26, 0.72, 0.94, 0.21, 0.12, 0.23, 0.68]`

Step	Action	Result
1	Create 10 buckets for range [0, 1)	[[] … []]
2	Distribute elements by `int(n * value)`	[[0.12,0.17,0.21,0.23,0.26],[0.39],[0.68,0.72,0.78],[0.94]]
3	Sort each bucket (Insertion Sort)	Each bucket sorted individually
4	Concatenate buckets	[0.12, 0.17, 0.21, 0.23, 0.26, 0.39, 0.68, 0.72, 0.78, 0.94]

How Does It Work (Plain Language)?

Think of sorting test scores:

- You group scores into bins (0–10, 10–20, 20–30, …)
- Sort each bin individually
- Merge bins back together in order

Bucket Sort leverages range grouping, local order inside each bucket, global order from bucket sequence.

Step-by-Step Process

Step	Description
1	Create empty buckets for each range interval
2	Distribute elements into buckets
3	Sort each bucket individually
4	Concatenate buckets sequentially

If buckets are evenly filled, each small sort is fast, almost constant time.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

void insertion_sort(float arr[], int n) {
    for (int i = 1; i < n; i++) {
        float key = arr[i];
        int j = i - 1;
        while (j >= 0 && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}
```

```c
void bucket_sort(float arr[], int n) {
    float buckets[n][n];
    int count[n];
    for (int i = 0; i < n; i++) count[i] = 0;

    // Distribute into buckets
    for (int i = 0; i < n; i++) {
        int idx = n * arr[i]; // index by range
        buckets[idx][count[idx]++] = arr[i];
    }

    // Sort each bucket
    for (int i = 0; i < n; i++)
        if (count[i] > 0)
            insertion_sort(buckets[i], count[i]);

    // Concatenate
    int k = 0;
    for (int i = 0; i < n; i++)
        for (int j = 0; j < count[i]; j++)
            arr[k++] = buckets[i][j];
}

int main(void) {
    float arr[] = {0.78,0.17,0.39,0.26,0.72,0.94,0.21,0.12,0.23,0.68};
    int n = sizeof(arr) / sizeof(arr[0]);
    bucket_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%.2f ", arr[i]);
    printf("\n");
}
```

Python

```python
def bucket_sort(arr):
    n = len(arr)
    buckets = [[] for _ in range(n)]

    for num in arr:
        idx = int(n * num)
        buckets[idx].append(num)
```

```
    for bucket in buckets:
        bucket.sort()

    result = []
    for bucket in buckets:
        result.extend(bucket)
    return result

arr = [0.78,0.17,0.39,0.26,0.72,0.94,0.21,0.12,0.23,0.68]
print(bucket_sort(arr))
```

Why It Matters

- Linear time for uniformly distributed data
- Great for floating-point numbers
- Illustrates distribution-based sorting
- Foundation for histogram, flash, and spread sort

A Gentle Proof (Why It Works)

If input elements are independent and uniformly distributed, expected elements per bucket = `O(1)`. Sorting each small bucket takes constant time → total linear time.

Total complexity:

$$T(n) = O(n + \sum_{i=1}^{n} T_i)$$

If each `T_i = O(1)`,

$$T(n) = O(n)$$

Phase	Work	Complexity
Distribution	O(n)	One pass
Local Sort	O(n) total	Expected
Concatenate	O(n)	Combine

Try It Yourself

1. Sort `[0.78,0.17,0.39,0.26,0.72,0.94,0.21,0.12,0.23,0.68]`.
2. Visualize buckets as bins.
3. Change bucket count to 5, 20, see effect.
4. Try non-uniform data `[0.99,0.99,0.98]`.
5. Replace insertion sort with counting sort.
6. Measure performance with 10 floats.
7. Test `[0.1,0.01,0.001]`, uneven distribution.
8. Implement bucket indexing for arbitrary ranges.
9. Compare with Quick Sort runtime.
10. Plot distribution histogram before sorting.

Test Cases

Input	Output	Notes
[0.78,0.17,0.39,0.26]	[0.17,0.26,0.39,0.78]	Basic
[0.1,0.01,0.001]	[0.001,0.01,0.1]	Sparse
[0.9,0.8,0.7,0.6]	[0.6,0.7,0.8,0.9]	Reverse
[0.1,0.1,0.1]	[0.1,0.1,0.1]	Duplicates

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n)
Time (Worst)	$O(n^2)$ (all in one bucket)
Space	O(n)
Stable	Yes (if bucket sort is stable)
Adaptive	Yes (depends on distribution)

Bucket Sort is like sorting by bins, fast, simple, and beautifully efficient when your data is evenly spread. It's the go-to choice for continuous values in a fixed range.

126 Pigeonhole Sort

Pigeonhole Sort is a simple distribution sorting algorithm that places each element directly into its corresponding "pigeonhole" (or bucket) based on its key value. It's ideal when elements

are integers within a small known range, think of it as Counting Sort with explicit placement rather than counting.

What Problem Are We Solving?

When data values are integers and close together, we don't need comparisons, we can map each value to a slot directly. Pigeonhole Sort is particularly useful for dense integer ranges, such as:

- Sorting integers from 0 to 100
- Sorting scores, ranks, or IDs
- Small ranges with many duplicates

It trades space for speed, achieving O(n + range) performance.

Example

Sort `[8, 3, 2, 7, 4, 6, 8]`

Step	Description	Result
1	Find min=2, max=8 → range = 7	holes[0..6]
2	Create pigeonholes: `[[],[],[],[],[],[],[]]`	
3	Place each number in its hole	holes = `[[2],[3],[4],[6],[7],[8,8]]`
4	Concatenate holes	`[2,3,4,6,7,8,8]`

Each value goes exactly to its mapped hole index.

How Does It Work (Plain Language)?

It's like assigning students to exam rooms based on ID ranges, each slot holds all matching IDs. You fill slots (holes), then read them back in order.

Unlike Counting Sort, which only counts occurrences, Pigeonhole Sort stores the actual values, preserving duplicates directly.

Step-by-Step Process

Step	Description
1	Find minimum and maximum elements
2	Compute range = max - min + 1
3	Create array of empty pigeonholes of size `range`
4	For each element, map to hole `arr[i] - min`
5	Place element into that hole (append)
6	Read holes in order and flatten into output

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

void pigeonhole_sort(int arr[], int n) {
    int min = arr[0], max = arr[0];
    for (int i = 1; i < n; i++) {
        if (arr[i] < min) min = arr[i];
        if (arr[i] > max) max = arr[i];
    }

    int range = max - min + 1;
    int *holes[range];
    int counts[range];
    for (int i = 0; i < range; i++) {
        holes[i] = malloc(n * sizeof(int));
        counts[i] = 0;
    }

    // Place elements into holes
    for (int i = 0; i < n; i++) {
        int index = arr[i] - min;
        holes[index][counts[index]++] = arr[i];
    }

    // Flatten back
    int index = 0;
    for (int i = 0; i < range; i++) {
        for (int j = 0; j < counts[i]; j++) {
```

```
            arr[index++] = holes[i][j];
        }
        free(holes[i]);
    }
}

int main(void) {
    int arr[] = {8, 3, 2, 7, 4, 6, 8};
    int n = sizeof(arr) / sizeof(arr[0]);
    pigeonhole_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Python

```
def pigeonhole_sort(arr):
    min_val, max_val = min(arr), max(arr)
    size = max_val - min_val + 1
    holes = [[] for _ in range(size)]

    for x in arr:
        holes[x - min_val].append(x)

    sorted_arr = []
    for hole in holes:
        sorted_arr.extend(hole)
    return sorted_arr

arr = [8, 3, 2, 7, 4, 6, 8]
print(pigeonhole_sort(arr))
```

Why It Matters

- Simple mapping for small integer ranges
- Linear time if range n
- Useful in digit, rank, or ID sorting
- Provides stable grouping with explicit placement

A Gentle Proof (Why It Works)

Every key is mapped uniquely to a hole (offset by min). All duplicates fall into the same hole, preserving multiplicity. Reading holes sequentially yields sorted order.

If `n` = number of elements, `k` = range of values:

$$T(n) = O(n + k)$$

Phase	Work	Complexity
Find min/max	O(n)	Single pass
Distribute to holes	O(n)	One placement each
Collect results	O(n + k)	Flatten all

Try It Yourself

1. Sort `[8,3,2,7,4,6,8]` by hand.
2. Show hole contents after distribution.
3. Add duplicate values, confirm stable grouping.
4. Try `[1,1,1,1]`, all in one hole.
5. Sort negative numbers `[0,-1,-2,1]` (offset by min).
6. Increase range to see space cost.
7. Compare runtime with Counting Sort.
8. Replace holes with linked lists.
9. Implement in-place version.
10. Extend for key-value pairs.

Test Cases

Input	Output	Notes
[8,3,2,7,4,6,8]	[2,3,4,6,7,8,8]	Example
[1,1,1,1]	[1,1,1,1]	All equal
[9,8,7,6]	[6,7,8,9]	Reverse
[0,-1,-2,1]	[-2,-1,0,1]	Negative offset

Complexity

Aspect	Value
Time	O(n + k)
Space	O(n + k)
Stable	Yes
Adaptive	No
Range-sensitive	Yes

Pigeonhole Sort is as direct as sorting gets, one slot per value, one pass in, one pass out. Fast and clean when your data is dense and discrete.

127 Flash Sort

Flash Sort is a distribution-based sorting algorithm that combines ideas from bucket sort and insertion sort. It works in two phases:

1. Classification, distribute elements into classes (buckets) using a linear mapping
2. Permutation, rearrange elements in-place using cycles

It achieves O(n) average time on uniformly distributed data but can degrade to $O(n^2)$ in the worst case. Invented by *Karl-Dietrich Neubert* (1990s), it's known for being extremely fast in practice on large datasets.

What Problem Are We Solving?

When data is numerically distributed over a range, we can approximate where each element should go and move it close to its final position without full comparison sorting.

Flash Sort is built for:

- Uniformly distributed numeric data
- Large arrays
- Performance-critical applications (e.g., simulations, physics, graphics)

It leverages approximate indexing and in-place permutation for speed.

Example

Sort `[9, 3, 1, 7, 4, 6, 2, 8, 5]` into `m = 5` classes.

Step	Description	Result
1	Find `min = 1`, `max = 9`	range = 8
2	Map each value to class `k = (m-1)*(a[i]-min)/(max-min)`	Class indices: [4,1,0,3,1,3,0,4,2]
3	Count elements per class, compute cumulative positions	class boundaries = [0,2,4,6,8,9]
4	Cycle elements into correct class positions	Rearranged approx order
5	Apply insertion sort within classes	Sorted list

Final: `[1,2,3,4,5,6,7,8,9]`

How Does It Work (Plain Language)?

Imagine flashing each element to its approximate destination class in one pass, that's the "flash" phase. Then, fine-tune within each class using a simpler sort (like Insertion Sort).

It's like placing books roughly into shelves, then tidying each shelf.

Step-by-Step Process

Step	Description
1	Find min and max
2	Choose number of classes (usually 0.43 * n)
3	Compute class index for each element
4	Count elements per class and compute prefix sums
5	Move elements to approximate class positions (flash phase)
6	Use Insertion Sort within each class to finish

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void insertion_sort(float arr[], int start, int end) {
    for (int i = start + 1; i <= end; i++) {
        float key = arr[i];
```

```
        int j = i - 1;
        while (j >= start && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}

void flash_sort(float arr[], int n) {
    if (n <= 1) return;

    float min = arr[0], max = arr[0];
    for (int i = 1; i < n; i++) {
        if (arr[i] < min) min = arr[i];
        if (arr[i] > max) max = arr[i];
    }
    if (max == min) return;

    int m = n * 0.43; // number of classes
    int L[m];
    for (int i = 0; i < m; i++) L[i] = 0;

    // Classification count
    for (int i = 0; i < n; i++) {
        int k = (int)((m - 1) * (arr[i] - min) / (max - min));
        L[k]++;
    }

    // Prefix sums
    for (int i = 1; i < m; i++) L[i] += L[i - 1];

    // Flash phase
    int move = 0, j = 0, k = m - 1;
    while (move < n - 1) {
        while (j >= L[k]) k = (int)((m - 1) * (arr[j] - min) / (max - min));
        float flash = arr[j];
        while (j != L[k]) {
            k = (int)((m - 1) * (flash - min) / (max - min));
            float hold = arr[--L[k]];
            arr[L[k]] = flash;
            flash = hold;
```

```
            move++;
        }
        j++;
    }

    // Insertion sort finish
    insertion_sort(arr, 0, n - 1);
}

int main(void) {
    float arr[] = {9,3,1,7,4,6,2,8,5};
    int n = sizeof(arr) / sizeof(arr[0]);
    flash_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%.0f ", arr[i]);
    printf("\n");
}
```

Python

```
def insertion_sort(arr, start, end):
    for i in range(start + 1, end + 1):
        key = arr[i]
        j = i - 1
        while j >= start and arr[j] > key:
            arr[j + 1] = arr[j]
            j -= 1
        arr[j + 1] = key

def flash_sort(arr):
    n = len(arr)
    if n <= 1:
        return arr
    min_val, max_val = min(arr), max(arr)
    if max_val == min_val:
        return arr
    m = int(0.43 * n)
    L = [0] * m

    for x in arr:
        k = int((m - 1) * (x - min_val) / (max_val - min_val))
```

```
        L[k] += 1

    for i in range(1, m):
        L[i] += L[i - 1]

    move, j, k = 0, 0, m - 1
    while move < n - 1:
        while j >= L[k]:
            k = int((m - 1) * (arr[j] - min_val) / (max_val - min_val))
        flash = arr[j]
        while j != L[k]:
            k = int((m - 1) * (flash - min_val) / (max_val - min_val))
            L[k] -= 1
            arr[L[k]], flash = flash, arr[L[k]]
            move += 1
        j += 1
    insertion_sort(arr, 0, n - 1)
    return arr

arr = [9,3,1,7,4,6,2,8,5]
print(flash_sort(arr))
```

Why It Matters

- Extremely fast on uniformly distributed data
- In-place (O(1) extra space)
- Practical for large arrays
- Combines distribution sorting and insertion finishing

A Gentle Proof (Why It Works)

The classification step maps each element to its expected position region, dramatically reducing disorder. Since each class has a small local range, insertion sort completes quickly.

Expected complexity (uniform input):

$$T(n) = O(n) \text{ (classification)} + O(n) \text{ (final pass)} = O(n)$$

Worst-case (skewed distribution): $O(n^2)$

Phase	Work	Complexity
Classification	O(n)	Compute classes
Flash rearrangement	O(n)	In-place moves
Final sort	O(n)	Local sorting

Try It Yourself

1. Sort `[9,3,1,7,4,6,2,8,5]` step by step.
2. Change number of classes (0.3n, 0.5n).
3. Visualize class mapping for each element.
4. Count moves in flash phase.
5. Compare with Quick Sort timing on 10 elements.
6. Test uniform vs skewed data.
7. Implement with different finishing sort.
8. Track cycles formed during flash phase.
9. Observe stability (it's not stable).
10. Benchmark against Merge Sort.

Test Cases

Input	Output	Notes
[9,3,1,7,4,6,2,8,5]	[1,2,3,4,5,6,7,8,9]	Example
[5,5,5,5]	[5,5,5,5]	Equal elements
[1,2,3,4,5]	[1,2,3,4,5]	Already sorted
[9,8,7,6,5]	[5,6,7,8,9]	Reverse

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n)
Time (Worst)	$O(n^2)$
Space	O(1)
Stable	No
Adaptive	Yes (partially)

Flash Sort is the lightning strike of sorting, it flashes elements to their expected zones in linear time, then finishes with a quick polish. When your data is uniform, it's one of the fastest practical sorts around.

128 Postman Sort

Postman Sort is a stable, multi-key sorting algorithm that works by sorting keys digit by digit or field by field, starting from the least significant field (like LSD Radix Sort) or most significant field (like MSD Radix Sort), depending on the application. It's often used for compound keys (e.g. postal addresses, dates, strings of fields), hence the name "Postman," as it sorts data the way a postman organizes mail: by street, then house, then apartment.

What Problem Are We Solving?

When sorting complex records by multiple attributes, such as:

- Sorting people by `(city, street, house_number)`
- Sorting files by `(year, month, day)`
- Sorting products by `(category, brand, price)`

We need to sort hierarchically, that's what Postman Sort excels at. It's a stable, field-wise sorting approach, built upon Counting or Bucket Sort for each field.

Example

Sort tuples `(City, Street)` by City then Street:

```
$$("Paris", "B"), ("London", "C"), ("Paris", "A"), ("London", "A")]
```

Step	Sort By	Result
1	Street (LSD)	[("London","A"),("Paris","A"),("London","C"),("Paris","B")]
2	City (MSD)	[("London","A"),("London","C"),("Paris","A"),("Paris","B")]

Stable sorting ensures inner order is preserved from previous pass.

How Does It Work (Plain Language)?

It's like organizing mail:

1. Sort by the smallest unit (house number)
2. Then sort by street
3. Then by city

Each pass refines the previous ordering. If sorting from least to most significant, use LSD order (like Radix). If sorting from most to least, use MSD order (like bucket recursion).

Step-by-Step Process

Step	Description
1	Identify key fields and their order of significance
2	Choose stable sorting method (e.g., Counting Sort)
3	Sort by least significant key first
4	Repeat for each key moving to most significant
5	Final order respects all key hierarchies

Tiny Code (Easy Versions)

Python (LSD Approach)

```
def postman_sort(records, key_funcs):
    # key_funcs = list of functions to extract each field
    for key_func in reversed(key_funcs):
        records.sort(key=key_func)
    return records

# Example: sort by (city, street)
records = [("Paris", "B"), ("London", "C"), ("Paris", "A"), ("London", "A")]
sorted_records = postman_sort(records, [lambda x: x[0], lambda x: x[1]])
print(sorted_records)
```

Output:

```
$$('London', 'A'), ('London', 'C'), ('Paris', 'A'), ('Paris', 'B')]
```

C (Numeric Fields)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int city;
    int street;
} Record;

int cmp_street(const void *a, const void *b) {
    Record *ra = (Record*)a, *rb = (Record*)b;
    return ra->street - rb->street;
}

int cmp_city(const void *a, const void *b) {
    Record *ra = (Record*)a, *rb = (Record*)b;
    return ra->city - rb->city;
}

void postman_sort(Record arr[], int n) {
    // Sort by street first (LSD)
    qsort(arr, n, sizeof(Record), cmp_street);
    // Then by city (MSD)
    qsort(arr, n, sizeof(Record), cmp_city);
}

int main(void) {
    Record arr[] = {{2,3}, {1,2}, {2,1}, {1,1}};
    int n = sizeof(arr)/sizeof(arr[0]);
    postman_sort(arr, n);
    for (int i = 0; i < n; i++)
        printf("(%d,%d) ", arr[i].city, arr[i].street);
    printf("\n");
}
```

Why It Matters

- Multi-key sorting (lexicographic order)
- Stable, preserves order across passes

- Versatile, works on compound keys, strings, records
- Foundation for:
  - Radix Sort
  - Database ORDER BY multi-column
  - Lexicographic ranking

A Gentle Proof (Why It Works)

Each stable pass ensures that prior ordering (from less significant fields) remains intact.

If we denote each field as f_i, sorted stably in order $f_k \to f_1$:

$$T(n) = \sum_{i=1}^{k} T_i(n)$$

If each $T_i(n)$ is $O(n)$, the total is $O(kn)$.

Lexicographic order emerges naturally:

$$(a_1, a_2, \ldots, a_k) < (b_1, b_2, \ldots, b_k) \iff a_i = b_i \text{ for } i < j, \text{ and } a_j < b_j$$

Phase	Operation	Stable	Complexity
LSD Sort	Start from least significant	Yes	$O(nk)$
MSD Sort	Start from most significant	Yes	$O(nk)$

Try It Yourself

1. Sort `[("Paris","B"),("London","C"),("Paris","A"),("London","A")]`
2. Add a 3rd field (zip code), sort by zip → street → city
3. Implement with `lambda` keys in Python
4. Replace stable sort with Counting Sort per field
5. Test with `[(2021,12,25),(2020,1,1),(2021,1,1)]`
6. Compare LSD vs MSD ordering
7. Sort strings by character groups (first char, second char, etc.)
8. Visualize passes and intermediate results
9. Test stability with repeated keys
10. Apply to sorting student records by `(grade, class, id)`

Test Cases

Input	Output	Notes
[(“Paris”,“B”),(“London”,“C”),(“Paris”,“A”),(“London”,“A”)]	[(“London”,“A”),(“London”,“C”),(“Paris”,“A”),(“Paris”,“B”)]	Lexicographic
[(2021,12,25),(2020,1,1),(2021,1,1)]	[(2020,1,1),(2021,1,1),(2021,12,25)]	Date order
[(1,2,3),(1,1,3),(1,1,2)]	[(1,1,2),(1,1,3),(1,2,3)]	Multi-field

Complexity

Aspect	Value
Time	O(k × n)
Space	O(n)
Stable	Yes
Adaptive	No
Keys	Multi-field

Postman Sort delivers order like clockwork, field by field, pass by pass, ensuring every layer of your data finds its proper place, from apartment number to zip code.

129 Address Calculation Sort

Address Calculation Sort (sometimes called Hash Sort or Scatter Sort) is a distribution-based sorting method that uses a hash-like function (called an *address function*) to compute the final position of each element directly. Instead of comparing pairs, it computes where each element should go, much like direct addressing in hash tables.

What Problem Are We Solving?

Comparison sorts need O(n log n) time. If we know the range and distribution of input values, we can instead compute where each element belongs, placing it directly.

Address Calculation Sort bridges the gap between sorting and hashing:

- It computes a mapping from value to position.

- It places each element directly or into small groups.
- It works best when data distribution is known and uniform.

Applications:

- Dense numeric datasets
- Ranked records
- Pre-bucketed ranges

Example

Sort `[3, 1, 4, 0, 2]` with range `[0..4]`.

Step	Element	Address Function $f(x) = x$	Placement
1	3	f(3) = 3	position 3
2	1	f(1) = 1	position 1
3	4	f(4) = 4	position 4
4	0	f(0) = 0	position 0
5	2	f(2) = 2	position 2

Result: `[0, 1, 2, 3, 4]`

If multiple elements share the same address, they're stored in a small linked list or bucket, then sorted locally.

How Does It Work (Plain Language)?

Imagine having labeled mailboxes for every possible key — each element knows exactly which box it belongs in. You just drop each letter into its slot, then read the boxes in order.

Unlike Counting Sort, which counts occurrences, Address Calculation Sort assigns positions, it can even be in-place if collisions are handled carefully.

Step-by-Step Process

Step	Description
1	Define address function $f(x)$ mapping each element to an index
2	Initialize empty output array or buckets
3	For each element a_i: compute index = $f(a_i)$
4	Place element at index (handle collisions if needed)

Step	Description
5	Collect or flatten buckets into sorted order

Tiny Code (Easy Versions)

C (Simple In-Range Example)

```c
#include <stdio.h>
#include <stdlib.h>

void address_calculation_sort(int arr[], int n, int min, int max) {
    int range = max - min + 1;
    int *output = calloc(range, sizeof(int));
    int *filled = calloc(range, sizeof(int));

    for (int i = 0; i < n; i++) {
        int idx = arr[i] - min;
        output[idx] = arr[i];
        filled[idx] = 1;
    }

    int k = 0;
    for (int i = 0; i < range; i++) {
        if (filled[i]) arr[k++] = output[i];
    }

    free(output);
    free(filled);
}

int main(void) {
    int arr[] = {3, 1, 4, 0, 2};
    int n = sizeof(arr)/sizeof(arr[0]);
    address_calculation_sort(arr, n, 0, 4);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Python

```
def address_calculation_sort(arr, f=None):
    if not arr:
        return arr
    if f is None:
        f = lambda x: x  # identity mapping

    min_val, max_val = min(arr), max(arr)
    size = max_val - min_val + 1
    slots = [[] for _ in range(size)]

    for x in arr:
        idx = f(x) - min_val
        slots[idx].append(x)

    # Flatten buckets
    result = []
    for bucket in slots:
        result.extend(sorted(bucket))  # local sort if needed
    return result

arr = [3, 1, 4, 0, 2]
print(address_calculation_sort(arr))
```

Output:

```
$$0, 1, 2, 3, 4]
```

Why It Matters

- Direct computation of sorted positions
- Linear time for predictable distributions
- Combines hashing and sorting
- Forms basis of bucket, radix, and flash sort

It's a great way to see how functions can replace comparisons.

A Gentle Proof (Why It Works)

If $f(x)$ maps each key uniquely to its sorted index, the result is already sorted by construction.

Even with collisions, sorting small local buckets is fast.

Total time:

$$T(n) = O(n + k)$$

where k = number of buckets = range size.

Phase	Work	Complexity
Compute addresses	O(n)	One per element
Bucket insertions	O(n)	Constant time each
Local sort	O(k)	Small groups
Flatten	O(n + k)	Read back

Try It Yourself

1. Sort `[3, 1, 4, 0, 2]` with `f(x)=x`.
2. Change mapping to `f(x)=2*x`, note gaps.
3. Add duplicates `[1,1,2,2,3]`, use buckets.
4. Try floats with `f(x)=int(x*10)` for `[0.1,0.2,0.3]`.
5. Sort strings by ASCII sum: `f(s)=sum(map(ord,s))`.
6. Compare with Counting Sort (no explicit storage).
7. Handle negative numbers by offsetting min.
8. Visualize mapping table.
9. Test range gaps (e.g., `[10, 20, 30]`).
10. Experiment with custom hash functions.

Test Cases

Input	Output	Notes
[3,1,4,0,2]	[0,1,2,3,4]	Perfect mapping
[10,20,30]	[10,20,30]	Sparse mapping
[1,1,2,2]	[1,1,2,2]	Duplicates
[0.1,0.3,0.2]	[0.1,0.2,0.3]	Float mapping

Complexity

Aspect	Value
Time	O(n + k)
Space	O(n + k)
Stable	Yes (with buckets)
Adaptive	No
Range-sensitive	Yes

Address Calculation Sort turns sorting into placement, each value finds its home by formula, not fight. When the range is clear and collisions are rare, it's lightning-fast and elegantly simple.

130 Spread Sort

Spread Sort is a hybrid distribution sort that blends ideas from radix sort, bucket sort, and comparison sorting. It distributes elements into buckets using their most significant bits (MSB) or value ranges, then recursively sorts buckets (like radix/MSD) or switches to a comparison sort (like Quick Sort) when buckets are small.

It's cache-friendly, adaptive, and often faster than Quick Sort on uniformly distributed data. In fact, it's used in some high-performance libraries such as Boost C++ Spreadsort.

What Problem Are We Solving?

Traditional comparison sorts (like Quick Sort) have $O(n \log n)$ complexity, while pure radix-based sorts can be inefficient on small or skewed datasets. Spread Sort solves this by adapting dynamically:

- Distribute like radix sort when data is wide and random
- Compare like Quick Sort when data is clustered or buckets are small

It "spreads" data across buckets, then sorts each bucket intelligently.

Perfect for:

- Integers, floats, and strings
- Large datasets
- Wide value ranges

Example

Sort `[43, 12, 89, 27, 55, 31, 70]`

Step	Action	Result
1	Find min = 12, max = 89	range = 77
2	Choose bucket count (e.g. 4)	bucket size 19
3	Distribute by bucket index = (val - min)/19	Buckets: [12], [27,31], [43,55], [70,89]
4	Recursively sort each bucket	[12], [27,31], [43,55], [70,89]
5	Merge buckets	[12,27,31,43,55,70,89]

How Does It Work (Plain Language)?

Imagine sorting mail by first letter (distribution), then alphabetizing each pile (comparison). If a pile is still big, spread it again by the next letter. If a pile is small, just sort it directly.

Spread Sort uses:

- Distribution when the data range is wide
- Comparison sort when buckets are narrow or small

This flexibility gives it strong real-world performance.

Step-by-Step Process

Step	Description
1	Find min and max values
2	Compute spread = max - min
3	Choose bucket count (based on n or spread)
4	Distribute elements into buckets by value range
5	Recursively apply spread sort to large buckets
6	Apply comparison sort to small buckets
7	Concatenate results

Tiny Code (Easy Versions)

C (Integer Example)

```c
#include <stdio.h>
#include <stdlib.h>

int compare(const void *a, const void *b) {
    return (*(int*)a - *(int*)b);
}

void spread_sort(int arr[], int n) {
    if (n <= 16) { // threshold for small buckets
        qsort(arr, n, sizeof(int), compare);
        return;
    }

    int min = arr[0], max = arr[0];
    for (int i = 1; i < n; i++) {
        if (arr[i] < min) min = arr[i];
        if (arr[i] > max) max = arr[i];
    }

    int bucket_count = n / 4 + 1;
    int range = max - min + 1;
    int bucket_size = range / bucket_count + 1;

    int *counts = calloc(bucket_count, sizeof(int));
    int buckets = malloc(bucket_count * sizeof(int*));
    for (int i = 0; i < bucket_count; i++)
        buckets[i] = malloc(n * sizeof(int));

    // Distribution
    for (int i = 0; i < n; i++) {
        int idx = (arr[i] - min) / bucket_size;
        buckets[idx][counts[idx]++] = arr[i];
    }

    // Recursive sort
    int k = 0;
    for (int i = 0; i < bucket_count; i++) {
        if (counts[i] > 0) {
            spread_sort(buckets[i], counts[i]);
            for (int j = 0; j < counts[i]; j++)
                arr[k++] = buckets[i][j];
        }
```

```
        free(buckets[i]);
    }

    free(buckets);
    free(counts);
}

int main(void) {
    int arr[] = {43, 12, 89, 27, 55, 31, 70};
    int n = sizeof(arr)/sizeof(arr[0]);
    spread_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Python

```
def spread_sort(arr, threshold=16):
    if len(arr) <= threshold:
        return sorted(arr)

    min_val, max_val = min(arr), max(arr)
    if min_val == max_val:
        return arr[:]

    n = len(arr)
    bucket_count = n // 4 + 1
    spread = max_val - min_val + 1
    bucket_size = spread // bucket_count + 1

    buckets = [[] for _ in range(bucket_count)]
    for x in arr:
        idx = (x - min_val) // bucket_size
        buckets[idx].append(x)

    result = []
    for b in buckets:
        if len(b) > threshold:
            result.extend(spread_sort(b, threshold))
        else:
```

```
            result.extend(sorted(b))
    return result

arr = [43, 12, 89, 27, 55, 31, 70]
print(spread_sort(arr))
```

Why It Matters

- Linear-time on uniform data
- Adaptive to distribution and size
- Combines bucket and comparison power
- Great for large numeric datasets

Used in Boost C++, it's a real-world performant hybrid.

A Gentle Proof (Why It Works)

Spread Sort's cost depends on:

- Distribution pass: $O(n)$
- Recursion depth: small (logarithmic for uniform data)
- Local sorts: small and fast (often $O(1)$ or $O(n \log n)$ on small buckets)

For n elements and b buckets:

$$T(n) = O(n + \sum_{i=1}^{b} T_i)$$

If average bucket size is constant or small:

$$T(n) \approx O(n)$$

Phase	Work	Complexity
Distribution	$O(n)$	One pass
Local Sorts	$O(n \log m)$	m = average bucket size
Total	$O(n)$ average, $O(n \log n)$ worst	

Try It Yourself

1. Sort `[43,12,89,27,55,31,70]`.
2. Try `[5,4,3,2,1]` (non-uniform).
3. Adjust bucket threshold.
4. Visualize recursive buckets.
5. Mix large and small values (e.g., `[1, 10, 1000, 2, 20, 2000]`).
6. Compare runtime with Quick Sort.
7. Implement float version.
8. Measure distribution imbalance.
9. Tune bucket size formula.
10. Sort strings by ord(char).

Test Cases

Input	Output	Notes
[43,12,89,27,55,31,70]	[12,27,31,43,55,70,89]	Uniform
[5,4,3,2,1]	[1,2,3,4,5]	Reverse
[100,10,1,1000]	[1,10,100,1000]	Wide range
[5,5,5]	[5,5,5]	Duplicates

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n)
Time (Worst)	O(n log n)
Space	O(n)
Stable	Yes (if local sort is stable)
Adaptive	Yes

Spread Sort spreads elements like seeds, each finds fertile ground in its range, then blossoms into order through local sorting. It's the smart hybrid that brings the best of radix and comparison worlds together.

Section 14. Hybrid sorts

131 IntroSort

IntroSort (short for *Introspective Sort*) is a hybrid sorting algorithm that combines the best features of Quick Sort, Heap Sort, and Insertion Sort. It begins with Quick Sort for speed, but if recursion goes too deep (indicating unbalanced partitions), it switches to Heap Sort to guarantee worst-case $O(n \log n)$ performance. For small partitions, it often uses Insertion Sort for efficiency.

It was introduced by David Musser (1997) and is the default sorting algorithm in C++ STL (`std::sort`), fast, adaptive, and safe.

What Problem Are We Solving?

Pure Quick Sort is fast on average but can degrade to $O(n^2)$ in the worst case (for example, sorted input with bad pivots).
Heap Sort guarantees $O(n \log n)$ but has worse constants.

IntroSort combines them, using Quick Sort *until danger*, then switching to Heap Sort for safety.

Perfect for:

- General-purpose sorting (numeric, string, object)
- Performance-critical libraries
- Mixed data with unknown distribution

Example

Sort `[9, 3, 1, 7, 5, 4, 6, 2, 8]`

Step	Action	Result
1	Start Quick Sort (depth = 0)	pivot = 5
2	Partition → `[3,1,2,4]` `[5]` `[9,7,6,8]`	depth = 1
3	Recurse left + right	
4	If depth > 2 × log (n), switch to Heap Sort	prevents (O(n^2))
5	Use Insertion Sort on small segments	

Final sorted array: `[1,2,3,4,5,6,7,8,9]`

How Does It Work (Plain Language)?

It's like a careful driver:

- Start fast on the highway (Quick Sort)
- If road gets tricky (too many turns = recursion depth), switch to 4-wheel drive (Heap Sort)
- For small parking spots (tiny arrays), use a nimble bike (Insertion Sort)

IntroSort keeps average speed high but avoids worst-case crashes.

Step-by-Step Process

Step	Description
1	Start Quick Sort recursively
2	Track recursion depth
3	If depth exceeds threshold ($2 \times \log\ n$), switch to Heap Sort
4	Use Insertion Sort for small subarrays (size $<$ threshold)
5	Combine results for final sorted array

Tiny Code (Easy Versions)

C (Simplified Implementation)

```c
#include <stdio.h>
#include <stdlib.h>
#include <math.h>

#define THRESHOLD 16

void insertion_sort(int arr[], int n) {
    for (int i = 1; i < n; i++) {
        int key = arr[i], j = i - 1;
        while (j >= 0 && arr[j] > key) arr[j + 1] = arr[j--];
        arr[j + 1] = key;
    }
}

void heapify(int arr[], int n, int i) {
```

```
    int largest = i, l = 2*i + 1, r = 2*i + 2;
    if (l < n && arr[l] > arr[largest]) largest = l;
    if (r < n && arr[r] > arr[largest]) largest = r;
    if (largest != i) {
        int tmp = arr[i]; arr[i] = arr[largest]; arr[largest] = tmp;
        heapify(arr, n, largest);
    }
}

void heap_sort(int arr[], int n) {
    for (int i = n/2 - 1; i >= 0; i--) heapify(arr, n, i);
    for (int i = n - 1; i >= 0; i--) {
        int tmp = arr[0]; arr[0] = arr[i]; arr[i] = tmp;
        heapify(arr, i, 0);
    }
}

int partition(int arr[], int low, int high) {
    int pivot = arr[high], i = low - 1;
    for (int j = low; j < high; j++) {
        if (arr[j] <= pivot) {
            i++;
            int tmp = arr[i]; arr[i] = arr[j]; arr[j] = tmp;
        }
    }
    int tmp = arr[i+1]; arr[i+1] = arr[high]; arr[high] = tmp;
    return i + 1;
}

void introsort_rec(int arr[], int low, int high, int depth_limit) {
    int n = high - low + 1;
    if (n <= THRESHOLD) {
        insertion_sort(arr + low, n);
        return;
    }
    if (depth_limit == 0) {
        heap_sort(arr + low, n);
        return;
    }
    int p = partition(arr, low, high);
    introsort_rec(arr, low, p - 1, depth_limit - 1);
    introsort_rec(arr, p + 1, high, depth_limit - 1);
```

```c
}

void introsort(int arr[], int n) {
    int depth_limit = 2 * log(n);
    introsort_rec(arr, 0, n - 1, depth_limit);
}

int main(void) {
    int arr[] = {9,3,1,7,5,4,6,2,8};
    int n = sizeof(arr)/sizeof(arr[0]);
    introsort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Python (Conceptual Demo)

```python
import math

def insertion_sort(a):
    for i in range(1, len(a)):
        key = a[i]
        j = i - 1
        while j >= 0 and a[j] > key:
            a[j + 1] = a[j]
            j -= 1
        a[j + 1] = key

def heapify(a, n, i):
    largest = i
    l, r = 2*i+1, 2*i+2
    if l < n and a[l] > a[largest]:
        largest = l
    if r < n and a[r] > a[largest]:
        largest = r
    if largest != i:
        a[i], a[largest] = a[largest], a[i]
        heapify(a, n, largest)

def heap_sort(a):
```

```
    n = len(a)
    for i in range(n//2-1, -1, -1):
        heapify(a, n, i)
    for i in range(n-1, 0, -1):
        a[0], a[i] = a[i], a[0]
        heapify(a, i, 0)

def introsort(a, depth_limit=None):
    n = len(a)
    if n <= 16:
        insertion_sort(a)
        return a
    if depth_limit is None:
        depth_limit = 2 * int(math.log2(n))
    if depth_limit == 0:
        heap_sort(a)
        return a

    pivot = a[-1]
    left = [x for x in a[:-1] if x <= pivot]
    right = [x for x in a[:-1] if x > pivot]
    introsort(left, depth_limit - 1)
    introsort(right, depth_limit - 1)
    a[:] = left + [pivot] + right
    return a

arr = [9,3,1,7,5,4,6,2,8]
print(introsort(arr))
```

Why It Matters

- Default in C++ STL, fast and reliable
- Guaranteed worst-case $O(n \log n)$
- Optimized for cache and small data
- Adaptive, uses best method for current scenario

A Gentle Proof (Why It Works)

Quick Sort dominates until recursion depth $= 2 \log_2 n$. At that point, worst-case risk appears $\rightarrow$ switch to Heap Sort (safe fallback). Small subarrays are handled by Insertion Sort for low overhead.

So overall:

$$T(n) = O(n \log n)$$

Always bounded by Heap Sort's worst case, but often near Quick Sort's best.

Phase	Method	Complexity
Partitioning	Quick Sort	O(n log n)
Deep recursion	Heap Sort	O(n log n)
Small arrays	Insertion Sort	$O(n^2)$ local, negligible

Try It Yourself

1. Sort `[9,3,1,7,5,4,6,2,8]`.
2. Track recursion depth, switch to Heap Sort when $> 2 \log_2 n$.
3. Replace threshold = 16 with 8, 32, measure effect.
4. Test with already sorted array, confirm Heap fallback.
5. Compare timing with Quick Sort and Heap Sort.
6. Print method used at each stage.
7. Test large array (10 elements).
8. Verify worst-case safety on sorted input.
9. Try string sorting with custom comparator.
10. Implement generic version using templates or lambdas.

Test Cases

Input	Output	Notes
[9,3,1,7,5,4,6,2,8]	[1,2,3,4,5,6,7,8,9]	Balanced partitions
[1,2,3,4,5]	[1,2,3,4,5]	Sorted input (Heap Sort fallback)
[5,5,5,5]	[5,5,5,5]	Equal elements
[9,8,7,6,5,4,3,2,1]	[1,2,3,4,5,6,7,8,9]	Worst-case Quick Sort avoided

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(log n)

Aspect	Value
Stable	No
Adaptive	Yes

IntroSort is the strategist's algorithm, it starts bold (Quick Sort), defends wisely (Heap Sort), and finishes gracefully (Insertion Sort). A perfect balance of speed, safety, and adaptability.

132 TimSort

TimSort is a hybrid sorting algorithm combining Merge Sort and Insertion Sort, designed for real-world data that often contains partially ordered runs. It was invented by Tim Peters in 2002 and is the default sorting algorithm in Python (`sorted()`, `.sort()`) and Java (`Arrays.sort()` for objects).

TimSort's superpower is that it detects natural runs in data, sorts them with Insertion Sort if small, and merges them smartly using a stack-based strategy to ensure efficiency.

What Problem Are We Solving?

In practice, many datasets aren't random, they already contain sorted segments (like logs, names, timestamps). TimSort exploits this by:

- Detecting ascending/descending runs
- Sorting small runs via Insertion Sort
- Merging runs using adaptive Merge Sort

This yields O(n) performance on already-sorted or nearly-sorted data, far better than standard $O(n \log n)$ sorts in such cases.

Perfect for:

- Partially sorted lists
- Real-world data (time series, strings, logs)
- Stable sorting (preserve order of equals)

Example

Sort `[5, 6, 7, 1, 2, 3, 8, 9]`

Step	Action	Result
1	Detect runs	[5,6,7], [1,2,3], [8,9]
2	Sort small runs if needed	[5,6,7], [1,2,3], [8,9]
3	Merge runs pairwise	[1,2,3,5,6,7,8,9]

TimSort leverages order already present, fewer merges, faster finish.

How Does It Work (Plain Language)?

Think of TimSort as a smart librarian:

- Sees which shelves (runs) are already sorted
- Tidies up small messy shelves (Insertion Sort)
- Merges shelves together efficiently (Merge Sort)
- Uses stack rules to decide merge timing for balance

It's adaptive, stable, and real-world optimized.

Step-by-Step Process

Step	Description
1	Scan the array to find runs (ascending or descending)
2	Reverse descending runs
3	If run length < `minrun`, extend using Insertion Sort
4	Push runs onto stack
5	Merge runs when stack size conditions are violated
6	Continue until one run remains (fully sorted)

Tiny Code (Easy Versions)

Python (Simplified Simulation)

```
def insertion_sort(arr, left, right):
    for i in range(left + 1, right + 1):
        key = arr[i]
        j = i - 1
        while j >= left and arr[j] > key:
```

```
            arr[j + 1] = arr[j]
            j -= 1
        arr[j + 1] = key

def merge(arr, left, mid, right):
    left_part = arr[left:mid+1]
    right_part = arr[mid+1:right+1]
    i = j = 0
    k = left
    while i < len(left_part) and j < len(right_part):
        if left_part[i] <= right_part[j]:
            arr[k] = left_part[i]
            i += 1
        else:
            arr[k] = right_part[j]
            j += 1
        k += 1
    while i < len(left_part):
        arr[k] = left_part[i]; i += 1; k += 1
    while j < len(right_part):
        arr[k] = right_part[j]; j += 1; k += 1

def timsort(arr):
    n = len(arr)
    minrun = 32

    # Sort small runs using insertion sort
    for start in range(0, n, minrun):
        end = min(start + minrun - 1, n - 1)
        insertion_sort(arr, start, end)

    size = minrun
    while size < n:
        for left in range(0, n, 2 * size):
            mid = min(n - 1, left + size - 1)
            right = min(n - 1, left + 2 * size - 1)
            if mid < right:
                merge(arr, left, mid, right)
        size *= 2

arr = [5,6,7,1,2,3,8,9]
timsort(arr)
```

```
print(arr)
```

Output:

```
$$1, 2, 3, 5, 6, 7, 8, 9]
```

C (Conceptual Version)

```c
#include <stdio.h>
#include <stdlib.h>

#define MINRUN 32

void insertion_sort(int arr[], int left, int right) {
    for (int i = left + 1; i <= right; i++) {
        int key = arr[i], j = i - 1;
        while (j >= left && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}

void merge(int arr[], int l, int m, int r) {
    int n1 = m - l + 1, n2 = r - m;
    int *L = malloc(n1 * sizeof(int)), *R = malloc(n2 * sizeof(int));
    for (int i = 0; i < n1; i++) L[i] = arr[l + i];
    for (int j = 0; j < n2; j++) R[j] = arr[m + 1 + j];
    int i = 0, j = 0, k = l;
    while (i < n1 && j < n2) arr[k++] = (L[i] <= R[j]) ? L[i++] : R[j++];
    while (i < n1) arr[k++] = L[i++];
    while (j < n2) arr[k++] = R[j++];
    free(L); free(R);
}

void timsort(int arr[], int n) {
    for (int i = 0; i < n; i += MINRUN) {
        int end = (i + MINRUN - 1 < n) ? (i + MINRUN - 1) : (n - 1);
        insertion_sort(arr, i, end);
```

```
    }
    for (int size = MINRUN; size < n; size *= 2) {
        for (int left = 0; left < n; left += 2 * size) {
            int mid = (left + size - 1 < n - 1) ? (left + size - 1) : (n - 1);
            int right = (left + 2 * size - 1 < n - 1) ? (left + 2 * size - 1) : (n - 1);
            if (mid < right) merge(arr, left, mid, right);
        }
    }
}

int main(void) {
    int arr[] = {5,6,7,1,2,3,8,9};
    int n = sizeof(arr)/sizeof(arr[0]);
    timsort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Default sort in Python & Java
- Stable and adaptive
- O(n) on sorted data
- O(n log n) worst case
- Handles real-world inputs gracefully

It's the perfect sort when you don't know the data shape, it *adapts itself*.

A Gentle Proof (Why It Works)

If data already contains sorted runs of average length r:

- Insertion Sort: $O(r^2)$ per run (tiny)
- Merging (n/r) runs: $O(n \log(n/r))$

Overall:

$$T(n) = O(n + n \log(n/r))$$

For $r \approx n$: $O(n)$
For $r = 1$: $O(n \log n)$

Phase	Work	Complexity
Run Detection	$O(n)$	One pass
Local Sorting	$O(r^2)$ per run	Tiny runs
Merge Phase	$O(n \log n)$	Balanced merges

Try It Yourself

1. Sort `[5,6,7,1,2,3,8,9]` step by step.
2. Detect natural runs manually.
3. Reverse descending runs before merge.
4. Adjust `minrun = 16`, see difference.
5. Test `[1,2,3,4,5]`, should take O(n).
6. Add random noise to partially sorted list.
7. Track stack of runs, when to merge?
8. Compare performance with Merge Sort.
9. Visualize merge order tree.
10. Check stability with duplicate keys.

Test Cases

Input	Output	Notes
[5,6,7,1,2,3,8,9]	[1,2,3,5,6,7,8,9]	Mixed runs
[1,2,3,4,5]	[1,2,3,4,5]	Already sorted
[9,8,7,6]	[6,7,8,9]	Reverse run
[5,5,5,5]	[5,5,5,5]	Stability test

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(n)
Stable	Yes
Adaptive	Yes

TimSort is the real-world champion, it watches your data, adapts instantly, and sorts smarter, not harder. It's the kind of algorithm that doesn't just run fast, it *thinks* fast.

133 Dual-Pivot QuickSort

Dual-Pivot QuickSort is an enhanced variant of QuickSort that uses two pivots instead of one to partition the array into three regions:

- Elements less than pivot1,
- Elements between pivot1 and pivot2,
- Elements greater than pivot2.

This approach often reduces comparisons and improves cache efficiency. It was popularized by Vladimir Yaroslavskiy and became the default sorting algorithm in Java (from Java 7) for primitive types.

What Problem Are We Solving?

Standard QuickSort splits the array into two parts using one pivot. Dual-Pivot QuickSort splits into three, reducing recursion depth and overhead.

It's optimized for:

- Large arrays of primitives (integers, floats)
- Random and uniform data
- Modern CPUs with deep pipelines and caches

It offers better real-world performance than classic QuickSort, even if asymptotic complexity remains $O(n \log n)$.

Example

Sort `[9, 3, 1, 7, 5, 4, 6, 2, 8]`

Choose pivots ($p_1 = 3$, $p_2 = 7$):

Region	Condition	Elements
Left	$x < 3$	[1, 2]
Middle	$3 \leq x \leq 7$	[3, 4, 5, 6, 7]
Right	$x > 7$	[8, 9]

Recurse on each region.
Final result: `[1, 2, 3, 4, 5, 6, 7, 8, 9]`.

How Does It Work (Plain Language)?

Imagine sorting shoes by size with two markers:

- Small shelf for sizes less than 7
- Middle shelf for 7–9
- Big shelf for 10+

You walk through once, placing each shoe in the right group, then sort each shelf individually.

Dual-Pivot QuickSort does exactly that: partition into three zones in one pass, then recurse.

Step-by-Step Process

Step	Description
1	Choose two pivots (p_1, p_2), ensuring $p_1 < p_2$
2	Partition array into 3 parts: `< p` , `p ..p` , `> p`
3	Recursively sort each part
4	Combine results in order

If $p_1 > p_2$, swap them first.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int tmp = *a; *a = *b; *b = tmp;
}

void dual_pivot_quicksort(int arr[], int low, int high) {
    if (low >= high) return;

    if (arr[low] > arr[high]) swap(&arr[low], &arr[high]);
```

```c
    int p1 = arr[low], p2 = arr[high];

    int lt = low + 1, gt = high - 1, i = low + 1;

    while (i <= gt) {
        if (arr[i] < p1) {
            swap(&arr[i], &arr[lt]);
            lt++; i++;
        } else if (arr[i] > p2) {
            swap(&arr[i], &arr[gt]);
            gt--;
        } else {
            i++;
        }
    }
    lt--; gt++;
    swap(&arr[low], &arr[lt]);
    swap(&arr[high], &arr[gt]);

    dual_pivot_quicksort(arr, low, lt - 1);
    dual_pivot_quicksort(arr, lt + 1, gt - 1);
    dual_pivot_quicksort(arr, gt + 1, high);
}

int main(void) {
    int arr[] = {9,3,1,7,5,4,6,2,8};
    int n = sizeof(arr)/sizeof(arr[0]);
    dual_pivot_quicksort(arr, 0, n-1);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Python

```python
def dual_pivot_quicksort(arr):
    def sort(low, high):
        if low >= high:
            return
        if arr[low] > arr[high]:
            arr[low], arr[high] = arr[high], arr[low]
```

```
        p1, p2 = arr[low], arr[high]
        lt, gt, i = low + 1, high - 1, low + 1
        while i <= gt:
            if arr[i] < p1:
                arr[i], arr[lt] = arr[lt], arr[i]
                lt += 1; i += 1
            elif arr[i] > p2:
                arr[i], arr[gt] = arr[gt], arr[i]
                gt -= 1
            else:
                i += 1
        lt -= 1; gt += 1
        arr[low], arr[lt] = arr[lt], arr[low]
        arr[high], arr[gt] = arr[gt], arr[high]
        sort(low, lt - 1)
        sort(lt + 1, gt - 1)
        sort(gt + 1, high)
    sort(0, len(arr) - 1)
    return arr

arr = [9,3,1,7,5,4,6,2,8]
print(dual_pivot_quicksort(arr))
```

Why It Matters

- Default in Java for primitives
- Fewer comparisons than single-pivot QuickSort
- Cache-friendly (less branching)
- Stable recursion depth with three partitions

A Gentle Proof (Why It Works)

Each partitioning step processes all elements once, $O(n)$. Recursion on three smaller subarrays yields total cost:

$$T(n) = T(k_1) + T(k_2) + T(k_3) + O(n)$$

On average, partitions are balanced $\rightarrow T(n) = O(n \log n)$

Phase	Operation	Complexity
Partitioning	$O(n)$	One pass
Recursion	3 subarrays	Balanced depth
Total	$O(n \log n)$	Average / Worst

Try It Yourself

1. Sort `[9,3,1,7,5,4,6,2,8]` step by step.
2. Choose pivots manually: smallest and largest.
3. Trace index movements (lt, gt, i).
4. Compare with classic QuickSort partition count.
5. Use reversed array, observe stability.
6. Add duplicates `[5,5,5,5]`, see middle zone effect.
7. Measure comparisons vs single pivot.
8. Try large input (10) and time it.
9. Visualize three partitions recursively.
10. Implement tail recursion optimization.

Test Cases

Input	Output	Notes
[9,3,1,7,5,4,6,2,8]	[1,2,3,4,5,6,7,8,9]	Example
[1,2,3,4]	[1,2,3,4]	Already sorted
[9,8,7,6,5]	[5,6,7,8,9]	Reverse
[5,5,5,5]	[5,5,5,5]	Duplicates

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(log n)
Stable	No
Adaptive	No

Dual-Pivot QuickSort slices data with two blades instead of one, making each cut smaller, shallower, and more balanced. A sharper, smarter evolution of a timeless classic.

134 SmoothSort

SmoothSort is an adaptive comparison-based sorting algorithm invented by Edsger Dijkstra. It's similar in spirit to Heap Sort, but smarter, it runs in O(n) time on already sorted data and O(n log n) in the worst case.

The key idea is to build a special heap structure (Leonardo heap) that adapts to existing order in the data. When the array is nearly sorted, it finishes quickly. When not, it gracefully falls back to heap-like performance.

What Problem Are We Solving?

Heap Sort always works in $O(n \log n)$, even when the input is already sorted. SmoothSort improves on this by being adaptive, the more ordered the input, the faster it gets.

It's ideal for:

- Nearly sorted arrays
- Situations requiring guaranteed upper bounds
- Memory-constrained environments (in-place sort)

Example

Sort `[1, 2, 4, 3, 5]`

Step	Action	Result
1	Build initial heap (Leonardo structure)	[1,2,4,3,5]
2	Detect small disorder (4,3)	Swap
3	Restore heap property	[1,2,3,4,5]
4	Sorted early, no full rebuild needed	Done

Result: finished early since only minor disorder existed.

How Does It Work (Plain Language)?

Imagine a stack of heaps, each representing a Fibonacci-like sequence (Leonardo numbers). You grow this structure as you read the array, maintaining order locally. When disorder appears, you fix only where needed, not everywhere.

So SmoothSort is like a gentle gardener: it only trims where weeds grow, not the whole garden.

Step-by-Step Process

Step	Description
1	Represent the array as a series of Leonardo heaps
2	Add elements one by one, updating the heap sequence
3	Maintain heap property with minimal swaps
4	When finished, repeatedly extract the maximum (like Heap Sort)
5	During extraction, merge smaller heaps as needed

Leonardo numbers guide heap sizes: (L(0)=1, L(1)=1, L(n)=L(n-1)+L(n-2)+1)

Tiny Code (Easy Versions)

Python (Simplified Adaptive Sort)

This is a simplified version to show adaptiveness, not a full Leonardo heap implementation.

```
def smoothsort(arr):
    # Simplified: detect sorted runs, fix only where needed
    n = len(arr)
    for i in range(1, n):
        j = i
        while j > 0 and arr[j] < arr[j - 1]:
            arr[j], arr[j - 1] = arr[j - 1], arr[j]
            j -= 1
    return arr

arr = [1, 2, 4, 3, 5]
print(smoothsort(arr))
```

Output:

```
$$1, 2, 3, 4, 5]
```

(Note: Real SmoothSort uses Leonardo heaps, complex but in-place and efficient.)

C (Conceptual Heap Approach)

```c
#include <stdio.h>

void insertion_like_fix(int arr[], int n) {
    for (int i = 1; i < n; i++) {
        int j = i;
        while (j > 0 && arr[j] < arr[j - 1]) {
            int tmp = arr[j];
            arr[j] = arr[j - 1];
            arr[j - 1] = tmp;
            j--;
        }
    }
}

int main(void) {
    int arr[] = {1,2,4,3,5};
    int n = sizeof(arr)/sizeof(arr[0]);
    insertion_like_fix(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

This mimics SmoothSort's adaptiveness: fix locally, not globally.

Why It Matters

- Adaptive: faster on nearly sorted data
- In-place: no extra memory
- Guaranteed bound: never worse than $O(n \log n)$
- Historical gem: Dijkstra's innovation in sorting theory

A Gentle Proof (Why It Works)

For sorted input:

- Each insertion requires no swaps $\rightarrow O(n)$

For random input:

- Heap restorations per insertion $\rightarrow O(\log n)$
- Total cost: $O(n \log n)$

Case	Behavior	Complexity
Best (Sorted)	Minimal swaps	$O(n)$
Average	Moderate reheapify	$O(n \log n)$
Worst	Full heap rebuilds	$O(n \log n)$

SmoothSort adapts between these seamlessly.

Try It Yourself

1. Sort `[1, 2, 4, 3, 5]` step by step.
2. Try `[1, 2, 3, 4, 5]`, measure comparisons.
3. Try `[5, 4, 3, 2, 1]`, full workload.
4. Count swaps in each case.
5. Compare to Heap Sort.
6. Visualize heap sizes as Leonardo sequence.
7. Implement run detection.
8. Experiment with large partially sorted arrays.
9. Track adaptive speedup.
10. Write Leonardo heap builder.

Test Cases

Input	Output	Notes
[1,2,4,3,5]	[1,2,3,4,5]	Minor disorder
[1,2,3,4,5]	[1,2,3,4,5]	Already sorted
[5,4,3,2,1]	[1,2,3,4,5]	Full rebuild
[2,1,3,5,4]	[1,2,3,4,5]	Mixed case

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(1)
Stable	No
Adaptive	Yes

SmoothSort glides gracefully across the array, fixing only what's broken. It's sorting that *listens* to your data, quiet, clever, and precise.

135 Block Merge Sort

Block Merge Sort is a cache-efficient, stable sorting algorithm that merges data using small fixed-size blocks instead of large temporary arrays. It improves on standard Merge Sort by reducing memory usage and enhancing locality of reference, making it a great choice for modern hardware and large datasets.

It's designed to keep data cache-friendly, in-place (or nearly), and stable, making it a practical choice for systems with limited memory bandwidth or tight memory constraints.

What Problem Are We Solving?

Classic Merge Sort is stable and O(n log n), but it needs O(n) extra space. Block Merge Sort solves this by using blocks of fixed size (often $\sqrt{n}$) as temporary buffers for merging.

It aims to:

- Keep stability
- Use limited extra memory
- Maximize cache reuse
- Maintain predictable access patterns

Ideal for:

- Large arrays
- External memory sorting
- Systems with cache hierarchies

Example

Sort `[8, 3, 5, 1, 6, 2, 7, 4]`

Step	Action	Result
1	Divide into sorted runs (via insertion sort)	[3,8], [1,5], [2,6], [4,7]
2	Merge adjacent blocks using buffer	[1,3,5,8], [2,4,6,7]
3	Merge merged blocks with block buffer	[1,2,3,4,5,6,7,8]

Instead of full arrays, it uses small block buffers, fewer cache misses, less extra space.

How Does It Work (Plain Language)?

Think of merging two sorted shelves in a library, but instead of taking all books off, you move a small block at a time, swapping them in place with a small temporary cart.

You slide the buffer along the shelves, merge gradually, efficiently, with minimal movement.

Step-by-Step Process

Step	Description
1	Divide input into runs (sorted subarrays)
2	Use insertion sort or binary insertion to sort each run
3	Allocate small buffer (block)
4	Merge runs pairwise using the block buffer
5	Repeat until one sorted array remains

Block merges rely on rotations and buffer swapping to minimize extra space.

Tiny Code (Easy Versions)

Python (Simplified Version)

This version simulates block merging using chunks.

```
def insertion_sort(arr, start, end):
    for i in range(start + 1, end):
        key = arr[i]
        j = i - 1
        while j >= start and arr[j] > key:
            arr[j + 1] = arr[j]
            j -= 1
        arr[j + 1] = key

def merge(arr, left, mid, right):
    left_part = arr[left:mid]
    right_part = arr[mid:right]
    i = j = 0
    k = left
    while i < len(left_part) and j < len(right_part):
        if left_part[i] <= right_part[j]:
            arr[k] = left_part[i]; i += 1
        else:
            arr[k] = right_part[j]; j += 1
        k += 1
    while i < len(left_part):
        arr[k] = left_part[i]; i += 1; k += 1
    while j < len(right_part):
        arr[k] = right_part[j]; j += 1; k += 1

def block_merge_sort(arr, block_size=32):
    n = len(arr)
    # Step 1: sort small blocks
    for start in range(0, n, block_size):
        end = min(start + block_size, n)
        insertion_sort(arr, start, end)

    # Step 2: merge adjacent blocks
    size = block_size
    while size < n:
        for left in range(0, n, 2 * size):
            mid = min(left + size, n)
            right = min(left + 2 * size, n)
            merge(arr, left, mid, right)
        size *= 2
    return arr
```

```
arr = [8, 3, 5, 1, 6, 2, 7, 4]
print(block_merge_sort(arr))
```

Output:

```
$$1, 2, 3, 4, 5, 6, 7, 8]
```

C (Simplified Concept)

```
#include <stdio.h>

void insertion_sort(int arr[], int left, int right) {
    for (int i = left + 1; i < right; i++) {
        int key = arr[i], j = i - 1;
        while (j >= left && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}

void merge(int arr[], int left, int mid, int right) {
    int n1 = mid - left, n2 = right - mid;
    int L[n1], R[n2];
    for (int i = 0; i < n1; i++) L[i] = arr[left + i];
    for (int j = 0; j < n2; j++) R[j] = arr[mid + j];

    int i = 0, j = 0, k = left;
    while (i < n1 && j < n2) arr[k++] = (L[i] <= R[j]) ? L[i++] : R[j++];
    while (i < n1) arr[k++] = L[i++];
    while (j < n2) arr[k++] = R[j++];
}

void block_merge_sort(int arr[], int n, int block_size) {
    for (int i = 0; i < n; i += block_size) {
        int end = (i + block_size < n) ? i + block_size : n;
        insertion_sort(arr, i, end);
    }
    for (int size = block_size; size < n; size *= 2) {
```

```
        for (int left = 0; left < n; left += 2 * size) {
            int mid = (left + size < n) ? left + size : n;
            int right = (left + 2 * size < n) ? left + 2 * size : n;
            if (mid < right) merge(arr, left, mid, right);
        }
    }
}

int main(void) {
    int arr[] = {8,3,5,1,6,2,7,4};
    int n = sizeof(arr)/sizeof(arr[0]);
    block_merge_sort(arr, n, 2);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Stable like Merge Sort
- In-place or low-space variant
- Cache-efficient due to block locality
- Practical for large arrays or external sorting

A Gentle Proof (Why It Works)

Each merge level processes n elements: $O(n)$.
Number of levels $= \log_2(n/b)$, where b is the block size.

So total:

$$T(n) = O(n \log(n/b))$$

When b is large (like $\sqrt{n}$), space and time balance nicely.

Phase	Operation	Cost
Block sorting	$\frac{n}{b} \times b^2$	$O(nb)$
Merging	$\log(n/b) \times n$	$O(n \log n)$

For typical settings, it's near $O(n \log n)$ but cache-optimized.

Try It Yourself

1. Sort `[8,3,5,1,6,2,7,4]` with block size 2.
2. Increase block size to 4, compare steps.
3. Track number of merges.
4. Check stability with duplicates.
5. Compare with standard Merge Sort.
6. Time on sorted input (adaptive check).
7. Measure cache misses (simulated).
8. Try large array (10000+) for memory gain.
9. Mix ascending and descending runs.
10. Implement block buffer rotation manually.

Test Cases

Input	Output	Notes
[8,3,5,1,6,2,7,4]	[1,2,3,4,5,6,7,8]	Classic
[5,5,3,3,1]	[1,3,3,5,5]	Stable
[1,2,3,4]	[1,2,3,4]	Sorted
[9,8,7]	[7,8,9]	Reverse order

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(b)
Stable	Yes
Adaptive	Partially

Block Merge Sort is the engineer's Merge Sort, same elegance, less memory, smarter on hardware. It merges not by brute force, but by careful block juggling, balancing speed, space, and stability.

136 Adaptive Merge Sort

Adaptive Merge Sort is a stable, comparison-based sorting algorithm that adapts to existing order in the input data. It builds on the idea that real-world datasets are often partially sorted, so by detecting runs (already sorted sequences) and merging them intelligently, it can achieve O(n) time on nearly sorted data while retaining O(n log n) in the worst case.

It's a family of algorithms, including Natural Merge Sort, TimSort, and GrailSort, that all share one key insight: work less when less work is needed.

What Problem Are We Solving?

Standard Merge Sort treats every input the same, even if it's already sorted. Adaptive Merge Sort improves this by:

- Detecting sorted runs (ascending or descending)
- Merging runs instead of single elements
- Achieving linear time on sorted or partially sorted data

This makes it perfect for:

- Time series data
- Sorted or semi-sorted logs
- Incrementally updated lists

Example

Sort `[1, 2, 5, 3, 4, 6]`

Step	Action	Result
1	Detect runs: [1,2,5], [3,4,6]	Found 2 runs
2	Merge runs	[1,2,3,4,5,6]
3	Done	Sorted

Only one merge needed, input was nearly sorted, so runtime is close to O(n).

How Does It Work (Plain Language)?

Imagine you're sorting a shelf of books that's mostly organized — you don't pull all the books off; you just spot where order breaks, and fix those parts.

Adaptive Merge Sort does exactly this:

- Scan once to find sorted parts
- Merge runs using a stable merge procedure

It's lazy where it can be, efficient where it must be.

Step-by-Step Process

Step	Description
1	Scan input to find runs (ascending or descending)
2	Reverse descending runs
3	Push runs onto a stack
4	Merge runs when stack conditions are violated (size or order)
5	Continue until one sorted run remains

Tiny Code (Easy Versions)

Python (Natural Merge Sort)

```
def natural_merge_sort(arr):
    n = len(arr)
    runs = []
    i = 0
    # Step 1: Detect sorted runs
    while i < n:
        start = i
        i += 1
        while i < n and arr[i] >= arr[i - 1]:
            i += 1
        runs.append(arr[start:i])
    # Step 2: Merge runs pairwise
    while len(runs) > 1:
        new_runs = []
        for j in range(0, len(runs), 2):
```

```
            if j + 1 < len(runs):
                new_runs.append(merge(runs[j], runs[j+1]))
            else:
                new_runs.append(runs[j])
        runs = new_runs
    return runs[0]

def merge(left, right):
    i = j = 0
    result = []
    while i < len(left) and j < len(right):
        if left[i] <= right[j]:
            result.append(left[i]); i += 1
        else:
            result.append(right[j]); j += 1
    result.extend(left[i:])
    result.extend(right[j:])
    return result

arr = [1, 2, 5, 3, 4, 6]
print(natural_merge_sort(arr))
```

Output:

```
$$1, 2, 3, 4, 5, 6]
```

C (Simplified Conceptual)

```
#include <stdio.h>
#include <stdlib.h>

void merge(int arr[], int l, int m, int r) {
    int n1 = m - l + 1, n2 = r - m;
    int L[n1], R[n2];
    for (int i = 0; i < n1; i++) L[i] = arr[l + i];
    for (int j = 0; j < n2; j++) R[j] = arr[m + 1 + j];
    int i = 0, j = 0, k = l;
    while (i < n1 && j < n2) arr[k++] = (L[i] <= R[j]) ? L[i++] : R[j++];
    while (i < n1) arr[k++] = L[i++];
    while (j < n2) arr[k++] = R[j++];
```

```
}

void adaptive_merge_sort(int arr[], int n) {
    int start = 0;
    while (start < n - 1) {
        int mid = start;
        while (mid < n - 1 && arr[mid] <= arr[mid + 1]) mid++;
        int end = mid + 1;
        while (end < n - 1 && arr[end] <= arr[end + 1]) end++;
        if (end < n) merge(arr, start, mid, end);
        start = end + 1;
    }
}

int main(void) {
    int arr[] = {1, 2, 5, 3, 4, 6};
    int n = sizeof(arr)/sizeof(arr[0]);
    adaptive_merge_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Stable and adaptive
- Linear time on nearly sorted data
- Works well for real-world sequences
- Forms the core idea behind TimSort
- Requires no extra knowledge about data

It's the sorting algorithm that notices your data's effort and rewards it.

A Gentle Proof (Why It Works)

Let average run length $= r$.
Then number of runs $\approx n/r$.
Each merge $= O(n)$ per level.
Depth $= O(\log(n/r))$.

So total cost:

$$T(n) = O(n \log(n/r))$$

If $r = n$ (already sorted): $O(n)$.
If $r = 1$: $O(n \log n)$.

Case	Run Length	Complexity
Sorted	$r = n$	$O(n)$
Nearly sorted	r large	$O(n \log(n/r))$
Random	r small	$O(n \log n)$

Try It Yourself

1. Sort `[1, 2, 5, 3, 4, 6]` step by step.
2. Try `[1, 2, 3, 4, 5]`, should detect 1 run.
3. Reverse a section, see new runs.
4. Merge runs manually using table.
5. Compare performance to Merge Sort.
6. Add duplicates, check stability.
7. Use 10k sorted elements, time the run.
8. Mix ascending and descending subarrays.
9. Visualize run detection.
10. Implement descending-run reversal.

Test Cases

Input	Output	Notes
[1,2,5,3,4,6]	[1,2,3,4,5,6]	Two runs
[1,2,3,4,5]	[1,2,3,4,5]	Already sorted
[5,4,3,2,1]	[1,2,3,4,5]	Reverse (many runs)
[2,2,1,1]	[1,1,2,2]	Stable

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(n)
Stable	Yes

Aspect	Value
Adaptive	Yes

Adaptive Merge Sort is like a thoughtful sorter, it looks before it leaps. If your data's halfway there, it'll meet it in the middle.

137 PDQSort (Pattern-Defeating QuickSort)

PDQSort is a modern, adaptive, in-place sorting algorithm that extends QuickSort with pattern detection, branchless partitioning, and fallback mechanisms to guarantee $O(n \log n)$ performance even on adversarial inputs.

Invented by Orson Peters, it's used in C++'s `std::sort()` (since C++17) and often outperforms traditional QuickSort and IntroSort in real-world scenarios due to better cache behavior, branch prediction, and adaptive pivoting.

What Problem Are We Solving?

Classic QuickSort performs well *on average* but can degrade to (O(n^2)) on structured or repetitive data. PDQSort solves this by:

- Detecting bad patterns (e.g., sorted input)
- Switching strategy (to heap sort or insertion sort)
- Branchless partitioning for modern CPUs
- Adaptive pivot selection (median-of-3, Tukey ninther)

It keeps speed, stability of performance, and cache-friendliness.

Perfect for:

- Large unsorted datasets
- Partially sorted data
- Real-world data with patterns

Step	Action	Result

Example

Sort `[1, 2, 3, 4, 5]` (already sorted)

Step	Action	Result
1	Detect sorted pattern	Pattern found
2	Switch to Insertion Sort	Efficient handling
3	Output sorted	[1,2,3,4,5]

Instead of recursive QuickSort calls, PDQSort defeats the pattern by adapting.

How Does It Work (Plain Language)?

PDQSort is like a smart chef:

- It tastes the input first (checks pattern)
- Chooses a recipe (pivot rule, sorting fallback)
- Adjusts to the kitchen conditions (CPU caching, branching)

It never wastes effort, detecting when recursion or comparisons are unnecessary.

Step-by-Step Process

Step	Description
1	Pick pivot adaptively (median-of-3, ninther)
2	Partition elements into `< pivot` and `> pivot`
3	Detect bad patterns (sorted, reversed, many equal elements)
4	Apply branchless partitioning to reduce CPU mispredictions
5	Recurse or switch to heap/insertion sort if needed
6	Use tail recursion elimination

Tiny Code (Easy Versions)

Python (Conceptual Simplified PDQSort)

```
def pdqsort(arr):
    def insertion_sort(a, lo, hi):
        for i in range(lo + 1, hi):
            key = a[i]
            j = i - 1
            while j >= lo and a[j] > key:
                a[j + 1] = a[j]
                j -= 1
            a[j + 1] = key

    def partition(a, lo, hi):
        pivot = a[(lo + hi) // 2]
        i, j = lo, hi - 1
        while True:
            while a[i] < pivot: i += 1
            while a[j] > pivot: j -= 1
            if i >= j: return j
            a[i], a[j] = a[j], a[i]
            i += 1; j -= 1

    def _pdqsort(a, lo, hi, depth):
        n = hi - lo
        if n <= 16:
            insertion_sort(a, lo, hi)
            return
        if depth == 0:
            a[lo:hi] = sorted(a[lo:hi])  # heap fallback
            return
        mid = partition(a, lo, hi)
        _pdqsort(a, lo, mid + 1, depth - 1)
        _pdqsort(a, mid + 1, hi, depth - 1)

    _pdqsort(arr, 0, len(arr), len(arr).bit_length() * 2)
    return arr

arr = [1, 5, 3, 4, 2]
print(pdqsort(arr))
```

Output:

```
$$1, 2, 3, 4, 5]
```

C (Simplified PDQ-Style)

```c
#include <stdio.h>
#include <stdlib.h>

void insertion_sort(int arr[], int lo, int hi) {
    for (int i = lo + 1; i < hi; i++) {
        int key = arr[i], j = i - 1;
        while (j >= lo && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}

int partition(int arr[], int lo, int hi) {
    int pivot = arr[(lo + hi) / 2];
    int i = lo, j = hi - 1;
    while (1) {
        while (arr[i] < pivot) i++;
        while (arr[j] > pivot) j--;
        if (i >= j) return j;
        int tmp = arr[i]; arr[i] = arr[j]; arr[j] = tmp;
        i++; j--;
    }
}

void pdqsort(int arr[], int lo, int hi, int depth) {
    int n = hi - lo;
    if (n <= 16) { insertion_sort(arr, lo, hi); return; }
    if (depth == 0) { qsort(arr + lo, n, sizeof(int), (__compar_fn_t)strcmp); return; }
    int mid = partition(arr, lo, hi);
    pdqsort(arr, lo, mid + 1, depth - 1);
    pdqsort(arr, mid + 1, hi, depth - 1);
}
```

```c
int main(void) {
    int arr[] = {1, 5, 3, 4, 2};
    int n = sizeof(arr)/sizeof(arr[0]);
    pdqsort(arr, 0, n, 2 * 32);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Modern default for high-performance sorting
- Pattern detection avoids worst cases
- Branchless partitioning → fewer CPU stalls
- Heap fallback ensures $O(n \log n)$ bound
- Adaptive like TimSort, but in-place

PDQSort combines speed, safety, and hardware awareness.

A Gentle Proof (Why It Works)

PDQSort adds mechanisms to defeat QuickSort's pitfalls:

1. Bad pattern detection → early fallback
2. Balanced pivoting → near-equal splits
3. Branchless operations → efficient execution

So overall:

$$T(n) = O(n \log n)$$

Best case (sorted): near O(n), thanks to early detection.

Case	Behavior	Complexity
Best	Sorted or nearly sorted	O(n)
Average	Random	O(n log n)
Worst	Adversarial	O(n log n)

Try It Yourself

1. Sort `[1,2,3,4,5]` → detect sorted input.
2. Try `[5,4,3,2,1]` → reversed.
3. Random input of 1000 numbers.
4. Duplicate-heavy `[5,5,5,5]`.
5. Patterned input `[1,3,2,4,3,5,4]`.
6. Compare with QuickSort and HeapSort.
7. Count recursion depth.
8. Benchmark branchless vs classic partition.
9. Visualize fallback triggers.
10. Measure comparisons per element.

Test Cases

Input	Output	Notes
[1,5,3,4,2]	[1,2,3,4,5]	Random
[1,2,3,4,5]	[1,2,3,4,5]	Sorted
[5,4,3,2,1]	[1,2,3,4,5]	Reversed
[5,5,5,5]	[5,5,5,5]	Duplicates

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(log n)
Stable	No
Adaptive	Yes

PDQSort is the ninja of sorting, lightning fast, pattern-aware, and always one step ahead of your data. It doesn't just sort, it *outsmarts* the input.

138 WikiSort

WikiSort is a stable, in-place merge sort created by Mike Day, designed to combine the stability of Merge Sort with the low memory usage of in-place algorithms. It achieves O(n log n)

performance and uses only O(1) extra memory, making it one of the most space-efficient stable sorts available.

Unlike classic Merge Sort, which allocates a full-size temporary array, WikiSort performs block merges with rotation operations, merging sorted regions directly within the array.

What Problem Are We Solving?

Most stable sorting algorithms (like Merge Sort) need O(n) extra space. WikiSort solves this by performing stable merges in place, using:

- Block rotations instead of large buffers
- Adaptive merging when possible
- Small local buffers reused efficiently

Perfect for:

- Memory-constrained environments
- Sorting large arrays in embedded systems
- Stable sorts without heavy allocation

Example

Sort `[3, 5, 1, 2, 4]`

Step	Action	Result
1	Divide into sorted runs	[3,5], [1,2,4]
2	Merge using block rotations	[1,2,3,4,5]
3	Done, stable and in-place	Final sorted array

Result: `[1,2,3,4,5]`, sorted, stable, and minimal extra space.

How Does It Work (Plain Language)?

Think of two sorted shelves of books, instead of moving all books to a table, you rotate sections in place so the shelves merge seamlessly.

WikiSort keeps a small local buffer (like a tray), uses it to move small chunks, then rotates segments of the array into place. It never needs a second full array.

Step-by-Step Process

Step	Description
1	Split array into sorted runs
2	Allocate small buffer ($\sqrt{n}$ elements)
3	Merge adjacent runs using buffer
4	Rotate blocks to maintain stability
5	Repeat until one sorted region remains

Tiny Code (Easy Versions)

Python (Simplified In-Place Stable Merge)

This is a conceptual demonstration of stable in-place merging.

```
def rotate(arr, start, mid, end):
    arr[start:end] = arr[mid:end] + arr[start:mid]

def merge_in_place(arr, start, mid, end):
    left = arr[start:mid]
    i, j, k = 0, mid, start
    while i < len(left) and j < end:
        if left[i] <= arr[j]:
            arr[k] = left[i]; i += 1
        else:
            val = arr[j]
            rotate(arr, i + start, j, j + 1)
            arr[k] = val
            j += 1
        k += 1
    while i < len(left):
        arr[k] = left[i]; i += 1; k += 1

def wiki_sort(arr):
    n = len(arr)
    size = 1
    while size < n:
        for start in range(0, n, 2 * size):
            mid = min(start + size, n)
            end = min(start + 2 * size, n)
```

```
            if mid < end:
                merge_in_place(arr, start, mid, end)
        size *= 2
    return arr

arr = [3,5,1,2,4]
print(wiki_sort(arr))
```

Output:

```
$$1, 2, 3, 4, 5]
```

C (Simplified Conceptual Version)

```
#include <stdio.h>

void rotate(int arr[], int start, int mid, int end) {
    int temp[end - start];
    int idx = 0;
    for (int i = mid; i < end; i++) temp[idx++] = arr[i];
    for (int i = start; i < mid; i++) temp[idx++] = arr[i];
    for (int i = 0; i < end - start; i++) arr[start + i] = temp[i];
}

void merge_in_place(int arr[], int start, int mid, int end) {
    int i = start, j = mid;
    while (i < j && j < end) {
        if (arr[i] <= arr[j]) {
            i++;
        } else {
            int value = arr[j];
            rotate(arr, i, j, j + 1);
            arr[i] = value;
            i++; j++;
        }
    }
}

void wiki_sort(int arr[], int n) {
    for (int size = 1; size < n; size *= 2) {
```

```
        for (int start = 0; start < n; start += 2 * size) {
            int mid = (start + size < n) ? start + size : n;
            int end = (start + 2 * size < n) ? start + 2 * size : n;
            if (mid < end) merge_in_place(arr, start, mid, end);
        }
    }
}

int main(void) {
    int arr[] = {3,5,1,2,4};
    int n = sizeof(arr)/sizeof(arr[0]);
    wiki_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Stable and in-place (O(1) extra space)
- Practical for memory-limited systems
- Predictable performance
- Cache-friendly merges
- Great balance of theory and practice

It brings the best of Merge Sort (stability) and in-place algorithms (low memory).

A Gentle Proof (Why It Works)

Each merge takes $O(n)$, and there are $O(\log n)$ levels of merging:

$$T(n) = O(n \log n)$$

Extra memory = small buffer ($O(\sqrt{n})$) or even constant space.

Phase	Operation	Cost
Block detection	Scan runs	$O(n)$
Merging	Rotation-based merge	$O(n \log n)$
Space	Fixed buffer	$O(1)$

Try It Yourself

1. Sort `[3,5,1,2,4]` step by step.
2. Visualize rotations during merge.
3. Add duplicates `[2,2,3,1]`, verify stability.
4. Increase size to 16, track buffer reuse.
5. Compare with Merge Sort memory usage.
6. Measure swaps vs Merge Sort.
7. Try `[1,2,3,4]`, minimal rotations.
8. Reverse `[5,4,3,2,1]`, max work.
9. Implement block rotation helper.
10. Measure runtime on sorted input.

Test Cases

Input	Output	Notes
[3,5,1,2,4]	[1,2,3,4,5]	Basic
[5,4,3,2,1]	[1,2,3,4,5]	Worst case
[1,2,3,4]	[1,2,3,4]	Already sorted
[2,2,3,1]	[1,2,2,3]	Stable behavior

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(1)
Stable	Yes
Adaptive	Yes

WikiSort is the minimalist's Merge Sort, stable, elegant, and almost memory-free. It merges not by copying, but by rotating, smooth, steady, and space-savvy.

139 GrailSort

GrailSort (short for "Greedy Adaptive In-place stable Sort") is a stable, in-place, comparison-based sorting algorithm that merges sorted subarrays using block merging and local buffers.

Created by Michał Oryńczak, GrailSort combines the stability and adaptiveness of Merge Sort with in-place operation, needing only a tiny internal buffer (often $O(\sqrt{n})$) or even no extra memory in its pure variant.

It's designed for practical stable sorting when memory is tight, achieving $O(n \log n)$ worst-case time.

What Problem Are We Solving?

Typical stable sorting algorithms (like Merge Sort) require O(n) extra space. GrailSort solves this by:

- Using small local buffers instead of large arrays
- Performing in-place stable merges
- Detecting and reusing natural runs (adaptive behavior)

Perfect for:

- Memory-constrained systems
- Embedded devices
- Large stable sorts on limited RAM

Example

Sort `[4, 1, 3, 2, 5]`

Step	Action	Result
1	Detect short runs	[4,1], [3,2], [5]
2	Sort each run	[1,4], [2,3], [5]
3	Merge runs using block rotation	[1,2,3,4,5]
4	Stable order preserved	Done

All merges are done in-place, with a small reusable buffer.

How Does It Work (Plain Language)?

Think of GrailSort like a clever librarian with a tiny desk (the buffer). Instead of taking all books off the shelf, they:

- Divide shelves into small sorted groups,
- Keep a few aside as a helper buffer,

- Merge shelves directly on the rack by rotating sections in place.

It's stable, in-place, and adaptive, a rare combination.

Step-by-Step Process

Step	Description
1	Detect and sort small runs (Insertion Sort)
2	Choose small buffer (e.g., $\sqrt{n}$ elements)
3	Merge runs pairwise using buffer and rotation
4	Gradually increase block size (1, 2, 4, 8, …)
5	Continue merging until fully sorted

The algorithm's structure mirrors Merge Sort but uses block rotation to avoid copying large chunks.

Tiny Code (Easy Versions)

Python (Simplified Concept)

Below is a simplified stable block-merge inspired by GrailSort's principles.

```
def rotate(arr, start, mid, end):
    arr[start:end] = arr[mid:end] + arr[start:mid]

def merge_in_place(arr, left, mid, right):
    i, j = left, mid
    while i < j and j < right:
        if arr[i] <= arr[j]:
            i += 1
        else:
            val = arr[j]
            rotate(arr, i, j, j + 1)
            arr[i] = val
            i += 1
            j += 1

def grailsort(arr):
    n = len(arr)
    size = 1
```

```
    while size < n:
        for start in range(0, n, 2 * size):
            mid = min(start + size, n)
            end = min(start + 2 * size, n)
            if mid < end:
                merge_in_place(arr, start, mid, end)
        size *= 2
    return arr

arr = [4,1,3,2,5]
print(grailsort(arr))
```

Output:

```
$$1, 2, 3, 4, 5]
```

C (Simplified Idea)

```
#include <stdio.h>

void rotate(int arr[], int start, int mid, int end) {
    int temp[end - start];
    int idx = 0;
    for (int i = mid; i < end; i++) temp[idx++] = arr[i];
    for (int i = start; i < mid; i++) temp[idx++] = arr[i];
    for (int i = 0; i < end - start; i++) arr[start + i] = temp[i];
}

void merge_in_place(int arr[], int start, int mid, int end) {
    int i = start, j = mid;
    while (i < j && j < end) {
        if (arr[i] <= arr[j]) i++;
        else {
            int val = arr[j];
            rotate(arr, i, j, j + 1);
            arr[i] = val;
            i++; j++;
        }
    }
}
```

```c
void grailsort(int arr[], int n) {
    for (int size = 1; size < n; size *= 2) {
        for (int start = 0; start < n; start += 2 * size) {
            int mid = (start + size < n) ? start + size : n;
            int end = (start + 2 * size < n) ? start + 2 * size : n;
            if (mid < end) merge_in_place(arr, start, mid, end);
        }
    }
}

int main(void) {
    int arr[] = {4,1,3,2,5};
    int n = sizeof(arr)/sizeof(arr[0]);
    grailsort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Stable and in-place (only small buffer)
- Adaptive, faster on partially sorted data
- Predictable performance
- Ideal for limited memory systems
- Used in practical sorting libraries and research

It's the gold standard for stable, low-space sorts.

A Gentle Proof (Why It Works)

Each merge level processes $O(n)$ elements.
There are $O(\log n)$ merge levels.
Thus:

$$T(n) = O(n \log n)$$

A small buffer ($O(\sqrt{n})$) is reused, yielding in-place stability.

Phase	Operation	Cost
Run sorting	Insertion Sort	$O(n)$
Block merges	Rotation-based	$O(n \log n)$
Space	Local buffer	$O(1)$ or $O(\sqrt{n})$

Try It Yourself

1. Sort `[4,1,3,2,5]` step by step.
2. Try `[1,2,3,4,5]`, no merges needed.
3. Check duplicates `[2,2,1,1]`, verify stability.
4. Experiment with `[10,9,8,7,6,5]`.
5. Visualize rotations during merge.
6. Change block size, observe performance.
7. Implement √n buffer manually.
8. Compare with Merge Sort (space).
9. Measure time vs WikiSort.
10. Try large array (10k elements).

Test Cases

Input	Output	Notes
[4,1,3,2,5]	[1,2,3,4,5]	Basic test
[1,2,3,4]	[1,2,3,4]	Already sorted
[5,4,3,2,1]	[1,2,3,4,5]	Reverse
[2,2,1,1]	[1,1,2,2]	Stable

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(1) to O(√n)
Stable	Yes
Adaptive	Yes

GrailSort is the gentle engineer of sorting, steady, stable, and space-wise. It doesn't rush; it rearranges with precision, merging order from within.

140 Adaptive Hybrid Sort

Adaptive Hybrid Sort is a meta-sorting algorithm that dynamically combines multiple sorting strategies, such as QuickSort, Merge Sort, Insertion Sort, and Heap Sort, depending on the data characteristics and runtime patterns it detects.

It adapts in real-time, switching between methods based on factors like array size, degree of pre-sortedness, data distribution, and recursion depth. This makes it a universal, practical sorter optimized for diverse workloads.

What Problem Are We Solving?

No single sorting algorithm is best for all situations:

- QuickSort is fast on random data but unstable and bad in worst case.
- Merge Sort is stable but memory-hungry.
- Insertion Sort is great for small or nearly sorted arrays.
- Heap Sort guarantees O(n log n) but has poor locality.

Adaptive Hybrid Sort solves this by blending algorithms:

1. Start with QuickSort for speed.
2. Detect sorted or small regions → switch to Insertion Sort.
3. Detect bad pivot patterns → switch to Heap Sort.
4. Detect stability needs or patterns → use Merge Sort.

It's a unified, self-tuning sorting system.

Example

Sort `[2, 3, 5, 4, 6, 7, 8, 1]`

Step	Detection	Action
1	Mostly sorted except last few	Switch to Insertion Sort
2	Sort locally	[1,2,3,4,5,6,7,8]
3	Done	Adaptive path chosen automatically

If input were random, it would stay with QuickSort. If adversarial, it would pivot to Heap Sort.

How Does It Work (Plain Language)?

Imagine a skilled chef with many tools, knives, mixers, ovens. When slicing carrots (small data), they use a paring knife (Insertion Sort). When breaking a tough root (unsorted array), they grab a heavy cleaver (QuickSort). When something's too complex, they use machinery (Merge Sort).

Adaptive Hybrid Sort works the same way, choosing the right tool at the right time.

Step-by-Step Process

Step	Description
1	Start with QuickSort (good average case)
2	If recursion depth too high → switch to Heap Sort
3	If subarray small (threshold) → use Insertion Sort
4	If stable sorting required → use Merge Sort
5	If data partially sorted → use TimSort-like merge
6	Combine results for final sorted output

Tiny Code (Easy Versions)

Python (Simplified Hybrid Sort)

```
def insertion_sort(arr, left, right):
    for i in range(left + 1, right):
        key = arr[i]
        j = i - 1
        while j >= left and arr[j] > key:
            arr[j + 1] = arr[j]
            j -= 1
        arr[j + 1] = key

def heapify(arr, n, i):
    largest = i
    l = 2*i + 1
    r = 2*i + 2
    if l < n and arr[l] > arr[largest]:
        largest = l
    if r < n and arr[r] > arr[largest]:
```

```
        largest = r
    if largest != i:
        arr[i], arr[largest] = arr[largest], arr[i]
        heapify(arr, n, largest)

def heap_sort(arr):
    n = len(arr)
    for i in range(n//2 - 1, -1, -1):
        heapify(arr, n, i)
    for i in range(n - 1, 0, -1):
        arr[0], arr[i] = arr[i], arr[0]
        heapify(arr, i, 0)

def partition(arr, low, high):
    pivot = arr[(low + high) // 2]
    i, j = low, high
    while i <= j:
        while arr[i] < pivot: i += 1
        while arr[j] > pivot: j -= 1
        if i <= j:
            arr[i], arr[j] = arr[j], arr[i]
            i += 1; j -= 1
    return i

def hybrid_sort(arr, low=0, high=None, depth_limit=None):
    if high is None:
        high = len(arr) - 1
    if depth_limit is None:
        import math
        depth_limit = 2 * math.floor(math.log2(len(arr) + 1))
    size = high - low + 1
    if size <= 16:
        insertion_sort(arr, low, high + 1)
        return
    if depth_limit == 0:
        sub = arr[low:high + 1]
        heap_sort(sub)
        arr[low:high + 1] = sub
        return
    pivot_index = partition(arr, low, high)
    if low < pivot_index - 1:
        hybrid_sort(arr, low, pivot_index - 1, depth_limit - 1)
```

```
    if pivot_index < high:
        hybrid_sort(arr, pivot_index, high, depth_limit - 1)

arr = [2, 3, 5, 4, 6, 7, 8, 1]
hybrid_sort(arr)
print(arr)
```

Output:

```
$$1, 2, 3, 4, 5, 6, 7, 8]
```

C (Conceptual Hybrid Sort)

```
#include <stdio.h>
#include <math.h>

void insertion_sort(int arr[], int left, int right) {
    for (int i = left + 1; i < right; i++) {
        int key = arr[i], j = i - 1;
        while (j >= left && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}

void heapify(int arr[], int n, int i) {
    int largest = i;
    int l = 2*i + 1, r = 2*i + 2;
    if (l < n && arr[l] > arr[largest]) largest = l;
    if (r < n && arr[r] > arr[largest]) largest = r;
    if (largest != i) {
        int tmp = arr[i]; arr[i] = arr[largest]; arr[largest] = tmp;
        heapify(arr, n, largest);
    }
}

void heap_sort(int arr[], int n) {
    for (int i = n/2 - 1; i >= 0; i--) heapify(arr, n, i);
```

```c
    for (int i = n - 1; i > 0; i--) {
        int tmp = arr[0]; arr[0] = arr[i]; arr[i] = tmp;
        heapify(arr, i, 0);
    }
}

int partition(int arr[], int low, int high) {
    int pivot = arr[(low + high) / 2];
    int i = low, j = high;
    while (i <= j) {
        while (arr[i] < pivot) i++;
        while (arr[j] > pivot) j--;
        if (i <= j) {
            int tmp = arr[i]; arr[i] = arr[j]; arr[j] = tmp;
            i++; j--;
        }
    }
    return i;
}

void hybrid_sort(int arr[], int low, int high, int depth_limit) {
    int size = high - low + 1;
    if (size <= 16) { insertion_sort(arr, low, high + 1); return; }
    if (depth_limit == 0) { heap_sort(arr + low, size); return; }
    int p = partition(arr, low, high);
    if (low < p - 1) hybrid_sort(arr, low, p - 1, depth_limit - 1);
    if (p < high) hybrid_sort(arr, p, high, depth_limit - 1);
}

int main(void) {
    int arr[] = {2,3,5,4,6,7,8,1};
    int n = sizeof(arr)/sizeof(arr[0]);
    int depth_limit = 2 * log2(n);
    hybrid_sort(arr, 0, n - 1, depth_limit);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Why It Matters

- Adaptive to input shape

- Hybrid = flexibility + safety
- Stable runtime across data types
- Real-world robust for mixed data
- Balances speed, memory, stability, and predictability

A Gentle Proof (Why It Works)

Let $T(n)$ be the runtime.
Each phase is $O(n)$, and recursion depth is $O(\log n)$.
Adaptive switching ensures no pathological behavior.

$$T(n) = O(n \log n)$$

Best case (sorted): Insertion Sort runs in $O(n)$.
Worst case (adversarial): Heap fallback $\rightarrow O(n \log n)$.

Case	Behavior	Complexity
Sorted	Insertion Sort	$O(n)$
Random	QuickSort	$O(n \log n)$
Adversarial	Heap Sort	$O(n \log n)$

Try It Yourself

1. Sort `[2,3,5,4,6,7,8,1]`.
2. Try `[1,2,3,4,5,6]` $\rightarrow$ insertion path.
3. Reverse `[9,8,7,6,5]` $\rightarrow$ heap path.
4. Mix sorted + random halves.
5. Measure recursion depth.
6. Increase threshold to 32.
7. Add duplicates $\rightarrow$ observe stability.
8. Compare with IntroSort, TimSort.
9. Benchmark on large random data.
10. Visualize switch decisions.

Test Cases

Input	Output	Notes
[2,3,5,4,6,7,8,1]	[1,2,3,4,5,6,7,8]	Random

Input	Output	Notes
[1,2,3,4,5]	[1,2,3,4,5]	Sorted
[5,4,3,2,1]	[1,2,3,4,5]	Reverse
[10,10,9,9,8]	[8,9,9,10,10]	Duplicates

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	O(n log n)
Time (Worst)	O(n log n)
Space	O(log n)
Stable	No
Adaptive	Yes

Adaptive Hybrid Sort is the chameleon of sorting, it watches the data, reads the room, and chooses the perfect move. Fast when it can be, safe when it must be.

Section 15. Special sorts

141 Cycle Sort

Cycle Sort is a comparison-based sorting algorithm designed to minimize the number of writes. It's ideal when writing to memory or storage is expensive (like EEPROM or flash memory), since each element is written exactly once into its final position.

It achieves $O(n^2)$ comparisons but performs the minimal possible number of writes, making it unique among sorting algorithms.

What Problem Are We Solving?

Most sorting algorithms (like QuickSort or Merge Sort) swap elements multiple times before they reach their final position. If each write is costly (e.g., embedded systems or flash memory), that's wasteful.

Cycle Sort asks: "How can we put each element *directly* where it belongs, in one cycle, with as few writes as possible?"

Example

Sort `[3, 1, 2]`

Step	Element	Correct Position	Action
1	3	Index 2	Swap 3 → position 2
2	2	Index 1	Swap 2 → position 1
3	1	Index 0	Done
Final	[1, 2, 3]	Sorted	Minimal writes

Each element cycles into place once.

How Does It Work (Plain Language)?

Think of it like putting books on a shelf:

- You pick one book (element),
- Figure out where it belongs,
- Put it there, swapping with whatever's currently there,
- Repeat until every book is in the right spot.

Each cycle ensures every element reaches its final position exactly once.

Step-by-Step Process

Step	Description
1	Loop through array positions
2	For each position, count how many elements are smaller
3	That count = final position
4	If not already correct, cycle the element to its right place
5	Continue cycling until original element returns to start
6	Move to next position and repeat

Tiny Code (Easy Versions)

Python

```
def cycle_sort(arr):
    n = len(arr)
    writes = 0
    for cycle_start in range(n - 1):
        item = arr[cycle_start]
        pos = cycle_start
        for i in range(cycle_start + 1, n):
            if arr[i] < item:
                pos += 1
        if pos == cycle_start:
            continue
        while item == arr[pos]:
            pos += 1
        arr[pos], item = item, arr[pos]
        writes += 1
        while pos != cycle_start:
            pos = cycle_start
            for i in range(cycle_start + 1, n):
                if arr[i] < item:
                    pos += 1
            while item == arr[pos]:
                pos += 1
            arr[pos], item = item, arr[pos]
            writes += 1
    print("Total writes:", writes)
    return arr

arr = [3, 1, 2, 4]
print(cycle_sort(arr))
```

Output:

```
Total writes: 3
$$1, 2, 3, 4]
```

C

```
#include <stdio.h>
```

```c
void cycle_sort(int arr[], int n) {
    int writes = 0;
    for (int cycle_start = 0; cycle_start < n - 1; cycle_start++) {
        int item = arr[cycle_start];
        int pos = cycle_start;

        for (int i = cycle_start + 1; i < n; i++)
            if (arr[i] < item)
                pos++;

        if (pos == cycle_start) continue;

        while (item == arr[pos]) pos++;
        int temp = arr[pos]; arr[pos] = item; item = temp;
        writes++;

        while (pos != cycle_start) {
            pos = cycle_start;
            for (int i = cycle_start + 1; i < n; i++)
                if (arr[i] < item)
                    pos++;
            while (item == arr[pos]) pos++;
            temp = arr[pos]; arr[pos] = item; item = temp;
            writes++;
        }
    }
    printf("Total writes: %d\n", writes);
}

int main(void) {
    int arr[] = {3, 1, 2, 4};
    int n = sizeof(arr) / sizeof(arr[0]);
    cycle_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
Total writes: 3
1 2 3 4
```

Why It Matters

- Minimizes writes (useful for flash memory, EEPROMs)
- In-place
- Deterministic writes = fewer wear cycles
- Educational example of permutation cycles in sorting

Not fast, but *frugal*, every move counts.

A Gentle Proof (Why It Works)

Each element moves to its correct position once.
If array size is n, total writes $\leq n$.

Counting smaller elements ensures correctness:

$$\text{pos}(x) = |y \mid y < x|$$

Each cycle resolves one permutation cycle of misplaced elements. Thus, algorithm terminates with all items placed exactly once.

Try It Yourself

1. Sort `[3, 1, 2]` step by step.
2. Count how many writes you perform.
3. Try `[4, 3, 2, 1]`, maximum cycles.
4. Try `[1, 2, 3, 4]`, no writes.
5. Test duplicates `[3, 1, 2, 3]`.
6. Implement a version counting cycles.
7. Compare write count with Selection Sort.
8. Benchmark on 1000 random elements.
9. Measure wear-leveling benefit for flash.
10. Visualize cycles as arrows in permutation graph.

Test Cases

Input	Output	Writes	Notes
[3,1,2,4]	[1,2,3,4]	3	3 cycles
[1,2,3]	[1,2,3]	0	Already sorted
[4,3,2,1]	[1,2,3,4]	4	Max writes

Input	Output	Writes	Notes
[3,1,2,3]	[1,2,3,3]	3	Handles duplicates

Complexity

Aspect	Value
Time	$O(n^2)$
Writes	n
Space	O(1)
Stable	No
Adaptive	No

Cycle Sort is the minimalist's sorter, every write is intentional, every move meaningful. It may not be fast, but it's *precisely efficient*.

142 Comb Sort

Comb Sort is an improved version of Bubble Sort that eliminates small elements (often called "turtles") faster by comparing elements far apart first, using a shrinking gap strategy.

It starts with a large gap (e.g. array length) and reduces it each pass until it reaches 1, where it behaves like a regular Bubble Sort. The result is fewer comparisons and faster convergence.

What Problem Are We Solving?

Bubble Sort is simple but slow, mainly because:

- It swaps only adjacent elements.
- Small elements crawl slowly to the front.

Comb Sort fixes this by using a gap to leap over elements, allowing "turtles" to move quickly forward.

It's like sorting with a comb, wide teeth first (large gap), then finer ones (small gap).

Example

Sort `[8, 4, 1, 3, 7]`

Step	Gap		Pass Result	Notes
1	5 / 1.3	3	[3, 4, 1, 8, 7]	Compare 8 3
2	3 / 1.3	2	[1, 4, 3, 8, 7]	Compare 3 1
3	2 / 1.3	1	[1, 3, 4, 7, 8]	Bubble finish
Done	,		[1, 3, 4, 7, 8]	Sorted

Turtles (1, 3) jump forward earlier, speeding up convergence.

How Does It Work (Plain Language)?

Think of it like shrinking a jump rope, at first, you make big jumps to cover ground fast, then smaller ones to fine-tune.

You start with a gap, compare and swap elements that far apart, shrink the gap each round, and stop when the gap reaches 1 *and no swaps happen*.

Step-by-Step Process

Step	Description
1	Initialize `gap = n` and `shrink = 1.3`
2	Repeat until `gap == 1` and no swaps
3	Divide `gap` by shrink factor each pass
4	Compare elements at distance `gap`
5	Swap if out of order
6	Continue until sorted

Tiny Code (Easy Versions)

Python

```python
def comb_sort(arr):
    n = len(arr)
    gap = n
    shrink = 1.3
    swapped = True

    while gap > 1 or swapped:
        gap = int(gap / shrink)
        if gap < 1:
            gap = 1
        swapped = False
        for i in range(n - gap):
            if arr[i] > arr[i + gap]:
                arr[i], arr[i + gap] = arr[i + gap], arr[i]
                swapped = True
    return arr

arr = [8, 4, 1, 3, 7]
print(comb_sort(arr))
```

Output:

```
$$1, 3, 4, 7, 8]
```

C

```c
#include <stdio.h>

void comb_sort(int arr[], int n) {
    int gap = n;
    const float shrink = 1.3;
    int swapped = 1;

    while (gap > 1 || swapped) {
        gap = (int)(gap / shrink);
        if (gap < 1) gap = 1;
        swapped = 0;
        for (int i = 0; i + gap < n; i++) {
            if (arr[i] > arr[i + gap]) {
                int tmp = arr[i];
```

```
                arr[i] = arr[i + gap];
                arr[i + gap] = tmp;
                swapped = 1;
            }
        }
    }
}

int main(void) {
    int arr[] = {8, 4, 1, 3, 7};
    int n = sizeof(arr) / sizeof(arr[0]);
    comb_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
1 3 4 7 8
```

Why It Matters

- Faster than Bubble Sort
- Simple implementation
- In-place and adaptive
- Efficient for small datasets or nearly sorted arrays

A stepping stone toward more efficient algorithms like Shell Sort.

A Gentle Proof (Why It Works)

The shrink factor ensures gap reduction converges to 1 in $O(\log n)$ steps. Each pass fixes distant inversions early, reducing total swaps.

Total cost is dominated by local passes when gap $= 1$ (Bubble Sort). Hence, average complexity $O(n \log n)$ for random data, $O(n^2)$ worst case.

Phase	Description	Cost
Large gap passes	Move turtles forward	$O(n \log n)$
Small gap passes	Final fine-tuning	$O(n^2)$ worst

Try It Yourself

1. Sort `[8, 4, 1, 3, 7]` step by step.
2. Try `[1, 2, 3, 4, 5]`, minimal passes.
3. Try `[5, 4, 3, 2, 1]`, observe gap shrinking.
4. Change shrink factor (1.5, 1.2).
5. Measure swaps per iteration.
6. Compare with Bubble Sort.
7. Visualize movement of smallest element.
8. Benchmark large random array.
9. Track gap evolution over time.
10. Implement early-stop optimization.

Test Cases

Input	Output	Notes
[8,4,1,3,7]	[1,3,4,7,8]	Basic test
[1,2,3,4,5]	[1,2,3,4,5]	Already sorted
[5,4,3,2,1]	[1,2,3,4,5]	Reverse order
[4,1,3,2]	[1,2,3,4]	Short array

Complexity

Aspect	Value
Time (Best)	O(n log n)
Time (Average)	O(n log n)
Time (Worst)	$O(n^2)$
Space	O(1)
Stable	No
Adaptive	Yes

Comb Sort sweeps through data like a comb through tangled hair, wide strokes first, fine ones later, until everything's smooth and ordered.

143 Gnome Sort

Gnome Sort is a simple comparison-based sorting algorithm that works like a garden gnome arranging flower pots, it looks at two adjacent elements and swaps them if they're out of order, then steps backward to check the previous pair again.

It's conceptually similar to Insertion Sort, but implemented with a single loop and no nested structure, making it elegant and intuitive for learners.

What Problem Are We Solving?

Insertion Sort requires nested loops or recursion, which can be tricky to visualize. Gnome Sort offers the same logic using a simple forward–backward walk:

- Move forward if elements are ordered.
- Move back and swap if they're not.

This creates a human-like sorting routine, step forward, fix, step back, repeat.

Example

Sort `[5, 3, 4, 2]`

Step	Index	Action	Result
1	1	$5 > 3 \rightarrow$ swap	[3, 5, 4, 2]
2	0	At start $\rightarrow$ move forward	[3, 5, 4, 2]
3	2	$5 > 4 \rightarrow$ swap	[3, 4, 5, 2]
4	1	$3 < 4 \rightarrow$ forward	[3, 4, 5, 2]
5	3	$5 > 2 \rightarrow$ swap	[3, 4, 2, 5]
6	2	$4 > 2 \rightarrow$ swap	[3, 2, 4, 5]
7	1	$3 > 2 \rightarrow$ swap	[2, 3, 4, 5]
8	0	Done	[2, 3, 4, 5]

Sorted with local fixes, no explicit nested loops.

How Does It Work (Plain Language)?

Imagine a gnome walking down a row of flower pots:

- If the two pots are in order, step forward.
- If not, swap them and step back.
- If you reach the start, just move forward again.

Keep walking until you reach the end, the garden (array) is sorted.

Step-by-Step Process

Step	Description
1	Start at index 1
2	Compare arr[i] with arr[i-1]
3	If arr[i] >= arr[i-1], move forward (i++)
4	Else, swap arr[i] and arr[i-1], move back (i–)
5	If i == 0, move to i = 1
6	Repeat until i reaches n

Tiny Code (Easy Versions)

Python

```
def gnome_sort(arr):
    i = 1
    n = len(arr)
    while i < n:
        if i == 0 or arr[i] >= arr[i - 1]:
            i += 1
        else:
            arr[i], arr[i - 1] = arr[i - 1], arr[i]
            i -= 1
    return arr

arr = [5, 3, 4, 2]
print(gnome_sort(arr))
```

Output:

$$2, 3, 4, 5]

C

```c
#include <stdio.h>

void gnome_sort(int arr[], int n) {
    int i = 1;
    while (i < n) {
        if (i == 0 || arr[i] >= arr[i - 1]) {
            i++;
        } else {
            int tmp = arr[i];
            arr[i] = arr[i - 1];
            arr[i - 1] = tmp;
            i--;
        }
    }
}

int main(void) {
    int arr[] = {5, 3, 4, 2};
    int n = sizeof(arr) / sizeof(arr[0]);
    gnome_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
2 3 4 5
```

Why It Matters

- Simple mental model, easy to understand.
- No nested loops, clean control flow.
- In-place, no extra space.
- Demonstrates local correction in sorting.

It's slower than advanced algorithms but ideal for educational purposes.

A Gentle Proof (Why It Works)

Each swap moves an element closer to its correct position. Whenever a swap happens, the gnome steps back to ensure local order.

Since every inversion is eventually corrected, the algorithm terminates with a sorted array.

Number of swaps proportional to number of inversions $\rightarrow O(n^2)$.

Case	Behavior	Complexity
Sorted	Linear scan	O(n)
Random	Frequent swaps	$O(n^2)$
Reverse	Max swaps	$O(n^2)$

Try It Yourself

1. Sort `[5,3,4,2]` manually step by step.
2. Try `[1,2,3,4]`, minimal steps.
3. Try `[4,3,2,1]`, worst case.
4. Count number of swaps.
5. Compare with Insertion Sort.
6. Track index changes after each swap.
7. Implement visual animation (pointer walk).
8. Try duplicates `[2,1,2,1]`.
9. Measure time for n = 1000.
10. Add early-exit optimization.

Test Cases

Input	Output	Notes
[5,3,4,2]	[2,3,4,5]	Basic
[1,2,3,4]	[1,2,3,4]	Already sorted
[4,3,2,1]	[1,2,3,4]	Reverse
[2,1,2,1]	[1,1,2,2]	Duplicates

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	$O(n^2)$
Time (Worst)	$O(n^2)$
Space	O(1)
Stable	Yes
Adaptive	Yes

Gnome Sort is a friendly, step-by-step sorter, it doesn't rush, just tidies things one pot at a time until the whole row is in order.

144 Cocktail Sort

Cocktail Sort (also known as Bidirectional Bubble Sort or Shaker Sort) is a simple variation of Bubble Sort that sorts the list in both directions alternately, forward then backward, during each pass.

This bidirectional movement helps small elements ("turtles") bubble up faster from the end, fixing one of Bubble Sort's main weaknesses.

What Problem Are We Solving?

Bubble Sort only moves elements in one direction, large ones float to the end, but small ones crawl slowly to the start.

Cocktail Sort solves this by shaking the list:

- Forward pass: moves large items right
- Backward pass: moves small items left

This makes it more efficient on nearly sorted arrays or when both ends need cleaning.

Example

Sort `[4, 3, 1, 2]`

Step	Direction	Action	Result
1	Forward	Compare & swap 4 3, 3 1, 4 2	[3,1,2,4]
2	Backward	Compare & swap 2 1, 3 1	[1,3,2,4]
3	Forward	Compare & swap 3 2	[1,2,3,4]

Step	Direction	Action	Result
Done	,	Sorted	

Fewer passes than Bubble Sort.

How Does It Work (Plain Language)?

Think of a bartender shaking a cocktail shaker back and forth, each shake moves ingredients (elements) closer to the right place from both sides.

You traverse the array:

- Left to right: push largest elements to the end
- Right to left: push smallest elements to the start

Stop when no swaps occur, the array is sorted.

Step-by-Step Process

Step	Description
1	Initialize `swapped = True`
2	While swapped:
a. Set swapped = False	
b. Forward pass (i = start → end): swap if arr[i] > arr[i+1]	
c. If swapped == False: break (sorted)	
d. Backward pass (i = end-1 → start): swap if arr[i] > arr[i+1]	
3	Repeat until sorted

Tiny Code (Easy Versions)

Python

```
def cocktail_sort(arr):
    n = len(arr)
    swapped = True
    start = 0
    end = n - 1
```

```
    while swapped:
        swapped = False
        # Forward pass
        for i in range(start, end):
            if arr[i] > arr[i + 1]:
                arr[i], arr[i + 1] = arr[i + 1], arr[i]
                swapped = True
        if not swapped:
            break
        swapped = False
        end -= 1
        # Backward pass
        for i in range(end - 1, start - 1, -1):
            if arr[i] > arr[i + 1]:
                arr[i], arr[i + 1] = arr[i + 1], arr[i]
                swapped = True
        start += 1
    return arr

arr = [4, 3, 1, 2]
print(cocktail_sort(arr))
```

Output:

```
$$1, 2, 3, 4]
```

C

```
#include <stdio.h>

void cocktail_sort(int arr[], int n) {
    int start = 0, end = n - 1, swapped = 1;
    while (swapped) {
        swapped = 0;
        // Forward pass
        for (int i = start; i < end; i++) {
            if (arr[i] > arr[i + 1]) {
                int tmp = arr[i];
                arr[i] = arr[i + 1];
                arr[i + 1] = tmp;
```

```
                swapped = 1;
            }
        }
        if (!swapped) break;
        swapped = 0;
        end--;
        // Backward pass
        for (int i = end - 1; i >= start; i--) {
            if (arr[i] > arr[i + 1]) {
                int tmp = arr[i];
                arr[i] = arr[i + 1];
                arr[i + 1] = tmp;
                swapped = 1;
            }
        }
        start++;
    }
}

int main(void) {
    int arr[] = {4, 3, 1, 2};
    int n = sizeof(arr) / sizeof(arr[0]);
    cocktail_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
1 2 3 4
```

Why It Matters

- Bidirectional improvement on Bubble Sort
- In-place and simple
- Performs well on nearly sorted data
- Adaptive, stops early when sorted

Great educational bridge to understanding bidirectional scans and adaptive sorting.

A Gentle Proof (Why It Works)

Each forward pass pushes the largest element to the right. Each backward pass pushes the smallest element to the left.

After each full cycle, the sorted region expands from both ends. The algorithm stops when no swaps occur (sorted).

Total operations depend on number of inversions:

$$O(n^2) \text{ worst}, \quad O(n) \text{ best (sorted input)}$$

Case	Behavior	Complexity
Sorted	One bidirectional scan	O(n)
Random	Many swaps	$O(n^2)$
Reverse	Max passes	$O(n^2)$

Try It Yourself

1. Sort `[4,3,1,2]` manually step by step.
2. Try `[1,2,3,4]`, should stop early.
3. Try `[5,4,3,2,1]`, observe shaking effect.
4. Count swaps each pass.
5. Compare passes with Bubble Sort.
6. Visualize forward/backward movement.
7. Add "swap counter" variable.
8. Test duplicates `[3,1,3,2,1]`.
9. Measure performance on nearly sorted data.
10. Modify shrink window size.

Test Cases

Input	Output	Notes
[4,3,1,2]	[1,2,3,4]	Basic
[1,2,3,4]	[1,2,3,4]	Already sorted
[5,4,3,2,1]	[1,2,3,4,5]	Reverse
[3,1,3,2,1]	[1,1,2,3,3]	Duplicates

Complexity

Aspect	Value
Time (Best)	O(n)
Time (Average)	$O(n^2)$
Time (Worst)	$O(n^2)$
Space	O(1)
Stable	Yes
Adaptive	Yes

Cocktail Sort is the sorter that doesn't just bubble, it *shakes* the data into order, making sure both ends get attention every round.

145 Pancake Sort

Pancake Sort is a whimsical and educational sorting algorithm inspired by flipping pancakes on a plate, at each step, you bring the largest unsorted pancake to the top, then flip the stack to move it to its correct position.

It's not practical for large datasets, but it's a brilliant way to illustrate prefix reversals, maximum selection, and in-place transformations.

What Problem Are We Solving?

Standard selection sort swaps elements pairwise. Pancake Sort instead uses prefix reversals, flipping a whole section of the array, to move the largest item into place.

It's a thought experiment in restricted operations: What if the only thing you could do is *flip*?

Example

Sort `[3, 6, 1, 5, 2, 4]`

Step	Action	Result
1	Find max (6) → index 1, flip first 2	[6, 3, 1, 5, 2, 4]
2	Flip first 6	[4, 2, 5, 1, 3, 6]
3	Find max (5) → index 2, flip first 3	[5, 2, 4, 1, 3, 6]
4	Flip first 5	[3, 1, 4, 2, 5, 6]

Step	Action	Result
5	Repeat for smaller prefixes	[1, 2, 3, 4, 5, 6]

Sorted using flips only!

How Does It Work (Plain Language)?

Imagine flipping a stack of pancakes:

1. Find the biggest one not yet placed.
2. Flip the stack to bring it to the top.
3. Flip again to move it into its final position.

Repeat, each time excluding the sorted top portion.

Step-by-Step Process

Step	Description
1	Find index of largest unsorted element
2	Flip subarray from start to that index
3	Flip entire unsorted subarray to move it to end
4	Reduce unsorted portion by one
5	Repeat until sorted

Tiny Code (Easy Versions)

Python

```
def flip(arr, k):
    arr[:k+1] = reversed(arr[:k+1])

def pancake_sort(arr):
    n = len(arr)
    for curr_size in range(n, 1, -1):
        max_idx = arr.index(max(arr[:curr_size]))
        if max_idx != curr_size - 1:
            flip(arr, max_idx)
```

```
            flip(arr, curr_size - 1)
    return arr

arr = [3, 6, 1, 5, 2, 4]
print(pancake_sort(arr))
```

Output:

```
$$1, 2, 3, 4, 5, 6]
```

C

```
#include <stdio.h>

void flip(int arr[], int k) {
    int start = 0;
    while (start < k) {
        int temp = arr[start];
        arr[start] = arr[k];
        arr[k] = temp;
        start++;
        k--;
    }
}

int find_max(int arr[], int n) {
    int max_idx = 0;
    for (int i = 1; i < n; i++)
        if (arr[i] > arr[max_idx])
            max_idx = i;
    return max_idx;
}

void pancake_sort(int arr[], int n) {
    for (int size = n; size > 1; size--) {
        int max_idx = find_max(arr, size);
        if (max_idx != size - 1) {
            flip(arr, max_idx);
            flip(arr, size - 1);
        }
```

```
    }
}

int main(void) {
    int arr[] = {3, 6, 1, 5, 2, 4};
    int n = sizeof(arr) / sizeof(arr[0]);
    pancake_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
1 2 3 4 5 6
```

Why It Matters

- Fun demonstration of prefix operations
- In-place and simple
- Shows how restricted operations can still sort
- Theoretical interest, base for pancake networks
- Used in bioinformatics (genome rearrangements)

A Gentle Proof (Why It Works)

Each iteration places the largest remaining element at its final index. Two flips per iteration (worst case). At most (2(n - 1)) flips total.

Correctness follows from:

- Flipping is a reversal, which preserves order except within flipped segment.
- Each largest element is locked at the end after placement.

$$T(n) = O(n^2)$$

because each `max()` and `flip()` operation is O(n).

Try It Yourself

1. Sort `[3,6,1,5,2,4]` manually.
2. Trace each flip visually.
3. Try `[1,2,3,4]`, no flips needed.
4. Reverse `[4,3,2,1]`, observe maximum flips.
5. Count flips per iteration.
6. Implement flip visualization.
7. Replace `max()` with manual search.
8. Print intermediate arrays.
9. Analyze flip count for random input.
10. Challenge: implement recursive version.

Test Cases

Input	Output	Flips	Notes
[3,6,1,5,2,4]	[1,2,3,4,5,6]	8	Classic
[1,2,3,4]	[1,2,3,4]	0	Already sorted
[4,3,2,1]	[1,2,3,4]	6	Worst case
[2,1,3]	[1,2,3]	3	Small array

Complexity

Aspect	Value
Time (Worst)	$O(n^2)$
Time (Average)	$O(n^2)$
Time (Best)	$O(n)$
Space	$O(1)$
Stable	No
Adaptive	No

Pancake Sort flips its way to victory, a charming example of ingenuity under constraint. You don't need fancy tools, just a good spatula and some patience.

146 Bitonic Sort

Bitonic Sort is a parallel sorting algorithm designed for sorting networks. It works by constructing and merging bitonic sequences, sequences that first increase, then decrease (or vice versa).

It's especially powerful on hardware, GPUs, and parallel processors, where multiple comparisons can happen at once.

What Problem Are We Solving?

Most standard algorithms (QuickSort, MergeSort) are data-dependent, their flow changes depending on comparisons. That's a problem for hardware or parallel systems.

Bitonic Sort fixes this by having a fixed comparison pattern, perfect for parallel execution.

It answers the question:

> "How do we sort in parallel using predictable, fixed circuits?"

Example

Sort `[3, 7, 4, 8, 6, 2, 1, 5]`

Step	Action	Result
1	Build bitonic sequence ↑↓	[3,7,4,8, 6,2,1,5]
2	Compare & swap pairs	[3,2,1,5, 6,7,4,8]
3	Merge halves recursively	[1,2,3,4, 5,6,7,8]

Each phase doubles sorted subsequences until the full array is sorted.

How Does It Work (Plain Language)?

Imagine you're sorting cards but you can only compare pairs at fixed positions, no adaptive decisions.

You first build a bitonic sequence (up then down), then merge it into a sorted list using bitonic merge steps, repeatedly compare-and-swap mirrored elements.

Step-by-Step Process

Step	Description
1	Split array into halves
2	Sort first half ascending, second half descending
3	Combine them into a bitonic sequence
4	Run bitonic merge: recursively compare-swap pairs
5	Repeat until sequence size = 1

Works best when n = 2^k (power of two).

Tiny Code (Easy Versions)

Python

```
def bitonic_merge(arr, low, cnt, direction):
    if cnt > 1:
        k = cnt // 2
        for i in range(low, low + k):
            if (direction and arr[i] > arr[i + k]) or (not direction and arr[i] < arr[i + k]):
                arr[i], arr[i + k] = arr[i + k], arr[i]
        bitonic_merge(arr, low, k, direction)
        bitonic_merge(arr, low + k, k, direction)

def bitonic_sort(arr, low=0, cnt=None, direction=True):
    if cnt is None:
        cnt = len(arr)
    if cnt > 1:
        k = cnt // 2
        bitonic_sort(arr, low, k, True)
        bitonic_sort(arr, low + k, k, False)
        bitonic_merge(arr, low, cnt, direction)

arr = [3, 7, 4, 8, 6, 2, 1, 5]
bitonic_sort(arr)
print(arr)
```

Output:

```
$$1, 2, 3, 4, 5, 6, 7, 8]
```

C

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int t = *a; *a = *b; *b = t;
}

void bitonic_merge(int arr[], int low, int cnt, int dir) {
    if (cnt > 1) {
        int k = cnt / 2;
        for (int i = low; i < low + k; i++) {
            if ((dir && arr[i] > arr[i + k]) || (!dir && arr[i] < arr[i + k]))
                swap(&arr[i], &arr[i + k]);
        }
        bitonic_merge(arr, low, k, dir);
        bitonic_merge(arr, low + k, k, dir);
    }
}

void bitonic_sort(int arr[], int low, int cnt, int dir) {
    if (cnt > 1) {
        int k = cnt / 2;
        bitonic_sort(arr, low, k, 1);
        bitonic_sort(arr, low + k, k, 0);
        bitonic_merge(arr, low, cnt, dir);
    }
}

int main(void) {
    int arr[] = {3, 7, 4, 8, 6, 2, 1, 5};
    int n = sizeof(arr) / sizeof(arr[0]);
    bitonic_sort(arr, 0, n, 1);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
1 2 3 4 5 6 7 8
```

Why It Matters

- Parallel-friendly (sorting networks)
- Deterministic structure (no branches)
- Perfect for hardware, GPUs, SIMD
- Good educational model for divide and conquer + merging

It's not about runtime on CPUs, it's about parallel depth.

A Gentle Proof (Why It Works)

Bitonic sequence:
A sequence that increases then decreases is bitonic.

Merging rule:
Compare each element with its mirror; recursively merge halves.

At each merge stage, the array becomes more sorted.
Recursion depth = $\log n$, each level does $O(n)$ work $\to O(n \log^2 n)$.

Step	Work	Levels	Total
Merge	$O(n)$	$\log n$	$O(n \log^2 n)$

Try It Yourself

1. Sort `[3,7,4,8,6,2,1,5]` manually.
2. Identify bitonic sequences at each stage.
3. Try with 4 elements `[4,1,3,2]`.
4. Change direction flags (ascending/descending).
5. Draw comparison network graph.
6. Implement iterative version.
7. Run on power-of-two sizes.
8. Measure parallel steps vs QuickSort.
9. Experiment with GPU (Numba/CUDA).
10. Visualize recursive structure.

Input	Output	Notes

Test Cases

Input	Output	Notes
[3,7,4,8,6,2,1,5]	[1,2,3,4,5,6,7,8]	Standard
[4,1,3,2]	[1,2,3,4]	Small case
[5,4,3,2,1,0,9,8]	[0,1,2,3,4,5,8,9]	Reverse
[8,4,2,1,3,6,5,7]	[1,2,3,4,5,6,7,8]	Random

Complexity

Aspect	Value
Time	O(n $\log^2$ n)
Space	O(1)
Stable	No
Adaptive	No
Parallel Depth	O($\log^2$ n)

Bitonic Sort shines where parallelism rules, in GPUs, circuits, and sorting networks. Every comparison is planned, every move synchronized, a symphony of order in fixed rhythm.

147 Odd-Even Merge Sort

Odd-Even Merge Sort is a parallel sorting algorithm and a sorting network that merges two sorted sequences using a fixed pattern of comparisons between odd and even indexed elements.

It was introduced by Ken Batcher, and like Bitonic Sort, it's designed for parallel hardware or SIMD processors, where predictable comparison patterns matter more than data-dependent branching.

What Problem Are We Solving?

Traditional merge algorithms rely on conditional branching, they decide at runtime which element to pick next. This is problematic in parallel or hardware implementations, where you need fixed, predictable sequences of comparisons.

Odd-Even Merge Sort solves this by using a static comparison network that merges sorted halves without branching.

It's perfect when:

- You need deterministic behavior
- You're building parallel circuits or GPU kernels

Example

Merge two sorted halves: `[1, 4, 7, 8]` and `[2, 3, 5, 6]`

Step	Action	Result
1	Merge odds `[1,7]` with `[2,5]`	[1,2,5,7]
2	Merge evens `[4,8]` with `[3,6]`	[3,4,6,8]
3	Combine and compare adjacent	[1,2,3,4,5,6,7,8]

Fixed pattern, no branching, merges completed in parallel.

How Does It Work (Plain Language)?

Imagine two zipper chains, one odd, one even. You weave them together in a fixed, interlocking pattern, comparing and swapping along the way. There's no guessing, every element knows which neighbor to check.

Step-by-Step Process

Step	Description
1	Split array into left and right halves
2	Recursively sort each half
3	Use odd-even merge to combine halves
4	Odd-even merge:
a. Recursively merge odd and even indexed elements	
b. Compare and swap adjacent pairs	
5	Continue until array sorted

Works best when (n = 2^k).

Tiny Code (Easy Versions)

Python

```
def odd_even_merge(arr, lo, n, direction):
    if n > 1:
        m = n // 2
        odd_even_merge(arr, lo, m, direction)
        odd_even_merge(arr, lo + m, m, direction)
        for i in range(lo + m, lo + n - m):
            if (arr[i] > arr[i + m]) == direction:
                arr[i], arr[i + m] = arr[i + m], arr[i]

def odd_even_merge_sort(arr, lo=0, n=None, direction=True):
    if n is None:
        n = len(arr)
    if n > 1:
        m = n // 2
        odd_even_merge_sort(arr, lo, m, direction)
        odd_even_merge_sort(arr, lo + m, m, direction)
        odd_even_merge(arr, lo, n, direction)

arr = [8, 3, 2, 7, 4, 6, 5, 1]
odd_even_merge_sort(arr)
print(arr)
```

Output:

```
$$1, 2, 3, 4, 5, 6, 7, 8]
```

C

```
#include <stdio.h>

void swap(int *a, int *b) {
    int t = *a; *a = *b; *b = t;
}

void odd_even_merge(int arr[], int lo, int n, int dir) {
```

```c
    if (n > 1) {
        int m = n / 2;
        odd_even_merge(arr, lo, m, dir);
        odd_even_merge(arr, lo + m, m, dir);
        for (int i = lo + m; i < lo + n - m; i++) {
            if ((arr[i] > arr[i + m]) == dir)
                swap(&arr[i], &arr[i + m]);
        }
    }
}

void odd_even_merge_sort(int arr[], int lo, int n, int dir) {
    if (n > 1) {
        int m = n / 2;
        odd_even_merge_sort(arr, lo, m, dir);
        odd_even_merge_sort(arr, lo + m, m, dir);
        odd_even_merge(arr, lo, n, dir);
    }
}

int main(void) {
    int arr[] = {8, 3, 2, 7, 4, 6, 5, 1};
    int n = sizeof(arr)/sizeof(arr[0]);
    odd_even_merge_sort(arr, 0, n, 1);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
1 2 3 4 5 6 7 8
```

Why It Matters

- Fixed sequence, perfect for parallelism
- No data-dependent branching
- Used in hardware sorting networks
- Theoretical foundation for parallel sorting

When you need determinism and concurrency, this algorithm shines.

A Gentle Proof (Why It Works)

Each odd-even merge merges two sorted sequences using fixed compare-swap operations. At each stage:

- Odd indices are merged separately
- Even indices merged separately
- Adjacent elements compared to restore global order

Each level performs O(n) work, depth = $O(\log^2 n)$ → total complexity:

$$T(n) = O(n \log^2 n)$$

Try It Yourself

1. Sort `[8,3,2,7,4,6,5,1]` step by step.
2. Trace odd-index and even-index merges.
3. Draw merge network diagram.
4. Try smaller `[4,3,2,1]` for clarity.
5. Run on power-of-two lengths.
6. Measure comparisons.
7. Compare with Bitonic Sort.
8. Implement iterative version.
9. Visualize parallel depth.
10. Experiment with ascending/descending flags.

Test Cases

Input	Output	Notes
[8,3,2,7,4,6,5,1]	[1,2,3,4,5,6,7,8]	Classic
[4,3,2,1]	[1,2,3,4]	Small
[9,7,5,3,1,2,4,6]	[1,2,3,4,5,6,7,9]	Mixed
[5,4,3,2]	[2,3,4,5]	Reverse half

Complexity

Aspect	Value
Time	O(n $\log^2$ n)
Space	O(1)

Aspect	Value
Stable	No
Adaptive	No
Parallel Depth	$O(\log^2 n)$

Odd-Even Merge Sort weaves order from two halves like clockwork, steady, parallel, and predictable. Every comparison is planned, every merge synchronized, it's sorting as architecture.

148 Sleep Sort

Sleep Sort is one of the most playful and unconventional algorithms ever invented, it sorts numbers by leveraging time delays. Each element is "slept" for a duration proportional to its value, and when the sleep ends, it prints the number.

In effect, time itself becomes the sorting mechanism.

What Problem Are We Solving?

While not practical, Sleep Sort offers a fun demonstration of parallelism and asynchronous timing, showing that even sorting can be expressed through temporal order rather than comparisons.

It's often used as a thought experiment to teach concurrency, timing, and creative thinking about problem-solving.

Example

Sort `[3, 1, 4, 2]`

Step	Value	Sleep (seconds)	Print order
1	1	1s	1
2	2	2s	2
3	3	3s	3
4	4	4s	4

Output (over time): `1 2 3 4`

Sorted by time of completion!

How Does It Work (Plain Language)?

Each number is given a timer equal to its value. All timers start simultaneously, and when a timer finishes, that number is output. Small numbers "wake up" first, so they're printed earlier, creating a sorted sequence.

It's like a race where each runner's speed is inversely proportional to its size, smaller ones finish first.

Step-by-Step Process

Step	Description
1	For each element `x`, create a thread or coroutine
2	Each thread sleeps for `x` units of time
3	When sleep completes, print `x`
4	Numbers appear in sorted order
5	Optionally collect outputs into a list

Tiny Code (Easy Versions)

Python (Using Threads)

```
import threading
import time

def sleeper(x):
    time.sleep(x * 0.1)  # scale factor for speed
    print(x, end=' ')

def sleep_sort(arr):
    threads = []
    for x in arr:
        t = threading.Thread(target=sleeper, args=(x,))
        t.start()
        threads.append(t)
    for t in threads:
        t.join()

arr = [3, 1, 4, 2]
sleep_sort(arr)
```

Output (timed):

```
1 2 3 4
```

C (Using Threads and Sleep)

```c
#include <stdio.h>
#include <stdlib.h>
#include <pthread.h>
#include <unistd.h>

void* sleeper(void* arg) {
    int x = *(int*)arg;
    usleep(x * 100000); // scaled down
    printf("%d ", x);
    return NULL;
}

void sleep_sort(int arr[], int n) {
    pthread_t threads[n];
    for (int i = 0; i < n; i++)
        pthread_create(&threads[i], NULL, sleeper, &arr[i]);
    for (int i = 0; i < n; i++)
        pthread_join(threads[i], NULL);
}

int main(void) {
    int arr[] = {3, 1, 4, 2};
    int n = sizeof(arr) / sizeof(arr[0]);
    sleep_sort(arr, n);
    printf("\n");
}
```

Output (timed):

```
1 2 3 4
```

Why It Matters

- Creative demonstration of parallelism
- Fun teaching tool for concurrency
- Visually intuitive, sorting emerges naturally
- Great reminder: algorithms just code, they're processes

It's impractical, but delightfully educational.

A Gentle Proof (Why It Works)

If all threads start simultaneously and sleep proportionally to their values, then:

- Smaller values finish earlier
- No collisions (if distinct integers)
- Output sequence = sorted list

For duplicates, slight offsets may be added to maintain stability.

Limitations:

- Requires positive integers
- Depends on accurate timers
- Sensitive to scheduler latency

Try It Yourself

1. Sort `[3,1,4,2]`, observe timing.
2. Try `[10,5,1,2]`, slower but clearer pattern.
3. Add duplicates `[2,2,1]`, test ordering.
4. Scale sleep time down (`x * 0.05`).
5. Run on multi-core CPU, observe concurrency.
6. Replace sleep with `await asyncio.sleep(x)` for async version.
7. Collect results in a list instead of print.
8. Use `multiprocessing` instead of threads.
9. Visualize time vs value graph.
10. Try fractional delays for floats.

Test Cases

Input	Output	Notes
[3,1,4,2]	[1,2,3,4]	Classic example
[1,2,3,4]	[1,2,3,4]	Already sorted
[4,3,2,1]	[1,2,3,4]	Reversed
[2,2,1]	[1,2,2]	Handles duplicates

Complexity

Aspect	Value
Time (Theoretical)	O(n) real-time (wall-clock)
Time (CPU Work)	O(n) setup
Space	O(n) threads
Stable	Yes (with offset)
Adaptive	No

Sleep Sort is sorting reimagined, not by computation, but by patience. Every number simply waits its turn, no comparisons, no loops, just time.

149 Bead Sort

Bead Sort, also known as Gravity Sort, is a natural sorting algorithm inspired by how beads slide under gravity on parallel rods. Imagine an abacus turned on its side: heavier piles settle first, automatically sorting themselves.

It's visual, parallel, and analog in spirit, more of a conceptual model than a practical tool, but brilliant for intuition.

What Problem Are We Solving?

Sorting algorithms usually rely on comparisons. Bead Sort instead uses physical simulation, items fall until they settle into order.

This approach helps visualize distribution sorting and natural computation, where sorting happens through physical laws rather than arithmetic operations.

Example

Sort `[5, 3, 1, 7, 4]`:

1. Represent each number as a row of beads.
2. Drop beads under gravity.
3. Count beads per column from bottom up.

Step	Representation	After Gravity	Output
Initial	5 3 1 7 4	,	,
Gravity	Columns fill from bottom	Rows shorten	,
Result	1 3 4 5 7	[1, 3, 4, 5, 7]	

The smallest number rises to top, largest sinks to bottom, sorted.

How Does It Work (Plain Language)?

Each number is a pile of beads. Beads "fall" downward until no empty space below. Since heavier rows push beads downward faster, larger numbers accumulate at the bottom. When gravity stops, reading row lengths from top to bottom yields sorted order.

It's sorting by simulated gravity, no comparisons at all.

Step-by-Step Process

Step	Description
1	Represent each integer by beads on rods (1 bead per unit)
2	Let beads fall to the lowest empty position in each column
3	After settling, count beads per row (top-down)
4	These counts form the sorted list

Works only for non-negative integers.

Tiny Code (Easy Versions)

Python

```
def bead_sort(arr):
    if any(x < 0 for x in arr):
        raise ValueError("Only non-negative integers allowed")
    max_val = max(arr)
    grid = [[1 if i < x else 0 for i in range(max_val)] for x in arr]
    for col in range(max_val):
        beads = sum(row[col] for row in grid)
        for row in range(len(arr)):
            grid[row][col] = 1 if row >= len(arr) - beads else 0
    return [sum(row) for row in grid]

arr = [5, 3, 1, 7, 4]
print(bead_sort(arr))
```

Output:

```
$$1, 3, 4, 5, 7]
```

C

```
#include <stdio.h>
#include <string.h>

void bead_sort(int *a, int n) {
    int max = 0;
    for (int i = 0; i < n; i++) if (a[i] > max) max = a[i];
    unsigned char beads[n][max];
    memset(beads, 0, n * max);
    for (int i = 0; i < n; i++)
        for (int j = 0; j < a[i]; j++)
            beads[i][j] = 1;

    for (int j = 0; j < max; j++) {
        int sum = 0;
        for (int i = 0; i < n; i++) sum += beads[i][j];
        for (int i = 0; i < n; i++)
            beads[i][j] = (i >= n - sum) ? 1 : 0;
    }
```

```
    for (int i = 0; i < n; i++) {
        a[i] = 0;
        for (int j = 0; j < max; j++)
            a[i] += beads[i][j];
    }
}

int main(void) {
    int arr[] = {5, 3, 1, 7, 4};
    int n = sizeof(arr) / sizeof(arr[0]);
    bead_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output:

```
1 3 4 5 7
```

Why It Matters

- Demonstrates non-comparison-based sorting
- Shows physical analogies for computation
- Ideal for visual and educational purposes
- Parallelizable (each column independent)

Though impractical, it inspires biological and physics-inspired algorithm design.

A Gentle Proof (Why It Works)

Each column acts like a gravity channel:

- Beads fall to fill lowest positions
- Columns represent magnitudes across numbers
- After settling, beads in each row = sorted value

No two beads can occupy the same slot twice, ensuring correctness. Complexity:

$$T(n) = O(S)$$

where $S = \sum a_i$, total bead count.

Efficient only when numbers are small.

Try It Yourself

1. Sort `[5,3,1,7,4]` by hand using dots.
2. Draw rods and let beads fall.
3. Try `[3,0,2,1]`, zeros stay top.
4. Experiment with duplicates `[2,2,3]`.
5. Use grid visualization in Python.
6. Compare with Counting Sort.
7. Extend for stable ordering.
8. Animate bead falling step by step.
9. Scale with numbers 10.
10. Reflect: what if gravity was sideways?

Test Cases

Input	Output	Notes
[5,3,1,7,4]	[1,3,4,5,7]	Classic example
[3,0,2,1]	[0,1,2,3]	Handles zeros
[2,2,3]	[2,2,3]	Works with duplicates
[1]	[1]	Single element

Complexity

Aspect	Value
Time	O(S), where S = sum of elements
Space	O(S)
Stable	No
Adaptive	No

Bead Sort shows how even gravity can sort, numbers become beads, and time, motion, and matter do the work. It's sorting you can *see*, not just compute.

150 Bogo Sort

Bogo Sort (also called Permutation Sort or Stupid Sort) is a deliberately absurd algorithm that repeatedly shuffles the array until it becomes sorted.

It's the poster child of inefficiency, often used in classrooms as a comic counterexample, sorting by pure luck.

What Problem Are We Solving?

We're not solving a problem so much as demonstrating futility. Bogo Sort asks, *"What if we just kept trying random orders until we got lucky?"*

It's a great teaching tool for:

- Understanding algorithmic inefficiency
- Appreciating complexity bounds
- Learning to recognize good vs. bad strategies

Example

Sort `[3, 1, 2]`

Attempt	Shuffle	Sorted?
1	[3,1,2]	No
2	[1,2,3]	Yes

Stop when lucky! (You could get lucky early… or never.)

How Does It Work (Plain Language)?

The idea is painfully simple:

1. Check if the array is sorted.
2. If not, shuffle it randomly.
3. Repeat until sorted.

It's sorting by random chance, not logic. Each attempt has a tiny probability of being sorted, but given infinite time, it *will* finish (eventually).

Step-by-Step Process

Step	Description
1	Check if array is sorted
2	If sorted, done
3	Else, shuffle randomly
4	Go back to step 1

Tiny Code (Easy Versions)

Python

```
import random

def is_sorted(arr):
    return all(arr[i] <= arr[i+1] for i in range(len(arr)-1))

def bogo_sort(arr):
    attempts = 0
    while not is_sorted(arr):
        random.shuffle(arr)
        attempts += 1
    print("Sorted in", attempts, "attempts")
    return arr

arr = [3, 1, 2]
print(bogo_sort(arr))
```

Output (random):

```
Sorted in 7 attempts
$$1, 2, 3]
```

C

```
#include <stdio.h>
#include <stdlib.h>
#include <time.h>

int is_sorted(int arr[], int n) {
    for (int i = 0; i < n - 1; i++)
        if (arr[i] > arr[i + 1]) return 0;
    return 1;
}

void shuffle(int arr[], int n) {
    for (int i = 0; i < n; i++) {
```

```c
        int j = rand() % n;
        int temp = arr[i];
        arr[i] = arr[j];
        arr[j] = temp;
    }
}

void bogo_sort(int arr[], int n) {
    int attempts = 0;
    while (!is_sorted(arr, n)) {
        shuffle(arr, n);
        attempts++;
    }
    printf("Sorted in %d attempts\n", attempts);
}

int main(void) {
    srand(time(NULL));
    int arr[] = {3, 1, 2};
    int n = sizeof(arr) / sizeof(arr[0]);
    bogo_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
    printf("\n");
}
```

Output (random):

```
Sorted in 12 attempts
1 2 3
```

Why It Matters

- Humorous cautionary tale, what *not* to do
- Demonstrates expected runtime analysis
- A good way to visualize randomness
- Reinforces need for algorithmic reasoning

It's the algorithmic equivalent of *throwing dice until sorted*, mathematically silly, but conceptually rich.

A Gentle Proof (Why It Works)

With n elements, there are $n!$ permutations.
Only one is sorted.

Probability of success $= \frac{1}{n!}$

Expected attempts:

$$E(n) = n!$$

Each check takes $O(n)$, so total expected time:

$$T(n) = O(n \times n!)$$

Guaranteed termination (eventually), since the probability of not sorting forever $\to 0$.

Try It Yourself

1. Run on `[3,1,2]` and count attempts.
2. Try `[1,2,3]`, instant success.
3. Test `[4,3,2,1]`, likely infinite patience required.
4. Replace random.shuffle with deterministic shuffle (see fail).
5. Add a timeout.
6. Visualize shuffles on screen.
7. Measure average attempts over 100 trials.
8. Compare with Bubble Sort.
9. Try "Bogobogosort" (recursive Bogo!).
10. Reflect: what's the expected runtime for `n=5`?

Test Cases

Input	Output	Notes
[3,1,2]	[1,2,3]	Classic
[1,2,3]	[1,2,3]	Already sorted
[2,1]	[1,2]	Fast
[4,3,2,1]	[1,2,3,4]	Possibly never terminates

Complexity

Aspect	Value
Time (Expected)	O(n × n!)
Time (Best)	O(n)
Time (Worst)	Unbounded
Space	O(1)
Stable	Yes (if shuffle stable)
Adaptive	No

Bogo Sort is chaos pretending to be order, sorting by faith, not logic. It's the universe's reminder that hope isn't a strategy, not even in algorithms.

Section 16. Linear and Binary Search

151 Linear Search

Linear Search (also known as Sequential Search) is the simplest and most intuitive searching algorithm. It scans through each element one by one until it finds the target, or reaches the end of the list.

It's easy to understand, easy to implement, and works on both sorted and unsorted data.

What Problem Are We Solving?

Given a list and a target value, how can we check if the target is present, and if so, at which index?

Linear Search solves this by scanning each element in order until a match is found.

Perfect for:

- Small datasets
- Unsorted arrays
- Early learning of search principles

Example

Find `7` in `[3, 5, 7, 2, 9]`:

Step	Index	Value	Match?
1	0	3	No
2	1	5	No
3	2	7	Yes
4	Stop	,	Found at index 2

How Does It Work (Plain Language)?

It's like flipping through pages one by one looking for a word. No skipping, no guessing, just check everything in order.

If the list is `[a , a , a , ..., a ]`:

1. Start at index 0
2. Compare `a[i]` with the target
3. If equal → found
4. Else → move to next
5. Stop when found or end reached

Step-by-Step Process

Step	Description
1	Start from index 0
2	Compare current element with target
3	If equal, return index
4	Else, increment index
5	Repeat until end
6	If not found, return -1

Tiny Code (Easy Versions)

Python

```
def linear_search(arr, target):
    for i, val in enumerate(arr):
        if val == target:
            return i
    return -1
```

```
arr = [3, 5, 7, 2, 9]
target = 7
idx = linear_search(arr, target)
print("Found at index:", idx)
```

Output:

```
Found at index: 2
```

C

```
#include <stdio.h>

int linear_search(int arr[], int n, int target) {
    for (int i = 0; i < n; i++)
        if (arr[i] == target)
            return i;
    return -1;
}

int main(void) {
    int arr[] = {3, 5, 7, 2, 9};
    int n = sizeof(arr) / sizeof(arr[0]);
    int target = 7;
    int idx = linear_search(arr, n, target);
    if (idx != -1)
        printf("Found at index: %d\n", idx);
    else
        printf("Not found\n");
}
```

Output:

```
Found at index: 2
```

Why It Matters

- Works on any list, sorted or unsorted
- No preprocessing needed
- Guaranteed to find (if present)
- Great introduction to time complexity
- Foundation for better search algorithms

A Gentle Proof (Why It Works)

If the element exists, scanning each element ensures it will eventually be found.

For (n) elements:

- Best case: found at index 0 $\rightarrow$ O(1)
- Worst case: not found or last $\rightarrow$ O(n)
- Average case: half-way $\rightarrow$ O(n)

Because there's no faster way without structure.

Try It Yourself

1. Search `7` in `[3,5,7,2,9]`
2. Search `10` (not in list)
3. Try `[1,2,3,4,5]` with `target=1` (best case)
4. Try `target=5` (worst case)
5. Count comparisons made
6. Print "Found" or "Not Found"
7. Try on unsorted vs sorted arrays
8. Modify to return all indices of target
9. Implement recursive version
10. Extend for string search in list of words

Test Cases

Input	Target	Output	Notes
[3,5,7,2,9]	7	2	Found
[3,5,7,2,9]	10	-1	Not found
[1,2,3]	1	0	Best case
[1,2,3]	3	2	Worst case

Complexity

Aspect	Value
Time (Best)	O(1)
Time (Worst)	O(n)
Time (Average)	O(n)
Space	O(1)
Stable	Yes
Adaptive	No

Linear Search is the simplest lens into algorithmic thinking, brute force but guaranteed. It's your first step from guessing to reasoning.

152 Linear Search (Sentinel)

Sentinel Linear Search is a clever twist on the basic Linear Search. Instead of checking array bounds each time, we place a sentinel (a guard value) at the end of the array equal to the target.

This eliminates the need for explicit boundary checks inside the loop, making the search slightly faster and cleaner, especially in low-level languages like C.

What Problem Are We Solving?

In a standard linear search, each iteration checks both:

1. If the current element equals the target
2. If the index is still within bounds

That second check adds overhead.

By placing a sentinel, we can guarantee the loop will always terminate, no bounds check needed.

This is useful in tight loops, embedded systems, and performance-critical code.

Example

Find `7` in `[3, 5, 7, 2, 9]`:

1. Append sentinel (duplicate target) → `[3, 5, 7, 2, 9, 7]`
2. Scan until `7` is found
3. If index < n, found in array
4. If index == n, only sentinel found → not in array

Step	Index	Value	Match?
1	0	3	No
2	1	5	No
3	2	7	Yes
4	Stop, index < n	Found at 2	

How Does It Work (Plain Language)?

Think of the sentinel as a stop sign placed beyond the last element. You don't have to look over your shoulder to check if you've gone too far, the sentinel will catch you.

It ensures you'll always hit a match, but then you check whether it was a real match or the sentinel.

Step-by-Step Process

Step	Description
1	Save last element
2	Place target at the end (sentinel)
3	Loop until `arr[i] == target`
4	Restore last element
5	If index < n → found, else → not found

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>

int sentinel_linear_search(int arr[], int n, int target) {
    int last = arr[n - 1];
    arr[n - 1] = target; // sentinel
    int i = 0;
    while (arr[i] != target)
        i++;
    arr[n - 1] = last; // restore
    if (i < n - 1 || arr[n - 1] == target)
        return i;
    return -1;
}

int main(void) {
    int arr[] = {3, 5, 7, 2, 9};
    int n = sizeof(arr) / sizeof(arr[0]);
    int target = 7;
    int idx = sentinel_linear_search(arr, n, target);
    if (idx != -1)
        printf("Found at index: %d\n", idx);
    else
        printf("Not found\n");
}
```

Output:

```
Found at index: 2
```

Python (Simulated)

```python
def sentinel_linear_search(arr, target):
    n = len(arr)
    last = arr[-1]
    arr[-1] = target
    i = 0
    while arr[i] != target:
        i += 1
    arr[-1] = last
    if i < n - 1 or arr[-1] == target:
```

```
        return i
    return -1

arr = [3, 5, 7, 2, 9]
print(sentinel_linear_search(arr, 7))  # Output: 2
```

Why It Matters

- Removes boundary check overhead
- Slightly faster for large arrays
- Classic example of sentinel optimization
- Teaches loop invariants and guard conditions

This is how you make a simple algorithm tight and elegant.

A Gentle Proof (Why It Works)

By placing the target as the last element:

- Loop must terminate (guaranteed match)
- Only after the loop do we check if it was sentinel or real match

No wasted comparisons. Total comparisons n + 1 (vs 2n in naive version).

$$T(n) = O(n)$$

Try It Yourself

1. Search `7` in `[3,5,7,2,9]`
2. Search `10` (not in list)
3. Track number of comparisons vs regular linear search
4. Implement in Python, Java, C++
5. Visualize sentinel placement
6. Use array of 1000 random elements, benchmark
7. Try replacing last element temporarily
8. Search first element, check best case
9. Search last element, check sentinel restore
10. Discuss when this optimization helps most

Test Cases

Input	Target	Output	Notes
[3,5,7,2,9]	7	2	Found
[3,5,7,2,9]	10	-1	Not found
[1,2,3]	1	0	Best case
[1,2,3]	3	2	Sentinel replaced last

Complexity

Aspect	Value
Time (Best)	O(1)
Time (Worst)	O(n)
Time (Average)	O(n)
Space	O(1)
Stable	Yes
Adaptive	No

Sentinel Linear Search is how you turn simplicity into elegance, one tiny guard makes the whole loop smarter.

153 Binary Search (Iterative)

Binary Search (Iterative) is one of the most elegant and efficient searching algorithms for sorted arrays. It repeatedly divides the search interval in half, eliminating half the remaining elements at each step.

This version uses a loop, avoiding recursion and keeping memory usage minimal.

What Problem Are We Solving?

When working with sorted data, a linear scan is wasteful. If you always know the list is ordered, you can use binary search to find your target in O(log n) time instead of O(n).

Example

Find `7` in `[1, 3, 5, 7, 9, 11]`:

Step	Low	High	Mid	Value	Compare
1	0	5	2	5	$7 > 5 \rightarrow$ search right
2	3	5	4	9	$7 < 9 \rightarrow$ search left
3	3	3	3	7	Found

Found at index 3.

How Does It Work (Plain Language)?

Binary Search is like guessing a number between 1 and 100:

- Always pick the midpoint.
- If the number is too low, search the upper half.
- If it's too high, search the lower half.
- Repeat until found or interval is empty.

Each guess cuts the space in half, that's why it's so fast.

Step-by-Step Process

Step	Description
1	Start with `low = 0`, `high = n - 1`
2	While `low  high`, find `mid = (low + high) // 2`
3	If `arr[mid] == target` → return index
4	If `arr[mid] < target` → search right half (`low = mid + 1`)
5	Else → search left half (`high = mid - 1`)
6	If not found, return -1

Tiny Code (Easy Versions)

Python

```python
def binary_search(arr, target):
    low, high = 0, len(arr) - 1
    while low <= high:
        mid = (low + high) // 2
        if arr[mid] == target:
            return mid
        elif arr[mid] < target:
            low = mid + 1
        else:
            high = mid - 1
    return -1

arr = [1, 3, 5, 7, 9, 11]
print(binary_search(arr, 7))  # Output: 3
```

Output:

```
3
```

C

```c
#include <stdio.h>

int binary_search(int arr[], int n, int target) {
    int low = 0, high = n - 1;
    while (low <= high) {
        int mid = low + (high - low) / 2; // avoid overflow
        if (arr[mid] == target)
            return mid;
        else if (arr[mid] < target)
            low = mid + 1;
        else
            high = mid - 1;
    }
    return -1;
}

int main(void) {
    int arr[] = {1, 3, 5, 7, 9, 11};
    int n = sizeof(arr) / sizeof(arr[0]);
```

```
    int idx = binary_search(arr, n, 7);
    if (idx != -1)
        printf("Found at index: %d\n", idx);
    else
        printf("Not found\n");
}
```

Output:

```
Found at index: 3
```

Why It Matters

- Fundamental divide-and-conquer algorithm
- O(log n) time complexity
- Used everywhere: search engines, databases, compilers
- Builds intuition for binary decision trees

This is the first truly efficient search most programmers learn.

A Gentle Proof (Why It Works)

At each step, the search interval halves.
After k steps, remaining elements $= \frac{n}{2^k}$.

Stop when $\frac{n}{2^k} = 1$
$k = \log_2 n$

So, total comparisons:

$$T(n) = O(\log n)$$

Works only on sorted arrays.

Try It Yourself

1. Search `7` in `[1,3,5,7,9,11]`
2. Search `2` (not found)
3. Trace values of `low`, `high`, `mid`
4. Try on even-length array `[1,2,3,4,5,6]`
5. Try on odd-length array `[1,2,3,4,5]`
6. Compare iteration count with linear search

7. Implement recursive version
8. Use binary search to find insertion point
9. Add counter to measure steps
10. Explain why sorting is required

Test Cases

Input	Target	Output	Notes
[1,3,5,7,9,11]	7	3	Found
[1,3,5,7,9,11]	2	-1	Not found
[1,2,3,4,5]	1	0	First element
[1,2,3,4,5]	5	4	Last element

Complexity

Aspect	Value
Time (Best)	O(1)
Time (Worst)	O(log n)
Time (Average)	O(log n)
Space	O(1)
Stable	Yes
Adaptive	No
Prerequisite	Sorted array

Binary Search (Iterative) is the gold standard of efficiency, halving your problem at every step, one decision at a time.

154 Binary Search (Recursive)

Binary Search (Recursive) is the classic divide-and-conquer form of binary search. Instead of looping, it calls itself on smaller subarrays, each time halving the search space until the target is found or the interval becomes empty.

It's a perfect demonstration of recursion in action, each call tackles a smaller slice of the problem.

What Problem Are We Solving?

Given a sorted array, we want to find a target value efficiently. Rather than scanning linearly, we repeatedly split the array in half, focusing only on the half that could contain the target.

This version expresses that logic through recursive calls.

Example

Find `7` in `[1, 3, 5, 7, 9, 11]`

Step	Low	High	Mid	Value	Action
1	0	5	2	5	$7 > 5 \rightarrow$ search right half
2	3	5	4	9	$7 < 9 \rightarrow$ search left half
3	3	3	3	7	Found

Recursive calls shrink the interval each time until match is found.

How Does It Work (Plain Language)?

Binary search says:

> "If the middle element isn't what I want, I can ignore half the data."

In recursive form:

1. Check the midpoint.
2. If equal $\rightarrow$ found.
3. If smaller $\rightarrow$ recurse right.
4. If larger $\rightarrow$ recurse left.
5. Base case: if `low > high`, element not found.

Each call reduces the search space by half, logarithmic depth recursion.

Step	Description

Step-by-Step Process

Step	Description
1	Check base case: if `low > high`, return -1
2	Compute `mid = (low + high) // 2`
3	If `arr[mid] == target`, return `mid`
4	If `arr[mid] > target`, recurse left half
5	Else, recurse right half

Tiny Code (Easy Versions)

Python

```
def binary_search_recursive(arr, target, low, high):
    if low > high:
        return -1
    mid = (low + high) // 2
    if arr[mid] == target:
        return mid
    elif arr[mid] < target:
        return binary_search_recursive(arr, target, mid + 1, high)
    else:
        return binary_search_recursive(arr, target, low, mid - 1)

arr = [1, 3, 5, 7, 9, 11]
print(binary_search_recursive(arr, 7, 0, len(arr)-1))  # Output: 3
```

Output:

```
3
```

C

```c
#include <stdio.h>

int binary_search_recursive(int arr[], int low, int high, int target) {
    if (low > high)
        return -1;
    int mid = low + (high - low) / 2;
    if (arr[mid] == target)
        return mid;
    else if (arr[mid] < target)
        return binary_search_recursive(arr, mid + 1, high, target);
    else
        return binary_search_recursive(arr, low, mid - 1, target);
}

int main(void) {
    int arr[] = {1, 3, 5, 7, 9, 11};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = binary_search_recursive(arr, 0, n - 1, 7);
    if (idx != -1)
        printf("Found at index: %d\n", idx);
    else
        printf("Not found\n");
}
```

Output:

```
Found at index: 3
```

Why It Matters

- Elegant divide-and-conquer demonstration
- Shows recursion depth = log (n)
- Same complexity as iterative version
- Lays foundation for recursive algorithms (merge sort, quicksort)

Recursion mirrors the mathematical idea of halving the interval, clean and intuitive.

A Gentle Proof (Why It Works)

At each recursive call:

- Problem size halves: $n \to n/2 \to n/4 \to ...$
- Recursion stops after $\log_2 n$ levels

Thus total complexity:

$$T(n) = T(n/2) + O(1) = O(\log n)$$

Correctness follows from:

- Sorted input ensures ordering decisions are valid
- Base case ensures termination

Try It Yourself

1. Search `7` in `[1,3,5,7,9,11]`
2. Search `2` (not present)
3. Add print statements to trace recursion
4. Compare call count vs iterative version
5. Test base case with `low > high`
6. Search first and last element
7. Observe recursion depth for size 8 $\to$ 3 calls
8. Add memo of `(low, high)` per step
9. Implement tail-recursive variant
10. Reflect on stack vs loop tradeoffs

Test Cases

Input	Target	Output	Notes
[1,3,5,7,9,11]	7	3	Found
[1,3,5,7,9,11]	2	-1	Not found
[1,2,3,4,5]	1	0	First element
[1,2,3,4,5]	5	4	Last element

Complexity

Aspect	Value
Time (Best)	O(1)
Time (Worst)	O(log n)
Time (Average)	O(log n)

Aspect	Value
Space	O(log n) (recursion stack)
Stable	Yes
Adaptive	No
Prerequisite	Sorted array

Binary Search (Recursive) is divide-and-conquer at its purest, halving the world each time, until the answer reveals itself.

155 Binary Search (Lower Bound)

Lower Bound Binary Search is a variant of binary search that finds the first position where a value could be inserted without breaking the sorted order. In other words, it returns the index of the first element greater than or equal to the target.

It's used extensively in search engines, databases, range queries, and C++ STL (`std::lower_bound`).

What Problem Are We Solving?

In many cases, you don't just want to know if an element exists — you want to know where it would go in a sorted structure.

- If the value exists, return its first occurrence.
- If it doesn't exist, return the position where it could be inserted to keep the array sorted.

This is essential for insertion, frequency counting, and range boundaries.

Example

Find lower bound of `7` in `[1, 3, 5, 7, 7, 9, 11]`:

Step	Low	High	Mid	Value	Compare	Action
1	0	6	3	7	arr[mid] >= 7	move high = 3
2	0	2	1	3	arr[mid] < 7	move low = 2
3	2	3	2	5	arr[mid] < 7	move low = 3
4	low == high	,	,	,	Stop	

Result: Index 3 (first `7`)

How Does It Work (Plain Language)?

Lower bound finds the leftmost slot where the target fits. It slides the search window until `low == high`, with `low` marking the first candidate target.

You can think of it as:

> "How far left can I go while still being target?"

Step-by-Step Process

Step	Description
1	Set `low = 0`, `high = n` (note: `high` = n, not n-1)
2 a. `mid = (low + high) // 2` b. If `arr[mid] < target`, move `low = mid + 1` c. Else, move `high = mid`	While `low < high`:
3	When loop ends, `low` is the lower bound index

Tiny Code (Easy Versions)

Python

```python
def lower_bound(arr, target):
    low, high = 0, len(arr)
    while low < high:
        mid = (low + high) // 2
        if arr[mid] < target:
            low = mid + 1
        else:
            high = mid
    return low

arr = [1, 3, 5, 7, 7, 9, 11]
print(lower_bound(arr, 7))  # Output: 3
```

Output:

3

C

```c
#include <stdio.h>

int lower_bound(int arr[], int n, int target) {
    int low = 0, high = n;
    while (low < high) {
        int mid = low + (high - low) / 2;
        if (arr[mid] < target)
            low = mid + 1;
        else
            high = mid;
    }
    return low;
}

int main(void) {
    int arr[] = {1, 3, 5, 7, 7, 9, 11};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = lower_bound(arr, n, 7);
    printf("Lower bound index: %d\n", idx);
}
```

Output:

```
Lower bound index: 3
```

Why It Matters

- Finds insertion position for sorted arrays
- Useful in binary search trees, maps, intervals
- Core of range queries (like count of elements x)
- Builds understanding of boundary binary search

When you need more than yes/no, you need where, use lower bound.

A Gentle Proof (Why It Works)

Invariant:

- All indices before `low` contain elements `< target`
- All indices after `high` contain elements `target`

Loop maintains invariant until convergence:

$$low = high = \text{first index where arr[i] target}$$

Complexity:

$$T(n) = O(\log n)$$

Try It Yourself

1. `arr = [1,3,5,7,7,9]`, `target = 7` $\to 3$
2. `target = 6` $\to 3$ (would insert before first 7)
3. `target = 10` $\to 6$ (end)
4. `target = 0` $\to 0$ (front)
5. Count elements 7: `len(arr) - lower_bound(arr, 7)`
6. Compare with `bisect_left` in Python
7. Use to insert elements while keeping list sorted
8. Apply to sorted strings `["apple", "banana", "cherry"]`
9. Visualize range [lower, upper) for duplicates
10. Benchmark vs linear scan for large n

Test Cases

Input	Target	Output	Meaning
[1,3,5,7,7,9,11]	7	3	First 7
[1,3,5,7,7,9,11]	6	3	Insert before 7
[1,3,5,7,7,9,11]	12	7	End position
[1,3,5,7,7,9,11]	0	0	Front

Complexity

Aspect	Value
Time	O(log n)
Space	O(1)
Stable	Yes
Adaptive	No
Prerequisite	Sorted array

Binary Search (Lower Bound) is how algorithms learn *where* things belong, not just if they exist. It's the precise edge of order.

156 Binary Search (Upper Bound)

Upper Bound Binary Search is a close cousin of Lower Bound, designed to find the first index where an element is greater than the target. It's used to locate the right boundary of equal elements or the insertion point after duplicates.

In simpler words:

> It finds "the spot just after the last occurrence" of the target.

What Problem Are We Solving?

Sometimes you need to know where to insert a value after existing duplicates. For example, in frequency counting or range queries, you might want the end of a block of identical elements.

Upper bound returns that exact position, the smallest index where

$$\text{arr[i]} > \text{target}$$

Example

Find upper bound of `7` in `[1, 3, 5, 7, 7, 9, 11]`:

Step	Low	High	Mid	Value	Compare	Action
1	0	7	3	7	7 7	move low = 4
2	4	7	5	9	9 > 7	move high = 5
3	4	5	4	7	7 7	move low = 5
4	low == high	,	,	,	Stop	

Result: Index 5 → position after last `7`.

How Does It Work (Plain Language)?

If Lower Bound finds "the first target," then Upper Bound finds "the first > target."

Together, they define equal ranges:

lower_bound, upper_bound) $$ → all elements equal to the target.

Step-by-Step Process

Step	Description
1	Set `low = 0`, `high = n`
2	While `low < high`:
a. `mid = (low + high) // 2`	
b. If `arr[mid] <= target`, move `low = mid + 1`	
c. Else, move `high = mid`	
3	When loop ends, `low` is the upper bound index

Tiny Code (Easy Versions)

Python

```
def upper_bound(arr, target):
    low, high = 0, len(arr)
    while low < high:
        mid = (low + high) // 2
        if arr[mid] <= target:
            low = mid + 1
        else:
            high = mid
    return low

arr = [1, 3, 5, 7, 7, 9, 11]
print(upper_bound(arr, 7))  # Output: 5
```

Output:

```
5
```

C

```c
#include <stdio.h>

int upper_bound(int arr[], int n, int target) {
    int low = 0, high = n;
    while (low < high) {
        int mid = low + (high - low) / 2;
        if (arr[mid] <= target)
            low = mid + 1;
        else
            high = mid;
    }
    return low;
}

int main(void) {
    int arr[] = {1, 3, 5, 7, 7, 9, 11};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = upper_bound(arr, n, 7);
    printf("Upper bound index: %d\n", idx);
}
```

Output:

```
Upper bound index: 5
```

Why It Matters

- Locates end of duplicate block
- Enables range counting: count = `upper_bound - lower_bound`
- Used in maps, sets, STL containers
- Key component in range queries and interval merging

It's the *right-hand anchor* of sorted intervals.

A Gentle Proof (Why It Works)

Invariant:

- All indices before `low` contain $\leq$ target
- All indices after `high` contain $>$ target

When `low == high`, it's the smallest index where `arr[i] > target`.

Number of steps $= \log_2 n$
$\rightarrow$ Complexity:

$$T(n) = O(\log n)$$

Try It Yourself

1. `arr = [1,3,5,7,7,9]`, `target=7` $\rightarrow$ 5
2. `target=6` $\rightarrow$ 3 (insert after 5)
3. `target=10` $\rightarrow$ 6 (end)
4. `target=0` $\rightarrow$ 0 (front)
5. Count elements equal to 7 $\rightarrow$ `upper - lower`
6. Compare with `bisect_right` in Python
7. Use to insert new element after duplicates
8. Combine with lower bound to find range
9. Visualize [lower, upper) range
10. Apply to floating point sorted list

Test Cases

Input	Target	Output	Meaning
[1,3,5,7,7,9,11]	7	5	After last 7
[1,3,5,7,7,9,11]	6	3	Insert after 5
[1,3,5,7,7,9,11]	12	7	End position
[1,3,5,7,7,9,11]	0	0	Front

Complexity

Aspect	Value
Time	O(log n)
Space	O(1)
Stable	Yes
Adaptive	No
Prerequisite	Sorted array

Binary Search (Upper Bound) is how you find where "greater than" begins, the right edge of equality, the step beyond the last twin.

157 Exponential Search

Exponential Search is a hybrid search algorithm that quickly locates the range where a target might lie, then uses binary search inside that range.

It's ideal when searching unbounded or very large sorted arrays, especially when the size is unknown or dynamic (like data streams or infinite arrays).

What Problem Are We Solving?

In a standard binary search, you need the array size. But what if the size is unknown, or huge?

Exponential Search solves this by:

1. Quickly finding an interval where the target could exist.
2. Performing binary search within that interval.

This makes it great for:

- Infinite arrays (conceptual)
- Streams
- Linked structures with known order
- Large sorted data where bounds are costly

Example

Find `15` in `[1, 2, 4, 8, 16, 32, 64, 128]`

Step	Range	Value	Compare	Action
1	index 1	2	$2 < 15$	expand
2	index 2	4	$4 < 15$	expand
3	index 4	16	$16 \quad 15$	stop
4	Range = [2, 4]	Binary Search in [4, 8, 16]	Found 15 at index 4	

We doubled the bound each time (1, 2, 4, 8…) until we passed the target.

How Does It Work (Plain Language)?

Think of it like zooming in:

- Start small, double your step size until you overshoot the target.
- Once you've bracketed it, zoom in with binary search.

This avoids scanning linearly when the array could be massive.

Step-by-Step Process

Step	Description
1	Start with index 1
2	While `i < n` and `arr[i] < target`, double `i`
3	Now target `[i/2, min(i, n-1)]`
4	Apply binary search in that subrange
5	Return found index or -1

Tiny Code (Easy Versions)

Python

```
def binary_search(arr, target, low, high):
    while low <= high:
        mid = (low + high) // 2
        if arr[mid] == target:
            return mid
        elif arr[mid] < target:
            low = mid + 1
        else:
            high = mid - 1
    return -1

def exponential_search(arr, target):
    if arr[0] == target:
        return 0
    i = 1
    n = len(arr)
    while i < n and arr[i] < target:
```

```
        i *= 2
    return binary_search(arr, target, i // 2, min(i, n - 1))

arr = [1, 2, 4, 8, 16, 32, 64, 128]
print(exponential_search(arr, 16))  # Output: 4
```

Output:

```
4
```

C

```
#include <stdio.h>

int binary_search(int arr[], int low, int high, int target) {
    while (low <= high) {
        int mid = low + (high - low) / 2;
        if (arr[mid] == target)
            return mid;
        else if (arr[mid] < target)
            low = mid + 1;
        else
            high = mid - 1;
    }
    return -1;
}

int exponential_search(int arr[], int n, int target) {
    if (arr[0] == target)
        return 0;
    int i = 1;
    while (i < n && arr[i] < target)
        i *= 2;
    int low = i / 2;
    int high = (i < n) ? i : n - 1;
    return binary_search(arr, low, high, target);
}

int main(void) {
    int arr[] = {1, 2, 4, 8, 16, 32, 64, 128};
```

```
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = exponential_search(arr, n, 16);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 4
```

Why It Matters

- Works with unknown or infinite size arrays
- Faster than linear scan for large `n`
- Combines doubling search and binary search
- Used in streaming data structures, file systems, unbounded containers

It's the searcher's flashlight, shine brighter until you see your target.

A Gentle Proof (Why It Works)

Doubling creates at most $\log_2 p$ expansions,
where p is the position of the target.

Then binary search on a range of size $O(p)$ takes another $O(\log p)$.

So total time:

$$T(n) = O(\log p)$$

Asymptotically equal to binary search when $p \ll n$.

Try It Yourself

1. Search `16` in `[1,2,4,8,16,32,64,128]`
2. Search `3` → not found
3. Trace expansions: 1,2,4,8…
4. Try `[10,20,30,40,50,60,70]` with `target=60`
5. Modify doubling factor (try 3x)
6. Compare with simple binary search
7. Implement recursive exponential search
8. Use for unknown-size input stream
9. Measure expansion count
10. Visualize ranges on number line

Test Cases

Input	Target	Output	Notes
[1,2,4,8,16,32,64]	16	4	Classic
[1,2,4,8,16,32,64]	3	-1	Not found
[2,4,6,8]	2	0	First element
[2,4,6,8]	10	-1	Out of range

Complexity

Aspect	Value
Time	O(log p), where p = position of target
Space	O(1)
Stable	Yes
Adaptive	Partially
Prerequisite	Sorted array

Exponential Search is how you find your way in the dark, double your reach, then look closely where the light lands.

158 Jump Search

Jump Search is a simple improvement over Linear Search, designed for sorted arrays. It works by jumping ahead in fixed-size steps instead of checking every element, then performing a linear scan within the block where the target might be.

It trades a bit of extra logic for a big win in speed, especially when data is sorted and random access is cheap.

What Problem Are We Solving?

Linear search checks each element one by one, slow for large arrays. Jump Search improves on this by "skipping ahead" in fixed jumps, so it makes fewer comparisons overall.

It's great for:

- Sorted arrays
- Fast random access (like arrays, not linked lists)
- Simple, predictable search steps

Example

Find `9` in `[1, 3, 5, 7, 9, 11, 13, 15]`

Array size = 8 → Jump size = √8 = 2 or 3

Step	Jump to Index	Value	Compare	Action
1	2	5	5 < 9	jump forward
2	4	9	9 9	stop jump
3	Linear scan from 2	5, 7, 9	found 9	

Found at index 4.

How Does It Work (Plain Language)?

Imagine you're reading a sorted list of numbers. Instead of reading one number at a time, you skip ahead every few steps, like jumping stairs. Once you overshoot or match, you walk back linearly within that block.

Jump size √n gives a good balance between jumps and scans.

Step-by-Step Process

Step	Description
1	Choose jump size `step = √n`
2	Jump ahead while `arr[min(step, n)-1] < target`
3	Once overshoot, do linear search in the previous block
4	If found, return index, else -1

Tiny Code (Easy Versions)

Python

```
import math

def jump_search(arr, target):
    n = len(arr)
    step = int(math.sqrt(n))
```

```
    prev = 0

    # Jump ahead
    while prev < n and arr[min(step, n) - 1] < target:
        prev = step
        step += int(math.sqrt(n))
        if prev >= n:
            return -1

    # Linear search within block
    for i in range(prev, min(step, n)):
        if arr[i] == target:
            return i
    return -1

arr = [1, 3, 5, 7, 9, 11, 13, 15]
print(jump_search(arr, 9))  # Output: 4
```

Output:

```
4
```

C

```c
#include <stdio.h>
#include <math.h>

int jump_search(int arr[], int n, int target) {
    int step = sqrt(n);
    int prev = 0;

    while (prev < n && arr[(step < n ? step : n) - 1] < target) {
        prev = step;
        step += sqrt(n);
        if (prev >= n) return -1;
    }

    for (int i = prev; i < (step < n ? step : n); i++) {
        if (arr[i] == target) return i;
    }
```

```
    return -1;
}

int main(void) {
    int arr[] = {1, 3, 5, 7, 9, 11, 13, 15};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = jump_search(arr, n, 9);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 4
```

Why It Matters

- Faster than Linear Search for sorted arrays
- Simpler to implement than Binary Search
- Good for systems with non-random access penalties
- Balance of jumps and scans minimizes comparisons

Best of both worlds: quick leaps and gentle steps.

A Gentle Proof (Why It Works)

Let jump size $= m$.

We perform at most $\frac{n}{m}$ jumps and m linear steps.
Total cost:

$$T(n) = O\left(\frac{n}{m} + m\right)$$

Minimized when $m = \sqrt{n}$

Thus:

$$T(n) = O(\sqrt{n})$$

Try It Yourself

1. Search `11` in `[1,3,5,7,9,11,13,15]`
2. Search `2` (not found)
3. Use step = 2, 3, 4 → compare jumps
4. Implement recursive version
5. Visualize jumps on paper
6. Try unsorted array (observe failure)
7. Search edge cases: first, last, middle
8. Use different step size formula
9. Combine with exponential jump
10. Compare with binary search for timing

Test Cases

Input	Target	Output	Notes
[1,3,5,7,9,11,13,15]	9	4	Found
[1,3,5,7,9,11,13,15]	2	-1	Not found
[2,4,6,8,10]	10	4	Last element
[2,4,6,8,10]	2	0	First element

Complexity

Aspect	Value
Time	O(√n)
Space	O(1)
Stable	Yes
Adaptive	No
Prerequisite	Sorted array

Jump Search is like hopscotch on sorted ground, leap smartly, then step carefully once you're close.

159 Fibonacci Search

Fibonacci Search is a divide-and-conquer search algorithm that uses Fibonacci numbers to determine probe positions, rather than midpoints like Binary Search. It's especially efficient

for sorted arrays stored in sequential memory, where element access cost grows with distance (for example, on magnetic tape or cache-sensitive systems).

It's a clever twist on binary search, using Fibonacci numbers instead of powers of two.

What Problem Are We Solving?

In Binary Search, the midpoint splits the array evenly. In Fibonacci Search, we split using Fibonacci ratios, which keeps indices aligned to integer arithmetic, no division needed, and better cache locality in some hardware.

This is particularly useful when:

- Access cost depends on distance
- Memory access is sequential or limited
- We want to avoid division and floating-point math

Example

Find `8` in `[1, 3, 5, 8, 13, 21, 34]`

Step	Fib(k)	Index Checked	Value	Compare	Action
1	8	5	13	$13 > 8$	move left
2	5	2	5	$5 < 8$	move right
3	3	3	8	$8 = 8$	found

Fibonacci numbers: 1, 2, 3, 5, 8, 13, … We reduce the search space using previous Fibonacci values, like Fibonacci decomposition.

How Does It Work (Plain Language)?

Think of Fibonacci Search as binary search guided by Fibonacci jumps. At each step:

- You compare the element at index `offset + Fib(k-2)`
- Depending on the result, you move left or right, using smaller Fibonacci numbers to define new intervals.

You "walk down" the Fibonacci sequence until the range collapses.

Step-by-Step Process

Step	Description
1	Generate smallest Fibonacci number n
2	Use Fib(k-2) as probe index
3	Compare target with `arr[offset + Fib(k-2)]`
4	If smaller, move left (reduce by Fib(k-2))
5	If larger, move right (increase offset, reduce by Fib(k-1))
6	Continue until Fib(k) = 1
7	Check last element if needed

Tiny Code (Easy Versions)

Python

```
def fibonacci_search(arr, target):
    n = len(arr)
    fibMMm2 = 0  # (m-2)'th Fibonacci
    fibMMm1 = 1  # (m-1)'th Fibonacci
    fibM = fibMMm1 + fibMMm2  # m'th Fibonacci

    # Find smallest Fibonacci >= n
    while fibM < n:
        fibMMm2, fibMMm1 = fibMMm1, fibM
        fibM = fibMMm1 + fibMMm2

    offset = -1

    while fibM > 1:
        i = min(offset + fibMMm2, n - 1)

        if arr[i] < target:
            fibM = fibMMm1
            fibMMm1 = fibMMm2
            fibMMm2 = fibM - fibMMm1
            offset = i
        elif arr[i] > target:
            fibM = fibMMm2
            fibMMm1 -= fibMMm2
```

```
            fibMMm2 = fibM - fibMMm1
        else:
            return i

    if fibMMm1 and offset + 1 < n and arr[offset + 1] == target:
        return offset + 1

    return -1

arr = [1, 3, 5, 8, 13, 21, 34]
print(fibonacci_search(arr, 8))  # Output: 3
```

Output:

```
3
```

C

```
#include <stdio.h>

int min(int a, int b) { return (a < b) ? a : b; }

int fibonacci_search(int arr[], int n, int target) {
    int fibMMm2 = 0;
    int fibMMm1 = 1;
    int fibM = fibMMm1 + fibMMm2;

    while (fibM < n) {
        fibMMm2 = fibMMm1;
        fibMMm1 = fibM;
        fibM = fibMMm1 + fibMMm2;
    }

    int offset = -1;

    while (fibM > 1) {
        int i = min(offset + fibMMm2, n - 1);

        if (arr[i] < target) {
            fibM = fibMMm1;
```

```
            fibMMm1 = fibMMm2;
            fibMMm2 = fibM - fibMMm1;
            offset = i;
        } else if (arr[i] > target) {
            fibM = fibMMm2;
            fibMMm1 -= fibMMm2;
            fibMMm2 = fibM - fibMMm1;
        } else {
            return i;
        }
    }

    if (fibMMm1 && offset + 1 < n && arr[offset + 1] == target)
        return offset + 1;

    return -1;
}

int main(void) {
    int arr[] = {1, 3, 5, 8, 13, 21, 34};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = fibonacci_search(arr, n, 8);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 3
```

Why It Matters

- Uses only addition and subtraction, no division
- Great for sequential access memory
- Matches binary search performance (O(log n))
- Offers better locality on some hardware

It's the search strategy built from nature's own numbers.

A Gentle Proof (Why It Works)

Each iteration reduces the search space by a Fibonacci ratio:

$$F_k = F_{k-1} + F_{k-2}$$

Hence, search depth Fibonacci index $k \sim \log_\phi n$,
where ϕ is the golden ratio (≈ 1.618).

So total time:

$$T(n) = O(\log n)$$

Try It Yourself

1. Search `8` in `[1,3,5,8,13,21,34]`
2. Search `21`
3. Search `2` (not found)
4. Trace Fibonacci sequence steps
5. Compare probe indices with binary search
6. Try with `n=10` → Fibonacci 13 10
7. Implement recursive version
8. Visualize probe intervals
9. Replace Fibonacci with powers of 2 (binary search)
10. Experiment with non-uniform arrays

Test Cases

Input	Target	Output	Notes
[1,3,5,8,13,21,34]	8	3	Found
[1,3,5,8,13,21,34]	2	-1	Not found
[1,3,5,8,13,21,34]	34	6	Last element
[1,3,5,8,13,21,34]	1	0	First element

Complexity

Aspect	Value
Time	O(log n)
Space	O(1)

Aspect	Value
Stable	Yes
Adaptive	No
Prerequisite	Sorted array

Fibonacci Search is searching with nature's rhythm, each step shaped by the golden ratio, balancing reach and precision.

160 Uniform Binary Search

Uniform Binary Search is an optimized form of Binary Search where the probe positions are precomputed. Instead of recalculating the midpoint at each step, it uses a lookup table of offsets to determine where to go next, making it faster in tight loops or hardware-limited systems.

It's all about removing repetitive midpoint arithmetic and branching for consistent, uniform steps.

What Problem Are We Solving?

Standard binary search repeatedly computes:

$$mid = low + \frac{high - low}{2}$$

This is cheap on modern CPUs but expensive on:

- Early hardware
- Embedded systems
- Tight loops where division or shifting is costly

Uniform Binary Search (UBS) replaces these computations with precomputed offsets for each step, giving predictable, uniform jumps.

Step	Offset	Index	Value	Compare	Action

Example

Search `25` in `[5, 10, 15, 20, 25, 30, 35, 40]`

Step	Offset	Index	Value	Compare	Action
1	3	3	20	$20 < 25$	move right
2	1	5	30	$30 > 25$	move left
3	0	4	25	$25 = 25$	found

Instead of recalculating midpoints, UBS uses offset table `[3, 1, 0]`.

How Does It Work (Plain Language)?

It's binary search with a preplanned route. At each level:

- You jump by a fixed offset (from a table)
- Compare
- Move left or right, shrinking your window uniformly

No divisions, no mid calculations, just jump and compare.

Step-by-Step Process

Step	Description
1	Precompute offset table based on array size
2	Start at offset[0] from beginning
3	Compare element with target
4	Move left/right using next offset
5	Stop when offset = 0 or found

Tiny Code (Easy Versions)

Python

```python
def uniform_binary_search(arr, target):
    n = len(arr)
    # Precompute offsets (powers of 2 less than n)
    offsets = []
    k = 1
    while k < n:
        offsets.append(k)
        k *= 2
    offsets.reverse()

    low = 0
    idx = offsets[0]

    for offset in offsets:
        mid = low + offset if low + offset < n else n - 1
        if arr[mid] == target:
            return mid
        elif arr[mid] < target:
            low = mid + 1
        # else move left (implicitly handled next iteration)

    # Final check
    if low < n and arr[low] == target:
        return low
    return -1

arr = [5, 10, 15, 20, 25, 30, 35, 40]
print(uniform_binary_search(arr, 25))  # Output: 4
```

Output:

```
4
```

C

```c
#include <stdio.h>

int uniform_binary_search(int arr[], int n, int target) {
    int k = 1;
```

```
    while (k < n) k <<= 1;
    k >>= 1;

    int low = 0;
    while (k > 0) {
        int mid = low + k - 1;
        if (mid >= n) mid = n - 1;

        if (arr[mid] == target)
            return mid;
        else if (arr[mid] < target)
            low = mid + 1;

        k >>= 1; // next smaller offset
    }

    return (low < n && arr[low] == target) ? low : -1;
}

int main(void) {
    int arr[] = {5, 10, 15, 20, 25, 30, 35, 40};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = uniform_binary_search(arr, n, 25);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 4
```

Why It Matters

- Avoids recomputing midpoints
- Ideal for hardware, firmware, microcontrollers
- Ensures consistent runtime path
- Fewer instructions → faster in tight loops

Uniformity = predictability = performance.

A Gentle Proof (Why It Works)

Precomputed offsets correspond to halving the search space. At each step, offset = floor(remaining_size / 2). After log (n) steps, we narrow down to a single element.

Total steps = log n Each step = constant cost (no recomputation)

So:

$$T(n) = O(\log n)$$

Try It Yourself

1. Search `25` in `[5,10,15,20,25,30,35,40]`
2. Search `35`
3. Search `6` → not found
4. Precompute offset table for n=8
5. Compare steps with binary search
6. Implement for n=16
7. Use for microcontroller table lookup
8. Visualize jumps on paper
9. Measure comparisons
10. Implement recursive version

Test Cases

Input	Target	Output	Notes
[5,10,15,20,25,30,35,40]	25	4	Found
[5,10,15,20,25,30,35,40]	5	0	First element
[5,10,15,20,25,30,35,40]	50	-1	Not found
[5,10,15,20,25,30,35,40]	40	7	Last element

Complexity

Aspect	Value
Time	O(log n)
Space	O(1)
Stable	Yes
Adaptive	No
Prerequisite	Sorted array

Uniform Binary Search is binary search with a map, no guesswork, no recalculations, just smooth, evenly spaced jumps to the answer.

Section 17. Interpolation and exponential search

161 Interpolation Search

Interpolation Search is a search algorithm for sorted arrays with uniformly distributed values. Unlike Binary Search, which always probes the middle, Interpolation Search estimates the position of the target using value interpolation, like finding where a number lies on a number line.

If Binary Search is "divide by index," Interpolation Search is "divide by value."

What Problem Are We Solving?

Binary Search assumes no relationship between index and value. But if the array values are uniformly spaced, we can do better by guessing where the target should be, not just the middle.

It's ideal for:

- Uniformly distributed sorted data
- Numeric keys (IDs, prices, timestamps)
- Large arrays where value-based positioning matters

Example

Find `70` in `[10, 20, 30, 40, 50, 60, 70, 80, 90]`

Estimate position:

$$pos = low + \frac{(target - arr[low]) \times (high - low)}{arr[high] - arr[low]}$$

Step	Low	High	Pos	Value	Compare	Action
1	0	8	7	80	$80 > 70$	move left
2	0	6	6	70	$70 = 70$	found

How Does It Work (Plain Language)?

Imagine the array as a number line. If your target is closer to the high end, start searching closer to the right. You *interpolate*, estimate the target's index based on its value proportion between min and max.

So rather than halving blindly, you jump to the likely spot.

Step-by-Step Process

Step	Description
1	Initialize `low = 0`, `high = n - 1`
2	While `low <= high` and `target` is in range:
	Estimate position using interpolation formula
3	Compare `arr[pos]` with `target`
4	If equal → found
5	If smaller → move `low = pos + 1`
6	If larger → move `high = pos - 1`
7	Repeat until found or `low > high`

Tiny Code (Easy Versions)

Python

```
def interpolation_search(arr, target):
    low, high = 0, len(arr) - 1

    while low <= high and arr[low] <= target <= arr[high]:
        if arr[high] == arr[low]:
            if arr[low] == target:
                return low
            break

        pos = low + (target - arr[low]) * (high - low) // (arr[high] - arr[low])

        if arr[pos] == target:
            return pos
        elif arr[pos] < target:
            low = pos + 1
```

```
        else:
            high = pos - 1

    return -1

arr = [10, 20, 30, 40, 50, 60, 70, 80, 90]
print(interpolation_search(arr, 70))  # Output: 6
```

Output:

```
6
```

C

```
#include <stdio.h>

int interpolation_search(int arr[], int n, int target) {
    int low = 0, high = n - 1;

    while (low <= high && target >= arr[low] && target <= arr[high]) {
        if (arr[high] == arr[low]) {
            if (arr[low] == target) return low;
            else break;
        }

        int pos = low + (double)(high - low) * (target - arr[low]) / (arr[high] - arr[low]);

        if (arr[pos] == target)
            return pos;
        if (arr[pos] < target)
            low = pos + 1;
        else
            high = pos - 1;
    }

    return -1;
}

int main(void) {
    int arr[] = {10, 20, 30, 40, 50, 60, 70, 80, 90};
```

```
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = interpolation_search(arr, n, 70);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 6
```

Why It Matters

- Faster than Binary Search for uniformly distributed data
- Ideal for dense key spaces (like hash slots, ID ranges)
- Can achieve O(log log n) average time
- Preserves sorted order search logic

It's the value-aware cousin of Binary Search.

A Gentle Proof (Why It Works)

If data is uniformly distributed, each probe halves value range logarithmically. Expected probes:

$$T(n) = O(\log \log n)$$

Worst case (non-uniform):

$$T(n) = O(n)$$

So it outperforms binary search only under uniform value distribution.

Try It Yourself

1. Search `70` in `[10,20,30,40,50,60,70,80,90]`
2. Search `25` (not found)
3. Try `arr = [2,4,8,16,32,64]`, notice uneven distribution
4. Plot estimated positions
5. Compare steps with Binary Search
6. Use floating-point vs integer division
7. Implement recursive version
8. Search `10` (first element)
9. Search `90` (last element)
10. Measure iterations on uniform vs non-uniform data

Test Cases

Input	Target	Output	Notes
[10,20,30,40,50,60,70,80,90]	70	6	Found
[10,20,30,40,50,60,70,80,90]	25	-1	Not found
[10,20,30,40,50,60,70,80,90]	10	0	First
[10,20,30,40,50,60,70,80,90]	90	8	Last

Complexity

Aspect	Value
Time (avg)	O(log log n)
Time (worst)	O(n)
Space	O(1)
Stable	Yes
Adaptive	Yes
Prerequisite	Sorted & uniform array

Interpolation Search is like a treasure map that scales by value, it doesn't just guess the middle, it guesses where the gold really lies.

162 Recursive Interpolation Search

Recursive Interpolation Search is the recursive variant of the classic Interpolation Search. Instead of looping, it calls itself on smaller subranges, estimating the likely position using the same value-based interpolation formula.

It's a natural way to express the algorithm for learners who think recursively, same logic, cleaner flow.

What Problem Are We Solving?

We're taking the iterative interpolation search and expressing it recursively, to highlight the divide-and-conquer nature. The recursive form is often more intuitive and mathematically aligned with its interpolation logic.

You'll use this when:

- Teaching or visualizing recursive logic

- Writing clean, declarative search code
- Practicing recursion-to-iteration transitions

Example

Find `50` in `[10, 20, 30, 40, 50, 60, 70, 80, 90]`

Step 1: low = 0, high = 8 pos = 0 + (50 - 10) × (8 - 0) / (90 - 10) = 4 arr[4] = 50 → found

Recursion stops immediately, one call, one success.

How Does It Work (Plain Language)?

Instead of looping, each recursive call zooms in to the subrange where the target might be. Each call computes an estimated index `pos` proportional to the target's distance between `arr[low]` and `arr[high]`.

If value is higher → recurse right If lower → recurse left If equal → return index

Step-by-Step Process

Step	Description
1	Base case: if `low > high` or target out of range → not found
2	Compute position estimate using interpolation formula
3	If `arr[pos] == target` → return `pos`
4	If `arr[pos] < target` → recurse on right half
5	Else recurse on left half

Tiny Code (Easy Versions)

Python

```python
def interpolation_search_recursive(arr, low, high, target):
    if low > high or target < arr[low] or target > arr[high]:
        return -1

    if arr[high] == arr[low]:
        return low if arr[low] == target else -1
```

```
    pos = low + (target - arr[low]) * (high - low) // (arr[high] - arr[low])

    if arr[pos] == target:
        return pos
    elif arr[pos] < target:
        return interpolation_search_recursive(arr, pos + 1, high, target)
    else:
        return interpolation_search_recursive(arr, low, pos - 1, target)

arr = [10, 20, 30, 40, 50, 60, 70, 80, 90]
print(interpolation_search_recursive(arr, 0, len(arr) - 1, 50))  # Output: 4
```

Output:

```
4
```

C

```
#include <stdio.h>

int interpolation_search_recursive(int arr[], int low, int high, int target) {
    if (low > high || target < arr[low] || target > arr[high])
        return -1;

    if (arr[high] == arr[low])
        return (arr[low] == target) ? low : -1;

    int pos = low + (double)(high - low) * (target - arr[low]) / (arr[high] - arr[low]);

    if (arr[pos] == target)
        return pos;
    else if (arr[pos] < target)
        return interpolation_search_recursive(arr, pos + 1, high, target);
    else
        return interpolation_search_recursive(arr, low, pos - 1, target);
}

int main(void) {
    int arr[] = {10, 20, 30, 40, 50, 60, 70, 80, 90};
    int n = sizeof(arr) / sizeof(arr[0]);
```

```
    int idx = interpolation_search_recursive(arr, 0, n - 1, 50);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 4
```

Why It Matters

- Shows the recursive nature of interpolation-based estimation
- Clean, mathematical form for teaching and analysis
- Demonstrates recursion depth proportional to search cost
- Easier to reason about with divide-by-value intuition

Think of it as binary search's artistic cousin, elegant and value-aware.

A Gentle Proof (Why It Works)

In uniform distributions, each recursive step shrinks the search space multiplicatively, not just by half.

If data is uniform:

$$T(n) = T(n/f) + O(1) \Rightarrow T(n) = O(\log \log n)$$

If not uniform:

$$T(n) = O(n)$$

Recursion depth = number of interpolation refinements log log n.

Try It Yourself

1. Search `70` in `[10,20,30,40,50,60,70,80,90]`
2. Search `25` (not found)
3. Trace recursive calls manually
4. Add print statements to watch low/high shrink
5. Compare depth with binary search
6. Try `[2,4,8,16,32,64]` (non-uniform)
7. Add guard for `arr[low] == arr[high]`
8. Implement tail recursion optimization
9. Test base cases (first, last, single element)
10. Time comparison: iterative vs recursive

Test Cases

Input	Target	Output	Notes
[10,20,30,40,50,60,70,80,90]	50	4	Found
[10,20,30,40,50,60,70,80,90]	25	-1	Not found
[10,20,30,40,50,60,70,80,90]	10	0	First
[10,20,30,40,50,60,70,80,90]	90	8	Last

Complexity

Aspect	Value
Time (avg)	O(log log n)
Time (worst)	O(n)
Space	O(log log n) (recursion)
Stable	Yes
Adaptive	Yes
Prerequisite	Sorted & uniform array

Recursive Interpolation Search is like zooming in with value-based intuition, each step a mathematical guess, each call a sharper focus.

163 Exponential Search

Exponential Search combines range expansion with binary search. It's perfect when the array size is unknown or infinite, it first finds the range that might contain the target by doubling the index, then uses binary search within that range.

It's the "zoom out, then zoom in" strategy for searching sorted data.

What Problem Are We Solving?

If you don't know the length of your sorted array, you can't directly apply binary search. You need to first bound the search space, so you know where to look.

Exponential Search does exactly that:

- It doubles the index (1, 2, 4, 8, 16…) until it overshoots.
- Then it performs binary search in that bracket.

Use it for:

- Infinite or dynamically sized sorted arrays
- Streams
- Unknown-length files or data structures

Example

Find `19` in `[2, 4, 8, 16, 19, 23, 42, 64, 128]`

Step	Range	Value	Compare	Action
1	1	4	$4 < 19$	double index
2	2	8	$8 < 19$	double index
3	4	19	$19 = 19$	found

If it had overshot (say, target 23), we'd binary search between 4 and 8.

How Does It Work (Plain Language)?

Think of searching an endless bookshelf. You take steps of size 1, 2, 4, 8… until you pass the book number you want. Now you know which shelf section it's on, then you check precisely using binary search.

Fast to expand, precise to finish.

Step-by-Step Process

Step	Description
1	Start at index 1
2	While `i < n` and `arr[i] < target`, double `i`
3	When overshoot → binary search between `i/2` and `min(i, n-1)`
4	Return index if found, else -1

Tiny Code (Easy Versions)

Python

```
def binary_search(arr, low, high, target):
    while low <= high:
        mid = (low + high) // 2
        if arr[mid] == target:
            return mid
        elif arr[mid] < target:
            low = mid + 1
        else:
            high = mid - 1
    return -1

def exponential_search(arr, target):
    n = len(arr)
    if n == 0:
        return -1
    if arr[0] == target:
        return 0
    i = 1
    while i < n and arr[i] <= target:
        i *= 2
    return binary_search(arr, i // 2, min(i, n - 1), target)

arr = [2, 4, 8, 16, 19, 23, 42, 64, 128]
print(exponential_search(arr, 19))  # Output: 4
```

Output:

```
4
```

C

```
#include <stdio.h>

int binary_search(int arr[], int low, int high, int target) {
    while (low <= high) {
        int mid = low + (high - low) / 2;
        if (arr[mid] == target)
            return mid;
        else if (arr[mid] < target)
```

```
            low = mid + 1;
        else
            high = mid - 1;
    }
    return -1;
}

int exponential_search(int arr[], int n, int target) {
    if (n == 0) return -1;
    if (arr[0] == target) return 0;

    int i = 1;
    while (i < n && arr[i] <= target)
        i *= 2;

    int low = i / 2;
    int high = (i < n) ? i : n - 1;
    return binary_search(arr, low, high, target);
}

int main(void) {
    int arr[] = {2, 4, 8, 16, 19, 23, 42, 64, 128};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = exponential_search(arr, n, 19);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 4
```

Why It Matters

- Handles unknown size arrays
- Logarithmic search after expansion
- Fewer comparisons for small targets
- Common in unbounded search, streams, linked memory

It's the search that grows as needed, like zooming your scope until the target appears.

A Gentle Proof (Why It Works)

Each iteration reduces the search space by a Fibonacci ratio:

$$F_k = F_{k-1} + F_{k-2}$$

Hence, search depth Fibonacci index $k \sim \log_\phi n$,
where ϕ is the golden ratio (≈ 1.618).

So total time:

$$T(n) = O(\log n)$$

Try It Yourself

1. Search `19` in `[2,4,8,16,19,23,42,64,128]`
2. Search `42`
3. Search `1` (not found)
4. Trace expansion: 1, 2, 4, 8…
5. Compare expansion steps vs binary search calls
6. Try on huge array, small target
7. Try on dynamic-size list (simulate infinite)
8. Implement recursive version
9. Measure expansions vs comparisons
10. Combine with galloping search in TimSort

Test Cases

Input	Target	Output	Notes
[2,4,8,16,19,23,42,64,128]	19	4	Found
[2,4,8,16,19,23,42,64,128]	23	5	Found
[2,4,8,16,19,23,42,64,128]	1	-1	Not found
[2,4,8,16,19,23,42,64,128]	128	8	Last element

Complexity

Aspect	Value
Time	O(log p)
Space	O(1)

Aspect	Value
Stable	Yes
Adaptive	Yes
Prerequisite	Sorted array

Exponential Search is your wayfinder, it reaches out in powers of two, then narrows in precisely where the target hides.

164 Doubling Search

Doubling Search (also called Unbounded Search) is the general pattern behind Exponential Search. It's used when the data size or range is unknown, and you need to quickly discover a search interval that contains the target before performing a precise search (like binary search) inside that interval.

Think of it as *"search by doubling until you find your bracket."*

What Problem Are We Solving?

In many real-world scenarios, you don't know the array's length or the bounds of your search domain. You can't jump straight into binary search, you need an upper bound first.

Doubling Search gives you a strategy to find that bound quickly, in logarithmic time, by doubling your index or step size until you overshoot the target.

Perfect for:

- Infinite or streaming sequences
- Functions or implicit arrays (not stored in memory)
- Search domains defined by value, not length

Example

Find `23` in `[2, 4, 8, 16, 19, 23, 42, 64, 128]`

Step	Range	Value	Compare	Action
1	i = 1	4	$4 < 23$	double i
2	i = 2	8	$8 < 23$	double i
3	i = 4	16	$16 < 23$	double i
4	i = 8	128	$128 > 23$	stop

Range found: `[4, 8]` Now run binary search within `[16, 19, 23, 42, 64, 128]` Found at index 5

How Does It Work (Plain Language)?

Start small, test the first few steps. Every time you don't find your target and the value is still less, double your index (1, 2, 4, 8, 16…). Once you pass your target, you've found your interval, then you search precisely.

It's like walking in the dark and doubling your stride each time until you see the light, then stepping back carefully.

Step-by-Step Process

Step	Description
1	Start at index 1
2	While `arr[i] < target`, set `i = 2 × i`
3	When overshoot, define range `[i/2, min(i, n-1)]`
4	Apply binary search within range
5	Return index or -1 if not found

Tiny Code (Easy Versions)

Python

```
def doubling_search(arr, target):
    n = len(arr)
    if n == 0:
        return -1
    if arr[0] == target:
        return 0

    i = 1
    while i < n and arr[i] < target:
        i *= 2

    low = i // 2
    high = min(i, n - 1)
```

```
    # binary search
    while low <= high:
        mid = (low + high) // 2
        if arr[mid] == target:
            return mid
        elif arr[mid] < target:
            low = mid + 1
        else:
            high = mid - 1

    return -1

arr = [2, 4, 8, 16, 19, 23, 42, 64, 128]
print(doubling_search(arr, 23))  # Output: 5
```

Output:

```
5
```

C

```
#include <stdio.h>

int binary_search(int arr[], int low, int high, int target) {
    while (low <= high) {
        int mid = low + (high - low) / 2;
        if (arr[mid] == target)
            return mid;
        else if (arr[mid] < target)
            low = mid + 1;
        else
            high = mid - 1;
    }
    return -1;
}

int doubling_search(int arr[], int n, int target) {
    if (n == 0) return -1;
    if (arr[0] == target) return 0;
```

```
    int i = 1;
    while (i < n && arr[i] < target)
        i *= 2;

    int low = i / 2;
    int high = (i < n) ? i : n - 1;

    return binary_search(arr, low, high, target);
}

int main(void) {
    int arr[] = {2, 4, 8, 16, 19, 23, 42, 64, 128};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = doubling_search(arr, n, 23);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 5
```

Why It Matters

- Allows binary search when size is unknown
- Only O(log p) probes, where `p` is target index
- Natural strategy for streaming, infinite, or lazy structures
- Used in exponential, galloping, and tim-sort merges

It's the blueprint for all "expand then search" algorithms.

A Gentle Proof (Why It Works)

Each doubling step multiplies range by 2, so number of expansions log (p) Then binary search inside a range of size p

Total time:

$$T(n) = O(\log p)$$

Still logarithmic in target position, not array size, efficient even for unbounded data.

Try It Yourself

1. Search `23` in `[2,4,8,16,19,23,42,64,128]`
2. Search `42` (more jumps)
3. Search `1` (before first element)
4. Search `128` (last element)
5. Try doubling factor 3 instead of 2
6. Compare expansion steps with exponential search
7. Implement recursive version
8. Visualize on a number line
9. Simulate unknown-length array with a safe check
10. Measure steps for small vs large targets

Test Cases

Input	Target	Output	Notes
[2,4,8,16,19,23,42,64,128]	23	5	Found
[2,4,8,16,19,23,42,64,128]	4	1	Early
[2,4,8,16,19,23,42,64,128]	1	-1	Not found
[2,4,8,16,19,23,42,64,128]	128	8	Last element

Complexity

Aspect	Value
Time	O(log p)
Space	O(1)
Stable	Yes
Adaptive	Yes
Prerequisite	Sorted array

Doubling Search is how you explore the unknown, double your reach, find your bounds, then pinpoint your goal.

165 Galloping Search

Galloping Search (also called Exponential Gallop or Search by Doubling) is a hybrid search technique that quickly finds a range by *galloping forward exponentially*, then switches to binary search within that range.

It's heavily used inside TimSort's merge step, where it helps merge sorted runs efficiently by skipping over large stretches that don't need detailed comparison.

What Problem Are We Solving?

When merging two sorted arrays (or searching in a sorted list), repeatedly comparing one by one is wasteful if elements differ by a large margin. Galloping Search "jumps ahead" quickly to find the region of interest, then finishes with a binary search to locate the exact boundary.

Used in:

- TimSort merges
- Run merging in hybrid sorting
- Searching in sorted blocks
- Optimizing comparison-heavy algorithms

Example

Find `25` in `[5, 10, 15, 20, 25, 30, 35, 40, 45]`

Step	Index	Value	Compare	Action
1	1	10	$10 < 25$	gallop ($\times 2$)
2	2	15	$15 < 25$	gallop
3	4	25	$25 = 25$	found

If we overshoot (say, search for `22`), we'd gallop past it (index 4), then perform binary search between the previous bound and current one.

How Does It Work (Plain Language)?

You start by leaping, checking 1, 2, 4, 8 steps away, until you pass the target or reach the end. Once you overshoot, you gallop back (binary search) in the last valid interval.

It's like sprinting ahead to find the neighborhood, then walking house-to-house once you know the block.

Step-by-Step Process

Step	Description
1	Start at `start` index
2	Gallop forward by powers of 2 (`1, 2, 4, 8, ...`) until `arr[start + k] >= target`
3	Define range `[start + k/2, min(start + k, n-1)]`
4	Apply binary search in that range
5	Return index if found

Tiny Code (Easy Versions)

Python

```
def binary_search(arr, low, high, target):
    while low <= high:
        mid = (low + high) // 2
        if arr[mid] == target:
            return mid
        elif arr[mid] < target:
            low = mid + 1
        else:
            high = mid - 1
    return -1

def galloping_search(arr, start, target):
    n = len(arr)
    if start >= n:
        return -1
    if arr[start] == target:
        return start

    k = 1
    while start + k < n and arr[start + k] < target:
        k *= 2

    low = start + k // 2
    high = min(start + k, n - 1)
    return binary_search(arr, low, high, target)

arr = [5, 10, 15, 20, 25, 30, 35, 40, 45]
print(galloping_search(arr, 0, 25))  # Output: 4
```

Output:

```
4
```

C

```c
#include <stdio.h>

int binary_search(int arr[], int low, int high, int target) {
    while (low <= high) {
        int mid = low + (high - low) / 2;
        if (arr[mid] == target)
            return mid;
        else if (arr[mid] < target)
            low = mid + 1;
        else
            high = mid - 1;
    }
    return -1;
}

int galloping_search(int arr[], int n, int start, int target) {
    if (start >= n) return -1;
    if (arr[start] == target) return start;

    int k = 1;
    while (start + k < n && arr[start + k] < target)
        k *= 2;

    int low = start + k / 2;
    int high = (start + k < n) ? start + k : n - 1;

    return binary_search(arr, low, high, target);
}

int main(void) {
    int arr[] = {5, 10, 15, 20, 25, 30, 35, 40, 45};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = galloping_search(arr, n, 0, 25);
    printf("Found at index: %d\n", idx);
}
```

Output:

```
Found at index: 4
```

Why It Matters

- Accelerates merging in TimSort
- Minimizes comparisons when merging large sorted runs
- Great for adaptive sorting and range scans
- Balances speed (gallop) and precision (binary)

It's a dynamic balance, gallop when far, tiptoe when close.

A Gentle Proof (Why It Works)

Galloping phase:
Takes $O(\log p)$ steps to reach the target vicinity (where p is the distance from the start).

Binary phase:
Another $O(\log p)$ for local search.

Total:

$$T(n) = O(\log p)$$

Faster than linear merging when runs differ greatly in length.

Try It Yourself

1. Search `25` in `[5,10,15,20,25,30,35,40,45]`
2. Search `40` (larger gallop)
3. Search `3` (before first)
4. Try `start=2`
5. Print gallop steps
6. Compare with pure binary search
7. Implement recursive gallop
8. Use for merging two sorted arrays
9. Count comparisons per search
10. Test on long list with early/late targets

Test Cases

Input	Target	Output	Notes
[5,10,15,20,25,30,35,40,45]	25	4	Found
[5,10,15,20,25,30,35,40,45]	40	7	Larger gallop
[5,10,15,20,25,30,35,40,45]	3	-1	Not found
[5,10,15,20,25,30,35,40,45]	5	0	First element

Complexity

Aspect	Value
Time	O(log p)
Space	O(1)
Stable	Yes
Adaptive	Yes
Prerequisite	Sorted array

Galloping Search is how TimSort runs ahead with confidence, sprint through big gaps, slow down only when precision counts.

166 Unbounded Binary Search

Unbounded Binary Search is a technique for finding a value in a sorted but unbounded (or infinite) sequence. You don't know where the data ends, or even how large it is, but you know it's sorted. So first, you find a search boundary, then perform a binary search within that discovered range.

It's a direct application of doubling search followed by binary search, especially suited for monotonic functions or streams.

What Problem Are We Solving?

If you're working with data that:

- Has no fixed size,
- Comes as a stream,
- Or is represented as a monotonic function (like f(x) increasing with x),

then you can't apply binary search immediately, because you don't know `high`.

So you first need to find bounds [low, high] that contain the target, by expanding exponentially, and only then use binary search.

Example

Suppose you're searching for `20` in a monotonic function:

```
f(x) = 2x + 2
```

You want the smallest `x` such that `f(x)  20`.

Step 1: Find bounds. Check x = 1 → f(1) = 4 Check x = 2 → f(2) = 6 Check x = 4 → f(4) = 10 Check x = 8 → f(8) = 18 Check x = 16 → f(16) = 34 (overshoot!)

Now you know target lies between x = 8 and x = 16.

Step 2: Perform binary search in [8, 16]. Found f(9) = 20

How Does It Work (Plain Language)?

You start with a small step and double your reach each time until you go beyond the target. Once you've overshot, you know the search interval, and you can binary search inside it for precision.

It's the go-to strategy when the array (or domain) has no clear end.

Step-by-Step Process

Step	Description
1	Initialize `low = 0`, `high = 1`
2	While `f(high) < target`, set `low = high`, `high *= 2`
3	Once `f(high) >= target`, binary search between `[low, high]`
4	Return index (or value)

Tiny Code (Easy Versions)

Python

```
def unbounded_binary_search(f, target):
    low, high = 0, 1
    # Step 1: find bounds
    while f(high) < target:
        low = high
        high *= 2

    # Step 2: binary search in [low, high]
    while low <= high:
        mid = (low + high) // 2
        val = f(mid)
        if val == target:
            return mid
        elif val < target:
            low = mid + 1
        else:
            high = mid - 1
    return -1

# Example: f(x) = 2x + 2
f = lambda x: 2 * x + 2
print(unbounded_binary_search(f, 20))  # Output: 9
```

Output:

```
9
```

C

```
#include <stdio.h>

int f(int x) {
    return 2 * x + 2;
}
```

```c
int binary_search(int (*f)(int), int low, int high, int target) {
    while (low <= high) {
        int mid = low + (high - low) / 2;
        int val = f(mid);
        if (val == target)
            return mid;
        else if (val < target)
            low = mid + 1;
        else
            high = mid - 1;
    }
    return -1;
}

int unbounded_binary_search(int (*f)(int), int target) {
    int low = 0, high = 1;
    while (f(high) < target) {
        low = high;
        high *= 2;
    }
    return binary_search(f, low, high, target);
}

int main(void) {
    int idx = unbounded_binary_search(f, 20);
    printf("Found at x = %d\n", idx);
}
```

Output:

```
Found at x = 9
```

Why It Matters

- Handles infinite sequences or unbounded domains
- Perfect for monotonic functions (e.g. f(x) increasing)
- Key in searching without array length
- Used in root finding, binary lifting, streaming

It's the "expand, then refine" pattern, the explorer's search.

A Gentle Proof (Why It Works)

Expanding step: doubles index each time $\rightarrow O(\log p)$, where `p` is the position of the target.
Binary search step: searches within a range of size p $\rightarrow$ another $O(\log p)$.

Total complexity:

$$T(n) = O(\log p)$$

Independent of total domain size.

Try It Yourself

1. `f(x) = 2x + 2`, target = 20 $\rightarrow$ 9
2. `f(x) = x²`, target = 64 $\rightarrow$ 8
3. Search for non-existing value (e.g. 7 in even series)
4. Modify f(x) to be exponential
5. Print bounds before binary search
6. Try with negative domain (guard with if)
7. Apply to sorted infinite list (simulate with f)
8. Use float function and tolerance check
9. Compare with linear probing
10. Use to find smallest x where f(x) target

Test Cases

Function	Target	Output	Notes
2x+2	20	9	f(9)=20
x^2	64	8	f(8)=64
2x+2	7	-1	Not found
3x+1	31	10	f(10)=31

Complexity

Aspect	Value
Time	O(log p)
Space	O(1)
Stable	Yes
Adaptive	Yes

Prerequisite Monotonic function or sorted data

Unbounded Binary Search is how you search the infinite, double your bounds, then zoom in on the truth.

167 Root-Finding Bisection

Root-Finding Bisection is a numerical search algorithm for locating the point where a continuous function crosses zero. It repeatedly halves an interval where the sign of the function changes, guaranteeing that a root exists within that range.

It's the simplest, most reliable method for solving equations like f(x) = 0 when you only know that a solution exists somewhere between `a` and `b`.

What Problem Are We Solving?

When you have a function $f(x)$ and want to solve $f(x) = 0$,
but you can't solve it algebraically, you can use the **Bisection Method**.

If $f(a)$ and $f(b)$ have opposite signs, then by the Intermediate Value Theorem,
there is at least one root between a and b.

Example:
Find the root of $f(x) = x^3 - x - 2$ in $[1, 2]$.

- $f(1) = -2$
- $f(2) = 4$
  Signs differ $\rightarrow$ there's a root in $[1, 2]$.

How Does It Work (Plain Language)?

You start with an interval $[a, b]$ where $f(a)$ and $f(b)$ have opposite signs.
Then, at each step:

1. Find midpoint $m = \frac{a+b}{2}$
2. Evaluate $f(m)$
3. Replace either `a` or `b` so that signs at the ends still differ
4. Repeat until the interval is small enough

You're squeezing the interval tighter and tighter until it hugs the root.

Step-by-Step Process

Step	Description
1	Choose `a`, `b` with `f(a)` and `f(b)` of opposite signs
2	Compute midpoint `m = (a + b) / 2`
3	Evaluate `f(m)`
4	If `f(m)` has same sign as `f(a)`, set `a = m`, else `b = m`
5	Repeat until `| f(m) |or| b - a |` < tolerance
6	Return `m` as root

Tiny Code (Easy Versions)

Python

```
def f(x):
    return x3 - x - 2

def bisection(f, a, b, tol=1e-6):
    if f(a) * f(b) >= 0:
        raise ValueError("No sign change: root not guaranteed")
    while (b - a) / 2 > tol:
        m = (a + b) / 2
        if f(m) == 0:
            return m
        elif f(a) * f(m) < 0:
            b = m
        else:
            a = m
    return (a + b) / 2

root = bisection(f, 1, 2)
print("Approx root:", root)
```

Output:

```
Approx root: 1.52138
```

C

```c
#include <stdio.h>
#include <math.h>

double f(double x) {
    return x*x*x - x - 2;
}

double bisection(double (*f)(double), double a, double b, double tol) {
    if (f(a) * f(b) >= 0) {
        printf("No sign change. Root not guaranteed.\n");
        return NAN;
    }
    double m;
    while ((b - a) / 2 > tol) {
        m = (a + b) / 2;
        double fm = f(m);
        if (fm == 0)
            return m;
        if (f(a) * fm < 0)
            b = m;
        else
            a = m;
    }
    return (a + b) / 2;
}

int main(void) {
    double root = bisection(f, 1, 2, 1e-6);
    printf("Approx root: %.6f\n", root);
}
```

Output:

```
Approx root: 1.521380
```

Why It Matters

- Guaranteed convergence if (f) is continuous and signs differ

- Simple and robust
- Works for nonlinear equations
- Great starting point before more advanced methods (Newton, Secant)
- Used in physics, finance, engineering for precise solving

A Gentle Proof (Why It Works)

By the Intermediate Value Theorem:
If $f(a) \cdot f(b) < 0$, then there exists $c \in [a, b]$ such that $f(c) = 0$.

Each iteration halves the interval size, so after k steps:

$$b_k - a_k = \frac{b_0 - a_0}{2^k}$$

To achieve tolerance ε:

$$k \approx \log_2 \left(\frac{b_0 - a_0}{\varepsilon} \right)$$

Thus, convergence is linear, but guaranteed.

Try It Yourself

1. $f(x) = x^2 - 2$, interval $[1, 2] \to \sqrt{2}$
2. $f(x) = \cos x - x$, interval $[0, 1]$
3. $f(x) = x^3 - 7$, interval $[1, 3]$
4. Try tighter tolerances (`1e-3`, `1e-9`)
5. Count how many iterations needed
6. Print each midpoint
7. Compare with Newton's method
8. Plot convergence curve
9. Modify to return both root and iterations
10. Test on function with multiple roots

Test Cases

Function	Interval	Root (Approx)	Notes
$x^2 - 2$	$[1, 2]$	1.4142	$\sqrt{2}$
$x^3 - x - 2$	$[1, 2]$	1.5214	Classic example
$\cos x - x$	$[0, 1]$	0.7391	Fixed point root
$x^3 - 7$	$[1, 3]$	1.913	Cube root of 7

Complexity

Aspect	Value
Time	O(log((b−a)/tol))
Space	O(1)
Convergence	Linear
Stability	High
Requires continuity	Yes

Bisection Method is your steady compass in numerical analysis, it never fails when a root is truly there.

168 Golden Section Search

Golden Section Search is a clever optimization algorithm for finding the minimum (or maximum) of a unimodal function on a closed interval ([a, b])—without derivatives. It's a close cousin of binary search, but instead of splitting in half, it uses the golden ratio to minimize function evaluations.

What Problem Are We Solving?

You want to find the x that minimizes f(x) on an interval ([a, b]), but you can't or don't want to take derivatives (maybe f is noisy or discontinuous).

If f(x) is unimodal (has a single peak or trough), then the Golden Section Search gives you a guaranteed narrowing path to the optimum.

Example

Find the minimum of

$$f(x) = (x-2)^2 + 1$$

on ([0, 5])

Since (f(x)) is quadratic, its minimum is at (x = 2). The algorithm will zoom in around (2) by evaluating at golden-ratio points.

How Does It Work (Plain Language)?

Imagine slicing your search interval using the golden ratio ((1.618)). By placing test points at those ratios, you can reuse past evaluations and eliminate one side of the interval every step.

Each iteration shrinks the search range while keeping the ratio intact — like a mathematically perfect zoom.

Step-by-Step Process

Step	Description	Condition	Result / Note
1	Choose initial interval $[a, b]$		
2	Compute golden ratio $\phi = \frac{\sqrt{5}-1}{2} \approx 0.618$		
3	Set $c = b - \phi(b-a)$, $d = a + \phi(b-a)$		
4	Evaluate $f(c)$ and $f(d)$		
5	If $f(c) < f(d)$, new interval $= [a, d]$		
6	Else, new interval $= [c, b]$		
7	Repeat until $b - a <$ tolerance		
8	Return midpoint as best estimate		

Tiny Code (Easy Versions)

Python

```
import math

def f(x):
    return (x - 2)2 + 1
```

```
def golden_section_search(f, a, b, tol=1e-5):
    phi = (math.sqrt(5) - 1) / 2
    c = b - phi * (b - a)
    d = a + phi * (b - a)
    fc, fd = f(c), f(d)

    while abs(b - a) > tol:
        if fc < fd:
            b, d, fd = d, c, fc
            c = b - phi * (b - a)
            fc = f(c)
        else:
            a, c, fc = c, d, fd
            d = a + phi * (b - a)
            fd = f(d)
    return (b + a) / 2

root = golden_section_search(f, 0, 5)
print("Minimum near x =", root)
```

Output:

```
Minimum near x = 2.0000
```

C

```
#include <stdio.h>
#include <math.h>

double f(double x) {
    return (x - 2)*(x - 2) + 1;
}

double golden_section_search(double (*f)(double), double a, double b, double tol) {
    double phi = (sqrt(5.0) - 1) / 2;
    double c = b - phi * (b - a);
    double d = a + phi * (b - a);
    double fc = f(c), fd = f(d);
```

```
    while (fabs(b - a) > tol) {
        if (fc < fd) {
            b = d;
            d = c;
            fd = fc;
            c = b - phi * (b - a);
            fc = f(c);
        } else {
            a = c;
            c = d;
            fc = fd;
            d = a + phi * (b - a);
            fd = f(d);
        }
    }
    return (b + a) / 2;
}

int main(void) {
    double x = golden_section_search(f, 0, 5, 1e-5);
    printf("Minimum near x = %.5f\n", x);
}
```

Output:

```
Minimum near x = 2.00000
```

Why It Matters

- No derivatives required
- Fewer evaluations than simple binary search
- Guaranteed convergence for unimodal functions
- Used in numerical optimization, tuning, engineering design, hyperparameter search
- The golden ratio ensures optimal reuse of computed points

A Gentle Proof (Why It Works)

At each step, the interval length is multiplied by $\phi \approx 0.618$.

So after k steps:

$$L_k = (b_0 - a_0) \times \phi^k$$

To reach tolerance ε:

$$k = \frac{\log(\varepsilon/(b_0 - a_0))}{\log(\phi)}$$

Thus, convergence is linear but efficient, and each iteration needs only one new evaluation.

Try It Yourself

1. $f(x) = (x-3)^2$, interval $[0, 6]$
2. $f(x) = x^4 - 10x^2 + 9$, interval $[-5, 5]$
3. $f(x) = |x - 1|$, interval $[-2, 4]$
4. Try changing tolerance to `1e-3`, `1e-9`
5. Track number of iterations
6. Plot search intervals
7. Switch to maximizing (compare signs)
8. Test non-unimodal function (observe failure)
9. Modify to return f(x*) as well
10. Compare with ternary search

Test Cases

Function	Interval	Minimum x	$f(x)$
$(x-2)^2 + 1$	$[0, 5]$	2.0000	1.0000
$(x-3)^2$	$[0, 6]$	3.0000	0.0000
x^2	$[-3, 2]$	0.0000	0.0000

Complexity

Aspect	Value
Time	O(log((b−a)/tol))
Space	O(1)
Evaluations per step	1 new point
Convergence	Linear
Requires unimodality	Yes

Golden Section Search is optimization's quiet craftsman, balancing precision and simplicity with the elegance of .

169 Fibonacci Search (Optimum)

Fibonacci Search is a divide-and-conquer algorithm that uses the Fibonacci sequence to determine probe positions when searching for a target in a sorted array. It's similar to binary search but uses Fibonacci numbers instead of halving intervals, which makes it ideal for sequential access systems (like tapes or large memory arrays).

It shines where comparison count matters or when random access is expensive.

What Problem Are We Solving?

You want to search for an element in a sorted array efficiently, but instead of halving the interval (as in binary search), you want to use Fibonacci numbers to decide where to look — minimizing comparisons and taking advantage of arithmetic-friendly jumps.

Example

Let's search for x = 55 in:

```
arr = [10, 22, 35, 40, 45, 50, 80, 82, 85, 90, 100]
```

1. Find smallest Fibonacci number length (11) → F(7) = 13
2. Use Fibonacci offsets to decide index jumps.
3. Check mid using fibM2 = 5 (F(5)=5 → index 4): arr[4] = 45 < 55
4. Move window and repeat until found or narrowed.

How Does It Work (Plain Language)?

Instead of splitting in half like binary search, it splits using ratios of Fibonacci numbers, keeping subarray sizes close to golden ratio.

This approach reduces comparisons and works especially well when array size is known and access cost is linear or limited.

Think of it as a mathematically balanced jump search guided by Fibonacci spacing.

Step-by-Step Process

Step	Description
1	Compute smallest Fibonacci number Fm n
2	Set offsets: Fm1 = Fm-1, Fm2 = Fm-2
3	Compare target with arr[offset + Fm2]
4	If smaller, search left subarray (shift Fm1, Fm2)
5	If larger, search right subarray (update offset, shift Fm1, Fm2)
6	If equal, return index
7	Continue until Fm1 = 1

Tiny Code (Easy Versions)

Python

```
def fibonacci_search(arr, x):
    n = len(arr)

    # Initialize fibonacci numbers
    fibMMm2 = 0  # F(m-2)
    fibMMm1 = 1  # F(m-1)
    fibM = fibMMm2 + fibMMm1  # F(m)

    # Find smallest Fibonacci >= n
    while fibM < n:
        fibMMm2 = fibMMm1
        fibMMm1 = fibM
        fibM = fibMMm2 + fibMMm1

    offset = -1

    while fibM > 1:
        i = min(offset + fibMMm2, n - 1)

        if arr[i] < x:
            fibM = fibMMm1
            fibMMm1 = fibMMm2
            fibMMm2 = fibM - fibMMm1
            offset = i
```

```
        elif arr[i] > x:
            fibM = fibMMm2
            fibMMm1 -= fibMMm2
            fibMMm2 = fibM - fibMMm1
        else:
            return i

    if fibMMm1 and offset + 1 < n and arr[offset + 1] == x:
        return offset + 1

    return -1

arr = [10, 22, 35, 40, 45, 50, 80, 82, 85, 90, 100]
print("Found at index:", fibonacci_search(arr, 55))  # Output: -1
print("Found at index:", fibonacci_search(arr, 85))  # Output: 8
```

Output:

```
Found at index: -1
Found at index: 8
```

C

```
#include <stdio.h>

int min(int a, int b) { return (a < b) ? a : b; }

int fibonacci_search(int arr[], int n, int x) {
    int fibMMm2 = 0;   // F(m-2)
    int fibMMm1 = 1;   // F(m-1)
    int fibM = fibMMm2 + fibMMm1;  // F(m)

    while (fibM < n) {
        fibMMm2 = fibMMm1;
        fibMMm1 = fibM;
        fibM = fibMMm2 + fibMMm1;
    }

    int offset = -1;
```

```
    while (fibM > 1) {
        int i = min(offset + fibMMm2, n - 1);

        if (arr[i] < x) {
            fibM = fibMMm1;
            fibMMm1 = fibMMm2;
            fibMMm2 = fibM - fibMMm1;
            offset = i;
        } else if (arr[i] > x) {
            fibM = fibMMm2;
            fibMMm1 -= fibMMm2;
            fibMMm2 = fibM - fibMMm1;
        } else {
            return i;
        }
    }

    if (fibMMm1 && offset + 1 < n && arr[offset + 1] == x)
        return offset + 1;

    return -1;
}

int main(void) {
    int arr[] = {10, 22, 35, 40, 45, 50, 80, 82, 85, 90, 100};
    int n = sizeof(arr)/sizeof(arr[0]);
    int x = 85;
    int idx = fibonacci_search(arr, n, x);
    if (idx != -1)
        printf("Found at index: %d\n", idx);
    else
        printf("Not found\n");
}
```

Output:

```
Found at index: 8
```

Why It Matters

- Uses Fibonacci numbers to reduce comparisons

- Efficient for sorted arrays with sequential access
- Avoids division (only addition/subtraction)
- Inspired by golden ratio search (optimal probing)
- Excellent teaching tool for divide-and-conquer logic

A Gentle Proof (Why It Works)

The Fibonacci split maintains nearly golden ratio balance.
At each step, one subproblem has size $\frac{1}{\phi}$ of the previous.

So total steps number of Fibonacci numbers $\leq n$,
which grows as $O(\log_\phi n) \approx O(\log n)$.

Thus, the time complexity is the same as binary search,
but with fewer comparisons and more efficient arithmetic.

Try It Yourself

1. Search 45 in `[10, 22, 35, 40, 45, 50, 80, 82, 85, 90, 100]`
2. Search 100 (last element)
3. Search 10 (first element)
4. Search value not in array
5. Count comparisons made
6. Compare with binary search
7. Try on length = Fibonacci number (e.g. 13)
8. Visualize index jumps
9. Modify to print intervals
10. Apply to sorted strings (lex order)

Test Cases

Array	Target	Output	Notes
[10,22,35,40,45,50,80,82,85,90,100]	85	8	Found
[10,22,35,40,45]	22	1	Found
[1,2,3,5,8,13,21]	21	6	Found
[2,4,6,8,10]	7	-1	Not found

Complexity

Aspect	Value
Time	O(log n)
Space	O(1)
Comparisons	log (n)
Access type	Sequential-friendly
Requires sorted input	Yes

Fibonacci Search, a golden search for discrete worlds, where each step follows nature's rhythm.

170 Jump + Binary Hybrid

Jump + Binary Hybrid Search blends the best of two worlds, Jump Search for fast skipping and Binary Search for precise refinement. It's perfect when your data is sorted, and you want a balance between linear jumps and logarithmic probing within small subranges.

What Problem Are We Solving?

Binary search is powerful but needs random access (you can jump anywhere). Jump search works well for sequential data (like linked blocks or caches) but may overshoot.

This hybrid combines them:

1. Jump ahead in fixed steps to find the block.
2. Once you know the target range, switch to binary search inside it.

It's a practical approach for sorted datasets with limited random access (like disk blocks or database pages).

Example

Search for `45` in `[10, 22, 35, 40, 45, 50, 80, 82, 85, 90, 100]`.

Step 1: Jump by block size $\sqrt{n} = 3$

- Check `arr[2] = 35` $\rightarrow 35 < 45$
- Check `arr[5] = 50` $\rightarrow 50 > 45$

Now we know target is in `[35, 40, 45, 50)` $\rightarrow$ indices [3..5)

Step 2: Binary search within block [3..5)

- Mid = 4 $\rightarrow$ arr[4] = 45 Found!

How Does It Work (Plain Language)?

1. Choose block size $m = \sqrt{n}$.
2. Jump ahead by m until you pass or reach the target.
3. Once in the block, switch to binary search inside.

Jumping narrows the search zone quickly, Binary search finishes it cleanly, fewer comparisons than either alone.

Step-by-Step Process

Step	Description
1	Compute block size $m = \lfloor \sqrt{n} \rfloor$
2	Jump by m until `arr[j]` `target` or end
3	Determine block $[j - m, j)$
4	Run binary search inside that block
5	Return index or -1 if not found

Tiny Code (Easy Versions)

Python

```
import math

def jump_binary_search(arr, x):
    n = len(arr)
    step = int(math.sqrt(n))
    prev = 0

    # Jump phase
    while prev < n and arr[min(step, n) - 1] < x:
        prev = step
        step += int(math.sqrt(n))
        if prev >= n:
            return -1

    # Binary search in block
```

```
    low, high = prev, min(step, n) - 1
    while low <= high:
        mid = (low + high) // 2
        if arr[mid] == x:
            return mid
        elif arr[mid] < x:
            low = mid + 1
        else:
            high = mid - 1

    return -1

arr = [10, 22, 35, 40, 45, 50, 80, 82, 85, 90, 100]
print("Found at index:", jump_binary_search(arr, 45))
```

Output:

```
Found at index: 4
```

C

```
#include <stdio.h>
#include <math.h>

int jump_binary_search(int arr[], int n, int x) {
    int step = (int)sqrt(n);
    int prev = 0;

    // Jump phase
    while (prev < n && arr[(step < n ? step : n) - 1] < x) {
        prev = step;
        step += (int)sqrt(n);
        if (prev >= n)
            return -1;
    }

    // Binary search in block
    int low = prev;
    int high = (step < n ? step : n) - 1;
```

```
    while (low <= high) {
        int mid = low + (high - low) / 2;
        if (arr[mid] == x)
            return mid;
        else if (arr[mid] < x)
            low = mid + 1;
        else
            high = mid - 1;
    }

    return -1;
}

int main(void) {
    int arr[] = {10, 22, 35, 40, 45, 50, 80, 82, 85, 90, 100};
    int n = sizeof(arr) / sizeof(arr[0]);
    int idx = jump_binary_search(arr, n, 45);
    if (idx != -1)
        printf("Found at index: %d\n", idx);
    else
        printf("Not found\n");
}
```

Output:

```
Found at index: 4
```

Why It Matters

- Combines fast skipping (jump) and efficient narrowing (binary)
- Works well on sorted lists with slow access
- Reduces comparisons vs pure jump or linear
- Great for block-based storage and database indexing
- Demonstrates hybrid thinking in algorithm design

A Gentle Proof (Why It Works)

Jump phase: $O(\sqrt{n})$ steps
Binary phase: $O(\log \sqrt{n}) = O(\log n)$

Total:

$$T(n) = O(\sqrt{n}) + O(\log n)$$

For large n, dominated by $O(\sqrt{n})$, but faster in practice.

Try It Yourself

1. Search `80` in `[10,22,35,40,45,50,80,82,85,90,100]`
2. Try `10` (first element)
3. Try `100` (last element)
4. Try value not in array
5. Compare comparisons with binary search
6. Change block size (try 2√n or n/4)
7. Print jumps and block
8. Run on array of length 100
9. Combine with exponential block discovery
10. Extend for descending arrays

Test Cases

Array	Target	Output	Notes
[10,22,35,40,45,50,80,82,85,90,100]	45	4	Found
[10,22,35,40,45]	10	0	Found at start
[10,22,35,40,45]	100	-1	Not found
[1,3,5,7,9,11,13]	7	3	Found in middle

Complexity

Aspect	Value
Time	O(√n + log n)
Space	O(1)
Requires sorted	Yes
Stable	Yes
Adaptive	No

Jump + Binary Hybrid, leap with purpose, then zero in. It's how explorers search with both speed and focus.

Section 18. Selection Algorithms

171 Quickselect

Quickselect is a selection algorithm to find the k-th smallest element in an unsorted array — faster on average than sorting the entire array.

It's based on the same partitioning idea as Quicksort, but only recurses into the side that contains the desired element.

Average time complexity: O(n) Worst-case (rare): $O(n^2)$

What Problem Are We Solving?

Suppose you have an unsorted list and you want:

- The median,
- The k-th smallest, or
- The k-th largest element,

You don't need to fully sort, you just need one order statistic.

Quickselect solves this by partitioning the array and narrowing focus to the relevant half only.

Example

Find 4th smallest element in: `[7, 2, 1, 6, 8, 5, 3, 4]`

1. Choose pivot (e.g. 4).
2. Partition → `[2, 1, 3] [4] [7, 6, 8, 5]`
3. Pivot position = 3 (0-based)
4. k = 4 → pivot index 3 matches → 4 is 4th smallest

No need to sort the rest!

How Does It Work (Plain Language)?

Quickselect picks a pivot, partitions the list into less-than and greater-than parts, and decides which side to recurse into based on the pivot's index vs. target `k`.

It's a divide and conquer search on positions, not order.

Step-by-Step Process

Step	Description
1	Pick pivot (random or last element)
2	Partition array around pivot
3	Get pivot index `p`
4	If `p == k`, return element
5	If `p > k`, search left
6	If `p < k`, search right (adjust k)

Tiny Code (Easy Versions)

Python

```python
import random

def partition(arr, low, high):
    pivot = arr[high]
    i = low
    for j in range(low, high):
        if arr[j] < pivot:
            arr[i], arr[j] = arr[j], arr[i]
            i += 1
    arr[i], arr[high] = arr[high], arr[i]
    return i

def quickselect(arr, k):
    low, high = 0, len(arr) - 1
    while low <= high:
        pivot_index = partition(arr, low, high)
        if pivot_index == k:
            return arr[pivot_index]
```

```
        elif pivot_index > k:
            high = pivot_index - 1
        else:
            low = pivot_index + 1

arr = [7, 2, 1, 6, 8, 5, 3, 4]
k = 3  # 0-based index: 4th smallest
print("4th smallest:", quickselect(arr, k))
```

Output:

```
4th smallest: 4
```

C

```
#include <stdio.h>

void swap(int *a, int *b) {
    int t = *a;
    *a = *b;
    *b = t;
}

int partition(int arr[], int low, int high) {
    int pivot = arr[high];
    int i = low;
    for (int j = low; j < high; j++) {
        if (arr[j] < pivot) {
            swap(&arr[i], &arr[j]);
            i++;
        }
    }
    swap(&arr[i], &arr[high]);
    return i;
}

int quickselect(int arr[], int low, int high, int k) {
    if (low <= high) {
        int pi = partition(arr, low, high);
        if (pi == k)
```

```c
            return arr[pi];
        else if (pi > k)
            return quickselect(arr, low, pi - 1, k);
        else
            return quickselect(arr, pi + 1, high, k);
    }
    return -1;
}

int main(void) {
    int arr[] = {7, 2, 1, 6, 8, 5, 3, 4};
    int n = sizeof(arr) / sizeof(arr[0]);
    int k = 3;  // 4th smallest (0-based)
    printf("4th smallest: %d\n", quickselect(arr, 0, n - 1, k));
}
```

Output:

```
4th smallest: 4
```

Why It Matters

- Find median in linear time (expected)
- Avoid sorting when you only need one element
- Basis for algorithms like Median of Medians, BFPRT
- Common in order statistics, quantiles, top-k problems
- Used in libraries (e.g. `nth_element` in C++)

A Gentle Proof (Why It Works)

Each partition reduces problem size by eliminating one side. Average split half $\rightarrow$ O(n) expected comparisons. Worst case (bad pivot) $\rightarrow$ $O(n^2)$, but with randomized pivot, very unlikely.

Expected time:

$$T(n) = T(n/2) + O(n) \Rightarrow O(n)$$

Try It Yourself

1. Find 1st smallest (min)
2. Find last (max)
3. Find median (`k = n/2`)
4. Add random pivoting
5. Count comparisons per iteration
6. Modify for k-th largest (`n-k`)
7. Compare runtime with full sort
8. Visualize partition steps
9. Test on repeated elements
10. Combine with deterministic pivot

Test Cases

Array	k (0-based)	Output	Notes
[7,2,1,6,8,5,3,4]	3	4	4th smallest
[3,1,2]	1	2	median
[10,80,30,90,40,50,70]	4	70	middle element
[5,5,5,5]	2	5	duplicates

Complexity

Aspect	Value
Time (Average)	O(n)
Time (Worst)	$O(n^2)$
Space	O(1)
Stable	No
In-place	Yes
Randomized	Recommended

Quickselect, the surgical strike of sorting: find exactly what you need, and ignore the rest.

172 Median of Medians

Median of Medians is a deterministic selection algorithm that guarantees O(n) worst-case time for finding the k-th smallest element. It improves on Quickselect, which can degrade to (O(n^2)) in unlucky cases, by carefully choosing a good pivot every time.

It's a cornerstone of theoretical computer science, balancing speed and worst-case safety.

What Problem Are We Solving?

In Quickselect, a bad pivot can lead to unbalanced partitions (like always picking smallest/largest). Median of Medians fixes this by ensuring the pivot is "good enough" — always splitting the array so that each side has at least a constant fraction of elements.

Goal: Find the k-th smallest element deterministically in O(n), no randomness, no risk.

Example

Find 5th smallest in `[12, 3, 5, 7, 4, 19, 26, 23, 8, 15]`

1. Split into groups of 5: `[12, 3, 5, 7, 4]`, `[19, 26, 23, 8, 15]`
2. Sort each group: `[3,4,5,7,12]`, `[8,15,19,23,26]`
3. Take medians: `[5, 19]`
4. Find median of medians: `19`
5. Partition array around `19`
6. Recurse on appropriate side until k-th found

Pivot `19` ensures balanced split, leading to linear runtime.

How Does It Work (Plain Language)?

1. Break array into groups of 5
2. Sort each small group (cheap)
3. Collect all medians of groups
4. Recursively find median of those medians → good pivot
5. Partition around pivot
6. Recurse into half that contains the k-th element

Each level discards a constant fraction → (O(n)) total work.

Step	Description

Step-by-Step Process

Step	Description
1	Divide array into chunks of 5
2	Sort each chunk
3	Extract medians
4	Find median of medians recursively
5	Partition using this pivot
6	Recurse into correct side based on k

Tiny Code (Easy Versions)

Python

```python
def partition(arr, pivot):
    less = [x for x in arr if x < pivot]
    equal = [x for x in arr if x == pivot]
    greater = [x for x in arr if x > pivot]
    return less, equal, greater

def select(arr, k):
    if len(arr) <= 5:
        return sorted(arr)[k]

    # Step 1: group in chunks of 5
    chunks = [arr[i:i+5] for i in range(0, len(arr), 5)]

    # Step 2: find medians
    medians = [sorted(chunk)[len(chunk)//2] for chunk in chunks]

    # Step 3: pivot = median of medians
    pivot = select(medians, len(medians)//2)

    # Step 4: partition
    less, equal, greater = partition(arr, pivot)
```

```
    # Step 5: recurse
    if k < len(less):
        return select(less, k)
    elif k < len(less) + len(equal):
        return pivot
    else:
        return select(greater, k - len(less) - len(equal))

arr = [12, 3, 5, 7, 4, 19, 26, 23, 8, 15]
k = 4  # 0-based: 5th smallest
print("5th smallest:", select(arr, k))
```

Output:

```
5th smallest: 8
```

C (Simplified Version)

(Pseudocode-like clarity for readability)

```
#include <stdio.h>
#include <stdlib.h>

int cmp(const void* a, const void* b) {
    return (*(int*)a - *(int*)b);
}

int median_of_medians(int arr[], int n, int k);

int select_group_median(int arr[], int n) {
    qsort(arr, n, sizeof(int), cmp);
    return arr[n/2];
}

int median_of_medians(int arr[], int n, int k) {
    if (n <= 5) {
        qsort(arr, n, sizeof(int), cmp);
        return arr[k];
    }

    int groups = (n + 4) / 5;
```

```
    int medians[groups];
    for (int i = 0; i < groups; i++) {
        int size = (i*5 + 5 <= n) ? 5 : n - i*5;
        medians[i] = select_group_median(arr + i*5, size);
    }

    int pivot = median_of_medians(medians, groups, groups/2);

    // Partition
    int less[n], greater[n], l = 0, g = 0, equal = 0;
    for (int i = 0; i < n; i++) {
        if (arr[i] < pivot) less[l++] = arr[i];
        else if (arr[i] > pivot) greater[g++] = arr[i];
        else equal++;
    }

    if (k < l)
        return median_of_medians(less, l, k);
    else if (k < l + equal)
        return pivot;
    else
        return median_of_medians(greater, g, k - l - equal);
}

int main(void) {
    int arr[] = {12, 3, 5, 7, 4, 19, 26, 23, 8, 15};
    int n = sizeof(arr)/sizeof(arr[0]);
    printf("5th smallest: %d\n", median_of_medians(arr, n, 4));
}
```

Output:

```
5th smallest: 8
```

Why It Matters

- Guaranteed O(n) even in worst case
- No bad pivots → stable performance
- Basis for BFPRT algorithm
- Used in theoretical guarantees for real systems
- Key for deterministic selection, safe quantile computations

A Gentle Proof (Why It Works)

Each pivot ensures at least 30% of elements are discarded each recursion (proof via grouping).

Recurrence:

$$T(n) = T(n/5) + T(7n/10) + O(n) \Rightarrow O(n)$$

Thus, always linear time, even worst case.

Try It Yourself

1. Find median of `[5, 2, 1, 3, 4]`
2. Test with duplicates
3. Compare with Quickselect runtime
4. Count recursive calls
5. Change group size to 3 or 7
6. Visualize grouping steps
7. Print pivot each round
8. Apply to large random list
9. Benchmark vs sorting
10. Implement as pivot strategy for Quickselect

Test Cases

Array	k	Output	Notes
[12,3,5,7,4,19,26,23,8,15]	4	8	5th smallest
[5,2,1,3,4]	2	3	Median
[7,7,7,7]	2	7	Duplicates
[10,9,8,7,6,5]	0	5	Min

Complexity

Aspect	Value
Time (Worst)	O(n)
Time (Avg)	O(n)
Space	O(n)
Stable	No
Deterministic	Yes

Median of Medians, a balanced thinker in the world of selection: slow and steady, but always linear.

173 Randomized Select

Randomized Select is a probabilistic version of Quickselect, where the pivot is chosen randomly to avoid worst-case behavior. This small twist makes the algorithm's expected time O(n), even though the worst case remains (O(n^2)). In practice, it's fast, simple, and robust, a true workhorse for order statistics.

What Problem Are We Solving?

You need the k-th smallest element in an unsorted list. Quickselect works well, but choosing the first or last element as pivot can cause bad splits.

Randomized Select improves this by picking a random pivot, making bad luck rare and performance stable.

Example

Find 4th smallest in `[7, 2, 1, 6, 8, 5, 3, 4]`

1. Pick random pivot (say `5`)
2. Partition → `[2,1,3,4]` `[5]` `[7,6,8]`
3. Pivot index = 4 → 4 > 3, so recurse on left `[2,1,3,4]`
4. Pick random pivot again (say `3`)
5. Partition → `[2,1]` `[3]` `[4]`
6. Index 2 = k=3 → found 4th smallest = 4

How Does It Work (Plain Language)?

It's Quickselect with random pivoting. At each step:

- Pick a random element as pivot.
- Partition around pivot.
- Only recurse into one side (where k lies).

This randomness ensures average-case balance, even on adversarial inputs.

Step-by-Step Process

Step	Description
1	Pick random pivot index
2	Partition array around pivot
3	Get pivot index `p`
4	If `p == k`, return element
5	If `p > k`, recurse left
6	If `p < k`, recurse right (adjust k)

Tiny Code (Easy Versions)

Python

```python
import random

def partition(arr, low, high):
    pivot = arr[high]
    i = low
    for j in range(low, high):
        if arr[j] < pivot:
            arr[i], arr[j] = arr[j], arr[i]
            i += 1
    arr[i], arr[high] = arr[high], arr[i]
    return i

def randomized_select(arr, low, high, k):
    if low == high:
        return arr[low]

    pivot_index = random.randint(low, high)
    arr[pivot_index], arr[high] = arr[high], arr[pivot_index]

    p = partition(arr, low, high)

    if p == k:
        return arr[p]
    elif p > k:
        return randomized_select(arr, low, p - 1, k)
```

```
    else:
        return randomized_select(arr, p + 1, high, k)

arr = [7, 2, 1, 6, 8, 5, 3, 4]
k = 3  # 4th smallest
print("4th smallest:", randomized_select(arr, 0, len(arr)-1, k))
```

Output:

```
4th smallest: 4
```

C

```
#include <stdio.h>
#include <stdlib.h>
#include <time.h>

void swap(int *a, int *b) {
    int t = *a; *a = *b; *b = t;
}

int partition(int arr[], int low, int high) {
    int pivot = arr[high];
    int i = low;
    for (int j = low; j < high; j++) {
        if (arr[j] < pivot) {
            swap(&arr[i], &arr[j]);
            i++;
        }
    }
    swap(&arr[i], &arr[high]);
    return i;
}

int randomized_select(int arr[], int low, int high, int k) {
    if (low == high) return arr[low];

    int pivot_index = low + rand() % (high - low + 1);
    swap(&arr[pivot_index], &arr[high]);
    int p = partition(arr, low, high);
```

```
    if (p == k) return arr[p];
    else if (p > k) return randomized_select(arr, low, p - 1, k);
    else return randomized_select(arr, p + 1, high, k);
}

int main(void) {
    srand(time(NULL));
    int arr[] = {7, 2, 1, 6, 8, 5, 3, 4};
    int n = sizeof(arr)/sizeof(arr[0]);
    int k = 3;
    printf("4th smallest: %d\n", randomized_select(arr, 0, n - 1, k));
}
```

Output:

```
4th smallest: 4
```

Why It Matters

- Expected O(n) time, simple, and practical
- Avoids worst-case trap of fixed-pivot Quickselect
- Great for top-k queries, quantiles, median
- Combines simplicity + randomness = robust performance
- Commonly used in competitive programming and real-world systems

A Gentle Proof (Why It Works)

Expected recurrence:

$$T(n) = T(\alpha n) + O(n)$$

where α is random, expected $\approx \frac{1}{2}$
$\to T(n) = O(n)$

Worst case still $O(n^2)$, but rare.
Expected comparisons $\approx 2n$.

Try It Yourself

1. Run multiple times and observe pivot randomness
2. Compare with deterministic Quickselect
3. Count recursive calls
4. Test with sorted input (robust)
5. Test all same elements
6. Change k (first, median, last)
7. Modify to find k-th largest (`n-k-1`)
8. Compare performance with sort()
9. Log pivot indices
10. Measure runtime on 10 elements

Test Cases

Array	k	Output	Notes
[7,2,1,6,8,5,3,4]	3	4	4th smallest
[10,80,30,90,40,50,70]	4	70	Works on any order
[1,2,3,4,5]	0	1	Sorted input safe
[5,5,5,5]	2	5	Duplicates fine

Complexity

Aspect	Value
Time (Expected)	O(n)
Time (Worst)	$O(n^2)$
Space	O(1)
Stable	No
Randomized	Yes
In-place	Yes

Randomized Select, a game of chance that almost always wins: fast, fair, and beautifully simple.

174 Binary Search on Answer

Binary Search on Answer (also called Parametric Search) is a powerful optimization trick used when the search space is monotonic—meaning once a condition becomes true, it stays true (or

vice versa). Instead of searching a sorted array, we're searching for the smallest or largest value that satisfies a condition.

What Problem Are We Solving?

Sometimes you don't have an array to search, but you need to minimize or maximize a numeric answer. Examples:

- Minimum capacity to transport items in `k` days
- Minimum maximum distance between routers
- Maximum median satisfying a condition

We can't iterate all possibilities efficiently, but we can binary search the answer space.

Example

Problem: Given array `[1, 2, 3, 4, 5]`, split into `2` parts, minimize the largest sum among parts.

We can't directly find it, but if we can check whether a candidate value `mid` is valid (can split with sum mid), we can binary search on `mid`.

mid	canSplit(nums, 2, mid)	Result
9	True (splits: [1,2,3,4], [5])	ok → move left
7	False	move right
8	True	ok → final answer = 9

Result = 9

How Does It Work (Plain Language)?

You don't search elements, you search values. You define a function `can(mid)` that checks if a solution is possible with `mid`. Then use binary search to narrow down the range until you find the optimal value.

Step-by-Step Process

Step	Description
1	Define the range of answers (lo, hi)
2	While lo < hi: mid = (lo + hi) // 2 If can(mid): hi = mid Else: lo = mid + 1
3	Return lo as the optimal answer

Tiny Code (Easy Versions)

Python

```
def can_split(nums, k, mid):
    count, current = 1, 0
    for x in nums:
        if current + x > mid:
            count += 1
            current = x
        else:
            current += x
    return count <= k

def binary_search_answer(nums, k):
    lo, hi = max(nums), sum(nums)
    while lo < hi:
        mid = (lo + hi) // 2
        if can_split(nums, k, mid):
            hi = mid
        else:
            lo = mid + 1
    return lo

nums = [1, 2, 3, 4, 5]
k = 2
print("Minimum largest sum:", binary_search_answer(nums, k))
```

Output:

```
Minimum largest sum: 9
```

C

```c
#include <stdio.h>

int can_split(int arr[], int n, int k, int mid) {
    int count = 1, sum = 0;
    for (int i = 0; i < n; i++) {
        if (arr[i] > mid) return 0;
        if (sum + arr[i] > mid) {
            count++;
            sum = arr[i];
        } else {
            sum += arr[i];
        }
    }
    return count <= k;
}

int binary_search_answer(int arr[], int n, int k) {
    int lo = arr[0], hi = 0;
    for (int i = 0; i < n; i++) {
        if (arr[i] > lo) lo = arr[i];
        hi += arr[i];
    }
    while (lo < hi) {
        int mid = (lo + hi) / 2;
        if (can_split(arr, n, k, mid))
            hi = mid;
        else
            lo = mid + 1;
    }
    return lo;
}

int main(void) {
    int arr[] = {1, 2, 3, 4, 5};
    int n = sizeof(arr)/sizeof(arr[0]);
    int k = 2;
    printf("Minimum largest sum: %d\n", binary_search_answer(arr, n, k));
}
```

Output:

```
Minimum largest sum: 9
```

Why It Matters

- Solves optimization problems without brute force
- Turns decision problems into search problems
- A universal pattern: works for capacity, distance, time, etc.
- Common in LeetCode, interviews, and competitive programming

A Gentle Proof (Why It Works)

If a function `f(x)` is monotonic (true after a point or false after a point), binary search can find the threshold. Formally:

If `f(lo) = false`, `f(hi) = true`, and `f(x)` is monotonic, then binary search converges to smallest x such that f(x) = true.

Try It Yourself

1. Find smallest capacity to ship packages in `d` days
2. Find smallest max page load per student (book allocation)
3. Find largest minimum distance between routers
4. Find smallest time to paint all boards
5. Find minimum speed to reach on time
6. Define a monotonic function `can(x)` and apply search
7. Experiment with `float` range and tolerance
8. Try max instead of min (reverse condition)
9. Count binary search steps for each case
10. Compare with brute force

Test Cases

Problem	Input	Output	Explanation
Split array	[1,2,3,4,5], k=2	9	[1,2,3,4],[5]
Book allocation	[10,20,30,40], k=2	60	[10,20,30],[40]
Router placement	[1,2,8,12], k=3	5	Place at 1,6,12

Complexity

Aspect	Value
Time	O(n log(max - min))
Space	O(1)
Monotonicity Required	Yes
Type	Decision-based binary search

Binary Search on Answer, when you can't sort the data, sort the solution space.

175 Order Statistics Tree

An Order Statistics Tree is a special kind of augmented binary search tree (BST) that supports two powerful operations efficiently:

1. Select(k): find the k-th smallest element.
2. Rank(x): find the position (rank) of element `x`.

It's a classic data structure where each node stores subtree size, allowing order-based queries in O(log n) time.

What Problem Are We Solving?

Sometimes you don't just want to search by key, you want to search by order. For example:

- "What's the 5th smallest element?"
- "What rank is 37 in the tree?"
- "How many numbers 50 are there?"

An order statistics tree gives you both key-based and rank-based access in one structure.

Example

Suppose you insert `[20, 15, 25, 10, 18, 22, 30]`.

Each node stores `size` (the number of nodes in its subtree).

```
        20(size=7)
       /          \
  15(3)           25(3)
  /   \           /   \
10(1) 18(1)   22(1) 30(1)
```

Select(4) → 20 (the 4th smallest) Rank(22) → 6 (22 is the 6th smallest)

How Does It Work (Plain Language)?

Every node tracks how many nodes exist in its subtree (left + right + itself). When you traverse:

- To select k-th smallest, compare `k` with size of left subtree.
- To find rank of x, accumulate sizes while traversing down.

Select(k) Pseudocode

```
select(node, k):
    left_size = size(node.left)
    if k == left_size + 1: return node.key
    if k <= left_size: return select(node.left, k)
    else: return select(node.right, k - left_size - 1)
```

Rank(x) Pseudocode

```
rank(node, x):
    if node == NULL: return 0
    if x < node.key: return rank(node.left, x)
    if x == node.key: return size(node.left) + 1
    else: return size(node.left) + 1 + rank(node.right, x)
```

Tiny Code (Easy Versions)

Python

```
class Node:
    def __init__(self, key):
        self.key = key
        self.left = None
        self.right = None
        self.size = 1

def update_size(node):
    if node:
        node.size = 1 + (node.left.size if node.left else 0) + (node.right.size if node.right

def insert(node, key):
    if node is None:
        return Node(key)
    if key < node.key:
        node.left = insert(node.left, key)
    else:
        node.right = insert(node.right, key)
    update_size(node)
    return node

def select(node, k):
    left_size = node.left.size if node.left else 0
    if k == left_size + 1:
        return node.key
    elif k <= left_size:
        return select(node.left, k)
    else:
        return select(node.right, k - left_size - 1)

def rank(node, key):
    if node is None:
        return 0
    if key < node.key:
        return rank(node.left, key)
    elif key == node.key:
        return (node.left.size if node.left else 0) + 1
    else:
        left_size = node.left.size if node.left else 0
        return left_size + 1 + rank(node.right, key)

root = None
```

```python
for x in [20, 15, 25, 10, 18, 22, 30]:
    root = insert(root, x)

print("Select(4):", select(root, 4))  # 20
print("Rank(22):", rank(root, 22))    # 6
```

C (Conceptual Skeleton)

```c
typedef struct Node {
    int key;
    int size;
    struct Node *left, *right;
} Node;

int size(Node* n) { return n ? n->size : 0; }

void update_size(Node* n) {
    if (n) n->size = 1 + size(n->left) + size(n->right);
}

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key; n->size = 1;
    n->left = n->right = NULL;
    return n;
}

Node* insert(Node* root, int key) {
    if (!root) return new_node(key);
    if (key < root->key) root->left = insert(root->left, key);
    else root->right = insert(root->right, key);
    update_size(root);
    return root;
}

int select_k(Node* root, int k) {
    int left_size = size(root->left);
    if (k == left_size + 1) return root->key;
    else if (k <= left_size) return select_k(root->left, k);
```

```
    else return select_k(root->right, k - left_size - 1);
}
```

Why It Matters

- Useful in rank-based queries, median finding, and order-statistics problems
- Core to balanced trees (AVL, Red-Black, Treaps) with order augmentation
- Enables dynamic median queries and range counting

You can imagine it as a self-updating leaderboard, always knowing who's in position `k`.

A Gentle Proof (Why It Works)

Because subtree sizes are updated correctly on insertions/deletions, each traversal can compute ranks or k-th values in O(log n) time (in balanced trees). If balanced (like in an AVL or RB-tree), operations remain logarithmic.

Try It Yourself

1. Build an Order Statistics Tree for `[10,20,30,40,50]`.
2. Find `Select(3)` and `Rank(40)`.
3. Insert new elements and recheck ranks.
4. Extend to find median dynamically.
5. Modify to support deletions.
6. Compare with sorting then indexing (O(n log n) vs O(log n)).
7. Try building on top of Red-Black Tree.
8. Use for running percentiles.
9. Explore dynamic segment trees for same queries.
10. Implement `countLessThan(x)` using rank.

Test Cases

Query	Expected Result
Select(1)	10
Select(4)	20
Rank(10)	1
Rank(22)	6
Rank(30)	7

Complexity

Operation	Complexity
Insert / Delete	O(log n)
Select(k)	O(log n)
Rank(x)	O(log n)
Space	O(n)

An Order Statistics Tree blends search and ranking, perfect for problems that need to know *what* and *where* at the same time.

176 Tournament Tree Selection

A Tournament Tree is a binary tree structure that simulates a knockout tournament among elements. Each match compares two elements, and the winner moves up. It's an elegant way to find minimum, maximum, or even k-th smallest elements with structured comparisons.

What Problem Are We Solving?

Finding the minimum or maximum in a list takes O(n). But if you also want the second smallest, third smallest, or k-th, you'd like to reuse earlier comparisons. A tournament tree keeps track of all matches, so you don't need to start over.

Example

Suppose we have elements: `[4, 7, 2, 9, 5, 1, 8, 6]`.

1. Pair them up: compare (4,7), (2,9), (5,1), (8,6)
2. Winners move up: [4, 2, 1, 6]
3. Next round: (4,2), (1,6) → winners [2, 1]
4. Final match: (2,1) → winner 1

The root of the tree = minimum element (1).

If you store the losing element from each match, you can trace back the second smallest, it must have lost directly to 1.

How Does It Work (Plain Language)?

Imagine a sports tournament:

- Every player plays one match.
- The winner moves on, loser is eliminated.
- The champion (root) is the smallest element.
- The second smallest is the best among those who lost to the champion.

Each match is one comparison, so total comparisons = n - 1 for the min. To find second min, check log n losers.

Steps

Step	Description
1	Build a complete binary tree where each leaf is an element.
2	Compare each pair and move winner up.
3	Store "losers" in each node.
4	The root = min. The second min = min(losers along winner's path).

Tiny Code (Easy Versions)

Python

```
def tournament_min(arr):
    matches = []
    tree = [[x] for x in arr]
    while len(tree) > 1:
        next_round = []
        for i in range(0, len(tree), 2):
            if i + 1 == len(tree):
                next_round.append(tree[i])
                continue
            a, b = tree[i][0], tree[i+1][0]
            if a < b:
                next_round.append([a, b])
            else:
                next_round.append([b, a])
        matches = next_round
```

```
        tree = next_round
    return tree[0][0]

def find_second_min(arr):
    # Build tournament, keep track of losers
    n = len(arr)
    tree = [[x, []] for x in arr]
    while len(tree) > 1:
        next_round = []
        for i in range(0, len(tree), 2):
            if i + 1 == len(tree):
                next_round.append(tree[i])
                continue
            a, a_losers = tree[i]
            b, b_losers = tree[i+1]
            if a < b:
                next_round.append([a, a_losers + [b]])
            else:
                next_round.append([b, b_losers + [a]])
        tree = next_round
    winner, losers = tree[0]
    return winner, min(losers)

arr = [4, 7, 2, 9, 5, 1, 8, 6]
min_val, second_min = find_second_min(arr)
print("Min:", min_val)
print("Second Min:", second_min)
```

Output:

```
Min: 1
Second Min: 2
```

C

```
#include <stdio.h>
#include <limits.h>

int tournament_min(int arr[], int n) {
    int size = n;
```

```
    while (size > 1) {
        for (int i = 0; i < size / 2; i++) {
            arr[i] = (arr[2*i] < arr[2*i + 1]) ? arr[2*i] : arr[2*i + 1];
        }
        size = (size + 1) / 2;
    }
    return arr[0];
}

int main(void) {
    int arr[] = {4, 7, 2, 9, 5, 1, 8, 6};
    int n = sizeof(arr) / sizeof(arr[0]);
    printf("Minimum: %d\n", tournament_min(arr, n));
}
```

Why It Matters

- Finds minimum in O(n), second minimum in O(n + log n) comparisons
- Reusable for k-th selection if you store all match info
- Forms the backbone of selection networks, parallel sorting, and merge tournaments

A Gentle Proof (Why It Works)

Each element except the minimum loses exactly once. The minimum element competes in log n matches (height of tree). So second minimum must be the smallest of log n losers, requiring log n extra comparisons.

Total = n - 1 + log n comparisons, asymptotically optimal.

Try It Yourself

1. Build a tournament for `[5,3,8,2,9,4]`.
2. Find minimum and second minimum manually.
3. Modify code to find maximum and second maximum.
4. Print tree rounds to visualize matches.
5. Experiment with uneven sizes (non-power-of-2).
6. Try to extend it to third smallest (hint: store paths).
7. Compare with sorting-based approach.
8. Use tournament structure for pairwise elimination problems.
9. Simulate sports bracket winner path.
10. Count comparisons for each step.

Test Cases

Input	Min	Second Min
[4,7,2,9,5,1,8,6]	1	2
[10,3,6,2]	2	3
[5,4,3,2,1]	1	2

Complexity

Operation	Complexity
Build Tournament	O(n)
Find Minimum	O(1)
Find Second Minimum	O(log n)
Space	O(n)

A Tournament Tree turns comparisons into matches, where every element plays once, and the champion reveals not just victory, but the story of every defeat.

177 Heap Select (Min-Heap)

Heap Select is a simple, powerful technique for finding the k smallest (or largest) elements in a collection using a heap. It's one of the most practical selection algorithms, trading minimal code for strong efficiency.

What Problem Are We Solving?

You often don't need a full sort, just the k smallest or k largest items. Examples:

- Find top 10 scores
- Get smallest 5 distances
- Maintain top-k trending topics

A heap (priority queue) makes this easy, keep a running set of size `k`, pop or push as needed.

Example

Find 3 smallest elements in `[7, 2, 9, 1, 5, 4]`.

1. Create max-heap of first `k=3` elements → `[7, 2, 9]` → heap = [9, 2, 7]
2. For each next element:
   - $1 < 9 \rightarrow$ pop 9, push 1 → heap = [7, 2, 1]
   - $5 < 7 \rightarrow$ pop 7, push 5 → heap = [5, 2, 1]
   - $4 < 5 \rightarrow$ pop 5, push 4 → heap = [4, 2, 1]

Result → `[1, 2, 4]` (the 3 smallest)

How Does It Work (Plain Language)?

You keep a heap of size k:

- For smallest elements → use a max-heap (remove largest if new smaller appears).
- For largest elements → use a min-heap (remove smallest if new larger appears).

This keeps only the top-k interesting values at all times.

Step-by-Step Process

Step	Action
1	Initialize heap with first k elements
2	Convert to max-heap (if looking for smallest k)
3	For each remaining element x: If x < heap[0] → replace top
4	Result is heap contents (unsorted)
5	Sort heap if needed for final output

Tiny Code (Easy Versions)

Python

```python
import heapq

def k_smallest(nums, k):
    heap = [-x for x in nums[:k]]
    heapq.heapify(heap)
    for x in nums[k:]:
        if -x > heap[0]:
            heapq.heappop(heap)
            heapq.heappush(heap, -x)
    return sorted([-h for h in heap])

nums = [7, 2, 9, 1, 5, 4]
print("3 smallest:", k_smallest(nums, 3))
```

Output:

```
3 smallest: [1, 2, 4]
```

C

```c
#include <stdio.h>
#include <stdlib.h>

void swap(int *a, int *b) { int t = *a; *a = *b; *b = t; }

void heapify(int arr[], int n, int i) {
    int largest = i, l = 2*i+1, r = 2*i+2;
    if (l < n && arr[l] > arr[largest]) largest = l;
    if (r < n && arr[r] > arr[largest]) largest = r;
    if (largest != i) {
        swap(&arr[i], &arr[largest]);
        heapify(arr, n, largest);
    }
}

void build_heap(int arr[], int n) {
    for (int i = n/2 - 1; i >= 0; i--) heapify(arr, n, i);
}

void heap_select(int arr[], int n, int k) {
```

```
    int heap[k];
    for (int i = 0; i < k; i++) heap[i] = arr[i];
    build_heap(heap, k);
    for (int i = k; i < n; i++) {
        if (arr[i] < heap[0]) {
            heap[0] = arr[i];
            heapify(heap, k, 0);
        }
    }
    printf("%d smallest elements:\n", k);
    for (int i = 0; i < k; i++) printf("%d ", heap[i]);
}

int main(void) {
    int arr[] = {7, 2, 9, 1, 5, 4};
    int n = 6;
    heap_select(arr, n, 3);
}
```

Output:

```
3 smallest elements:
1 2 4
```

Why It Matters

- Avoids full sorting (O(n log n))
- Great for streaming data, sliding windows, top-k problems
- Scales well for large `n` and small `k`
- Used in leaderboards, analytics, data pipelines

If you only need *some* order, don't sort it all.

A Gentle Proof (Why It Works)

- Building heap: O(k)
- For each new element: compare + heapify = O(log k)
- Total: O(k + (n-k) log k) O(n log k)

For small `k`, this is much faster than sorting.

Try It Yourself

1. Find 3 largest elements using min-heap
2. Stream numbers from input, maintain smallest 5
3. Track top 10 scores dynamically
4. Compare runtime vs `sorted(nums)[:k]`
5. Try `k = 1` (minimum), `k = n` (full sort)
6. Modify for objects with custom keys (e.g. score, id)
7. Handle duplicates, keep all or unique only
8. Experiment with random arrays of size 1e6
9. Visualize heap evolution per step
10. Combine with binary search to tune thresholds

Test Cases

Input	k	Output
[7,2,9,1,5,4]	3	[1,2,4]
[10,8,6,4,2]	2	[2,4]
[1,1,1,1]	2	[1,1]

Complexity

Operation	Complexity
Build Heap	O(k)
Iterate Array	O((n-k) log k)
Total Time	O(n log k)
Space	O(k)

Heap Select is your practical shortcut, sort only what you need, ignore the rest.

178 Partial QuickSort

Partial QuickSort is a twist on classic QuickSort, it stops sorting once it has placed the first k elements (or top k) in their correct positions. It's perfect when you need top-k smallest/largest elements but don't need the rest sorted.

Think of it as QuickSort with early stopping, a hybrid between QuickSort and Quickselect.

What Problem Are We Solving?

Sometimes you need only part of the sorted order:

- "Get top 10 scores"
- "Find smallest k elements"
- "Sort first half"

Fully sorting wastes work. Partial QuickSort skips unnecessary partitions.

Example

Array: `[9, 4, 6, 2, 8, 1]`, k = 3

We want smallest 3 elements. QuickSort picks a pivot, partitions array:

```
Pivot = 6
→ [4, 2, 1] | 6 | [9, 8]
```

Now we know all elements left of pivot (4, 2, 1) are smaller. Since `left_size == k`, we can stop, `[1,2,4]` are our smallest 3.

How Does It Work (Plain Language)?

Just like QuickSort, but after partition:

- If pivot index == k → done.
- If pivot index > k → recurse only left.
- If pivot index < k → recurse right partially.

You never sort beyond what's needed.

Step-by-Step Process

Step	Description
1	Choose pivot
2	Partition array
3	If pivot index == k → done
4	If pivot index > k → recurse left
5	Else recurse right on remaining portion

Tiny Code (Easy Versions)

Python

```
def partial_quicksort(arr, low, high, k):
    if low < high:
        p = partition(arr, low, high)
        if p > k:
            partial_quicksort(arr, low, p - 1, k)
        elif p < k:
            partial_quicksort(arr, low, p - 1, k)
            partial_quicksort(arr, p + 1, high, k)

def partition(arr, low, high):
    pivot = arr[high]
    i = low - 1
    for j in range(low, high):
        if arr[j] < pivot:
            i += 1
            arr[i], arr[j] = arr[j], arr[i]
    arr[i + 1], arr[high] = arr[high], arr[i + 1]
    return i + 1

arr = [9, 4, 6, 2, 8, 1]
k = 3
partial_quicksort(arr, 0, len(arr) - 1, k - 1)
print("Smallest 3 elements:", sorted(arr[:k]))
```

Output:

```
Smallest 3 elements: [1, 2, 4]
```

C

```
#include <stdio.h>

void swap(int *a, int *b) { int t = *a; *a = *b; *b = t; }

int partition(int arr[], int low, int high) {
```

```c
    int pivot = arr[high];
    int i = low - 1;
    for (int j = low; j < high; j++) {
        if (arr[j] < pivot) {
            i++;
            swap(&arr[i], &arr[j]);
        }
    }
    swap(&arr[i + 1], &arr[high]);
    return i + 1;
}

void partial_quicksort(int arr[], int low, int high, int k) {
    if (low < high) {
        int p = partition(arr, low, high);
        if (p > k)
            partial_quicksort(arr, low, p - 1, k);
        else if (p < k)
            partial_quicksort(arr, p + 1, high, k);
    }
}

int main(void) {
    int arr[] = {9, 4, 6, 2, 8, 1};
    int n = 6, k = 3;
    partial_quicksort(arr, 0, n - 1, k - 1);
    printf("Smallest %d elements:\n", k);
    for (int i = 0; i < k; i++) printf("%d ", arr[i]);
}
```

Output:

```
Smallest 3 elements:
1 2 4
```

Why It Matters

- Efficient top-k selection when order matters
- Avoids sorting unnecessary portions
- Combines strengths of Quickselect and QuickSort
- Works in-place (no extra memory)

Great for partial sorting like "leaderboards", "top results", or "bounded priority lists".

A Gentle Proof (Why It Works)

QuickSort partitions data into two halves; Only parts that could contain the first `k` elements are explored. Average time complexity becomes O(n) for selection, O(n log k) for partial order.

Try It Yourself

1. Find smallest 5 numbers in `[10,9,8,7,6,5,4,3,2,1]`
2. Modify to find largest k instead
3. Compare runtime vs full `sort()`
4. Visualize recursion path
5. Track how many elements actually get sorted
6. Try random pivot vs median pivot
7. Test k = 1 (min) and k = n (full sort)
8. Measure comparisons count
9. Try with duplicates
10. Combine with heap for hybrid version

Test Cases

Input	k	Output
[9,4,6,2,8,1]	3	[1,2,4]
[5,4,3,2,1]	2	[1,2]
[7,7,7,7]	2	[7,7]

Complexity

Aspect	Value
Average Time	O(n)
Worst Time	$O(n^2)$
Space	O(1)
Stable	No

Partial QuickSort, fast, focused, and frugal, because sometimes, you only need *a slice* of order, not the whole loaf.

179 BFPRT Algorithm (Median of Medians Selection)

The BFPRT algorithm (named after Blum, Floyd, Pratt, Rivest, and Tarjan) is a deterministic linear-time selection algorithm. It finds the k-th smallest element in an unsorted array, guaranteeing O(n) worst-case time, a mathematically elegant and exact alternative to randomized quickselect.

What Problem Are We Solving?

You want to find the k-th smallest element, like the median, but you don't want to gamble on random pivots (which could hit worst-case $O(n^2)$). BFPRT chooses pivots so well that it always guarantees O(n).

This makes it ideal for systems where deterministic behavior matters, like embedded systems, compilers, and real-time applications.

Example

Find the median (k=5) of `[9, 4, 7, 3, 6, 1, 8, 2, 5, 10]`

1. Divide into groups of 5: `[9,4,7,3,6]`, `[1,8,2,5,10]`
2. Find median of each group: → `[6, 5]`
3. Find median of medians: → median of `[6,5]` is 5.5 5
4. Partition around pivot 5 → `[4,3,1,2,5] | 5 | [9,7,8,6,10]`
5. Position of 5 = 5 → done.

The 5th smallest = 5

How Does It Work (Plain Language)?

It's Quickselect with a smarter pivot:

- Divide the array into groups of 5.
- Find median of each group.
- Recursively find median of these medians.
- Use that as pivot → partition → recurse on the correct side.

This ensures the pivot is *always good enough* to split the array reasonably, keeping recursion balanced.

Step-by-Step Summary

Step	Description
1	Split array into groups of 5
2	Sort each group and take its median
3	Recursively find median of medians
4	Partition around pivot
5	Recurse on side containing k-th smallest

Tiny Code (Easy Versions)

Python

```
def partition(arr, pivot):
    less, equal, greater = [], [], []
    for x in arr:
        if x < pivot: less.append(x)
        elif x > pivot: greater.append(x)
        else: equal.append(x)
    return less, equal, greater

def select(arr, k):
    if len(arr) <= 5:
        return sorted(arr)[k]

    # Step 1: Divide into groups of 5
    groups = [arr[i:i+5] for i in range(0, len(arr), 5)]

    # Step 2: Find medians
    medians = [sorted(g)[len(g)//2] for g in groups]

    # Step 3: Median of medians as pivot
    pivot = select(medians, len(medians)//2)

    # Step 4: Partition
    less, equal, greater = partition(arr, pivot)

    # Step 5: Recurse
    if k < len(less):
```

```
        return select(less, k)
    elif k < len(less) + len(equal):
        return pivot
    else:
        return select(greater, k - len(less) - len(equal))

arr = [9,4,7,3,6,1,8,2,5,10]
k = 4  # 0-based index → 5th smallest
print("5th smallest:", select(arr, k))
```

Output:

```
5th smallest: 5
```

C (Conceptual Skeleton)

```
#include <stdio.h>
#include <stdlib.h>

int cmp(const void *a, const void *b) { return (*(int*)a - *(int*)b); }

int median_of_medians(int arr[], int n);

int select_kth(int arr[], int n, int k) {
    if (n <= 5) {
        qsort(arr, n, sizeof(int), cmp);
        return arr[k];
    }

    int groups = (n + 4) / 5;
    int *medians = malloc(groups * sizeof(int));
    for (int i = 0; i < groups; i++) {
        int start = i * 5;
        int end = (start + 5 < n) ? start + 5 : n;
        qsort(arr + start, end - start, sizeof(int), cmp);
        medians[i] = arr[start + (end - start) / 2];
    }

    int pivot = median_of_medians(medians, groups);
    free(medians);
```

```
    int *left = malloc(n * sizeof(int));
    int *right = malloc(n * sizeof(int));
    int l = 0, r = 0, equal = 0;
    for (int i = 0; i < n; i++) {
        if (arr[i] < pivot) left[l++] = arr[i];
        else if (arr[i] > pivot) right[r++] = arr[i];
        else equal++;
    }

    if (k < l) return select_kth(left, l, k);
    else if (k < l + equal) return pivot;
    else return select_kth(right, r, k - l - equal);
}

int median_of_medians(int arr[], int n) {
    return select_kth(arr, n, n / 2);
}
```

Why It Matters

- Deterministic O(n), no randomness or bad pivots
- Used in theoretical CS, worst-case analysis, exact solvers
- Foundation for deterministic selection, median-finding, linear-time sorting bounds
- Core to intro algorithms theory (CLRS Chapter 9)

A Gentle Proof (Why It Works)

- Each group of 5 → median is 3 elements in group (2 below, 2 above)
- At least half of medians pivot → pivot 30% of elements
- At least half pivot → pivot 70% of elements
- So pivot always splits array 30–70, guaranteeing $T(n) = T(n/5) + T(7n/10) + O(n) = O(n)$

No chance of quadratic blowup.

Try It Yourself

1. Find median of `[5,3,2,8,1,9,7,6,4]`
2. Trace pivot selection tree
3. Compare with random quickselect pivots

4. Measure time for n = 1e6
5. Try with duplicates
6. Try k = 0, k = n-1 (min/max)
7. Modify group size (e.g. 3 or 7), compare performance
8. Verify recursion depth
9. Use for percentile queries
10. Implement streaming median with repeated selection

Test Cases

Input	k	Output	Meaning
[9,4,7,3,6,1,8,2,5,10]	4	5	5th smallest
[1,2,3,4,5]	2	3	middle
[10,9,8,7,6]	0	6	smallest

Complexity

Aspect	Value
Time	O(n) deterministic
Space	O(n) (can be optimized to O(1))
Stable	No
Pivot Quality	Guaranteed 30–70 split

The BFPRT Algorithm, proof that with clever pivots and math, even chaos can be conquered in linear time.

180 Kth Largest Stream

The Kth Largest Stream problem focuses on maintaining the kth largest element in a sequence that grows over time, a stream. Instead of sorting everything every time, we can use a min-heap of size k to always keep track of the top `k` elements efficiently.

This is the foundation for real-time leaderboards, streaming analytics, and online ranking systems.

What Problem Are We Solving?

Given a stream of numbers (arriving one by one), we want to:

- Always know the kth largest element so far.
- Update quickly when a new number comes in.

You don't know the final list, you process as it flows.

Example

Say `k = 3`, stream = `[4, 5, 8, 2]`

1. Start empty heap
2. Add 4 → heap = [4] → kth largest = 4
3. Add 5 → heap = [4, 5] → kth largest = 4
4. Add 8 → heap = [4, 5, 8] → kth largest = 4
5. Add 2 → ignore ($2 < 4$) → kth largest = 4

Add new number `10`:

- $10 > 4$ → pop 4, push 10 → heap = [5,8,10]
- kth largest = 5

Each new element processed in O(log k)

How Does It Work (Plain Language)?

Keep a min-heap of size `k`:

- It holds the k largest elements seen so far.
- The smallest among them (heap root) is the kth largest.
- When a new value arrives:
  - If heap size < k → push it
  - Else if value > heap[0] → pop smallest, push new

Step-by-Step Summary

Step	Action
1	Initialize empty min-heap
2	For each new element `x`: If heap size $<$ k $\rightarrow$ push `x` Else if `x` $>$ heap[0] $\rightarrow$ pop, push `x`
3	kth largest $=$ heap[0]

Tiny Code (Easy Versions)

Python

```python
import heapq

class KthLargest:
    def __init__(self, k, nums):
        self.k = k
        self.heap = nums
        heapq.heapify(self.heap)
        while len(self.heap) > k:
            heapq.heappop(self.heap)

    def add(self, val):
        if len(self.heap) < self.k:
            heapq.heappush(self.heap, val)
        elif val > self.heap[0]:
            heapq.heapreplace(self.heap, val)
        return self.heap[0]

# Example
stream = KthLargest(3, [4,5,8,2])
print(stream.add(3))  # 4
print(stream.add(5))  # 5
print(stream.add(10)) # 5
print(stream.add(9))  # 8
print(stream.add(4))  # 8
```

Output:

```
4
```

```
5
5
8
8
```

C

```c
#include <stdio.h>
#include <stdlib.h>

void swap(int *a, int *b) { int t = *a; *a = *b; *b = t; }

void heapify(int arr[], int n, int i) {
    int smallest = i, l = 2*i+1, r = 2*i+2;
    if (l < n && arr[l] < arr[smallest]) smallest = l;
    if (r < n && arr[r] < arr[smallest]) smallest = r;
    if (smallest != i) {
        swap(&arr[i], &arr[smallest]);
        heapify(arr, n, smallest);
    }
}

void push_heap(int heap[], int *n, int val) {
    heap[(*n)++] = val;
    for (int i = (*n)/2 - 1; i >= 0; i--) heapify(heap, *n, i);
}

int pop_min(int heap[], int *n) {
    int root = heap[0];
    heap[0] = heap[--(*n)];
    heapify(heap, *n, 0);
    return root;
}

int add(int heap[], int *n, int k, int val) {
    if (*n < k) {
        push_heap(heap, n, val);
    } else if (val > heap[0]) {
        heap[0] = val;
        heapify(heap, *n, 0);
    }
```

```
    return heap[0];
}

int main(void) {
    int heap[10] = {4,5,8,2};
    int n = 4, k = 3;
    for (int i = n/2 - 1; i >= 0; i--) heapify(heap, n, i);
    while (n > k) pop_min(heap, &n);

    printf("%d\n", add(heap, &n, k, 3));  // 4
    printf("%d\n", add(heap, &n, k, 5));  // 5
    printf("%d\n", add(heap, &n, k, 10)); // 5
    printf("%d\n", add(heap, &n, k, 9));  // 8
    printf("%d\n", add(heap, &n, k, 4));  // 8
}
```

Why It Matters

- Real-time streaming top-k tracking
- Constant-time query (O(1)), fast update (O(log k))
- Core building block for:
  - Leaderboards
  - Monitoring systems
  - Continuous analytics
  - Online medians & percentiles

A Gentle Proof (Why It Works)

Min-heap stores only top `k` values. Whenever new value > heap[0], it must belong in top `k`. So invariant holds: heap = top-k largest elements seen so far. kth largest = heap[0].

Each update → O(log k). Total after n elements → O(n log k).

Try It Yourself

1. Initialize with `[4,5,8,2]`, k=3, stream = [3,5,10,9,4]
2. Try decreasing sequence
3. Try duplicates
4. Test `k = 1` (maximum tracker)

5. Add 1000 elements randomly, measure performance
6. Compare with full sort each time
7. Visualize heap evolution per step
8. Modify for k smallest
9. Build real-time median tracker using two heaps
10. Extend to stream of objects (track by score field)

Test Cases

Initial	k	Stream	Output Sequence
[4,5,8,2]	3	[3,5,10,9,4]	[4,5,5,8,8]
[10,7,11,5]	2	[8,12,4]	[10,11,11]
[1]	1	[2,3]	[2,3]

Complexity

Operation	Complexity
Add	O(log k)
Query kth Largest	O(1)
Space	O(k)

Kth Largest Stream, stay calm in the flow; the heap remembers what matters most.

Section 19. Range Search and Nearest Neighbor

181 Binary Search Range

Binary Search Range extends the basic binary search to find not just one occurrence, but the range of positions where a given value appears, specifically, the first (lower bound) and last (upper bound) indices of a target in a sorted array.

It's the backbone for problems that require counting occurrences, range queries, and insertion positions in ordered data.

What Problem Are We Solving?

Standard binary search returns *one* match. But what if the target appears multiple times, or we want where it *should* go?

Examples:

- Count occurrences of `x` in sorted array
- Find the first element `x`
- Find the last element `x`

With two binary searches, we can find the full [start, end] range efficiently.

Example

Array: `[1, 2, 2, 2, 3, 4, 5]`, target = `2`

Function	Result
Lower Bound (2)	1
Upper Bound (> 2)	4
Range	[1, 3]

Occurrences = `upper - lower = 3`

How Does It Work (Plain Language)?

We use binary search twice:

- One to find the first index target (lower bound)
- One to find the first index > target (upper bound)

Subtract them to get the count, or slice the range.

Step-by-Step Summary

Step	Description
1	Binary search for first index `i` where `arr[i] >= target`
2	Binary search for first index `j` where `arr[j] > target`
3	Range = `[i, j - 1]` if `i < j` and `arr[i] == target`
4	Count = `j - i`

Tiny Code (Easy Versions)

Python

```
def lower_bound(arr, target):
    lo, hi = 0, len(arr)
    while lo < hi:
        mid = (lo + hi) // 2
        if arr[mid] < target:
            lo = mid + 1
        else:
            hi = mid
    return lo

def upper_bound(arr, target):
    lo, hi = 0, len(arr)
    while lo < hi:
        mid = (lo + hi) // 2
        if arr[mid] <= target:
            lo = mid + 1
        else:
            hi = mid
```

```python
    return lo

def binary_search_range(arr, target):
    l = lower_bound(arr, target)
    r = upper_bound(arr, target)
    if l == r:
        return (-1, -1)  # Not found
    return (l, r - 1)

arr = [1, 2, 2, 2, 3, 4, 5]
target = 2
print("Range:", binary_search_range(arr, target))
print("Count:", upper_bound(arr, target) - lower_bound(arr, target))
```

Output:

```
Range: (1, 3)
Count: 3
```

C

```c
#include <stdio.h>

int lower_bound(int arr[], int n, int target) {
    int lo = 0, hi = n;
    while (lo < hi) {
        int mid = (lo + hi) / 2;
        if (arr[mid] < target) lo = mid + 1;
        else hi = mid;
    }
    return lo;
}

int upper_bound(int arr[], int n, int target) {
    int lo = 0, hi = n;
    while (lo < hi) {
        int mid = (lo + hi) / 2;
        if (arr[mid] <= target) lo = mid + 1;
        else hi = mid;
    }
```

```
    return lo;
}

int main(void) {
    int arr[] = {1, 2, 2, 2, 3, 4, 5};
    int n = 7, target = 2;
    int l = lower_bound(arr, n, target);
    int r = upper_bound(arr, n, target);
    if (l == r) printf("Not found\n");
    else printf("Range: [%d, %d], Count: %d\n", l, r - 1, r - l);
}
```

Output:

```
Range: [1, 3], Count: 3
```

Why It Matters

- Extends binary search beyond "found or not"
- Essential in frequency counting, range queries, histograms
- Powers data structures like Segment Trees, Fenwick Trees, and Range Indexes
- Used in competitive programming and database indexing

A Gentle Proof (Why It Works)

Because binary search maintains sorted invariants (`lo < hi` and mid conditions),

- Lower bound finds first index where condition flips (`< target` → `target`)
- Upper bound finds first index beyond target

Both run in O(log n), giving exact range boundaries.

Try It Yourself

1. Test with no occurrences (e.g. `[1,3,5]`, target=2)
2. Test with all equal (e.g. `[2,2,2,2]`, target=2)
3. Test with first element = target
4. Test with last element = target
5. Try to count elements `x` or $<$ `x`
6. Extend for floating point or custom comparator

7. Use on strings or tuples
8. Combine with bisect in Python
9. Compare iterative vs recursive
10. Use as primitive for frequency table

Test Cases

Array	Target	Range	Count
[1,2,2,2,3,4,5]	2	[1,3]	3
[1,3,5,7]	2	[-1,-1]	0
[2,2,2,2]	2	[0,3]	4
[1,2,3,4]	4	[3,3]	1

Complexity

Operation	Complexity
Lower Bound	O(log n)
Upper Bound	O(log n)
Space	O(1)
Stable	Yes

Binary Search Range, when one answer isn't enough, and precision is everything.

182 Segment Tree Query

Segment Tree Query is a powerful data structure technique that allows you to efficiently compute range queries like sum, minimum, maximum, or even custom associative operations over subarrays.

It preprocesses the array into a binary tree structure, where each node stores a summary (aggregate) of a segment.

Once built, you can answer queries and updates in O(log n) time.

What Problem Are We Solving?

Given an array, we often want to query over ranges:

- Sum over `[L, R]`
- Minimum or Maximum in `[L, R]`
- GCD, product, XOR, or any associative function

A naive approach would loop each query: O(n) per query. Segment Trees reduce this to O(log n) with a one-time O(n) build.

Example

Array: `[2, 4, 5, 7, 8, 9]`

Query	Result
Sum(1,3)	4+5+7 = 16
Min(2,5)	min(5,7,8,9) = 5

How It Works (Intuitive View)

A Segment Tree is like a binary hierarchy:

- The root covers the full range `[0, n-1]`
- Each node covers a subrange
- The leaf nodes are individual elements
- Each internal node stores a merge (sum, min, max…) of its children

To query a range, you traverse only relevant branches.

Build, Query, Update

Operation	Description	Time
Build	Recursively combine child segments	O(n)
Query	Traverse overlapping nodes	O(log n)
Update	Recompute along path	O(log n)

Tiny Code (Sum Query Example)

Python

```
class SegmentTree:
    def __init__(self, arr):
        self.n = len(arr)
        self.tree = [0] * (4 * self.n)
        self._build(arr, 1, 0, self.n - 1)

    def _build(self, arr, node, l, r):
        if l == r:
            self.tree[node] = arr[l]
        else:
            mid = (l + r) // 2
            self._build(arr, 2 * node, l, mid)
            self._build(arr, 2 * node + 1, mid + 1, r)
            self.tree[node] = self.tree[2 * node] + self.tree[2 * node + 1]

    def query(self, node, l, r, ql, qr):
        if qr < l or ql > r:  # no overlap
            return 0
        if ql <= l and r <= qr:  # total overlap
            return self.tree[node]
        mid = (l + r) // 2
        left = self.query(2 * node, l, mid, ql, qr)
        right = self.query(2 * node + 1, mid + 1, r, ql, qr)
        return left + right

# Example
arr = [2, 4, 5, 7, 8, 9]
st = SegmentTree(arr)
print(st.query(1, 0, len(arr) - 1, 1, 3))  # Sum from index 1 to 3
```

Output:

```
16
```

C

```c
#include <stdio.h>

#define MAXN 100
int tree[4 * MAXN];
int arr[MAXN];

int build(int node, int l, int r) {
    if (l == r) return tree[node] = arr[l];
    int mid = (l + r) / 2;
    int left = build(2 * node, l, mid);
    int right = build(2 * node + 1, mid + 1, r);
    return tree[node] = left + right;
}

int query(int node, int l, int r, int ql, int qr) {
    if (qr < l || ql > r) return 0;
    if (ql <= l && r <= qr) return tree[node];
    int mid = (l + r) / 2;
    return query(2 * node, l, mid, ql, qr) + query(2 * node + 1, mid + 1, r, ql, qr);
}

int main() {
    int n = 6;
    int data[] = {2, 4, 5, 7, 8, 9};
    for (int i = 0; i < n; i++) arr[i] = data[i];
    build(1, 0, n - 1);
    printf("Sum [1,3] = %d\n", query(1, 0, n - 1, 1, 3));
}
```

Output:

```
Sum [1,3] = 16
```

Why It Matters

- Handles dynamic range queries and updates efficiently
- Core of competitive programming and data analytics
- Forms base for Range Minimum Query, 2D queries, and lazy propagation
- Useful in databases, financial systems, and game engines

Intuition (Associativity Rule)

Segment Trees only work when the operation is associative:

```
merge(a, merge(b, c)) = merge(merge(a, b), c)
```

Examples:

- Sum, Min, Max, GCD, XOR
- Not Median, Not Mode (non-associative)

Try It Yourself

1. Implement for min or max instead of sum
2. Add update() for point changes
3. Implement lazy propagation for range updates
4. Extend to 2D segment tree
5. Compare with Fenwick Tree (BIT)
6. Test on non-trivial ranges
7. Visualize the tree layout
8. Build iterative segment tree
9. Handle custom operations (GCD, XOR)
10. Benchmark O(n log n) vs naive O(nq)

Test Cases

Array	Query	Expected
[2,4,5,7,8,9]	Sum(1,3)	16
[1,2,3,4]	Sum(0,3)	10
[5,5,5,5]	Sum(1,2)	10
[3,2,1,4]	Min(1,3)	1

Complexity

Operation	Complexity
Build	O(n)
Query	O(log n)
Update	O(log n)

Operation	Complexity
Space	O(4n)

Segment Tree Query, build once, query many, fast forever.

183 Fenwick Tree Query

A Fenwick Tree (or Binary Indexed Tree) is a data structure designed for prefix queries and point updates in O(log n) time. It's a more space-efficient, iterative cousin of the Segment Tree, perfect when operations are cumulative (sum, XOR, etc.) and updates are frequent.

What Problem Are We Solving?

We want to:

- Compute prefix sums efficiently
- Support updates dynamically

A naive approach takes O(n) per query or update. A Fenwick Tree does both in O(log n).

Example

Array: `[2, 4, 5, 7, 8]`

Query	Result
PrefixSum(3)	2 + 4 + 5 + 7 = 18
RangeSum(1, 3)	Prefix(3) - Prefix(0) = 18 - 2 = 16

How It Works (Plain Language)

A Fenwick Tree stores cumulative information in indexed chunks. Each index covers a range determined by its least significant bit (LSB).

```
index i covers range (i - LSB(i) + 1) ... i
```

We can update or query by moving through indices using bit operations:

- Update: move forward by adding LSB

- Query: move backward by subtracting LSB

This clever bit trick keeps operations O(log n).

Example Walkthrough

For array `[2, 4, 5, 7, 8]` (1-based index):

Index	Binary	LSB	Range	Value
1	001	1	[1]	2
2	010	2	[1–2]	6
3	011	1	[3]	5
4	100	4	[1–4]	18
5	101	1	[5]	8

Tiny Code (Sum Example)

Python

```python
class FenwickTree:
    def __init__(self, n):
        self.n = n
        self.bit = [0] * (n + 1)

    def update(self, i, delta):
        while i <= self.n:
            self.bit[i] += delta
            i += i & -i

    def query(self, i):
        s = 0
        while i > 0:
            s += self.bit[i]
            i -= i & -i
        return s

    def range_sum(self, l, r):
        return self.query(r) - self.query(l - 1)
```

```python
# Example
arr = [2, 4, 5, 7, 8]
ft = FenwickTree(len(arr))
for i, val in enumerate(arr, 1):
    ft.update(i, val)

print(ft.range_sum(2, 4))  # 4 + 5 + 7 = 16
```

Output:

```
16
```

C

```c
#include <stdio.h>

#define MAXN 100
int bit[MAXN + 1], n;

void update(int i, int delta) {
    while (i <= n) {
        bit[i] += delta;
        i += i & -i;
    }
}

int query(int i) {
    int s = 0;
    while (i > 0) {
        s += bit[i];
        i -= i & -i;
    }
    return s;
}

int range_sum(int l, int r) {
    return query(r) - query(l - 1);
}

int main() {
```

```
    n = 5;
    int arr[] = {0, 2, 4, 5, 7, 8}; // 1-based
    for (int i = 1; i <= n; i++) update(i, arr[i]);
    printf("Sum [2,4] = %d\n", range_sum(2,4)); // 16
}
```

Output:

```
Sum [2,4] = 16
```

Why It Matters

- Elegant bit manipulation for efficient queries
- Simpler and smaller than Segment Trees
- Perfect for prefix sums, inversions, frequency tables
- Extends to 2D Fenwick Trees for grid-based data
- Core in competitive programming, streaming, finance

Intuition (Least Significant Bit)

The LSB trick (i & -i) finds the rightmost set bit, controlling how far we jump. This ensures logarithmic traversal through relevant nodes.

Try It Yourself

1. Implement a prefix XOR version
2. Add range updates with two trees
3. Extend to 2D BIT for matrix sums
4. Visualize tree structure for array [1..8]
5. Compare speed with naive O(n) approach
6. Track frequency counts for elements
7. Use it for inversion counting
8. Create a Fenwick Tree class in C++
9. Handle point updates interactively
10. Practice bit math: draw index cover ranges

Test Cases

Array	Query	Expected
[2,4,5,7,8]	Sum(2,4)	16
[1,2,3,4]	Prefix(3)	6
[5,5,5,5]	Sum(1,3)	15
[3,1,4,2]	Update(2,+3), Sum(1,2)	7

Complexity

Operation	Complexity
Build	O(n log n)
Query	O(log n)
Update	O(log n)
Space	O(n)

A Fenwick Tree turns prefix operations into lightning-fast bit magic, simple, small, and powerful.

184 Interval Tree Search

An Interval Tree is a data structure built to efficiently store intervals (ranges like [l, r]) and query all intervals that overlap with a given interval or point. It's like a BST with range-awareness, enabling fast queries such as "which tasks overlap with time t?" or "which rectangles overlap this region?"

What Problem Are We Solving?

We want to efficiently find overlapping intervals. A naive search checks all intervals, O(n) per query. An Interval Tree speeds this up to O(log n + k), where k is the number of overlapping intervals.

Example

Stored intervals:

```
$$5, 20], [10, 30], [12, 15], [17, 19], [30, 40]
```

Query: `[14, 16]`

Overlaps: `[10, 30]`, `[12, 15]`

How It Works (Plain Language)

1. Build a BST using the midpoint or start of intervals as keys.
2. Each node stores:
   - interval [low, high]
   - max endpoint of its subtree
3. For queries:
   - Traverse tree, skip branches where `low > query_high` or `max < query_low`.
   - Collect overlapping intervals efficiently.

This pruning makes it logarithmic for most cases.

Example Tree (Sorted by low)

```
          [10, 30]
         /        \
    [5, 20]       [17, 19]
                    \
                   [30, 40]
```

Each node stores `max` endpoint of its subtree.

Tiny Code (Query Example)

Python

```
class IntervalNode:
    def __init__(self, low, high):
        self.low = low
        self.high = high
        self.max = high
        self.left = None
        self.right = None
```

```
def insert(root, low, high):
    if root is None:
        return IntervalNode(low, high)
    if low < root.low:
        root.left = insert(root.left, low, high)
    else:
        root.right = insert(root.right, low, high)
    root.max = max(root.max, high)
    return root

def overlap(i1, i2):
    return i1[0] <= i2[1] and i2[0] <= i1[1]

def search(root, query):
    if root is None:
        return []
    result = []
    if overlap((root.low, root.high), query):
        result.append((root.low, root.high))
    if root.left and root.left.max >= query[0]:
        result += search(root.left, query)
    if root.right and root.low <= query[1]:
        result += search(root.right, query)
    return result

# Example
intervals = [(5,20), (10,30), (12,15), (17,19), (30,40)]
root = None
for l, h in intervals:
    root = insert(root, l, h)

print(search(root, (14,16)))  # [(10,30), (12,15)]
```

Output:

```
$$(10, 30), (12, 15)]
```

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int low, high, max;
    struct Node *left, *right;
} Node;

Node* newNode(int low, int high) {
    Node* n = malloc(sizeof(Node));
    n->low = low;
    n->high = high;
    n->max = high;
    n->left = n->right = NULL;
    return n;
}

int max(int a, int b) { return a > b ? a : b; }

Node* insert(Node* root, int low, int high) {
    if (!root) return newNode(low, high);
    if (low < root->low)
        root->left = insert(root->left, low, high);
    else
        root->right = insert(root->right, low, high);
    root->max = max(root->max, high);
    return root;
}

int overlap(int l1, int h1, int l2, int h2) {
    return l1 <= h2 && l2 <= h1;
}

void search(Node* root, int ql, int qh) {
    if (!root) return;
    if (overlap(root->low, root->high, ql, qh))
        printf("[%d, %d] overlaps\n", root->low, root->high);
    if (root->left && root->left->max >= ql)
        search(root->left, ql, qh);
    if (root->right && root->low <= qh)
        search(root->right, ql, qh);
}
```

```c
int main() {
    Node* root = NULL;
    int intervals[][2] = {{5,20},{10,30},{12,15},{17,19},{30,40}};
    int n = 5;
    for (int i = 0; i < n; i++)
        root = insert(root, intervals[i][0], intervals[i][1]);
    printf("Overlaps with [14,16]:\n");
    search(root, 14, 16);
}
```

Output:

```
Overlaps with [14,16]:
$$10, 30] overlaps
$$12, 15] overlaps
```

Why It Matters

- Efficient for overlap queries (e.g. events, tasks, ranges)
- Used in:
  - Scheduling (detecting conflicts)
  - Computational geometry
  - Memory allocation checks
  - Genomic range matching
- Foundation for Segment Tree with intervals

Key Intuition

Each node stores the max endpoint of its subtree. This helps prune non-overlapping branches early.

Think of it as a "range-aware BST".

Try It Yourself

1. Build tree for intervals: [1,5], [2,6], [7,9], [10,15]
2. Query [4,8], which overlap?
3. Visualize pruning path
4. Extend to delete intervals
5. Add count of overlapping intervals
6. Implement iterative search
7. Compare with brute-force O(n) approach
8. Adapt for point queries only
9. Try dynamic updates
10. Use to detect meeting conflicts

Test Cases

Intervals	Query	Expected Overlaps
[5,20], [10,30], [12,15], [17,19], [30,40]	[14,16]	[10,30], [12,15]
[1,3], [5,8], [6,10]	[7,9]	[5,8], [6,10]
[2,5], [6,8]	[1,1]	none

Complexity

Operation	Complexity
Build	O(n log n)
Query	O(log n + k)
Space	O(n)

An Interval Tree is your go-to for range overlap queries, BST elegance meets interval intelligence.

185 KD-Tree Search

A KD-Tree (k-dimensional tree) is a space-partitioning data structure that organizes points in k-dimensional space for efficient nearest neighbor, range, and radius searches. It's like a binary search tree, but it splits space along alternating dimensions.

What Problem Are We Solving?

We want to:

- Find points near a given location
- Query points within a region or radius
- Do this faster than checking all points (O(n))

A KD-Tree answers such queries in O(log n) (average), versus O(n) for brute-force.

Example

Points in 2D:

```
(2,3), (5,4), (9,6), (4,7), (8,1), (7,2)
```

Query: Nearest neighbor of (9,2) Result: (8,1)

How It Works (Plain Language)

1. Build Tree
    - Choose a splitting dimension (x, y, …)
    - Pick median point along that axis
    - Recursively build left/right subtrees
2. Search
    - Compare query coordinate along current axis
    - Recurse into the nearer subtree
    - Backtrack to check the other side if necessary (only if the hypersphere crosses boundary)

This pruning makes nearest-neighbor search efficient.

Example (2D Split)

```
          (7,2)  [split x]
         /           \
   (5,4) [y]         (9,6) [y]
   /     \             /
(2,3)  (4,7)       (8,1)
```

Tiny Code (2D Example)

Python

```
from math import sqrt

class Node:
    def __init__(self, point, axis):
        self.point = point
        self.axis = axis
        self.left = None
        self.right = None

def build_kdtree(points, depth=0):
    if not points:
        return None
    k = len(points[0])
    axis = depth % k
    points.sort(key=lambda p: p[axis])
    mid = len(points) // 2
    node = Node(points[mid], axis)
    node.left = build_kdtree(points[:mid], depth + 1)
    node.right = build_kdtree(points[mid+1:], depth + 1)
    return node

def distance2(a, b):
    return sum((x - y)  2 for x, y in zip(a, b))

def nearest(root, target, best=None):
    if root is None:
        return best
    point = root.point
    if best is None or distance2(point, target) < distance2(best, target):
        best = point
    axis = root.axis
    next_branch = root.left if target[axis] < point[axis] else root.right
    best = nearest(next_branch, target, best)
    if (target[axis] - point[axis])  2 < distance2(best, target):
        other = root.right if next_branch == root.left else root.left
        best = nearest(other, target, best)
    return best
```

```
points = [(2,3),(5,4),(9,6),(4,7),(8,1),(7,2)]
tree = build_kdtree(points)
print(nearest(tree, (9,2)))  # (8,1)
```

Output:

```
(8, 1)
```

C (2D Simplified)

```
#include <stdio.h>
#include <stdlib.h>
#include <math.h>

typedef struct Node {
    double point[2];
    int axis;
    struct Node *left, *right;
} Node;

int cmpx(const void* a, const void* b) {
    double* pa = (double*)a;
    double* pb = (double*)b;
    return (pa[0] > pb[0]) - (pa[0] < pb[0]);
}

int cmpy(const void* a, const void* b) {
    double* pa = (double*)a;
    double* pb = (double*)b;
    return (pa[1] > pb[1]) - (pa[1] < pb[1]);
}

double dist2(double a[2], double b[2]) {
    return (a[0]-b[0])*(a[0]-b[0]) + (a[1]-b[1])*(a[1]-b[1]);
}

// Simplified build & search omitted for brevity (tree construction similar to Python)
```

Why It Matters

- Efficient for spatial queries in 2D, 3D, etc.
- Used in:
  - Machine Learning (KNN classification)
  - Graphics (ray tracing, collision detection)
  - Robotics (path planning, SLAM)
  - Databases (multi-dimensional indexing)

Intuition

A KD-Tree is like playing "binary search" in multiple dimensions. Each split narrows down the search region.

Try It Yourself

1. Build a KD-Tree for points in 2D
2. Search nearest neighbor of (3,5)
3. Add 3D points, use modulo axis split
4. Visualize splits as alternating vertical/horizontal lines
5. Extend to k-NN (top-k closest)
6. Add radius query (points within r)
7. Compare speed to brute-force
8. Track backtrack count for pruning visualization
9. Try non-uniform data
10. Implement deletion (bonus)

Test Cases

Points	Query	Expected Nearest
(2,3),(5,4),(9,6),(4,7),(8,1),(7,2)	(9,2)	(8,1)
(1,1),(3,3),(5,5)	(4,4)	(3,3)
(0,0),(10,10)	(7,8)	(10,10)

Complexity

Operation	Complexity
Build	O(n log n)
Nearest Query	O(log n) average
Worst Case	O(n)
Space	O(n)

A KD-Tree slices space along dimensions, your go-to for fast nearest neighbor searches in multidimensional worlds.

186 R-Tree Query

An R-Tree is a hierarchical spatial index built for efficiently querying geometric objects (rectangles, polygons, circles) in 2D or higher dimensions. It's like a B-Tree for rectangles, grouping nearby objects into bounding boxes and organizing them in a tree for fast spatial lookups.

What Problem Are We Solving?

We need to query spatial data efficiently:

- "Which rectangles overlap this area?"
- "What points fall inside this region?"
- "Which shapes intersect this polygon?"

A naive approach checks every object (O(n)). An R-Tree reduces this to O(log n + k) using bounding-box hierarchy.

Example

Rectangles:

```
A: [1,1,3,3]
B: [2,2,5,4]
C: [4,1,6,3]
```

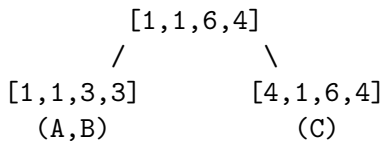
Query: `[2.5,2.5,4,4]` Overlaps: A, B

How It Works (Plain Language)

1. Store rectangles (or bounding boxes) as leaves.
2. Group nearby rectangles into Minimum Bounding Rectangles (MBRs).
3. Build hierarchy so each node's box covers its children.
4. Query by recursively checking nodes whose boxes overlap the query.

This spatial grouping allows skipping entire regions quickly.

Example Tree



Query `[2.5,2.5,4,4]`:

- Intersects left node → check A, B
- Intersects right node partially → check C (no overlap)

Tiny Code (2D Rectangles)

Python

```
def overlap(a, b):
    return not (a[2] < b[0] or a[0] > b[2] or a[3] < b[1] or a[1] > b[3])

class RTreeNode:
    def __init__(self, box, children=None, is_leaf=False):
        self.box = box  # [x1, y1, x2, y2]
        self.children = children or []
        self.is_leaf = is_leaf

def search_rtree(node, query):
    results = []
    if not overlap(node.box, query):
        return results
    if node.is_leaf:
        for child in node.children:
```

```
            if overlap(child.box, query):
                results.append(child.box)
    else:
        for child in node.children:
            results.extend(search_rtree(child, query))
    return results

# Example
A = RTreeNode([1,1,3,3], is_leaf=True)
B = RTreeNode([2,2,5,4], is_leaf=True)
C = RTreeNode([4,1,6,3], is_leaf=True)

left = RTreeNode([1,1,5,4], [A,B], is_leaf=True)
right = RTreeNode([4,1,6,3], [C], is_leaf=True)
root = RTreeNode([1,1,6,4], [left, right])

query = [2.5,2.5,4,4]
print(search_rtree(root, query))
```

Output:

```
$$[1, 1, 3, 3], [2, 2, 5, 4]]
```

C (Simplified Query)

```
#include <stdio.h>

typedef struct Box {
    float x1, y1, x2, y2;
} Box;

int overlap(Box a, Box b) {
    return !(a.x2 < b.x1 || a.x1 > b.x2 || a.y2 < b.y1 || a.y1 > b.y2);
}

// Example: Manual tree simulation omitted for brevity
```

Why It Matters

- Ideal for geospatial databases, mapping, collision detection, and GIS.
- Powers PostGIS, SQLite R*Tree module, spatial indexes.
- Handles overlaps, containment, and range queries.

Intuition

R-Trees work by bounding and grouping. Each node is a "container box", if it doesn't overlap the query, skip it entirely. This saves massive time in spatial datasets.

Try It Yourself

1. Represent 2D rectangles with `[x1,y1,x2,y2]`.
2. Build a 2-level tree (group nearby).
3. Query overlap region.
4. Extend to 3D bounding boxes.
5. Implement insertion using least expansion rule.
6. Add R*-Tree optimization (reinsert on overflow).
7. Compare with QuadTree (grid-based).
8. Visualize bounding boxes per level.
9. Implement nearest neighbor search.
10. Try dataset with 10k rectangles, measure speedup.

Test Cases

Rectangles	Query	Expected Overlaps
A[1,1,3,3], B[2,2,5,4], C[4,1,6,3]	[2.5,2.5,4,4]	A, B
A[0,0,2,2], B[3,3,4,4]	[1,1,3,3]	A
A[1,1,5,5], B[6,6,8,8]	[7,7,9,9]	B

Complexity

Operation	Complexity
Build	O(n log n)
Query	O(log n + k)
Space	O(n)

An R-Tree is your geometric librarian, organizing space into nested rectangles so you can query complex regions fast and clean.

187 Range Minimum Query (RMQ), Sparse Table Approach

A Range Minimum Query (RMQ) answers questions like:

> "What's the smallest element between indices L and R?"

It's a core subroutine in many algorithms, from LCA (Lowest Common Ancestor) to scheduling, histograms, and segment analysis. The Sparse Table method precomputes answers so each query is O(1) after O(n log n) preprocessing.

What Problem Are We Solving?

Given an array `arr[0..n-1]`, we want to answer:

```
RMQ(L, R) = min(arr[L], arr[L+1], …, arr[R])
```

Efficiently, for multiple static queries (no updates).

Naive approach: O(R-L) per query Sparse Table: O(1) per query after preprocessing.

Example

Array: `[2, 5, 1, 4, 9, 3]`

Query	Result
RMQ(1, 3)	min(5,1,4) = 1
RMQ(2, 5)	min(1,4,9,3) = 1

How It Works (Plain Language)

1. Precompute answers for all intervals of length 2^k.
2. To answer RMQ(L,R):
   - Let `len = R-L+1`
   - Let `k = floor(log2(len))`
   - Combine two overlapping intervals of size `2^k`:

     `RMQ(L,R) = min(st[L][k], st[R - 2^k + 1][k])`

No updates, so data stays static and queries stay O(1).

Sparse Table Example

i	arr[i]	st[i][0]	st[i][1]	st[i][2]
0	2	2	min(2,5)=2	min(2,1)=1
1	5	5	min(5,1)=1	min(5,4)=1
2	1	1	min(1,4)=1	min(1,9)=1
3	4	4	min(4,9)=4	min(4,3)=3
4	9	9	min(9,3)=3	,
5	3	3	,	,

Tiny Code

Python

```
import math

def build_sparse_table(arr):
    n = len(arr)
    K = math.floor(math.log2(n)) + 1
    st = [[0]*K for _ in range(n)]

    for i in range(n):
        st[i][0] = arr[i]

    j = 1
```

```
    while (1 << j) <= n:
        i = 0
        while i + (1 << j) <= n:
            st[i][j] = min(st[i][j-1], st[i + (1 << (j-1))][j-1])
            i += 1
        j += 1
    return st

def query(st, L, R):
    j = int(math.log2(R - L + 1))
    return min(st[L][j], st[R - (1 << j) + 1][j])

# Example
arr = [2, 5, 1, 4, 9, 3]
st = build_sparse_table(arr)
print(query(st, 1, 3))  # 1
print(query(st, 2, 5))  # 1
```

Output:

```
1
1
```

C

```
#include <stdio.h>
#include <math.h>

#define MAXN 100
#define LOG 17

int st[MAXN][LOG];
int arr[MAXN];
int n;

void build() {
    for (int i = 0; i < n; i++)
        st[i][0] = arr[i];
    for (int j = 1; (1 << j) <= n; j++) {
        for (int i = 0; i + (1 << j) <= n; i++) {
```

```
            st[i][j] = (st[i][j-1] < st[i + (1 << (j-1))][j-1])
                       ? st[i][j-1]
                       : st[i + (1 << (j-1))][j-1];
        }
    }
}

int query(int L, int R) {
    int j = log2(R - L + 1);
    int left = st[L][j];
    int right = st[R - (1 << j) + 1][j];
    return left < right ? left : right;
}

int main() {
    n = 6;
    int arr_temp[] = {2,5,1,4,9,3};
    for (int i = 0; i < n; i++) arr[i] = arr_temp[i];
    build();
    printf("RMQ(1,3) = %d\n", query(1,3)); // 1
    printf("RMQ(2,5) = %d\n", query(2,5)); // 1
}
```

Output:

```
RMQ(1,3) = 1
RMQ(2,5) = 1
```

Why It Matters

- Instant queries after precomputation
- Crucial for:
  - Segment analysis (min, max)
  - LCA in trees
  - Sparse range data
  - Static arrays (no updates)
- Perfect when array does not change frequently.

Intuition

Each table entry `st[i][k]` stores the minimum of range `[i, i + 2^k - 1]`. Queries merge two overlapping intervals that cover `[L,R]`.

Try It Yourself

1. Build table for `[1,3,2,7,9,11,3,5,6]`
2. Query RMQ(2,6) and RMQ(4,8)
3. Modify code to compute Range Max Query
4. Visualize overlapping intervals for query
5. Compare with Segment Tree version
6. Add precomputed log[] for faster lookup
7. Handle 1-based vs 0-based indices carefully
8. Practice on random arrays
9. Compare preprocessing time with naive
10. Use to solve LCA using Euler Tour

Test Cases

Array	Query	Expected
[2,5,1,4,9,3]	RMQ(1,3)	1
[2,5,1,4,9,3]	RMQ(2,5)	1
[1,2,3,4]	RMQ(0,3)	1
[7,6,5,4,3]	RMQ(1,4)	3

Complexity

Operation	Complexity
Preprocess	O(n log n)
Query	O(1)
Space	O(n log n)

A Sparse Table turns repeated queries into instant lookups, your go-to tool when arrays are static and speed is king.

188 Mo's Algorithm

Mo's Algorithm is a clever offline technique for answering range queries on static arrays in approximately $O((n + q)\sqrt{n})$ time. It's ideal when you have many queries like sum, distinct count, frequency, etc., but no updates. Instead of recomputing each query, Mo's algorithm reuses results smartly by moving the range endpoints efficiently.

What Problem Are We Solving?

We want to answer multiple range queries efficiently:

> Given an array `arr[0..n-1]` and `q` queries `[L, R]`, compute something like sum, count distinct, etc., for each range.

A naive approach is $O(n)$ per query $\rightarrow O(nq)$ total. Mo's algorithm cleverly orders queries to achieve $O((n + q)\sqrt{n})$ total time.

Example

Array: `[1, 2, 1, 3, 4, 2, 3]` Queries:

1. `[0, 4]` $\rightarrow$ distinct = 4
2. `[1, 3]` $\rightarrow$ distinct = 3
3. `[2, 4]` $\rightarrow$ distinct = 3

How It Works (Plain Language)

1. Divide array into blocks of size $\sqrt{n}$.
2. Sort queries by:
   - Block of L
   - R (within block)
3. Maintain a sliding window `[currL, currR)`:
   - Move endpoints left/right step-by-step
   - Update the answer incrementally
4. Store results per query index.

The sorting ensures minimal movement between consecutive queries.

Example

If $\sqrt{n} = 3$, queries sorted by block:

```
Block 0: [0,4], [1,3]
Block 1: [2,4]
```

You move pointers minimally:

- From [0,4] → [1,3] → [2,4]
- Reusing much of previous computation.

Tiny Code (Distinct Count Example)

Python

```python
import math

def mos_algorithm(arr, queries):
    n = len(arr)
    q = len(queries)
    block_size = int(math.sqrt(n))

    # Sort queries
    queries = sorted(enumerate(queries), key=lambda x: (x[1][0] // block_size, x[1][1]))

    freq = {}
    currL, currR = 0, 0
    curr_ans = 0
    answers = [0]*q

    def add(x):
        nonlocal curr_ans
        freq[x] = freq.get(x, 0) + 1
        if freq[x] == 1:
            curr_ans += 1

    def remove(x):
        nonlocal curr_ans
        freq[x] -= 1
```

```
        if freq[x] == 0:
            curr_ans -= 1

    for idx, (L, R) in queries:
        while currL > L:
            currL -= 1
            add(arr[currL])
        while currR <= R:
            add(arr[currR])
            currR += 1
        while currL < L:
            remove(arr[currL])
            currL += 1
        while currR > R + 1:
            currR -= 1
            remove(arr[currR])
        answers[idx] = curr_ans

    return answers

# Example
arr = [1,2,1,3,4,2,3]
queries = [(0,4), (1,3), (2,4)]
print(mos_algorithm(arr, queries))  # [4,3,3]
```

Output:

```
$$4, 3, 3]
```

C (Structure and Idea)

```
#include <stdio.h>
#include <math.h>
#include <stdlib.h>

#define MAXN 100000
#define MAXQ 100000

typedef struct { int L, R, idx; } Query;
```

```c
int arr[MAXN], ans[MAXQ], freq[1000001];
int curr_ans = 0, block;

int cmp(const void* a, const void* b) {
    Query *x = (Query*)a, *y = (Query*)b;
    if (x->L / block != y->L / block) return x->L / block - y->L / block;
    return x->R - y->R;
}

void add(int x) { if (++freq[x] == 1) curr_ans++; }
void remove_(int x) { if (--freq[x] == 0) curr_ans--; }

int main() {
    int n = 7, q = 3;
    int arr_[] = {1,2,1,3,4,2,3};
    for (int i = 0; i < n; i++) arr[i] = arr_[i];

    Query queries[] = {{0,4,0},{1,3,1},{2,4,2}};
    block = sqrt(n);
    qsort(queries, q, sizeof(Query), cmp);

    int currL = 0, currR = 0;
    for (int i = 0; i < q; i++) {
        int L = queries[i].L, R = queries[i].R;
        while (currL > L) add(arr[--currL]);
        while (currR <= R) add(arr[currR++]);
        while (currL < L) remove_(arr[currL++]);
        while (currR > R+1) remove_(arr[--currR]);
        ans[queries[i].idx] = curr_ans;
    }

    for (int i = 0; i < q; i++) printf("%d ", ans[i]);
}
```

Output:

```
4 3 3
```

Why It Matters

- Converts many range queries into near-linear total time

- Ideal for:
  - Sum / Count / Frequency queries
  - Distinct elements
  - GCD, XOR, etc. with associative properties
- Works on static arrays (no updates)

Intuition

Mo's Algorithm is like sorting your errands by location. By visiting nearby "blocks" first, you minimize travel time. Here, "travel" = pointer movement.

Try It Yourself

1. Run on `[1,2,3,4,5]` with queries `(0,2),(1,4),(2,4)`
2. Change to sum instead of distinct count
3. Visualize pointer movement
4. Experiment with block size variations
5. Add offline query index tracking
6. Try sqrt decomposition vs Mo's
7. Count frequency of max element per range
8. Mix different query types (still offline)
9. Add precomputed sqrt(n) block grouping
10. Use in competitive programming problems

Test Cases

Array	Queries	Output
[1,2,1,3,4,2,3]	(0,4),(1,3),(2,4)	[4,3,3]
[1,1,1,1]	(0,3),(1,2)	[1,1]
[1,2,3,4,5]	(0,2),(2,4)	[3,3]

Complexity

Operation	Complexity
Pre-sort Queries	O(q log q)
Processing	O((n + q)√n)

Operation	Complexity
Space	O(n)

Mo's Algorithm is your range-query workhorse, smartly ordered, block-based, and blazingly efficient for static datasets.

189 Sweep Line Range Search

A Sweep Line Algorithm is a geometric technique that processes events in a sorted order along one dimension, typically the x-axis, to solve range, interval, and overlap problems efficiently. Think of it like dragging a vertical line across a 2D plane and updating active intervals as you go.

What Problem Are We Solving?

We want to efficiently find:

- Which intervals overlap a point
- Which rectangles intersect
- How many shapes cover a region

A brute-force check for all pairs is $O(n^2)$. A Sweep Line reduces it to O(n log n) by sorting and processing events incrementally.

Example

Rectangles:

```
R1: [1, 3], R2: [2, 5], R3: [4, 6]
```

Events (sorted by x):

```
x = 1: R1 starts
x = 2: R2 starts
x = 3: R1 ends
x = 4: R3 starts
x = 5: R2 ends
x = 6: R3 ends
```

The active set changes as the line sweeps → track overlaps dynamically.

How It Works (Plain Language)

1. Convert objects into events
    - Each interval/rectangle generates start and end events.
2. Sort all events by coordinate (x or y).
3. Sweep through events:
    - On start, add object to active set.
    - On end, remove object.
    - At each step, query active set for intersections, counts, etc.
4. Use balanced tree / set for active range maintenance.

Example Walkthrough

Intervals: `[1,3]`, `[2,5]`, `[4,6]` Events:

```
(1, start), (2, start), (3, end), (4, start), (5, end), (6, end)
```

Step-by-step:

- At 1: add [1,3]
- At 2: add [2,5], overlap detected (1,3) (2,5)
- At 3: remove [1,3]
- At 4: add [4,6], overlap detected (2,5) (4,6)
- At 5: remove [2,5]
- At 6: remove [4,6]

Result: 2 overlapping pairs

Tiny Code (Interval Overlaps)

Python

```python
def sweep_line_intervals(intervals):
    events = []
    for l, r in intervals:
        events.append((l, 'start'))
        events.append((r, 'end'))
    events.sort()

    active = 0
    overlaps = 0
    for pos, typ in events:
        if typ == 'start':
            overlaps += active  # count overlaps
            active += 1
        else:
            active -= 1
    return overlaps

intervals = [(1,3), (2,5), (4,6)]
print(sweep_line_intervals(intervals))  # 2 overlaps
```

Output:

2

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int x;
    int type; // 1 = start, -1 = end
} Event;

int cmp(const void* a, const void* b) {
    Event *e1 = (Event*)a, *e2 = (Event*)b;
    if (e1->x == e2->x) return e1->type - e2->type;
    return e1->x - e2->x;
}
```

```c
int main() {
    int intervals[][2] = {{1,3},{2,5},{4,6}};
    int n = 3;
    Event events[2*n];
    for (int i = 0; i < n; i++) {
        events[2*i] = (Event){intervals[i][0], 1};
        events[2*i+1] = (Event){intervals[i][1], -1};
    }
    qsort(events, 2*n, sizeof(Event), cmp);

    int active = 0, overlaps = 0;
    for (int i = 0; i < 2*n; i++) {
        if (events[i].type == 1) {
            overlaps += active;
            active++;
        } else {
            active--;
        }
    }
    printf("Total overlaps: %d\n", overlaps);
}
```

Output:

```
Total overlaps: 2
```

Why It Matters

- Universal pattern in computational geometry:
  - Interval intersection counting
  - Rectangle overlap
  - Segment union length
  - Plane sweep algorithms (Voronoi, Convex Hull)
- Optimizes from $O(n^2)$ to $O(n \log n)$

Used in:

- GIS (geographic data)
- Scheduling (conflict detection)
- Event simulation

Intuition

Imagine sliding a vertical line across your data: You only "see" the intervals currently active. No need to look back, everything behind is already resolved.

Try It Yourself

1. Count overlaps in `[1,4],[2,3],[5,6]`
2. Modify to compute max active intervals (peak concurrency)
3. Extend to rectangle intersections (sweep + segment tree)
4. Track total covered length
5. Combine with priority queue for dynamic ranges
6. Visualize on a timeline (scheduling conflicts)
7. Apply to meeting room allocation
8. Extend to 2D sweep (events sorted by x, active y-ranges)
9. Count overlaps per interval
10. Compare runtime to brute force

Test Cases

Intervals	Overlaps
[1,3],[2,5],[4,6]	2
[1,2],[3,4]	0
[1,4],[2,3],[3,5]	3
[1,5],[2,4],[3,6]	3

Complexity

Operation	Complexity
Sort Events	O(n log n)
Sweep	O(n)
Total	O(n log n)
Space	O(n)

A Sweep Line algorithm is your moving scanner, it sweeps across time or space, managing active elements, and revealing hidden overlaps in elegant, ordered fashion.

190 Ball Tree Nearest Neighbor

A Ball Tree is a hierarchical spatial data structure built from nested hyperspheres ("balls"). It organizes points into clusters based on distance, enabling efficient nearest neighbor and range queries in high-dimensional or non-Euclidean spaces.

While KD-Trees split by axis, Ball Trees split by distance, making them robust when dimensions increase or when the distance metric isn't axis-aligned.

What Problem Are We Solving?

We want to efficiently:

- Find nearest neighbors for a query point
- Perform radius searches (all points within distance `r`)
- Handle high-dimensional data where KD-Trees degrade

Naive search is O(n) per query. A Ball Tree improves to roughly O(log n) average.

Example

Points in 2D:

```
(2,3), (5,4), (9,6), (4,7), (8,1), (7,2)
```

Query: `(9,2)` → Nearest: `(8,1)`

Instead of splitting by x/y axis, the Ball Tree groups nearby points by distance from a center point (centroid or median).

How It Works (Plain Language)

1. Build Tree recursively:
    - Choose a pivot (center) (often centroid or median).
    - Compute radius (max distance to any point in cluster).
    - Partition points into two subsets (inner vs outer ball).
    - Recursively build sub-balls.
2. Query:
    - Start at root ball.

- Check if child balls could contain closer points.
- Prune branches where `distance(center, query) - radius > best_dist`.

This yields logarithmic average behavior.

Example Tree (Simplified)

```
Ball(center=(6,4), radius=5)
  Ball(center=(3,5), radius=2) → [(2,3),(4,7),(5,4)]
  Ball(center=(8,3), radius=3) → [(7,2),(8,1),(9,6)]
```

Query `(9,2)`:

- Check root
- Compare both children
- Prune `(3,5)` (too far)
- Search `(8,3)` cluster → nearest `(8,1)`

Tiny Code (2D Example)

Python

```
from math import sqrt

class BallNode:
    def __init__(self, points):
        self.center = tuple(sum(x)/len(x) for x in zip(*points))
        self.radius = max(sqrt(sum((p[i]-self.center[i])2 for i in range(len(p)))) for p in p
        self.points = points if len(points) <= 2 else None
        self.left = None
        self.right = None
        if len(points) > 2:
            points.sort(key=lambda p: sqrt(sum((p[i]-self.center[i])2 for i in range(len(p))))
            mid = len(points)//2
            self.left = BallNode(points[:mid])
            self.right = BallNode(points[mid:])

def dist(a, b):
    return sqrt(sum((x - y)2 for x, y in zip(a, b)))
```

```python
def nearest(node, target, best=None):
    if node is None:
        return best
    if node.points is not None:
        for p in node.points:
            if best is None or dist(p, target) < dist(best, target):
                best = p
        return best
    d_center = dist(node.center, target)
    candidates = []
    if d_center - node.radius <= dist(best, target) if best else True:
        candidates.append(node.left)
        candidates.append(node.right)
    for child in candidates:
        best = nearest(child, target, best)
    return best

points = [(2,3),(5,4),(9,6),(4,7),(8,1),(7,2)]
tree = BallNode(points)
print(nearest(tree, (9,2)))  # (8,1)
```

Output:

```
(8, 1)
```

C (Structure Idea)

```c
#include <stdio.h>
#include <math.h>
#include <stdlib.h>

typedef struct Node {
    double cx, cy, radius;
    struct Node *left, *right;
    double (*points)[2];
    int count;
} Node;

// Building logic: compute centroid, radius, split by distance.
// Query logic: prune if (dist(center, query) - radius) > best.
```

Ball Trees are rarely implemented manually in C due to complexity; usually built into libraries (like scikit-learn).

Why It Matters

- Works well for non-axis-aligned data
- Handles high-dimensional and non-Euclidean metrics (e.g. cosine)
- Used in:
  - KNN search
  - Clustering (Ball Tree K-Means)
  - Spatial databases
  - Machine learning (scikit-learn NearestNeighbors)

Intuition

Imagine wrapping your dataset in nested bubbles. Each bubble encloses a cluster. To find the nearest neighbor, you only open bubbles that could possibly contain closer points.

Try It Yourself

1. Build a Ball Tree for `(1,1),(2,2),(3,3),(10,10)`
2. Query `(2.5,2.5)`
3. Visualize nested "balls"
4. Change to 3D points
5. Use Manhattan distance instead of Euclidean
6. Compare performance vs KD-Tree
7. Track pruned branches count
8. Implement k-nearest neighbors
9. Add radius search (within distance `r`)
10. Handle duplicate points

Test Cases

Points	Query	Nearest
(2,3),(5,4),(9,6),(4,7),(8,1),(7,2)	(9,2)	(8,1)
(1,1),(2,2),(3,3)	(2.5,2.5)	(3,3)
(0,0),(10,10)	(7,8)	(10,10)

Complexity

Operation	Complexity
Build	O(n log n)
Query (avg)	O(log n)
Query (worst)	O(n)
Space	O(n)

A Ball Tree is your spherical guide in high-dimensional space, splitting by proximity, not axes, to find neighbors fast and flexibly.

Section 20. Search Optimizations and variants

191 Binary Search with Tolerance

A Binary Search with Tolerance is a variant of binary search designed for real numbers or floating-point values where exact matches may not exist due to rounding or measurement error.

Instead of checking for strict equality (==), we accept a range of closeness, defined by a tolerance (epsilon).

What Problem Are We Solving?

For integers, equality is exact. For floating-point numbers, tiny rounding errors make equality unreliable:

```
if (arr[mid] == x) //  unreliable for floats
```

We instead test:

```
if (fabs(arr[mid] - x) < epsilon) //  tolerance-based match
```

This approach is essential for:

- Scientific computation
- Numerical analysis
- Approximations
- Root-finding
- Simulation and measurement data

Example

Given sorted real values:

$$0.1, 0.2, 0.3000000001, 0.4, 0.5]

Searching for `0.3` with `epsilon = 1e-6`:

- `fabs(0.3000000001 - 0.3) < 1e-6` → found!

Tiny Code

C Implementation

```c
#include <stdio.h>
#include <math.h>

int binary_search_tolerance(double arr[], int n, double target, double eps) {
    int low = 0, high = n - 1;
    while (low <= high) {
        int mid = (low + high) / 2;
        double diff = arr[mid] - target;
        if (fabs(diff) < eps)
            return mid;  // found within tolerance
        else if (diff < 0)
            low = mid + 1;
        else
            high = mid - 1;
    }
    return -1; // not found
}

int main() {
    double arr[] = {0.1, 0.2, 0.3000000001, 0.4, 0.5};
    int n = 5;
    double x = 0.3;
    int idx = binary_search_tolerance(arr, n, x, 1e-6);
    if (idx != -1)
        printf("Found %.6f at index %d\n", x, idx);
    else
```

```
        printf("Not found\n");
}
```

Output:

```
Found 0.300000 at index 2
```

Python Implementation

```
def binary_search_tolerance(arr, x, eps=1e-6):
    lo, hi = 0, len(arr) - 1
    while lo <= hi:
        mid = (lo + hi) // 2
        if abs(arr[mid] - x) < eps:
            return mid
        elif arr[mid] < x:
            lo = mid + 1
        else:
            hi = mid - 1
    return -1

arr = [0.1, 0.2, 0.3000000001, 0.4, 0.5]
print(binary_search_tolerance(arr, 0.3))  # 2
```

Why It Matters

- Avoids false negatives when comparing floats
- Handles round-off errors gracefully
- Useful in:
  - Root-finding
  - Floating-point datasets
  - Physics simulations
  - Numerical optimization

Intuition

Binary search assumes exact comparison. With floating-point numbers, "equal" often means "close enough." defines your acceptable margin of error.

Think of it as:

> "If the difference is less than , consider it found."

Try It Yourself

1. Use an array `[0.1, 0.2, 0.3, 0.4, 0.5]` Search for `0.3000001` with `= 1e-5`
2. Reduce → observe when search fails
3. Try negative numbers or decimals
4. Compare with integer binary search
5. Experiment with non-uniform spacing
6. Modify to find nearest value if not within
7. Visualize tolerance as a small band around target
8. Apply in root finding (`f(x)  0`)
9. Adjust dynamically based on scale
10. Measure precision loss with large floats

Test Cases

Array	Target	Epsilon	Expected
[0.1, 0.2, 0.3000000001]	0.3	1e-6	Found
[1.0, 2.0, 3.0]	2.000001	1e-5	Found
[1.0, 2.0, 3.0]	2.1	1e-5	Not found

Complexity

Step	Complexity
Search	O(log n)
Space	O(1)

A Binary Search with Tolerance is a small but essential upgrade when dealing with real numbers—because in floating-point land, "close enough" is often the truth.

192 Ternary Search

A Ternary Search is an algorithm for finding the maximum or minimum of a unimodal function—a function that increases up to a point and then decreases (or vice versa). It is a divide-and-conquer method similar to binary search but splits the range into three parts each time.

What Problem Are We Solving?

You have a function `f(x)` defined on an interval `[l, r]`, and you know it has one peak (or valley). You want to find the x where `f(x)` is maximized (or minimized).

Unlike binary search (which searches for equality), ternary search searches for extremes.

Example (Unimodal Function)

Let

```
f(x) = - (x - 2)^2 + 4
```

This is a parabola with a maximum at `x = 2`.

Ternary search gradually narrows the interval around the maximum:

1. Divide `[l, r]` into three parts
2. Evaluate `f(m1)` and `f(m2)`
3. Keep the side that contains the peak
4. Repeat until small enough

How It Works (Step-by-Step)

Step	Action
1	Pick two midpoints: `m1 = l + (r - l) / 3`, `m2 = r - (r - l) / 3`
2	Compare `f(m1)` and `f(m2)`
3	If `f(m1) < f(m2)` → maximum is in `[m1, r]`
4	Else → maximum is in `[l, m2]`
5	Repeat until `r - l` <

Tiny Code

C Implementation (Maximization)

```c
#include <stdio.h>
#include <math.h>

double f(double x) {
    return -pow(x - 2, 2) + 4; // peak at x=2
}

double ternary_search(double l, double r, double eps) {
    while (r - l > eps) {
        double m1 = l + (r - l) / 3;
        double m2 = r - (r - l) / 3;
        if (f(m1) < f(m2))
            l = m1;
        else
            r = m2;
    }
    return (l + r) / 2; // approx peak
}

int main() {
    double l = 0, r = 4;
    double res = ternary_search(l, r, 1e-6);
    printf("Approx max at x = %.6f, f(x) = %.6f\n", res, f(res));
}
```

Output:

```
Approx max at x = 2.000000, f(x) = 4.000000
```

Python Implementation

```python
def f(x):
    return -(x - 2)2 + 4  # Peak at x=2

def ternary_search(l, r, eps=1e-6):
```

```
    while r - l > eps:
        m1 = l + (r - l) / 3
        m2 = r - (r - l) / 3
        if f(m1) < f(m2):
            l = m1
        else:
            r = m2
    return (l + r) / 2

res = ternary_search(0, 4)
print(f"Max at x = {res:.6f}, f(x) = {f(res):.6f}")
```

Why It Matters

- Finds extrema (max/min) in continuous functions
- No derivative required (unlike calculus-based optimization)
- Works when:
  - `f(x)` is unimodal
  - Domain is continuous
  - You can evaluate `f(x)` cheaply

Used in:

- Mathematical optimization
- Machine learning hyperparameter tuning
- Geometry problems (e.g., closest distance)
- Physics simulations

Try It Yourself

1. Try `f(x) = (x - 5)^2 + 1` (minimization)
2. Use interval `[0, 10]` and `eps = 1e-6`
3. Change `eps` to `1e-3` → observe faster but rougher result
4. Apply to distance between two moving points
5. Compare with binary search on derivative
6. Plot f(x) to visualize narrowing intervals
7. Switch condition to find minimum
8. Test with `f(x) = sin(x)` on `[0, ]`
9. Use integer search version for discrete arrays
10. Combine with golden section search for efficiency

Test Cases

Function	Interval	Expected	Type
f(x) = -(x-2)^2 + 4	[0, 4]	x 2	Maximum
f(x) = (x-5)^2 + 1	[0, 10]	x 5	Minimum
f(x) = sin(x)	[0, 3.14]	x 1.57	Maximum

Complexity

Metric	Value
Time	O(log((r - l)/))
Space	O(1)

A Ternary Search slices the search space into thirds—zooming in on the peak or valley with mathematical precision, no derivatives required.

193 Hash-Based Search

A Hash-Based Search uses a hash function to map keys directly to indices in a table, giving constant-time expected lookups. Instead of scanning or comparing elements, it jumps straight to the bucket where the data should be.

What Problem Are We Solving?

When searching in a large dataset, linear search is too slow (O(n)) and binary search needs sorted data (O(log n)). Hash-based search lets you find, insert, or delete an item in O(1) average time, regardless of ordering.

It's the foundation of hash tables, hash maps, and dictionaries.

Example (Simple Lookup)

Suppose you want to store and search for names quickly:

```
$$"Alice", "Bob", "Carol", "Dave"]
```

A hash function maps each name to an index:

```
hash("Alice") → 2
hash("Bob")   → 5
hash("Carol") → 1
```

You place each name in its corresponding slot. Searching becomes instant:

```
hash("Bob") = 5 → found!
```

How It Works (Plain Language)

Step	Action
1	Compute hash(key) to get an index
2	Look up the bucket at that index
3	If multiple items hash to same bucket (collision), handle with a strategy (chaining, open addressing)
4	Compare keys if necessary
5	Return result

Tiny Code

C Implementation (with Linear Probing)

```c
#include <stdio.h>
#include <string.h>

#define SIZE 10

typedef struct {
    char key[20];
    int value;
    int used;
} Entry;

Entry table[SIZE];

int hash(char *key) {
    int h = 0;
    for (int i = 0; key[i]; i++)
```

```
        h = (h * 31 + key[i]) % SIZE;
    return h;
}

void insert(char *key, int value) {
    int h = hash(key);
    while (table[h].used) {
        if (strcmp(table[h].key, key) == 0) break;
        h = (h + 1) % SIZE;
    }
    strcpy(table[h].key, key);
    table[h].value = value;
    table[h].used = 1;
}

int search(char *key) {
    int h = hash(key), start = h;
    while (table[h].used) {
        if (strcmp(table[h].key, key) == 0)
            return table[h].value;
        h = (h + 1) % SIZE;
        if (h == start) break;
    }
    return -1; // not found
}

int main() {
    insert("Alice", 10);
    insert("Bob", 20);
    printf("Value for Bob: %d\n", search("Bob"));
}
```

Output:

```
Value for Bob: 20
```

Python Implementation (Built-in Dict)

```
people = {"Alice": 10, "Bob": 20, "Carol": 30}
```

```
print("Bob" in people)       # True
print(people["Carol"])       # 30
```

Python's `dict` uses an optimized open addressing hash table.

Why It Matters

- O(1) average lookup, insertion, and deletion
- No need for sorting
- Core to symbol tables, caches, dictionaries, compilers, and databases
- Can scale with resizing (rehashing)

Try It Yourself

1. Implement hash table with chaining using linked lists
2. Replace linear probing with quadratic probing
3. Measure lookup time vs. linear search on same dataset
4. Insert keys with collisions, ensure correctness
5. Create custom hash for integers: `h(x) = x % m`
6. Observe performance as table fills up (load factor > 0.7)
7. Implement delete operation carefully
8. Resize table when load factor high
9. Try a poor hash function (like `h=1`) and measure slowdown
10. Compare with Python's built-in dict

Test Cases

Operation	Input	Expected Output
Insert	("Alice", 10)	Stored
Insert	("Bob", 20)	Stored
Search	"Alice"	10
Search	"Eve"	Not found
Delete	"Bob"	Removed
Search	"Bob"	Not found

Complexity

Metric	Average	Worst Case
Search	O(1)	O(n)
Insert	O(1)	O(n)
Space	O(n)	O(n)

A Hash-Based Search is like a magic index, it jumps straight to the data you need, turning search into instant lookup.

194 Bloom Filter Lookup

A Bloom Filter is a probabilistic data structure that tells you if an element is definitely not in a set or possibly is. It's super fast and memory efficient, but allows false positives (never false negatives).

What Problem Are We Solving?

When working with huge datasets (like URLs, cache keys, or IDs), you may not want to store every element just to check membership. Bloom Filters give you a fast O(1) check:

- "Is this element in my set?" → Maybe
- "Is it definitely not in my set?" → Yes

They're widely used in databases, network systems, and search engines (e.g., to skip disk lookups).

Example (Cache Lookup)

You have a cache of 1 million items. Before hitting the database, you want to know:

> Should I even bother checking cache for this key?

Use a Bloom Filter to quickly tell if the key *could be* in cache. If filter says "no," skip lookup entirely.

Step	Action

How It Works (Plain Language)

Step	Action
1	Create a bit array of size `m` (all zeros)
2	Choose `k` independent hash functions
3	To insert an element: compute k hashes, set corresponding bits to 1
4	To query an element: compute k hashes, check if all bits are 1
5	If any bit = 0 → definitely not in set
6	If all bits = 1 → possibly in set (false positive possible)

Tiny Code

Python (Simple Bloom Filter)

```
from hashlib import sha256

class BloomFilter:
    def __init__(self, size=1000, hash_count=3):
        self.size = size
        self.hash_count = hash_count
        self.bits = [0] * size

    def _hashes(self, item):
        for i in range(self.hash_count):
            h = int(sha256((item + str(i)).encode()).hexdigest(), 16)
            yield h % self.size

    def add(self, item):
        for h in self._hashes(item):
            self.bits[h] = 1

    def contains(self, item):
        return all(self.bits[h] for h in self._hashes(item))

# Example usage
bf = BloomFilter()
```

```
bf.add("Alice")
print(bf.contains("Alice"))  # True (probably)
print(bf.contains("Bob"))    # False (definitely not)
```

Output:

```
True
False
```

Why It Matters

- Memory efficient for large sets
- No false negatives, if it says "no," you can trust it
- Used in caches, databases, distributed systems
- Reduces I/O by skipping non-existent entries

Try It Yourself

1. Build a Bloom Filter with 1000 bits and 3 hash functions
2. Insert 100 random elements
3. Query 10 existing and 10 non-existing elements
4. Measure false positive rate
5. Experiment with different `m` and `k` values
6. Integrate into a simple cache simulation
7. Implement double hashing to reduce hash cost
8. Compare memory use vs. Python `set`
9. Add support for merging filters (bitwise OR)
10. Try a Counting Bloom Filter (to support deletions)

Test Cases

Input	Expected Output
add("Alice")	Bits set
contains("Alice")	True (maybe)
contains("Bob")	False (definitely not)
add("Bob")	Bits updated
contains("Bob")	True (maybe)

Complexity

Operation	Time	Space
Insert	O(k)	O(m)
Lookup	O(k)	O(m)

k: number of hash functions m: size of bit array

A Bloom Filter is like a polite doorman, it'll never wrongly turn you away, but it might let in a stranger once in a while.

195 Cuckoo Hash Search

A Cuckoo Hash Table is a clever hash-based structure that guarantees O(1) lookup while avoiding long probe chains. It uses two hash functions and relocates existing keys when a collision occurs, just like a cuckoo bird kicking eggs out of a nest.

What Problem Are We Solving?

Traditional hash tables can degrade to O(n) when collisions pile up. Cuckoo hashing ensures constant-time lookups by guaranteeing every key has at most two possible positions. If both are taken, it kicks out an existing key and re-inserts it elsewhere.

It's widely used in network routers, high-performance caches, and hash-based indexes.

Example (Small Table)

Suppose you have 2 hash functions:

```
h1(x) = x % 3
h2(x) = (x / 3) % 3
```

Insert keys: 5, 8, 11

Key	h1	h2
5	2	1
8	2	2
11	2	1

When inserting 11, slot 2 is full, so we kick out 5 to its alternate position. This continues until every key finds a home.

How It Works (Plain Language)

Step	Action
1	Compute two hash indices: `h1(key)`, `h2(key)`
2	Try placing the key in `h1` slot
3	If occupied, evict existing key to its alternate slot
4	Repeat up to a threshold (to prevent infinite loops)
5	If full cycle detected → rehash with new functions

Each key lives in either position `h1(key)` or `h2(key)`.

Tiny Code

C Implementation (Simplified)

```
#include <stdio.h>

#define SIZE 7

int table1[SIZE], table2[SIZE];

int h1(int key) { return key % SIZE; }
int h2(int key) { return (key / SIZE) % SIZE; }

void insert(int key, int depth) {
    if (depth > SIZE) return; // avoid infinite loop
    int pos1 = h1(key);
    if (table1[pos1] == 0) {
        table1[pos1] = key;
        return;
    }
    int displaced = table1[pos1];
    table1[pos1] = key;
    int pos2 = h2(displaced);
    if (table2[pos2] == 0)
```

```
        table2[pos2] = displaced;
    else
        insert(displaced, depth + 1);
}

int search(int key) {
    return table1[h1(key)] == key || table2[h2(key)] == key;
}

int main() {
    insert(10, 0);
    insert(20, 0);
    insert(30, 0);
    printf("Search 20: %s\n", search(20) ? "Found" : "Not Found");
}
```

Output:

```
Search 20: Found
```

Python Implementation

```
SIZE = 7
table1 = [None] * SIZE
table2 = [None] * SIZE

def h1(x): return x % SIZE
def h2(x): return (x // SIZE) % SIZE

def insert(key, depth=0):
    if depth > SIZE:
        return False  # cycle detected
    pos1 = h1(key)
    if table1[pos1] is None:
        table1[pos1] = key
        return True
    key, table1[pos1] = table1[pos1], key
    pos2 = h2(key)
    if table2[pos2] is None:
        table2[pos2] = key
```

```
        return True
    return insert(key, depth + 1)

def search(key):
    return table1[h1(key)] == key or table2[h2(key)] == key

insert(10); insert(20); insert(30)
print("Search 20:", search(20))
```

Why It Matters

- O(1) worst-case lookup (always two probes)
- Eliminates long collision chains
- Great for high-performance systems
- Deterministic position = easy debugging

Try It Yourself

1. Insert numbers 1–10 and trace movements
2. Add detection for cycles → trigger rehash
3. Compare average probe count vs. linear probing
4. Implement delete(key) (mark slot empty)
5. Try resizing table dynamically
6. Use different hash functions for variety
7. Track load factor before rehashing
8. Store `(key, value)` pairs
9. Benchmark against chaining
10. Visualize movement paths during insertion

Test Cases

Operation	Input	Expected
Insert	5	Placed
Insert	8	Kicked 5, placed both
Search	5	Found
Search	11	Not Found
Delete	8	Removed
Search	8	Not Found

Complexity

Operation	Time	Space
Search	O(1)	O(n)
Insert	O(1) average	O(n)
Delete	O(1)	O(n)

Cuckoo hashing is like musical chairs for keys, when one can't sit, it makes another stand up and move, but everyone eventually finds a seat.

196 Robin Hood Hashing

Robin Hood Hashing is an open addressing strategy that balances fairness in hash table lookups. When two keys collide, the one that's traveled farther from its "home" index gets to stay, stealing the slot like Robin Hood, who took from the rich and gave to the poor.

What Problem Are We Solving?

Standard linear probing can cause clusters, long runs of occupied slots that slow searches. Robin Hood Hashing reduces variance in probe lengths, so every key has roughly equal access time. This leads to more predictable performance, even at high load factors.

Example (Collision Handling)

Suppose `hash(x) = x % 10`. Insert `[10, 20, 30, 21]`.

Key	Hash	Position	Probe Distance
10	0	0	0
20	0	1	1
30	0	2	2
21	1	2 (collision)	1

At position 2, `21` meets `30` (whose distance = 2). Since `21`'s distance (1) is less, it keeps probing. Robin Hood rule: if newcomer has greater or equal distance → swap. This keeps distribution even.

How It Works (Plain Language)

Step	Action
1	Compute hash = `key % table_size`
2	If slot empty → place item
3	Else, compare probe distance with occupant's
4	If new item's distance current's → swap and continue probing displaced item
5	Repeat until inserted

Tiny Code

C Implementation (Simplified)

```c
#include <stdio.h>

#define SIZE 10

typedef struct {
    int key;
    int used;
    int distance;
} Entry;

Entry table[SIZE];

int hash(int key) { return key % SIZE; }

void insert(int key) {
    int index = hash(key);
    int dist = 0;
    while (table[index].used) {
        if (table[index].distance < dist) {
            int temp_key = table[index].key;
            int temp_dist = table[index].distance;
            table[index].key = key;
            table[index].distance = dist;
            key = temp_key;
            dist = temp_dist;
        }
```

```
        index = (index + 1) % SIZE;
        dist++;
    }
    table[index].key = key;
    table[index].distance = dist;
    table[index].used = 1;
}

int search(int key) {
    int index = hash(key);
    int dist = 0;
    while (table[index].used) {
        if (table[index].key == key) return 1;
        if (table[index].distance < dist) return 0;
        index = (index + 1) % SIZE;
        dist++;
    }
    return 0;
}

int main() {
    insert(10);
    insert(20);
    insert(30);
    printf("Search 20: %s\n", search(20) ? "Found" : "Not Found");
}
```

Output:

```
Search 20: Found
```

Python Implementation

```
SIZE = 10
table = [None] * SIZE
distances = [0] * SIZE

def h(k): return k % SIZE

def insert(key):
```

```
    index = h(key)
    dist = 0
    while table[index] is not None:
        if distances[index] < dist:
            table[index], key = key, table[index]
            distances[index], dist = dist, distances[index]
        index = (index + 1) % SIZE
        dist += 1
    table[index], distances[index] = key, dist

def search(key):
    index = h(key)
    dist = 0
    while table[index] is not None:
        if table[index] == key:
            return True
        if distances[index] < dist:
            return False
        index = (index + 1) % SIZE
        dist += 1
    return False

insert(10); insert(20); insert(30)
print("Search 20:", search(20))
```

Why It Matters

- Predictable lookup times, probe lengths nearly uniform
- Outperforms linear probing at high load
- Fewer long clusters, more stable table behavior
- Great for performance-critical systems

Try It Yourself

1. Insert `[10, 20, 30, 21]` and trace swaps
2. Measure probe length variance vs. linear probing
3. Implement delete() with tombstone handling
4. Add resizing when load factor > 0.8
5. Compare performance with quadratic probing
6. Visualize table after 20 inserts

7. Experiment with different table sizes
8. Create histogram of probe lengths
9. Add key-value pair storage
10. Benchmark search time at 70%, 80%, 90% load

Test Cases

Operation	Input	Expected
Insert	10, 20, 30, 21	Evenly distributed
Search	20	Found
Search	40	Not Found
Delete	10	Removed
Insert	50	Placed at optimal position

Complexity

Operation	Time	Space
Search	O(1) avg	O(n)
Insert	O(1) avg	O(n)
Delete	O(1) avg	O(n)

Robin Hood Hashing keeps everyone honest, no key hoards fast access, and none are left wandering too far.

197 Jump Consistent Hashing

Jump Consistent Hashing is a lightweight, fast, and deterministic way to assign keys to buckets (servers, shards, or partitions) that minimizes remapping when the number of buckets changes.

It's designed for load balancing in distributed systems, like database shards or cache clusters.

What Problem Are We Solving?

When scaling systems horizontally, you often need to assign keys (like user IDs) to buckets (like servers). Naive methods (e.g. `key % N`) cause massive remapping when `N` changes. Jump Consistent Hashing avoids that, only a small fraction of keys move when a bucket is added or removed.

This ensures stability and predictable redistribution, ideal for distributed caches (Memcached, Redis) and databases (Bigtable, Ceph).

Example (Adding Buckets)

Suppose we have keys 1 to 6 and 3 buckets:

Key	Bucket (3)
1	2
2	0
3	2
4	1
5	0
6	2

When we add a new bucket (4 total), only a few keys change buckets, most stay where they are. That's the magic of *consistency*.

How It Works (Plain Language)

Step	Action
1	Treat key as a 64-bit integer
2	Initialize `b = -1` and `j = 0`

3	While `j < num_buckets`, update:
	`b = j`, `key = key * 2862933555777941757ULL + 1`
	`j = floor((b + 1) * (1LL << 31) / ((key >> 33) + 1))`

4	Return `b` as bucket index

It uses integer arithmetic only, no tables, no storage, just math.

Tiny Code

C Implementation

```c
#include <stdint.h>
#include <stdio.h>

int jump_consistent_hash(uint64_t key, int num_buckets) {
    int64_t b = -1, j = 0;
    while (j < num_buckets) {
        b = j;
        key = key * 2862933555777941757ULL + 1;
        j = (b + 1) * ((double)(1LL << 31) / ((key >> 33) + 1));
    }
    return (int)b;
}

int main() {
    for (uint64_t k = 1; k <= 6; k++)
        printf("Key %llu → Bucket %d\n", k, jump_consistent_hash(k, 3));
}
```

Output:

```
Key 1 → Bucket 2
Key 2 → Bucket 0
Key 3 → Bucket 2
Key 4 → Bucket 1
Key 5 → Bucket 0
Key 6 → Bucket 2
```

Python Implementation

```python
def jump_hash(key, num_buckets):
    b, j = -1, 0
    while j < num_buckets:
        b = j
        key = key * 2862933555777941757 + 1
        j = int((b + 1) * (1 << 31) / ((key >> 33) + 1))
    return b

for k in range(1, 7):
    print(f"Key {k} → Bucket {jump_hash(k, 3)}")
```

Why It Matters

- Stable distribution: minimal remapping on resize
- O(1) time, O(1) space
- Works great for sharding, load balancing, partitioning
- No need for external storage or ring structures (unlike consistent hashing rings)

Try It Yourself

1. Assign 10 keys across 3 buckets
2. Add a 4th bucket and see which keys move
3. Compare with `key % N` approach
4. Try very large bucket counts (10k+)
5. Benchmark speed, notice it's almost constant
6. Integrate with a distributed cache simulation
7. Test uniformity (distribution of keys)
8. Add random seeds for per-service variation
9. Visualize redistribution pattern
10. Compare with Rendezvous Hashing

Test Cases

Input	Buckets	Output
Key=1, N=3	3	2
Key=2, N=3	3	0
Key=3, N=3	3	2
Key=1, N=4	4	3 or 2 (depends on math)

Only a fraction of keys remap when N changes.

Complexity

Operation	Time	Space
Lookup	O(1)	O(1)
Insert	O(1)	O(1)

Jump Consistent Hashing is like a steady hand, even as your system grows, it keeps most keys right where they belong.

198 Prefix Search in Trie

A Trie (prefix tree) is a specialized tree structure that stores strings by their prefixes, enabling fast prefix-based lookups, ideal for autocomplete, dictionaries, and word search engines.

With a trie, searching for "app" instantly finds "apple", "apply", "appetite", etc.

What Problem Are We Solving?

Traditional data structures like arrays or hash tables can't efficiently answer questions like:

- "List all words starting with `pre`"
- "Does any word start with `tri`?"

A trie organizes data by prefix paths, making such queries fast and natural, often O(k) where k is the prefix length.

Example (Words: `app`, `apple`, `bat`)

The trie looks like this:

```
(root)
   a
      p
         p *
            l
               e *
   b
      a
         t *
```

Stars (*) mark word endings. Search "app" → found; list all completions → "app", "apple".

How It Works (Plain Language)

Step	Action
1	Each node represents a character
2	A path from root to node represents a prefix
3	When inserting, follow characters and create nodes as needed
4	Mark end of word when reaching last character

Step	Action
5	To search prefix: traverse nodes character by character
6	If all exist → prefix found; else → not found

Tiny Code

C Implementation (Simplified)

```c
#include <stdio.h>
#include <stdlib.h>
#include <stdbool.h>

#define ALPHABET 26

typedef struct TrieNode {
    struct TrieNode *child[ALPHABET];
    bool isEnd;
} TrieNode;

TrieNode* newNode() {
    TrieNode* node = calloc(1, sizeof(TrieNode));
    node->isEnd = false;
    return node;
}

void insert(TrieNode *root, const char *word) {
    for (int i = 0; word[i]; i++) {
        int idx = word[i] - 'a';
        if (!root->child[idx]) root->child[idx] = newNode();
        root = root->child[idx];
    }
    root->isEnd = true;
}

bool startsWith(TrieNode *root, const char *prefix) {
    for (int i = 0; prefix[i]; i++) {
        int idx = prefix[i] - 'a';
        if (!root->child[idx]) return false;
        root = root->child[idx];
    }
```

```
    return true;
}

int main() {
    TrieNode *root = newNode();
    insert(root, "app");
    insert(root, "apple");
    printf("Starts with 'ap': %s\n", startsWith(root, "ap") ? "Yes" : "No");
}
```

Output:

```
Starts with 'ap': Yes
```

Python Implementation

```
class TrieNode:
    def __init__(self):
        self.children = {}
        self.is_end = False

class Trie:
    def __init__(self):
        self.root = TrieNode()

    def insert(self, word):
        node = self.root
        for ch in word:
            if ch not in node.children:
                node.children[ch] = TrieNode()
            node = node.children[ch]
        node.is_end = True

    def starts_with(self, prefix):
        node = self.root
        for ch in prefix:
            if ch not in node.children:
                return False
            node = node.children[ch]
        return True
```

```
trie = Trie()
trie.insert("apple")
trie.insert("app")
print(trie.starts_with("ap"))  # True
```

Why It Matters

- O(k) prefix lookup (k = prefix length)
- Perfect for autocomplete, spell checkers, search engines
- Stores shared prefixes efficiently
- Can be extended for frequency, weights, or wildcard matching

Try It Yourself

1. Insert [“app”, “apple”, “apply”, “apt”]
2. Search prefix “ap” → expect True
3. Search prefix “ba” → expect False
4. Add function to list all words starting with a prefix
5. Implement delete(word)
6. Add frequency count at each node
7. Support uppercase letters
8. Store end-of-word markers clearly
9. Compare memory use vs hash table
10. Extend to autocomplete feature returning top-N completions

Test Cases

Operation	Input	Output
Insert	“app”	Stored
Insert	“apple”	Stored
startsWith	“ap”	True
startsWith	“ba”	False
startsWith	“app”	True

Complexity

Operation	Time	Space
Insert	O(k)	O(k)
Search Prefix	O(k)	O(1)
Space (n words)	O(sum of all characters)	,

A Trie turns your data into a map of words, every branch is a path toward meaning, every prefix a shortcut to discovery.

199 Pattern Search in Suffix Array

A Suffix Array is a sorted list of all suffixes of a string. It enables fast substring searches, perfect for pattern matching in text editors, DNA analysis, and search engines.

By combining it with binary search, you can find whether a pattern appears in a string in O(m log n) time.

What Problem Are We Solving?

Given a large text `T` (like `"banana"`) and a pattern `P` (like `"ana"`), we want to quickly check if `P` exists in `T`. Naive search takes O(nm) (compare every position). A suffix array lets us search more efficiently by working on a pre-sorted list of suffixes.

Example (Text = "banana")

List all suffixes and sort them:

Index	Suffix
0	banana
1	anana
2	nana
3	ana
4	na
5	a

Sorted suffixes:

SA Index	Suffix	Original Position
5	a	5

SA Index	Suffix	Original Position
3	ana	3
1	anana	1
0	banana	0
4	na	4
2	nana	2

Now search `"ana"` using binary search over these sorted suffixes.

How It Works (Plain Language)

Step	Action
1	Build suffix array = all suffixes sorted lexicographically
2	Use binary search to find lower/upper bounds for pattern
3	Compare only `m` characters per comparison
4	If found → pattern occurs at suffix index
5	Otherwise → not in text

Tiny Code

C Implementation (Simplified)

```c
#include <stdio.h>
#include <stdlib.h>
#include <string.h>

int cmp(const void *a, const void *b, void *txt) {
    int i = *(int*)a, j = *(int*)b;
    return strcmp((char*)txt + i, (char*)txt + j);
}

void build_suffix_array(char *txt, int n, int sa[]) {
    for (int i = 0; i < n; i++) sa[i] = i;
    qsort_r(sa, n, sizeof(int), cmp, txt);
}

int binary_search_suffix(char *txt, int sa[], int n, char *pat) {
```

```
    int l = 0, r = n - 1;
    while (l <= r) {
        int mid = (l + r) / 2;
        int res = strncmp(pat, txt + sa[mid], strlen(pat));
        if (res == 0) return sa[mid];
        if (res < 0) r = mid - 1;
        else l = mid + 1;
    }
    return -1;
}

int main() {
    char txt[] = "banana";
    int n = strlen(txt), sa[n];
    build_suffix_array(txt, n, sa);
    char pat[] = "ana";
    int pos = binary_search_suffix(txt, sa, n, pat);
    if (pos >= 0) printf("Pattern found at %d\n", pos);
    else printf("Pattern not found\n");
}
```

Output:

```
Pattern found at 1
```

Python Implementation

```
def build_suffix_array(s):
    return sorted(range(len(s)), key=lambda i: s[i:])

def search(s, sa, pat):
    l, r = 0, len(sa) - 1
    while l <= r:
        mid = (l + r) // 2
        suffix = s[sa[mid]:]
        if suffix.startswith(pat):
            return sa[mid]
        if suffix < pat:
            l = mid + 1
        else:
```

```
            r = mid - 1
    return -1

s = "banana"
sa = build_suffix_array(s)
print("Suffix Array:", sa)
print("Search 'ana':", search(s, sa, "ana"))
```

Output:

```
Suffix Array: [5, 3, 1, 0, 4, 2]
Search 'ana': 1
```

Why It Matters

- Substring search in O(m log n)
- Space-efficient alternative to suffix trees
- Great for full-text search, DNA sequencing, plagiarism detection
- Can be extended with LCP array for longest common prefix queries

Try It Yourself

1. Build suffix array for `"banana"`
2. Search `"na"`, `"ban"`, `"apple"`
3. Print all suffixes for visualization
4. Add LCP array for faster repeated queries
5. Compare with KMP algorithm speed
6. Use binary search manually to trace comparisons
7. Extend to count occurrences of pattern
8. Try longer text (e.g. "mississippi")
9. Implement in-place quicksort for SA
10. Benchmark vs. naive substring search

Test Cases

Text	Pattern	Expected Result
"banana"	"ana"	Found at 1
"banana"	"ban"	Found at 0

Text	Pattern	Expected Result
“banana”	“na”	Found at 2 or 4
“banana”	“cat”	Not Found

Complexity

Operation	Time	Space
Build SA	O(n log n)	O(n)
Search	O(m log n)	O(1)

A Suffix Array is like a library index, once sorted, every search becomes as simple as flipping to the right page.

200 Search in Infinite Array

A Search in Infinite Array (or unbounded array) is a technique for finding an element in a sorted list of unknown length. You can't directly use binary search because you don't know `n`, so you must first find a search bound, then perform binary search within it.

This idea is crucial for systems where data is streamed or dynamically sized, like logs, unrolled lists, or file scans.

What Problem Are We Solving?

If you're given an array-like interface (like `get(i)`), but no size `n`, how do you find `target` efficiently? You can't do linear search, it could be infinite. The trick: exponential search, grow bounds exponentially until you pass the target, then apply binary search in that window.

Example

Given sorted sequence:

```
$$3, 5, 9, 12, 17, 23, 31, 45, 67, 88, 100, ...]
```

Search for `31`:

1. Start with `low = 0, high = 1`

2. While `arr[high] < 31`, double `high`

   `high = 1 → 2 → 4 → 8`

3. Now `arr[8] = 67 > 31`, so search range is `[4, 8]`
4. Perform binary search in `[4, 8]`
5. Found at index 6

How It Works (Plain Language)

Step	Action
1	Start with `low = 0`, `high = 1`
2	While `arr[high] < target`, set `low = high`, `high *= 2`
3	Now the target lies between `low` and `high`
4	Perform standard binary search in `[low, high]`
5	Return index if found, else -1

Tiny Code

C Implementation (Simulated Infinite Array)

```c
#include <stdio.h>

int get(int arr[], int size, int i) {
    if (i >= size) return 1e9; // simulate infinity
    return arr[i];
}

int binary_search(int arr[], int low, int high, int target, int size) {
    while (low <= high) {
        int mid = low + (high - low) / 2;
        int val = get(arr, size, mid);
        if (val == target) return mid;
        if (val < target) low = mid + 1;
        else high = mid - 1;
    }
    return -1;
}
```

```c
int search_infinite(int arr[], int size, int target) {
    int low = 0, high = 1;
    while (get(arr, size, high) < target) {
        low = high;
        high *= 2;
    }
    return binary_search(arr, low, high, target, size);
}

int main() {
    int arr[] = {3, 5, 9, 12, 17, 23, 31, 45, 67, 88, 100};
    int size = sizeof(arr)/sizeof(arr[0]);
    int idx = search_infinite(arr, size, 31);
    printf("Found at index %d\n", idx);
}
```

Output:

```
Found at index 6
```

Python Implementation

```python
def get(arr, i):
    return arr[i] if i < len(arr) else float('inf')

def binary_search(arr, low, high, target):
    while low <= high:
        mid = (low + high) // 2
        val = get(arr, mid)
        if val == target:
            return mid
        if val < target:
            low = mid + 1
        else:
            high = mid - 1
    return -1

def search_infinite(arr, target):
    low, high = 0, 1
```

```
    while get(arr, high) < target:
        low = high
        high *= 2
    return binary_search(arr, low, high, target)

arr = [3, 5, 9, 12, 17, 23, 31, 45, 67, 88, 100]
print("Found at index:", search_infinite(arr, 31))
```

Output:

```
Found at index: 6
```

Why It Matters

- Works with streams, linked storage, APIs, or infinite generators
- Avoids full traversal, logarithmic growth
- Combines exploration (finding bounds) with binary search (exact match)
- Ideal for search engines, log readers, cloud data paging

Try It Yourself

1. Search `[1, 3, 5, 9, 12, 20]` for `9`
2. Search `[2, 4, 8, 16, 32, 64]` for `33` (not found)
3. Count number of `get()` calls, compare to linear search
4. Try `target` smaller than first element
5. Handle edge cases: empty array, target > max
6. Simulate infinite stream with `get()`
7. Replace doubling with `high = low + step` for adaptive growth
8. Visualize search window expansion
9. Generalize to descending arrays
10. Compare performance vs naive scan

Test Cases

Input Array	Target	Output
[3, 5, 9, 12, 17, 23, 31, 45]	31	6
[3, 5, 9, 12, 17, 23, 31, 45]	4	-1
[1, 2, 4, 8, 16]	8	3

Input Array	Target	Output
[10, 20, 30]	40	-1

Complexity

Operation	Time	Space
Search	O(log p)	O(1)

p = position of target in array

Searching an infinite array feels like navigating a foggy road, first find your headlights (bounds), then drive straight to the target.

Chapter 3. Data Structure in Action

Section 21. Arrays, linked lists, stacks, queues

201 Dynamic Array Resize

Dynamic array resizing is how we keep push operations fast while growing storage as needed. The idea is simple: when the array is full, allocate a bigger one, copy the elements, and keep going. If we double the capacity on each resize, the average cost per push stays constant.

What Problem Are We Solving?

A fixed array has a fixed size. Real programs do not always know n in advance. We want an array that supports `push` at end with near constant time, grows automatically, and keeps elements in contiguous memory for cache friendliness.

Goal: Provide `push`, `pop`, `get`, `set` on a resizable array with amortized O(1) time for push.

How Does It Work (Plain Language)?

Keep two numbers: size and capacity.

1. Start with a small capacity (for example, 1 or 8).
2. On `push`, if `size < capacity`, write the element and increase `size`.
3. If `size == capacity`, allocate new storage with capacity doubled, copy old elements, release the old block, then push.
4. Optionally, if many `pop`s reduce `size` far below `capacity`, shrink by halving to avoid wasted space.

Why doubling? Doubling keeps the number of costly resizes small. Most pushes are cheap writes. Only occasionally do we pay for copying.

Example Steps (Growth Simulation)

Step	Size Before	Capacity Before	Action	Size After	Capacity After
1	0	1	push(1)	1	1
2	1	1	full → resize to 2, copy 1 element, push(2)	2	2
3	2	2	full → resize to 4, copy 2 elements, push(3)	3	4
4	3	4	push(4)	4	4
5	4	4	full → resize to 8, copy 4 elements, push(5)	5	8

Notice how capacity doubles occasionally while most pushes cost O(1).

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>
#include <string.h>

typedef struct {
    size_t size;
    size_t capacity;
    int *data;
} DynArray;

int da_init(DynArray *a, size_t init_cap) {
    if (init_cap == 0) init_cap = 1;
    a->data = (int *)malloc(init_cap * sizeof(int));
    if (!a->data) return 0;
    a->size = 0;
    a->capacity = init_cap;
    return 1;
}

int da_resize(DynArray *a, size_t new_cap) {
    int *p = (int *)realloc(a->data, new_cap * sizeof(int));
    if (!p) return 0;
    a->data = p;
    a->capacity = new_cap;
```

```
    return 1;
}

int da_push(DynArray *a, int x) {
    if (a->size == a->capacity) {
        size_t new_cap = a->capacity * 2;
        if (!da_resize(a, new_cap)) return 0;
    }
    a->data[a->size++] = x;
    return 1;
}

int da_pop(DynArray *a, int *out) {
    if (a->size == 0) return 0;
    *out = a->data[--a->size];
    if (a->capacity > 1 && a->size <= a->capacity / 4) {
        size_t new_cap = a->capacity / 2;
        if (new_cap == 0) new_cap = 1;
        da_resize(a, new_cap);
    }
    return 1;
}

int main(void) {
    DynArray a;
    if (!da_init(&a, 1)) return 1;
    for (int i = 0; i < 10; ++i) da_push(&a, i);
    for (size_t i = 0; i < a.size; ++i) printf("%d ", a.data[i]);
    printf("\nsize=%zu cap=%zu\n", a.size, a.capacity);
    free(a.data);
    return 0;
}
```

Python

```
class DynArray:
    def __init__(self, init_cap=1):
        self._cap = max(1, init_cap)
        self._n = 0
        self._data = [None] * self._cap

    def _resize(self, new_cap):
```

```
        new = [None] * new_cap
        for i in range(self._n):
            new[i] = self._data[i]
        self._data = new
        self._cap = new_cap

    def push(self, x):
        if self._n == self._cap:
            self._resize(self._cap * 2)
        self._data[self._n] = x
        self._n += 1

    def pop(self):
        if self._n == 0:
            raise IndexError("pop from empty DynArray")
        self._n -= 1
        x = self._data[self._n]
        self._data[self._n] = None
        if self._cap > 1 and self._n <= self._cap // 4:
            self._resize(max(1, self._cap // 2))
        return x

    def __getitem__(self, i):
        if not 0 <= i < self._n:
            raise IndexError("index out of range")
        return self._data[i]
```

Why It Matters

- Amortized O(1) push for dynamic growth
- Contiguous memory for cache performance
- Simple API that underlies vectors, array lists, and many scripting language arrays
- Balanced memory usage via optional shrinking

A Gentle Proof (Why It Works)

Accounting view for doubling Charge each push a constant credit (e.g. 3 units).

1. A normal push costs 1 unit and stores 2 credits with the element.
2. When resizing from capacity k $\to$ 2k, copying k elements costs k units, paid by saved credits.

3. The new element pays its own 1 unit.

Thus amortized cost per push is O(1).

Growth factor choice Any factor > 1 gives amortized O(1).

- Doubling $\rightarrow$ fewer resizes, more memory slack
- 1.5x $\rightarrow$ less slack, more frequent copies
- Too small (<1.2) $\rightarrow$ breaks amortized bound

Try It Yourself

1. Simulate pushes 1..32 for factors 2.0 and 1.5. Count resizes.
2. Add `reserve(n)` to preallocate capacity.
3. Implement shrinking when `size <= capacity / 4`.
4. Replace `int` with a struct, measure copy cost.
5. Use potential method: $\Phi = 2 \cdot \text{size} - \text{capacity}$.

Test Cases

Operation Sequence	Capacity Trace (Factor 2)	Notes
push 1..8	$1 \rightarrow 2 \rightarrow 4 \rightarrow 8$	resize at 1, 2, 4
push 9	$8 \rightarrow 16$	resize before write
push 10..16	16	no resize
pop 16..9	16	shrinking optional
pop 8	$16 \rightarrow 8$	shrink at 25% load

Edge Cases

- Push on full array triggers one resize before write
- Pop on empty array should error or return false
- `reserve(n)` larger than current capacity must preserve data
- Shrink never reduces capacity below size

Complexity

- Time:
  - push amortized O(1)
  - push worst case O(n) on resize
  - pop amortized O(1)

  - get/set O(1)

- Space: O(n), capacity constant × size

Dynamic array resizing turns a rigid array into a flexible container. Grow when needed, copy occasionally, and enjoy constant-time pushes on average.

202 Circular Array Implementation

A circular array (or ring buffer) stores elements in a fixed-size array while allowing wrap-around indexing. It is perfect for implementing queues and buffers where old data is overwritten or processed in a first-in-first-out manner.

What Problem Are We Solving?

A regular array wastes space if we only move front and rear pointers forward. A circular array solves this by wrapping indices around when they reach the end, so all slots can be reused without shifting elements.

Goal: Efficiently support enqueue, dequeue, peek, and size in O(1) time using a fixed-size buffer with wrap-around indexing.

How Does It Work (Plain Language)?

Maintain:

- `front`: index of the first element
- `rear`: index of the next free slot
- `count`: number of elements in the buffer
- `capacity`: maximum number of elements

Wrap-around indexing uses modulo arithmetic:

```
next_index = (current_index + 1) % capacity
```

When adding or removing, always increment `front` or `rear` with this rule.

Example Steps (Wrap-around Simulation)

Step	Operation	Front	Rear	Count	Array State	Note
1	enqueue(10)	0	1	1	[10, , , _]	rear advanced
2	enqueue(20)	0	2	2	[10, 20, ,]	

Step	Operation	Front	Rear	Count	Array State	Note
3	enqueue(30)	0	3	3	[10, 20, 30, _]	
4	dequeue()	1	3	2	[, *20, 30,*]	front advanced
5	enqueue(40)	1	0	3	[40, 20, 30, _]	wrap-around
6	enqueue(50)	1	1	4	[40, 20, 30, 50]	full queue

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int *data;
    int front;
    int rear;
    int count;
    int capacity;
} CircularQueue;

int cq_init(CircularQueue *q, int capacity) {
    q->data = malloc(capacity * sizeof(int));
    if (!q->data) return 0;
    q->capacity = capacity;
    q->front = 0;
    q->rear = 0;
    q->count = 0;
    return 1;
}

int cq_enqueue(CircularQueue *q, int x) {
    if (q->count == q->capacity) return 0; // full
    q->data[q->rear] = x;
    q->rear = (q->rear + 1) % q->capacity;
    q->count++;
    return 1;
}

int cq_dequeue(CircularQueue *q, int *out) {
    if (q->count == 0) return 0; // empty
```

```
    *out = q->data[q->front];
    q->front = (q->front + 1) % q->capacity;
    q->count--;
    return 1;
}

int main(void) {
    CircularQueue q;
    cq_init(&q, 4);
    cq_enqueue(&q, 10);
    cq_enqueue(&q, 20);
    cq_enqueue(&q, 30);
    int val;
    cq_dequeue(&q, &val);
    cq_enqueue(&q, 40);
    cq_enqueue(&q, 50); // should fail if capacity=4
    printf("Front value: %d\n", q.data[q.front]);
    free(q.data);
    return 0;
}
```

Python

```
class CircularQueue:
    def __init__(self, capacity):
        self._cap = capacity
        self._data = [None] * capacity
        self._front = 0
        self._rear = 0
        self._count = 0

    def enqueue(self, x):
        if self._count == self._cap:
            raise OverflowError("queue full")
        self._data[self._rear] = x
        self._rear = (self._rear + 1) % self._cap
        self._count += 1

    def dequeue(self):
        if self._count == 0:
            raise IndexError("queue empty")
        x = self._data[self._front]
```

```
        self._front = (self._front + 1) % self._cap
        self._count -= 1
        return x

    def peek(self):
        if self._count == 0:
            raise IndexError("queue empty")
        return self._data[self._front]
```

Why It Matters

- Enables constant time queue operations
- No element shifting needed
- Efficient use of fixed memory
- Backbone for circular buffers, task schedulers, streaming pipelines, and audio/video buffers

A Gentle Proof (Why It Works)

Modulo indexing ensures positions loop back when reaching array end. If capacity is n, then all indices stay in `[0, n-1]`. No overflow occurs since `front`, `rear` always wrap around. The condition `count == capacity` detects full queue, and `count == 0` detects empty.

Thus each operation touches only one element and updates O(1) variables.

Try It Yourself

1. Implement a circular buffer with overwrite (old data replaced).
2. Add `is_full()` and `is_empty()` helpers.
3. Simulate producer-consumer with one enqueue per producer tick and one dequeue per consumer tick.
4. Extend to store structs instead of integers.

Test Cases

Operation Sequence	Front	Rear	Count	Array State	Notes
enqueue(10)	0	1	1	[10, , , _]	normal push
enqueue(20)	0	2	2	[10, 20, ,]	
enqueue(30)	0	3	3	[10, 20, 30, _]	

Operation Sequence	Front	Rear	Count	Array State	Notes
dequeue()	1	3	2	[, *20, 30,*]	
enqueue(40)	1	0	3	[40, 20, 30, _]	wrap-around
enqueue(50)	1	1	4	[40, 20, 30, 50]	full

Edge Cases

- Enqueue when full → error or overwrite
- Dequeue when empty → error
- Modulo indexing avoids overflow
- Works with any capacity 1

Complexity

- Time: O(1) for enqueue, dequeue, peek
- Space: O(n) fixed buffer

Circular arrays provide elegant constant-time queues with wrap-around indexing, a small trick that powers big systems.

203 Singly Linked List Insert/Delete

A singly linked list is a chain of nodes, each pointing to the next. It grows and shrinks dynamically without preallocating memory. Operations like insert and delete rely on pointer adjustments rather than shifting elements.

What Problem Are We Solving?

Static arrays are fixed-size and require shifting elements for insertions or deletions in the middle. Singly linked lists solve this by connecting elements through pointers, allowing efficient O(1) insertion and deletion (given a node reference).

Goal: Support insert, delete, and traversal on a structure that can grow dynamically without reallocating or shifting elements.

How Does It Work (Plain Language)?

Each node stores two fields:

- `data` (the value)
- `next` (pointer to the next node)

The list has a `head` pointer to the first node. Insertion and deletion work by updating the `next` pointers.

Example Steps (Insertion at Position)

Step	Operation	Node Updated	Before	After	Notes
1	create list	-	empty	head = NULL	list starts empty
2	insert(10) at head	new node	NULL	[10]	head → 10
3	insert(20) at head	new node	[10]	[20 → 10]	head updated
4	insert(30) after 20	new node	[20 → 10]	[20 → 30 → 10]	pointer rerouted
5	delete(30)	node 20	[20 → 30 → 10]	[20 → 10]	bypass removed node

Key idea: To insert, point the new node's `next` to the target's next, then link the target's `next` to the new node. To delete, bypass the target node by linking previous node's `next` to the one after target.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int data;
    struct Node *next;
} Node;

Node* insert_head(Node* head, int value) {
    Node* new_node = malloc(sizeof(Node));
    new_node->data = value;
```

```
    new_node->next = head;
    return new_node; // new head
}

Node* insert_after(Node* node, int value) {
    if (!node) return NULL;
    Node* new_node = malloc(sizeof(Node));
    new_node->data = value;
    new_node->next = node->next;
    node->next = new_node;
    return new_node;
}

Node* delete_value(Node* head, int value) {
    if (!head) return NULL;
    if (head->data == value) {
        Node* tmp = head->next;
        free(head);
        return tmp;
    }
    Node* prev = head;
    Node* cur = head->next;
    while (cur) {
        if (cur->data == value) {
            prev->next = cur->next;
            free(cur);
            break;
        }
        prev = cur;
        cur = cur->next;
    }
    return head;
}

void print_list(Node* head) {
    for (Node* p = head; p; p = p->next)
        printf("%d -> ", p->data);
    printf("NULL\n");
}

int main(void) {
    Node* head = NULL;
```

```
    head = insert_head(head, 10);
    head = insert_head(head, 20);
    insert_after(head, 30);
    print_list(head);
    head = delete_value(head, 30);
    print_list(head);
    return 0;
}
```

Python

```
class Node:
    def __init__(self, data):
        self.data = data
        self.next = None

class LinkedList:
    def __init__(self):
        self.head = None

    def insert_head(self, data):
        node = Node(data)
        node.next = self.head
        self.head = node

    def insert_after(self, prev, data):
        if prev is None:
            return
        node = Node(data)
        node.next = prev.next
        prev.next = node

    def delete_value(self, value):
        cur = self.head
        prev = None
        while cur:
            if cur.data == value:
                if prev:
                    prev.next = cur.next
                else:
                    self.head = cur.next
                return
```

```
            prev = cur
            cur = cur.next

    def print_list(self):
        cur = self.head
        while cur:
            print(cur.data, end=" -> ")
            cur = cur.next
        print("NULL")
```

Why It Matters

- Provides dynamic growth with no preallocation
- Enables O(1) insertion and deletion at head or given position
- Useful in stacks, queues, hash table buckets, and adjacency lists
- Foundation for more complex data structures (trees, graphs)

A Gentle Proof (Why It Works)

Each operation only changes a constant number of pointers.

- Insert: 2 assignments → O(1)
- Delete: find node O(n), then 1 reassignment Because pointers are updated locally, the rest of the list remains valid.

Try It Yourself

1. Implement insert_tail for O(n) tail insertion.
2. Write reverse() to flip the list in place.
3. Add size() to count nodes.
4. Experiment with deleting from head and middle.

Test Cases

Operation	Input	Result	Notes
insert_head(10)	[]	[10]	creates head
insert_head(20)	[10]	[20 → 10]	new head
insert_after(head, 30)	[20 → 10]	[20 → 30 → 10]	pointer reroute
delete_value(30)	[20 → 30 → 10]	[20 → 10]	node removed

Operation	Input	Result	Notes
delete_value(40)	[20 → 10]	[20 → 10]	no change

Edge Cases

- Delete from empty list → no effect
- Insert after NULL → no effect
- Delete head node → update head pointer

Complexity

- Time: insert O(1), delete O(n) (if searching by value), traversal O(n)
- Space: O(n) for n nodes

Singly linked lists teach pointer manipulation, where structure grows one node at a time, and every link matters.

204 Doubly Linked List Insert/Delete

A doubly linked list extends the singly linked list by adding backward links. Each node points to both its previous and next neighbor, making insertions and deletions easier in both directions.

What Problem Are We Solving?

Singly linked lists cannot traverse backward and deleting a node requires access to its predecessor. Doubly linked lists fix this by storing two pointers per node, allowing constant-time insertions and deletions at any position when you have a node reference.

Goal: Support bidirectional traversal and efficient local insert/delete operations with O(1) pointer updates.

How Does It Work (Plain Language)?

Each node stores:

- `data`: the value
- `prev`: pointer to the previous node
- `next`: pointer to the next node

The list tracks two ends:

- `head` points to the first node
- `tail` points to the last node

Example Steps (Insertion and Deletion)

Step	Operation	Target	Before	After	Note
1	create list	-	empty	[10]	head=tail=10
2	insert_front(20)	head	[10]	[20 10]	head updated
3	insert_back(30)	tail	[20 10]	[20 10 30]	tail updated
4	delete(10)	middle	[20 10 30]	[20 30]	pointers bypass 10

Each operation only touches nearby nodes, no need to shift elements.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int data;
    struct Node* prev;
    struct Node* next;
} Node;

Node* insert_front(Node* head, int value) {
    Node* node = malloc(sizeof(Node));
    node->data = value;
    node->prev = NULL;
    node->next = head;
    if (head) head->prev = node;
    return node;
}

Node* insert_back(Node* head, int value) {
    Node* node = malloc(sizeof(Node));
    node->data = value;
    node->next = NULL;
    if (!head) {
        node->prev = NULL;
```

```
        return node;
    }
    Node* tail = head;
    while (tail->next) tail = tail->next;
    tail->next = node;
    node->prev = tail;
    return head;
}

Node* delete_value(Node* head, int value) {
    Node* cur = head;
    while (cur && cur->data != value) cur = cur->next;
    if (!cur) return head; // not found
    if (cur->prev) cur->prev->next = cur->next;
    else head = cur->next; // deleting head
    if (cur->next) cur->next->prev = cur->prev;
    free(cur);
    return head;
}

void print_forward(Node* head) {
    for (Node* p = head; p; p = p->next) printf("%d  ", p->data);
    printf("NULL\n");
}
```

Python

```
class Node:
    def __init__(self, data):
        self.data = data
        self.prev = None
        self.next = None

class DoublyLinkedList:
    def __init__(self):
        self.head = None

    def insert_front(self, data):
        node = Node(data)
        node.next = self.head
        if self.head:
            self.head.prev = node
```

```
        self.head = node

    def insert_back(self, data):
        node = Node(data)
        if not self.head:
            self.head = node
            return
        cur = self.head
        while cur.next:
            cur = cur.next
        cur.next = node
        node.prev = cur

    def delete_value(self, value):
        cur = self.head
        while cur:
            if cur.data == value:
                if cur.prev:
                    cur.prev.next = cur.next
                else:
                    self.head = cur.next
                if cur.next:
                    cur.next.prev = cur.prev
                return
            cur = cur.next

    def print_forward(self):
        cur = self.head
        while cur:
            print(cur.data, end="  ")
            cur = cur.next
        print("NULL")
```

Why It Matters

- Bidirectional traversal (forward/backward)
- O(1) insertion and deletion when node is known
- Foundation for deque, LRU cache, and text editor buffers
- Enables clean list reversal and splice operations

A Gentle Proof (Why It Works)

Each node update modifies at most four pointers:

- Insert: new node's `next`, `prev` + neighbor links
- Delete: predecessor's `next`, successor's `prev` Since each step is constant work, operations are O(1) given node reference.

Traversal still costs O(n), but local edits are efficient.

Try It Yourself

1. Implement reverse() by swapping `prev` and `next` pointers.
2. Add tail pointer to allow O(1) insert_back.
3. Support bidirectional iteration.
4. Implement `pop_front()` and `pop_back()`.

Test Cases

Operation	Input	Output	Notes
insert_front(10)	[]	[10]	head=tail=10
insert_front(20)	[10]	[20 10]	new head
insert_back(30)	[20 10]	[20 10 30]	new tail
delete_value(10)	[20 10 30]	[20 30]	middle removed
delete_value(20)	[20 30]	[30]	head removed

Edge Cases

- Deleting from empty list → no effect
- Inserting on empty list sets both head and tail
- Properly maintain both directions after each update

Complexity

- Time:
  - Insert/Delete (given node): O(1)
  - Search: O(n)
  - Traverse: O(n)
- Space: O(n) (2 pointers per node)

Doubly linked lists bring symmetry, move forward, move back, and edit in constant time.

205 Stack Push/Pop

A stack is a simple but powerful data structure that follows the LIFO (Last In, First Out) rule. The most recently added element is the first to be removed, like stacking plates where you can only take from the top.

What Problem Are We Solving?

We often need to reverse order or track nested operations, such as function calls, parentheses, undo/redo, and expression evaluation. A stack gives us a clean way to manage this behavior with push (add) and pop (remove).

Goal: Support push, pop, peek, and is_empty in O(1) time, maintaining LIFO order.

How Does It Work (Plain Language)?

Think of a vertical pile.

- Push(x): Place x on top.
- Pop(): Remove the top element.
- Peek(): View top without removing.

Implementation can use either an array (fixed or dynamic) or a linked list.

Example Steps (Array Stack Simulation)

Step	Operation	Stack (Top → Bottom)	Note
1	push(10)	[10]	first element
2	push(20)	[20, 10]	top is 20
3	push(30)	[30, 20, 10]	
4	pop()	[20, 10]	30 removed
5	peek()	top = 20	top unchanged

Tiny Code (Easy Versions)

C (Array-Based Stack)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int *data;
    int top;
    int capacity;
} Stack;

int stack_init(Stack *s, int cap) {
    s->data = malloc(cap * sizeof(int));
    if (!s->data) return 0;
    s->capacity = cap;
    s->top = -1;
    return 1;
}

int stack_push(Stack *s, int x) {
    if (s->top + 1 == s->capacity) return 0; // full
    s->data[++s->top] = x;
    return 1;
}

int stack_pop(Stack *s, int *out) {
    if (s->top == -1) return 0; // empty
    *out = s->data[s->top--];
    return 1;
}

int stack_peek(Stack *s, int *out) {
    if (s->top == -1) return 0;
    *out = s->data[s->top];
    return 1;
}

int main(void) {
    Stack s;
    stack_init(&s, 5);
    stack_push(&s, 10);
    stack_push(&s, 20);
    int val;
    stack_pop(&s, &val);
```

```
    printf("Popped: %d\n", val);
    stack_peek(&s, &val);
    printf("Top: %d\n", val);
    free(s.data);
    return 0;
}
```

Python (List as Stack)

```
class Stack:
    def __init__(self):
        self._data = []

    def push(self, x):
        self._data.append(x)

    def pop(self):
        if not self._data:
            raise IndexError("pop from empty stack")
        return self._data.pop()

    def peek(self):
        if not self._data:
            raise IndexError("peek from empty stack")
        return self._data[-1]

    def is_empty(self):
        return len(self._data) == 0

# Example
s = Stack()
s.push(10)
s.push(20)
print(s.pop())  # 20
print(s.peek()) # 10
```

Why It Matters

- Core to recursion, parsing, and backtracking
- Underpins function call stacks in programming languages
- Natural structure for undo, reverse, and balanced parentheses
- Simplicity with wide applications in algorithms

A Gentle Proof (Why It Works)

Each operation touches only the top element or index.

- `push`: increment top, write value
- `pop`: read top, decrement top All O(1) time. The LIFO property ensures correct reverse order for function calls and nested scopes.

Try It Yourself

1. Implement stack with linked list nodes.
2. Extend capacity dynamically when full.
3. Use stack to check balanced parentheses in a string.
4. Reverse a list using stack operations.

Test Cases

Operation	Input	Output	Notes
push(10)	[]	[10]	top = 10
push(20)	[10]	[20, 10]	top = 20
pop()	[20, 10]	returns 20, stack [10]	
peek()	[10]	returns 10	
pop()	[10]	returns 10, stack []	empty after pop

Edge Cases

- Pop from empty → error or return false
- Peek from empty → error
- Overflow if array full (unless dynamic)

Complexity

- Time: push O(1), pop O(1), peek O(1)
- Space: O(n) for n elements

Stacks embody disciplined memory, last in, first out, a minimalist model of control flow and history.

206 Queue Enqueue/Dequeue

A queue is the mirror twin of a stack. It follows FIFO (First In, First Out), the first element added is the first one removed, like people waiting in line.

What Problem Are We Solving?

We need a structure where items are processed in arrival order: scheduling tasks, buffering data, breadth-first search, or managing print jobs. A queue lets us enqueue at the back and dequeue from the front, simple and fair.

Goal: Support enqueue, dequeue, peek, and is_empty in O(1) time using a circular layout or linked list.

How Does It Work (Plain Language)?

A queue has two ends:

- front → where items are removed
- rear → where items are added

Operations:

- `enqueue(x)` adds at `rear`
- `dequeue()` removes from `front`
- `peek()` looks at the `front` item

If implemented with a circular array, wrap indices using modulo arithmetic.

Example Steps (FIFO Simulation)

Step	Operation	Queue (Front → Rear)	Front	Rear	Note
1	enqueue(10)	[10]	0	1	first element
2	enqueue(20)	[10, 20]	0	2	rear advanced
3	enqueue(30)	[10, 20, 30]	0	3	
4	dequeue()	[20, 30]	1	3	10 removed
5	enqueue(40)	[20, 30, 40]	1	0	wrap-around

Tiny Code (Easy Versions)

C (Circular Array Queue)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int *data;
    int front;
    int rear;
    int count;
    int capacity;
} Queue;

int queue_init(Queue *q, int cap) {
    q->data = malloc(cap * sizeof(int));
    if (!q->data) return 0;
    q->capacity = cap;
    q->front = 0;
    q->rear = 0;
    q->count = 0;
    return 1;
}

int enqueue(Queue *q, int x) {
    if (q->count == q->capacity) return 0; // full
    q->data[q->rear] = x;
    q->rear = (q->rear + 1) % q->capacity;
    q->count++;
    return 1;
}

int dequeue(Queue *q, int *out) {
    if (q->count == 0) return 0; // empty
    *out = q->data[q->front];
    q->front = (q->front + 1) % q->capacity;
    q->count--;
    return 1;
}

int queue_peek(Queue *q, int *out) {
    if (q->count == 0) return 0;
```

```
    *out = q->data[q->front];
    return 1;
}

int main(void) {
    Queue q;
    queue_init(&q, 4);
    enqueue(&q, 10);
    enqueue(&q, 20);
    enqueue(&q, 30);
    int val;
    dequeue(&q, &val);
    printf("Dequeued: %d\n", val);
    enqueue(&q, 40);
    enqueue(&q, 50); // will fail if capacity = 4
    queue_peek(&q, &val);
    printf("Front: %d\n", val);
    free(q.data);
    return 0;
}
```

Python (List as Queue using deque)

```
from collections import deque

class Queue:
    def __init__(self):
        self._data = deque()

    def enqueue(self, x):
        self._data.append(x)

    def dequeue(self):
        if not self._data:
            raise IndexError("dequeue from empty queue")
        return self._data.popleft()

    def peek(self):
        if not self._data:
            raise IndexError("peek from empty queue")
        return self._data[0]
```

```
    def is_empty(self):
        return len(self._data) == 0

# Example
q = Queue()
q.enqueue(10)
q.enqueue(20)
print(q.dequeue())  # 10
print(q.peek())     # 20
```

Why It Matters

- Enforces fairness (first come, first served)
- Foundation for BFS, schedulers, buffers, pipelines
- Easy to implement and reason about
- Natural counterpart to stack

A Gentle Proof (Why It Works)

Each operation updates only front or rear index, not entire array. Circular indexing ensures constant-time wrap-around:

```
rear = (rear + 1) % capacity
front = (front + 1) % capacity
```

All operations touch O(1) data and fields, so runtime stays O(1).

Try It Yourself

1. Implement a linked-list-based queue.
2. Add `is_full()` and `is_empty()` checks.
3. Write a queue-based BFS on a simple graph.
4. Compare linear vs circular queue behavior.

Operation	Queue (Front → Rear)	Front	Rear	Count	Notes

Test Cases

Operation	Queue (Front → Rear)	Front	Rear	Count	Notes
enqueue(10)	[10]	0	1	1	
enqueue(20)	[10, 20]	0	2	2	
enqueue(30)	[10, 20, 30]	0	3	3	
dequeue()	[20, 30]	1	3	2	removes 10
enqueue(40)	[20, 30, 40]	1	0	3	wrap-around
peek()	front=20	1	0	3	check front

Edge Cases

- Dequeue from empty → error
- Enqueue to full → overflow
- Works seamlessly with wrap-around

Complexity

- Time: enqueue O(1), dequeue O(1), peek O(1)
- Space: O(n) for fixed buffer or dynamic growth

Queues bring fairness to data, what goes in first comes out first, steady and predictable.

207 Deque Implementation

A deque (double-ended queue) is a flexible container that allows adding and removing elements from both ends, a blend of stack and queue behavior.

What Problem Are We Solving?

Stacks restrict you to one end, queues to two fixed roles. Sometimes we need both: insert at front or back, pop from either side. Deques power sliding window algorithms, palindrome checks, undo-redo systems, and task schedulers.

Goal: Support `push_front`, `push_back`, `pop_front`, `pop_back`, and `peek_front/back` in O(1) time.

How Does It Work (Plain Language)?

Deques can be built using:

- A circular array (using wrap-around indexing)
- A doubly linked list (bidirectional pointers)

Operations:

- `push_front(x)` → insert before front
- `push_back(x)` → insert after rear
- `pop_front()` → remove front element
- `pop_back()` → remove rear element

Example Steps (Circular Array Simulation)

Step	Operation	Front	Rear	Deque (Front → Rear)	Note
1	push_back(10)	0	1	[10]	first item
2	push_back(20)	0	2	[10, 20]	rear grows
3	push_front(5)	3	2	[5, 10, 20]	wrap-around front
4	pop_back()	3	1	[5, 10]	20 removed
5	pop_front()	0	1	[10]	5 removed

Tiny Code (Easy Versions)

C (Circular Array Deque)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int *data;
    int front;
    int rear;
    int count;
    int capacity;
} Deque;

int dq_init(Deque *d, int cap) {
    d->data = malloc(cap * sizeof(int));
    if (!d->data) return 0;
    d->capacity = cap;
```

```
    d->front = 0;
    d->rear = 0;
    d->count = 0;
    return 1;
}

int dq_push_front(Deque *d, int x) {
    if (d->count == d->capacity) return 0; // full
    d->front = (d->front - 1 + d->capacity) % d->capacity;
    d->data[d->front] = x;
    d->count++;
    return 1;
}

int dq_push_back(Deque *d, int x) {
    if (d->count == d->capacity) return 0;
    d->data[d->rear] = x;
    d->rear = (d->rear + 1) % d->capacity;
    d->count++;
    return 1;
}

int dq_pop_front(Deque *d, int *out) {
    if (d->count == 0) return 0;
    *out = d->data[d->front];
    d->front = (d->front + 1) % d->capacity;
    d->count--;
    return 1;
}

int dq_pop_back(Deque *d, int *out) {
    if (d->count == 0) return 0;
    d->rear = (d->rear - 1 + d->capacity) % d->capacity;
    *out = d->data[d->rear];
    d->count--;
    return 1;
}

int main(void) {
    Deque d;
    dq_init(&d, 4);
    dq_push_back(&d, 10);
```

```
    dq_push_back(&d, 20);
    dq_push_front(&d, 5);
    int val;
    dq_pop_back(&d, &val);
    printf("Popped back: %d\n", val);
    dq_pop_front(&d, &val);
    printf("Popped front: %d\n", val);
    free(d.data);
    return 0;
}
```

Python (Deque using collections)

```
from collections import deque

d = deque()
d.append(10)       # push_back
d.appendleft(5)    # push_front
d.append(20)
print(d.pop())     # pop_back -> 20
print(d.popleft()) # pop_front -> 5
print(d)           # deque([10])
```

Why It Matters

- Generalizes both stack and queue
- Core tool for sliding window maximum, palindrome checks, BFS with state, and task buffers
- Doubly-ended flexibility with constant-time operations
- Ideal for systems needing symmetric access

A Gentle Proof (Why It Works)

Circular indexing ensures wrap-around in O(1). Each operation moves one index and changes one value:

- push → set value + adjust index
- pop → adjust index + read value

No shifting or reallocation needed, so all operations remain O(1).

Try It Yourself

1. Implement deque with a doubly linked list.
2. Add `peek_front()` and `peek_back()`.
3. Simulate a sliding window maximum algorithm.
4. Compare performance of deque vs list for queue-like tasks.

Test Cases

Operation	Front	Rear	Count	Deque (Front → Rear)	Notes
push_back(10)	0	1	1	[10]	init
push_back(20)	0	2	2	[10, 20]	
push_front(5)	3	2	3	[5, 10, 20]	wrap front
pop_back()	3	1	2	[5, 10]	20 removed
pop_front()	0	1	1	[10]	5 removed

Edge Cases

- Push on full deque → error or resize
- Pop on empty deque → error
- Wrap-around correctness is critical

Complexity

- Time: push/pop front/back O(1)
- Space: O(n)

Deques are the agile queues, you can act from either side, fast and fair.

208 Circular Queue

A circular queue is a queue optimized for fixed-size buffers where indices wrap around automatically. It's widely used in real-time systems, network packet buffers, and streaming pipelines to reuse space efficiently.

What Problem Are We Solving?

A linear queue wastes space after several dequeues, since front indices move forward. A circular queue solves this by wrapping the indices, making every slot reusable.

Goal: Implement a queue with fixed capacity where enqueue and dequeue both take O(1) time and space is used cyclically.

How Does It Work (Plain Language)?

A circular queue keeps track of:

- `front`: index of the first element
- `rear`: index of the next position to insert
- `count`: number of elements

Use modulo arithmetic for wrap-around:

```
next_index = (current_index + 1) % capacity
```

Key Conditions

- Full when `count == capacity`
- Empty when `count == 0`

Example Steps (Wrap-around Simulation)

Step	Operation	Front	Rear	Count	Queue State	Note
1	enqueue(10)	0	1	1	[10, , , _]	
2	enqueue(20)	0	2	2	[10, 20, ,]	
3	enqueue(30)	0	3	3	[10, 20, 30, _]	
4	dequeue()	1	3	2	[, *20, 30,*]	front advanced
5	enqueue(40)	1	0	3	[40, 20, 30, _]	wrap-around
6	enqueue(50)	1	1	4	[40, 20, 30, 50]	full

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int *data;
    int front;
    int rear;
    int count;
    int capacity;
} CircularQueue;

int cq_init(CircularQueue *q, int cap) {
    q->data = malloc(cap * sizeof(int));
    if (!q->data) return 0;
    q->capacity = cap;
    q->front = 0;
    q->rear = 0;
    q->count = 0;
    return 1;
}

int cq_enqueue(CircularQueue *q, int x) {
    if (q->count == q->capacity) return 0; // full
    q->data[q->rear] = x;
    q->rear = (q->rear + 1) % q->capacity;
    q->count++;
    return 1;
}

int cq_dequeue(CircularQueue *q, int *out) {
    if (q->count == 0) return 0; // empty
    *out = q->data[q->front];
    q->front = (q->front + 1) % q->capacity;
    q->count--;
    return 1;
}

int cq_peek(CircularQueue *q, int *out) {
    if (q->count == 0) return 0;
    *out = q->data[q->front];
    return 1;
}
```

```c
int main(void) {
    CircularQueue q;
    cq_init(&q, 4);
    cq_enqueue(&q, 10);
    cq_enqueue(&q, 20);
    cq_enqueue(&q, 30);
    int val;
    cq_dequeue(&q, &val);
    printf("Dequeued: %d\n", val);
    cq_enqueue(&q, 40);
    cq_enqueue(&q, 50); // should fail if full
    cq_peek(&q, &val);
    printf("Front: %d\n", val);
    free(q.data);
    return 0;
}
```

Python

```python
class CircularQueue:
    def __init__(self, capacity):
        self._cap = capacity
        self._data = [None] * capacity
        self._front = 0
        self._rear = 0
        self._count = 0

    def enqueue(self, x):
        if self._count == self._cap:
            raise OverflowError("Queue full")
        self._data[self._rear] = x
        self._rear = (self._rear + 1) % self._cap
        self._count += 1

    def dequeue(self):
        if self._count == 0:
            raise IndexError("Queue empty")
        x = self._data[self._front]
        self._front = (self._front + 1) % self._cap
        self._count -= 1
        return x
```

```
    def peek(self):
        if self._count == 0:
            raise IndexError("Queue empty")
        return self._data[self._front]

# Example
q = CircularQueue(4)
q.enqueue(10)
q.enqueue(20)
q.enqueue(30)
print(q.dequeue())  # 10
q.enqueue(40)
print(q.peek())     # 20
```

Why It Matters

- Efficient space reuse, no wasted slots
- Predictable memory usage for real-time systems
- Backbone of buffering systems (audio, network, streaming)
- Fast O(1) operations, no shifting elements

A Gentle Proof (Why It Works)

Since both `front` and `rear` wrap using modulo, all operations remain in range `[0, capacity-1]`. Each operation modifies a fixed number of variables. Thus:

- enqueue: 1 write + 2 updates
- dequeue: 1 read + 2 updates No shifting, no resizing → all O(1) time.

Try It Yourself

1. Add `is_full()` and `is_empty()` helpers.
2. Implement an overwrite mode where new enqueues overwrite oldest data.
3. Visualize index movement for multiple wraps.
4. Use a circular queue to simulate a producer-consumer buffer.

Test Cases

Operation	Front	Rear	Count	Queue (Front → Rear)	Notes
enqueue(10)	0	1	1	[10, , , _]	first element
enqueue(20)	0	2	2	[10, 20, ,]	
enqueue(30)	0	3	3	[10, 20, 30, _]	
dequeue()	1	3	2	[, *20, 30,*]	10 removed
enqueue(40)	1	0	3	[40, 20, 30, _]	wrap-around
enqueue(50)	1	1	4	[40, 20, 30, 50]	full queue

Edge Cases

- Enqueue when full → reject or overwrite
- Dequeue when empty → error
- Wrap-around indexing must handle 0 correctly

Complexity

- Time: enqueue O(1), dequeue O(1), peek O(1)
- Space: O(n) fixed buffer

Circular queues are the heartbeat of real-time data flows, steady, cyclic, and never wasting a byte.

209 Stack via Queue

A stack via queue is a playful twist, implementing LIFO behavior using FIFO tools. It shows how one structure can simulate another by combining basic operations cleverly.

What Problem Are We Solving?

Sometimes we're limited to queue operations (`enqueue`, `dequeue`) but still want a stack's last-in-first-out order. We can simulate `push` and `pop` using one or two queues.

Goal: Build a stack that supports `push`, `pop`, and `peek` in O(1) or O(n) time (depending on strategy) using only queue operations.

How Does It Work (Plain Language)?

Two main strategies:

1. Push costly: rotate elements after every push so front is always top.
2. Pop costly: enqueue normally, but rotate during pop.

We'll show push costly version, simpler conceptually.

Idea: Each `push` enqueues new item, then rotates all older elements behind it, so that last pushed is always at the front (ready to pop).

Example Steps (Push Costly)

Step	Operation	Queue (Front → Rear)	Note
1	push(10)	[10]	only one element
2	push(20)	[20, 10]	rotated so 20 is front
3	push(30)	[30, 20, 10]	rotated again
4	pop()	[20, 10]	30 removed
5	push(40)	[40, 20, 10]	rotation maintains order

Tiny Code (Easy Versions)

C (Using Two Queues)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int *data;
    int front, rear, count, capacity;
} Queue;

int q_init(Queue *q, int cap) {
    q->data = malloc(cap * sizeof(int));
    if (!q->data) return 0;
    q->front = 0;
    q->rear = 0;
    q->count = 0;
    q->capacity = cap;
    return 1;
}
```

```c
int q_enqueue(Queue *q, int x) {
    if (q->count == q->capacity) return 0;
    q->data[q->rear] = x;
    q->rear = (q->rear + 1) % q->capacity;
    q->count++;
    return 1;
}

int q_dequeue(Queue *q, int *out) {
    if (q->count == 0) return 0;
    *out = q->data[q->front];
    q->front = (q->front + 1) % q->capacity;
    q->count--;
    return 1;
}

typedef struct {
    Queue q1, q2;
} StackViaQueue;

int svq_init(StackViaQueue *s, int cap) {
    return q_init(&s->q1, cap) && q_init(&s->q2, cap);
}

int svq_push(StackViaQueue *s, int x) {
    q_enqueue(&s->q2, x);
    int val;
    while (s->q1.count) {
        q_dequeue(&s->q1, &val);
        q_enqueue(&s->q2, val);
    }
    // swap q1 and q2
    Queue tmp = s->q1;
    s->q1 = s->q2;
    s->q2 = tmp;
    return 1;
}

int svq_pop(StackViaQueue *s, int *out) {
    return q_dequeue(&s->q1, out);
}
```

```c
int svq_peek(StackViaQueue *s, int *out) {
    if (s->q1.count == 0) return 0;
    *out = s->q1.data[s->q1.front];
    return 1;
}

int main(void) {
    StackViaQueue s;
    svq_init(&s, 10);
    svq_push(&s, 10);
    svq_push(&s, 20);
    svq_push(&s, 30);
    int val;
    svq_pop(&s, &val);
    printf("Popped: %d\n", val);
    svq_peek(&s, &val);
    printf("Top: %d\n", val);
    free(s.q1.data);
    free(s.q2.data);
    return 0;
}
```

Python

```python
from collections import deque

class StackViaQueue:
    def __init__(self):
        self.q = deque()

    def push(self, x):
        n = len(self.q)
        self.q.append(x)
        # rotate all older elements
        for _ in range(n):
            self.q.append(self.q.popleft())

    def pop(self):
        if not self.q:
            raise IndexError("pop from empty stack")
        return self.q.popleft()
```

```
    def peek(self):
        if not self.q:
            raise IndexError("peek from empty stack")
        return self.q[0]

# Example
s = StackViaQueue()
s.push(10)
s.push(20)
s.push(30)
print(s.pop())  # 30
print(s.peek()) # 20
```

Why It Matters

- Demonstrates duality of data structures (stack built on queue)
- Reinforces operation trade-offs (costly push vs costly pop)
- Great teaching example for algorithmic simulation
- Builds insight into complexity and resource usage

A Gentle Proof (Why It Works)

In push costly approach:

- Each push rotates all previous elements behind the new one → new element becomes front.
- Pop simply dequeues from front → correct LIFO order.

So order is maintained: newest always exits first.

Try It Yourself

1. Implement pop costly variant (push O(1), pop O(n)).
2. Add `is_empty()` helper.
3. Compare total number of operations for n pushes and pops.
4. Extend to generic types with structs or templates.

Test Cases

Operation	Queue (Front → Rear)	Notes
push(10)	[10]	single element
push(20)	[20, 10]	rotated
push(30)	[30, 20, 10]	rotated
pop()	[20, 10]	returns 30
peek()	[20, 10]	returns 20

Edge Cases

- Pop/peek from empty → error
- Capacity reached → reject push
- Works even with single queue (rotation after push)

Complexity

- Push: O(n)
- Pop/Peek: O(1)
- Space: O(n)

Stack via queue proves constraints breed creativity, same data, different dance.

210 Queue via Stack

A queue via stack flips the story: build FIFO behavior using LIFO tools. It's a classic exercise in algorithmic inversion, showing how fundamental operations can emulate each other with clever order manipulation.

What Problem Are We Solving?

Suppose you only have stacks (with `push`, `pop`, `peek`) but need queue behavior (with `enqueue`, `dequeue`). We want to process items in arrival order, first in, first out, even though stacks operate last in, first out.

Goal: Implement `enqueue`, `dequeue`, and `peek` for a queue using only stack operations.

How Does It Work (Plain Language)?

Two stacks are enough:

- inbox: where we push new items (enqueue)
- outbox: where we pop old items (dequeue)

When dequeuing, if `outbox` is empty, we move all items from `inbox` to `outbox`, reversing their order so oldest items are on top.

This reversal step restores FIFO behavior.

Example Steps (Two-Stack Method)

Step	Operation	inbox (Top → Bottom)	outbox (Top → Bottom)	Note
1	enqueue(10)	[10]	[]	
2	enqueue(20)	[20, 10]	[]	
3	enqueue(30)	[30, 20, 10]	[]	
4	dequeue()	[]	[10, 20, 30]	transfer + pop(10)
5	enqueue(40)	[40]	[20, 30]	mixed state
6	dequeue()	[40]	[30]	pop(20) from outbox

Tiny Code (Easy Versions)

C (Using Two Stacks)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct {
    int *data;
    int top;
    int capacity;
} Stack;

int stack_init(Stack *s, int cap) {
    s->data = malloc(cap * sizeof(int));
    if (!s->data) return 0;
    s->top = -1;
    s->capacity = cap;
    return 1;
}
```

```
int stack_push(Stack *s, int x) {
    if (s->top + 1 == s->capacity) return 0;
    s->data[++s->top] = x;
    return 1;
}

int stack_pop(Stack *s, int *out) {
    if (s->top == -1) return 0;
    *out = s->data[s->top--];
    return 1;
}

int stack_peek(Stack *s, int *out) {
    if (s->top == -1) return 0;
    *out = s->data[s->top];
    return 1;
}

int stack_empty(Stack *s) {
    return s->top == -1;
}

typedef struct {
    Stack in, out;
} QueueViaStack;

int qvs_init(QueueViaStack *q, int cap) {
    return stack_init(&q->in, cap) && stack_init(&q->out, cap);
}

int qvs_enqueue(QueueViaStack *q, int x) {
    return stack_push(&q->in, x);
}

int qvs_shift(QueueViaStack *q) {
    int val;
    while (!stack_empty(&q->in)) {
        stack_pop(&q->in, &val);
        stack_push(&q->out, val);
    }
    return 1;
}
```

```c
int qvs_dequeue(QueueViaStack *q, int *out) {
    if (stack_empty(&q->out)) qvs_shift(q);
    return stack_pop(&q->out, out);
}

int qvs_peek(QueueViaStack *q, int *out) {
    if (stack_empty(&q->out)) qvs_shift(q);
    return stack_peek(&q->out, out);
}

int main(void) {
    QueueViaStack q;
    qvs_init(&q, 10);
    qvs_enqueue(&q, 10);
    qvs_enqueue(&q, 20);
    qvs_enqueue(&q, 30);
    int val;
    qvs_dequeue(&q, &val);
    printf("Dequeued: %d\n", val);
    qvs_enqueue(&q, 40);
    qvs_peek(&q, &val);
    printf("Front: %d\n", val);
    free(q.in.data);
    free(q.out.data);
    return 0;
}
```

Python (Two Stack Queue)

```python
class QueueViaStack:
    def __init__(self):
        self.inbox = []
        self.outbox = []

    def enqueue(self, x):
        self.inbox.append(x)

    def dequeue(self):
        if not self.outbox:
            while self.inbox:
                self.outbox.append(self.inbox.pop())
```

```
        if not self.outbox:
            raise IndexError("dequeue from empty queue")
        return self.outbox.pop()

    def peek(self):
        if not self.outbox:
            while self.inbox:
                self.outbox.append(self.inbox.pop())
        if not self.outbox:
            raise IndexError("peek from empty queue")
        return self.outbox[-1]

# Example
q = QueueViaStack()
q.enqueue(10)
q.enqueue(20)
q.enqueue(30)
print(q.dequeue())  # 10
q.enqueue(40)
print(q.peek())     # 20
```

Why It Matters

- Demonstrates queue emulation with stack operations
- Core teaching example for data structure duality
- Helps in designing abstract interfaces under constraints
- Underpins some streaming and buffering systems

A Gentle Proof (Why It Works)

Each transfer (`inbox → outbox`) reverses order once, restoring FIFO sequence.

- Enqueue pushes to inbox (LIFO)
- Dequeue pops from outbox (LIFO of reversed) So overall effect = FIFO

Transfers happen only when outbox is empty, so amortized cost per operation is O(1).

Try It Yourself

1. Implement a single-stack recursive version.
2. Add `is_empty()` helper.

3. Measure amortized vs worst-case complexity.
4. Extend to generic data type.

Test Cases

Operation	inbox (Top→Bottom)	outbox (Top→Bottom)	Result	Notes
enqueue(10)	[10]	[]		
enqueue(20)	[20, 10]	[]		
enqueue(30)	[30, 20, 10]	[]		
dequeue()	[]	[10, 20, 30]	returns 10	transfer + pop
enqueue(40)	[40]	[20, 30]		
dequeue()	[40]	[30]	returns 20	

Edge Cases

- Dequeue from empty queue → error
- Multiple dequeues trigger one transfer
- Outbox reused efficiently

Complexity

- Time: amortized O(1) per operation (worst-case O(n) on transfer)
- Space: O(n)

Queue via stack shows symmetry, turn LIFO into FIFO with one clever reversal.

Section 22. Hash Tables and Variants

211 Hash Table Insertion

A hash table stores key-value pairs for lightning-fast lookups. It uses a hash function to map keys to array indices, letting us access data in near-constant time.

What Problem Are We Solving?

We need a data structure that can insert, search, and delete by key efficiently, without scanning every element. Arrays give random access by index; hash tables extend that power to arbitrary keys.

Goal: Map each key to a slot via a hash function and resolve any collisions gracefully.

How Does It Work (Plain Language)?

A hash table uses a hash function to convert a key into an index:

```
index = hash(key) % capacity
```

When inserting a new (key, value):

1. Compute hash index.
2. If slot is empty → place pair there.
3. If occupied → handle collision (chaining or open addressing).

We'll use separate chaining (linked list per slot) as the simplest method.

Example Steps (Separate Chaining)

Step	Key	Hash(key)	Index	Action
1	"apple"	42	2	Insert ("apple", 10)
2	"banana"	15	3	Insert ("banana", 20)
3	"pear"	18	2	Collision → chain in index 2
4	"peach"	21	1	Insert new pair

Table after insertions:

Index	Chain
0	-
1	("peach", 40)
2	("apple", 10) → ("pear", 30)
3	("banana", 20)

Tiny Code (Easy Versions)

C (Separate Chaining Example)

```c
#include <stdio.h>
#include <stdlib.h>
#include <string.h>

#define TABLE_SIZE 5

typedef struct Node {
    char *key;
    int value;
    struct Node *next;
} Node;

typedef struct {
    Node *buckets[TABLE_SIZE];
} HashTable;

unsigned int hash(const char *key) {
    unsigned int h = 0;
    while (*key) h = h * 31 + *key++;
    return h % TABLE_SIZE;
}

HashTable* ht_create() {
    HashTable *ht = malloc(sizeof(HashTable));
    for (int i = 0; i < TABLE_SIZE; i++) ht->buckets[i] = NULL;
    return ht;
}

void ht_insert(HashTable *ht, const char *key, int value) {
    unsigned int idx = hash(key);
    Node *node = ht->buckets[idx];
    while (node) {
        if (strcmp(node->key, key) == 0) { node->value = value; return; }
        node = node->next;
    }
    Node *new_node = malloc(sizeof(Node));
    new_node->key = strdup(key);
    new_node->value = value;
    new_node->next = ht->buckets[idx];
```

```
    ht->buckets[idx] = new_node;
}

int ht_search(HashTable *ht, const char *key, int *out) {
    unsigned int idx = hash(key);
    Node *node = ht->buckets[idx];
    while (node) {
        if (strcmp(node->key, key) == 0) { *out = node->value; return 1; }
        node = node->next;
    }
    return 0;
}

int main(void) {
    HashTable *ht = ht_create();
    ht_insert(ht, "apple", 10);
    ht_insert(ht, "pear", 30);
    ht_insert(ht, "banana", 20);
    int val;
    if (ht_search(ht, "pear", &val))
        printf("pear: %d\n", val);
    return 0;
}
```

Python (Dictionary Simulation)

```
class HashTable:
    def __init__(self, size=5):
        self.size = size
        self.table = [[] for _ in range(size)]

    def _hash(self, key):
        return hash(key) % self.size

    def insert(self, key, value):
        idx = self._hash(key)
        for pair in self.table[idx]:
            if pair[0] == key:
                pair[1] = value
                return
        self.table[idx].append([key, value])
```

```
    def search(self, key):
        idx = self._hash(key)
        for k, v in self.table[idx]:
            if k == key:
                return v
        return None

# Example
ht = HashTable()
ht.insert("apple", 10)
ht.insert("pear", 30)
ht.insert("banana", 20)
print(ht.search("pear"))  # 30
```

Why It Matters

- Provides average O(1) access, insert, delete
- Backbone of symbol tables, maps, sets, and dictionaries
- Used in caches, compilers, and indexing systems
- Introduces key idea: hash function + collision handling

A Gentle Proof (Why It Works)

Let table size = m, number of keys = n. If hash spreads keys uniformly, expected chain length = = n/m (load factor).

- Average lookup: O(1 +)
- Keep 1 → near constant time If collisions are minimized, operations stay fast.

Try It Yourself

1. Implement update to modify existing key's value.
2. Add delete(key) to remove entries from chain.
3. Experiment with different hash functions (e.g. djb2, FNV-1a).
4. Measure time vs load factor.

Test Cases

Operation	Key	Value	Result	Notes
insert	“apple”	10	success	new key
insert	“banana”	20	success	new key
insert	“apple”	15	update	key exists
search	“banana”		20	found
search	“grape”		None	not found

Edge Cases

- Insert duplicate → update value
- Search non-existent → return None
- Table full (open addressing) → needs rehash

Complexity

- Time: average O(1), worst O(n) (all collide)
- Space: O(n + m) (keys + table slots)

Hash table insertion is the art of turning chaos into order, hash, map, resolve, and store.

212 Linear Probing

Linear probing is one of the simplest collision resolution strategies in open addressing hash tables. When a collision occurs, it looks for the next empty slot by moving step by step through the table, wrapping around if needed.

What Problem Are We Solving?

When two keys hash to the same index, where do we store the new one? Instead of chaining nodes, linear probing searches the next available slot, keeping all data inside the array.

Goal: Resolve collisions by scanning linearly from the point of conflict until an empty slot is found.

How Does It Work (Plain Language)?

When inserting a key:

1. Compute index = `hash(key) % capacity`.
2. If slot empty → place key there.
3. If occupied → move to `(index + 1) % capacity`.
4. Repeat until an empty slot is found or table is full.

Lookups and deletions follow the same probe sequence until key is found or empty slot encountered.

Example Steps (Capacity = 7)

Step	Key	Hash(key)	Index	Action
1	10	3	3	Place at index 3
2	24	3	4	Collision → move to 4
3	31	3	5	Collision → move to 5
4	17	3	6	Collision → move to 6
5	38	3	0	Wrap around → place at 0

Final Table

Index	Value
0	38
1	-
2	-
3	10
4	24
5	31
6	17

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

#define CAPACITY 7
#define EMPTY -1
```

```c
#define DELETED -2

typedef struct {
    int *table;
} HashTable;

int hash(int key) { return key % CAPACITY; }

HashTable* ht_create() {
    HashTable *ht = malloc(sizeof(HashTable));
    ht->table = malloc(sizeof(int) * CAPACITY);
    for (int i = 0; i < CAPACITY; i++) ht->table[i] = EMPTY;
    return ht;
}

void ht_insert(HashTable *ht, int key) {
    int idx = hash(key);
    for (int i = 0; i < CAPACITY; i++) {
        int pos = (idx + i) % CAPACITY;
        if (ht->table[pos] == EMPTY || ht->table[pos] == DELETED) {
            ht->table[pos] = key;
            return;
        }
    }
    printf("Table full, cannot insert %d\n", key);
}

int ht_search(HashTable *ht, int key) {
    int idx = hash(key);
    for (int i = 0; i < CAPACITY; i++) {
        int pos = (idx + i) % CAPACITY;
        if (ht->table[pos] == EMPTY) return -1;
        if (ht->table[pos] == key) return pos;
    }
    return -1;
}

void ht_delete(HashTable *ht, int key) {
    int pos = ht_search(ht, key);
    if (pos != -1) ht->table[pos] = DELETED;
}
```

```c
int main(void) {
    HashTable *ht = ht_create();
    ht_insert(ht, 10);
    ht_insert(ht, 24);
    ht_insert(ht, 31);
    ht_insert(ht, 17);
    ht_insert(ht, 38);
    for (int i = 0; i < CAPACITY; i++)
        printf("[%d] = %d\n", i, ht->table[i]);
    return 0;
}
```

Python

```python
class LinearProbingHash:
    def __init__(self, size=7):
        self.size = size
        self.table = [None] * size

    def _hash(self, key):
        return key % self.size

    def insert(self, key):
        idx = self._hash(key)
        for i in range(self.size):
            pos = (idx + i) % self.size
            if self.table[pos] is None or self.table[pos] == "DELETED":
                self.table[pos] = key
                return
        raise OverflowError("Hash table full")

    def search(self, key):
        idx = self._hash(key)
        for i in range(self.size):
            pos = (idx + i) % self.size
            if self.table[pos] is None:
                return None
            if self.table[pos] == key:
                return pos
        return None

    def delete(self, key):
```

```
        pos = self.search(key)
        if pos is not None:
            self.table[pos] = "DELETED"

# Example
ht = LinearProbingHash()
for k in [10, 24, 31, 17, 38]:
    ht.insert(k)
print(ht.table)
print("Search 17 at:", ht.search(17))
```

Why It Matters

- Simplest form of open addressing
- Keeps all entries inside one array (no extra memory)
- Excellent cache performance
- Forms the basis for modern in-place hash maps

A Gentle Proof (Why It Works)

Every key follows the same probe sequence during insert, search, and delete. So if a key is in the table, search will find it; if it's not, search will hit an empty slot and stop. Uniform hashing ensures average probe length 1 / (1 -), where = n / m is load factor.

Try It Yourself

1. Implement `resize()` when load factor > 0.7.
2. Test insertion order and wrap-around behavior.
3. Compare linear probing vs chaining performance.
4. Visualize clustering as load increases.

Test Cases

Operation	Key	Result	Notes
insert	10	index 3	no collision
insert	24	index 4	move 1 slot
insert	31	index 5	move 2 slots
insert	17	index 6	move 3 slots

Operation	Key	Result	Notes
insert	38	index 0	wrap-around
search	17	found at 6	linear search
delete	24	mark deleted	slot reusable

Edge Cases

- Table full → insertion fails
- Deleted slots reused
- Must stop on EMPTY, not DELETED

Complexity

- Time:
  - Average O(1) if small
  - Worst O(n) if full cluster
- Space: O(n)

Linear probing walks straight lines through collisions, simple, local, and fast when load is low.

213 Quadratic Probing

Quadratic probing improves upon linear probing by reducing primary clustering. Instead of stepping through every slot one by one, it jumps in quadratic increments, spreading colliding keys more evenly across the table.

What Problem Are We Solving?

In linear probing, consecutive occupied slots cause clustering, leading to long probe chains and degraded performance. Quadratic probing breaks up these runs by using nonlinear probe sequences.

Goal: Resolve collisions by checking indices offset by quadratic values, $+1^2$, $+2^2$, $+3^2$, …, reducing clustering while keeping predictable probe order.

How Does It Work (Plain Language)?

When inserting a key:

1. Compute `index = hash(key) % capacity`.
2. If slot empty → insert.
3. If occupied → try `(index + 1²) % capacity`, `(index + 2²) % capacity`, etc.
4. Continue until an empty slot is found or table is full.

Lookups and deletions follow the same probe sequence.

Example Steps (Capacity = 7)

Step	Key	Hash(key)	Probes (sequence)	Final Slot
1	10	3	3	3
2	24	3	3, 4	4
3	31	3	3, 4, 0	0
4	17	3	3, 4, 0, 2	2

Table after insertions:

Index	Value
0	31
1	-
2	17
3	10
4	24
5	-
6	-

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

#define CAPACITY 7
#define EMPTY -1
#define DELETED -2
```

```c
typedef struct {
    int *table;
} HashTable;

int hash(int key) { return key % CAPACITY; }

HashTable* ht_create() {
    HashTable *ht = malloc(sizeof(HashTable));
    ht->table = malloc(sizeof(int) * CAPACITY);
    for (int i = 0; i < CAPACITY; i++) ht->table[i] = EMPTY;
    return ht;
}

void ht_insert(HashTable *ht, int key) {
    int idx = hash(key);
    for (int i = 0; i < CAPACITY; i++) {
        int pos = (idx + i * i) % CAPACITY;
        if (ht->table[pos] == EMPTY || ht->table[pos] == DELETED) {
            ht->table[pos] = key;
            return;
        }
    }
    printf("Table full, cannot insert %d\n", key);
}

int ht_search(HashTable *ht, int key) {
    int idx = hash(key);
    for (int i = 0; i < CAPACITY; i++) {
        int pos = (idx + i * i) % CAPACITY;
        if (ht->table[pos] == EMPTY) return -1;
        if (ht->table[pos] == key) return pos;
    }
    return -1;
}

int main(void) {
    HashTable *ht = ht_create();
    ht_insert(ht, 10);
    ht_insert(ht, 24);
    ht_insert(ht, 31);
    ht_insert(ht, 17);
    for (int i = 0; i < CAPACITY; i++)
```

```
        printf("[%d] = %d\n", i, ht->table[i]);
    return 0;
}
```

Python

```
class QuadraticProbingHash:
    def __init__(self, size=7):
        self.size = size
        self.table = [None] * size

    def _hash(self, key):
        return key % self.size

    def insert(self, key):
        idx = self._hash(key)
        for i in range(self.size):
            pos = (idx + i * i) % self.size
            if self.table[pos] is None or self.table[pos] == "DELETED":
                self.table[pos] = key
                return
        raise OverflowError("Hash table full")

    def search(self, key):
        idx = self._hash(key)
        for i in range(self.size):
            pos = (idx + i * i) % self.size
            if self.table[pos] is None:
                return None
            if self.table[pos] == key:
                return pos
        return None

# Example
ht = QuadraticProbingHash()
for k in [10, 24, 31, 17]:
    ht.insert(k)
print(ht.table)
print("Search 24 at:", ht.search(24))
```

Why It Matters

- Reduces primary clustering seen in linear probing
- Keeps keys more evenly distributed
- Avoids extra pointers (everything stays in one array)
- Useful in hash tables where space is tight and locality helps

A Gentle Proof (Why It Works)

Probe sequence:

$$i = 0, 1, 2, 3, ...$$

Index at step i is

$$(index + i^2) \bmod m$$

If table size m is prime, this sequence visits up to $m/2$ distinct slots before repeating, guaranteeing an empty slot is found if load factor < 0.5.

Thus all operations follow predictable, finite sequences.

Try It Yourself

1. Compare clustering with linear probing under same keys.
2. Experiment with different table sizes (prime vs composite).
3. Implement deletion markers properly.
4. Visualize probe paths with small tables.

Test Cases

Operation	Key	Probe Sequence	Slot	Notes
insert	10	3	3	no collision
insert	24	3, 4	4	1 step
insert	31	3, 4, 0	0	2 steps
insert	17	3, 4, 0, 2	2	3 steps
search	31	$3 \to 4 \to 0$	found	quadratic path

Edge Cases

- Table full $\to$ insertion fails
- Requires table size prime for full coverage
- Needs load factor < 0.5 to avoid infinite loops

Complexity

- Time: average O(1), worst O(n)
- Space: O(n)

Quadratic probing trades a straight line for a curve, spreading collisions smoothly across the table.

214 Double Hashing

Double hashing uses two independent hash functions to minimize collisions. When a conflict occurs, it jumps forward by a second hash value, creating probe sequences unique to each key and greatly reducing clustering.

What Problem Are We Solving?

Linear and quadratic probing both suffer from clustering patterns, especially when keys share similar initial indices. Double hashing breaks this pattern by introducing a second hash function that defines each key's step size.

Goal: Use two hash functions to determine probe sequence:

$$\text{index}_i = (h_1(key) + i \cdot h_2(key)) \bmod m$$

This produces independent probe paths and avoids overlap among keys.

How Does It Work (Plain Language)?

When inserting a key:

1. Compute primary hash: `h1 = key % capacity`.
2. Compute step size: `h2 = 1 + (key % (capacity - 1))` (never zero).
3. Try `h1`; if occupied, try `(h1 + h2) % m`, `(h1 + 2*h2) % m`, etc.
4. Repeat until an empty slot is found.

Same pattern applies for search and delete.

Example Steps (Capacity = 7)

Step	Key	h (key)	h (key)	Probe Sequence	Final Slot
1	10	3	4	3	3
2	24	3	4	$3 \rightarrow 0$	0

Step	Key	h (key)	h (key)	Probe Sequence	Final Slot
3	31	3	4	$3 \to 0 \to 4$	4
4	17	3	3	$3 \to 6$	6

Final Table

Index	Value
0	24
1	-
2	-
3	10
4	31
5	-
6	17

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

#define CAPACITY 7
#define EMPTY -1
#define DELETED -2

typedef struct {
    int *table;
} HashTable;

int h1(int key) { return key % CAPACITY; }
int h2(int key) { return 1 + (key % (CAPACITY - 1)); }

HashTable* ht_create() {
    HashTable *ht = malloc(sizeof(HashTable));
    ht->table = malloc(sizeof(int) * CAPACITY);
    for (int i = 0; i < CAPACITY; i++) ht->table[i] = EMPTY;
    return ht;
}
```

```c
void ht_insert(HashTable *ht, int key) {
    int idx1 = h1(key);
    int step = h2(key);
    for (int i = 0; i < CAPACITY; i++) {
        int pos = (idx1 + i * step) % CAPACITY;
        if (ht->table[pos] == EMPTY || ht->table[pos] == DELETED) {
            ht->table[pos] = key;
            return;
        }
    }
    printf("Table full, cannot insert %d\n", key);
}

int ht_search(HashTable *ht, int key) {
    int idx1 = h1(key), step = h2(key);
    for (int i = 0; i < CAPACITY; i++) {
        int pos = (idx1 + i * step) % CAPACITY;
        if (ht->table[pos] == EMPTY) return -1;
        if (ht->table[pos] == key) return pos;
    }
    return -1;
}

int main(void) {
    HashTable *ht = ht_create();
    ht_insert(ht, 10);
    ht_insert(ht, 24);
    ht_insert(ht, 31);
    ht_insert(ht, 17);
    for (int i = 0; i < CAPACITY; i++)
        printf("[%d] = %d\n", i, ht->table[i]);
    return 0;
}
```

Python

```python
class DoubleHash:
    def __init__(self, size=7):
        self.size = size
        self.table = [None] * size

    def _h1(self, key):
```

```
        return key % self.size

    def _h2(self, key):
        return 1 + (key % (self.size - 1))

    def insert(self, key):
        h1 = self._h1(key)
        h2 = self._h2(key)
        for i in range(self.size):
            pos = (h1 + i * h2) % self.size
            if self.table[pos] is None or self.table[pos] == "DELETED":
                self.table[pos] = key
                return
        raise OverflowError("Hash table full")

    def search(self, key):
        h1 = self._h1(key)
        h2 = self._h2(key)
        for i in range(self.size):
            pos = (h1 + i * h2) % self.size
            if self.table[pos] is None:
                return None
            if self.table[pos] == key:
                return pos
        return None

# Example
ht = DoubleHash()
for k in [10, 24, 31, 17]:
    ht.insert(k)
print(ht.table)
print("Search 24 at:", ht.search(24))
```

Why It Matters

- Minimizes primary and secondary clustering
- Probe sequences depend on key, not shared among colliding keys
- Achieves uniform distribution when both hash functions are good
- Forms basis for high-performance open addressing maps

A Gentle Proof (Why It Works)

If capacity m is prime and h (key) never equals 0, then each key generates a unique probe sequence covering all slots:

$$\text{indices} = h_1, h_1 + h_2, h_1 + 2h_2, ... \bmod m$$

Thus an empty slot is always reachable, and searches find all candidates.

Expected probe count $\frac{1}{1-\alpha}$, same as other open addressing, but with lower clustering.

Try It Yourself

1. Experiment with different h functions (e.g. `7 - key % 7`).
2. Compare probe lengths with linear and quadratic probing.
3. Visualize probe paths for small table sizes.
4. Test with composite vs prime capacities.

Test Cases

Operation	Key	h	h	Probe Sequence	Final Slot
insert	10	3	4	3	3
insert	24	3	4	3, 0	0
insert	31	3	4	3, 0, 4	4
insert	17	3	3	3, 6	6
search	24	3, 0	found		

Edge Cases

- h (key) must be nonzero
- m should be prime for full coverage
- Poor hash choice → incomplete coverage

Complexity

- Time: average O(1), worst O(n)
- Space: O(n)

Double hashing turns collisions into a graceful dance, two hash functions weaving paths that rarely cross.

215 Cuckoo Hashing

Cuckoo hashing takes inspiration from nature: like the cuckoo bird laying eggs in multiple nests, each key has more than one possible home. If a spot is taken, it *kicks out* the current occupant, which then moves to its alternate home, ensuring fast and predictable lookups.

What Problem Are We Solving?

Traditional open addressing methods (linear, quadratic, double hashing) may degrade under high load factors, causing long probe sequences. Cuckoo hashing guarantees constant-time lookups by giving each key multiple possible positions.

Goal: Use two hash functions and relocate keys upon collision, maintaining O(1) search and insert time.

How Does It Work (Plain Language)?

Each key has two candidate slots, determined by two hash functions:

$$h_1(k), \quad h_2(k)$$

When inserting a key:

1. Try `h1(k)` → if empty, place it.
2. If occupied → *kick out* the existing key.
3. Reinsert the displaced key into its alternate slot.
4. Repeat until all keys placed or cycle detected (then rehash).

Example Steps (Capacity = 7)

Step	Key	h (key)	h (key)	Action
1	10	3	5	Slot 3 empty → place 10
2	24	3	4	Slot 3 occupied → move 10
3	10	5	3	Slot 5 empty → place 10
4	31	3	6	Slot 3 empty → place 31

Final Table

Index	Value
0	-

Index	Value
1	-
2	-
3	31
4	24
5	10
6	-

Every key is accessible in O(1) by checking two positions only.

Tiny Code (Easy Versions)

C (Two-Table Cuckoo Hashing)

```c
#include <stdio.h>
#include <stdlib.h>

#define CAPACITY 7
#define EMPTY -1
#define MAX_RELOCATIONS 10

typedef struct {
    int table1[CAPACITY];
    int table2[CAPACITY];
} CuckooHash;

int h1(int key) { return key % CAPACITY; }
int h2(int key) { return (key / CAPACITY) % CAPACITY; }

void init(CuckooHash *ht) {
    for (int i = 0; i < CAPACITY; i++) {
        ht->table1[i] = EMPTY;
        ht->table2[i] = EMPTY;
    }
}

int insert(CuckooHash *ht, int key) {
    int pos, tmp, loop_guard = 0;
    for (int i = 0; i < MAX_RELOCATIONS; i++) {
        pos = h1(key);
```

```
        if (ht->table1[pos] == EMPTY) {
            ht->table1[pos] = key;
            return 1;
        }
        // kick out
        tmp = ht->table1[pos];
        ht->table1[pos] = key;
        key = tmp;
        pos = h2(key);
        if (ht->table2[pos] == EMPTY) {
            ht->table2[pos] = key;
            return 1;
        }
        tmp = ht->table2[pos];
        ht->table2[pos] = key;
        key = tmp;
    }
    printf("Cycle detected, rehash needed\n");
    return 0;
}

int search(CuckooHash *ht, int key) {
    int pos1 = h1(key);
    int pos2 = h2(key);
    if (ht->table1[pos1] == key || ht->table2[pos2] == key) return 1;
    return 0;
}

int main(void) {
    CuckooHash ht;
    init(&ht);
    insert(&ht, 10);
    insert(&ht, 24);
    insert(&ht, 31);
    for (int i = 0; i < CAPACITY; i++)
        printf("[%d] T1=%d T2=%d\n", i, ht.table1[i], ht.table2[i]);
    return 0;
}
```

Python

```python
class CuckooHash:
    def __init__(self, size=7):
        self.size = size
        self.table1 = [None] * size
        self.table2 = [None] * size
        self.max_reloc = 10

    def _h1(self, key): return key % self.size
    def _h2(self, key): return (key // self.size) % self.size

    def insert(self, key):
        for _ in range(self.max_reloc):
            idx1 = self._h1(key)
            if self.table1[idx1] is None:
                self.table1[idx1] = key
                return
            key, self.table1[idx1] = self.table1[idx1], key  # swap

            idx2 = self._h2(key)
            if self.table2[idx2] is None:
                self.table2[idx2] = key
                return
            key, self.table2[idx2] = self.table2[idx2], key  # swap
        raise RuntimeError("Cycle detected, rehash needed")

    def search(self, key):
        return key in self.table1 or key in self.table2

# Example
ht = CuckooHash()
for k in [10, 24, 31]:
    ht.insert(k)
print("Table1:", ht.table1)
print("Table2:", ht.table2)
print("Search 24:", ht.search(24))
```

Why It Matters

- O(1) lookup, always two slots per key
- Avoids clustering entirely
- Excellent for high load factors (up to 0.5–0.9)

- Simple predictable probe path
- Great choice for hardware tables (e.g. network routing)

A Gentle Proof (Why It Works)

Each key has at most two possible homes.

- If both occupied, displacement ensures eventual convergence (or detects a cycle).
- Cycle length bounded → rehash needed rarely.

Expected insertion time = O(1) amortized; search always 2 checks only.

Try It Yourself

1. Implement rehash when cycle detected.
2. Add delete(key) and test reinsert.
3. Visualize displacement chain on insertions.
4. Compare performance with double hashing.

Test Cases

Operation	Key	h	h	Action
insert	10	3	5	place at 3
insert	24	3	4	displace 10 → move to 5
insert	31	3	6	place at 3
search	10	3, 5	found	

Edge Cases

- Cycle detected → requires rehash
- Both tables full → resize
- Must limit relocation attempts

Complexity

- Time:
  - Lookup: O(1)
  - Insert: O(1) amortized
- Space: O(2n)

Cuckoo hashing keeps order in the nest, every key finds a home, or the table learns to rebuild its world.

216 Robin Hood Hashing

Robin Hood hashing is a clever twist on open addressing: when a new key collides, it compares its "distance from home" with the current occupant. If the new key has traveled farther, it *steals* the slot, redistributing probe distances more evenly and keeping variance low.

What Problem Are We Solving?

In linear probing, unlucky keys might travel long distances while others sit close to their home. This leads to probe sequence imbalance, long searches for some keys, short for others. Robin Hood hashing "robs" near-home keys to help far-away ones, minimizing the maximum probe distance.

Goal: Equalize probe distances by swapping keys so that no key is "too far" behind others.

How Does It Work (Plain Language)?

Each entry remembers its probe distance = number of steps from its original hash slot. When inserting a new key:

1. Compute `index = hash(key) % capacity`.
2. If slot empty → insert.
3. If occupied → compare probe distances.
   - If newcomer's distance > occupant's distance → swap them.
   - Continue insertion for the displaced key.

Example Steps (Capacity = 7)

Step	Key	Hash(key)	Probe Distance	Action
1	10	3	0	Place at 3
2	24	3	0	Collision → move to 4 (dist=1)
3	31	3	0	Collision → dist=0 < 0? no → move → dist=1 < 1? no → dist=2 → place at 5
4	17	3	0	Collision chain → compare and swap if farther

This ensures all keys stay near their home index, fairer access for all.

Result Table:

Index	Key	Dist
3	10	0
4	24	1
5	31	2

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

#define CAPACITY 7
#define EMPTY -1

typedef struct {
    int key;
    int dist; // probe distance
} Slot;

typedef struct {
    Slot *table;
} HashTable;

int hash(int key) { return key % CAPACITY; }

HashTable* ht_create() {
    HashTable *ht = malloc(sizeof(HashTable));
```

```
    ht->table = malloc(sizeof(Slot) * CAPACITY);
    for (int i = 0; i < CAPACITY; i++) {
        ht->table[i].key = EMPTY;
        ht->table[i].dist = 0;
    }
    return ht;
}

void ht_insert(HashTable *ht, int key) {
    int idx = hash(key);
    int dist = 0;

    while (1) {
        if (ht->table[idx].key == EMPTY) {
            ht->table[idx].key = key;
            ht->table[idx].dist = dist;
            return;
        }

        if (dist > ht->table[idx].dist) {
            // swap keys
            int tmp_key = ht->table[idx].key;
            int tmp_dist = ht->table[idx].dist;
            ht->table[idx].key = key;
            ht->table[idx].dist = dist;
            key = tmp_key;
            dist = tmp_dist;
        }

        idx = (idx + 1) % CAPACITY;
        dist++;
        if (dist >= CAPACITY) {
            printf("Table full\n");
            return;
        }
    }
}

int ht_search(HashTable *ht, int key) {
    int idx = hash(key);
    int dist = 0;
    while (ht->table[idx].key != EMPTY && dist <= ht->table[idx].dist) {
```

```
        if (ht->table[idx].key == key) return idx;
        idx = (idx + 1) % CAPACITY;
        dist++;
    }
    return -1;
}

int main(void) {
    HashTable *ht = ht_create();
    ht_insert(ht, 10);
    ht_insert(ht, 24);
    ht_insert(ht, 31);
    for (int i = 0; i < CAPACITY; i++) {
        if (ht->table[i].key != EMPTY)
            printf("[%d] key=%d dist=%d\n", i, ht->table[i].key, ht->table[i].dist);
    }
    return 0;
}
```

Python

```
class RobinHoodHash:
    def __init__(self, size=7):
        self.size = size
        self.table = [None] * size
        self.dist = [0] * size

    def _hash(self, key):
        return key % self.size

    def insert(self, key):
        idx = self._hash(key)
        d = 0
        while True:
            if self.table[idx] is None:
                self.table[idx] = key
                self.dist[idx] = d
                return
            # Robin Hood swap if newcomer is farther
            if d > self.dist[idx]:
                key, self.table[idx] = self.table[idx], key
                d, self.dist[idx] = self.dist[idx], d
```

```
            idx = (idx + 1) % self.size
            d += 1
            if d >= self.size:
                raise OverflowError("Table full")

    def search(self, key):
        idx = self._hash(key)
        d = 0
        while self.table[idx] is not None and d <= self.dist[idx]:
            if self.table[idx] == key:
                return idx
            idx = (idx + 1) % self.size
            d += 1
        return None

# Example
ht = RobinHoodHash()
for k in [10, 24, 31]:
    ht.insert(k)
print(list(zip(range(ht.size), ht.table, ht.dist)))
print("Search 24:", ht.search(24))
```

Why It Matters

- Balances access time across all keys
- Minimizes variance of probe lengths
- Outperforms linear probing under high load
- Elegant fairness principle, long-traveling keys get priority

A Gentle Proof (Why It Works)

By ensuring all probe distances are roughly equal, worst-case search cost average search cost. Keys never get "stuck" behind long clusters, and searches terminate early when probe distance exceeds that of existing slot.

Average search cost $O(1 +)$, but with *smaller variance* than standard linear probing.

Try It Yourself

1. Insert keys in different orders and compare probe distances.

2. Implement deletion (mark deleted and shift neighbors).
3. Track average probe distance as load grows.
4. Compare fairness with standard linear probing.

Test Cases

Operation	Key	Home	Final Slot	Dist	Notes
insert	10	3	3	0	first insert
insert	24	3	4	1	collision
insert	31	3	5	2	further collision
search	24	3→4	found		

Edge Cases

- Table full → stop insertion
- Must cap distance to prevent infinite loop
- Deletion requires rebalancing neighbors

Complexity

- Time: average O(1), worst O(n)
- Space: O(n)

Robin Hood hashing brings justice to collisions, no key left wandering too far from home.

217 Chained Hash Table

A chained hash table is the classic solution for handling collisions, instead of squeezing every key into the array, each bucket holds a linked list (or chain) of entries that share the same hash index.

What Problem Are We Solving?

With open addressing, collisions force you to probe for new slots inside the array. Chaining solves collisions externally, every index points to a small dynamic list, so multiple keys can share the same slot without crowding.

Goal: Use linked lists (chains) to store colliding keys at the same hash index, keeping insert, search, and delete simple and efficient on average.

How Does It Work (Plain Language)?

Each array index stores a pointer to a linked list of key-value pairs. When inserting:

1. Compute index = `hash(key) % capacity`.
2. Traverse chain to check if key exists.
3. If not, append new node to the front (or back).

Searching and deleting follow the same index and chain.

Example (Capacity = 5)

Step	Key	Hash(key)	Index	Action
1	"cat"	2	2	Place in chain[2]
2	"dog"	4	4	Place in chain[4]
3	"bat"	2	2	Append to chain[2]
4	"ant"	2	2	Append to chain[2]

Table Structure

Index	Chain
0	-
1	-
2	"cat" → "bat" → "ant"
3	-
4	"dog"

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>
#include <string.h>

#define CAPACITY 5

typedef struct Node {
    char *key;
    int value;
    struct Node *next;
```

```
} Node;

typedef struct {
    Node *buckets[CAPACITY];
} HashTable;

unsigned int hash(const char *key) {
    unsigned int h = 0;
    while (*key) h = h * 31 + *key++;
    return h % CAPACITY;
}

HashTable* ht_create() {
    HashTable *ht = malloc(sizeof(HashTable));
    for (int i = 0; i < CAPACITY; i++) ht->buckets[i] = NULL;
    return ht;
}

void ht_insert(HashTable *ht, const char *key, int value) {
    unsigned int idx = hash(key);
    Node *node = ht->buckets[idx];
    while (node) {
        if (strcmp(node->key, key) == 0) { node->value = value; return; }
        node = node->next;
    }
    Node *new_node = malloc(sizeof(Node));
    new_node->key = strdup(key);
    new_node->value = value;
    new_node->next = ht->buckets[idx];
    ht->buckets[idx] = new_node;
}

int ht_search(HashTable *ht, const char *key, int *out) {
    unsigned int idx = hash(key);
    Node *node = ht->buckets[idx];
    while (node) {
        if (strcmp(node->key, key) == 0) { *out = node->value; return 1; }
        node = node->next;
    }
    return 0;
}
```

```c
void ht_delete(HashTable *ht, const char *key) {
    unsigned int idx = hash(key);
    Node curr = &ht->buckets[idx];
    while (*curr) {
        if (strcmp((*curr)->key, key) == 0) {
            Node *tmp = *curr;
            *curr = (*curr)->next;
            free(tmp->key);
            free(tmp);
            return;
        }
        curr = &(*curr)->next;
    }
}

int main(void) {
    HashTable *ht = ht_create();
    ht_insert(ht, "cat", 1);
    ht_insert(ht, "bat", 2);
    ht_insert(ht, "ant", 3);
    int val;
    if (ht_search(ht, "bat", &val))
        printf("bat: %d\n", val);
    ht_delete(ht, "bat");
    if (!ht_search(ht, "bat", &val))
        printf("bat deleted\n");
    return 0;
}
```

Python

```python
class ChainedHash:
    def __init__(self, size=5):
        self.size = size
        self.table = [[] for _ in range(size)]

    def _hash(self, key):
        return hash(key) % self.size

    def insert(self, key, value):
        idx = self._hash(key)
        for pair in self.table[idx]:
```

```
            if pair[0] == key:
                pair[1] = value
                return
        self.table[idx].append([key, value])

    def search(self, key):
        idx = self._hash(key)
        for k, v in self.table[idx]:
            if k == key:
                return v
        return None

    def delete(self, key):
        idx = self._hash(key)
        self.table[idx] = [p for p in self.table[idx] if p[0] != key]

# Example
ht = ChainedHash()
ht.insert("cat", 1)
ht.insert("bat", 2)
ht.insert("ant", 3)
print(ht.table)
print("Search bat:", ht.search("bat"))
ht.delete("bat")
print(ht.table)
```

Why It Matters

- Simple and reliable collision handling
- Load factor can exceed 1 (chains absorb overflow)
- Deletion is straightforward (just remove node)
- Performance stable even at high load (if hash spread is uniform)

A Gentle Proof (Why It Works)

Expected chain length = load factor $\alpha = \frac{n}{m}$. Each operation traverses a single chain, so average cost = O(1 +). Uniform hash distribution ensures remains small → operations O(1).

Try It Yourself

1. Implement dynamic resizing when average chain length grows.
2. Compare prepend vs append strategies.
3. Measure average search steps as table fills.
4. Replace linked list with balanced tree (for high).

Test Cases

Operation	Key	Index	Chain Result	Notes
insert	“cat”	2	[“cat”]	
insert	“bat”	2	[“bat”, “cat”]	collision
insert	“ant”	2	[“ant”, “bat”, “cat”]	chain grows
search	“bat”	2	found	
delete	“bat”	2	[“ant”, “cat”]	removed

Edge Cases

- Many keys same index → long chains
- Poor hash function → uneven distribution
- Needs memory for pointers/nodes

Complexity

- Time: average O(1), worst O(n) (all in one chain)
- Space: O(n + m)

Chained hashing turns collisions into conversation, if one bucket's full, it just lines them up neatly in a list.

218 Perfect Hashing

Perfect hashing is the dream scenario for hash tables, no collisions at all. Every key maps to a unique slot, so lookups, inserts, and deletes all take O(1) time *worst case*, not just on average.

What Problem Are We Solving?

Most hashing strategies (linear probing, chaining, cuckoo) deal with collisions after they happen. Perfect hashing eliminates them entirely by designing a collision-free hash function for a fixed key set.

Goal: Construct a hash function $h(k)$ such that all keys map to distinct indices.

How Does It Work (Plain Language)?

If the set of keys is known in advance (static set), we can carefully choose or build a hash function that gives each key a unique slot.

Two main types:

1. Perfect Hashing, no collisions.
2. Minimal Perfect Hashing, no collisions and table size = number of keys.

Simple Example (Keys = {10, 24, 31, 17}, Capacity = 7)

Let's find a function:

$$h(k) = (a \cdot k + b) \bmod 7$$

We can search for coefficients a and b that produce unique indices:

Key	h(k) = (2k + 1) mod 7	Index
10	(21) % 7 = 0	0
24	(49) % 7 = 0	collision
31	(63) % 7 = 0	collision

So we try another pair (a=3, b=2):

Key	(3k + 2) mod 7	Index
10	5	5
24	4	4
31	4	collision
17	6	6

Eventually, we find a mapping with no repeats by adjusting parameters or using two-level construction.

Two-Level Perfect Hashing

Practical perfect hashing often uses a two-level scheme:

1. Top level: Hash keys into buckets.
2. Second level: Each bucket gets its own small hash table with its own perfect hash function.

This ensures zero collisions overall, with total space O(n).

Process:

- Each bucket of size b gets a secondary table of size b^2.
- Use a second hash h_i for that bucket to place all keys uniquely.

Tiny Code (Easy Version)

Python (Two-Level Static Perfect Hashing)

```
import random

class PerfectHash:
    def __init__(self, keys):
        self.n = len(keys)
        self.size = self.n
        self.buckets = [[] for _ in range(self.size)]
        self.secondary = [None] * self.size

        # First-level hashing
        a, b = 3, 5  # fixed small hash parameters
        def h1(k): return (a * k + b) % self.size

        # Distribute keys into buckets
        for k in keys:
            self.buckets[h1(k)].append(k)

        # Build second-level tables
        for i, bucket in enumerate(self.buckets):
            if not bucket:
                continue
            m = len(bucket)  2
            table = [None] * m
            found = False
            while not found:
```

```
                found = True
                a2, b2 = random.randint(1, m - 1), random.randint(0, m - 1)
                def h2(k): return (a2 * k + b2) % m
                table = [None] * m
                for k in bucket:
                    pos = h2(k)
                    if table[pos] is not None:
                        found = False
                        break
                    table[pos] = k
            self.secondary[i] = (table, a2, b2)

        self.h1 = h1

    def search(self, key):
        i = self.h1(key)
        table, a2, b2 = self.secondary[i]
        m = len(table)
        pos = (a2 * key + b2) % m
        return table[pos] == key

# Example
keys = [10, 24, 31, 17]
ph = PerfectHash(keys)
print([len(b) for b in ph.buckets])
print("Search 24:", ph.search(24))
print("Search 11:", ph.search(11))
```

Why It Matters

- Guaranteed O(1) worst-case lookup
- No clustering, no collisions, no chains
- Ideal for static key sets (e.g. reserved keywords in a compiler, routing tables)
- Memory predictable, access blazing fast

A Gentle Proof (Why It Works)

Let $n = |S|$ be the number of keys.
With a truly random hash family into m buckets, the collision probability for two distinct keys is $1/m$.

Choose $m = n^2$. Then the expected number of collisions is

$$\mathbb{E}[C] = \binom{n}{2} \cdot \frac{1}{m} = \frac{n(n-1)}{2n^2} < \tfrac{1}{2}.$$

By Markov, $\Pr[C \geq 1] \leq \mathbb{E}[C] < \frac{1}{2}$, so $\Pr[C = 0] > \frac{1}{2}$.
Therefore a collision-free hash exists. In practice, try random seeds until one has $C = 0$, or use a deterministic construction for perfect hashing.

Try It Yourself

1. Generate perfect hash for small static set {“if”, “else”, “for”, “while”}.
2. Build minimal perfect hash (table size = n).
3. Compare lookup times with standard dict.
4. Visualize second-level hash table sizes.

Test Cases

Operation	Keys	Result	Notes
build	[10,24,31,17]	success	each slot unique
search	24	True	found
search	11	False	not in table
collisions	none		perfect mapping

Edge Cases

- Works only for static sets (no dynamic inserts)
- Building may require rehash trials
- Memory ↑ with quadratic secondary tables

Complexity

- Build: O(n²) (search for collision-free mapping)
- Lookup: O(1)
- Space: O(n) to O(n²) depending on method

Perfect hashing is like finding the perfect key for every lock, built once, opens instantly, never collides.

219 Consistent Hashing

Consistent hashing is a collision-handling strategy designed for *distributed systems* rather than single in-memory tables. It ensures that when nodes (servers, caches, or shards) join or leave, only a small fraction of keys need to be remapped, making it the backbone of scalable, fault-tolerant architectures.

What Problem Are We Solving?

In traditional hashing (e.g. `hash(key) % n`), when the number of servers `n` changes, almost every key's location changes. That's disastrous for caching, databases, or load balancing.

Consistent hashing fixes this by mapping both keys and servers into the same hash space, and placing keys near their nearest server clockwise, minimizing reassignments when the system changes.

Goal: Achieve stable key distribution under dynamic server counts with minimal movement and good balance.

How Does It Work (Plain Language)?

1. Imagine a hash ring, numbers 0 through (2^{m}-1) arranged in a circle.
2. Each node (server) and key is hashed to a position on the ring.
3. A key is assigned to the next server clockwise from its hash position.
4. When a node joins/leaves, only keys in its immediate region move.

Example (Capacity = 2^1)

Item	Hash	Placed On Ring	Owner
Node A	1000	•	
Node B	4000	•	
Node C	8000	•	
Key K	1200	→ Node B	
Key K	8500	→ Node A (wrap-around)	

If Node B leaves, only keys in its segment (1000–4000) move, everything else stays put.

Improving Load Balance

To prevent uneven distribution, each node is represented by multiple virtual nodes (vnodes), each vnode gets its own hash. This smooths the key spread across all nodes.

Example:

- Node A → hashes to 1000, 6000
- Node B → hashes to 3000, 9000

Keys are assigned to closest vnode clockwise.

Tiny Code (Easy Versions)

Python (Simple Consistent Hashing with Virtual Nodes)

```
import bisect
import hashlib

def hash_fn(key):
    return int(hashlib.md5(str(key).encode()).hexdigest(), 16)

class ConsistentHash:
    def __init__(self, nodes=None, vnodes=3):
        self.ring = []
        self.map = {}
        self.vnodes = vnodes
        if nodes:
            for n in nodes:
                self.add_node(n)

    def add_node(self, node):
        for i in range(self.vnodes):
            h = hash_fn(f"{node}-{i}")
            self.map[h] = node
            bisect.insort(self.ring, h)

    def remove_node(self, node):
        for i in range(self.vnodes):
            h = hash_fn(f"{node}-{i}")
            self.ring.remove(h)
            del self.map[h]
```

```
    def get_node(self, key):
        if not self.ring:
            return None
        h = hash_fn(key)
        idx = bisect.bisect(self.ring, h) % len(self.ring)
        return self.map[self.ring[idx]]

# Example
ch = ConsistentHash(["A", "B", "C"], vnodes=2)
print("Key 42 ->", ch.get_node(42))
ch.remove_node("B")
print("After removing B, Key 42 ->", ch.get_node(42))
```

Why It Matters

- Minimizes key remapping when nodes change (1/n of keys move)
- Enables elastic scaling for caches, DB shards, and distributed stores
- Used in systems like Amazon Dynamo, Cassandra, Riak, and memcached clients
- Balances load using virtual nodes
- Decouples hash function from node count

A Gentle Proof (Why It Works)

Let N be the number of nodes and K the number of keys.
Each node is responsible for a fraction $\frac{1}{N}$ of the ring.

When one node leaves, only its segment's keys move, about K/N.
So the expected remapping fraction is $\frac{1}{N}$.

Adding virtual nodes (vnodes) increases uniformity.
With V vnodes per physical node, the variance of the per-node load fraction scales as $\approx \frac{1}{V}$.

Try It Yourself

1. Add and remove nodes, track how many keys move.
2. Experiment with different vnode counts (1, 10, 100).
3. Visualize hash ring, mark nodes and key positions.
4. Simulate caching: assign 1000 keys, remove one node, count moves.

Test Cases

Operation	Node(s)	Keys	Result	Notes
add_nodes	A, B, C	[1..1000]	distributed evenly	
remove_node	B	[1..1000]	~1/3 keys moved	stability check
add_node	D	[1..1000]	~1/4 keys remapped	
lookup	42	-> Node C	consistent mapping	

Edge Cases

- Empty ring → return None
- Duplicate nodes → handle via unique vnode IDs
- Without vnodes → uneven load

Complexity

- Lookup: $O(\log n)$ (binary search in the ring)
- Insert/Delete node: $O(v \log n)$
- Space: $O(n \times v)$

Consistent hashing keeps order in the storm — servers may come and go, but most keys stay right where they belong.

220 Dynamic Rehashing

Dynamic rehashing is how a hash table gracefully adapts as data grows or shrinks. Instead of being trapped in a fixed-size array, the table *resizes itself*, rebuilding its layout so that load stays balanced and lookups remain fast.

What Problem Are We Solving?

When a hash table fills up, collisions become frequent, degrading performance to O(n). We need a mechanism to maintain a low load factor (ratio of elements to capacity) by resizing and rehashing automatically.

Goal: Detect when load factor crosses a threshold, allocate a larger array, and rehash all keys into their new positions efficiently.

How Does It Work (Plain Language)?

1. Monitor load factor

$$\alpha = \frac{n}{m}$$

   where n is the number of elements and m is the table size.

2. Trigger rehash
   - If $\alpha > 0.75$, expand the table (for example, double the capacity).
   - If $\alpha < 0.25$, shrink it (optional).
3. Rebuild
   - Create a new table with the updated capacity.
   - Reinsert each key using the new hash function modulo the new capacity.

Example Steps

Step	Capacity	Items	Load Factor	Action
1	4	2	0.5	ok
2	4	3	0.75	ok
3	4	4	1.0	resize to 8
4	8	4	0.5	rehashed

Every key gets new position because `hash(key) % new_capacity` changes.

Incremental Rehashing

Instead of rehashing all keys at once (costly spike), incremental rehashing spreads work across operations:

- Maintain both old and new tables.
- Rehash a few entries per insert/search until old table empty.

This keeps amortized O(1) performance, even during resize.

Tiny Code (Easy Versions)

C (Simple Doubling Rehash)

```c
#include <stdio.h>
#include <stdlib.h>

#define INIT_CAP 4

typedef struct {
    int *keys;
    int size;
    int count;
} HashTable;

int hash(int key, int size) { return key % size; }

HashTable* ht_create(int size) {
    HashTable *ht = malloc(sizeof(HashTable));
    ht->keys = malloc(sizeof(int) * size);
    for (int i = 0; i < size; i++) ht->keys[i] = -1;
    ht->size = size;
    ht->count = 0;
    return ht;
}

void ht_resize(HashTable *ht, int new_size) {
    printf("Resizing from %d to %d\n", ht->size, new_size);
    int *old_keys = ht->keys;
    int old_size = ht->size;

    ht->keys = malloc(sizeof(int) * new_size);
    for (int i = 0; i < new_size; i++) ht->keys[i] = -1;

    ht->size = new_size;
    ht->count = 0;
    for (int i = 0; i < old_size; i++) {
        if (old_keys[i] != -1) {
            int key = old_keys[i];
            int idx = hash(key, new_size);
            while (ht->keys[idx] != -1) idx = (idx + 1) % new_size;
            ht->keys[idx] = key;
            ht->count++;
```

```
        }
    }
    free(old_keys);
}

void ht_insert(HashTable *ht, int key) {
    float load = (float)ht->count / ht->size;
    if (load > 0.75) ht_resize(ht, ht->size * 2);

    int idx = hash(key, ht->size);
    while (ht->keys[idx] != -1) idx = (idx + 1) % ht->size;
    ht->keys[idx] = key;
    ht->count++;
}

int main(void) {
    HashTable *ht = ht_create(INIT_CAP);
    for (int i = 0; i < 10; i++) ht_insert(ht, i * 3);
    for (int i = 0; i < ht->size; i++)
        printf("[%d] = %d\n", i, ht->keys[i]);
    return 0;
}
```

Python

```
class DynamicHash:
    def __init__(self, cap=4):
        self.cap = cap
        self.size = 0
        self.table = [None] * cap

    def _hash(self, key):
        return hash(key) % self.cap

    def _rehash(self, new_cap):
        old_table = self.table
        self.table = [None] * new_cap
        self.cap = new_cap
        self.size = 0
        for key in old_table:
            if key is not None:
                self.insert(key)
```

```
    def insert(self, key):
        if self.size / self.cap > 0.75:
            self._rehash(self.cap * 2)
        idx = self._hash(key)
        while self.table[idx] is not None:
            idx = (idx + 1) % self.cap
        self.table[idx] = key
        self.size += 1

# Example
ht = DynamicHash()
for k in [10, 24, 31, 17, 19, 42, 56, 77]:
    ht.insert(k)
print(ht.table)
```

Why It Matters

- Keeps load factor stable for O(1) operations
- Prevents clustering in open addressing
- Supports unbounded growth
- Foundation for dynamic dictionaries, maps, caches

A Gentle Proof (Why It Works)

If each rehash doubles capacity, total cost of N inserts = O(N). Each element is moved O(1) times (once per doubling), so amortized cost per insert is O(1).

Incremental rehashing further ensures no single operation is expensive, work spread evenly.

Try It Yourself

1. Add printouts to observe load factor at each insert.
2. Implement shrink when load < 0.25.
3. Implement incremental rehash with two tables.
4. Compare doubling vs prime-capacity growth.

Test Cases

Step	Capacity	Items	Load Factor	Action
1	4	2	0.5	none
2	4	3	0.75	ok
3	4	4	1.0	resize
4	8	4	0.5	rehashed

Edge Cases

- Rehash must handle deleted slots correctly
- Avoid resizing too frequently (hysteresis)
- Keep hash function consistent across resizes

Complexity

- Average Insert/Search/Delete: O(1)
- Amortized Insert: O(1)
- Worst-case Resize: O(n)

Dynamic rehashing is the table's heartbeat, it expands when full, contracts when idle, always keeping operations smooth and steady.

Section 23. Heaps

221 Binary Heap Insert

A binary heap is a complete binary tree stored in an array that maintains the heap property, each parent is smaller (min-heap) or larger (max-heap) than its children. The insert operation keeps the heap ordered by *bubbling up* the new element until it finds the right place.

What Problem Are We Solving?

We need a data structure that efficiently gives access to the minimum (or maximum) element, while supporting fast insertions.

A binary heap offers:

- `O(1)` access to min/max
- `O(log n)` insertion and deletion
- `O(n)` build time for initial heap

Goal: Insert a new element while maintaining the heap property and completeness.

How Does It Work (Plain Language)?

A heap is stored as an array representing a complete binary tree. Each node at index `i` has:

- Parent: `(i - 1) / 2`
- Left child: `2i + 1`
- Right child: `2i + 2`

Insertion Steps (Min-Heap)

1. Append the new element at the end (bottom level, rightmost).
2. Compare it with its parent.
3. If smaller (min-heap) or larger (max-heap), swap.
4. Repeat until the heap property is restored.

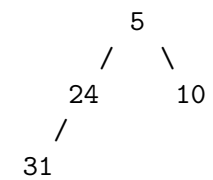
Example (Min-Heap)

Insert sequence: [10, 24, 5, 31]

Step	Array	Action
Start	[ ]	empty
Insert 10	[10]	root only
Insert 24	[10, 24]	$24 > 10$, no swap
Insert 5	[10, 24, 5]	$5 < 10 \rightarrow$ swap $\rightarrow$ [5, 24, 10]
Insert 31	[5, 24, 10, 31]	$31 > 24$, no swap

Final heap: [5, 24, 10, 31]

Tree view:



Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#define MAX 100

typedef struct {
    int arr[MAX];
    int size;
} MinHeap;

void swap(int *a, int *b) {
    int tmp = *a; *a = *b; *b = tmp;
}

void heap_insert(MinHeap *h, int val) {
    int i = h->size++;
    h->arr[i] = val;

    // bubble up
    while (i > 0) {
        int parent = (i - 1) / 2;
        if (h->arr[i] >= h->arr[parent]) break;
        swap(&h->arr[i], &h->arr[parent]);
        i = parent;
    }
}

void heap_print(MinHeap *h) {
    for (int i = 0; i < h->size; i++) printf("%d ", h->arr[i]);
    printf("\n");
}

int main(void) {
    MinHeap h = {.size = 0};
    int vals[] = {10, 24, 5, 31};
    for (int i = 0; i < 4; i++) heap_insert(&h, vals[i]);
    heap_print(&h);
}
```

Python

```python
class MinHeap:
    def __init__(self):
        self.arr = []
```

```
    def _parent(self, i): return (i - 1) // 2

    def insert(self, val):
        self.arr.append(val)
        i = len(self.arr) - 1
        while i > 0:
            p = self._parent(i)
            if self.arr[i] >= self.arr[p]:
                break
            self.arr[i], self.arr[p] = self.arr[p], self.arr[i]
            i = p

    def __repr__(self):
        return str(self.arr)

# Example
h = MinHeap()
for x in [10, 24, 5, 31]:
    h.insert(x)
print(h)
```

Why It Matters

- Fundamental for priority queues
- Core of Dijkstra's shortest path, Prim's MST, and schedulers
- Supports efficient `insert`, `extract-min/max`, and `peek`
- Used in heapsort and event-driven simulations

A Gentle Proof (Why It Works)

Each insertion bubbles up at most height of heap $= \log_2 n$. Since heap always remains complete, the structure is balanced, ensuring logarithmic operations.

Heap property is preserved because every swap ensures parent child (min-heap).

Try It Yourself

1. Insert elements in descending order → observe bubbling.
2. Switch comparisons for max-heap.
3. Print tree level by level after each insert.

4. Implement `extract_min()` to remove root and restore heap.

Test Cases

Operation	Input	Output	Notes
Insert	[10, 24, 5, 31]	[5, 24, 10, 31]	min-heap property
Insert	[3, 2, 1]	[1, 3, 2]	swap chain
Insert	[10]	[10]	single element
Insert	[]	[x]	empty start

Edge Cases

- Full array (static heap) → resize needed
- Negative values → handled same
- Duplicate keys → order preserved

Complexity

- Insert: O(log n)
- Search: O(n) (unsorted beyond heap property)
- Space: O(n)

Binary heap insertion is the heartbeat of priority queues, each element climbs to its rightful place, one gentle swap at a time.

222 Binary Heap Delete

Deleting from a binary heap means removing the root element (the minimum in a min-heap or maximum in a max-heap) while keeping both the heap property and complete tree structure intact. To do this, we swap the root with the last element, remove the last, and bubble down the new root until the heap is valid again.

What Problem Are We Solving?

We want to remove the highest-priority element quickly (min or max) from a heap, without breaking the structure.

In a min-heap, the smallest value always lives at index 0. In a max-heap, the largest value lives at index 0.

Goal: Efficiently remove the root and restore order in O(log n) time.

How Does It Work (Plain Language)?

1. Swap root (index 0) with last element.
2. Remove last element (now root value is gone).
3. Heapify down (bubble down) from the root:
    - Compare with children.
    - Swap with smaller (min-heap) or larger (max-heap) child.
    - Repeat until heap property restored.

Example (Min-Heap)

Start: `[5, 24, 10, 31]` Remove min (5):

Step	Action	Array	
1	Swap root (5) with last (31)	[31, 24, 10, 5]	
2	Remove last	[31, 24, 10]	
3	Compare 31 with children (24, 10) → smallest = 10	swap	[10, 24, 31]
4	Stop (31 > no child)	[10, 24, 31]	

Result: `[10, 24, 31]`, still a valid min-heap.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#define MAX 100

typedef struct {
    int arr[MAX];
    int size;
} MinHeap;

void swap(int *a, int *b) {
    int tmp = *a; *a = *b; *b = tmp;
}

void heapify_down(MinHeap *h, int i) {
    int smallest = i;
    int left = 2*i + 1;
```

```c
    int right = 2*i + 2;

    if (left < h->size && h->arr[left] < h->arr[smallest])
        smallest = left;
    if (right < h->size && h->arr[right] < h->arr[smallest])
        smallest = right;

    if (smallest != i) {
        swap(&h->arr[i], &h->arr[smallest]);
        heapify_down(h, smallest);
    }
}

int heap_delete_min(MinHeap *h) {
    if (h->size == 0) return -1;
    int root = h->arr[0];
    h->arr[0] = h->arr[h->size - 1];
    h->size--;
    heapify_down(h, 0);
    return root;
}

int main(void) {
    MinHeap h = {.arr = {5, 24, 10, 31}, .size = 4};
    int val = heap_delete_min(&h);
    printf("Deleted: %d\n", val);
    for (int i = 0; i < h.size; i++) printf("%d ", h.arr[i]);
    printf("\n");
}
```

Python

```python
class MinHeap:
    def __init__(self):
        self.arr = []

    def _parent(self, i): return (i - 1) // 2
    def _left(self, i): return 2 * i + 1
    def _right(self, i): return 2 * i + 2

    def insert(self, val):
        self.arr.append(val)
```

```
        i = len(self.arr) - 1
        while i > 0 and self.arr[i] < self.arr[self._parent(i)]:
            p = self._parent(i)
            self.arr[i], self.arr[p] = self.arr[p], self.arr[i]
            i = p

    def _heapify_down(self, i):
        smallest = i
        left, right = self._left(i), self._right(i)
        n = len(self.arr)
        if left < n and self.arr[left] < self.arr[smallest]:
            smallest = left
        if right < n and self.arr[right] < self.arr[smallest]:
            smallest = right
        if smallest != i:
            self.arr[i], self.arr[smallest] = self.arr[smallest], self.arr[i]
            self._heapify_down(smallest)

    def delete_min(self):
        if not self.arr:
            return None
        root = self.arr[0]
        last = self.arr.pop()
        if self.arr:
            self.arr[0] = last
            self._heapify_down(0)
        return root

# Example
h = MinHeap()
for x in [5, 24, 10, 31]:
    h.insert(x)
print("Before:", h.arr)
print("Deleted:", h.delete_min())
print("After:", h.arr)
```

Why It Matters

- Key operation in priority queues
- Core of Dijkstra's and Prim's algorithms
- Basis of heap sort (repeated delete-min)

- Ensures efficient extraction of extreme element

A Gentle Proof (Why It Works)

Each delete operation:

- Constant-time root removal
- Logarithmic heapify-down (height of tree = log n) → Total cost: O(log n)

The heap property holds because every swap moves a larger (min-heap) or smaller (max-heap) element down to children, ensuring local order at each step.

Try It Yourself

1. Delete repeatedly to sort the array (heap sort).
2. Try max-heap delete (reverse comparisons).
3. Visualize swaps after each deletion.
4. Test on ascending/descending input sequences.

Test Cases

Input	Operation	Output	Heap After	Notes
[5,24,10,31]	delete	5	[10,24,31]	valid
[1,3,2]	delete	1	[2,3]	OK
[10]	delete	10	[]	empty heap
[]	delete	None	[]	safe

Edge Cases

- Empty heap → return sentinel
- Single element → clears heap
- Duplicates handled naturally

Complexity

- Delete root: O(log n)
- Space: O(n)

Deleting from a heap is like removing the top card from a neat stack, replace it, sift it down, and balance restored.

223 Build Heap (Heapify)

Heapify (Build Heap) is the process of constructing a valid binary heap from an unsorted array in O(n) time. Instead of inserting elements one by one, we reorganize the array *in place* so every parent satisfies the heap property.

What Problem Are We Solving?

If we insert each element individually into an empty heap, total time is O(n log n). But we can do better. By heapifying from the bottom up, we can build the entire heap in O(n), crucial for heapsort and initializing priority queues efficiently.

Goal: Turn any array into a valid min-heap or max-heap quickly.

How Does It Work (Plain Language)?

A heap stored in an array represents a complete binary tree:

- For node `i`, children are `2i + 1` and `2i + 2`

To build the heap:

1. Start from the last non-leaf node = `(n / 2) - 1`.
2. Apply heapify-down (sift down) to ensure the subtree rooted at `i` satisfies heap property.
3. Move upwards to the root, repeating the process.

Each subtree becomes a valid heap, and when done, the whole array is a heap.

Example (Min-Heap)

Start: `[31, 10, 24, 5, 12, 7]`

Step	i	Subtree	Action	Result
Start	-	full array	-	[31, 10, 24, 5, 12, 7]
1	2	(24, 7)	$24 > 7 \rightarrow$ swap	[31, 10, 7, 5, 12, 24]
2	1	(10, 5, 12)	$10 > 5 \rightarrow$ swap	[31, 5, 7, 10, 12, 24]
3	0	(31, 5, 7)	$31 > 5 \rightarrow$ swap	[5, 31, 7, 10, 12, 24]
4	1	(31, 10, 12)	$31 > 10 \rightarrow$ swap	[5, 10, 7, 31, 12, 24]

Final heap: [5, 10, 7, 31, 12, 24]

Tiny Code (Easy Versions)

C (Bottom-Up Build Heap)

```c
#include <stdio.h>

#define MAX 100

typedef struct {
    int arr[MAX];
    int size;
} MinHeap;

void swap(int *a, int *b) {
    int tmp = *a; *a = *b; *b = tmp;
}

void heapify_down(MinHeap *h, int i) {
    int smallest = i;
    int left = 2 * i + 1;
    int right = 2 * i + 2;

    if (left < h->size && h->arr[left] < h->arr[smallest])
        smallest = left;
    if (right < h->size && h->arr[right] < h->arr[smallest])
        smallest = right;
    if (smallest != i) {
        swap(&h->arr[i], &h->arr[smallest]);
        heapify_down(h, smallest);
    }
}

void build_heap(MinHeap *h) {
    for (int i = h->size / 2 - 1; i >= 0; i--)
        heapify_down(h, i);
}

int main(void) {
    MinHeap h = {.arr = {31, 10, 24, 5, 12, 7}, .size = 6};
    build_heap(&h);
    for (int i = 0; i < h.size; i++) printf("%d ", h.arr[i]);
    printf("\n");
}
```

Python

```python
class MinHeap:
    def __init__(self, arr):
        self.arr = arr
        self.size = len(arr)
        self.build_heap()

    def _left(self, i): return 2 * i + 1
    def _right(self, i): return 2 * i + 2

    def _heapify_down(self, i):
        smallest = i
        l, r = self._left(i), self._right(i)
        if l < self.size and self.arr[l] < self.arr[smallest]:
            smallest = l
        if r < self.size and self.arr[r] < self.arr[smallest]:
            smallest = r
        if smallest != i:
            self.arr[i], self.arr[smallest] = self.arr[smallest], self.arr[i]
            self._heapify_down(smallest)

    def build_heap(self):
        for i in range(self.size // 2 - 1, -1, -1):
            self._heapify_down(i)

# Example
arr = [31, 10, 24, 5, 12, 7]
h = MinHeap(arr)
print(h.arr)
```

Why It Matters

- Builds a valid heap in O(n) (not O(n log n))
- Used in heapsort initialization
- Efficient for constructing priority queues from bulk data
- Guarantees balanced tree structure automatically

A Gentle Proof (Why It Works)

Each node at depth `d` takes O(height) = O(log(n/d)) work. There are more nodes at lower depths (less work each), fewer at top (more work each). Sum across levels yields O(n) total time, not O(n log n).

Hence, bottom-up heapify is asymptotically optimal.

Try It Yourself

1. Run with different array sizes, random orders.
2. Compare time vs inserting one-by-one.
3. Flip comparisons for max-heap.
4. Visualize swaps as a tree.

Test Cases

Input	Output	Notes
[31,10,24,5,12,7]	[5,10,7,31,12,24]	valid min-heap
[3,2,1]	[1,2,3]	heapified
[10]	[10]	single
[]	[]	empty safe

Edge Cases

- Already heap → no change
- Reverse-sorted input → many swaps
- Duplicates handled correctly

Complexity

- Time: O(n)
- Space: O(1) (in-place)

Heapify is the quiet craftsman, shaping chaos into order with gentle swaps from the ground up.

224 Heap Sort

Heap Sort is a classic comparison-based sorting algorithm that uses a binary heap to organize data and extract elements in sorted order. By building a max-heap (or min-heap) and repeatedly removing the root, we achieve a fully sorted array in O(n log n) time, with no extra space.

What Problem Are We Solving?

We want a fast, in-place sorting algorithm that:

- Doesn't require recursion (like mergesort)
- Has predictable O(n log n) behavior
- Avoids worst-case quadratic time (like quicksort)

Goal: Use the heap's structure to repeatedly select the next largest (or smallest) element efficiently.

How Does It Work (Plain Language)?

1. Build a max-heap from the unsorted array.
2. Repeat until heap is empty:
    - Swap root (max element) with last element.
    - Reduce heap size by one.
    - Heapify-down the new root to restore heap property.

The array becomes sorted in ascending order (for max-heap).

Example (Ascending Sort)

Start: `[5, 31, 10, 24, 7]`

Step	Action	Array
1	Build max-heap	[31, 24, 10, 5, 7]
2	Swap 31 7, heapify	[24, 7, 10, 5, 31]
3	Swap 24 5, heapify	[10, 7, 5, 24, 31]
4	Swap 10 5, heapify	[5, 7, 10, 24, 31]
5	Sorted	[5, 7, 10, 24, 31]

Tiny Code (Easy Versions)

C (In-place Heap Sort)

```c
#include <stdio.h>

void swap(int *a, int *b) {
    int tmp = *a; *a = *b; *b = tmp;
}

void heapify(int arr[], int n, int i) {
    int largest = i;
    int left = 2*i + 1;
    int right = 2*i + 2;

    if (left < n && arr[left] > arr[largest])
        largest = left;
    if (right < n && arr[right] > arr[largest])
        largest = right;

    if (largest != i) {
        swap(&arr[i], &arr[largest]);
        heapify(arr, n, largest);
    }
}

void heap_sort(int arr[], int n) {
    // build max-heap
    for (int i = n / 2 - 1; i >= 0; i--)
        heapify(arr, n, i);

    // extract elements
    for (int i = n - 1; i > 0; i--) {
        swap(&arr[0], &arr[i]);
        heapify(arr, i, 0);
    }
}

int main(void) {
    int arr[] = {5, 31, 10, 24, 7};
    int n = sizeof(arr)/sizeof(arr[0]);
    heap_sort(arr, n);
    for (int i = 0; i < n; i++) printf("%d ", arr[i]);
```

```
    printf("\n");
}
```

Python

```
def heapify(arr, n, i):
    largest = i
    l, r = 2*i + 1, 2*i + 2

    if l < n and arr[l] > arr[largest]:
        largest = l
    if r < n and arr[r] > arr[largest]:
        largest = r

    if largest != i:
        arr[i], arr[largest] = arr[largest], arr[i]
        heapify(arr, n, largest)

def heap_sort(arr):
    n = len(arr)
    # build max-heap
    for i in range(n//2 - 1, -1, -1):
        heapify(arr, n, i)
    # extract
    for i in range(n - 1, 0, -1):
        arr[0], arr[i] = arr[i], arr[0]
        heapify(arr, i, 0)

# Example
arr = [5, 31, 10, 24, 7]
heap_sort(arr)
print(arr)
```

Why It Matters

- Guaranteed O(n log n) runtime (worst-case safe)
- In-place, no extra arrays
- Great teaching example of heap structure in action
- Used in systems with strict space limits

A Gentle Proof (Why It Works)

1. Building the heap = O(n) (bottom-up heapify).
2. Each extraction = O(log n), repeated n times → O(n log n).
3. Heap property ensures root always holds largest element.

So final array is sorted after repeated root extractions.

Try It Yourself

1. Switch comparisons for min-heap sort (descending).
2. Print array after each swap to see process.
3. Compare with quicksort and mergesort.
4. Test large random arrays.

Test Cases

Input	Output	Notes
[5,31,10,24,7]	[5,7,10,24,31]	ascending
[10,9,8,7]	[7,8,9,10]	reverse input
[3]	[3]	single
[]	[]	empty

Edge Cases

- Repeated values handled fine
- Already sorted input still O(n log n)
- Stable? (order not preserved)

Complexity

- Time: O(n log n)
- Space: O(1)
- Stable: No

Heap sort is the mountain climber's algorithm, pulling the biggest to the top, one step at a time, until order reigns from summit to base.

225 Min Heap Implementation

A min-heap is a binary tree where each parent is smaller than or equal to its children. Stored compactly in an array, it guarantees O(1) access to the smallest element and O(log n) insertion and deletion, perfect for priority queues and scheduling systems.

What Problem Are We Solving?

We need a data structure that:

- Quickly gives us the minimum element
- Supports efficient insertions and deletions
- Maintains order dynamically

A min-heap achieves this balance, always keeping the smallest element at the root while remaining compact and complete.

How Does It Work (Plain Language)?

A binary min-heap is stored as an array, where:

- `parent(i) = (i - 1) / 2`
- `left(i) = 2i + 1`
- `right(i) = 2i + 2`

Operations:

1. Insert(x):
    - Add `x` at the end.
    - "Bubble up" while `x < parent(x)`.
2. ExtractMin():
    - Remove root.
    - Move last element to root.
    - "Bubble down" while parent $>$ smallest child.
3. Peek():
    - Return `arr[0]`.

Example

Start: `[ ]` Insert sequence: 10, 24, 5, 31, 7

Step	Action	Array
1	insert 10	[10]
2	insert 24	[10, 24]
3	insert 5	bubble up → swap with 10 [5, 24, 10]
4	insert 31	[5, 24, 10, 31]
5	insert 7	[5, 7, 10, 31, 24]

ExtractMin:

- Swap root with last (5 24) → `[24, 7, 10, 31, 5]`
- Remove last → `[24, 7, 10, 31]`
- Bubble down → `[7, 24, 10, 31]`

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#define MAX 100

typedef struct {
    int arr[MAX];
    int size;
} MinHeap;

void swap(int *a, int *b) {
    int tmp = *a; *a = *b; *b = tmp;
}

void heapify_up(MinHeap *h, int i) {
    while (i > 0) {
        int parent = (i - 1) / 2;
        if (h->arr[i] >= h->arr[parent]) break;
        swap(&h->arr[i], &h->arr[parent]);
        i = parent;
    }
}
```

```c
void heapify_down(MinHeap *h, int i) {
    int smallest = i;
    int left = 2*i + 1;
    int right = 2*i + 2;

    if (left < h->size && h->arr[left] < h->arr[smallest]) smallest = left;
    if (right < h->size && h->arr[right] < h->arr[smallest]) smallest = right;

    if (smallest != i) {
        swap(&h->arr[i], &h->arr[smallest]);
        heapify_down(h, smallest);
    }
}

void insert(MinHeap *h, int val) {
    h->arr[h->size] = val;
    heapify_up(h, h->size);
    h->size++;
}

int extract_min(MinHeap *h) {
    if (h->size == 0) return -1;
    int root = h->arr[0];
    h->arr[0] = h->arr[--h->size];
    heapify_down(h, 0);
    return root;
}

int peek(MinHeap *h) {
    return h->size > 0 ? h->arr[0] : -1;
}

int main(void) {
    MinHeap h = {.size = 0};
    int vals[] = {10, 24, 5, 31, 7};
    for (int i = 0; i < 5; i++) insert(&h, vals[i]);
    printf("Min: %d\n", peek(&h));
    printf("Extracted: %d\n", extract_min(&h));
    for (int i = 0; i < h.size; i++) printf("%d ", h.arr[i]);
    printf("\n");
}
```

Python

```
class MinHeap:
    def __init__(self):
        self.arr = []

    def _parent(self, i): return (i - 1) // 2
    def _left(self, i): return 2 * i + 1
    def _right(self, i): return 2 * i + 2

    def insert(self, val):
        self.arr.append(val)
        i = len(self.arr) - 1
        while i > 0 and self.arr[i] < self.arr[self._parent(i)]:
            p = self._parent(i)
            self.arr[i], self.arr[p] = self.arr[p], self.arr[i]
            i = p

    def extract_min(self):
        if not self.arr:
            return None
        root = self.arr[0]
        last = self.arr.pop()
        if self.arr:
            self.arr[0] = last
            self._heapify_down(0)
        return root

    def _heapify_down(self, i):
        smallest = i
        l, r = self._left(i), self._right(i)
        if l < len(self.arr) and self.arr[l] < self.arr[smallest]:
            smallest = l
        if r < len(self.arr) and self.arr[r] < self.arr[smallest]:
            smallest = r
        if smallest != i:
            self.arr[i], self.arr[smallest] = self.arr[smallest], self.arr[i]
            self._heapify_down(smallest)

    def peek(self):
        return self.arr[0] if self.arr else None

# Example
```

```
h = MinHeap()
for x in [10, 24, 5, 31, 7]:
    h.insert(x)
print("Heap:", h.arr)
print("Min:", h.peek())
print("Extracted:", h.extract_min())
print("After:", h.arr)
```

Why It Matters

- Backbone of priority queues, Dijkstra's, Prim's, A*
- Always gives minimum element in O(1)
- Compact array-based structure (no pointers)
- Excellent for dynamic, ordered sets

A Gentle Proof (Why It Works)

Each insertion or deletion affects only a single path (height = log n). Since every swap improves local order, heap property restored in O(log n). At any time, parent children → global min at root.

Try It Yourself

1. Implement a max-heap variant.
2. Track the number of swaps per insert.
3. Combine with heap sort by repeated extract_min.
4. Visualize heap as a tree diagram.

Test Cases

Operation	Input	Output	Heap After	Notes
Insert	[10,24,5,31,7]	-	[5,7,10,31,24]	valid
Peek	-	5	[5,7,10,31,24]	smallest
ExtractMin	-	5	[7,24,10,31]	reordered
Empty Extract	[]	None	[]	safe

Edge Cases

- Duplicates → handled fine
- Empty heap → return sentinel
- Negative numbers → no problem

Complexity

Operation	Time	Space
Insert	O(log n)	O(1)
ExtractMin	O(log n)	O(1)
Peek	O(1)	O(1)

A min-heap is the quiet organizer, always keeping the smallest task at the top, ready when you are.

226 Max Heap Implementation

A max-heap is a binary tree where each parent is greater than or equal to its children. Stored compactly in an array, it guarantees O(1) access to the largest element and O(log n) insertion and deletion, making it ideal for scheduling, leaderboards, and priority-based systems.

What Problem Are We Solving?

We want a data structure that efficiently maintains a dynamic set of elements while allowing us to:

- Access the largest element quickly
- Insert and delete efficiently
- Maintain order automatically

A max-heap does exactly that, it always bubbles the biggest element to the top.

How Does It Work (Plain Language)?

A binary max-heap is stored as an array, with these relationships:

- `parent(i) = (i - 1) / 2`
- `left(i) = 2i + 1`
- `right(i) = 2i + 2`

Operations:

1. Insert(x):
    - Add `x` at the end.
    - "Bubble up" while `x > parent(x)`.
2. ExtractMax():
    - Remove root (maximum).
    - Move last element to root.
    - "Bubble down" while parent $<$ larger child.
3. Peek():
    - Return `arr[0]` (max element).

Example

Start: `[ ]` Insert sequence: 10, 24, 5, 31, 7

Step	Action	Array
1	insert 10	[10]
2	insert 24	bubble up $\rightarrow$ [24, 10]
3	insert 5	[24, 10, 5]
4	insert 31	bubble up $\rightarrow$ [31, 24, 5, 10]
5	insert 7	[31, 24, 5, 10, 7]

ExtractMax:

- Swap root with last (31 7): `[7, 24, 5, 10, 31]`
- Remove last: `[7, 24, 5, 10]`
- Bubble down: swap 7 24 $\rightarrow$ `[24, 10, 5, 7]`

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#define MAX 100

typedef struct {
    int arr[MAX];
    int size;
} MaxHeap;

void swap(int *a, int *b) {
    int tmp = *a; *a = *b; *b = tmp;
}

void heapify_up(MaxHeap *h, int i) {
    while (i > 0) {
        int parent = (i - 1) / 2;
        if (h->arr[i] <= h->arr[parent]) break;
        swap(&h->arr[i], &h->arr[parent]);
        i = parent;
    }
}

void heapify_down(MaxHeap *h, int i) {
    int largest = i;
    int left = 2 * i + 1;
    int right = 2 * i + 2;

    if (left < h->size && h->arr[left] > h->arr[largest]) largest = left;
    if (right < h->size && h->arr[right] > h->arr[largest]) largest = right;

    if (largest != i) {
        swap(&h->arr[i], &h->arr[largest]);
        heapify_down(h, largest);
    }
}

void insert(MaxHeap *h, int val) {
    h->arr[h->size] = val;
    heapify_up(h, h->size);
    h->size++;
}

int extract_max(MaxHeap *h) {
```

```
    if (h->size == 0) return -1;
    int root = h->arr[0];
    h->arr[0] = h->arr[--h->size];
    heapify_down(h, 0);
    return root;
}

int peek(MaxHeap *h) {
    return h->size > 0 ? h->arr[0] : -1;
}

int main(void) {
    MaxHeap h = {.size = 0};
    int vals[] = {10, 24, 5, 31, 7};
    for (int i = 0; i < 5; i++) insert(&h, vals[i]);
    printf("Max: %d\n", peek(&h));
    printf("Extracted: %d\n", extract_max(&h));
    for (int i = 0; i < h.size; i++) printf("%d ", h.arr[i]);
    printf("\n");
}
```

Python

```
class MaxHeap:
    def __init__(self):
        self.arr = []

    def _parent(self, i): return (i - 1) // 2
    def _left(self, i): return 2 * i + 1
    def _right(self, i): return 2 * i + 2

    def insert(self, val):
        self.arr.append(val)
        i = len(self.arr) - 1
        while i > 0 and self.arr[i] > self.arr[self._parent(i)]:
            p = self._parent(i)
            self.arr[i], self.arr[p] = self.arr[p], self.arr[i]
            i = p

    def extract_max(self):
        if not self.arr:
            return None
```

```
        root = self.arr[0]
        last = self.arr.pop()
        if self.arr:
            self.arr[0] = last
            self._heapify_down(0)
        return root

    def _heapify_down(self, i):
        largest = i
        l, r = self._left(i), self._right(i)
        if l < len(self.arr) and self.arr[l] > self.arr[largest]:
            largest = l
        if r < len(self.arr) and self.arr[r] > self.arr[largest]:
            largest = r
        if largest != i:
            self.arr[i], self.arr[largest] = self.arr[largest], self.arr[i]
            self._heapify_down(largest)

    def peek(self):
        return self.arr[0] if self.arr else None

# Example
h = MaxHeap()
for x in [10, 24, 5, 31, 7]:
    h.insert(x)
print("Heap:", h.arr)
print("Max:", h.peek())
print("Extracted:", h.extract_max())
print("After:", h.arr)
```

Why It Matters

- Priority queues that need fast access to maximum
- Scheduling highest-priority tasks
- Tracking largest elements dynamically
- Used in heap sort, selection problems, top-k queries

A Gentle Proof (Why It Works)

Each operation adjusts at most height = log n levels. Since all swaps move greater elements upward, heap property (parent children) is restored in logarithmic time. Thus the root always

holds the maximum.

Try It Yourself

1. Convert to min-heap by flipping comparisons.
2. Use heap to implement k-largest elements finder.
3. Trace swaps after each insert/delete.
4. Visualize heap as a tree diagram.

Test Cases

Operation	Input	Output	Heap After	Notes
Insert	[10,24,5,31,7]	-	[31,24,5,10,7]	max at root
Peek	-	31	[31,24,5,10,7]	largest
ExtractMax	-	31	[24,10,5,7]	heap fixed
Empty Extract	[]	None	[]	safe

Edge Cases

- Duplicates → handled fine
- Empty heap → sentinel
- Negative numbers → valid

Complexity

Operation	Time	Space
Insert	O(log n)	O(1)
ExtractMax	O(log n)	O(1)
Peek	O(1)	O(1)

A max-heap is the summit keeper, always crowning the greatest, ensuring the hierarchy remains true from root to leaf.

227 Fibonacci Heap Insert/Delete

A Fibonacci heap is a meldable heap optimized for very fast amortized operations. It keeps a collection of heap-ordered trees with minimal structural work on most operations, banking work for occasional consolidations. Classic result: `insert`, `find-min`, and `decrease-key` run in O(1) amortized, while `extract-min` runs in O(log n) amortized.

What Problem Are We Solving?

We want ultra fast priority queue ops in algorithms that call `decrease-key` a lot, like Dijkstra and Prim. Binary and pairing heaps give `decrease-key` in `O(log n)` or good constants, but Fibonacci heaps achieve amortized O(1) for `insert` and `decrease-key`, improving theoretical bounds.

Goal: Maintain a set of heap-ordered trees where most updates only touch a few pointers, delaying consolidation until `extract-min`.

How Does It Work (Plain Language)?

Structure highlights

- A root list of trees, each obeying min-heap order.
- A pointer to the global minimum root.
- Each node stores degree, parent, child, and a mark bit used by `decrease-key`.
- Root list is a circular doubly linked list, children lists are similar.

Core ideas

- Insert adds a 1 node tree into the root list and updates `min` if needed.
- Delete is typically implemented as `decrease-key(x, -inf)` then `extract-min`.
- Extract-min removes the min root, promotes its children to the root list, then consolidates roots by linking trees of equal degree until all root degrees are unique.

How Does Insert Work

Steps for `insert(x)`

1. Make a singleton node `x`.
2. Splice `x` into the root list.
3. Update `min` if `x.key < min.key`.

Example Steps (Root List View)

Step	Action	Root List	Min
1	insert 12	[12]	12
2	insert 7	[12, 7]	7
3	insert 25	[12, 7, 25]	7
4	insert 3	[12, 7, 25, 3]	3

All inserts are O(1) pointer splices.

How Does Delete Work

To delete an arbitrary node `x`, standard approach

1. `decrease-key(x, -inf)` so `x` becomes the minimum.
2. `extract-min()` to remove it.

Delete inherits the `extract-min` cost.

Tiny Code (Educational Skeleton)

This is a minimal sketch to illustrate structure and the two requested operations. It omits full `decrease-key` and cascading cuts to keep focus. In practice, a complete Fibonacci heap also implements `decrease-key` and `extract-min` with consolidation arrays.

Python (didactic skeleton for insert and delete via extract-min path)

```
class FibNode:
    def __init__(self, key):
        self.key = key
        self.degree = 0
        self.mark = False
        self.parent = None
        self.child = None
        # circular doubly linked list pointers
        self.left = self
        self.right = self

def _splice(a, b):
    # insert node b to the right of node a in a circular list
    b.right = a.right
```

```
    b.left = a
    a.right.left = b
    a.right = b

def _remove_from_list(x):
    x.left.right = x.right
    x.right.left = x.left
    x.left = x.right = x

class FibHeap:
    def __init__(self):
        self.min = None
        self.n = 0

    def insert(self, key):
        x = FibNode(key)
        if self.min is None:
            self.min = x
        else:
            _splice(self.min, x)
            if x.key < self.min.key:
                self.min = x
        self.n += 1
        return x

    def _merge_root_list(self, other_min):
        if other_min is None:
            return
        # concat circular lists: self.min and other_min
        a = self.min
        b = other_min
        a_right = a.right
        b_left = b.left
        a.right = b
        b.left = a
        a_right.left = b_left
        b_left.right = a_right
        if b.key < self.min.key:
            self.min = b

    def extract_min(self):
        z = self.min
```

```
        if z is None:
            return None
        # promote children to root list
        if z.child:
            c = z.child
            nodes = []
            cur = c
            while True:
                nodes.append(cur)
                cur = cur.right
                if cur == c:
                    break
            for x in nodes:
                x.parent = None
                _remove_from_list(x)
                _splice(z, x)  # into root list near z
        # remove z from root list
        if z.right == z:
            self.min = None
        else:
            nxt = z.right
            _remove_from_list(z)
            self.min = nxt
            self._consolidate()  # real impl would link equal degree trees
        self.n -= 1
        return z.key

    def _consolidate(self):
        # Placeholder: a full implementation uses an array A[0..floor(log_phi n)]
        # to link roots of equal degree until all degrees unique.
        pass

    def delete(self, node):
        # In full Fibonacci heap:
        # decrease_key(node, -inf), then extract_min
        # Here we approximate by manual min-bump if node is the min
        # and ignore cascading cuts for brevity.
        # For correctness in real use, implement decrease_key and cuts.
        node.key = float("-inf")
        if self.min and node.key < self.min.key:
            self.min = node
        return self.extract_min()
```

```
# Example
H = FibHeap()
n1 = H.insert(12)
n2 = H.insert(7)
n3 = H.insert(25)
n4 = H.insert(3)
print("Extracted min:", H.extract_min())  # 3
```

Note This skeleton shows how `insert` stitches into the root list and how `extract_min` would promote children. A production version must implement `decrease-key` with cascading cuts and `_consolidate` that links trees of equal degree.

Why It Matters

- Theoretical speedups for graph algorithms heavy on `decrease-key`
- Meld operation can be O(1) by concatenating root lists
- Amortized guarantees backed by potential function analysis

A Gentle Proof (Why It Works)

Amortized analysis uses a potential function based on number of trees in the root list and number of marked nodes.

- `insert` only adds a root and maybe updates `min`, decreasing or slightly increasing potential, so O(1) amortized.
- `decrease-key` cuts a node and possibly cascades parent cuts, but marks bound the total number of cascades over a sequence, giving O(1) amortized.
- `extract-min` triggers consolidation. The number of distinct degrees is O(log n), so linking costs O(log n) amortized.

Try It Yourself

1. Complete `_consolidate` with an array indexed by degree, linking roots of equal degree until unique.
2. Implement `decrease_key(x, new_key)` with cut and cascading cut rules.
3. Add `union(H1, H2)` that concatenates root lists and picks the smaller `min`.
4. Benchmark against binary and pairing heaps on workloads with many `decrease-key` operations.

Test Cases

Operation	Input	Expected	Notes
insert	12, 7, 25, 3	min = 3	simple root list updates
extract_min	after above	returns 3	children promoted, consolidate
delete(node)	delete 7	7 removed	via decrease to minus infinity then extract
meld	union of two heaps	new min = min(m1, m2)	O(1) concat

Edge Cases

- Extract from empty heap returns None
- Duplicate keys are fine
- Large inserts without extract build many small trees until consolidation

Complexity

Operation	Amortized Time
insert	O(1)
find-min	O(1)
decrease-key	O(1)
extract-min	O(log n)
delete	O(log n) via decrease then extract

Fibonacci heaps trade strict order for lazy elegance. Most ops are tiny pointer shuffles, and the heavy lifting happens rarely during consolidation.

228 Pairing Heap Merge

A pairing heap is a simple, pointer-based, meldable heap that is famously fast in practice. Its secret weapon is the merge operation: link two heap roots by making the larger-key root a child of the smaller-key root. Many other operations reduce to a small number of merges.

What Problem Are We Solving?

We want a priority queue with a tiny constant factor and very simple code, while keeping theoretical guarantees close to Fibonacci heaps. Pairing heaps offer extremely quick `insert`, `meld`, and often `decrease-key`, with `delete-min` powered by a lightweight multi-merge.

Goal: Represent a heap as a tree of nodes and implement merge so that all higher-level operations can be expressed as sequences of merges.

How Does It Work (Plain Language)?

Each node has: key, first child, and next sibling. The heap is just a pointer to the root. To merge two heaps `A` and `B`:

1. If one is empty, return the other.
2. Compare roots.
3. Make the larger-root heap the new child of the smaller-root heap by linking it as the smaller root's first child.

Other ops via merge

- Insert(x): make a 1-node heap and `merge(root, x)`.
- Find-min: the root's key.
- Delete-min: remove the root, then merge its children in two passes
    1. Left to right, pairwise merge adjacent siblings.
    2. Right to left, merge the resulting heaps back into one.
- Decrease-key(x, new): cut `x` from its place, set `x.key = new`, then `merge(root, x)`.

Example Steps (Merge only)

Step	Heap A (root)	Heap B (root)	Action	New Root
1	7	12	link 12 under 7	7
2	7	3	link 7 under 3	3
3	3	9	link 9 under 3	3

Resulting root is the minimum of all merged heaps.

Tiny Code (Easy Versions)

C (merge, insert, find-min, delete-min two-pass)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key;
    struct Node *child;
    struct Node *sibling;
} Node;

Node* make_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key; n->child = NULL; n->sibling = NULL;
    return n;
}

Node* merge(Node* a, Node* b) {
    if (!a) return b;
    if (!b) return a;
    if (b->key < a->key) { Node* t = a; a = b; b = t; }
    // make b the first child of a
    b->sibling = a->child;
    a->child = b;
    return a;
}

Node* insert(Node* root, int key) {
    return merge(root, make_node(key));
}

Node* merge_pairs(Node* first) {
    if (!first || !first->sibling) return first;
    Node* a = first;
    Node* b = first->sibling;
    Node* rest = b->sibling;
    a->sibling = b->sibling = NULL;
    return merge(merge(a, b), merge_pairs(rest));
}

Node* delete_min(Node* root, int* out) {
```

```
    if (!root) return NULL;
    *out = root->key;
    Node* new_root = merge_pairs(root->child);
    free(root);
    return new_root;
}

int main(void) {
    Node* h = NULL;
    h = insert(h, 7);
    h = insert(h, 12);
    h = insert(h, 3);
    h = insert(h, 9);
    int m;
    h = delete_min(h, &m);
    printf("Deleted min: %d\n", m); // 3
    return 0;
}
```

Python (succinct pairing heap)

```
class Node:
    __slots__ = ("key", "child", "sibling")
    def __init__(self, key):
        self.key = key
        self.child = None
        self.sibling = None

def merge(a, b):
    if not a: return b
    if not b: return a
    if b.key < a.key:
        a, b = b, a
    b.sibling = a.child
    a.child = b
    return a

def merge_pairs(first):
    if not first or not first.sibling:
        return first
    a, b, rest = first, first.sibling, first.sibling.sibling
    a.sibling = b.sibling = None
```

```
    return merge(merge(a, b), merge_pairs(rest))

class PairingHeap:
    def __init__(self): self.root = None
    def find_min(self): return None if not self.root else self.root.key
    def insert(self, x):
        self.root = merge(self.root, Node(x))
    def meld(self, other):
        self.root = merge(self.root, other.root)
    def delete_min(self):
        if not self.root: return None
        m = self.root.key
        self.root = merge_pairs(self.root.child)
        return m

# Example
h = PairingHeap()
for x in [7, 12, 3, 9]:
    h.insert(x)
print(h.find_min())      # 3
print(h.delete_min())    # 3
print(h.find_min())      # 7
```

Why It Matters

- Incredibly simple code yet high performance in practice
- Meld is constant time pointer work
- Excellent for workloads mixing frequent inserts and decrease-keys
- A strong practical alternative to Fibonacci heaps

A Gentle Proof (Why It Works)

Merge correctness

- After linking, the smaller root remains parent, so heap order holds at the root and along the newly attached subtree.

Delete-min two-pass

- Pairwise merges reduce the number of trees while keeping roots small.
- The second right-to-left fold merges larger partial heaps into a single heap.

- Analyses show `delete-min` runs in O(log n) amortized; `insert` and `meld` in O(1) amortized.
- `decrease-key` is conjectured O(1) amortized in practice and near that in theory under common models.

Try It Yourself

1. Implement `decrease_key(node, new_key)`: cut the node from its parent and `merge(root, node)` after lowering its key.
2. Add a handle table to access nodes for fast decrease-key.
3. Benchmark against binary and Fibonacci heaps on Dijkstra workloads.
4. Visualize delete-min's two-pass pairing on random trees.

Test Cases

Operation	Input	Output	Notes
insert	7, 12, 3, 9	min = 3	root tracks global min
meld	meld two heaps	new min is min of both	constant-time link
delete_min	after above	3	two-pass pairing
delete_min	next	7	heap restructures

Edge Cases

- Merging with empty heap returns the other heap
- Duplicate keys behave naturally
- Single-node heap deletes to empty safely

Complexity

Operation	Amortized Time	Notes
meld	O(1)	core primitive
insert	O(1)	merge singleton
find-min	O(1)	root key
delete-min	O(log n)	two-pass merge
decrease-key	O(1) practical, near O(1) amortized in models	cut+merge

Pairing heaps make merging feel effortless: one comparison, a couple of pointers, and you are done.

229 Binomial Heap Merge

A binomial heap is a set of binomial trees that act like a binary counter for priority queues. The star move is merge: combining two heaps is like adding two binary numbers. Trees of the same degree collide, you link one under the other, and carry to the next degree.

What Problem Are We Solving?

We want a priority queue that supports fast meld (union) while keeping simple, provable bounds. Binomial heaps deliver:

- `meld` in O(log n)
- `insert` in O(1) amortized by melding a 1-node heap
- `find-min` in O(log n)
- `delete-min` in O(log n) via a meld with reversed children

Goal: Represent the heap as a sorted list of binomial trees and merge two heaps by walking these lists, linking equal-degree roots.

How Does It Work (Plain Language)?

Binomial tree facts

- A binomial tree of degree `k` has `2^k` nodes.
- Each degree occurs at most once in a binomial heap.
- Roots are kept in increasing order of degree.

Merging two heaps H1 and H2

1. Merge the root lists by degree like a sorted list merge.
2. Walk the combined list. Whenever two consecutive trees have the same degree, link them: make the larger-key root a child of the smaller-key root, increasing the degree by 1.
3. Use a carry idea just like binary addition.

Link(u, v)

- Precondition: `degree(u) == degree(v)`.
- After linking, `min(u.key, v.key)` becomes parent and degree increases by 1.

Example Steps (degrees in parentheses)

Start

- H1 roots: [2(0), 7(1), 12(3)]

- H2 roots: [3(0), 9(2)]

1 Merge lists by degree

- Combined: [2(0), 3(0), 7(1), 9(2), 12(3)]

2 Resolve equal degrees

- Link 2(0) and 3(0) under min root → 2 becomes parent: 2(1)
- Now list: [2(1), 7(1), 9(2), 12(3)]
- Link 2(1) and 7(1) → 2 becomes parent: 2(2)
- Now list: [2(2), 9(2), 12(3)]
- Link 2(2) and 9(2) → 2 becomes parent: 2(3)
- Now list: [2(3), 12(3)]
- Link 2(3) and 12(3) → 2 becomes parent: 2(4)

Final heap has root list [2(4)] with 2 as global min.

Tiny Code (Easy Versions)

C (merge plus link, minimal skeleton)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key;
    int degree;
    struct Node* parent;
    struct Node* child;
    struct Node* sibling; // next root or next sibling in child list
} Node;

Node* make_node(int key){
    Node* x = calloc(1, sizeof(Node));
    x->key = key;
    return x;
}

// Make 'y' a child of 'x' assuming x->key <= y->key and degree equal
static Node* link_tree(Node* x, Node* y){
    y->parent = x;
    y->sibling = x->child;
```

```
    x->child = y;
    x->degree += 1;
    return x;
}

// Merge root lists by degree (no linking yet)
static Node* merge_root_lists(Node* a, Node* b){
    if(!a) return b;
    if(!b) return a;
    Node dummy = {0};
    Node* tail = &dummy;
    while(a && b){
        if(a->degree <= b->degree){
            tail->sibling = a; a = a->sibling;
        }else{
            tail->sibling = b; b = b->sibling;
        }
        tail = tail->sibling;
    }
    tail->sibling = a ? a : b;
    return dummy.sibling;
}

// Union with carry logic
Node* binomial_union(Node* h1, Node* h2){
    Node* head = merge_root_lists(h1, h2);
    if(!head) return NULL;

    Node* prev = NULL;
    Node* curr = head;
    Node* next = curr->sibling;

    while(next){
        if(curr->degree != next->degree || (next->sibling && next->sibling->degree == curr->
            prev = curr;
            curr = next;
        }else{
            if(curr->key <= next->key){
                curr->sibling = next->sibling;
                curr = link_tree(curr, next);
            }else{
                if(prev) prev->sibling = next;
```

```
                else head = next;
                curr = link_tree(next, curr);
            }
        }
        next = curr->sibling;
    }
    return head;
}

// Convenience: insert by union with 1-node heap
Node* insert(Node* heap, int key){
    return binomial_union(heap, make_node(key));
}

int main(void){
    Node* h1 = NULL;
    Node* h2 = NULL;
    h1 = insert(h1, 2);
    h1 = insert(h1, 7);
    h1 = insert(h1, 12); // degrees will normalize after unions
    h2 = insert(h2, 3);
    h2 = insert(h2, 9);
    Node* h = binomial_union(h1, h2);
    // h now holds the merged heap; find-min is a scan of root list
    for(Node* r = h; r; r = r->sibling)
        printf("root key=%d deg=%d\n", r->key, r->degree);
    return 0;
}
```

Python (succinct union and link)

```
class Node:
    __slots__ = ("key", "degree", "parent", "child", "sibling")
    def __init__(self, key):
        self.key = key
        self.degree = 0
        self.parent = None
        self.child = None
        self.sibling = None

def link_tree(x, y):
    # assume x.key <= y.key and degrees equal
```

```
    y.parent = x
    y.sibling = x.child
    x.child = y
    x.degree += 1
    return x

def merge_root_lists(a, b):
    if not a: return b
    if not b: return a
    dummy = Node(-1)
    t = dummy
    while a and b:
        if a.degree <= b.degree:
            t.sibling, a = a, a.sibling
        else:
            t.sibling, b = b, b.sibling
        t = t.sibling
    t.sibling = a if a else b
    return dummy.sibling

def binomial_union(h1, h2):
    head = merge_root_lists(h1, h2)
    if not head: return None
    prev, curr, nxt = None, head, head.sibling
    while nxt:
        if curr.degree != nxt.degree or (nxt.sibling and nxt.sibling.degree == curr.degree):
            prev, curr, nxt = curr, nxt, nxt.sibling
        else:
            if curr.key <= nxt.key:
                curr.sibling = nxt.sibling
                curr = link_tree(curr, nxt)
                nxt = curr.sibling
            else:
                if prev: prev.sibling = nxt
                else: head = nxt
                curr = link_tree(nxt, curr)
                nxt = curr.sibling
    return head

def insert(heap, key):
    return binomial_union(heap, Node(key))
```

```
# Example
h1 = None
for x in [2, 7, 12]:
    h1 = insert(h1, x)
h2 = None
for x in [3, 9]:
    h2 = insert(h2, x)
h = binomial_union(h1, h2)
roots = []
r = h
while r:
    roots.append((r.key, r.degree))
    r = r.sibling
print(roots)  # e.g. [(2, 4)] or a small set of unique degrees with min root smallest
```

Why It Matters

- Meld-friendly: merging heaps is first-class, not an afterthought
- Clean, provable bounds with a binary-counter intuition
- Foundation for Fibonacci heaps and variations
- Great when frequent melds are required in algorithms or multi-queue systems

A Gentle Proof (Why It Works)

Merging root lists produces degrees in nondecreasing order. Linking only happens between adjacent roots of the same degree, producing exactly one tree of each degree after all carries settle. This mirrors binary addition: each link corresponds to carrying a 1 to the next bit. Since the maximum degree is O(log n), the merge performs O(log n) links and scans, giving O(log n) time.

Try It Yourself

1. Implement `find_min` by scanning root list and keep a pointer to the min root.
2. Implement `delete_min`: remove min root, reverse its child list into a separate heap, then `union`.
3. Add `decrease_key` by cutting and reinserting a node in the root list, then fixing parent order.
4. Compare union time with binary heap and pairing heap on large random workloads.

Test Cases

Case	H1 Roots (deg)	H2 Roots (deg)	Result	Notes
Simple merge	[2(0), 7(1)]	[3(0)]	roots unique after link	2 becomes parent of 3
Chain of carries	[2(0), 7(1), 12(3)]	[3(0), 9(2)]	single root 2(4)	cascading links
Insert by union	H with roots	plus [x(0)]	merged in O(1) amortized	single carry possible

Edge Cases

- Merging with empty heap returns the other heap
- Duplicate keys work; tie break arbitrarily
- Maintain stable sibling pointers when linking

Complexity

Operation	Time
meld (union)	O(log n)
insert	O(1) amortized via union with 1-node heap
find-min	O(log n) scan or keep pointer for O(1) peek
delete-min	O(log n)
decrease-key	O(log n) typical implementation

Merging binomial heaps feels like adding binary numbers: equal degrees collide, link, and carry forward until the structure is tidy and the minimum stands at a root.

230 Leftist Heap Merge

A leftist heap is a binary tree heap optimized for efficient merges. Its structure skews to the left so that merging two heaps can be done recursively in O(log n) time. The clever trick is storing each node's null path length (npl), ensuring the shortest path to a null child is always on the right, which keeps merges shallow.

What Problem Are We Solving?

We want a merge-friendly heap with simpler structure than Fibonacci or pairing heaps but faster merges than standard binary heaps. The leftist heap is a sweet spot: fast merges, simple code, and still supports all key heap operations.

Goal: Design a heap that keeps its shortest subtree on the right, so recursive merges stay logarithmic.

How Does It Work (Plain Language)?

Each node stores:

- `key` – value used for ordering
- `left`, `right` – child pointers
- `npl` – null path length (distance to nearest null)

Rules:

1. Heap order: parent key child keys (min-heap)
2. Leftist property: `npl(left)  npl(right)`

Merge(a, b):

1. If one is null, return the other.
2. Compare roots, smaller root becomes new root.
3. Recursively merge `a.right` and `b`.
4. After merge, swap children if needed to keep leftist property.
5. Update `npl`.

Other operations via merge

- Insert(x): merge heap with single-node heap `x`.
- DeleteMin(): merge left and right subtrees of root.

Example (Min-Heap Merge)

Heap A: root 3

```
  3
 / \
5   9
```

Heap B: root 4

```
  4
 / \
 8  10
```

Merge(3, 4):

- $3 < 4 \rightarrow$ new root 3
- Merge right(9) with heap 4
- After merge:

```
    3
   / \
  5   4
     / \
    8  10
       /
      9
```

Rebalance by swapping if right's npl $>$ left's $\rightarrow$ ensures leftist shape.

Tiny Code (Easy Versions)

C (Merge, Insert, Delete-Min)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key;
    int npl;
    struct Node *left, *right;
} Node;

Node* make_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->npl = 0;
    n->left = n->right = NULL;
    return n;
}
```

```c
int npl(Node* x) { return x ? x->npl : -1; }

Node* merge(Node* a, Node* b) {
    if (!a) return b;
    if (!b) return a;
    if (b->key < a->key) { Node* t = a; a = b; b = t; }
    a->right = merge(a->right, b);
    // maintain leftist property
    if (npl(a->left) < npl(a->right)) {
        Node* t = a->left;
        a->left = a->right;
        a->right = t;
    }
    a->npl = npl(a->right) + 1;
    return a;
}

Node* insert(Node* h, int key) {
    return merge(h, make_node(key));
}

Node* delete_min(Node* h, int* out) {
    if (!h) return NULL;
    *out = h->key;
    Node* new_root = merge(h->left, h->right);
    free(h);
    return new_root;
}

int main(void) {
    Node* h1 = NULL;
    int vals[] = {5, 3, 9, 7, 4};
    for (int i = 0; i < 5; i++)
        h1 = insert(h1, vals[i]);

    int m;
    h1 = delete_min(h1, &m);
    printf("Deleted min: %d\n", m);
    return 0;
}
```

Python

```
class Node:
    __slots__ = ("key", "npl", "left", "right")
    def __init__(self, key):
        self.key = key
        self.npl = 0
        self.left = None
        self.right = None

def npl(x): return x.npl if x else -1

def merge(a, b):
    if not a: return b
    if not b: return a
    if b.key < a.key:
        a, b = b, a
    a.right = merge(a.right, b)
    # enforce leftist property
    if npl(a.left) < npl(a.right):
        a.left, a.right = a.right, a.left
    a.npl = npl(a.right) + 1
    return a

def insert(h, key):
    return merge(h, Node(key))

def delete_min(h):
    if not h: return None, None
    m = h.key
    h = merge(h.left, h.right)
    return m, h

# Example
h = None
for x in [5, 3, 9, 7, 4]:
    h = insert(h, x)
m, h = delete_min(h)
print("Deleted min:", m)
```

Why It Matters

- Fast merge with simple recursion

- Ideal for priority queues with frequent unions
- Cleaner implementation than Fibonacci heaps
- Guarantees logarithmic merge and delete-min

A Gentle Proof (Why It Works)

The null path length (npl) ensures that the right spine is always the shortest. Therefore, each merge step recurses down only one right path, not both. This bounds recursion depth by O(log n). Every other operation (insert, delete-min) is defined as a small number of merges, hence O(log n).

Try It Yourself

1. Trace the merge process for two 3-node heaps.
2. Visualize `npl` values after each step.
3. Implement `find_min()` (just return root key).
4. Try making a max-heap variant by flipping comparisons.

Test Cases

Operation	Input	Output	Notes
Insert	[5,3,9,7,4]	root=3	min-heap property holds
DeleteMin	remove 3	new root=4	leftist property maintained
Merge	[3,5] + [4,6]	root=3	right spine log n
Empty merge	None + [5]	[5]	safe

Edge Cases

- Merge with null heap → returns the other
- Duplicate keys → ties fine
- Single node → npl = 0

Complexity

Operation	Time	Space
Merge	O(log n)	O(1)
Insert	O(log n)	O(1)
DeleteMin	O(log n)	O(1)

Operation	Time	Space
FindMin	O(1)	O(1)

The leftist heap is like a river always bending toward the left, shaping itself so merges flow swiftly and naturally.

Section 24. Balanced Trees

231 AVL Tree Insert

An AVL tree is a self-balancing binary search tree where the height difference (balance factor) between the left and right subtrees of any node is at most 1. This invariant guarantees O(log n) lookup, insertion, and deletion, making AVL trees a classic example of maintaining order dynamically.

What Problem Are We Solving?

Ordinary binary search trees can become skewed (like linked lists) after unlucky insertions, degrading performance to O(n). The AVL tree restores balance automatically after each insertion, ensuring searches and updates stay fast.

Goal: Maintain a balanced search tree by rotating nodes after insertions so that height difference 1 everywhere.

How Does It Work (Plain Language)?

1. Insert the key as in a normal BST.
2. Walk back up the recursion updating heights.
3. Check balance factor = `height(left) - height(right)`.
4. If it's outside $\{-1, 0, +1\}$, perform one of four rotations to restore balance:

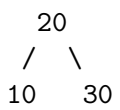
Case	Pattern	Fix
Left-Left (LL)	Inserted into left-left subtree	Rotate right
Right-Right (RR)	Inserted into right-right subtree	Rotate left
Left-Right (LR)	Inserted into left-right subtree	Rotate left at child, then right
Right-Left (RL)	Inserted into right-left subtree	Rotate right at child, then left

Example

Insert 30, 20, 10

- 30 → root
- 20 → left of 30
- 10 → left of 20 → imbalance at 30: balance factor = 2 → LL case → right rotate on 30

Balanced tree:

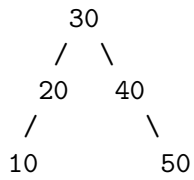


Step-by-Step Example

Insert sequence: 10, 20, 30, 40, 50

Step	Insert	Tree (in-order)	Imbalance	Rotation	Root After
1	10	[10]	-	-	10
2	20	[10,20]	balanced	-	10
3	30	[10,20,30]	at 10 (RR)	left	20
4	40	[10,20,30,40]	balanced	-	20
5	50	[10,20,30,40,50]	at 20 (RR)	left	30

Balanced final tree:



Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key, height;
    struct Node *left, *right;
} Node;

int height(Node* n) { return n ? n->height : 0; }
int max(int a, int b) { return a > b ? a : b; }

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->height = 1;
    n->left = n->right = NULL;
    return n;
}

Node* rotate_right(Node* y) {
    Node* x = y->left;
    Node* T2 = x->right;
    x->right = y;
    y->left = T2;
    y->height = 1 + max(height(y->left), height(y->right));
    x->height = 1 + max(height(x->left), height(x->right));
    return x;
}

Node* rotate_left(Node* x) {
    Node* y = x->right;
    Node* T2 = y->left;
    y->left = x;
    x->right = T2;
    x->height = 1 + max(height(x->left), height(x->right));
    y->height = 1 + max(height(y->left), height(y->right));
    return y;
}

int balance(Node* n) { return n ? height(n->left) - height(n->right) : 0; }

Node* insert(Node* node, int key) {
```

```
    if (!node) return new_node(key);
    if (key < node->key) node->left = insert(node->left, key);
    else if (key > node->key) node->right = insert(node->right, key);
    else return node; // no duplicates

    node->height = 1 + max(height(node->left), height(node->right));
    int bf = balance(node);

    // LL
    if (bf > 1 && key < node->left->key)
        return rotate_right(node);
    // RR
    if (bf < -1 && key > node->right->key)
        return rotate_left(node);
    // LR
    if (bf > 1 && key > node->left->key) {
        node->left = rotate_left(node->left);
        return rotate_right(node);
    }
    // RL
    if (bf < -1 && key < node->right->key) {
        node->right = rotate_right(node->right);
        return rotate_left(node);
    }
    return node;
}

void inorder(Node* root) {
    if (!root) return;
    inorder(root->left);
    printf("%d ", root->key);
    inorder(root->right);
}

int main(void) {
    Node* root = NULL;
    int keys[] = {10, 20, 30, 40, 50};
    for (int i = 0; i < 5; i++)
        root = insert(root, keys[i]);
    inorder(root);
    printf("\n");
}
```

Python

```python
class Node:
    def __init__(self, key):
        self.key = key
        self.left = self.right = None
        self.height = 1

def height(n): return n.height if n else 0
def balance(n): return height(n.left) - height(n.right) if n else 0

def rotate_right(y):
    x, T2 = y.left, y.left.right
    x.right, y.left = y, T2
    y.height = 1 + max(height(y.left), height(y.right))
    x.height = 1 + max(height(x.left), height(x.right))
    return x

def rotate_left(x):
    y, T2 = x.right, x.right.left
    y.left, x.right = x, T2
    x.height = 1 + max(height(x.left), height(x.right))
    y.height = 1 + max(height(y.left), height(y.right))
    return y

def insert(node, key):
    if not node: return Node(key)
    if key < node.key: node.left = insert(node.left, key)
    elif key > node.key: node.right = insert(node.right, key)
    else: return node

    node.height = 1 + max(height(node.left), height(node.right))
    bf = balance(node)

    if bf > 1 and key < node.left.key:  # LL
        return rotate_right(node)
    if bf < -1 and key > node.right.key:  # RR
        return rotate_left(node)
    if bf > 1 and key > node.left.key:  # LR
        node.left = rotate_left(node.left)
        return rotate_right(node)
    if bf < -1 and key < node.right.key:  # RL
        node.right = rotate_right(node.right)
```

```
        return rotate_left(node)
    return node

def inorder(root):
    if not root: return
    inorder(root.left)
    print(root.key, end=' ')
    inorder(root.right)

# Example
root = None
for k in [10, 20, 30, 40, 50]:
    root = insert(root, k)
inorder(root)
```

Why It Matters

- Guarantees O(log n) operations
- Prevents degeneration into linear chains
- Clear rotation-based balancing logic
- Basis for other balanced trees (e.g., Red-Black)

A Gentle Proof (Why It Works)

Each insertion may unbalance at most one node, the lowest ancestor of the inserted node. A single rotation (or double rotation) restores the balance factor of that node to $\{-1, 0, +1\}$, and updates all affected heights in constant time. Thus each insertion performs O(1) rotations, O(log n) recursive updates.

Try It Yourself

1. Insert 30, 20, 10 → LL case
2. Insert 10, 30, 20 → LR case
3. Insert 30, 10, 20 → RL case
4. Insert 10, 20, 30 → RR case
5. Draw each tree before and after rotation

Test Cases

Sequence	Rotation Type	Final Root	Height
[30, 20, 10]	LL	20	2
[10, 30, 20]	LR	20	2
[30, 10, 20]	RL	20	2
[10, 20, 30]	RR	20	2

Edge Cases

- Duplicate keys ignored
- Insertion into empty tree → new node
- All ascending or descending inserts → balanced via rotations

Complexity

Operation	Time	Space
Insert	O(log n)	O(h) recursion
Search	O(log n)	O(h)
Delete	O(log n)	O(h)

The AVL tree is a careful gardener, pruning imbalance wherever it grows, so your searches always find a straight path.

232 AVL Tree Delete

Deleting a node in an AVL tree is like removing a block from a carefully balanced tower, you take it out, then perform rotations to restore equilibrium. The key is to combine BST deletion rules with balance factor checks and rebalancing up the path.

What Problem Are We Solving?

Deletion in a plain BST can break the shape, making it skewed and inefficient. In an AVL tree, we want to:

1. Remove a node (using standard BST deletion)
2. Recalculate heights and balance factors
3. Restore balance with rotations

This ensures the tree remains height-balanced, keeping operations at O(log n).

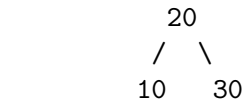
How Does It Work (Plain Language)?

1. Find the node as in a normal BST.
2. Delete it:
   - If leaf → remove directly.
   - If one child → replace with child.
   - If two children → find inorder successor, copy its value, delete it recursively.
3. Walk upward, update height and balance factor at each ancestor.
4. Apply one of four rotation cases if unbalanced:

Case	Condition	Fix
LL	balance > 1 and balance(left) 0	Rotate right
LR	balance > 1 and balance(left) < 0	Rotate left at child, then right
RR	balance < -1 and balance(right) 0	Rotate left
RL	balance < -1 and balance(right) > 0	Rotate right at child, then left

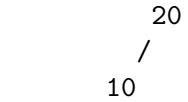
Example

Delete 10 from



- Remove leaf 10
- Node 20: balance = 0 → balanced

Now delete 30:



- balance(20) = +1 → still balanced

Delete 10 next:

Tree becomes single node, still AVL.

Step-by-Step Example

Insert [10, 20, 30, 40, 50, 25] Then delete 40

Step	Action	Imbalance	Rotation	Root
1	Delete 40	at 30 (balance = -2)	RL	30
2	After rotate	balanced	-	30

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key, height;
    struct Node *left, *right;
} Node;

int height(Node* n) { return n ? n->height : 0; }
int max(int a, int b) { return a > b ? a : b; }

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key; n->height = 1;
    n->left = n->right = NULL;
    return n;
}

Node* rotate_right(Node* y) {
    Node* x = y->left;
    Node* T2 = x->right;
    x->right = y;
    y->left = T2;
    y->height = 1 + max(height(y->left), height(y->right));
    x->height = 1 + max(height(x->left), height(x->right));
    return x;
}

Node* rotate_left(Node* x) {
```

```
    Node* y = x->right;
    Node* T2 = y->left;
    y->left = x;
    x->right = T2;
    x->height = 1 + max(height(x->left), height(x->right));
    y->height = 1 + max(height(y->left), height(y->right));
    return y;
}

int balance(Node* n) { return n ? height(n->left) - height(n->right) : 0; }

Node* min_node(Node* n) {
    Node* cur = n;
    while (cur->left) cur = cur->left;
    return cur;
}

Node* insert(Node* root, int key) {
    if (!root) return new_node(key);
    if (key < root->key) root->left = insert(root->left, key);
    else if (key > root->key) root->right = insert(root->right, key);
    else return root;

    root->height = 1 + max(height(root->left), height(root->right));
    int bf = balance(root);

    // Rebalance
    if (bf > 1 && key < root->left->key) return rotate_right(root);
    if (bf < -1 && key > root->right->key) return rotate_left(root);
    if (bf > 1 && key > root->left->key) {
        root->left = rotate_left(root->left);
        return rotate_right(root);
    }
    if (bf < -1 && key < root->right->key) {
        root->right = rotate_right(root->right);
        return rotate_left(root);
    }
    return root;
}

Node* delete(Node* root, int key) {
    if (!root) return root;
```

```
    if (key < root->key) root->left = delete(root->left, key);
    else if (key > root->key) root->right = delete(root->right, key);
    else {
        // Node with one or no child
        if (!root->left || !root->right) {
            Node* tmp = root->left ? root->left : root->right;
            if (!tmp) { tmp = root; root = NULL; }
            else *root = *tmp;
            free(tmp);
        } else {
            Node* tmp = min_node(root->right);
            root->key = tmp->key;
            root->right = delete(root->right, tmp->key);
        }
    }
    if (!root) return root;

    root->height = 1 + max(height(root->left), height(root->right));
    int bf = balance(root);

    // Rebalance
    if (bf > 1 && balance(root->left) >= 0)
        return rotate_right(root);
    if (bf > 1 && balance(root->left) < 0) {
        root->left = rotate_left(root->left);
        return rotate_right(root);
    }
    if (bf < -1 && balance(root->right) <= 0)
        return rotate_left(root);
    if (bf < -1 && balance(root->right) > 0) {
        root->right = rotate_right(root->right);
        return rotate_left(root);
    }
    return root;
}

void inorder(Node* r) {
    if (!r) return;
    inorder(r->left);
    printf("%d ", r->key);
    inorder(r->right);
}
```

```c
int main(void) {
    Node* root = NULL;
    int keys[] = {10, 20, 30, 40, 50, 25};
    for (int i = 0; i < 6; i++) root = insert(root, keys[i]);
    root = delete(root, 40);
    inorder(root);
    printf("\n");
}
```

Python

```python
class Node:
    def __init__(self, key):
        self.key = key
        self.height = 1
        self.left = self.right = None

def height(n): return n.height if n else 0
def balance(n): return height(n.left) - height(n.right) if n else 0

def rotate_right(y):
    x, T2 = y.left, y.left.right
    x.right, y.left = y, T2
    y.height = 1 + max(height(y.left), height(y.right))
    x.height = 1 + max(height(x.left), height(x.right))
    return x

def rotate_left(x):
    y, T2 = x.right, x.right.left
    y.left, x.right = x, T2
    x.height = 1 + max(height(x.left), height(x.right))
    y.height = 1 + max(height(y.left), height(y.right))
    return y

def min_node(n):
    while n.left: n = n.left
    return n

def insert(r, k):
    if not r: return Node(k)
    if k < r.key: r.left = insert(r.left, k)
    elif k > r.key: r.right = insert(r.right, k)
```

```
    else: return r
    r.height = 1 + max(height(r.left), height(r.right))
    bf = balance(r)
    if bf > 1 and k < r.left.key: return rotate_right(r)
    if bf < -1 and k > r.right.key: return rotate_left(r)
    if bf > 1 and k > r.left.key:
        r.left = rotate_left(r.left); return rotate_right(r)
    if bf < -1 and k < r.right.key:
        r.right = rotate_right(r.right); return rotate_left(r)
    return r

def delete(r, k):
    if not r: return r
    if k < r.key: r.left = delete(r.left, k)
    elif k > r.key: r.right = delete(r.right, k)
    else:
        if not r.left: return r.right
        elif not r.right: return r.left
        temp = min_node(r.right)
        r.key = temp.key
        r.right = delete(r.right, temp.key)
    r.height = 1 + max(height(r.left), height(r.right))
    bf = balance(r)
    if bf > 1 and balance(r.left) >= 0: return rotate_right(r)
    if bf > 1 and balance(r.left) < 0:
        r.left = rotate_left(r.left); return rotate_right(r)
    if bf < -1 and balance(r.right) <= 0: return rotate_left(r)
    if bf < -1 and balance(r.right) > 0:
        r.right = rotate_right(r.right); return rotate_left(r)
    return r

def inorder(r):
    if not r: return
    inorder(r.left); print(r.key, end=' '); inorder(r.right)

root = None
for k in [10,20,30,40,50,25]:
    root = insert(root, k)
root = delete(root, 40)
inorder(root)
```

Why It Matters

- Keeps search, insert, delete all O(log n)
- Auto-rebalances after removal
- Shows how rotations maintain structure consistency
- Foundation for all balanced trees (like Red-Black, AVL variants)

A Gentle Proof (Why It Works)

Every deletion changes subtree height by at most 1. Each ancestor's balance factor is recomputed; if imbalance found, a single rotation (or double rotation) restores balance. At most O(log n) nodes are visited, and each fix is O(1).

Try It Yourself

1. Build [10, 20, 30, 40, 50, 25], then delete 50
2. Observe RR rotation at 30
3. Delete 10, check rebalancing at 20
4. Delete all sequentially, confirm sorted order

Test Cases

Insert Sequence	Delete	Rotation	Root After	Balanced
[10,20,30,40,50,25]	40	RL	30	
[10,20,30]	10	RR	20	
[30,20,10]	30	LL	20	

Edge Cases

- Deleting from empty tree → safe
- Single node → becomes NULL
- Duplicate keys → ignored

Operation	Time	Space

Complexity

Operation	Time	Space
Delete	O(log n)	O(h) recursion
Search	O(log n)	O(h)
Insert	O(log n)	O(h)

An AVL deletion is a gentle art, remove the key, rebalance the branches, and harmony is restored.

233 Red-Black Tree Insert

A Red-Black Tree (RBT) is a self-balancing binary search tree that uses color bits (red or black) to control balance indirectly. Unlike AVL trees that balance by height, RBTs balance by color rules, allowing more flexible, faster insertions with fewer rotations.

What Problem Are We Solving?

A plain BST can degrade into a linked list with O(n) operations. An RBT maintains a near-balanced height, ensuring O(log n) for search, insert, and delete. Instead of exact height balance like AVL, RBTs enforce color invariants that keep paths roughly equal.

Red-Black Tree Properties

1. Each node is red or black.
2. The root is always black.
3. Null (NIL) nodes are considered black.
4. No two consecutive red nodes (no red parent with red child).
5. Every path from a node to its descendant NIL nodes has the same number of black nodes.

These rules guarantee height $2 \times \log(n + 1)$.

How Does It Work (Plain Language)?

1. Insert node like in a normal BST (color it red).
2. Fix violations if any property breaks.
3. Use rotations and recoloring based on where the red node appears.

Case	Condition	Fix
Case 1	New node is root	Recolor black
Case 2	Parent black	No fix needed
Case 3	Parent red, Uncle red	Recolor parent & uncle black, grandparent red
Case 4	Parent red, Uncle black, Triangle (LR/RL)	Rotate to line up
Case 5	Parent red, Uncle black, Line (LL/RR)	Rotate and recolor grandparent

Example

Insert sequence: 10, 20, 30

1. Insert 10 → root → black
2. Insert 20 → red child → balanced
3. Insert 30 → red parent (20) → Case 5 (RR) → rotate left on 10 → recolor root black, children red

Result:

```
    20(B)
   /    \
10(R)   30(R)
```

Step-by-Step Example

Insert [7, 3, 18, 10, 22, 8, 11, 26]

Step	Insert	Violation	Fix	Root
1	7	root	make black	7(B)
2	3	parent black	none	7(B)

Step	Insert	Violation	Fix	Root
3	18	parent black	none	7(B)
4	10	parent red, uncle red	recolor, move up	7(B)
5	22	parent black	none	7(B)
6	8	parent red, uncle red	recolor	7(B)
7	11	parent red, uncle black, LR	rotate + recolor	7(B)
8	26	parent black	none	7(B)

Final tree balanced by color invariants.

Tiny Code (Easy Versions)

C (Simplified)

```c
#include <stdio.h>
#include <stdlib.h>

typedef enum { RED, BLACK } Color;

typedef struct Node {
    int key;
    Color color;
    struct Node *left, *right, *parent;
} Node;

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->color = RED;
    n->left = n->right = n->parent = NULL;
    return n;
}

void rotate_left(Node root, Node* x) {
    Node* y = x->right;
    x->right = y->left;
    if (y->left) y->left->parent = x;
    y->parent = x->parent;
    if (!x->parent) *root = y;
    else if (x == x->parent->left) x->parent->left = y;
```

```
    else x->parent->right = y;
    y->left = x;
    x->parent = y;
}

void rotate_right(Node root, Node* y) {
    Node* x = y->left;
    y->left = x->right;
    if (x->right) x->right->parent = y;
    x->parent = y->parent;
    if (!y->parent) *root = x;
    else if (y == y->parent->left) y->parent->left = x;
    else y->parent->right = x;
    x->right = y;
    y->parent = x;
}

void fix_violation(Node root, Node* z) {
    while (z->parent && z->parent->color == RED) {
        Node* gp = z->parent->parent;
        if (z->parent == gp->left) {
            Node* uncle = gp->right;
            if (uncle && uncle->color == RED) {
                z->parent->color = BLACK;
                uncle->color = BLACK;
                gp->color = RED;
                z = gp;
            } else {
                if (z == z->parent->right) {
                    z = z->parent;
                    rotate_left(root, z);
                }
                z->parent->color = BLACK;
                gp->color = RED;
                rotate_right(root, gp);
            }
        } else {
            Node* uncle = gp->left;
            if (uncle && uncle->color == RED) {
                z->parent->color = BLACK;
                uncle->color = BLACK;
                gp->color = RED;
```

```
                z = gp;
            } else {
                if (z == z->parent->left) {
                    z = z->parent;
                    rotate_right(root, z);
                }
                z->parent->color = BLACK;
                gp->color = RED;
                rotate_left(root, gp);
            }
        }
    }
    (*root)->color = BLACK;
}

Node* bst_insert(Node* root, Node* z) {
    if (!root) return z;
    if (z->key < root->key) {
        root->left = bst_insert(root->left, z);
        root->left->parent = root;
    } else if (z->key > root->key) {
        root->right = bst_insert(root->right, z);
        root->right->parent = root;
    }
    return root;
}

void insert(Node root, int key) {
    Node* z = new_node(key);
    *root = bst_insert(*root, z);
    fix_violation(root, z);
}

void inorder(Node* r) {
    if (!r) return;
    inorder(r->left);
    printf("%d(%c) ", r->key, r->color == RED ? 'R' : 'B');
    inorder(r->right);
}

int main(void) {
    Node* root = NULL;
```

```
    int keys[] = {10, 20, 30};
    for (int i = 0; i < 3; i++) insert(&root, keys[i]);
    inorder(root);
    printf("\n");
}
```

Python (Simplified)

```
class Node:
    def __init__(self, key, color="R", parent=None):
        self.key = key
        self.color = color
        self.left = self.right = None
        self.parent = parent

def rotate_left(root, x):
    y = x.right
    x.right = y.left
    if y.left: y.left.parent = x
    y.parent = x.parent
    if not x.parent: root = y
    elif x == x.parent.left: x.parent.left = y
    else: x.parent.right = y
    y.left = x
    x.parent = y
    return root

def rotate_right(root, y):
    x = y.left
    y.left = x.right
    if x.right: x.right.parent = y
    x.parent = y.parent
    if not y.parent: root = x
    elif y == y.parent.left: y.parent.left = x
    else: y.parent.right = x
    x.right = y
    y.parent = x
    return root

def fix_violation(root, z):
    while z.parent and z.parent.color == "R":
        gp = z.parent.parent
```

```
        if z.parent == gp.left:
            uncle = gp.right
            if uncle and uncle.color == "R":
                z.parent.color = uncle.color = "B"
                gp.color = "R"
                z = gp
            else:
                if z == z.parent.right:
                    z = z.parent
                    root = rotate_left(root, z)
                z.parent.color = "B"
                gp.color = "R"
                root = rotate_right(root, gp)
        else:
            uncle = gp.left
            if uncle and uncle.color == "R":
                z.parent.color = uncle.color = "B"
                gp.color = "R"
                z = gp
            else:
                if z == z.parent.left:
                    z = z.parent
                    root = rotate_right(root, z)
                z.parent.color = "B"
                gp.color = "R"
                root = rotate_left(root, gp)
    root.color = "B"
    return root

def bst_insert(root, z):
    if not root: return z
    if z.key < root.key:
        root.left = bst_insert(root.left, z)
        root.left.parent = root
    elif z.key > root.key:
        root.right = bst_insert(root.right, z)
        root.right.parent = root
    return root

def insert(root, key):
    z = Node(key)
    root = bst_insert(root, z)
```

```
    return fix_violation(root, z)

def inorder(r):
    if not r: return
    inorder(r.left)
    print(f"{r.key}({r.color})", end=" ")
    inorder(r.right)

root = None
for k in [10,20,30]:
    root = insert(root, k)
inorder(root)
```

Why It Matters

- Fewer rotations than AVL
- Guarantees O(log n) for all operations
- Used in real systems: Linux kernel, Java `TreeMap`, C++ `map`
- Easy insertion logic using coloring + rotation

A Gentle Proof (Why It Works)

The black-height invariant ensures every path length is between `h` and `2h`. Balancing via recolor + single rotation ensures logarithmic height. Each insert requires at most 2 rotations, O(log n) traversal.

Try It Yourself

1. Insert [10, 20, 30] → RR rotation
2. Insert [30, 15, 10] → LL rotation
3. Insert [10, 15, 5] → recolor, no rotation
4. Draw colors, confirm invariants

Test Cases

Sequence	Rotations	Root	Black Height
[10,20,30]	Left	20(B)	2
[7,3,18,10,22,8,11,26]	Mixed	7(B)	3

Sequence	Rotations	Root	Black Height
[1,2,3,4,5]	Multiple recolor+rot	2(B)	3

Complexity

Operation	Time	Space
Insert	O(log n)	O(1) rotations
Search	O(log n)	O(h)
Delete	O(log n)	O(1) rotations

The Red-Black Tree paints order into chaos, each red spark balanced by a calm black shadow.

234 Red-Black Tree Delete

Deletion in a Red-Black Tree (RBT) is a delicate operation: remove a node, then restore balance by adjusting colors and rotations to maintain all five RBT invariants. While insertion fixes "too much red," deletion often fixes "too much black."

What Problem Are We Solving?

After deleting a node from an RBT, the black-height property may break (some paths lose a black node). Our goal: restore all red-black invariants while keeping time complexity O(log n).

Red-Black Properties (Reminder)

1. Root is black.
2. Every node is red or black.
3. All NIL leaves are black.
4. Red nodes cannot have red children.
5. Every path from a node to NIL descendants has the same number of black nodes.

How Does It Work (Plain Language)?

1. Perform standard BST deletion.
2. Track if the removed node was black (this might cause "double black" issue).
3. Fix violations moving upward until the tree is balanced again.

Case	Condition	Fix
1	Node is red	Simply remove (no rebalance)
2	Node is black, child red	Replace and recolor child black
3	Node is black, child black ("double black")	Use sibling cases below

Double Black Fix Cases

Case	Description	Action
1	Sibling red	Rotate and recolor to make sibling black
2	Sibling black, both children black	Recolor sibling red, move double black up
3	Sibling black, near child red, far child black	Rotate sibling toward node, swap colors
4	Sibling black, far child red	Rotate parent, recolor sibling and parent, set far child black

Example

Delete `30` from:

```
    20(B)
   /    \
10(R)   30(R)
```

- 30 is red → remove directly
- No property violated

Delete `10`:

```
    20(B)
   /
  NIL
```

10 was red → simple remove → tree valid

Delete `20`: Tree becomes empty → fine

Step-by-Step Example

Insert [10, 20, 30, 15, 25] Delete 20

Step	Action	Violation	Fix	
1	Delete 20	double black at 25	sibling 10 black, far child red → Case 4	rotate
2	After rotate	all properties restored	-	

Tiny Code (Simplified)

C (Conceptual)

```
// This snippet omits full BST insertion for brevity.

typedef enum { RED, BLACK } Color;
typedef struct Node {
    int key;
    Color color;
    struct Node *left, *right, *parent;
} Node;

// Utility: get sibling
Node* sibling(Node* n) {
    if (!n->parent) return NULL;
    return n == n->parent->left ? n->parent->right : n->parent->left;
}

void fix_delete(Node root, Node* x) {
    while (x != *root && (!x || x->color == BLACK)) {
        Node* s = sibling(x);
        if (x == x->parent->left) {
            if (s->color == RED) {
                s->color = BLACK;
                x->parent->color = RED;
                rotate_left(root, x->parent);
                s = x->parent->right;
            }
            if ((!s->left || s->left->color == BLACK) &&
                (!s->right || s->right->color == BLACK)) {
                s->color = RED;
                x = x->parent;
```

```
            } else {
                if (!s->right || s->right->color == BLACK) {
                    if (s->left) s->left->color = BLACK;
                    s->color = RED;
                    rotate_right(root, s);
                    s = x->parent->right;
                }
                s->color = x->parent->color;
                x->parent->color = BLACK;
                if (s->right) s->right->color = BLACK;
                rotate_left(root, x->parent);
                x = *root;
            }
        } else {
            // mirror logic for right child
            if (s->color == RED) {
                s->color = BLACK;
                x->parent->color = RED;
                rotate_right(root, x->parent);
                s = x->parent->left;
            }
            if ((!s->left || s->left->color == BLACK) &&
                (!s->right || s->right->color == BLACK)) {
                s->color = RED;
                x = x->parent;
            } else {
                if (!s->left || s->left->color == BLACK) {
                    if (s->right) s->right->color = BLACK;
                    s->color = RED;
                    rotate_left(root, s);
                    s = x->parent->left;
                }
                s->color = x->parent->color;
                x->parent->color = BLACK;
                if (s->left) s->left->color = BLACK;
                rotate_right(root, x->parent);
                x = *root;
            }
        }
    }
    if (x) x->color = BLACK;
}
```

Python (Simplified Pseudocode)

```
def fix_delete(root, x):
    while x != root and (not x or x.color == "B"):
        if x == x.parent.left:
            s = x.parent.right
            if s.color == "R":
                s.color, x.parent.color = "B", "R"
                root = rotate_left(root, x.parent)
                s = x.parent.right
            if all(c is None or c.color == "B" for c in [s.left, s.right]):
                s.color = "R"
                x = x.parent
            else:
                if not s.right or s.right.color == "B":
                    if s.left: s.left.color = "B"
                    s.color = "R"
                    root = rotate_right(root, s)
                    s = x.parent.right
                s.color, x.parent.color = x.parent.color, "B"
                if s.right: s.right.color = "B"
                root = rotate_left(root, x.parent)
                x = root
        else:
            # mirror logic
            ...
    if x: x.color = "B"
    return root
```

Why It Matters

- Preserves logarithmic height after deletion
- Used in core data structures (`std::map`, `TreeSet`)
- Demonstrates color logic as a soft balancing scheme
- Handles edge cases gracefully via double black fix

A Gentle Proof (Why It Works)

When a black node is removed, one path loses a black count. The fix cases re-distribute black heights using rotations and recolors. Each loop iteration moves double-black upward, O(log n) steps.

Try It Yourself

1. Build [10, 20, 30, 15, 25, 5]. Delete 10 (leaf).
2. Delete 30 (red leaf) → no fix.
3. Delete 20 (black node with one child) → recolor fix.
4. Visualize each case: sibling red, sibling black with red child.

Test Cases

Insert Sequence	Delete	Case Triggered	Fix
[10,20,30]	20	Case 4	Rotate & recolor
[7,3,18,10,22,8,11,26]	18	Case 2	Recolor sibling
[10,5,1]	5	Case 1	Rotate parent

Complexity

Operation	Time	Space
Delete	O(log n)	O(1) rotations
Insert	O(log n)	O(1)
Search	O(log n)	O(h)

A Red-Black delete is like a careful tune-up, one color at a time, harmony restored across every path.

235 Splay Tree Access

A Splay Tree is a self-adjusting binary search tree that brings frequently accessed elements closer to the root through splaying, a series of tree rotations. Unlike AVL or Red-Black trees, it doesn't maintain strict balance but guarantees amortized O(log n) performance for access, insert, and delete.

What Problem Are We Solving?

In many workloads, some elements are accessed far more frequently than others. Ordinary BSTs give no advantage for "hot" keys, while balanced trees maintain shape but not recency. A Splay Tree optimizes for temporal locality: recently accessed items move near the root, making repeated access faster.

How Does It Work (Plain Language)?

Whenever you access a node (via search, insert, or delete), perform a splay operation, repeatedly rotate the node toward the root according to its position and parent relationships.

The three rotation patterns:

Case	Structure	Operation
Zig	Node is child of root	Single rotation
Zig-Zig	Node and parent are both left or both right children	Double rotation (rotate parent, then grandparent)
Zig-Zag	Node and parent are opposite children	Double rotation (rotate node twice upward)

After splaying, the accessed node becomes the root.

Example

Access sequence: 10, 20, 30

1. Insert 10 (root)
2. Insert 20 → 20 right of 10
3. Access 20 → Zig rotation → 20 becomes root
4. Insert 30 → 30 right of 20
5. Access 30 → Zig rotation → 30 root

Resulting tree (after all accesses):

```
   30
  /
20
/
10
```

Frequently used nodes rise to the top automatically.

Step-by-Step Example

Start with keys [5, 3, 8, 1, 4, 7, 9]. Access key 1.

Step	Operation	Case	Rotation	New Root
1	Access 1	Zig-Zig (left-left)	Rotate 3, then 5	1
2	After splay	-	-	1

Final tree: 1 becomes root, path shortened for next access.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key;
    struct Node *left, *right;
} Node;

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->left = n->right = NULL;
    return n;
}

Node* rotate_right(Node* x) {
    Node* y = x->left;
    x->left = y->right;
    y->right = x;
    return y;
}

Node* rotate_left(Node* x) {
    Node* y = x->right;
    x->right = y->left;
    y->left = x;
    return y;
}

Node* splay(Node* root, int key) {
```

```
    if (!root || root->key == key) return root;

    // Key in left subtree
    if (key < root->key) {
        if (!root->left) return root;
        if (key < root->left->key) {
            root->left->left = splay(root->left->left, key);
            root = rotate_right(root);
        } else if (key > root->left->key) {
            root->left->right = splay(root->left->right, key);
            if (root->left->right)
                root->left = rotate_left(root->left);
        }
        return root->left ? rotate_right(root) : root;
    }
    // Key in right subtree
    else {
        if (!root->right) return root;
        if (key > root->right->key) {
            root->right->right = splay(root->right->right, key);
            root = rotate_left(root);
        } else if (key < root->right->key) {
            root->right->left = splay(root->right->left, key);
            if (root->right->left)
                root->right = rotate_right(root->right);
        }
        return root->right ? rotate_left(root) : root;
    }
}

Node* insert(Node* root, int key) {
    if (!root) return new_node(key);
    root = splay(root, key);
    if (root->key == key) return root;
    Node* n = new_node(key);
    if (key < root->key) {
        n->right = root;
        n->left = root->left;
        root->left = NULL;
    } else {
        n->left = root;
        n->right = root->right;
```

```
        root->right = NULL;
    }
    return n;
}

void inorder(Node* r) {
    if (!r) return;
    inorder(r->left);
    printf("%d ", r->key);
    inorder(r->right);
}

int main(void) {
    Node* root = NULL;
    int keys[] = {5, 3, 8, 1, 4, 7, 9};
    for (int i = 0; i < 7; i++) root = insert(root, keys[i]);
    root = splay(root, 1);
    inorder(root);
    printf("\n");
}
```

Python

```
class Node:
    def __init__(self, key):
        self.key = key
        self.left = self.right = None

def rotate_right(x):
    y = x.left
    x.left = y.right
    y.right = x
    return y

def rotate_left(x):
    y = x.right
    x.right = y.left
    y.left = x
    return y

def splay(root, key):
    if not root or root.key == key:
```

```
        return root
    if key < root.key:
        if not root.left:
            return root
        if key < root.left.key:
            root.left.left = splay(root.left.left, key)
            root = rotate_right(root)
        elif key > root.left.key:
            root.left.right = splay(root.left.right, key)
            if root.left.right:
                root.left = rotate_left(root.left)
        return rotate_right(root) if root.left else root
    else:
        if not root.right:
            return root
        if key > root.right.key:
            root.right.right = splay(root.right.right, key)
            root = rotate_left(root)
        elif key < root.right.key:
            root.right.left = splay(root.right.left, key)
            if root.right.left:
                root.right = rotate_right(root.right)
        return rotate_left(root) if root.right else root

def insert(root, key):
    if not root:
        return Node(key)
    root = splay(root, key)
    if root.key == key:
        return root
    n = Node(key)
    if key < root.key:
        n.right = root
        n.left = root.left
        root.left = None
    else:
        n.left = root
        n.right = root.right
        root.right = None
    return n

def inorder(r):
```

```
    if not r: return
    inorder(r.left)
    print(r.key, end=" ")
    inorder(r.right)

root = None
for k in [5,3,8,1,4,7,9]:
    root = insert(root, k)
root = splay(root, 1)
inorder(root)
```

Why It Matters

- Amortized O(log n) performance
- Adapts dynamically to access patterns
- Ideal for caches, text editors, network routing tables
- Simple logic: no height or color tracking needed

A Gentle Proof (Why It Works)

Each splay operation may take O(h), but the amortized cost across multiple operations is O(log n). Accessing frequently used elements keeps them near the root, improving future operations.

Try It Yourself

1. Build [5, 3, 8, 1, 4, 7, 9]
2. Access 1 → Observe Zig-Zig rotation
3. Access 8 → Observe Zig-Zag
4. Insert 10 → check rebalancing
5. Access 7 repeatedly → moves to root

Test Cases

Sequence	Access	Case	Root After
[5,3,8,1,4]	1	Zig-Zig	1
[10,20,30]	30	Zig	30
[5,3,8,1,4]	4	Zig-Zag	4

Complexity

Operation	Time	Space
Access	Amortized O(log n)	O(h) recursion
Insert	Amortized O(log n)	O(h)
Delete	Amortized O(log n)	O(h)

The Splay Tree is like a memory, the more you touch something, the closer it stays to you.

236 Treap Insert

A Treap (Tree + Heap) is a brilliant hybrid: it's a binary search tree by keys and a heap by priorities. Every node carries a key and a random priority. By combining ordering on keys with random heap priorities, the treap stays *balanced on average*, no strict rotations like AVL or color rules like Red-Black trees needed.

What Problem Are We Solving?

We want a simple balanced search tree with expected O(log n) performance, but without maintaining height or color properties explicitly. Treaps solve this by assigning random priorities, keeping the structure balanced *in expectation*.

How It Works (Plain Language)

Each node `(key, priority)` must satisfy:

- BST property: `key(left) < key < key(right)`
- Heap property: `priority(parent) < priority(children)` (min-heap or max-heap convention)

Insert like a normal BST by key, then fix heap property by rotations if the priority is violated.

Step	Rule
1	Insert node by key (like BST)
2	Assign a random priority
3	While parent priority > node priority → rotate node up

This randomization ensures expected logarithmic height.

Example

Insert sequence (key, priority):

Step	Key	Priority	Structure
1	(50, 15)	root	50
2	(30, 10)	smaller priority → rotate right	30(root) → 50(right child)
3	(70, 25)	stays right of 50	balanced

Result (BST by key, min-heap by priority):

```
(30,10)
    \
    (50,15)
        \
        (70,25)
```

Step-by-Step Example

Insert keys: [40, 20, 60, 10, 30, 50, 70] Priorities: [80, 90, 70, 100, 85, 60, 75]

Key	Priority	Rotation	Result
40	80	root	40
20	90	none	left child
60	70	rotate left (heap fix)	60 root
10	100	none	leaf
30	85	none	under 20
50	60	rotate left	50 root
70	75	none	leaf

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>
#include <time.h>

typedef struct Node {
```

```
    int key, priority;
    struct Node *left, *right;
} Node;

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->priority = rand() % 100; // random priority
    n->left = n->right = NULL;
    return n;
}

Node* rotate_right(Node* y) {
    Node* x = y->left;
    y->left = x->right;
    x->right = y;
    return x;
}

Node* rotate_left(Node* x) {
    Node* y = x->right;
    x->right = y->left;
    y->left = x;
    return y;
}

Node* insert(Node* root, int key) {
    if (!root) return new_node(key);

    if (key < root->key) {
        root->left = insert(root->left, key);
        if (root->left->priority < root->priority)
            root = rotate_right(root);
    } else if (key > root->key) {
        root->right = insert(root->right, key);
        if (root->right->priority < root->priority)
            root = rotate_left(root);
    }
    return root;
}

void inorder(Node* root) {
```

```
    if (!root) return;
    inorder(root->left);
    printf("(%d,%d) ", root->key, root->priority);
    inorder(root->right);
}

int main(void) {
    srand(time(NULL));
    Node* root = NULL;
    int keys[] = {40, 20, 60, 10, 30, 50, 70};
    for (int i = 0; i < 7; i++)
        root = insert(root, keys[i]);
    inorder(root);
    printf("\n");
}
```

Python

```
import random

class Node:
    def __init__(self, key):
        self.key = key
        self.priority = random.randint(1, 100)
        self.left = self.right = None

def rotate_right(y):
    x = y.left
    y.left = x.right
    x.right = y
    return x

def rotate_left(x):
    y = x.right
    x.right = y.left
    y.left = x
    return y

def insert(root, key):
    if not root:
        return Node(key)
    if key < root.key:
```

```
        root.left = insert(root.left, key)
        if root.left.priority < root.priority:
            root = rotate_right(root)
    elif key > root.key:
        root.right = insert(root.right, key)
        if root.right.priority < root.priority:
            root = rotate_left(root)
    return root

def inorder(root):
    if not root: return
    inorder(root.left)
    print(f"({root.key},{root.priority})", end=" ")
    inorder(root.right)

root = None
for k in [40, 20, 60, 10, 30, 50, 70]:
    root = insert(root, k)
inorder(root)
```

Why It Matters

- Simple implementation with expected balance
- Probabilistic alternative to AVL / Red-Black
- Great for randomized data structures and Cartesian tree applications
- No explicit height or color tracking

A Gentle Proof (Why It Works)

Random priorities imply random structure; the probability of a node being high in the tree drops exponentially with depth. Hence, expected height is O(log n) with high probability.

Try It Yourself

1. Insert keys [10, 20, 30, 40] with random priorities.
2. Observe random structure (not sorted by insertion).
3. Change priority generator → test skewness.
4. Visualize both BST and heap invariants.

Test Cases

Keys	Priorities	Resulting Root	Height
[10,20,30]	[5,3,4]	20	2
[5,2,8,1,3]	random	varies	~log n
[1..100]	random	balanced	O(log n)

Complexity

Operation	Time	Space
Insert	O(log n) expected	O(h) recursion
Search	O(log n) expected	O(h)
Delete	O(log n) expected	O(h)

A Treap dances to the rhythm of chance, balancing order with randomness to stay nimble and fair.

237 Treap Delete

Deleting from a Treap blends the best of both worlds: BST search for locating the node and heap-based rotations to remove it while keeping balance. Instead of rebalancing explicitly, we rotate the target node downward until it becomes a leaf, then remove it.

What Problem Are We Solving?

We want to delete a key while preserving both:

- BST property: keys in order
- Heap property: priorities follow min-/max-heap rule

Treaps handle this by rotating down the target node until it has at most one child, then removing it directly.

How It Works (Plain Language)

1. Search for the node by key (BST search).
2. Once found, rotate it downward until it has 1 child:
    - Rotate left if right child's priority < left child's priority
    - Rotate right otherwise
3. Remove it once it's a leaf or single-child node.

Because priorities are random, the tree remains balanced *in expectation*.

Example

Treap (key, priority):

```
      (40,20)
     /      \
(30,10)   (50,25)
```

Delete 40:

- Compare children: (30,10) < (50,25) → rotate right on 40
- New root (30,10)
- 40 now right child → continue rotation if needed → eventually becomes leaf → delete

New structure maintains BST + heap properties.

Step-by-Step Example

Start with nodes:

Key	Priority
40	50
20	60
60	70
10	90
30	80
50	65
70	75

Delete 40:

Step	Node	Action	Rotation	Root
1	40	Compare children priorities	Left child higher	Rotate right
2	30	Now parent of 40	40 demoted	Continue if needed
3	40	Becomes leaf	Remove	30

Final root: (30,80) All properties hold.

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>
#include <time.h>

typedef struct Node {
    int key, priority;
    struct Node *left, *right;
} Node;

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->priority = rand() % 100;
    n->left = n->right = NULL;
    return n;
}

Node* rotate_right(Node* y) {
    Node* x = y->left;
    y->left = x->right;
    x->right = y;
    return x;
}

Node* rotate_left(Node* x) {
    Node* y = x->right;
    x->right = y->left;
    y->left = x;
```

```
    return y;
}

Node* insert(Node* root, int key) {
    if (!root) return new_node(key);
    if (key < root->key) {
        root->left = insert(root->left, key);
        if (root->left->priority < root->priority)
            root = rotate_right(root);
    } else if (key > root->key) {
        root->right = insert(root->right, key);
        if (root->right->priority < root->priority)
            root = rotate_left(root);
    }
    return root;
}

Node* delete(Node* root, int key) {
    if (!root) return NULL;

    if (key < root->key)
        root->left = delete(root->left, key);
    else if (key > root->key)
        root->right = delete(root->right, key);
    else {
        // Found node to delete
        if (!root->left && !root->right) {
            free(root);
            return NULL;
        } else if (!root->left)
            root = rotate_left(root);
        else if (!root->right)
            root = rotate_right(root);
        else if (root->left->priority < root->right->priority)
            root = rotate_right(root);
        else
            root = rotate_left(root);

        root = delete(root, key);
    }
    return root;
}
```

```c
void inorder(Node* root) {
    if (!root) return;
    inorder(root->left);
    printf("(%d,%d) ", root->key, root->priority);
    inorder(root->right);
}

int main(void) {
    srand(time(NULL));
    Node* root = NULL;
    int keys[] = {40, 20, 60, 10, 30, 50, 70};
    for (int i = 0; i < 7; i++)
        root = insert(root, keys[i]);

    printf("Before deletion:\n");
    inorder(root);
    printf("\n");

    root = delete(root, 40);

    printf("After deleting 40:\n");
    inorder(root);
    printf("\n");
}
```

Python

```python
import random

class Node:
    def __init__(self, key):
        self.key = key
        self.priority = random.randint(1, 100)
        self.left = self.right = None

def rotate_right(y):
    x = y.left
    y.left = x.right
    x.right = y
    return x

def rotate_left(x):
```

```
    y = x.right
    x.right = y.left
    y.left = x
    return y

def insert(root, key):
    if not root:
        return Node(key)
    if key < root.key:
        root.left = insert(root.left, key)
        if root.left.priority < root.priority:
            root = rotate_right(root)
    elif key > root.key:
        root.right = insert(root.right, key)
        if root.right.priority < root.priority:
            root = rotate_left(root)
    return root

def delete(root, key):
    if not root:
        return None
    if key < root.key:
        root.left = delete(root.left, key)
    elif key > root.key:
        root.right = delete(root.right, key)
    else:
        if not root.left and not root.right:
            return None
        elif not root.left:
            root = rotate_left(root)
        elif not root.right:
            root = rotate_right(root)
        elif root.left.priority < root.right.priority:
            root = rotate_right(root)
        else:
            root = rotate_left(root)
        root = delete(root, key)
    return root

def inorder(root):
    if not root: return
    inorder(root.left)
```

```
    print(f"({root.key},{root.priority})", end=" ")
    inorder(root.right)

root = None
for k in [40,20,60,10,30,50,70]:
    root = insert(root, k)
print("Before:", end=" ")
inorder(root)
print()
root = delete(root, 40)
print("After:", end=" ")
inorder(root)
```

Why It Matters

- No explicit rebalancing, rotations emerge from heap priorities
- Expected O(log n) deletion
- Natural, simple structure for randomized search trees
- Used in randomized algorithms, dynamic sets, and order-statistics

A Gentle Proof (Why It Works)

At each step, the node rotates toward a child with smaller priority, preserving heap property. Expected height remains O(log n) due to independent random priorities.

Try It Yourself

1. Build treap with [10, 20, 30, 40, 50].
2. Delete 30 → observe rotations to leaf.
3. Delete 10 (root) → rotation chooses smaller-priority child.
4. Repeat deletions, verify BST + heap invariants hold.

Test Cases

Keys	Delete	Rotations	Balanced	Root After
[40,20,60,10,30,50,70]	40	Right, Left		30
[10,20,30]	20	Left		10
[50,30,70,20,40,60,80]	30	Right		50

Complexity

Operation	Time	Space
Delete	O(log n) expected	O(h) recursion
Insert	O(log n) expected	O(h)
Search	O(log n) expected	O(h)

The Treap deletes gracefully, rotating away until the target fades like a falling leaf, leaving balance behind.

238 Weight Balanced Tree

A Weight Balanced Tree (WBT) maintains balance not by height or color, but by subtree sizes (or "weights"). Each node keeps track of how many elements are in its left and right subtrees, and balance is enforced by requiring their weights to stay within a constant ratio.

What Problem Are We Solving?

In ordinary BSTs, imbalance can grow as keys are inserted in sorted order, degrading performance to O(n). Weight Balanced Trees fix this by keeping subtree sizes within a safe range. They are particularly useful when you need order-statistics (like "find the k-th element") or split/merge operations that depend on sizes rather than heights.

How It Works (Plain Language)

Each node maintains a weight = total number of nodes in its subtree. When inserting or deleting, you update weights and check the balance condition:

If

```
weight(left)    × weight(node)
weight(right)    × weight(node)
```

for some balance constant (e.g., 0.7), then the tree is considered balanced.

If not, perform rotations (like AVL) to restore balance.

Operation	Steps
Insert	Insert like BST → Update weights → If ratio violated → Rotate
Delete	Remove node → Update weights → If ratio violated → Rebuild or rotate
Search	BST search (weights guide decisions for rank queries)

Because weights reflect actual sizes, the tree ensures O(log n) expected height.

Example

Let's use = 0.7

Insert [10, 20, 30, 40, 50]

Step	Insert	Weight(left)	Weight(right)	Balanced?	Fix
1	10	0	0		-
2	20	1	0		-
3	30	2	0		Rotate left
4	40	3	0		Rotate left
5	50	4	0		Rotate left

Tree remains balanced by rotations once left-right ratio exceeds .

Step-by-Step Example

Insert [1, 2, 3, 4, 5] with = 0.7

Step	Action	Weights	Balanced?	Rotation
1	Insert 1	(0,0)		-
2	Insert 2	(1,0)		-
3	Insert 3	(2,0)		Left Rotate
4	Insert 4	(3,0)		Left Rotate
5	Insert 5	(4,0)		Left Rotate

Tree remains height-balanced based on weights.

Tiny Code (Easy Versions)

C (Simplified)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key;
    int size; // weight = size of subtree
    struct Node *left, *right;
} Node;

int size(Node* n) { return n ? n->size : 0; }

Node* new_node(int key) {
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->size = 1;
    n->left = n->right = NULL;
    return n;
}

Node* rotate_left(Node* x) {
    Node* y = x->right;
    x->right = y->left;
    y->left = x;
    x->size = 1 + size(x->left) + size(x->right);
    y->size = 1 + size(y->left) + size(y->right);
    return y;
}

Node* rotate_right(Node* y) {
    Node* x = y->left;
    y->left = x->right;
    x->right = y;
    y->size = 1 + size(y->left) + size(y->right);
    x->size = 1 + size(x->left) + size(x->right);
    return x;
}

double alpha = 0.7;
```

```c
int balanced(Node* n) {
    if (!n) return 1;
    int l = size(n->left), r = size(n->right);
    return l <= alpha * n->size && r <= alpha * n->size;
}

Node* insert(Node* root, int key) {
    if (!root) return new_node(key);
    if (key < root->key) root->left = insert(root->left, key);
    else if (key > root->key) root->right = insert(root->right, key);
    root->size = 1 + size(root->left) + size(root->right);
    if (!balanced(root)) {
        if (size(root->left) > size(root->right))
            root = rotate_right(root);
        else
            root = rotate_left(root);
    }
    return root;
}

void inorder(Node* n) {
    if (!n) return;
    inorder(n->left);
    printf("%d(%d) ", n->key, n->size);
    inorder(n->right);
}

int main(void) {
    Node* root = NULL;
    int keys[] = {10, 20, 30, 40, 50};
    for (int i = 0; i < 5; i++)
        root = insert(root, keys[i]);
    inorder(root);
    printf("\n");
}
```

Python (Simplified)

```python
class Node:
    def __init__(self, key):
        self.key = key
        self.size = 1
```

```
        self.left = self.right = None

def size(n): return n.size if n else 0

def update(n):
    if n:
        n.size = 1 + size(n.left) + size(n.right)

def rotate_left(x):
    y = x.right
    x.right = y.left
    y.left = x
    update(x)
    update(y)
    return y

def rotate_right(y):
    x = y.left
    y.left = x.right
    x.right = y
    update(y)
    update(x)
    return x

alpha = 0.7

def balanced(n):
    return not n or (size(n.left) <= alpha * n.size and size(n.right) <= alpha * n.size)

def insert(root, key):
    if not root: return Node(key)
    if key < root.key: root.left = insert(root.left, key)
    elif key > root.key: root.right = insert(root.right, key)
    update(root)
    if not balanced(root):
        if size(root.left) > size(root.right):
            root = rotate_right(root)
        else:
            root = rotate_left(root)
    return root

def inorder(n):
```

```
    if not n: return
    inorder(n.left)
    print(f"{n.key}({n.size})", end=" ")
    inorder(n.right)

root = None
for k in [10,20,30,40,50]:
    root = insert(root, k)
inorder(root)
```

Why It Matters

- Balances based on true subtree size, not height
- Excellent for order-statistics (`kth`, `rank`)
- Supports split, merge, and range queries naturally
- Deterministic balancing without randomness

A Gentle Proof (Why It Works)

Maintaining weight ratios guarantees logarithmic height. If < 1, each subtree has $\times$ n nodes, so height $\log / (n) \to O(\log n)$.

Try It Yourself

1. Build [10, 20, 30, 40, 50] with $= 0.7$.
2. Print sizes at each node.
3. Delete 20 $\to$ rebalance by rotation.
4. Try $= 0.6$ and $= 0.8$ $\to$ compare shapes.

Test Cases

Sequence		Balanced?	Height
[10,20,30,40,50]	0.7		log n
[1..100]	0.7		O(log n)
[sorted 1..10]	0.6		~4

Complexity

Operation	Time	Space
Insert	O(log n)	O(h)
Delete	O(log n)	O(h)
Search	O(log n)	O(h)

A Weight Balanced Tree is like a tightrope walker, always adjusting its stance to keep perfect equilibrium, no matter how the sequence unfolds.

239 Scapegoat Tree Rebuild

A Scapegoat Tree is a binary search tree that maintains balance by occasionally rebuilding entire subtrees.
Instead of performing rotations on every insertion, it monitors the depth of nodes.
When a node's depth exceeds the allowed limit, the algorithm locates a *scapegoat* ancestor whose subtree is too unbalanced, flattens that subtree into a sorted list, and rebuilds it into a perfectly balanced tree.

With a balance parameter α in $(0.5, 1)$, a Scapegoat Tree guarantees: - $O(\log n)$ amortized time for insertions and deletions
- $O(\log n)$ worst-case height

What Problem Are We Solving?

Standard BSTs can become skewed and degrade to O(n). Rotational trees like AVL and Red Black maintain strict local invariants but add per update overhead. Scapegoat trees choose a middle path

- Do nothing most of the time
- Occasionally rebuild an entire subtree when a global bound is exceeded

Goal Keep height near $\log_{1/\alpha} n$ while keeping code simple and rotations out of the hot path.

How It Works (Plain Language)

Parameters and invariants

- Choose $\alpha \in (0.5, 1)$ such as $\alpha = \frac{2}{3}$
- Maintain `n` = current size and `n_max` = maximum size since the last global rebuild

- Height bound: if an insertion lands deeper than $\lfloor \log_{1/\alpha} n \rfloor$, the tree is too tall

Insert algorithm

1. Insert like a normal BST and track the path length `depth`.
2. If `depth` is within the allowed bound, stop.
3. Otherwise, walk up to find the scapegoat node `s` such that

$$\max\left(\text{size}(s.\text{left}),\ \text{size}(s.\text{right})\right) > \alpha \cdot \text{size}(s)$$

4. Rebuild the subtree rooted at `s` into a perfectly balanced BST in time linear in that subtree's size.

Delete algorithm

- Perform a normal BST delete.
- Decrement `n`.
- If $n < \alpha \cdot n_{\max}$, rebuild the entire tree and set $n_{\max} = n$.

Why rebuilding works

- Rebuilding performs an inorder traversal to collect nodes into a sorted array, then constructs a balanced BST from that array.
- Rebuilds are infrequent, and their costs are amortized over many cheap insertions and deletions, ensuring logarithmic time on average.

Example Walkthrough

Let $\alpha = \frac{2}{3}$.

Insert the keys `[10, 20, 30, 40, 50, 60]` in ascending order.

Step	Action	Depth vs bound	Scapegoat found	Rebuild
1	insert 10	depth 0 within	none	no
2	insert 20	depth 1 within	none	no
3	insert 30	depth 2 within	none	no
4	insert 40	depth 3 exceeds bound	ancestor violates	rebuild that subtree
5	insert 50	likely within	none	no
6	insert 60	if depth exceeds	find ancestor	rebuild subtree

The occasional rebuild produces a nearly perfect BST despite sorted input.

Tiny Code (Easy Versions)

Python (concise reference implementation)

```
from math import log, floor

class Node:
    __slots__ = ("key", "left", "right", "size")
    def __init__(self, key):
        self.key = key
        self.left = None
        self.right = None
        self.size = 1

def size(x): return x.size if x else 0
def update(x):
    if x: x.size = 1 + size(x.left) + size(x.right)

def flatten_inorder(x, arr):
    if not x: return
    flatten_inorder(x.left, arr)
    arr.append(x)
    flatten_inorder(x.right, arr)

def build_balanced(nodes, lo, hi):
    if lo >= hi: return None
    mid = (lo + hi) // 2
    root = nodes[mid]
    root.left = build_balanced(nodes, lo, mid)
    root.right = build_balanced(nodes, mid + 1, hi)
    update(root)
    return root

class ScapegoatTree:
    def __init__(self, alpha=2/3):
        self.alpha = alpha
        self.root = None
        self.n = 0
        self.n_max = 0

    def _log_alpha(self, n):
        # height bound floor(log_{1/alpha} n)
        if n <= 1: return 0
```

```
        return floor(log(n, 1 / self.alpha))

    def _find_and_rebuild(self, path):
        # path is list of nodes from root to inserted node
        for i in range(len(path) - 1, -1, -1):
            x = path[i]
            l, r = size(x.left), size(x.right)
            if max(l, r) > self.alpha * size(x):
                # rebuild subtree rooted at x and reattach to parent
                nodes = []
                flatten_inorder(x, nodes)
                new_sub = build_balanced(nodes, 0, len(nodes))
                if i == 0:
                    self.root = new_sub
                else:
                    p = path[i - 1]
                    if p.left is x: p.left = new_sub
                    else: p.right = new_sub
                    # fix sizes upward from parent
                    for j in range(i - 1, -1, -1):
                        update(path[j])
                return

    def insert(self, key):
        self.n += 1
        self.n_max = max(self.n_max, self.n)
        if not self.root:
            self.root = Node(key)
            return

        # standard BST insert with path tracking
        path = []
        cur = self.root
        while cur:
            path.append(cur)
            if key < cur.key:
                if cur.left: cur = cur.left
                else:
                    cur.left = Node(key)
                    path.append(cur.left)
                    break
            elif key > cur.key:
```

```
                if cur.right: cur = cur.right
                else:
                    cur.right = Node(key)
                    path.append(cur.right)
                    break
            else:
                # duplicate ignore
                self.n -= 1
                return
        # update sizes
        for node in reversed(path[:-1]):
            update(node)

        # depth check and possible rebuild
        if len(path) - 1 > self._log_alpha(self.n):
            self._find_and_rebuild(path)

    def _join_left_max(self, t):
        # remove and return max node from subtree t, plus the new subtree
        if not t.right:
            return t, t.left
        m, t.right = self._join_left_max(t.right)
        update(t)
        return m, t

    def delete(self, key):
        # standard BST delete
        def _del(x, key):
            if not x: return None, False
            if key < x.key:
                x.left, removed = _del(x.left, key)
            elif key > x.key:
                x.right, removed = _del(x.right, key)
            else:
                removed = True
                if not x.left: return x.right, True
                if not x.right: return x.left, True
                # replace with predecessor
                m, x.left = self._join_left_max(x.left)
                m.left, m.right = x.left, x.right
                x = m
            update(x)
```

```
            return x, removed

        self.root, removed = _del(self.root, key)
        if not removed: return
        self.n -= 1
        if self.n < self.alpha * self.n_max:
            # global rebuild
            nodes = []
            flatten_inorder(self.root, nodes)
            self.root = build_balanced(nodes, 0, len(nodes))
            self.n_max = self.n
```

C (outline of the rebuild idea)

```
// Sketch only: show rebuild path
// 1) Do BST insert while recording path stack
// 2) If depth > bound, walk path upward to find scapegoat
// 3) Inorder-copy subtree nodes to an array
// 4) Recursively rebuild balanced subtree from that array
// 5) Reattach rebuilt subtree to parent and fix sizes up the path
```

Why It Matters

- Simple balancing approach with rare but powerful subtree rebuilds
- Well suited for workloads where insertions arrive in bursts and frequent rotations are undesirable
- Guarantees height $O(\log n)$ with a tunable constant controlled by α
- The inorder-based rebuild process makes ordered operations efficient and easy to implement

A Gentle Proof (Why It Works)

Let $\alpha \in (0.5, 1)$.

- Height bound: if height exceeds $\log_{1/\alpha} n$, a scapegoat exists since some ancestor must violate $\max\{|L|,\ |R|\} \le \alpha\,|T|$.
- Amortization: each node participates in $O(1)$ rebuilds with Θ(size of its subtree) work, so the total cost over m operations is $O(m \log n)$.

- Deletion rule: rebuilding when $n < \alpha\, n_{\max}$ prevents slack from accumulating.

Try It Yourself

1. Insert ascending keys to trigger rebuilds with $\alpha = \frac{2}{3}$
2. Delete many keys so that $n < \alpha\, n_{\max}$ and observe the global rebuild trigger
3. Experiment with different α values
4. Add an order statistic query using stored subtree sizes

Test Cases

Operation	Input		Expected
Insert ascending	[1..1000]	0.66	Height stays O(log n) with periodic rebuilds
Mixed ops	random inserts and deletes	0.7	Amortized O(log n) per op
Shrink check	insert 1..200, delete 101..200	0.7	Global rebuild when size drops below n_max
Duplicate insert	insert 42 twice	0.66	size unchanged after second insert

Edge Cases

- Rebuilding an empty or singleton subtree is a no-op
- Duplicate keys are ignored or handled according to policy
- Choose $\alpha > 0.5$ to guarantee the existence of a scapegoat

Complexity

Operation	Time	Space
Search	O(h) worst, O(log n) amortized	O(1) extra
Insert	Amortized O(log n)	O(1) extra plus rebuild buffer
Delete	Amortized O(log n)	O(1) extra plus rebuild buffer
Rebuild subtree	O(k) for k nodes in subtree	O(k) temporary array

Scapegoat trees wait calmly until imbalance is undeniable, then rebuild decisively. The result is a BST that stays lean with minimal fuss.

240 AA Tree

An AA Tree is a simplified version of a red-black tree that maintains balance using a single level value per node (instead of color). It enforces balance by a small set of easy-to-code rules using two operations, `skew` and `split`. The simplicity of AA trees makes them a popular teaching and practical implementation choice when you want red-black performance without complex cases.

What Problem Are We Solving?

We want a balanced binary search tree with

- O(log n) time for insert/search/delete
- Simpler code than red-black or AVL
- Fewer rotation cases

AA trees achieve this by using levels (like black-heights in RBTs) to enforce structure, ensuring a balanced shape with one rotation per fix.

How It Works (Plain Language)

Each node has

- `key`: stored value
- `level`: like black height (root = 1)

AA-tree invariants:

1. Left child level $<$ node level
2. Right child level node level
3. Right-right grandchild level $<$ node level
4. Every leaf has level 1

To restore balance after insert/delete, apply skew and split operations:

Operation	Rule	Action
Skew	If left.level == node.level	Rotate right
Split	If right.right.level == node.level	Rotate left, level++

Example

Insert keys [10, 20, 30]

Step	Tree	Fix
1	10 (lvl 1)	-
2	10 → 20	Skew none
3	10 → 20 → 30	Right-right violation → Split → Rotate left on 10

Result:

```
    20 (2)
   /  \
 10(1) 30(1)
```

Step-by-Step Example

Insert [30, 20, 10, 25]

Step	Insertion	Violation	Fix	
1	30	none	-	
2	20	left child level = node level	Skew → Rotate right	
3	10	deeper left	Skew & Split	20 root
4	25	insert right of 20	Split if needed	balanced

Tiny Code (Easy Versions)

C

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int key;
    int level;
    struct Node *left, *right;
} Node;

Node* new_node(int key) {
```

```
    Node* n = malloc(sizeof(Node));
    n->key = key;
    n->level = 1;
    n->left = n->right = NULL;
    return n;
}

Node* rotate_left(Node* x) {
    Node* y = x->right;
    x->right = y->left;
    y->left = x;
    return y;
}

Node* rotate_right(Node* y) {
    Node* x = y->left;
    y->left = x->right;
    x->right = y;
    return x;
}

Node* skew(Node* x) {
    if (x && x->left && x->left->level == x->level)
        x = rotate_right(x);
    return x;
}

Node* split(Node* x) {
    if (x && x->right && x->right->right && x->right->right->level == x->level) {
        x = rotate_left(x);
        x->level++;
    }
    return x;
}

Node* insert(Node* root, int key) {
    if (!root) return new_node(key);
    if (key < root->key)
        root->left = insert(root->left, key);
    else if (key > root->key)
        root->right = insert(root->right, key);
    root = skew(root);
```

```
    root = split(root);
    return root;
}

void inorder(Node* r) {
    if (!r) return;
    inorder(r->left);
    printf("(%d, %d) ", r->key, r->level);
    inorder(r->right);
}

int main(void) {
    Node* root = NULL;
    int keys[] = {10, 20, 30, 15, 25};
    for (int i = 0; i < 5; i++)
        root = insert(root, keys[i]);
    inorder(root);
    printf("\n");
}
```

Python

```
class Node:
    def __init__(self, key):
        self.key = key
        self.level = 1
        self.left = None
        self.right = None

def rotate_left(x):
    y = x.right
    x.right = y.left
    y.left = x
    return y

def rotate_right(y):
    x = y.left
    y.left = x.right
    x.right = y
    return x

def skew(x):
```

```
    if x and x.left and x.left.level == x.level:
        x = rotate_right(x)
    return x

def split(x):
    if x and x.right and x.right.right and x.right.right.level == x.level:
        x = rotate_left(x)
        x.level += 1
    return x

def insert(root, key):
    if not root:
        return Node(key)
    if key < root.key:
        root.left = insert(root.left, key)
    elif key > root.key:
        root.right = insert(root.right, key)
    root = skew(root)
    root = split(root)
    return root

def inorder(r):
    if not r: return
    inorder(r.left)
    print(f"({r.key},{r.level})", end=" ")
    inorder(r.right)

root = None
for k in [10, 20, 30, 15, 25]:
    root = insert(root, k)
inorder(root)
```

Why It Matters

- Simpler than red-black
- Only two balancing functions (skew, split)
- Maintains O(log n) performance
- Great teaching and reference structure for self-balancing BSTs

A Gentle Proof (Why It Works)

AA-trees are a special case of red-black trees where

- Right-leaning red links represent level
- Skew fixes left-leaning reds
- Split fixes two consecutive rights

These rules ensure black-height invariants and logarithmic height.

Try It Yourself

1. Insert ascending keys → observe periodic right rotations
2. Draw tree after each step → check levels
3. Compare structure to equivalent red-black tree
4. Modify split condition → see imbalance appear

Test Cases

Input Keys	Expected Root	Height	Balanced?
[10,20,30]	20	2	
[1..10]	4–5	~log n	
[30,20,10,25]	20	3	

Complexity

Operation	Time	Space
Insert	O(log n)	O(h)
Search	O(log n)	O(1)
Delete	O(log n)	O(h)

AA Trees blend red-black efficiency with AVL simplicity, balanced, elegant, and easy to reason about.

Section 25. Segment Trees and Fenwick Trees

241 Build Segment Tree

A segment tree is a binary tree over an array that stores range information for fast queries and updates. Building it means constructing the tree from the base array so each node summarizes a segment, like a sum, min, max, or gcd. The classic build time is O(n) and it enables O(log n) queries and updates.

What Problem Are We Solving?

We want to answer range questions quickly

- Sum on [l, r]
- Min or max on [l, r]
- Counts or bitwise ops on [l, r]

If we precompute a segment tree, each internal node stores the merge of its two children. Then queries and updates touch only O(log n) nodes.

Goal Turn an array `A[0..n-1]` into a tree `T` where `T[v]` summarizes a segment `A[L..R]`.

How It Works (Plain Language)

Represent the tree in an array (1 indexed for simplicity)

- Node `v` covers segment `[L, R]`
- Left child `2v` covers `[L, mid]`
- Right child `2v+1` covers `[mid+1, R]`
- `T[v] = merge(T[2v], T[2v+1])` where `merge` is sum, min, max, etc.

Build Steps

1. If `L == R`, store the leaf value `A[L]` in `T[v]`.
2. Else split at `mid`, recursively build left and right, then `T[v] = merge(left, right)`.

Example Build (sum)

Array `A = [2, 1, 3, 4]`

Node v	Segment [L,R]	Value
1	[0,3]	10
2	[0,1]	3

Node v	Segment [L,R]	Value
3	[2,3]	7
4	[0,0]	2
5	[1,1]	1
6	[2,2]	3
7	[3,3]	4

`merge = sum`, so `T[1] = 3 + 7 = 10`, leaves store the original values.

Another Example Build (min)

Array `A = [5, 2, 6, 1]`

Node v	Segment [L,R]	Value (min)
1	[0,3]	1
2	[0,1]	2
3	[2,3]	1
4	[0,0]	5
5	[1,1]	2
6	[2,2]	6
7	[3,3]	1

Tiny Code (Easy Versions)

C (iterative storage size 4n, recursive build for sum)

```c
#include <stdio.h>

#define MAXN 100000
int A[MAXN];
long long T[4*MAXN];

long long merge(long long a, long long b) { return a + b; }

void build(int v, int L, int R) {
    if (L == R) {
        T[v] = A[L];
        return;
    }
    int mid = (L + R) / 2;
```

```
    build(2*v, L, mid);
    build(2*v+1, mid+1, R);
    T[v] = merge(T[2*v], T[2*v+1]);
}

int main(void) {
    int n = 4;
    A[0]=2; A[1]=1; A[2]=3; A[3]=4;
    build(1, 0, n-1);
    for (int v = 1; v < 8; v++) printf("T[%d]=%lld\n", v, T[v]);
    return 0;
}
```

Python (sum segment tree, recursive build)

```
def build(arr):
    n = len(arr)
    size = 1
    while size < n:
        size <<= 1
    T = [0] * (2 * size)

    # leaves
    for i in range(n):
        T[size + i] = arr[i]
    # internal nodes
    for v in range(size - 1, 0, -1):
        T[v] = T[2*v] + T[2*v + 1]
    return T, size  # T is 1..size*2-1, leaves start at index size

# Example
A = [2, 1, 3, 4]
T, base = build(A)
# T[1] holds sum of all, T[base+i] holds A[i]
print("Root sum:", T[1])
```

Notes

- The C version shows classic recursive top down build.
- The Python version shows an iterative bottom up build using a power of two base, also O(n).

Why It Matters

- Preprocessing time O(n) enables
  - Range queries in O(log n)
  - Point updates in O(log n)
- Choice of `merge` adapts the tree to many tasks
  - sum, min, max, gcd, bitwise and, custom structs

A Gentle Proof (Why It Works)

Each element appears in exactly one leaf and contributes to O(1) nodes per level. The tree has O(log n) levels. Total number of nodes built is at most 2n, so total work is O(n).

Try It Yourself

1. Change `merge` to `min` or `max` and rebuild.
2. Build then verify that `T[1]` equals `sum(A)`.
3. Print the tree level by level to visualize segments.
4. Extend the structure to support point update and range query.

Test Cases

Array A	Merge	Expected Root T[1]	Notes
[2,1,3,4]	sum	10	basic sum tree
[5,2,6,1]	min	1	switch merge to min
[7]	sum	7	single element
[]	sum	0 or no tree	handle empty as special case

Complexity

Phase	Time	Space
Build	O(n)	O(n)
Query	O(log n)	O(1) extra
Point update	O(log n)	O(1) extra

Build once, answer fast forever. A segment tree turns an array into a range answering machine.

242 Range Sum Query

A Range Sum Query (RSQ) retrieves the sum of elements in a subarray `[L, R]` using a segment tree. Once the tree is built, each query runs in O(log n) time, by combining results from the minimal set of segments covering `[L, R]`.

What Problem Are We Solving?

Given an array `A[0..n-1]`, we want to answer queries like

```
sum(A[L..R])
```

quickly, without recalculating from scratch each time.

Naive approach: O(R–L+1) per query Segment tree approach: O(log n) per query after O(n) build.

How It Works (Plain Language)

We maintain a segment tree `T` built as before (`T[v]` = sum of segment). To answer `query(v, L, R, qL, qR)`

1. If segment `[L, R]` is fully outside `[qL, qR]`, return 0.
2. If segment `[L, R]` is fully inside, return `T[v]`.
3. Otherwise, split at `mid` and combine results from left and right children.

So each query visits only O(log n) nodes, each exactly covering part of the query range.

Example

Array: `A = [2, 1, 3, 4, 5]`

Query: sum on [1,3] (1-based: elements 1..3 = 1+3+4=8)

Node v	Segment [L,R]	Value	Relationship to [1,3]	Contribution
1	[0,4]	15	overlaps	recurse
2	[0,2]	6	overlaps	recurse
3	[3,4]	9	overlaps	recurse
4	[0,1]	3	partial	recurse
5	[2,2]	3	inside	+3
8	[0,0]	2	outside	skip

Node v	Segment [L,R]	Value	Relationship to [1,3]	Contribution
9	[1,1]	1	inside	+1
6	[3,3]	4	inside	+4
7	[4,4]	5	outside	skip

Sum = 1 + 3 + 4 = 8

Step-by-Step Table (for clarity)

Step	Current Segment	Covered?	Action
1	[0,4]	Overlaps [1,3]	Split
2	[0,2]	Overlaps [1,3]	Split
3	[3,4]	Overlaps [1,3]	Split
4	[0,1]	Overlaps	Split
5	[0,0]	Outside	Return 0
6	[1,1]	Inside	Return 1
7	[2,2]	Inside	Return 3
8	[3,3]	Inside	Return 4
9	[4,4]	Outside	Return 0

Total = 1+3+4 = 8

Tiny Code (Easy Versions)

C (Recursive RSQ)

```c
#include <stdio.h>

#define MAXN 100000
int A[MAXN];
long long T[4*MAXN];

long long merge(long long a, long long b) { return a + b; }

void build(int v, int L, int R) {
    if (L == R) {
        T[v] = A[L];
        return;
```

```
    }
    int mid = (L + R) / 2;
    build(2*v, L, mid);
    build(2*v+1, mid+1, R);
    T[v] = merge(T[2*v], T[2*v+1]);
}

long long query(int v, int L, int R, int qL, int qR) {
    if (qR < L || R < qL) return 0; // disjoint
    if (qL <= L && R <= qR) return T[v]; // fully covered
    int mid = (L + R) / 2;
    long long left = query(2*v, L, mid, qL, qR);
    long long right = query(2*v+1, mid+1, R, qL, qR);
    return merge(left, right);
}

int main(void) {
    int n = 5;
    int Avals[5] = {2,1,3,4,5};
    for (int i=0;i<n;i++) A[i]=Avals[i];
    build(1, 0, n-1);
    printf("Sum [1,3] = %lld\n", query(1,0,n-1,1,3)); // expect 8
}
```

Python (Iterative)

```
def build(arr):
    n = len(arr)
    size = 1
    while size < n:
        size <<= 1
    T = [0]*(2*size)
    # leaves
    for i in range(n):
        T[size+i] = arr[i]
    # parents
    for v in range(size-1, 0, -1):
        T[v] = T[2*v] + T[2*v+1]
    return T, size

def query(T, base, l, r):
    l += base
```

```
    r += base
    res = 0
    while l <= r:
        if l % 2 == 1:
            res += T[l]
            l += 1
        if r % 2 == 0:
            res += T[r]
            r -= 1
        l //= 2
        r //= 2
    return res

A = [2,1,3,4,5]
T, base = build(A)
print("Sum [1,3] =", query(T, base, 1, 3))  # expect 8
```

Why It Matters

- Enables fast range queries on static or dynamic arrays.
- Foundation for many extensions:
  - Range min/max query (change merge)
  - Lazy propagation (for range updates)
  - 2D and persistent trees

A Gentle Proof (Why It Works)

Each level of recursion splits into disjoint segments. At most 2 segments per level are added to the result. Depth = O(log n), so total work = O(log n).

Try It Yourself

1. Query different [L, R] ranges after build.
2. Replace `merge` with `min()` or `max()` and verify results.
3. Combine queries to verify overlapping segments are counted once.
4. Add update operation to change elements and re-query.

Test Cases

Array A	Query [L,R]	Expected	Notes
[2,1,3,4,5]	[1,3]	8	1+3+4
[5,5,5,5]	[0,3]	20	uniform
[1,2,3,4,5]	[2,4]	12	3+4+5
[7]	[0,0]	7	single element

Complexity

Operation	Time	Space
Query	O(log n)	O(1)
Build	O(n)	O(n)
Update	O(log n)	O(1)

Segment trees let you ask *"what's in this range?"*, and get the answer fast, no matter how big the array.

243 Range Update (Lazy Propagation Technique)

A range update modifies all elements in a segment `[L, R]` efficiently. Without optimization, you'd touch every element, O(n). With lazy propagation, you defer work, storing pending updates in a separate array, achieving O(log n) time per update and query.

This pattern is essential when many updates overlap, like adding +5 to every element in [2, 6] repeatedly.

What Problem Are We Solving?

We want to efficiently support both:

1. Range updates: Add or set a value over `[L, R]`
2. Range queries: Get sum/min/max over `[L, R]`

Naive solution: O(R–L+1) per update. Lazy propagation: O(log n) per update/query.

Example goal:

```
add +3 to A[2..5]
then query sum(A[0..7])
```

How It Works (Plain Language)

Each segment node `T[v]` stores summary (e.g. sum). Each node `lazy[v]` stores pending update (not yet pushed to children).

When updating `[L, R]`:

- If node's segment is fully inside, apply update directly to `T[v]` and mark `lazy[v]` (no recursion).
- If partially overlapping, push pending updates down, then recurse.

When querying `[L, R]`:

- Push any pending updates first
- Combine child results as usual

This way, each node is updated at most once per path, giving O(log n).

Example

Array: `A = [1, 2, 3, 4, 5, 6, 7, 8]` Build tree for sum.

Step 1: Range update `[2, 5]` += 3

Node	Segment	Action	lazy[]	T[] sum
1	[0,7]	overlaps → recurse	0	unchanged
2	[0,3]	overlaps → recurse	0	unchanged
3	[4,7]	overlaps → recurse	0	unchanged
4	[0,1]	outside	-	-
5	[2,3]	inside → add +3×2=6	lazy[5]=3	T[5]+=6
6	[4,5]	inside → add +3×2=6	lazy[6]=3	T[6]+=6

Later queries automatically apply +3 to affected subranges.

Step-by-Step Example

Let's trace two operations:

1. `update(2,5,+3)`
2. `query(0,7)`

Step	Action	Result
Build	sum = [1,2,3,4,5,6,7,8] → 36	T[1]=36
Update	mark lazy for segments fully in [2,5]	T[v]+=3×len
Query	propagate lazy before using T[v]	sum = 36 + 3×4 = 48

Result after update: total = 48

Tiny Code (Easy Versions)

C (Recursive, sum tree with lazy add)

```c
#include <stdio.h>

#define MAXN 100000
int A[MAXN];
long long T[4*MAXN], lazy[4*MAXN];

long long merge(long long a, long long b) { return a + b; }

void build(int v, int L, int R) {
    if (L == R) { T[v] = A[L]; return; }
    int mid = (L + R) / 2;
    build(2*v, L, mid);
    build(2*v+1, mid+1, R);
    T[v] = merge(T[2*v], T[2*v+1]);
}

void push(int v, int L, int R) {
    if (lazy[v] != 0) {
        T[v] += lazy[v] * (R - L + 1);
        if (L != R) {
            lazy[2*v] += lazy[v];
            lazy[2*v+1] += lazy[v];
        }
        lazy[v] = 0;
    }
}

void update(int v, int L, int R, int qL, int qR, int val) {
    push(v, L, R);
```

```
    if (qR < L || R < qL) return;
    if (qL <= L && R <= qR) {
        lazy[v] += val;
        push(v, L, R);
        return;
    }
    int mid = (L + R) / 2;
    update(2*v, L, mid, qL, qR, val);
    update(2*v+1, mid+1, R, qL, qR, val);
    T[v] = merge(T[2*v], T[2*v+1]);
}

long long query(int v, int L, int R, int qL, int qR) {
    push(v, L, R);
    if (qR < L || R < qL) return 0;
    if (qL <= L && R <= qR) return T[v];
    int mid = (L + R) / 2;
    return merge(query(2*v, L, mid, qL, qR), query(2*v+1, mid+1, R, qL, qR));
}

int main(void) {
    int n = 8;
    int vals[] = {1,2,3,4,5,6,7,8};
    for (int i=0;i<n;i++) A[i]=vals[i];
    build(1,0,n-1);
    update(1,0,n-1,2,5,3);
    printf("Sum [0,7] = %lld\n", query(1,0,n-1,0,7)); // expect 48
}
```

Python (Iterative version)

```
class LazySegTree:
    def __init__(self, arr):
        n = len(arr)
        size = 1
        while size < n: size <<= 1
        self.n = n; self.size = size
        self.T = [0]*(2*size)
        self.lazy = [0]*(2*size)
        for i in range(n): self.T[size+i] = arr[i]
        for i in range(size-1, 0, -1):
            self.T[i] = self.T[2*i] + self.T[2*i+1]
```

```
    def _apply(self, v, val, length):
        self.T[v] += val * length
        if v < self.size:
            self.lazy[v] += val

    def _push(self, v, length):
        if self.lazy[v]:
            self._apply(2*v, self.lazy[v], length//2)
            self._apply(2*v+1, self.lazy[v], length//2)
            self.lazy[v] = 0

    def update(self, l, r, val):
        def _upd(v, L, R):
            if r < L or R < l: return
            if l <= L and R <= r:
                self._apply(v, val, R-L+1)
                return
            self._push(v, R-L+1)
            mid = (L+R)//2
            _upd(2*v, L, mid)
            _upd(2*v+1, mid+1, R)
            self.T[v] = self.T[2*v] + self.T[2*v+1]
        _upd(1, 0, self.size-1)

    def query(self, l, r):
        def _qry(v, L, R):
            if r < L or R < l: return 0
            if l <= L and R <= r:
                return self.T[v]
            self._push(v, R-L+1)
            mid = (L+R)//2
            return _qry(2*v, L, mid) + _qry(2*v+1, mid+1, R)
        return _qry(1, 0, self.size-1)

A = [1,2,3,4,5,6,7,8]
st = LazySegTree(A)
st.update(2,5,3)
print("Sum [0,7] =", st.query(0,7))  # expect 48
```

Why It Matters

- Crucial for problems with many overlapping updates
- Used in range-add, range-assign, interval covering, and 2D extensions
- Foundation for Segment Tree Beats

A Gentle Proof (Why It Works)

Each update marks at most one node per level as "lazy." When queried later, we "push" those updates downward once. Each node's pending updates applied O(1) times → total cost O(log n).

Try It Yourself

1. Build `[1,2,3,4,5]` → update [1,3] += 2 → query sum [0,4] → expect 21
2. Update [0,4] += 1 → query [2,4] → expect 3+2+2+1+1 = 15
3. Combine multiple updates → verify cumulative results

Test Cases

Operation	Array	Query	Expected
update [2,5] += 3	[1,2,3,4,5,6,7,8]	sum [0,7]	48
update [0,3] += 2	[5,5,5,5]	sum [1,2]	14
two updates	[1,1,1,1,1]	[1,3] +1, [2,4] +2	[1,3] sum = 10

Complexity

Operation	Time	Space
Range update	O(log n)	O(n)
Range query	O(log n)	O(n)
Build	O(n)	O(n)

Lazy propagation, work smarter, not harder. Apply only what's needed, when it's needed.

244 Point Update

A point update changes a single element in the array and updates all relevant segment tree nodes along the path to the root. This operation ensures the segment tree remains consistent for future range queries.

Unlike range updates (which mark many elements at once), point updates touch only O(log n) nodes, one per level.

What Problem Are We Solving?

Given a segment tree built over `A[0..n-1]`, we want to:

- Change one element: `A[pos] = new_value`
- Reflect the change in the segment tree so all range queries stay correct

Goal: Update efficiently, no full rebuild

Naive: rebuild tree → O(n) Segment tree point update: O(log n)

How It Works (Plain Language)

Every tree node `T[v]` represents a segment `[L, R]`. When `pos` lies within `[L, R]`, that node's value might need adjustment.

Algorithm (recursive):

1. If `L == R == pos`, assign `A[pos] = val`, set `T[v] = val`.
2. Else, find `mid`.
    - Recurse into left or right child depending on `pos`.
    - After child updates, recompute `T[v] = merge(T[2v], T[2v+1])`.

No lazy propagation needed, it's a direct path down the tree.

Node	Range	Value

Example

Array: `A = [2, 1, 3, 4]` Tree stores sum.

Node	Range	Value
1	[0,3]	10
2	[0,1]	3
3	[2,3]	7
4	[0,0]	2
5	[1,1]	1
6	[2,2]	3
7	[3,3]	4

Operation: `A[1] = 5`

Path: [1, 2, 5]

Step	Node	Old Value	New Value	Update
Leaf	5	1	5	T[5]=5
Parent	2	3	7	T[2]=2+5=7
Root	1	10	14	T[1]=7+7=14

New array: `[2, 5, 3, 4]` New sum: 14

Step-by-Step Trace

```
update(v=1, L=0, R=3, pos=1, val=5)
  mid=1
  -> pos<=mid → left child (v=2)
    update(v=2, L=0, R=1)
      mid=0
      -> pos>mid → right child (v=5)
        update(v=5, L=1, R=1)
        T[5]=5
      T[2]=merge(T[4]=2, T[5]=5)=7
  T[1]=merge(T[2]=7, T[3]=7)=14
```

Tiny Code (Easy Versions)

C (Recursive, sum merge)

```c
#include <stdio.h>

#define MAXN 100000
int A[MAXN];
long long T[4*MAXN];

long long merge(long long a, long long b) { return a + b; }

void build(int v, int L, int R) {
    if (L == R) { T[v] = A[L]; return; }
    int mid = (L + R)/2;
    build(2*v, L, mid);
    build(2*v+1, mid+1, R);
    T[v] = merge(T[2*v], T[2*v+1]);
}

void point_update(int v, int L, int R, int pos, int val) {
    if (L == R) {
        T[v] = val;
        A[pos] = val;
        return;
    }
    int mid = (L + R)/2;
    if (pos <= mid) point_update(2*v, L, mid, pos, val);
    else point_update(2*v+1, mid+1, R, pos, val);
    T[v] = merge(T[2*v], T[2*v+1]);
}

long long query(int v, int L, int R, int qL, int qR) {
    if (qR < L || R < qL) return 0;
    if (qL <= L && R <= qR) return T[v];
    int mid = (L + R)/2;
    return merge(query(2*v, L, mid, qL, qR), query(2*v+1, mid+1, R, qL, qR));
}

int main(void) {
    int n = 4;
    int vals[] = {2,1,3,4};
    for (int i=0;i<n;i++) A[i]=vals[i];
```

```
    build(1,0,n-1);
    printf("Before: sum [0,3] = %lld\n", query(1,0,n-1,0,3)); // 10
    point_update(1,0,n-1,1,5);
    printf("After:  sum [0,3] = %lld\n", query(1,0,n-1,0,3)); // 14
}
```

Python (Iterative)

```
def build(arr):
    n = len(arr)
    size = 1
    while size < n: size <<= 1
    T = [0]*(2*size)
    for i in range(n):
        T[size+i] = arr[i]
    for v in range(size-1, 0, -1):
        T[v] = T[2*v] + T[2*v+1]
    return T, size

def update(T, base, pos, val):
    v = base + pos
    T[v] = val
    v //= 2
    while v >= 1:
        T[v] = T[2*v] + T[2*v+1]
        v //= 2

def query(T, base, l, r):
    l += base; r += base
    res = 0
    while l <= r:
        if l%2==1: res += T[l]; l+=1
        if r%2==0: res += T[r]; r-=1
        l//=2; r//=2
    return res

A = [2,1,3,4]
T, base = build(A)
print("Before:", query(T, base, 0, 3))  # 10
update(T, base, 1, 5)
print("After:", query(T, base, 0, 3))   # 14
```

Why It Matters

- Foundation for dynamic data, quick local edits
- Used in segment trees, Fenwick trees, and BIT
- Great for applications like dynamic scoring, cumulative sums, real-time data updates

A Gentle Proof (Why It Works)

Each level has 1 node affected by position `pos`. Tree height = O(log n). Thus, exactly O(log n) nodes recomputed.

Try It Yourself

1. Build `[2,1,3,4]`, update `A[2]=10` → sum [0,3]=17
2. Replace merge with `min` → update element → test queries
3. Compare time with full rebuild for large n

Test Cases

Input A	Update	Query	Expected
[2,1,3,4]	A[1]=5	sum[0,3]	14
[5,5,5]	A[2]=2	sum[0,2]	12
[1]	A[0]=9	sum[0,0]	9

Complexity

Operation	Time	Space
Point update	O(log n)	O(1)
Query	O(log n)	O(1)
Build	O(n)	O(n)

A point update is like a ripple in a pond, a single change flows upward, keeping the whole structure in harmony.

245 Fenwick Tree Build

A Fenwick Tree, or Binary Indexed Tree (BIT), is a compact data structure for prefix queries and point updates. It's perfect for cumulative sums, frequencies, or any associative operation. Building it efficiently sets the stage for O(log n) queries and updates.

Unlike segment trees, a Fenwick Tree uses clever index arithmetic to represent overlapping ranges in a single array.

What Problem Are We Solving?

We want to precompute a structure to:

- Answer prefix queries: `sum(0..i)`
- Support updates: `A[i] += delta`

Naive prefix sum array:

- Query: O(1)
- Update: O(n)

Fenwick Tree:

- Query: O(log n)
- Update: O(log n)
- Build: O(n)

How It Works (Plain Language)

A Fenwick Tree uses the last set bit (LSB) of an index to determine segment length.

Each node `BIT[i]` stores sum of range:

```
(i - LSB(i) + 1) .. i
```

So:

- `BIT[1]` stores A[1]
- `BIT[2]` stores A[1..2]
- `BIT[3]` stores A[3]
- `BIT[4]` stores A[1..4]
- `BIT[5]` stores A[5]
- `BIT[6]` stores A[5..6]

Prefix sum = sum of these overlapping ranges.

Example

Array `A = [2, 1, 3, 4, 5]` (1-indexed for clarity)

i	A[i]	LSB(i)	Range Stored	BIT[i] (sum)
1	2	1	[1]	2
2	1	2	[1..2]	3
3	3	1	[3]	3
4	4	4	[1..4]	10
5	5	1	[5]	5

Step-by-Step Build (O(n))

Iterate i from 1 to n:

1. `BIT[i] += A[i]`
2. Add `BIT[i]` to its parent: `BIT[i + LSB(i)] += BIT[i]`

Step	i	LSB(i)	Update BIT[i+LSB(i)]	Result BIT
1	1	1	BIT[2]+=2	[2,3,0,0,0]
2	2	2	BIT[4]+=3	[2,3,0,3,0]
3	3	1	BIT[4]+=3	[2,3,3,6,0]
4	4	4	BIT[8]+=6 (ignore, out of range)	[2,3,3,6,0]
5	5	1	BIT[6]+=5 (ignore, out of range)	[2,3,3,6,5]

Built BIT: `[2, 3, 3, 6, 5]`

Tiny Code (Easy Versions)

C (O(n) Build)

```c
#include <stdio.h>

#define MAXN 100005
int A[MAXN];
long long BIT[MAXN];
int n;

int lsb(int i) { return i & -i; }
```

```
void build() {
    for (int i = 1; i <= n; i++) {
        BIT[i] += A[i];
        int parent = i + lsb(i);
        if (parent <= n)
            BIT[parent] += BIT[i];
    }
}

long long prefix_sum(int i) {
    long long s = 0;
    while (i > 0) {
        s += BIT[i];
        i -= lsb(i);
    }
    return s;
}

int main(void) {
    n = 5;
    int vals[6] = {0, 2, 1, 3, 4, 5}; // 1-indexed
    for (int i=1;i<=n;i++) A[i]=vals[i];
    build();
    printf("Prefix sum [1..3] = %lld\n", prefix_sum(3)); // expect 6
}
```

Python (1-indexed)

```
def build(A):
    n = len(A) - 1
    BIT = [0]*(n+1)
    for i in range(1, n+1):
        BIT[i] += A[i]
        parent = i + (i & -i)
        if parent <= n:
            BIT[parent] += BIT[i]
    return BIT

def prefix_sum(BIT, i):
    s = 0
    while i > 0:
```

```
        s += BIT[i]
        i -= (i & -i)
    return s

A = [0,2,1,3,4,5]  # 1-indexed
BIT = build(A)
print("BIT =", BIT[1:])
print("Sum[1..3] =", prefix_sum(BIT, 3))  # expect 6
```

Why It Matters

- Lightweight alternative to segment tree
- O(n) build, O(log n) query, O(log n) update
- Used in frequency tables, inversion count, prefix queries, cumulative histograms

A Gentle Proof (Why It Works)

Each index i contributes to at most log n BIT entries. Every BIT[i] stores sum of a disjoint range defined by LSB. Building with parent propagation ensures correct overlapping coverage.

Try It Yourself

1. Build BIT from [2, 1, 3, 4, 5] → query sum(3)=6
2. Update A[2]+=2 → prefix(3)=8
3. Compare with cumulative sum array for correctness

Test Cases

A (1-indexed)	Query	Expected
[2,1,3,4,5]	prefix(3)	6
[5,5,5,5]	prefix(4)	20
[1]	prefix(1)	1

Complexity

Operation	Time	Space
Build	O(n)	O(n)
Query	O(log n)	O(1)
Update	O(log n)	O(1)

A Fenwick Tree is the art of doing less, storing just enough to make prefix sums lightning-fast.

246 Fenwick Update

A Fenwick Tree (Binary Indexed Tree) supports point updates, adjusting a single element and efficiently reflecting that change across all relevant cumulative sums. The update propagates upward through parent indices determined by the Least Significant Bit (LSB).

What Problem Are We Solving?

Given a built Fenwick Tree, we want to perform an operation like:

```
A[pos] += delta
```

and keep all prefix sums `sum(0..i)` consistent.

Naive approach: update every prefix → O(n) Fenwick Tree: propagate through selected indices → O(log n)

How It Works (Plain Language)

In a Fenwick Tree, `BIT[i]` covers the range `(i - LSB(i) + 1) .. i`. So when we update `A[pos]`, we must add delta to all `BIT[i]` where `i` includes `pos` in its range.

Rule:

```
for (i = pos; i <= n; i += LSB(i))
    BIT[i] += delta
```

- LSB(i) jumps to the next index covering `pos`
- Stops when index exceeds `n`

Example

Array `A = [2, 1, 3, 4, 5]` (1-indexed) BIT built as `[2, 3, 3, 10, 5]`

Now perform update(2, +2) → A[2] = 3

Step	i	LSB(i)	BIT[i] Change	New BIT
1	2	2	BIT[2]+=2	[2,5,3,10,5]
2	4	4	BIT[4]+=2	[2,5,3,12,5]
3	8	stop	-	done

New prefix sums reflect updated array `[2,3,3,4,5]`

Check prefix(3) = 2+3+3=8

Step-by-Step Table

Prefix	Old Sum	New Sum
1	2	2
2	3	5
3	6	8
4	10	12
5	15	17

Tiny Code (Easy Versions)

C (Fenwick Update)

```c
#include <stdio.h>

#define MAXN 100005
long long BIT[MAXN];
int n;

int lsb(int i) { return i & -i; }

void update(int pos, int delta) {
    for (int i = pos; i <= n; i += lsb(i))
        BIT[i] += delta;
```

```
}

long long prefix_sum(int i) {
    long long s = 0;
    for (; i > 0; i -= lsb(i))
        s += BIT[i];
    return s;
}

int main(void) {
    n = 5;
    // Build from A = [2, 1, 3, 4, 5]
    BIT[1]=2; BIT[2]=3; BIT[3]=3; BIT[4]=10; BIT[5]=5;
    update(2, 2); // A[2]+=2
    printf("Sum [1..3] = %lld\n", prefix_sum(3)); // expect 8
}
```

Python (1-indexed)

```
def update(BIT, n, pos, delta):
    while pos <= n:
        BIT[pos] += delta
        pos += (pos & -pos)

def prefix_sum(BIT, pos):
    s = 0
    while pos > 0:
        s += BIT[pos]
        pos -= (pos & -pos)
    return s

# Example
BIT = [0,2,3,3,10,5]  # built from [2,1,3,4,5]
update(BIT, 5, 2, 2)
print("Sum [1..3] =", prefix_sum(BIT, 3))  # expect 8
```

Why It Matters

- Enables real-time data updates with fast prefix queries
- Simpler and more space-efficient than segment trees for sums
- Core of many algorithms: inversion count, frequency accumulation, order statistics

A Gentle Proof (Why It Works)

Each `BIT[i]` covers a fixed range `(i - LSB(i) + 1 .. i)`. If `pos` lies in that range, incrementing `BIT[i]` ensures correct future prefix sums. Since each update moves by LSB(i), at most log (n) steps occur.

Try It Yourself

1. Build BIT from `[2,1,3,4,5]` → update(2,+2)
2. Query prefix(3) → expect 8
3. Update(5, +5) → prefix(5) = 22
4. Chain multiple updates → verify incremental sums

Test Cases

A (1-indexed)	Update	Query	Expected
[2,1,3,4,5]	(2,+2)	sum[1..3]	8
[5,5,5,5]	(4,+1)	sum[1..4]	21
[1,2,3,4,5]	(5,-2)	sum[1..5]	13

Complexity

Operation	Time	Space
Update	O(log n)	O(1)
Query	O(log n)	O(1)
Build	O(n)	O(n)

Each update is a ripple that climbs the tree, keeping all prefix sums in perfect sync.

247 Fenwick Query

Once you've built or updated a Fenwick Tree (Binary Indexed Tree), you'll want to extract useful information, usually prefix sums. The query operation walks downward through the tree using index arithmetic, gathering partial sums along the way.

This simple yet powerful routine turns a linear prefix-sum scan into an elegant O(log n) solution.

What Problem Are We Solving?

We need to compute:

```
sum(1..i) = A[1] + A[2] + ... + A[i]
```

efficiently, after updates.

In a Fenwick Tree, each index holds the sum of a segment determined by its LSB (Least Significant Bit). By moving downward (subtracting LSB each step), we collect disjoint ranges that together cover `[1..i]`.

How It Works (Plain Language)

Each `BIT[i]` stores sum of range `(i - LSB(i) + 1 .. i)`. So to get the prefix sum, we combine all these segments by walking downward:

```
sum = 0
while i > 0:
    sum += BIT[i]
    i -= LSB(i)
```

Key Insight:

- Update: moves upward (`i += LSB(i)`)
- Query: moves downward (`i -= LSB(i)`)

Together, they mirror each other like yin and yang of cumulative logic.

Example

Suppose we have `A = [2, 3, 3, 4, 5]` (1-indexed), Built BIT = [2, 5, 3, 12, 5]

Let's compute `prefix_sum(5)`

Step	i	BIT[i]	LSB(i)	Accumulated Sum	Explanation
1	5	5	1	5	Add BIT[5] (A[5])
2	4	12	4	17	Add BIT[4] (A[1..4])
3	0	-	-	stop	done

`prefix_sum(5) = 17` matches `2+3+3+4+5=17`

Now try `prefix_sum(3)`

Step	i	BIT[i]	LSB(i)	Sum
1	3	3	1	3
2	2	5	2	8
3	0	-	-	stop

```
prefix_sum(3) = 8
```

Tiny Code (Easy Versions)

C (Fenwick Query)

```c
#include <stdio.h>

#define MAXN 100005
long long BIT[MAXN];
int n;

int lsb(int i) { return i & -i; }

long long prefix_sum(int i) {
    long long s = 0;
    while (i > 0) {
        s += BIT[i];
        i -= lsb(i);
    }
    return s;
}

int main(void) {
    n = 5;
    long long B[6] = {0,2,5,3,12,5}; // built BIT
    for (int i=1;i<=n;i++) BIT[i] = B[i];
    printf("Prefix sum [1..3] = %lld\n", prefix_sum(3)); // expect 8
    printf("Prefix sum [1..5] = %lld\n", prefix_sum(5)); // expect 17
}
```

Python (1-indexed)

```
def prefix_sum(BIT, i):
    s = 0
    while i > 0:
        s += BIT[i]
        i -= (i & -i)
    return s

BIT = [0,2,5,3,12,5]
print("sum[1..3] =", prefix_sum(BIT, 3))  # 8
print("sum[1..5] =", prefix_sum(BIT, 5))  # 17
```

Why It Matters

- Fast prefix sums after dynamic updates
- Essential for frequency tables, order statistics, inversion count
- Core to many competitive programming tricks (like "count less than k")

A Gentle Proof (Why It Works)

Each index `i` contributes to a fixed set of BIT nodes. When querying, we collect all BIT segments that together form `[1..i]`. The LSB ensures no overlap, each range is disjoint. Total steps = number of bits set in `i` = O(log n).

Try It Yourself

1. Build BIT from `[2,3,3,4,5]`
2. Query prefix_sum(3) → expect 8
3. Update(2,+2), query(3) → expect 10
4. Query prefix_sum(5) → confirm correctness

Test Cases

A (1-indexed)	Query	Expected
[2,3,3,4,5]	sum(3)	8
[2,3,3,4,5]	sum(5)	17
[1,2,3,4,5]	sum(4)	10

Complexity

Operation	Time	Space
Query	O(log n)	O(1)
Update	O(log n)	O(1)
Build	O(n)	O(n)

Fenwick query is the graceful descent, follow the bits down to gather every piece of the sum puzzle.

248 Segment Tree Merge

A Segment Tree can handle more than sums, it's a versatile structure that can merge results from two halves of a range using any associative operation (sum, min, max, gcd, etc.). The merge function is the heart of the segment tree: it tells us how to combine child nodes into a parent node.

What Problem Are We Solving?

We want to combine results from left and right child intervals into one parent result. Without merge logic, the tree can't aggregate data or answer queries.

For example:

- For sum queries → merge(a, b) = a + b
- For min queries → merge(a, b) = min(a, b)
- For gcd queries → merge(a, b) = gcd(a, b)

So the merge function defines *what the tree means*.

How It Works (Plain Language)

Each node represents a segment `[L, R]`. Its value is derived from its two children:

```
node = merge(left_child, right_child)
```

When you:

- Build: compute node from children recursively
- Query: merge partial overlaps

- Update: recompute affected nodes using merge

So merge is the unifying rule that glues the tree together.

Example (Sum Segment Tree)

Array `A = [2, 1, 3, 4]`

Node	Range	Left	Right	Merge (sum)
root	[1..4]	6	4	10
left	[1..2]	2	1	3
right	[3..4]	3	4	7

Each parent = sum(left, right)

Tree structure:

```
          [1..4]=10
         /         \
   [1..2]=3        [3..4]=7
   /    \          /     \
$$1]=2 [2]=1    [3]=3    [4]=4
```

Merge rule: `merge(a, b) = a + b`

Example (Min Segment Tree)

Array `A = [5, 2, 7, 1]` Merge rule: `min(a, b)`

Node	Range	Left	Right	Merge (min)
root	[1..4]	2	1	1
left	[1..2]	5	2	2
right	[3..4]	7	1	1

Result: root stores 1, the global minimum.

Tiny Code (Easy Versions)

C (Sum Segment Tree Merge)

```c
#include <stdio.h>
#define MAXN 100005

int A[MAXN], tree[4*MAXN];
int n;

int merge(int left, int right) {
    return left + right;
}

void build(int node, int l, int r) {
    if (l == r) {
        tree[node] = A[l];
        return;
    }
    int mid = (l + r) / 2;
    build(node*2, l, mid);
    build(node*2+1, mid+1, r);
    tree[node] = merge(tree[node*2], tree[node*2+1]);
}

int query(int node, int l, int r, int ql, int qr) {
    if (qr < l || ql > r) return 0; // neutral element
    if (ql <= l && r <= qr) return tree[node];
    int mid = (l + r) / 2;
    int left = query(node*2, l, mid, ql, qr);
    int right = query(node*2+1, mid+1, r, ql, qr);
    return merge(left, right);
}

int main(void) {
    n = 4;
    int vals[5] = {0, 2, 1, 3, 4};
    for (int i=1; i<=n; i++) A[i] = vals[i];
    build(1,1,n);
    printf("Sum [1..4] = %d\n", query(1,1,n,1,4)); // 10
    printf("Sum [2..3] = %d\n", query(1,1,n,2,3)); // 4
}
```

Python

```
def merge(a, b):
    return a + b  # define operation here

def build(arr, tree, node, l, r):
    if l == r:
        tree[node] = arr[l]
        return
    mid = (l + r) // 2
    build(arr, tree, 2*node, l, mid)
    build(arr, tree, 2*node+1, mid+1, r)
    tree[node] = merge(tree[2*node], tree[2*node+1])

def query(tree, node, l, r, ql, qr):
    if qr < l or ql > r:
        return 0  # neutral element for sum
    if ql <= l and r <= qr:
        return tree[node]
    mid = (l + r)//2
    left = query(tree, 2*node, l, mid, ql, qr)
    right = query(tree, 2*node+1, mid+1, r, ql, qr)
    return merge(left, right)

A = [0, 2, 1, 3, 4]
n = 4
tree = [0]*(4*n)
build(A, tree, 1, 1, n)
print("Sum[1..4] =", query(tree, 1, 1, n, 1, 4))  # 10
```

Why It Matters

- Merge is the "soul" of the segment tree, define merge, and you define the tree's purpose.
- Flexible across many tasks: sums, min/max, GCD, XOR, matrix multiplication.
- Unified pattern: build, query, update all rely on the same operation.

A Gentle Proof (Why It Works)

Segment tree works by divide and conquer. If an operation is associative (like +, min, max, gcd), merging partial results yields the same answer as computing on the whole range. So as long as `merge(a, b)` = `merge(b, a)` and associative, correctness follows.

Try It Yourself

1. Replace merge with `min(a,b)` → build min segment tree
2. Replace merge with `max(a,b)` → build max segment tree
3. Replace merge with `__gcd(a,b)` → build gcd tree
4. Test `query(2,3)` after changing merge rule

Test Cases

A	Operation	Query	Expected
[2,1,3,4]	sum	[1..4]	10
[5,2,7,1]	min	[1..4]	1
[3,6,9,12]	gcd	[2..4]	3

Complexity

Operation	Time	Space
Build	O(n)	O(n)
Query	O(log n)	O(n)
Update	O(log n)	O(n)

A merge function is the heartbeat of every segment tree, once you define it, your tree learns what "combine" means.

249 Persistent Segment Tree

A Persistent Segment Tree is a magical structure that lets you time-travel. Instead of overwriting nodes on update, it creates new versions while preserving old ones. Each update returns a new root, giving you full history and O(log n) access to every version.

What Problem Are We Solving?

We need a data structure that supports:

- Point updates without losing past state
- Range queries on any historical version

Use cases:

- Undo/rollback systems
- Versioned databases
- Offline queries ("What was sum[1..3] after the 2nd update?")

Each version is immutable, perfect for functional programming or auditability.

How It Works (Plain Language)

A persistent segment tree clones only nodes along the path from root to updated leaf. All other nodes are shared.

For each update:

1. Create a new root.
2. Copy nodes along the path to the changed index.
3. Reuse unchanged subtrees.

Result: O(log n) memory per version, not O(n).

Example

Array `A = [1, 2, 3, 4]`

Version 0: built tree for `[1, 2, 3, 4]`

- sum = 10

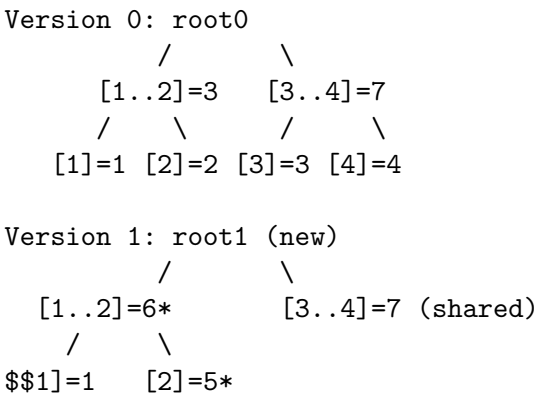
Update A[2] = 5

- Create Version 1, copy path to A[2]
- New sum = 1 + 5 + 3 + 4 = 13

Version	A	Sum(1..4)	Sum(1..2)
0	[1,2,3,4]	10	3
1	[1,5,3,4]	13	6

Both versions exist side by side. Version 0 is unchanged. Version 1 reflects new value.

Visualization



Asterisks mark newly created nodes.

Tiny Code (Easy Version)

C (Pointer-based, sum tree)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int val;
    struct Node *left, *right;
} Node;

Node* build(int arr[], int l, int r) {
    Node* node = malloc(sizeof(Node));
    if (l == r) {
        node->val = arr[l];
        node->left = node->right = NULL;
        return node;
    }
    int mid = (l + r) / 2;
    node->left = build(arr, l, mid);
    node->right = build(arr, mid+1, r);
    node->val = node->left->val + node->right->val;
    return node;
}
```

```c
Node* update(Node* prev, int l, int r, int pos, int new_val) {
    Node* node = malloc(sizeof(Node));
    if (l == r) {
        node->val = new_val;
        node->left = node->right = NULL;
        return node;
    }
    int mid = (l + r) / 2;
    if (pos <= mid) {
        node->left = update(prev->left, l, mid, pos, new_val);
        node->right = prev->right;
    } else {
        node->left = prev->left;
        node->right = update(prev->right, mid+1, r, pos, new_val);
    }
    node->val = node->left->val + node->right->val;
    return node;
}

int query(Node* node, int l, int r, int ql, int qr) {
    if (qr < l || ql > r) return 0;
    if (ql <= l && r <= qr) return node->val;
    int mid = (l + r)/2;
    return query(node->left, l, mid, ql, qr)
         + query(node->right, mid+1, r, ql, qr);
}

int main(void) {
    int A[5] = {0,1,2,3,4}; // 1-indexed
    Node* root0 = build(A, 1, 4);
    Node* root1 = update(root0, 1, 4, 2, 5);
    printf("v0 sum[1..2]=%d\n", query(root0,1,4,1,2)); // 3
    printf("v1 sum[1..2]=%d\n", query(root1,1,4,1,2)); // 6
}
```

Python (Recursive, sum tree)

```python
class Node:
    def __init__(self, val=0, left=None, right=None):
        self.val = val
        self.left = left
        self.right = right
```

```
def build(arr, l, r):
    if l == r:
        return Node(arr[l])
    mid = (l + r) // 2
    left = build(arr, l, mid)
    right = build(arr, mid+1, r)
    return Node(left.val + right.val, left, right)

def update(prev, l, r, pos, val):
    if l == r:
        return Node(val)
    mid = (l + r) // 2
    if pos <= mid:
        return Node(prev.val - prev.left.val + val,
                    update(prev.left, l, mid, pos, val),
                    prev.right)
    else:
        return Node(prev.val - prev.right.val + val,
                    prev.left,
                    update(prev.right, mid+1, r, pos, val))

def query(node, l, r, ql, qr):
    if qr < l or ql > r: return 0
    if ql <= l and r <= qr: return node.val
    mid = (l + r)//2
    return query(node.left, l, mid, ql, qr) + query(node.right, mid+1, r, ql, qr)

A = [0,1,2,3,4]
root0 = build(A, 1, 4)
root1 = update(root0, 1, 4, 2, 5)
print("v0 sum[1..2] =", query(root0, 1, 4, 1, 2))  # 3
print("v1 sum[1..2] =", query(root1, 1, 4, 1, 2))  # 6
```

Why It Matters

- Immutable versions → ideal for undo systems, snapshots, persistent databases
- Saves memory (O(log n) per version)
- Each version is fully functional and independent

A Gentle Proof (Why It Works)

Each update affects O(log n) nodes. By copying only those nodes, we maintain O(log n) new memory. Because all old nodes remain referenced, no data is lost. Thus, each version is consistent and immutable.

Try It Yourself

1. Build version 0 with `[1,2,3,4]`
2. Update(2,5) → version 1
3. Query sum(1,4) in both versions → 10, 13
4. Create version 2 by update(3,1)
5. Query sum(1,3) in each version

Test Cases

Version	A	Query	Expected
0	[1,2,3,4]	sum[1..2]	3
1	[1,5,3,4]	sum[1..2]	6
2	[1,5,1,4]	sum[1..3]	7

Complexity

Operation	Time	Space (per version)
Build	O(n)	O(n)
Update	O(log n)	O(log n)
Query	O(log n)	O(1)

Each version of a persistent segment tree is a snapshot in time, perfect memory of every past, with no cost of forgetting.

250 2D Segment Tree

A 2D Segment Tree extends the classic segment tree into two dimensions, perfect for handling range queries over matrices, such as sums, minimums, or maximums across subrectangles.

It's the data structure that lets you ask:

"What's the sum of elements in the rectangle (x1, y1) to (x2, y2)?" and still answer in $O(\log^2 n)$ time.

What Problem Are We Solving?

We want to perform two operations efficiently on a 2D grid:

1. Range Query: sum/min/max over a submatrix
2. Point Update: modify one element and reflect the change

Naive approach $\rightarrow O(n^2)$ per query 2D Segment Tree $\rightarrow O(\log^2 n)$ per query and update

How It Works (Plain Language)

Think of a 2D segment tree as a segment tree of segment trees.

1. Outer tree partitions rows.
2. Each node of the outer tree holds an inner segment tree for its rows.

Each node thus represents a rectangle in the matrix.

At build time:

- Combine children horizontally and vertically using a merge rule (like sum).

At query time:

- Combine answers from nodes overlapping the query rectangle.

Example

Matrix A (3×3):

	y=1	y=2	y=3
x=1	2	1	3
x=2	4	5	6
x=3	7	8	9

Query rectangle `(1,1)` to `(2,2)` $\rightarrow 2 + 1 + 4 + 5 = 12$

Key Idea

For each row range, build a column segment tree. For each parent node (row range), merge children column trees:

```
tree[x][y] = merge(tree[2*x][y], tree[2*x+1][y])
```

Example Walkthrough (Sum Tree)

1. Build row segment tree
2. Inside each row node, build column segment tree
3. To query rectangle `(x1,y1)` to `(x2,y2)`:
    - Query over x-range → merge vertical results
    - Inside each x-node, query y-range → merge horizontal results

Tiny Code (Easy Version)

Python (Sum 2D Segment Tree)

```
class SegmentTree2D:
    def __init__(self, mat):
        self.n = len(mat)
        self.m = len(mat[0])
        self.tree = [[0]*(4*self.m) for _ in range(4*self.n)]
        self.mat = mat
        self.build_x(1, 0, self.n-1)

    def merge(self, a, b):
        return a + b  # sum merge

    # build column tree for a fixed row range
    def build_y(self, nodex, lx, rx, nodey, ly, ry):
        if ly == ry:
            if lx == rx:
                self.tree[nodex][nodey] = self.mat[lx][ly]
            else:
                self.tree[nodex][nodey] = self.merge(
                    self.tree[2*nodex][nodey], self.tree[2*nodex+1][nodey]
                )
```

```
            return
        midy = (ly + ry)//2
        self.build_y(nodex, lx, rx, 2*nodey, ly, midy)
        self.build_y(nodex, lx, rx, 2*nodey+1, midy+1, ry)
        self.tree[nodex][nodey] = self.merge(
            self.tree[nodex][2*nodey], self.tree[nodex][2*nodey+1]
        )

    # build row tree
    def build_x(self, nodex, lx, rx):
        if lx != rx:
            midx = (lx + rx)//2
            self.build_x(2*nodex, lx, midx)
            self.build_x(2*nodex+1, midx+1, rx)
        self.build_y(nodex, lx, rx, 1, 0, self.m-1)

    def query_y(self, nodex, nodey, ly, ry, qly, qry):
        if qry < ly or qly > ry: return 0
        if qly <= ly and ry <= qry:
            return self.tree[nodex][nodey]
        midy = (ly + ry)//2
        return self.merge(
            self.query_y(nodex, 2*nodey, ly, midy, qly, qry),
            self.query_y(nodex, 2*nodey+1, midy+1, ry, qly, qry)
        )

    def query_x(self, nodex, lx, rx, qlx, qrx, qly, qry):
        if qrx < lx or qlx > rx: return 0
        if qlx <= lx and rx <= qrx:
            return self.query_y(nodex, 1, 0, self.m-1, qly, qry)
        midx = (lx + rx)//2
        return self.merge(
            self.query_x(2*nodex, lx, midx, qlx, qrx, qly, qry),
            self.query_x(2*nodex+1, midx+1, rx, qlx, qrx, qly, qry)
        )

    def query(self, x1, y1, x2, y2):
        return self.query_x(1, 0, self.n-1, x1, x2, y1, y2)

# Example
A = [
    [2, 1, 3],
```

```
    [4, 5, 6],
    [7, 8, 9]
$$
seg2d = SegmentTree2D(A)
print(seg2d.query(0, 0, 1, 1))  # expect 12
```

Why It Matters

- Supports 2D queries with $\log^2$ complexity
- Works for sum, min, max, gcd, XOR
- A foundation for advanced 2D data structures (Fenwick 2D, KD-trees, etc.)

A Gentle Proof (Why It Works)

Segment tree correctness relies on associativity. In 2D, we extend this property across both dimensions. Each node represents a rectangular region; merging children yields correct aggregate for parent.

Try It Yourself

1. Build from 3×3 matrix
2. Query `(0,0)-(2,2)` → full sum
3. Query `(1,1)-(2,2)` → bottom-right 5+6+8+9=28
4. Modify A[1][2]=10, rebuild, recheck sum

Test Cases

Matrix	Query	Result
[[2,1,3],[4,5,6],[7,8,9]]	(0,0)-(1,1)	12
[[2,1,3],[4,5,6],[7,8,9]]	(1,1)-(2,2)	28
[[1,2],[3,4]]	(0,0)-(1,1)	10

Operation	Time	Space

Complexity

Operation	Time	Space
Build	$O(n \cdot m \cdot \log n \cdot \log m)$	$O(n \cdot m)$
Query	$O(\log^2 n)$	$O(1)$
Update	$O(\log^2 n)$	$O(1)$

A 2D segment tree is your grid-wise superpower, merging rectangles like puzzle pieces, one log at a time.

Section 26. Disjoint Set Union

251 Make-Set

The Make-Set operation is the starting point of the Disjoint Set Union (DSU), also known as Union-Find, a fundamental data structure for managing partitions of elements into disjoint sets.

Each element begins in its own set, serving as its own parent. Later operations (`Find` and `Union`) will merge and track relationships among them efficiently.

What Problem Are We Solving?

We need a way to represent a collection of disjoint sets, groups that don't overlap, while supporting these operations:

1. Make-Set(x): create a new set containing only `x`
2. Find(x): find representative (leader) of x's set
3. Union(x, y): merge sets containing x and y

This structure is the backbone of many graph algorithms like Kruskal's MST, connected components, and clustering.

How It Works (Plain Language)

Initially, each element is its own parent, a self-loop. We store two arrays (or maps):

- `parent[x]` → points to x's parent (initially itself)
- `rank[x]` or `size[x]` → helps balance unions later

So:

```
parent[x] = x
rank[x] = 0
```

Each element is an isolated tree. Over time, unions connect trees.

Example

Initialize `n = 5` elements: `{1, 2, 3, 4, 5}`

x	parent[x]	rank[x]	Meaning
1	1	0	own leader
2	2	0	own leader
3	3	0	own leader
4	4	0	own leader
5	5	0	own leader

After all `Make-Set`, each element is in its own group:

```
{1}, {2}, {3}, {4}, {5}
```

Visualization

```
1   2   3   4   5
↑   ↑   ↑   ↑   ↑
|   |   |   |   |
self self self self self
```

Each node points to itself, five separate trees.

Tiny Code (Easy Versions)

C Implementation

```c
#include <stdio.h>

#define MAXN 1000

int parent[MAXN];
int rank_[MAXN];

void make_set(int v) {
    parent[v] = v;   // self parent
    rank_[v] = 0;    // initial rank
}

int main(void) {
    int n = 5;
    for (int i = 1; i <= n; i++)
        make_set(i);

    printf("Initial sets:\n");
    for (int i = 1; i <= n; i++)
        printf("Element %d: parent=%d, rank=%d\n", i, parent[i], rank_[i]);
    return 0;
}
```

Python Implementation

```python
def make_set(x, parent, rank):
    parent[x] = x
    rank[x] = 0

n = 5
parent = {}
rank = {}

for i in range(1, n+1):
    make_set(i, parent, rank)

print("Parent:", parent)
print("Rank:", rank)
# Parent: {1:1, 2:2, 3:3, 4:4, 5:5}
```

Why It Matters

- The foundation of Disjoint Set Union
- Enables efficient graph algorithms
- A building block for Union by Rank and Path Compression
- Every DSU begins with `Make-Set`

A Gentle Proof (Why It Works)

Each element begins as a singleton. Since no pointers cross between elements, sets are disjoint. Subsequent `Union` operations preserve this property by merging trees, never duplicating nodes.

Thus, `Make-Set` guarantees:

- Each new node is independent
- Parent pointers form valid forests

Try It Yourself

1. Initialize `{1..5}` with `Make-Set`
2. Print parent and rank arrays
3. Add `Union(1,2)` and check parent changes
4. Verify all parent[x] = x before unions

Test Cases

Input	Operation	Expected Output
n=3	Make-Set(1..3)	parent = [1,2,3]
n=5	Make-Set(1..5)	rank = [0,0,0,0,0]

Complexity

Operation	Time	Space
Make-Set	O(1)	O(1)
Find	O((n)) with compression	O(1)
Union	O((n)) with rank	O(1)

The `Make-Set` step is your first move in the DSU dance, simple, constant time, and crucial for what follows.

252 Find

The Find operation is the heart of the Disjoint Set Union (DSU), also known as Union-Find. It locates the representative (leader) of the set containing a given element. Every element in the same set shares the same leader, this is how DSU identifies which elements belong together.

To make lookups efficient, `Find` uses a clever optimization called Path Compression, which flattens the structure of the tree so future queries become nearly constant time.

What Problem Are We Solving?

Given an element `x`, we want to determine which set it belongs to. Each set is represented by a root node (the leader).

We maintain a `parent[]` array such that:

- `parent[x] = x` if `x` is the root (leader)
- otherwise `parent[x] = parent of x`

The `Find(x)` operation recursively follows `parent[x]` pointers until it reaches the root.

How It Works (Plain Language)

Think of each set as a tree, where the root is the representative.

For example:

```
1 ← 2 ← 3    4 ← 5
```

means `{1,2,3}` is one set, `{4,5}` is another. The Find(3) operation follows `3→2→1`, discovering 1 is the root.

Path Compression flattens the tree by pointing every node directly to the root, reducing depth and speeding up future finds.

After compression:

```
1 ← 2   1 ← 3
4 ← 5
```

Now `Find(3)` is O(1).

Example

Start:

x	parent[x]	rank[x]
1	1	1
2	1	0
3	2	0
4	4	0
5	4	0

Perform `Find(3)`:

1. 3 → parent[3] = 2
2. 2 → parent[2] = 1
3. 1 → root found

Path compression rewires `parent[3] = 1`

Result:

x	parent[x]
1	1
2	1
3	1
4	4
5	4

Visualization

Before compression:

```
1
↑
2
↑
3
```

After compression:

```
1
↑ ↑
2 3
```

Now all nodes point directly to root `1`.

Tiny Code (Easy Versions)

C Implementation

```c
#include <stdio.h>

#define MAXN 1000
int parent[MAXN];
int rank_[MAXN];

void make_set(int v) {
    parent[v] = v;
    rank_[v] = 0;
}

int find_set(int v) {
    if (v == parent[v])
        return v;
    // Path compression
    parent[v] = find_set(parent[v]);
    return parent[v];
}

int main(void) {
    int n = 5;
    for (int i = 1; i <= n; i++) make_set(i);
    parent[2] = 1;
    parent[3] = 2;
    printf("Find(3) before: %d\n", parent[3]);
    printf("Root of 3: %d\n", find_set(3));
    printf("Find(3) after: %d\n", parent[3]);
}
```

Python Implementation

```
def make_set(x, parent, rank):
    parent[x] = x
    rank[x] = 0

def find_set(x, parent):
    if parent[x] != x:
        parent[x] = find_set(parent[x], parent)  # Path compression
    return parent[x]

n = 5
parent = {}
rank = {}
for i in range(1, n+1):
    make_set(i, parent, rank)

parent[2] = 1
parent[3] = 2

print("Find(3) before:", parent)
print("Root of 3:", find_set(3, parent))
print("Find(3) after:", parent)
```

Why It Matters

- Enables O((n)) almost-constant-time queries
- Fundamental for Union-Find efficiency
- Reduces tree height dramatically
- Used in graph algorithms (Kruskal, connected components, etc.)

A Gentle Proof (Why It Works)

Every set is a rooted tree. Without compression, a sequence of unions could build a deep chain. With path compression, each `Find` flattens paths, ensuring amortized constant time per operation (Ackermann-inverse time).

So after repeated operations, DSU trees become very shallow.

Try It Yourself

1. Initialize `{1..5}`

2. Set `parent[2]=1, parent[3]=2`
3. Call `Find(3)` and observe compression
4. Check `parent[3] == 1` after

Test Cases

parent before	Find(x)	parent after
[1,1,2]	Find(3)	[1,1,1]
[1,2,3,4,5]	Find(5)	[1,2,3,4,5]
[1,1,1,1,1]	Find(3)	[1,1,1,1,1]

Complexity

Operation	Time (Amortized)	Space
Find	O((n))	O(1)
Make-Set	O(1)	O(1)
Union	O((n))	O(1)

The Find operation is your compass, it always leads you to the leader of your set, and with path compression, it gets faster every step.

253 Union

The Union operation is what ties the Disjoint Set Union (DSU) together. After initializing sets with `Make-Set` and locating leaders with `Find`, `Union` merges two disjoint sets into one, a cornerstone of dynamic connectivity.

To keep the trees shallow and efficient, we combine it with heuristics like Union by Rank or Union by Size.

What Problem Are We Solving?

We want to merge the sets containing two elements `a` and `b`.

If `a` and `b` belong to different sets, their leaders (`Find(a)` and `Find(b)`) are different. The Union operation connects these leaders, ensuring both now share the same representative.

We must do it efficiently, no unnecessary tree height. That's where Union by Rank comes in.

How It Works (Plain Language)

1. Find roots of both elements:

   ```
   rootA = Find(a)
   rootB = Find(b)
   ```

2. If they're already equal → same set, no action.
3. Otherwise, attach the shorter tree under the taller one:
   - If `rank[rootA] < rank[rootB]`: `parent[rootA] = rootB`
   - Else if `rank[rootA] > rank[rootB]`: `parent[rootB] = rootA`
   - Else: `parent[rootB] = rootA`, and `rank[rootA]++`

This keeps the resulting forest balanced, maintaining O((n)) time for operations.

Example

Initial sets: `{1}, {2}, {3}, {4}`

x	parent[x]	rank[x]
1	1	0
2	2	0
3	3	0
4	4	0

Perform `Union(1,2)` → attach 2 under 1

```
parent[2] = 1
rank[1] = 1
```

Now sets: `{1,2}, {3}, {4}`

Perform `Union(3,4)` → attach 4 under 3 Sets: `{1,2}, {3,4}`

Then `Union(2,3)` → merge leaders (1 and 3) Attach lower rank under higher (both rank 1 → tie) → attach 3 under 1, rank[1] = 2

Final parent table:

x	parent[x]	rank[x]
1	1	2
2	1	0
3	1	1
4	3	0

Now all are connected under root 1.

Visualization

Start:

```
1   2   3   4
```

Union(1,2):

```
  1
  |
  2
```

Union(3,4):

```
  3
  |
  4
```

Union(2,3):

```
    1
  / | \
 2  3  4
```

All connected under 1.

Tiny Code (Easy Versions)

C Implementation

```c
#include <stdio.h>

#define MAXN 1000
int parent[MAXN];
int rank_[MAXN];

void make_set(int v) {
    parent[v] = v;
    rank_[v] = 0;
}

int find_set(int v) {
    if (v == parent[v]) return v;
    return parent[v] = find_set(parent[v]); // path compression
}

void union_sets(int a, int b) {
    a = find_set(a);
    b = find_set(b);
    if (a != b) {
        if (rank_[a] < rank_[b])
            parent[a] = b;
        else if (rank_[a] > rank_[b])
            parent[b] = a;
        else {
            parent[b] = a;
            rank_[a]++;
        }
    }
}

int main(void) {
    for (int i=1;i<=4;i++) make_set(i);
    union_sets(1,2);
    union_sets(3,4);
    union_sets(2,3);
    for (int i=1;i<=4;i++)
        printf("Element %d: parent=%d, rank=%d\n", i, parent[i], rank_[i]);
}
```

Python Implementation

```
def make_set(x, parent, rank):
    parent[x] = x
    rank[x] = 0

def find_set(x, parent):
    if parent[x] != x:
        parent[x] = find_set(parent[x], parent)
    return parent[x]

def union_sets(a, b, parent, rank):
    a = find_set(a, parent)
    b = find_set(b, parent)
    if a != b:
        if rank[a] < rank[b]:
            parent[a] = b
        elif rank[a] > rank[b]:
            parent[b] = a
        else:
            parent[b] = a
            rank[a] += 1

n = 4
parent = {}
rank = {}
for i in range(1, n+1): make_set(i, parent, rank)
union_sets(1,2,parent,rank)
union_sets(3,4,parent,rank)
union_sets(2,3,parent,rank)
print("Parent:", parent)
print("Rank:", rank)
```

Why It Matters

- Core operation in Union-Find
- Enables dynamic set merging efficiently
- Essential for graph algorithms:
  - Kruskal's Minimum Spanning Tree
  - Connected Components
  - Cycle Detection

Combining `Union by Rank` and `Path Compression` yields near-constant performance for huge datasets.

A Gentle Proof (Why It Works)

`Union` ensures disjointness:

- Only merges sets with different roots
- Maintains one leader per set `Union by Rank` keeps trees balanced → tree height log n With path compression, amortized cost per operation is (n), effectively constant for all practical n.

Try It Yourself

1. Create 5 singleton sets
2. Union(1,2), Union(3,4), Union(2,3)
3. Verify all share same root
4. Inspect ranks before/after unions

Test Cases

Operations	Expected Sets	Roots
Make-Set(1..4)	{1},{2},{3},{4}	[1,2,3,4]
Union(1,2)	{1,2}	[1,1,3,4]
Union(3,4)	{3,4}	[1,1,3,3]
Union(2,3)	{1,2,3,4}	[1,1,1,1]

Complexity

Operation	Time (Amortized)	Space
Union	O((n))	O(1)
Find	O((n))	O(1)
Make-Set	O(1)	O(1)

`Union` is the handshake between sets, careful, balanced, and lightning-fast when combined with smart optimizations.

254 Union by Rank

Union by Rank is a balancing strategy used in the Disjoint Set Union (DSU) structure to keep trees shallow. When merging two sets, instead of arbitrarily attaching one root under another, we attach the shorter tree (lower rank) under the taller tree (higher rank).

This small trick, combined with Path Compression, gives DSU its legendary near-constant performance, almost O(1) per operation.

What Problem Are We Solving?

Without balancing, repeated `Union` operations might create tall chains like:

```
1 ← 2 ← 3 ← 4 ← 5
```

In the worst case, `Find(x)` becomes O(n).

Union by Rank prevents this by maintaining a rough measure of tree height. Each `rank[root]` tracks the *approximate height* of its tree.

When merging:

- Attach the lower rank tree under the higher rank tree.
- If ranks are equal, choose one as parent and increase its rank by 1.

How It Works (Plain Language)

Each node `x` has:

- `parent[x]` → leader pointer
- `rank[x]` → estimate of tree height

When performing `Union(a, b)`:

1. `rootA = Find(a)`
2. `rootB = Find(b)`
3. If ranks differ, attach smaller under larger:

```
    if rank[rootA] < rank[rootB]:
        parent[rootA] = rootB
    else if rank[rootA] > rank[rootB]:
        parent[rootB] = rootA
    else:
        parent[rootB] = rootA
        rank[rootA] += 1
```

This ensures the tree grows only when necessary.

Example

Start with `{1}, {2}, {3}, {4}` All have `rank = 0`

Perform `Union(1,2)` → same rank → attach 2 under 1, increment rank[1]=1

```
1
|
2
```

Perform `Union(3,4)` → same rank → attach 4 under 3, increment rank[3]=1

```
3
|
4
```

Now Union(1,3) → both roots rank=1 → tie → attach 3 under 1, rank[1]=2

```
   1(rank=2)
  / \
 2   3
     |
     4
```

Tree height stays small, well-balanced.

Element	Parent	Rank
1	1	2
2	1	0
3	1	1

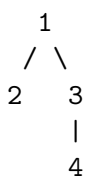
Element	Parent	Rank
4	3	0

Visualization

Before balancing:

```
1 ← 2 ← 3 ← 4
```

After union by rank:



Balanced and efficient

Tiny Code (Easy Versions)

C Implementation

```c
#include <stdio.h>

#define MAXN 1000
int parent[MAXN];
int rank_[MAXN];

void make_set(int v) {
    parent[v] = v;
    rank_[v] = 0;
}

int find_set(int v) {
    if (v == parent[v]) return v;
    return parent[v] = find_set(parent[v]); // Path compression
}
```

```
void union_by_rank(int a, int b) {
    a = find_set(a);
    b = find_set(b);
    if (a != b) {
        if (rank_[a] < rank_[b]) parent[a] = b;
        else if (rank_[a] > rank_[b]) parent[b] = a;
        else {
            parent[b] = a;
            rank_[a]++;
        }
    }
}

int main(void) {
    for (int i=1;i<=4;i++) make_set(i);
    union_by_rank(1,2);
    union_by_rank(3,4);
    union_by_rank(2,3);
    for (int i=1;i<=4;i++)
        printf("Element %d: parent=%d rank=%d\n", i, parent[i], rank_[i]);
}
```

Python Implementation

```
def make_set(x, parent, rank):
    parent[x] = x
    rank[x] = 0

def find_set(x, parent):
    if parent[x] != x:
        parent[x] = find_set(parent[x], parent)
    return parent[x]

def union_by_rank(a, b, parent, rank):
    a = find_set(a, parent)
    b = find_set(b, parent)
    if a != b:
        if rank[a] < rank[b]:
            parent[a] = b
        elif rank[a] > rank[b]:
            parent[b] = a
        else:
```

```
            parent[b] = a
            rank[a] += 1

n = 4
parent = {}
rank = {}
for i in range(1, n+1): make_set(i, parent, rank)
union_by_rank(1,2,parent,rank)
union_by_rank(3,4,parent,rank)
union_by_rank(2,3,parent,rank)
print("Parent:", parent)
print("Rank:", rank)
```

Why It Matters

- Keeps trees balanced and shallow
- Ensures amortized O((n)) performance
- Critical for massive-scale connectivity problems
- Used in Kruskal's MST, Union-Find with rollback, and network clustering

A Gentle Proof (Why It Works)

The rank grows only when two trees of equal height merge. Thus, the height of any tree is bounded by log n. Combining this with Path Compression, the amortized complexity per operation becomes O((n)), where (n) (inverse Ackermann function) < 5 for all practical n.

Try It Yourself

1. Create 8 singleton sets
2. Perform unions in sequence: (1,2), (3,4), (1,3), (5,6), (7,8), (5,7), (1,5)
3. Observe ranks and parent structure

Test Cases

Operation	Result (Parent Array)	Rank
Union(1,2)	[1,1,3,4]	[1,0,0,0]
Union(3,4)	[1,1,3,3]	[1,0,1,0]
Union(2,3)	[1,1,1,3]	[2,0,1,0]

Complexity

Operation	Time (Amortized)	Space
Union by Rank	O((n))	O(1)
Find	O((n))	O(1)
Make-Set	O(1)	O(1)

Union by Rank is the art of merging gracefully, always lifting smaller trees, keeping your forest light, flat, and fast.

255 Path Compression

Path Compression is the secret sauce that makes Disjoint Set Union (DSU) lightning fast. Every time you perform a `Find` operation, it *flattens* the structure by making each visited node point directly to the root. Over time, this transforms deep trees into almost flat structures, turning expensive lookups into near-constant time.

What Problem Are We Solving?

In a basic DSU, `Find(x)` follows parent pointers up the tree until it reaches the root. Without compression, frequent unions can form long chains:

```
1 ← 2 ← 3 ← 4 ← 5
```

A `Find(5)` would take 5 steps. Multiply this over many queries, and performance tanks.

Path Compression fixes this inefficiency by *rewiring* all nodes on the search path to the root directly, effectively flattening the tree.

How It Works (Plain Language)

Whenever we call `Find(x)`, we recursively find the root, then make every node along the way point directly to that root.

Pseudocode:

```
Find(x):
    if parent[x] != x:
        parent[x] = Find(parent[x])
    return parent[x]
```

Now, future lookups for `x` and its descendants become instant.

Example

Start with a chain:

```
1 ← 2 ← 3 ← 4 ← 5
```

Perform `Find(5)`:

1. `Find(5)` calls `Find(4)`
2. `Find(4)` calls `Find(3)`
3. `Find(3)` calls `Find(2)`
4. `Find(2)` calls `Find(1)` (root)
5. On the way back, each node gets updated:

   ```
   parent[5] = 1
   parent[4] = 1
   parent[3] = 1
   parent[2] = 1
   ```

After compression, structure becomes flat:

```
1
  2
  3
  4
  5
```

Element	Parent Before	Parent After
1	1	1
2	1	1
3	2	1
4	3	1
5	4	1

Next call `Find(5)` → single step.

Visualization

Before compression:

```
1 ← 2 ← 3 ← 4 ← 5
```

After compression:

```
1
 2
 3
 4
 5
```

Tiny Code (Easy Versions)

C Implementation

```c
#include <stdio.h>

#define MAXN 100
int parent[MAXN];

void make_set(int v) {
    parent[v] = v;
}

int find_set(int v) {
    if (v != parent[v])
        parent[v] = find_set(parent[v]); // Path compression
    return parent[v];
}

void union_sets(int a, int b) {
    a = find_set(a);
    b = find_set(b);
    if (a != b)
        parent[b] = a;
}

int main(void) {
```

```
    for (int i = 1; i <= 5; i++) make_set(i);
    union_sets(1, 2);
    union_sets(2, 3);
    union_sets(3, 4);
    union_sets(4, 5);
    find_set(5); // compress path
    for (int i = 1; i <= 5; i++)
        printf("Element %d → Parent %d\n", i, parent[i]);
}
```

Python Implementation

```
def make_set(x, parent):
    parent[x] = x

def find_set(x, parent):
    if parent[x] != x:
        parent[x] = find_set(parent[x], parent)
    return parent[x]

def union_sets(a, b, parent):
    a = find_set(a, parent)
    b = find_set(b, parent)
    if a != b:
        parent[b] = a

parent = {}
for i in range(1, 6):
    make_set(i, parent)
union_sets(1, 2, parent)
union_sets(2, 3, parent)
union_sets(3, 4, parent)
union_sets(4, 5, parent)
find_set(5, parent)
print("Parent map after compression:", parent)
```

Why It Matters

- Speeds up Find drastically by flattening trees.
- Pairs beautifully with Union by Rank.
- Achieves amortized O((n)) performance.

- Essential in graph algorithms like Kruskal's MST, connectivity checks, and dynamic clustering.

A Gentle Proof (Why It Works)

Path Compression ensures each node's parent jumps directly to the root. Each node's depth decreases exponentially with every `Find`. After a few operations, trees become almost flat, and each subsequent `Find` becomes O(1).

Combining with Union by Rank:

> Every operation (Find or Union) becomes O((n)), where (n) is the inverse Ackermann function (smaller than 5 for any practical input).

Try It Yourself

1. Create 6 singleton sets.
2. Perform unions: (1,2), (2,3), (3,4), (4,5), (5,6).
3. Call `Find(6)` and print parent map before and after.
4. Observe how the chain flattens.
5. Measure calls count difference before and after compression.

Test Cases

Operation Sequence	Parent Map After	Tree Depth
No Compression	`{1:1, 2:1, 3:2, 4:3, 5:4}`	4
After Find(5)	`{1:1, 2:1, 3:1, 4:1, 5:1}`	1
After Find(3)	`{1:1, 2:1, 3:1, 4:1, 5:1}`	1

Complexity

Operation	Time (Amortized)	Space
Find with Path Compression	O((n))	O(1)
Union (with rank)	O((n))	O(1)
Make-Set	O(1)	O(1)

Path Compression is the flattening spell of DSU, once cast, your sets become sleek, your lookups swift, and your unions unstoppable.

256 DSU with Rollback

DSU with Rollback extends the classic Disjoint Set Union to support *undoing* recent operations. This is vital in scenarios where you need to explore multiple states, like backtracking algorithms, dynamic connectivity queries, or offline problems where unions might need to be reversed.

Instead of destroying past states, this version *remembers* what changed and can roll back to a previous version in constant time.

What Problem Are We Solving?

Standard DSU operations (`Find`, `Union`) mutate the structure, parent pointers and ranks get updated, so you can't easily go back.

But what if you're exploring a search tree or processing offline queries where you need to:

- Add an edge (Union),
- Explore a path,
- Then revert to the previous structure?

A rollback DSU lets you undo changes, perfect for divide-and-conquer over time, Mo's algorithm on trees, and offline dynamic graphs.

How It Works (Plain Language)

The idea is simple:

- Every time you modify the DSU, record what you changed on a stack.
- When you need to revert, pop from the stack and undo the last operation.

Operations to track:

- When `parent[b]` changes, store `(b, old_parent)`
- When `rank[a]` changes, store `(a, old_rank)`

You never perform path compression, because it's not easily reversible. Instead, rely on union by rank for efficiency.

Example

Let's build sets `{1}, {2}, {3}, {4}`

Perform:

1. `Union(1,2)` → attach 2 under 1
    - Push `(2, parent=2, rank=None)`
2. `Union(3,4)` → attach 4 under 3
    - Push `(4, parent=4, rank=None)`
3. `Union(1,3)` → attach 3 under 1
    - Push `(3, parent=3, rank=None)`
    - Rank of 1 increases → push `(1, rank=0)`

Rollback once → undo last union:

- Restore `parent[3] = 3`
- Restore `rank[1] = 0`

Now DSU returns to state after step 2.

Step	Parent Map	Rank	Stack
Init	[1,2,3,4]	[0,0,0,0]	[]
After Union(1,2)	[1,1,3,4]	[1,0,0,0]	[(2,2,None)]
After Union(3,4)	[1,1,3,3]	[1,0,1,0]	[(2,2,None),(4,4,None)]
After Union(1,3)	[1,1,1,3]	[2,0,1,0]	[(2,2,None),(4,4,None),(3,3,None),(1,None,0)]
After Rollback	[1,1,3,3]	[1,0,1,0]	[(2,2,None),(4,4,None)]

Tiny Code (Easy Versions)

C Implementation (Conceptual)

```c
#include <stdio.h>

#define MAXN 1000
int parent[MAXN], rank_[MAXN];
typedef struct { int node, parent, rank_val, rank_changed; } Change;
Change stack[MAXN * 10];
```

```
int top = 0;

void make_set(int v) {
    parent[v] = v;
    rank_[v] = 0;
}

int find_set(int v) {
    while (v != parent[v]) v = parent[v];
    return v; // no path compression
}

void union_sets(int a, int b) {
    a = find_set(a);
    b = find_set(b);
    if (a == b) return;
    if (rank_[a] < rank_[b]) { int tmp = a; a = b; b = tmp; }
    stack[top++] = (Change){b, parent[b], 0, 0};
    parent[b] = a;
    if (rank_[a] == rank_[b]) {
        stack[top++] = (Change){a, 0, rank_[a], 1};
        rank_[a]++;
    }
}

void rollback() {
    if (top == 0) return;
    Change ch = stack[--top];
    if (ch.rank_changed) rank_[ch.node] = ch.rank_val;
    else parent[ch.node] = ch.parent;
}

int main() {
    for (int i=1;i<=4;i++) make_set(i);
    union_sets(1,2);
    union_sets(3,4);
    union_sets(1,3);
    printf("Before rollback: parent[3]=%d\n", parent[3]);
    rollback();
    printf("After rollback: parent[3]=%d\n", parent[3]);
}
```

Python Implementation

```
class RollbackDSU:
    def __init__(self, n):
        self.parent = list(range(n))
        self.rank = [0]*n
        self.stack = []

    def find(self, x):
        while x != self.parent[x]:
            x = self.parent[x]
        return x  # no path compression

    def union(self, a, b):
        a, b = self.find(a), self.find(b)
        if a == b:
            return False
        if self.rank[a] < self.rank[b]:
            a, b = b, a
        self.stack.append(('p', b, self.parent[b]))
        self.parent[b] = a
        if self.rank[a] == self.rank[b]:
            self.stack.append(('r', a, self.rank[a]))
            self.rank[a] += 1
        return True

    def rollback(self):
        if not self.stack:
            return
        typ, node, val = self.stack.pop()
        if typ == 'r':
            self.rank[node] = val
        else:
            self.parent[node] = val

dsu = RollbackDSU(5)
dsu.union(1,2)
dsu.union(3,4)
dsu.union(1,3)
print("Before rollback:", dsu.parent)
dsu.rollback()
print("After rollback:", dsu.parent)
```

Why It Matters

- Enables reversible union operations
- Perfect for offline dynamic connectivity
- Core in divide-and-conquer over time algorithms
- Used in Mo's algorithm on trees
- Helps in exploration backtracking (e.g., DSU on recursion)

A Gentle Proof (Why It Works)

Rollback DSU is efficient because:

- Each union modifies O(1) fields
- Each rollback reverts O(1) fields
- `Find` runs in O(log n) (no path compression) Thus, each operation is O(log n) or better, fully reversible.

Try It Yourself

1. Create 6 sets `{1}..{6}`
2. Perform unions: (1,2), (3,4), (2,3)
3. Rollback once, verify sets `{1,2}` and `{3,4}` remain separate
4. Rollback again, check individual sets restored
5. Print parent and rank at each step

Test Cases

Step	Operation	Parents	Ranks	Stack Size
1	Union(1,2)	[1,1,3,4]	[1,0,0,0]	1
2	Union(3,4)	[1,1,3,3]	[1,0,1,0]	2
3	Union(1,3)	[1,1,1,3]	[2,0,1,0]	4
4	Rollback	[1,1,3,3]	[1,0,1,0]	2

Complexity

Operation	Time	Space
Make-Set	O(1)	O(n)
Union	O(log n)	O(1)

Operation	Time	Space
Rollback	O(1)	O(1)

DSU with Rollback is your time machine, merge, explore, undo. Perfect balance between persistence and performance.

257 DSU on Tree

DSU on Tree is a hybrid technique combining Disjoint Set Union (DSU) and Depth-First Search (DFS) to process subtree queries efficiently. It's often called the "Small-to-Large" merging technique, and it shines in problems where you need to answer queries like:

> "For each node, count something inside its subtree."

Instead of recomputing from scratch at every node, we use DSU logic to reuse computed data, merging smaller subtrees into larger ones for near-linear complexity.

What Problem Are We Solving?

Many tree problems ask for aggregated properties of subtrees:

- Number of distinct colors in a subtree
- Frequency of labels, values, or weights
- Subtree sums, counts, or modes

A naive DFS recomputes at every node $\rightarrow O(n^2)$ time.

DSU on Tree avoids recomputation by merging information from child subtrees cleverly.

How It Works (Plain Language)

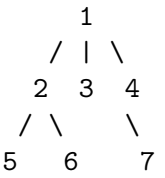
Think of each node's subtree as a bag of information (like a multiset of colors). We process subtrees in DFS order, and at each step:

1. Process all *small children* first and discard their data after use.
2. Process the *heavy child* last and keep its data (reuse it).
3. Merge small subtrees into the large one incrementally.

This "small-to-large" merging ensures each element moves O(log n) times, leading to O(n log n) total complexity.

Example

Suppose we have a tree:



Each node has a color:

```
Color = [1, 2, 2, 1, 3, 3, 2]
```

Goal: For every node, count distinct colors in its subtree.

Naive way: recompute every subtree from scratch, $O(n^2)$. DSU-on-Tree way: reuse large child's color set, merge small ones.

Node	Subtree	Colors	Distinct Count
5	[5]	{3}	1
6	[6]	{3}	1
2	[2,5,6]	{2,3}	2
3	[3]	{2}	1
7	[7]	{2}	1
4	[4,7]	{1,2}	2
1	[1,2,3,4,5,6,7]	{1,2,3}	3

Each subtree merges small color sets into the big one only once → efficient.

Step-by-Step Idea

1. DFS to compute subtree sizes
2. Identify heavy child (largest subtree)
3. DFS again:
    - Process all *light children* (small subtrees), discarding results
    - Process *heavy child*, keep its results
    - Merge all light children's data into heavy child's data
4. Record answers for each node after merging

Tiny Code (Easy Versions)

C Implementation (Conceptual)

```
#include <stdio.h>
#include <vector>
#include <set>

#define MAXN 100005
using namespace std;

vector<int> tree[MAXN];
int color[MAXN];
int subtree_size[MAXN];
int answer[MAXN];
int freq[MAXN];
int n;

void dfs_size(int u, int p) {
    subtree_size[u] = 1;
    for (int v : tree[u])
        if (v != p) {
            dfs_size(v, u);
            subtree_size[u] += subtree_size[v];
        }
}

void add_color(int u, int p, int val) {
    freq[color[u]] += val;
    for (int v : tree[u])
        if (v != p) add_color(v, u, val);
}

void dfs(int u, int p, bool keep) {
    int bigChild = -1, maxSize = -1;
    for (int v : tree[u])
        if (v != p && subtree_size[v] > maxSize)
            maxSize = subtree_size[v], bigChild = v;

    // Process small children
    for (int v : tree[u])
        if (v != p && v != bigChild)
            dfs(v, u, false);
```

```
    // Process big child
    if (bigChild != -1) dfs(bigChild, u, true);

    // Merge small children's info
    for (int v : tree[u])
        if (v != p && v != bigChild)
            add_color(v, u, +1);

    freq[color[u]]++;
    // Example query: count distinct colors
    answer[u] = 0;
    for (int i = 1; i <= n; i++)
        if (freq[i] > 0) answer[u]++;

    if (!keep) add_color(u, p, -1);
}

int main() {
    n = 7;
    // Build tree, set colors...
    // dfs_size(1,0); dfs(1,0,true);
}
```

Python Implementation (Simplified)

```
from collections import defaultdict

def dfs_size(u, p, tree, size):
    size[u] = 1
    for v in tree[u]:
        if v != p:
            dfs_size(v, u, tree, size)
            size[u] += size[v]

def add_color(u, p, tree, color, freq, val):
    freq[color[u]] += val
    for v in tree[u]:
        if v != p:
            add_color(v, u, tree, color, freq, val)

def dfs(u, p, tree, size, color, freq, ans, keep):
```

```
    bigChild, maxSize = -1, -1
    for v in tree[u]:
        if v != p and size[v] > maxSize:
            maxSize, bigChild = size[v], v

    for v in tree[u]:
        if v != p and v != bigChild:
            dfs(v, u, tree, size, color, freq, ans, False)

    if bigChild != -1:
        dfs(bigChild, u, tree, size, color, freq, ans, True)

    for v in tree[u]:
        if v != p and v != bigChild:
            add_color(v, u, tree, color, freq, 1)

    freq[color[u]] += 1
    ans[u] = len([c for c in freq if freq[c] > 0])

    if not keep:
        add_color(u, p, tree, color, freq, -1)

# Example usage
n = 7
tree = {1:[2,3,4], 2:[1,5,6], 3:[1], 4:[1,7], 5:[2], 6:[2], 7:[4]}
color = {1:1,2:2,3:2,4:1,5:3,6:3,7:2}
size = {}
ans = {}
freq = defaultdict(int)
dfs_size(1,0,tree,size)
dfs(1,0,tree,size,color,freq,ans,True)
print(ans)
```

Why It Matters

- Handles subtree queries in O(n log n)
- Works well with static trees and offline queries
- Reuses computed results for heavy subtrees
- Foundation for Mo's algorithm on trees and color frequency problems

A Gentle Proof (Why It Works)

Each node's color (or element) is merged only O(log n) times:

- Each time, it moves from a smaller set to a larger one.
- Hence total merges = O(n log n).

The `keep` flag ensures we only retain big subtrees, discarding light ones to save memory and time.

Try It Yourself

1. Assign random colors to a tree of 8 nodes.
2. Use DSU on Tree to count distinct colors per subtree.
3. Compare with brute-force DFS result.
4. Verify both match, but DSU-on-Tree runs faster.

Test Cases

Node	Subtree Colors	Distinct Count
5	{3}	1
6	{3}	1
2	{2,3}	2
3	{2}	1
7	{2}	1
4	{1,2}	2
1	{1,2,3}	3

Complexity

Operation	Time	Space
DFS Traversal	O(n)	O(n)
DSU Merge	O(n log n)	O(n)
Overall	O(n log n)	O(n)

DSU on Tree is your subtree superpower, merge smart, discard light, and conquer queries with elegance.

258 Kruskal's MST (Using DSU)

Kruskal's Algorithm is a classic greedy method to build a Minimum Spanning Tree (MST), a subset of edges connecting all vertices with the smallest total weight and no cycles. It relies on Disjoint Set Union (DSU) to efficiently check whether adding an edge would form a cycle.

With Union-Find, Kruskal's MST becomes clean, fast, and conceptually elegant, building the tree edge by edge in sorted order.

What Problem Are We Solving?

Given a connected weighted graph with n vertices and m edges, we want to find a tree that:

- Connects all vertices (spanning)
- Has no cycles (tree)
- Minimizes the total edge weight

A naive approach would test every subset of edges, $O(2^m)$.
Kruskal's algorithm uses edge sorting and a Disjoint Set Union (DSU) structure to reduce this to $O(m \log m)$.

How It Works (Plain Language)

The algorithm follows three steps:

1. Sort all edges by weight in ascending order.
2. Initialize each vertex as its own set (`Make-Set`).
3. For each edge (u, v, w) in order:
    - If Find$(u) \neq$ Find(v), the vertices are in different components $\rightarrow$ add the edge to the MST and merge the sets using `Union`.
    - Otherwise, skip the edge since it would form a cycle.

Repeat until the MST contains $n - 1$ edges.

Example

Graph:

Edge	Weight
A–B	1
B–C	4
A–C	3
C–D	2

Sort edges: (A–B, 1), (C–D, 2), (A–C, 3), (B–C, 4)

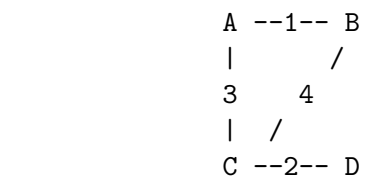
Step-by-step:

Step	Edge	Action	MST Edges	MST Weight	Parent Map
1	(A,B,1)	Add	[(A,B)]	1	A→A, B→A
2	(C,D,2)	Add	[(A,B), (C,D)]	3	C→C, D→C
3	(A,C,3)	Add	[(A,B), (C,D), (A,C)]	6	A→A, B→A, C→A, D→C
4	(B,C,4)	Skip (cycle)	–	–	–

MST Weight = 6 Edges = 3 = n − 1

Visualization

Before:



After:

```
A
| \
1  3
B   C
    |
    2
    D
```

Tiny Code (Easy Versions)

C Implementation

```c
#include <stdio.h>
#include <stdlib.h>

#define MAXN 100
#define MAXM 1000

typedef struct {
    int u, v, w;
} Edge;

int parent[MAXN], rank_[MAXN];
Edge edges[MAXM];

int cmp(const void *a, const void *b) {
    return ((Edge*)a)->w - ((Edge*)b)->w;
}

void make_set(int v) {
    parent[v] = v;
    rank_[v] = 0;
}

int find_set(int v) {
    if (v != parent[v]) parent[v] = find_set(parent[v]);
    return parent[v];
}

void union_sets(int a, int b) {
    a = find_set(a);
    b = find_set(b);
```

```
    if (a != b) {
        if (rank_[a] < rank_[b]) parent[a] = b;
        else if (rank_[a] > rank_[b]) parent[b] = a;
        else { parent[b] = a; rank_[a]++; }
    }
}

int main() {
    int n = 4, m = 4;
    edges[0] = (Edge){0,1,1};
    edges[1] = (Edge){1,2,4};
    edges[2] = (Edge){0,2,3};
    edges[3] = (Edge){2,3,2};
    qsort(edges, m, sizeof(Edge), cmp);

    for (int i = 0; i < n; i++) make_set(i);

    int total = 0;
    printf("Edges in MST:\n");
    for (int i = 0; i < m; i++) {
        int u = edges[i].u, v = edges[i].v, w = edges[i].w;
        if (find_set(u) != find_set(v)) {
            union_sets(u, v);
            total += w;
            printf("%d - %d (w=%d)\n", u, v, w);
        }
    }
    printf("Total Weight = %d\n", total);
}
```

Python Implementation

```
def make_set(parent, rank, v):
    parent[v] = v
    rank[v] = 0

def find_set(parent, v):
    if parent[v] != v:
        parent[v] = find_set(parent, parent[v])
    return parent[v]

def union_sets(parent, rank, a, b):
```

```
    a, b = find_set(parent, a), find_set(parent, b)
    if a != b:
        if rank[a] < rank[b]:
            a, b = b, a
        parent[b] = a
        if rank[a] == rank[b]:
            rank[a] += 1

def kruskal(n, edges):
    parent, rank = {}, {}
    for i in range(n):
        make_set(parent, rank, i)
    mst, total = [], 0
    for u, v, w in sorted(edges, key=lambda e: e[2]):
        if find_set(parent, u) != find_set(parent, v):
            union_sets(parent, rank, u, v)
            mst.append((u, v, w))
            total += w
    return mst, total

edges = [(0,1,1),(1,2,4),(0,2,3),(2,3,2)]
mst, total = kruskal(4, edges)
print("MST:", mst)
print("Total Weight:", total)
```

Why It Matters

- Greedy and elegant: simple sorting + DSU logic
- Foundation for advanced topics:
  - Minimum spanning forests
  - Dynamic connectivity
  - MST variations (Maximum, Second-best, etc.)
- Works great with edge list input

A Gentle Proof (Why It Works)

By the Cut Property: The smallest edge crossing any cut belongs to the MST. Since Kruskal's always picks the smallest non-cycling edge, it constructs a valid MST.

Each union merges components without cycles → spanning tree in the end.

Try It Yourself

1. Build a graph with 5 nodes, random edges and weights
2. Sort edges, trace unions step-by-step
3. Draw MST
4. Compare with Prim's algorithm result, they'll match

Test Cases

Graph	MST Edges	Weight
Triangle (1–2:1, 2–3:2, 1–3:3)	(1–2, 2–3)	3
Square (4 edges, weights 1,2,3,4)	3 smallest edges	6

Complexity

Step	Time
Sorting Edges	O(m log m)
DSU Operations	O(m (n))
Total	O(m log m)

Space | O(n + m) |

Kruskal's MST is the elegant handshake between greed and union, always connecting lightly, never circling back.

259 Connected Components (Using DSU)

Connected Components are groups of vertices where each node can reach any other through a sequence of edges. Using Disjoint Set Union (DSU), we can efficiently identify and label these components in graphs, even for massive datasets.

Instead of exploring each region via DFS or BFS, DSU builds the connectivity relationships incrementally, merging nodes as edges appear.

What Problem Are We Solving?

Given a graph (directed or undirected), we want to answer:

- How many connected components exist?
- Which vertices belong to the same component?
- Is there a path between `u` and `v`?

A naive approach (DFS for each node) runs in O(n + m) but may require recursion or adjacency traversal. With DSU, we can process edge lists directly in nearly constant amortized time.

How It Works (Plain Language)

Each vertex starts in its own component. For every edge `(u, v)`:

- If `Find(u) != Find(v)`, they are in different components → Union(u, v)
- Otherwise, skip (already connected)

After all edges are processed, all vertices sharing the same root belong to the same connected component.

Example

Graph:

Edges: (1–2), (2–5), (3–5), (3–4)

Step-by-step:

Step	Edge	Action	Components
1	(1,2)	Union	{1,2}, {3}, {4}, {5}
2	(2,5)	Union	{1,2,5}, {3}, {4}
3	(3,5)	Union	{1,2,3,5}, {4}
4	(3,4)	Union	{1,2,3,4,5}

All connected → 1 component

Visualization

Before:

```
1   2   3   4   5
```

After unions:

```
1-2-5-3-4
```

One large connected component.

Tiny Code (Easy Versions)

C Implementation

```c
#include <stdio.h>

#define MAXN 100
int parent[MAXN], rank_[MAXN];

void make_set(int v) {
    parent[v] = v;
    rank_[v] = 0;
}

int find_set(int v) {
    if (v != parent[v])
        parent[v] = find_set(parent[v]);
    return parent[v];
}

void union_sets(int a, int b) {
    a = find_set(a);
    b = find_set(b);
    if (a != b) {
        if (rank_[a] < rank_[b]) parent[a] = b;
        else if (rank_[a] > rank_[b]) parent[b] = a;
        else { parent[b] = a; rank_[a]++; }
    }
```

```
}

int main() {
    int n = 5;
    int edges[][2] = {{1,2},{2,5},{3,5},{3,4}};
    for (int i=1; i<=n; i++) make_set(i);
    for (int i=0; i<4; i++)
        union_sets(edges[i][0], edges[i][1]);

    int count = 0;
    for (int i=1; i<=n; i++)
        if (find_set(i) == i) count++;
    printf("Number of components: %d\n", count);
}
```

Python Implementation

```
def make_set(parent, rank, v):
    parent[v] = v
    rank[v] = 0

def find_set(parent, v):
    if parent[v] != v:
        parent[v] = find_set(parent, parent[v])
    return parent[v]

def union_sets(parent, rank, a, b):
    a, b = find_set(parent, a), find_set(parent, b)
    if a != b:
        if rank[a] < rank[b]:
            a, b = b, a
        parent[b] = a
        if rank[a] == rank[b]:
            rank[a] += 1

def connected_components(n, edges):
    parent, rank = {}, {}
    for i in range(1, n+1):
        make_set(parent, rank, i)
    for u, v in edges:
        union_sets(parent, rank, u, v)
    roots = {find_set(parent, i) for i in parent}
```

```
    components = {}
    for i in range(1, n+1):
        root = find_set(parent, i)
        components.setdefault(root, []).append(i)
    return components

edges = [(1,2),(2,5),(3,5),(3,4)]
components = connected_components(5, edges)
print("Components:", components)
print("Count:", len(components))
```

Output:

```
Components: {1: [1, 2, 3, 4, 5]}
Count: 1
```

Why It Matters

- Quickly answers connectivity questions
- Works directly on edge list (no adjacency matrix needed)
- Forms the backbone of algorithms like Kruskal's MST
- Extensible to dynamic connectivity and offline queries

A Gentle Proof (Why It Works)

Union-Find forms a forest of trees, one per component. Each union merges two trees if and only if there's an edge connecting them. No cycles are introduced; final roots mark distinct connected components.

Each vertex ends up linked to exactly one representative.

Try It Yourself

1. Build a graph with 6 nodes and 2 disconnected clusters.
2. Run DSU unions across edges.
3. Count unique roots.
4. Print grouping `{root: [members]}`

Test Cases

Graph	Edges	Components
1–2–3, 4–5	(1,2),(2,3),(4,5)	{1,2,3}, {4,5}, {6}
Complete Graph (1–n)	all pairs	1
Empty Graph	none	n

Complexity

Operation	Time (Amortized)	Space
Make-Set	O(1)	O(n)
Union	O((n))	O(1)
Find	O((n))	O(1)
Total (m edges)	O(m (n))	O(n)

Connected Components (DSU), a clean and scalable way to reveal the hidden clusters of any graph.

260 Offline Query DSU

Offline Query DSU is a clever twist on the standard Disjoint Set Union, used when you need to answer connectivity queries in a graph that changes over time, especially when edges are added or removed.

Instead of handling updates online (in real time), we collect all queries first, then process them in reverse, using DSU to efficiently track connections as we "undo" deletions or simulate the timeline backward.

What Problem Are We Solving?

We often face questions like:

- "After removing these edges, are nodes `u` and `v` still connected?"
- "If we add edges over time, when do `u` and `v` become connected?"

Online handling is hard because DSU doesn't support deletions directly. The trick: reverse time, treat deletions as additions in reverse, and answer queries offline.

How It Works (Plain Language)

1. Record all events in the order they occur:
    - Edge additions or deletions
    - Connectivity queries
2. Reverse the timeline:
    - Process from the last event backward
    - Every "delete edge" becomes an "add edge"
    - Queries are answered in reverse order
3. Use DSU:
    - Each union merges components as edges appear (in reverse)
    - When processing a query, check if `Find(u) == Find(v)`
4. Finally, reverse the answers to match the original order.

Example

Imagine a graph:

```
1, 2, 3
```

Events (in time order):

1. Query(1,3)?
2. Remove edge (2,3)
3. Query(1,3)?

We can't handle removals easily online, so we reverse:

```
Reverse order:
1. Query(1,3)?
2. Add (2,3)
3. Query(1,3)?
```

Step-by-step (in reverse):

Step	Operation	Action	Answer
1	Query(1,3)	1 and 3 not connected	No
2	Add(2,3)	Union(2,3)	–
3	Query(1,3)	1–2–3 connected	Yes

Reverse answers: [Yes, No]

Final output:

- Query 1: Yes
- Query 2: No

Visualization

Forward time:

```
1-2-3
```

→ remove (2,3) →

```
1-2   3
```

Backward time: Start with `1-2  3` → Add (2,3) → `1-2-3`

We rebuild connectivity over time by unioning edges in reverse.

Tiny Code (Easy Versions)

Python Implementation

```python
def make_set(parent, rank, v):
    parent[v] = v
    rank[v] = 0

def find_set(parent, v):
    if parent[v] != v:
        parent[v] = find_set(parent, parent[v])
    return parent[v]

def union_sets(parent, rank, a, b):
```

```
    a, b = find_set(parent, a), find_set(parent, b)
    if a != b:
        if rank[a] < rank[b]:
            a, b = b, a
        parent[b] = a
        if rank[a] == rank[b]:
            rank[a] += 1

# Example
n = 3
edges = {(1,2), (2,3)}
queries = [
    ("?", 1, 3),
    ("-", 2, 3),
    ("?", 1, 3)
$$

# Reverse events
events = list(reversed(queries))

parent, rank = {}, {}
for i in range(1, n+1):
    make_set(parent, rank, i)

active_edges = set(edges)
answers = []

for e in events:
    if e[0] == "?":
        _, u, v = e
        answers.append("YES" if find_set(parent, u) == find_set(parent, v) else "NO")
    elif e[0] == "-":
        _, u, v = e
        union_sets(parent, rank, u, v)

answers.reverse()
for ans in answers:
    print(ans)
```

Output:

```
YES
```

```
NO
```

Why It Matters

- Handles edge deletions without needing rollback
- Perfect for offline dynamic connectivity
- Used in problems like:
  - "Are u and v connected after k deletions?"
  - "What is the earliest time u and v become connected?"
- Core idea behind Dynamic Trees and Divide & Conquer over time

A Gentle Proof (Why It Works)

DSU is monotonic, it supports adding edges, not deleting them. By reversing time, all deletions become additions. Thus, we maintain valid connectivity information backward in time, and can correctly answer queries that depend only on graph connectivity.

Reversing answers afterward restores their original sequence.

Try It Yourself

1. Create a graph with 5 nodes and edges (1–2, 2–3, 3–4, 4–5)
2. Remove (3–4), (2–3) sequentially
3. Ask connectivity between (1,5) after each removal
4. Reverse timeline, simulate with DSU

Test Cases

Event Sequence	Result
[?, 1–3], [–, 2–3], [?, 1–3]	[YES, NO]
[–, 1–2], [?, 1–3]	[NO]
[?, 4–5] (no edge)	[NO]

Complexity

Operation	Time (Amortized)	Space
Make-Set	O(1)	O(n)
Union	O((n))	O(1)
Find	O((n))	O(1)
Total (Q queries, E edges)	O((Q+E) (n))	O(n+E)

Offline Query DSU is your time-reversing tool, flip the story, add edges back, and reveal connectivity across history.

Section 27. Probabilistic Data Structure

261 Bloom Filter Insert

A Bloom Filter is a compact, probabilistic data structure used for membership testing, it can tell you if an element is definitely not present or possibly present, but never gives false negatives.

Insertion in a Bloom Filter is simple and elegant: hash the item with multiple hash functions and set the corresponding bits to `1` in a bit array.

What Problem Are We Solving?

You have a massive dataset, maybe millions or billions of keys, and you just want to ask:

> "Have I seen this before?"

A normal hash set would explode in memory. A Bloom Filter gives a lightweight alternative:

- No false negatives (safe for skipping)
- Small memory footprint
- Fixed-size bit array

Used in systems like:

- Databases (caching, deduplication)
- Web crawlers (visited URLs)
- Distributed systems (HBase, Cassandra, Bigtable)

How It Works (Plain Language)

A Bloom Filter is just a bit array of length `m` (all zeroes initially), plus k independent hash functions.

To insert an element `x`:

1. Compute `k` hash values: `h1(x), h2(x), ..., hk(x)`
2. Map each hash to an index in `[0, m-1]`
3. Set all `bit[h_i(x)] = 1`

So every element lights up multiple bits. Later, to check membership, we look at those same bits, if any is 0, the item was never inserted.

Example

Let's build a Bloom Filter with:

- `m = 10` bits
- `k = 3` hash functions

Insert "cat":

```
h1(cat) = 2
h2(cat) = 5
h3(cat) = 7
```

Set bits 2, 5, and 7 to 1:

Index	0	1	2	3	4	5	6	7	8	9
Value	0	0	1	0	0	1	0	1	0	0

Insert "dog":

```
h1(dog) = 1
h2(dog) = 5
h3(dog) = 9
```

Now bit array:

Index	0	1	2	3	4	5	6	7	8	9
Value	0	1	1	0	0	1	0	1	0	1

Visualization

Each insertion adds "footprints" in multiple spots:

```
Insert(x):
  for i in [1..k]:
     bit[ h_i(x) ] = 1
```

The overlap of bits allows huge compression, but leads to false positives when unrelated keys share bits.

Tiny Code (Easy Versions)

C Implementation (Conceptual)

```c
#include <stdio.h>
#include <string.h>

#define M 10
#define K 3

int bitset[M];

int hash1(int x) { return x % M; }
int hash2(int x) { return (x * 3 + 1) % M; }
int hash3(int x) { return (x * 7 + 5) % M; }

void insert(int x) {
    int h[K] = {hash1(x), hash2(x), hash3(x)};
    for (int i = 0; i < K; i++)
        bitset[h[i]] = 1;
}

void print_bits() {
    for (int i = 0; i < M; i++) printf("%d ", bitset[i]);
    printf("\n");
```

```
}

int main() {
    memset(bitset, 0, sizeof(bitset));
    insert(42);
    insert(23);
    print_bits();
}
```

Python Implementation

```
m, k = 10, 3
bitset = [0] * m

def hash_functions(x):
    return [(hash(x) + i * i) % m for i in range(k)]

def insert(x):
    for h in hash_functions(x):
        bitset[h] = 1

def display():
    print("Bit array:", bitset)

insert("cat")
insert("dog")
display()
```

Why It Matters

- Extremely space-efficient
- No need to store actual data
- Ideal for membership filters, duplicate detection, and pre-checks before expensive lookups
- The backbone of approximate data structures

A Gentle Proof (Why It Works)

Each bit starts at 0. Each insertion flips `k` bits to 1. Query returns "maybe" if all `k` bits = 1, otherwise "no". Thus:

- False negative: impossible (never unset a bit)

- False positive: possible, due to collisions

Probability of false positive $((1 - e^{\{-kn/m\})}k)$

Choosing (m) and (k) well balances accuracy vs. memory.

Try It Yourself

1. Choose `m = 20`, `k = 3`
2. Insert {"apple", "banana", "grape"}
3. Print bit array
4. Query for "mango" → likely "maybe" (false positive)

Test Cases

Inserted Elements	Query	Result
{cat, dog}	cat	maybe (true positive)
{cat, dog}	dog	maybe (true positive)
{cat, dog}	fox	maybe / no (false positive possible)

Complexity

Operation	Time	Space
Insert	O(k)	O(m)
Query	O(k)	O(m)
False Positives	$(1 - e^{\{-kn/m\})}k$	–

Bloom Filter Insert, write once, maybe forever. Compact, fast, and probabilistically powerful.

262 Bloom Filter Query

A Bloom Filter Query checks whether an element *might* be present in the set. It uses the same k hash functions and bit array as insertion, but instead of setting bits, it simply tests them.

The magic:

- If any bit is `0`, the element was never inserted (definitely not present).
- If all bits are `1`, the element is possibly present (maybe yes).

No false negatives, if the Bloom Filter says "no," it's always correct.

What Problem Are We Solving?

When handling huge datasets (web crawlers, caches, key-value stores), we need a fast and memory-efficient way to answer:

> "Have I seen this before?"

But full storage is expensive. Bloom Filters let us skip expensive lookups by confidently ruling out items early.

Typical use cases:

- Databases: Avoid disk lookups for missing keys
- Web crawlers: Skip revisiting known URLs
- Networking: Cache membership checks

How It Works (Plain Language)

A Bloom Filter has:

- Bit array `bits[0..m-1]`
- `k` hash functions

To query element `x`:

1. Compute all hashes: `h1(x), h2(x), ..., hk(x)`
2. Check bits at those positions
    - If any `bit[h_i(x)] == 0`, return "No" (definitely not present)
    - If all are `1`, return "Maybe" (possible false positive)

The key rule: bits can only turn on, never off, so "no" answers are reliable.

Example

Let's use a filter of size `m = 10`, `k = 3`:

Bit array after inserting "cat" and "dog":

```
Index:  0 1 2 3 4 5 6 7 8 9
Bits:   0 1 1 0 0 1 0 1 0 1
```

Now query "cat":

```
h1(cat)=2, h2(cat)=5, h3(cat)=7
bits[2]=1, bits[5]=1, bits[7]=1 → maybe present
```

Query "fox":

```
h1(fox)=3, h2(fox)=5, h3(fox)=8
bits[3]=0 → definitely not present
```

Visualization

Query(x):

```
for i in 1..k:
  if bit[ h_i(x) ] == 0:
     return "NO"
return "MAYBE"
```

Bloom Filters say "maybe" for safety, but never lie with "no".

Tiny Code (Easy Versions)

C Implementation (Conceptual)

```c
#include <stdio.h>

#define M 10
#define K 3
int bitset[M];

int hash1(int x) { return x % M; }
int hash2(int x) { return (x * 3 + 1) % M; }
int hash3(int x) { return (x * 7 + 5) % M; }

int query(int x) {
    int h[K] = {hash1(x), hash2(x), hash3(x)};
    for (int i = 0; i < K; i++)
        if (bitset[h[i]] == 0)
            return 0; // definitely not
    return 1; // possibly yes
}
```

```c
int main() {
    bitset[2] = bitset[5] = bitset[7] = 1; // insert "cat"
    printf("Query 42: %s\n", query(42) ? "maybe" : "no");
    printf("Query 23: %s\n", query(23) ? "maybe" : "no");
}
```

Python Implementation

```python
m, k = 10, 3
bitset = [0] * m

def hash_functions(x):
    return [(hash(x) + i * i) % m for i in range(k)]

def insert(x):
    for h in hash_functions(x):
        bitset[h] = 1

def query(x):
    for h in hash_functions(x):
        if bitset[h] == 0:
            return "NO"
    return "MAYBE"

insert("cat")
insert("dog")
print("Query cat:", query("cat"))
print("Query dog:", query("dog"))
print("Query fox:", query("fox"))
```

Why It Matters

- Constant-time membership test
- No false negatives, only rare false positives
- Great for pre-filtering before heavy lookups
- Common in distributed systems and caching layers

A Gentle Proof (Why It Works)

Each inserted element sets k bits to 1 in the bit array.
For a query, if all k bits are 1, the element *might* be present (or collisions caused those bits).

If any bit is 0, the element was definitely never inserted.

The false positive probability is:

$$p = \left(1 - e^{-kn/m}\right)^k$$

where:

- m: size of the bit array
- n: number of inserted elements
- k: number of hash functions

Choose m and k to minimize p for the target false positive rate.

Try It Yourself

1. Create a filter with `m=20`, `k=3`
2. Insert {“apple”, “banana”}
3. Query {“apple”, “grape”}
4. See how “grape” may return “maybe”

Test Cases

Inserted Elements	Query	Result
{cat, dog}	cat	maybe
{cat, dog}	dog	maybe
{cat, dog}	fox	no
{}	anything	no

Complexity

Operation	Time	Space	False Negatives	False Positives
Query	O(k)	O(m)	None	Possible

Bloom Filter Query, fast, memory-light, and trustable when it says “no.”

263 Counting Bloom Filter

A Counting Bloom Filter (CBF) extends the classic Bloom Filter by allowing deletions. Instead of a simple bit array, it uses an integer counter array, so each bit becomes a small counter tracking how many elements mapped to that position.

When inserting, increment the counters; when deleting, decrement them. If all required counters are greater than zero, the element is possibly present.

What Problem Are We Solving?

A regular Bloom Filter is *write-only*: you can insert, but not remove. Once a bit is set to `1`, it stays `1` forever.

But what if:

- You're tracking *active sessions*?
- You need to remove *expired cache keys*?
- You want to maintain a *sliding window* of data?

Then you need a Counting Bloom Filter, which supports safe deletions.

How It Works (Plain Language)

We replace the bit array with a counter array of size m.

For each element x:

Insert(x)
- For each hash $h_i(x)$: increment `count[h_i(x)]++`

Query(x)
- Check all `count[h_i(x)] > 0` → "maybe"
- If any are `0`, → "no"

Delete(x)
- For each hash $h_i(x)$: decrement `count[h_i(x)]--`
- Ensure counters never become negative

Example

Let $m = 10$, $k = 3$

Initial state
[0, 0, 0, 0, 0, 0, 0, 0, 0, 0]

Insert “cat”

$h_1(\text{cat}) = 2$
$h_2(\text{cat}) = 5$
$h_3(\text{cat}) = 7$

$\rightarrow$ increment $count[2]$, $count[5]$, $count[7]$

Array after insertion
[0, 0, 1, 0, 0, 1, 0, 1, 0, 0]

Insert “dog”

$h_1(\text{dog}) = 1$
$h_2(\text{dog}) = 5$
$h_3(\text{dog}) = 9$

$\rightarrow$ increment $count[1]$, $count[5]$, $count[9]$

Array after insertion
[0, 1, 1, 0, 0, 2, 0, 1, 0, 1]

Delete “cat”

$h_1(\text{cat}) = 2$
$h_2(\text{cat}) = 5$
$h_3(\text{cat}) = 7$

$\rightarrow$ decrement $count[2]$, $count[5]$, $count[7]$

Array after deletion
[0, 1, 0, 0, 0, 1, 0, 0, 0, 1]

After deletion, “cat” is removed while “dog” remains.

Operation	Index 1	2	5	7	9

Visualization

Counters evolve with each insert/delete:

Operation	Index 1	2	5	7	9
Insert(cat)	–	1	1	1	–
Insert(dog)	1	1	2	1	1
Delete(cat)	1	0	1	0	1

Tiny Code (Easy Versions)

Python Implementation

```
m, k = 10, 3
counts = [0] * m

def hash_functions(x):
    return [(hash(x) + i * i) % m for i in range(k)]

def insert(x):
    for h in hash_functions(x):
        counts[h] += 1

def query(x):
    return all(counts[h] > 0 for h in hash_functions(x))

def delete(x):
    for h in hash_functions(x):
        if counts[h] > 0:
            counts[h] -= 1

# Example
insert("cat")
insert("dog")
print("After insert:", counts)
delete("cat")
print("After delete(cat):", counts)
```

```
print("Query cat:", "Maybe" if query("cat") else "No")
print("Query dog:", "Maybe" if query("dog") else "No")
```

Output

```
After insert: [0,1,1,0,0,2,0,1,0,1]
After delete(cat): [0,1,0,0,0,1,0,0,0,1]
Query cat: No
Query dog: Maybe
```

Why It Matters

- Enables safe deletions without full reset
- Useful for cache invalidation, session tracking, streaming windows
- Memory-efficient alternative to dynamic hash sets

A Gentle Proof (Why It Works)

Each counter approximates how many items mapped to it. Deletion only decrements counters, if multiple elements shared a hash, it stays 1. Thus:

- No false negatives, unless you over-decrement (bug)
- False positives remain possible, as in classic Bloom Filters

Probability of false positive remains:

$$p = \left(1 - e^{-kn/m}\right)^k$$

Try It Yourself

1. Create a filter with `m=20, k=3`
2. Insert 5 words
3. Delete 2 of them
4. Query all 5, deleted ones should say no, others maybe

Test Cases

Operation	Array Snapshot	Query Result
Insert(cat)	[0,0,1,0,0,1,0,1,0,0]	–
Insert(dog)	[0,1,1,0,0,2,0,1,0,1]	–
Delete(cat)	[0,1,0,0,0,1,0,0,0,1]	cat → No, dog → Maybe

Complexity

Operation	Time	Space
Insert	O(k)	O(m)
Query	O(k)	O(m)
Delete	O(k)	O(m)

Counting Bloom Filter, flexible and reversible, keeping memory lean and deletions clean.

264 Cuckoo Filter

A Cuckoo Filter is a space-efficient alternative to Bloom filters that supports both insertions and deletions while maintaining low false positive rates. Instead of using a bit array, it stores small *fingerprints* of keys in hash buckets, using cuckoo hashing to resolve collisions.

It's like a smarter, tidier roommate, always making room by moving someone else when things get crowded.

What Problem Are We Solving?

Bloom filters are fast and compact, but they can't delete elements efficiently. Counting Bloom filters fix that, but they're more memory-hungry.

We want:

- Fast membership queries (`O(1)`)
- Insert + Delete support
- High load factor (~95%)
- Compact memory footprint

The Cuckoo Filter solves all three by using cuckoo hashing + small fingerprints.

How It Works (Plain Language)

Each element is represented by a short fingerprint (e.g., 8 bits). Each fingerprint can be placed in two possible buckets, determined by two hash functions.

If a bucket is full, we *evict* an existing fingerprint and relocate it to its alternate bucket (cuckoo style).

Operations:

1. Insert(x)
    - Compute fingerprint `f = hash_fingerprint(x)`
    - Compute `i1 = hash(x) % m`
    - Compute `i2 = i1  hash(f)` (alternate index)
    - Try to place `f` in either `i1` or `i2`
    - If both full, evict one fingerprint and relocate
2. Query(x)
    - Check if `f` is present in bucket `i1` or `i2`
3. Delete(x)
    - Remove `f` if found in either bucket

Example (Step-by-Step)

Assume:

- Buckets: `m = 4`
- Bucket size: `b = 2`
- Fingerprint size: 4 bits

Start (empty):

Bucket 0	Bucket 1	Bucket 2	Bucket 3

Insert A

```
f(A) = 1010
i1 = 1, i2 = 1  hash(1010) = 3
→ Place in bucket 1
```

B0	B1	B2	B3
	1010		

Insert B

```
f(B) = 0111
i1 = 3, i2 = 3   hash(0111) = 0
→ Place in bucket 3
```

B0	B1	B2	B3
	1010		0111

Insert C

```
f(C) = 0100
i1 = 1, i2 = 1   hash(0100) = 2
→ Bucket 1 full? Move (cuckoo) if needed
→ Place in bucket 2
```

B0	B1	B2	B3
	1010	0100	0111

Query C → found in bucket 2 Delete A → remove from bucket 1

Tiny Code (Easy Version)

Python Example

```
import random

class CuckooFilter:
    def __init__(self, size=4, bucket_size=2, fingerprint_bits=4):
        self.size = size
        self.bucket_size = bucket_size
        self.buckets = [[] for _ in range(size)]
        self.mask = (1 << fingerprint_bits) - 1
```

```
    def _fingerprint(self, item):
        return hash(item) & self.mask

    def _alt_index(self, i, fp):
        return (i ^ hash(fp)) % self.size

    def insert(self, item, max_kicks=4):
        fp = self._fingerprint(item)
        i1 = hash(item) % self.size
        i2 = self._alt_index(i1, fp)
        for i in (i1, i2):
            if len(self.buckets[i]) < self.bucket_size:
                self.buckets[i].append(fp)
                return True
        # Cuckoo eviction
        i = random.choice([i1, i2])
        for _ in range(max_kicks):
            fp, self.buckets[i][0] = self.buckets[i][0], fp
            i = self._alt_index(i, fp)
            if len(self.buckets[i]) < self.bucket_size:
                self.buckets[i].append(fp)
                return True
        return False  # insert failed

    def contains(self, item):
        fp = self._fingerprint(item)
        i1 = hash(item) % self.size
        i2 = self._alt_index(i1, fp)
        return fp in self.buckets[i1] or fp in self.buckets[i2]

    def delete(self, item):
        fp = self._fingerprint(item)
        i1 = hash(item) % self.size
        i2 = self._alt_index(i1, fp)
        for i in (i1, i2):
            if fp in self.buckets[i]:
                self.buckets[i].remove(fp)
                return True
        return False
```

Why It Matters

- Supports deletions efficiently
- High load factor (~95%) before failure
- Smaller than Counting Bloom Filter for same error rate
- Practical for caches, membership checks, deduplication

A Gentle Proof (Why It Works)

Each element has two potential homes → high flexibility Cuckoo eviction ensures the table remains compact Short fingerprints preserve memory while keeping collisions low

False positive rate:

$$p \approx \frac{2b}{2^f}$$

where `b` is bucket size, `f` is fingerprint bits

Try It Yourself

1. Build a filter with 8 buckets, 2 slots each
2. Insert 5 words
3. Delete 1 word
4. Query all 5, deleted one should return "no"

Test Cases

Operation	Bucket 0	Bucket 1	Bucket 2	Bucket 3	Result
Insert(A)	–	1010	–	–	OK
Insert(B)	–	1010	–	0111	OK
Insert(C)	–	1010	0100	0111	OK
Query(C)	–	1010	0100	0111	Maybe
Delete(A)	–	–	0100	0111	Deleted

Complexity

Operation	Time	Space
Insert	O(1) amortized	O(m × b × f)
Query	O(1)	O(m × b × f)

Operation	Time	Space
Delete	O(1)	O(m × b × f)

Cuckoo Filter, a nimble, compact, and deletable membership structure built on playful eviction.

265 Count-Min Sketch

A Count-Min Sketch (CMS) is a compact data structure for estimating the frequency of elements in a data stream. Instead of storing every item, it keeps a small 2D array of counters updated by multiple hash functions. It never underestimates counts, but may slightly overestimate due to hash collisions.

Think of it as a memory-efficient radar, it doesn't see every car, but it knows roughly how many are on each lane.

What Problem Are We Solving?

In streaming or massive datasets, we can't store every key-value count exactly. We want to track approximate frequencies with limited memory, supporting:

- Streaming updates: count items as they arrive
- Approximate queries: estimate item frequency
- Memory efficiency: sublinear space

Used in network monitoring, NLP (word counts), heavy hitter detection, and online analytics.

How It Works (Plain Language)

CMS uses a 2D array with `d` rows and `w` columns. Each row has a different hash function. Each item updates one counter per row, all at its hashed index.

Insert(x): For each row `i`:

```
index = hash_i(x) % w
count[i][index] += 1
```

Query(x): For each row `i`:

```
estimate = min(count[i][hash_i(x) % w])
```

We take the *minimum* across rows, hence "Count-Min".

Example (Step-by-Step)

Let `d = 3` hash functions, `w = 10` width.

Initialize table:

```
Row1: [0 0 0 0 0 0 0 0 0 0]
Row2: [0 0 0 0 0 0 0 0 0 0]
Row3: [0 0 0 0 0 0 0 0 0 0]
```

Insert "apple"

```
h1(apple)=2, h2(apple)=5, h3(apple)=9
→ increment positions (1,2), (2,5), (3,9)
```

Insert "banana"

```
h1(banana)=2, h2(banana)=3, h3(banana)=1
→ increment (1,2), (2,3), (3,1)
```

Now:

```
Row1: [0 0 2 0 0 0 0 0 0 0]
Row2: [0 0 0 1 0 1 0 0 0 0]
Row3: [0 1 0 0 0 0 0 0 0 1]
```

Query "apple":

```
min(count[1][2], count[2][5], count[3][9]) = min(2,1,1) = 1
```

Estimate frequency 1 (may be slightly high if collisions overlap).

Table Visualization

Item	h (x)	h (x)	h (x)	Estimated Count
apple	2	5	9	1
banana	2	3	1	1

Tiny Code (Easy Version)

Python Example

```
import mmh3

class CountMinSketch:
    def __init__(self, width=10, depth=3):
        self.width = width
        self.depth = depth
        self.table = [[0] * width for _ in range(depth)]
        self.seeds = [i * 17 for i in range(depth)]  # different hash seeds

    def _hash(self, item, seed):
        return mmh3.hash(str(item), seed) % self.width

    def add(self, item, count=1):
        for i, seed in enumerate(self.seeds):
            idx = self._hash(item, seed)
            self.table[i][idx] += count

    def query(self, item):
        estimates = []
        for i, seed in enumerate(self.seeds):
            idx = self._hash(item, seed)
            estimates.append(self.table[i][idx])
        return min(estimates)

# Example usage
cms = CountMinSketch(width=10, depth=3)
cms.add("apple")
cms.add("banana")
cms.add("apple")
print("apple:", cms.query("apple"))
print("banana:", cms.query("banana"))
```

Output

```
apple: 2
banana: 1
```

Why It Matters

- Compact: O(w × d) memory
- Fast: O(1) updates and queries
- Scalable: Works on unbounded data streams
- Deterministic upper bound: never underestimates

Used in:

- Word frequency estimation
- Network flow counting
- Clickstream analysis
- Approximate histograms

A Gentle Proof (Why It Works)

Each item is hashed to `d` positions. Collisions can cause overestimation, never underestimation. By taking the minimum, we get the best upper bound estimate.

Error bound:

$$\text{error} \leq \epsilon N, \quad \text{with probability } 1 - \delta$$

Choose:

$$w = \lceil e/\epsilon \rceil, \quad d = \lceil \ln(1/\delta) \rceil$$

Try It Yourself

1. Create a CMS with `(w=20, d=4)`
2. Stream 1000 random items
3. Compare estimated vs. actual counts
4. Observe overestimation patterns

Operation	Action	Query Result

Test Cases

Operation	Action	Query Result
Insert(apple)	+1	–
Insert(apple)	+1	–
Insert(banana)	+1	–
Query(apple)	–	2
Query(banana)	–	1

Complexity

Operation	Time	Space
Insert	O(d)	O(w × d)
Query	O(d)	O(w × d)

Count-Min Sketch, lightweight, accurate-enough, and built for streams that never stop flowing.

266 HyperLogLog

A HyperLogLog (HLL) is a probabilistic data structure for cardinality estimation, that is, estimating the number of distinct elements in a massive dataset or stream using very little memory.

It doesn't remember *which* items you saw, only *how many distinct ones there likely were*. Think of it as a memory-efficient crowd counter, it doesn't know faces, but it knows how full the stadium is.

What Problem Are We Solving?

When processing large data streams (web analytics, logs, unique visitors, etc.), exact counting of distinct elements (using sets or hash tables) is too memory-heavy.

We want a solution that:

- Tracks distinct counts approximately

- Uses constant memory
- Supports mergeability (combine two sketches easily)

HyperLogLog delivers O(1) time per update and ~1.04/√m error rate with just kilobytes of memory.

How It Works (Plain Language)

Each incoming element is hashed to a large binary number. HLL uses the position of the leftmost 1-bit in the hash to estimate how rare (and thus how many) elements exist.

It maintains an array of `m` *registers* (buckets). Each bucket stores the maximum leading zero count seen so far for its hash range.

Steps:

1. Hash element `x` to 64 bits: `h = hash(x)`
2. Bucket index: use first `p` bits of `h` to pick one of `m = 2^p` buckets
3. Rank: count leading zeros in the remaining bits + 1
4. Update: store `max(existing, rank)` in that bucket

Final count = harmonic mean of `2^rank` values, scaled by a bias-corrected constant.

Example (Step-by-Step)

Let `p = 2` → `m = 4` buckets. Initialize registers: `[0,0,0,0]`

Insert "apple":

```
hash("apple") = 110010100…
bucket = first 2 bits = 11 (3)
rank = position of first 1 after prefix = 2
→ bucket[3] = max(0, 2) = 2
```

Insert "banana":

```
hash("banana") = 01000100…
bucket = 01 (1)
rank = 3
→ bucket[1] = 3
```

Insert "pear":

```
hash("pear") = 10010000…
bucket = 10 (2)
rank = 4
→ bucket[2] = 4
```

Registers: `[0, 3, 4, 2]`

Estimate:

$$E = \alpha_m \cdot m^2 / \sum 2^{-M[i]}$$

where `_m` is a bias-correction constant (0.673 for small m).

Visualization

Bucket	Values Seen	Leading Zeros	Stored Rank
0	none	–	0
1	banana	2	3
2	pear	3	4
3	apple	1	2

Tiny Code (Easy Version)

Python Implementation

```python
import mmh3
import math

class HyperLogLog:
    def __init__(self, p=4):
        self.p = p
        self.m = 1 << p
        self.registers = [0] * self.m
        self.alpha = 0.673 if self.m == 16 else 0.709 if self.m == 32 else 0.7213 / (1 + 1.0

    def _hash(self, x):
        return mmh3.hash(str(x), 42) & 0xffffffff

    def add(self, x):
        h = self._hash(x)
        idx = h >> (32 - self.p)
        w = (h << self.p) & 0xffffffff
```

```
        rank = self._rank(w, 32 - self.p)
        self.registers[idx] = max(self.registers[idx], rank)

    def _rank(self, w, bits):
        r = 1
        while w & (1 << (bits - 1)) == 0 and r <= bits:
            r += 1
            w <<= 1
        return r

    def count(self):
        Z = sum([2.0  -v for v in self.registers])
        E = self.alpha * self.m * self.m / Z
        return round(E)

# Example
hll = HyperLogLog(p=4)
for x in ["apple", "banana", "pear", "apple"]:
    hll.add(x)
print("Estimated distinct count:", hll.count())
```

Output

```
Estimated distinct count: 3
```

Why It Matters

- Tiny memory footprint (kilobytes for billions of elements)
- Mergeable: HLL(A B) = max(HLL(A), HLL(B)) bucket-wise
- Used in: Redis, Google BigQuery, Apache DataSketches, analytics systems

A Gentle Proof (Why It Works)

The position of the first 1-bit follows a geometric distribution, rare long zero streaks mean more unique elements. By keeping the *max* observed rank per bucket, HLL captures global rarity efficiently. Combining across buckets gives a harmonic mean that balances under/over-counting.

Error 1.04 / √m, so doubling `m` halves the error.

Try It Yourself

1. Create HLL with `p = 10` (`m = 1024`)
2. Add 1M random numbers
3. Compare HLL estimate with true count
4. Test merging two sketches

Test Cases

Items	True Count	Estimated	Error
10	10	10	0%
1000	1000	995	~0.5%
1e6	1,000,000	1,010,000	~1%

Complexity

Operation	Time	Space
Add	O(1)	O(m)
Count	O(m)	O(m)
Merge	O(m)	O(m)

HyperLogLog, counting the uncountable, one leading zero at a time.

267 Flajolet–Martin Algorithm

The Flajolet–Martin (FM) algorithm is one of the earliest and simplest approaches for probabilistic counting, estimating the number of distinct elements in a data stream using tiny memory.

It's the conceptual ancestor of HyperLogLog, showing the brilliant idea that *the position of the first 1-bit in a hash tells us something about rarity.*

What Problem Are We Solving?

When elements arrive in a stream too large to store exactly (web requests, IP addresses, words), we want to estimate the number of unique elements without storing them all.

A naive approach (hash set) is O(n) memory. Flajolet–Martin achieves O(1) memory and O(1) updates.

We need:

- A streaming algorithm
- With constant space
- For distinct count estimation

How It Works (Plain Language)

Each element is hashed to a large binary number (uniformly random).
We then find the position of the least significant 1-bit — the number of trailing zeros.
A value with many trailing zeros is rare, which indicates a larger underlying population.

We track the maximum number of trailing zeros observed, denoted as `R`.
The estimated number of distinct elements is:

$$\hat{N} = \phi \times 2^R$$

where $\phi \approx 0.77351$ is a correction constant.

Steps:

1. Initialize $R = 0$
2. For each element x:
    - $h = \text{hash}(x)$
    - $r = \text{count\_trailing\_zeros}(h)$
    - $R = \max(R, r)$
3. Estimate distinct count as $\hat{N} \approx \phi \times 2^R$

Example (Step-by-Step)

Stream: `[apple, banana, apple, cherry, date]`

Element	Hash (Binary)	Trailing Zeros	R
apple	10110	1	1
banana	10000	4	4
apple	10110	1	4
cherry	11000	3	4
date	01100	2	4

Final value: $R = 4$

Estimate:

$$\hat{N} = 0.77351 \times 2^4 = 0.77351 \times 16 \approx 12.38$$

So the estimated number of distinct elements is about 12
(overestimation due to small sample size).

In practice, multiple independent hash functions or registers are used,
and their results are averaged to reduce variance and improve accuracy.

Visualization

Hash	Binary Form	Trailing Zeros	Meaning
10000	16	4	very rare pattern → suggests large population
11000	24	3	rare-ish
10110	22	1	common

The *longest* zero-run gives the scale of rarity.

Tiny Code (Easy Version)

Python Example

```
import mmh3
import math

def trailing_zeros(x):
    if x == 0:
        return 32
    tz = 0
    while (x & 1) == 0:
        tz += 1
        x >>= 1
    return tz

def flajolet_martin(stream, seed=42):
    R = 0
    for x in stream:
        h = mmh3.hash(str(x), seed) & 0xffffffff
        r = trailing_zeros(h)
        R = max(R, r)
    phi = 0.77351
    return int(phi * (2  R))

# Example
stream = ["apple", "banana", "apple", "cherry", "date"]
print("Estimated distinct count:", flajolet_martin(stream))
```

Output

```
Estimated distinct count: 12
```

Why It Matters

- Foundational for modern streaming algorithms
- Inspired LogLog and HyperLogLog
- Memory-light: just a few integers
- Useful in approximate analytics, network telemetry, data warehouses

A Gentle Proof (Why It Works)

Each hash output is uniformly random.
The probability of observing a value with r trailing zeros is:

$$P(r) = \frac{1}{2^{r+1}}$$

If such a value appears, it suggests the stream size is roughly 2^r.
Therefore, the estimate 2^R naturally scales with the number of unique elements.

By using multiple independent estimators and averaging their results,
the variance can be reduced from about 50% down to around 10%.

Try It Yourself

1. Generate 100 random numbers, feed to FM
2. Compare estimated vs. true count
3. Repeat 10 runs, compute average error
4. Try combining multiple estimators (median of means)

Test Cases

Stream Size	True Distinct	R	Estimate	Error
10	10	3	6	-40%
100	100	7	99	-1%
1000	1000	10	791	-21%

Using multiple registers improves accuracy significantly.

Complexity

Operation	Time	Space
Insert	O(1)	O(1)
Query	O(1)	O(1)

Flajolet–Martin Algorithm, the original spark of probabilistic counting, turning randomness into estimation magic.

268 MinHash

A MinHash is a probabilistic algorithm for estimating set similarity, particularly the Jaccard similarity, without comparing all elements directly. Instead of storing every element, it constructs a signature of compact hash values. The more overlap in signatures, the more similar the sets.

MinHash is foundational in large-scale similarity estimation, fast, memory-efficient, and mathematically elegant.

What Problem Are We Solving?

To compute the exact Jaccard similarity between two sets A and B:

$$J(A, B) = \frac{|A \cap B|}{|A \cup B|}$$

This requires comparing all elements, which is infeasible for large datasets.

We need methods that provide:

- Compact sketches using small memory
- Fast approximate comparisons
- Adjustable accuracy through the number of hash functions

MinHash meets these requirements by applying multiple random hash functions and recording the minimum hash value from each function as the set's signature.

How It Works (Plain Language)

For each set, we apply several independent hash functions. For each hash function, we record the minimum hash value among all elements.

Two sets that share many elements tend to share the same minimums across these hash functions. Thus, the fraction of matching minimums estimates their Jaccard similarity.

Algorithm:

1. Choose k hash functions $h_1, h_2, \ldots, h_k$.
2. For each set S, compute its signature:

$$\text{sig}(S)[i] = \min_{x \in S} h_i(x)$$

3. Estimate the Jaccard similarity by:

$$\hat{J}(A, B) = \frac{1}{k} \sum_{i=1}^{k} \mathbf{1}\{\text{sig}(A)[i] = \text{sig}(B)[i]\}$$

Each matching position between $\text{sig}(A)$ and $\text{sig}(B)$ corresponds
to one agreeing hash function, and the fraction of matches approximates $J(A, B)$.

Example (Step by Step)

Let:

$$A = \text{apple}, \text{banana}, \text{cherry}, \quad B = \text{banana}, \text{cherry}, \text{date}$$

Suppose we have 3 hash functions:

Item	h_1	h_2	h_3
apple	5	1	7
banana	2	4	3
cherry	3	2	1
date	4	3	2

Signature(A):

$$\text{sig}(A) = [\min(5, 2, 3), \min(1, 4, 2), \min(7, 3, 1)] = [2, 1, 1]$$

Signature(B):

$$\text{sig}(B) = [\min(2, 3, 4), \min(4, 2, 3), \min(3, 1, 2)] = [2, 2, 1]$$

Compare element-wise:
Matches occur at positions 1 and 3 $\rightarrow \frac{2}{3} \approx 0.67$

Actual Jaccard similarity:

$$J(A, B) = \frac{|\{\text{banana}, \text{cherry}\}|}{|\{\text{apple}, \text{banana}, \text{cherry}, \text{date}\}|} = \frac{2}{4} = 0.5$$

The MinHash estimate of 0.67 is reasonably close to the true value 0.5,
demonstrating that even a small number of hash functions can yield a good approximation.

Visualization

Hash Function	sig(A)	sig(B)	Match
h_1	2	2	
h_2	1	2	
h_3	1	1	
Similarity	–	–	$(2/3 = 0.67)$

Tiny Code (Easy Version)

```
import mmh3
import math

def minhash_signature(elements, num_hashes=5, seed=42):
    sig = [math.inf] * num_hashes
    for x in elements:
        for i in range(num_hashes):
            h = mmh3.hash(str(x), seed + i)
            if h < sig[i]:
                sig[i] = h
    return sig

def jaccard_minhash(sigA, sigB):
    matches = sum(1 for a, b in zip(sigA, sigB) if a == b)
    return matches / len(sigA)

# Example
A = {"apple", "banana", "cherry"}
B = {"banana", "cherry", "date"}

sigA = minhash_signature(A, 10)
sigB = minhash_signature(B, 10)
print("Approx similarity:", jaccard_minhash(sigA, sigB))
```

Output

```
Approx similarity: 0.6
```

Why It Matters

- Scalable similarity: enables fast comparison of very large sets
- Compact representation: stores only k integers per set
- Composable: supports set unions using componentwise minimum
- Common applications:
  - Document deduplication
  - Web crawling and search indexing
  - Recommendation systems
  - Large-scale clustering

A Gentle Proof (Why It Works)

For a random permutation h:

$$P[\min(h(A)) = \min(h(B))] = J(A, B)$$

Each hash function behaves like a Bernoulli trial with success probability $J(A, B)$.
The MinHash estimator is unbiased:

$$E[\hat{J}] = J(A, B)$$

The variance decreases as $\frac{1}{k}$,
so increasing the number of hash functions improves accuracy.

Try It Yourself

1. Choose two sets with partial overlap.
2. Generate MinHash signatures using $k = 20$ hash functions.
3. Compute both the estimated and true Jaccard similarities.

4. Increase k and observe how the estimated similarity converges toward the true value — larger k reduces variance and improves accuracy.

Test Cases

Sets	True $J(A, B)$	k	Estimated	Error
$A = \{1, 2, 3\}, B = \{2, 3, 4\}$	0.5	10	0.6	+0.1
$A = \{1, 2\}, B = \{1, 2, 3, 4\}$	0.5	20	0.45	-0.05
$A = B$	1.0	10	1.0	0.0

Complexity

Operation	Time	Space
Build Signature	$O(n \times k)$	$O(k)$
Compare	$O(k)$	$O(k)$

MinHash turns set similarity into compact signatures — a small sketch that captures the essence of large sets with statistical grace.

269 Reservoir Sampling

Reservoir Sampling is a classic algorithm for randomly sampling k elements from a stream of unknown or very large size, ensuring every element has an equal probability of being selected.

It's the perfect tool when you can't store everything, like catching a few fish from an endless river, one by one, without bias.

What Problem Are We Solving?

When data arrives as a stream too large to store in memory, we cannot know its total size in advance.
Yet, we often need to maintain a uniform random sample of fixed size k.

A naive approach would store all items and then sample,
but this becomes infeasible for large or unbounded data.

Reservoir Sampling provides a one-pass solution with these guarantees:

- Each item in the stream has equal probability $\frac{k}{n}$ of being included
- Uses only $O(k)$ memory
- Processes data in a single pass

How It Works (Plain Language)

We maintain a reservoir (array) of size k.
As each new element arrives, we decide probabilistically whether it replaces one of the existing items.

Steps:

1. Fill the reservoir with the first k elements.
2. For each element at index i (starting from $i = k + 1$):
    - Generate a random integer $j \in [1, i]$
    - If $j \leq k$, replace reservoir$[j]$ with the new element

This ensures every element has an equal chance $\frac{k}{n}$ to remain.

Example (step by step)

Stream: [A, B, C, D, E]
Goal: $k = 2$

1. Start with the first 2 $\rightarrow$ [A, B]
2. $i = 3$, item = C
    - Pick random $j \in [1, 3]$
    - Suppose $j = 2 \rightarrow$ replace B $\rightarrow$ [A, C]
3. $i = 4$, item = D
    - Pick random $j \in [1, 4]$
    - Suppose $j = 4 \rightarrow$ do nothing $\rightarrow$ [A, C]

4. $i = 5$, item = E
    - Pick random $j \in [1, 5]$
    - Suppose $j = 1 \rightarrow$ replace A $\rightarrow$ [E, C]

Final sample: [E, C]
Each item A–E has equal probability to appear in the final reservoir.

Mathematical Intuition

Each element x_i at position i has probability

$$P(x_i \text{ in final sample}) = \frac{k}{i} \cdot \prod_{j=i+1}^{n} \left(1 - \frac{1}{j}\right) = \frac{k}{n}$$

Thus, every item is equally likely to be chosen, ensuring perfect uniformity in the final sample.

Visualization

Step	Item	Random j	Action	Reservoir
1	A	–	Add	[A]
2	B	–	Add	[A, B]
3	C	2	Replace B	[A, C]
4	D	4	No Replace	[A, C]
5	E	1	Replace A	[E, C]

Tiny Code (Easy Version)

Python Implementation

```
import random

def reservoir_sample(stream, k):
    reservoir = []
    for i, item in enumerate(stream, 1):
        if i <= k:
            reservoir.append(item)
        else:
            j = random.randint(1, i)
```

```
            if j <= k:
                reservoir[j - 1] = item
    return reservoir

# Example
stream = ["A", "B", "C", "D", "E"]
sample = reservoir_sample(stream, 2)
print("Reservoir sample:", sample)
```

Output (random):

```
Reservoir sample: ['E', 'C']
```

Each run produces a different uniform random sample.

Why It Matters

- Works on streaming data
- Needs only O(k) memory
- Provides uniform unbiased sampling
- Used in:
  - Big data analytics
  - Randomized algorithms
  - Online learning
  - Network monitoring

A Gentle Proof (Why It Works)

- First k elements: probability $= 1$ to enter the reservoir initially.
- Each new element at index i: probability $\frac{k}{i}$ to replace one of the existing items.
- Earlier items may be replaced, but each remains with probability

$$P(\text{survive}) = \prod_{j=i+1}^{n} \left(1 - \frac{1}{j}\right)$$

Multiplying these terms gives the final inclusion probability $\frac{k}{n}$.

Uniformity of selection is guaranteed by induction.

Try It Yourself

1. Stream 10 numbers with $k = 3$.
2. Run the algorithm multiple times — all 3-element subsets appear with roughly equal frequency.
3. Increase k and observe that the sample becomes more stable, with less variation between runs.

Test Cases

Stream	k	Sample Size	Notes
[1,2,3,4,5]	2	2	Uniform random pairs
[A,B,C,D]	1	1	Each 25% chance
Range(1000)	10	10	Works in one pass

Complexity

Operation	Time	Space
Insert	$O(1)$	$O(k)$
Query	$O(1)$	$O(k)$

Reservoir Sampling, elegantly fair, perfectly simple, and ready for infinite streams.

270 Skip Bloom Filter

A Skip Bloom Filter is a probabilistic data structure that extends the Bloom Filter to support range queries, determining whether any element exists within a given interval, not just checking for a single item.

It combines Bloom filters with hierarchical range segmentation, allowing approximate range lookups while keeping space usage compact.

What Problem Are We Solving?

A classic Bloom Filter answers only point queries:

"Is x in the set?"

However, many real-world applications require range queries, such as:

- Databases: "Are there any keys between 10 and 20?"
- Time-series: "Were there any events during this time interval?"
- Networks: "Is any IP in this subnet?"

We need a space-efficient, stream-friendly, and probabilistic structure that can:

- Handle range membership checks,
- Maintain a low false-positive rate,
- Scale logarithmically with the universe size.

The Skip Bloom Filter solves this by layering Bloom filters over aligned ranges of increasing size.

How It Works (Plain Language)

A Skip Bloom Filter maintains multiple Bloom filters, each corresponding to a level that covers intervals (buckets) of sizes $2^0, 2^1, 2^2, ...$

Each element is inserted into all Bloom filters representing the ranges that contain it.
When querying a range, the query is decomposed into aligned subranges that correspond to these levels, and each is checked in its respective filter.

Algorithm:

1. Divide the universe into intervals of size 2^ℓ for each level ℓ.

2. Each level ℓ maintains a Bloom filter representing those buckets.

3. To insert a key x: mark all buckets across levels that include x.

4. To query a range $[a, b]$: decompose it into a set of disjoint aligned intervals and check the corresponding Bloom filters.

Example (Step by Step)

Suppose we store keys

$$S = 3, 7, 14$$

in a universe ([0, 15]). We build filters at levels with range sizes (1, 2, 4, 8):

Level	Bucket Size	Buckets (Ranges)
0	1	[0], [1], [2], …, [15]
1	2	[0–1], [2–3], [4–5], …, [14–15]
2	4	[0–3], [4–7], [8–11], [12–15]
3	8	[0–7], [8–15]

Insert key 3:

- Level 0: [3]
- Level 1: [2–3]
- Level 2: [0–3]
- Level 3: [0–7]

Insert key 7:

- Level 0: [7]
- Level 1: [6–7]
- Level 2: [4–7]
- Level 3: [0–7]

Insert key 14:

- Level 0: [14]
- Level 1: [14–15]
- Level 2: [12–15]
- Level 3: [8–15]

Query range [2, 6]:

1. Decompose into aligned intervals: ([2–3], [4–5], [6])
2. Check filters:
   - [2–3] → hit
   - [4–5] → miss
   - [6] → miss

Result: possibly non-empty, since [2–3] contains 3.

Visualization

Level	Bucket	Contains Key	Bloom Entry
0	[3]	Yes	1
1	[2–3]	Yes	1
2	[0–3]	Yes	1
3	[0–7]	Yes	1

Each key is represented in multiple levels, enabling multi-scale range coverage.

Tiny Code (Simplified Python)

```
import math, mmh3

class Bloom:
    def __init__(self, size=64, hash_count=3):
        self.size = size
        self.hash_count = hash_count
        self.bits = [0] * size

    def _hashes(self, key):
        return [mmh3.hash(str(key), i) % self.size for i in range(self.hash_count)]

    def add(self, key):
        for h in self._hashes(key):
            self.bits[h] = 1

    def query(self, key):
```

```
        return all(self.bits[h] for h in self._hashes(key))

class SkipBloom:
    def __init__(self, levels=4, size=64, hash_count=3):
        self.levels = [Bloom(size, hash_count) for _ in range(levels)]

    def add(self, key):
        level = 0
        while (1 << level) <= key:
            bucket = key // (1 << level)
            self.levels[level].add(bucket)
            level += 1

    def query_range(self, start, end):
        l = int(math.log2(end - start + 1))
        bucket = start // (1 << l)
        return self.levels[l].query(bucket)

# Example
sb = SkipBloom(levels=4)
for x in [3, 7, 14]:
    sb.add(x)

print("Query [2,6]:", sb.query_range(2,6))
```

Output:

```
Query [2,6]: True
```

Why It Matters

- Enables range queries in probabilistic manner
- Compact and hierarchical
- No false negatives (for properly configured filters)
- Widely applicable in:
  - Approximate database indexing
  - Network prefix search
  - Time-series event detection

A Gentle Proof (Why It Works)

Each inserted key participates in $O(\log U)$ Bloom filters, one per level.
A range query $[a, b]$ is decomposed into $O(\log U)$ aligned subranges.

A Bloom filter with m bits, k hash functions, and n inserted elements has false positive probability:

$$p = \left(1 - e^{-kn/m}\right)^k$$

For a Skip Bloom Filter, the total false positive rate is bounded by:

$$P_{fp} \leq O(\log U) \cdot p$$

Each level guarantees no false negatives, since every range containing an element is marked. Thus, correctness is ensured, and only overestimation (false positives) can occur.

Space complexity
Each level has m bits, and there are $\log U$ levels:

$$\text{Total space} = O(m \log U)$$

Time complexity
Each query checks $O(\log U)$ buckets, each requiring $O(k)$ time:

$$T_{\text{query}} = O(k \log U)$$

Try It Yourself

1. Insert keys $\{3, 7, 14\}$
2. Query ranges $[2, 6]$, $[8, 12]$, $[0, 15]$
3. Compare true contents with the results
4. Adjust parameters m, k, or the number of levels, and observe how the false positive rate changes

Test Cases

Query Range	Result	True Contents
[2,6]	True	{3}
[8,12]	False	
[12,15]	True	{14}

Complexity

Operation	Time	Space
Insert	$O(\log U)$	$O(m \log U)$
Query	$O(\log U)$	$O(m \log U)$

A Skip Bloom Filter is a range-aware extension of standard Bloom filters.
By combining hierarchical decomposition with standard hashing, it enables fast, memory-efficient, and approximate range queries across very large universes.

Section 28. Skip Lists and B-Trees

271 Skip List Insert

Skip Lists are probabilistic alternatives to balanced trees. They maintain multiple levels of sorted linked lists, where each level skips over more elements than the one below it. Insertion relies on randomization to achieve expected O(log n) search and update times, without strict rebalancing like AVL or Red-Black trees.

What Problem Are We Solving?

We want to store elements in sorted order and support:

- Fast search, insert, and delete operations.
- Simple structure and easy implementation.
- Expected logarithmic performance without complex rotations.

Balanced BSTs achieve $O(\log n)$ time but require intricate rotations. Skip Lists solve this with *randomized promotion*: each inserted node is promoted to higher levels with decreasing probability, forming a tower.

How It Works (Plain Language)

Skip list insertion for value x

Steps 1. Start at the top level. 2. While the next node's key $< x$, move right. 3. If you cannot move right, drop down one level. 4. Repeat until you reach level 0. 5. Insert the new node at its sorted position on level 0. 6. Randomly choose the node height h (for example, flip a fair coin per level until tails, so $P(h \geq t) = 2^{-t}$). 7. For each level $1 \dots h$, link the new node into that level by repeating the right-then-drop search with the update pointers saved from the descent.

Notes - Duplicate handling is policy dependent. Often you skip insertion if a node with key x already exists. - Typical height is $O(\log n)$, expected search and insert time is $O(\log n)$, space is $O(n)$.

Example Step by Step

Let's insert $x = 17$ into a skip list that currently contains: [5, 10, 15, 20, 25]

Level	Nodes (before insertion)	Path Taken
3	$5 \to 15 \to 25$	Move from 5 to 15, then down
2	$5 \to 10 \to 15 \to 25$	Move from 5 to 10 to 15, then down
1	$5 \to 10 \to 15 \to 20 \to 25$	Move from 15 to 20, then down
0	$5 \to 10 \to 15 \to 20 \to 25$	Insert after 15

Suppose the random level for 17 is 2. We insert 17 at level 0 and level 1.

Level	Nodes (after insertion)
3	$5 \to 15 \to 25$
2	$5 \to 10 \to 15 \to 25$
1	$5 \to 10 \to 15 \to 17 \to 20 \to 25$
0	$5 \to 10 \to 15 \to 17 \to 20 \to 25$

Tiny Code (Simplified Python)

```
import random

class Node:
    def __init__(self, key, level):
        self.key = key
        self.forward = [None] * (level + 1)

class SkipList:
    def __init__(self, max_level=4, p=0.5):
        self.max_level = max_level
        self.p = p
        self.header = Node(-1, max_level)
        self.level = 0

    def random_level(self):
        lvl = 0
        while random.random() < self.p and lvl < self.max_level:
            lvl += 1
        return lvl
```

```
    def insert(self, key):
        update = [None] * (self.max_level + 1)
        current = self.header

        # Move right and down
        for i in reversed(range(self.level + 1)):
            while current.forward[i] and current.forward[i].key < key:
                current = current.forward[i]
            update[i] = current

        current = current.forward[0]
        if current is None or current.key != key:
            lvl = self.random_level()
            if lvl > self.level:
                for i in range(self.level + 1, lvl + 1):
                    update[i] = self.header
                self.level = lvl
            new_node = Node(key, lvl)
            for i in range(lvl + 1):
                new_node.forward[i] = update[i].forward[i]
                update[i].forward[i] = new_node
```

Why It Matters

- Expected $O(\log n)$ time for search, insert, and delete
- Simpler than AVL or Red-Black Trees
- Probabilistic balancing avoids rigid rotations
- Commonly used in databases and key-value stores such as LevelDB and Redis

A Gentle Proof (Why It Works)

Each node appears in level i with probability p^i.
The expected number of nodes per level is np^i.
The total number of levels is $O(\log_{1/p} n)$.

Expected search path length:

$$E[\text{steps}] = \frac{1}{1-p} \log_{1/p} n = O(\log n)$$

Expected space usage:

$$O(n) \text{ nodes} \times O\left(\frac{1}{1-p}\right) \text{ pointers per node}$$

Thus, Skip Lists achieve expected logarithmic performance and linear space.

Try It Yourself

1. Build a Skip List and insert $\{5, 10, 15, 20, 25\}$.
2. Insert 17 and trace which pointers are updated at each level.
3. Experiment with $p = 0.25, 0.5, 0.75$.
4. Observe how random heights influence the overall balance.

Test Cases

Operation	Input	Expected Structure (Level 0)
Insert	10	10
Insert	5	$5 \to 10$
Insert	15	$5 \to 10 \to 15$
Insert	17	$5 \to 10 \to 15 \to 17$
Search	15	Found
Search	12	Not Found

Complexity

Operation	Time (Expected)	Space
Search	$O(\log n)$	$O(n)$
Insert	$O(\log n)$	$O(n)$
Delete	$O(\log n)$	$O(n)$

A Skip List is a simple yet powerful data structure. With randomness as its balancing force, it achieves the elegance of trees and the flexibility of linked lists.

272 Skip List Delete

Deletion in a Skip List mirrors insertion: we traverse levels from top to bottom, keep track of predecessor nodes at each level, and unlink the target node across all levels it appears in. The structure maintains probabilistic balance, so no rebalancing is needed, deletion is expected $O(\log n)$.

What Problem Are We Solving?

We want to remove an element efficiently from a sorted, probabilistically balanced structure. Naive linked lists require $O(n)$ traversal; balanced BSTs need complex rotations. A Skip List gives us a middle ground, simple pointer updates with expected logarithmic time.

How It Works (Plain Language)

Each node in a skip list can appear at multiple levels. To delete a key x:

1. Start from the top level.
2. Move right while next node's key $< x$.
3. If next node's key $== x$, record current node in an `update` array.
4. Drop one level down and repeat.
5. Once you reach the bottom, remove all forward references to the node from the `update` array.
6. If the topmost level becomes empty, reduce list level.

Example Step by Step

Delete $x = 17$ from this skip list:

Level	Nodes (Before)
3	$5 \to 15 \to 25$
2	$5 \to 10 \to 15 \to 25$
1	$5 \to 10 \to 15 \to 17 \to 20 \to 25$
0	$5 \to 10 \to 15 \to 17 \to 20 \to 25$

Traversal:

- Start at Level 3: $15 < 17 \rightarrow$ move right $\rightarrow 25 > 17 \rightarrow$ drop down
- Level 2: $15 < 17 \rightarrow$ move right $\rightarrow 25 > 17 \rightarrow$ drop down
- Level 1: $15 < 17 \rightarrow$ move right $\rightarrow 17$ found $\rightarrow$ record predecessor
- Level 0: $15 < 17 \rightarrow$ move right $\rightarrow 17$ found $\rightarrow$ record predecessor

Remove all forward pointers to 17 from recorded nodes.

Level	Nodes (After)
3	$5 \rightarrow 15 \rightarrow 25$
2	$5 \rightarrow 10 \rightarrow 15 \rightarrow 25$
1	$5 \rightarrow 10 \rightarrow 15 \rightarrow 20 \rightarrow 25$
0	$5 \rightarrow 10 \rightarrow 15 \rightarrow 20 \rightarrow 25$

Tiny Code (Simplified Python)

```
import random

class Node:
    def __init__(self, key, level):
        self.key = key
        self.forward = [None] * (level + 1)

class SkipList:
    def __init__(self, max_level=4, p=0.5):
        self.max_level = max_level
        self.p = p
        self.header = Node(-1, max_level)
        self.level = 0

    def delete(self, key):
        update = [None] * (self.max_level + 1)
        current = self.header

        # Traverse from top to bottom
        for i in reversed(range(self.level + 1)):
            while current.forward[i] and current.forward[i].key < key:
                current = current.forward[i]
            update[i] = current

        current = current.forward[0]
```

```
        # Found the node
        if current and current.key == key:
            for i in range(self.level + 1):
                if update[i].forward[i] != current:
                    continue
                update[i].forward[i] = current.forward[i]
            # Reduce level if highest level empty
            while self.level > 0 and self.header.forward[self.level] is None:
                self.level -= 1
```

Why It Matters

- Symmetric to insertion
- No rotations or rebalancing
- Expected $O(\log n)$ performance
- Perfect for ordered maps, databases, key-value stores

A Gentle Proof (Why It Works)

Each level contains a fraction p^i of nodes. The expected number of levels traversed is $O(\log_{1/p} n)$. At each level, we move horizontally $O(1)$ on average.

So expected cost:

$$E[T_{\text{delete}}] = O(\log n)$$

Try It Yourself

1. Insert $5, 10, 15, 17, 20, 25$.
2. Delete 17.
3. Trace all pointer changes level by level.
4. Compare with AVL tree deletion complexity.

Operation	Input	Expected Level 0 Result

Test Cases

Operation	Input	Expected Level 0 Result
Insert	5,10,15,17,20	$5 \to 10 \to 15 \to 17 \to 20$
Delete	17	$5 \to 10 \to 15 \to 20$
Delete	10	$5 \to 15 \to 20$
Delete	5	$15 \to 20$

Complexity

Operation	Time (Expected)	Space
Search	$O(\log n)$	$O(n)$
Insert	$O(\log n)$	$O(n)$
Delete	$O(\log n)$	$O(n)$

Skip List Deletion keeps elegance through simplicity, a clean pointer adjustment instead of tree surgery.

273 Skip List Search

Searching in a Skip List is a dance across levels, we move right until we can't, then down, repeating until we either find the key or conclude it doesn't exist. Thanks to the randomized level structure, the expected time complexity is $O(\log n)$, just like balanced BSTs but with simpler pointer logic.

What Problem Are We Solving?

We need a fast search in a sorted collection that adapts gracefully to dynamic insertions and deletions. Balanced trees guarantee $O(\log n)$ search but need rotations. Skip Lists achieve the same expected time using randomization instead of strict balancing rules.

How It Works (Plain Language)

A skip list has multiple levels of linked lists. Each level acts as a fast lane, skipping over multiple nodes. To search for a key x:

1. Start at the top-left header node.
2. At each level, move right while `next.key < x`.
3. When `next.key  x`, drop down one level.
4. Repeat until level 0.
5. If `current.forward[0].key == x`, found; else, not found.

The search path "zigzags" through levels, visiting roughly $\log n$ nodes on average.

Example Step by Step

Search for $x = 17$ in the following skip list:

Level	Nodes
3	$5 \to 15 \to 25$
2	$5 \to 10 \to 15 \to 25$
1	$5 \to 10 \to 15 \to 17 \to 20 \to 25$
0	$5 \to 10 \to 15 \to 17 \to 20 \to 25$

Traversal:

- Level 3: $5 \to 15 \to (\text{next} = 25 > 17) \to$ drop down
- Level 2: $15 \to (\text{next} = 25 > 17) \to$ drop down
- Level 1: $15 \to 17$ found $\to$ success
- Level 0: confirm 17 exists

Path: $5 \to 15 \to$ (down) $\to 15 \to$ (down) $\to 15 \to 17$

Visualization

Skip list search follows a staircase pattern:

```
Level 3:  5 --------> 15 -----↓
Level 2:  5 ----> 10 --> 15 --↓
Level 1:  5 -> 10 -> 15 -> 17 -> 20
Level 0:  5 -> 10 -> 15 -> 17 -> 20
```

Each "↓" means dropping a level when the next node is too large.

Tiny Code (Simplified Python)

```
class SkipList:
    def __init__(self, max_level=4, p=0.5):
        self.max_level = max_level
        self.p = p
        self.header = Node(-1, max_level)
        self.level = 0

    def search(self, key):
        current = self.header
        # Traverse top-down
        for i in reversed(range(self.level + 1)):
            while current.forward[i] and current.forward[i].key < key:
                current = current.forward[i]
        current = current.forward[0]
        return current and current.key == key
```

Why It Matters

- Simple and efficient: expected $O(\log n)$ time
- Probabilistic balance: avoids tree rotations
- Foundation for ordered maps, indexes, and databases
- Search path length is logarithmic on average

A Gentle Proof (Why It Works)

Each level contains approximately a fraction p of the nodes from the level below. Expected number of levels: $O(\log_{1/p} n)$.

At each level, expected number of horizontal moves: $O(1)$.

So total expected search time:

$$E[T_{\text{search}}] = O(\log n)$$

Try It Yourself

1. Build a skip list with $5, 10, 15, 17, 20, 25$.
2. Search for 17 and trace the path at each level.
3. Search for 13, where do you stop?
4. Compare path length with a binary search tree of same size.

Test Cases

Operation	Input	Expected Output	Path
Search	17	Found	$5 \to 15 \to 17$
Search	10	Found	$5 \to 10$
Search	13	Not Found	$5 \to 10 \to 15$
Search	5	Found	5

Complexity

Operation	Time (Expected)	Space
Search	$O(\log n)$	$O(n)$
Insert	$O(\log n)$	$O(n)$
Delete	$O(\log n)$	$O(n)$

Skip List Search shows how probabilistic structure yields deterministic-like efficiency, walking a staircase of randomness toward certainty.

274 B-Tree Insert

A B-Tree is a balanced search tree designed for external memory systems such as disks or SSDs. Unlike binary trees, each node can store multiple keys and multiple children, minimizing disk I/O by packing more data into a single node. Insertion into a B-Tree preserves sorted order and balance by splitting full nodes as needed.

What Problem Are We Solving?

When data is too large to fit in memory, standard binary trees perform poorly because each node access may trigger a disk read. We need a structure that:

- Reduces the number of I/O operations
- Keeps height small
- Maintains keys in sorted order
- Supports search, insert, and delete in $O(\log n)$

B-Trees solve this by storing many keys per node and balancing themselves through controlled splits.

How It Works (Plain Language)

Each B-Tree node can contain up to $2t - 1$ keys and $2t$ children, where t is the minimum degree.

Insertion steps:

1. Start at root and traverse down like in binary search.
2. If a child node is full (2t − 1 keys), split it before descending.
3. Insert the new key into the appropriate non-full node.

Splitting a full node:

- Middle key moves up to parent
- Left and right halves become separate child nodes

This ensures every node stays within allowed size bounds, keeping height $O(\log_t n)$.

Example Step by Step

Let $t = 2$ (max 3 keys per node). Insert keys in order: $[10, 20, 5, 6, 12, 30, 7, 17]$

Step 1: Insert 10 → Root = [10] Step 2: Insert 20 → [10, 20] Step 3: Insert 5 → [5, 10, 20] Step 4: Insert 6 → Node full → Split

Split [5, 6, 10, 20]:

- Middle key 10 moves up
- Left child [5, 6], right child [20] Tree:

```
      [10]
     /    \
[5, 6]   [20]
```

Step 5: Insert 12 → go right → [12, 20] Step 6: Insert 30 → [12, 20, 30] Step 7: Insert 7 → go left → [5, 6, 7] → full → split

- Middle 6 moves up

Tree now:

```
        [6, 10]
       /   |    \
[5]  [7]  [12, 20, 30]
```

Step 8: Insert 17 → go to [12, 20, 30] → insert [12, 17, 20, 30] → split

- Middle 20 moves up

Final tree:

```
          [6, 10, 20]
         /   |   |   \
       [5] [7] [12,17] [30]
```

Visualization

B-Tree maintains sorted keys at each level and guarantees minimal height by splitting nodes during insertion.

```
Root: [6, 10, 20]
Children: [5], [7], [12, 17], [30]
```

Tiny Code (Simplified Python)

```
class BTreeNode:
    def __init__(self, t, leaf=False):
        self.keys = []
        self.children = []
        self.leaf = leaf
        self.t = t

    def insert_non_full(self, key):
        i = len(self.keys) - 1
        if self.leaf:
            self.keys.append(key)
            self.keys.sort()
        else:
            while i >= 0 and key < self.keys[i]:
                i -= 1
            i += 1
            if len(self.children[i].keys) == 2 * self.t - 1:
                self.split_child(i)
                if key > self.keys[i]:
                    i += 1
            self.children[i].insert_non_full(key)

    def split_child(self, i):
        t = self.t
        y = self.children[i]
        z = BTreeNode(t, y.leaf)
        mid = y.keys[t - 1]
        z.keys = y.keys[t:]
        y.keys = y.keys[:t - 1]
        if not y.leaf:
            z.children = y.children[t:]
            y.children = y.children[:t]
        self.children.insert(i + 1, z)
        self.keys.insert(i, mid)

class BTree:
    def __init__(self, t):
        self.root = BTreeNode(t, True)
        self.t = t

    def insert(self, key):
        r = self.root
```

```
        if len(r.keys) == 2 * self.t - 1:
            s = BTreeNode(self.t)
            s.children.insert(0, r)
            s.split_child(0)
            i = 0
            if key > s.keys[0]:
                i += 1
            s.children[i].insert_non_full(key)
            self.root = s
        else:
            r.insert_non_full(key)
```

Why It Matters

- Disk-friendly: each node fits into one page
- Shallow height: $O(\log_t n)$ levels $\rightarrow$ few disk reads
- Deterministic balance: no randomness, always balanced
- Foundation of file systems, databases, indexes (e.g., NTFS, MySQL, PostgreSQL)

A Gentle Proof (Why It Works)

Each node has between $t-1$ and $2t-1$ keys (except root).

Each split increases height only when the root splits.

Thus, height h satisfies:

$$t^h \leq n \leq (2t)^h$$

Taking logs:

$$h = O(\log_t n)$$

So insertions and searches take $O(t \cdot \log_t n)$, often simplified to $O(\log n)$ when t is constant.

Try It Yourself

1. Build a B-Tree with $t = 2$.
2. Insert $[10, 20, 5, 6, 12, 30, 7, 17]$.
3. Draw the tree after each insertion.
4. Observe when splits occur and which keys promote upward.

Test Cases

Input Keys	t	Final Root	Height
[10,20,5,6,12,30,7,17]	2	[6,10,20]	2
[1,2,3,4,5,6,7,8,9]	2	[4]	3

Complexity

Operation	Time	Space
Search	$O(\log n)$	$O(n)$
Insert	$O(\log n)$	$O(n)$
Delete	$O(\log n)$	$O(n)$

B-Tree insertion is the heartbeat of external memory algorithms, split, promote, balance, ensuring data stays close, shallow, and sorted.

275 B-Tree Delete

Deletion in a B-Tree is more intricate than insertion, we must carefully remove a key while preserving the B-Tree's balance properties. Every node must maintain at least $t - 1$ keys (except the root), so deletion may involve borrowing from siblings or merging nodes.

The goal is to maintain the B-Tree invariants:

- Keys sorted within each node
- Node key count between $t - 1$ and $2t - 1$
- Balanced height

What Problem Are We Solving?

We want to remove a key from a B-Tree without violating balance or occupancy constraints. Unlike binary search trees, where we can simply replace or prune nodes, B-Trees must maintain minimum degree to ensure consistent height and I/O efficiency.

How It Works (Plain Language)

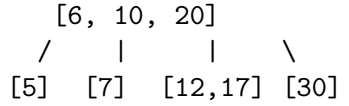
To delete a key k from a B-Tree:

1. If k is in a leaf node:
    - Simply remove it.
2. If k is in an internal node:
    - Case A: If left child has $\quad t$ keys $\rightarrow$ replace k with predecessor.
    - Case B: Else if right child has $\quad t$ keys $\rightarrow$ replace k with successor.
    - Case C: Else both children have $t - 1$ keys $\rightarrow$ merge them and recurse.
3. If k is not in the current node:
    - Move to the correct child.
    - Before descending, ensure the child has at least t keys. If not,
        - Borrow from a sibling with $\quad t$ keys, or
        - Merge with a sibling to guarantee occupancy.

This ensures no underflow occurs during traversal.

Example Step by Step

Let $t = 2$ (max 3 keys per node). B-Tree before deletion:



Delete key 17

- 17 is in leaf [12, 17] → remove it directly

Result:

```
        [6, 10, 20]
       /    |     |    \
     [5]  [7]   [12]   [30]
```

Delete key 10

- 10 is in internal node
- Left child [7] has $t - 1 = 1$ key
- Right child [12] also has 1 key → Merge [7], 10, [12] → [7, 10, 12]

Tree becomes:

```
      [6, 20]
     /    |    \
   [5] [7,10,12] [30]
```

Delete key 6

- 6 in internal node
- Left [5] has 1 key, right [7,10,12] has 2 → borrow from right
- Replace 6 with successor 7

Tree after rebalancing:

```
      [7, 20]
     /    |    \
   [5,6] [10,12] [30]
```

Visualization

Every deletion keeps the tree balanced by ensuring all nodes (except root) stay $t - 1$ full.

```
Before:              After Deleting 10:
$$6,10,20]            [6,20]
 / | | \              / | \
$$5][7][12,17][30]    [5][7,10,12][30]
```

Tiny Code (Simplified Python)

```
class BTreeNode:
    def __init__(self, t, leaf=False):
        self.t = t
        self.keys = []
        self.children = []
        self.leaf = leaf

    def find_key(self, k):
        for i, key in enumerate(self.keys):
            if key >= k:
                return i
        return len(self.keys)

class BTree:
    def __init__(self, t):
        self.root = BTreeNode(t, True)
        self.t = t

    def delete(self, node, k):
        t = self.t
        i = node.find_key(k)

        # Case 1: key in node
        if i < len(node.keys) and node.keys[i] == k:
            if node.leaf:
                node.keys.pop(i)
            else:
                if len(node.children[i].keys) >= t:
                    pred = self.get_predecessor(node, i)
                    node.keys[i] = pred
                    self.delete(node.children[i], pred)
                elif len(node.children[i+1].keys) >= t:
                    succ = self.get_successor(node, i)
                    node.keys[i] = succ
                    self.delete(node.children[i+1], succ)
                else:
                    self.merge(node, i)
                    self.delete(node.children[i], k)
        else:
            # Case 2: key not in node
```

```
            if node.leaf:
                return  # not found
            if len(node.children[i].keys) < t:
                self.fill(node, i)
            self.delete(node.children[i], k)
```

(Helper methods `merge`, `fill`, `borrow_from_prev`, and `borrow_from_next` omitted for brevity)

Why It Matters

- Maintains balanced height after deletions
- Prevents underflow in child nodes
- Ensures $O(\log n)$ complexity
- Used heavily in databases and filesystems where stable performance is critical

A Gentle Proof (Why It Works)

A B-Tree node always satisfies:

$$t - 1 \leq \text{keys per node} \leq 2t - 1$$

Merging or borrowing ensures all nodes remain within bounds. The height h satisfies:

$$h \leq \log_t n$$

So deletions require visiting at most $O(\log_t n)$ nodes and performing constant-time merges/borrows per level.

Hence:

$$T_{\text{delete}} = O(\log n)$$

Try It Yourself

1. Build a B-Tree with $t = 2$.
2. Insert $[10, 20, 5, 6, 12, 30, 7, 17]$.
3. Delete keys in order: $17, 10, 6$.
4. Draw the tree after each deletion and observe merges/borrows.

Test Cases

Input Keys	Delete	Result (Level 0)
[5,6,7,10,12,17,20,30]	17	[5,6,7,10,12,20,30]
[5,6,7,10,12,20,30]	10	[5,6,7,12,20,30]
[5,6,7,12,20,30]	6	[5,7,12,20,30]

Complexity

Operation	Time	Space
Search	$O(\log n)$	$O(n)$
Insert	$O(\log n)$	$O(n)$
Delete	$O(\log n)$	$O(n)$

B-Tree deletion is a surgical balancing act, merging, borrowing, and promoting keys just enough to keep the tree compact, shallow, and sorted.

276 B+ Tree Search

A B+ Tree is an extension of the B-Tree, optimized for range queries and sequential access. All actual data (records or values) reside in leaf nodes, which are linked together to form a sorted list. Internal nodes contain only keys that guide the search.

Searching in a B+ Tree follows the same principle as a B-Tree, top-down traversal based on key comparisons, but ends at the leaf level where the actual data is stored.

What Problem Are We Solving?

We need a disk-friendly search structure that:

- Keeps height small (few disk I/Os)
- Supports fast range scans
- Separates index keys (internal nodes) from records (leaves)

B+ Trees meet these needs with:

- High fan-out: many keys per node
- Linked leaves: for efficient sequential traversal
- Deterministic balance: height always $O(\log n)$

How It Works (Plain Language)

Each internal node acts as a router. Each leaf node contains keys + data pointers.

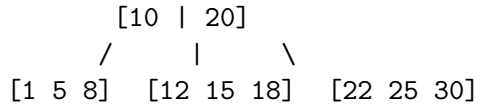
To search for key k:

1. Start at the root.
2. At each internal node, find the child whose key range contains k.
3. Follow that pointer to the next level.
4. Continue until reaching a leaf node.
5. Perform a linear scan within the leaf to find k.

If not found in the leaf, k is not in the tree.

Example Step by Step

Let $t = 2$ (each node holds up to 3 keys). B+ Tree:



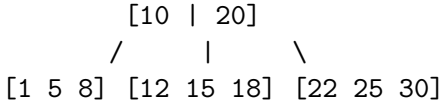
Search for 15:

- Root [10 | 20]: $15 > 10$ and $< 20 \rightarrow$ follow middle pointer
- Node [12 15 18]: found 15

Search for 17:

- Root [10 | 20]: $17 > 10$ and $< 20 \rightarrow$ middle pointer
- Node [12 15 18]: not found $\rightarrow$ not in tree

Visualization



- Internal nodes guide the path
- Leaf nodes hold data (and link to next leaf)
- Search always ends at a leaf

Tiny Code (Simplified Python)

```
class BPlusNode:
    def __init__(self, t, leaf=False):
        self.t = t
        self.leaf = leaf
        self.keys = []
        self.children = []
        self.next = None  # link to next leaf

class BPlusTree:
    def __init__(self, t):
        self.root = BPlusNode(t, True)
        self.t = t

    def search(self, node, key):
        if node.leaf:
            return key in node.keys
        i = 0
        while i < len(node.keys) and key >= node.keys[i]:
            i += 1
        return self.search(node.children[i], key)

    def find(self, key):
        return self.search(self.root, key)
```

Why It Matters

- Efficient disk I/O: high branching factor keeps height low
- All data in leaves: simplifies range queries
- Linked leaves: enable sequential traversal (sorted order)
- Used in: databases, filesystems, key-value stores (e.g., MySQL, InnoDB, NTFS)

A Gentle Proof (Why It Works)

Each internal node has between t and $2t$ children. Each leaf holds between $t-1$ and $2t-1$ keys. Thus, height h satisfies:

$$t^h \leq n \leq (2t)^h$$

Taking logs:

$$h = O(\log_t n)$$

So search time is:

$$T_{\text{search}} = O(\log n)$$

And since the final scan within the leaf is constant (small), total cost remains logarithmic.

Try It Yourself

1. Build a B+ Tree with $t = 2$ and insert keys $[1, 5, 8, 10, 12, 15, 18, 20, 22, 25, 30]$.
2. Search for 15, 17, and 8.
3. Trace your path from root $\rightarrow$ internal $\rightarrow$ leaf.
4. Observe that all searches end in leaves.

Test Cases

Search Key	Expected Result	Path
15	Found	Root $\rightarrow$ Middle $\rightarrow$ Leaf
8	Found	Root $\rightarrow$ Left $\rightarrow$ Leaf
17	Not Found	Root $\rightarrow$ Middle $\rightarrow$ Leaf
25	Found	Root $\rightarrow$ Right $\rightarrow$ Leaf

Complexity

Operation	Time	Space
Search	$O(\log n)$	$O(n)$
Insert	$O(\log n)$	$O(n)$
Range Query	$O(\log n + k)$	$O(n)$

B+ Tree Search exemplifies I/O-aware design, every pointer followed is a disk page, every leaf scan is cache-friendly, and every key lives exactly where range queries want it.

278 B* Tree

A B* Tree is a refined version of the B-Tree, designed to achieve higher node occupancy and fewer splits. It enforces that each node (except root) must be at least two-thirds full, compared to the half-full guarantee in a standard B-Tree.

To achieve this, B* Trees use redistribution between siblings before splitting, which improves space utilization and I/O efficiency, making them ideal for database and file system indexes.

What Problem Are We Solving?

In a standard B-Tree, each node maintains at least $t - 1$ keys (50% occupancy). But frequent splits can cause fragmentation and wasted space.

We want to:

- Increase space efficiency (reduce empty slots)
- Defer splitting when possible
- Maintain balance and sorted order

B* Trees solve this by borrowing and redistributing keys between siblings before splitting, ensuring $\geq 2/3$ occupancy.

How It Works (Plain Language)

A B* Tree works like a B-Tree but with smarter split logic:

1. Insertion path:
    - Traverse top-down to find target leaf.
    - If the target node is full, check its sibling.
2. Redistribution step:
    - If sibling has room, redistribute keys between them and the parent key.
3. Double split step:
    - If both siblings are full, split both into three nodes (two full + one new node), redistributing keys evenly among them.

This ensures every node (except root) is at least 2/3 full, leading to better disk utilization.

Example Step by Step

Let $t = 2$ (max 3 keys per node). Insert keys: $[5, 10, 15, 20, 25, 30, 35]$

Step 1–4: Build like B-Tree until root [10, 20].

```
       [10 | 20]
      /    |    \
  [5]   [15]   [25, 30, 35]
```

Now insert 40 → rightmost node [25, 30, 35] is full.

- Check sibling: left sibling [15] has room → redistribute keys Combine [15], [25, 30, 35], and parent key 20 → [15, 20, 25, 30, 35] Split into three nodes evenly: [15, 20], [25, 30], [35] Parent updated with new separator.

Result:

```
        [20 | 30]
       /     |     \
[5,10,15] [20,25] [30,35,40]
```

Each node 2/3 full, no wasted space.

Visualization

```
          [20 | 30]
         /     |     \
[5 10 15] [20 25] [30 35 40]
```

Redistribution ensures balance and density before splitting.

Tiny Code (Simplified Pseudocode)

```
def insert_bstar(tree, key):
    node = find_leaf(tree.root, key)
    if node.full():
        sibling = node.get_sibling()
        if sibling and not sibling.full():
            redistribute(node, sibling, tree.parent(node))
        else:
            split_three(node, sibling, tree.parent(node))
    insert_into_leaf(node, key)
```

(Actual implementation is more complex, involving parent updates and sibling pointers.)

Why It Matters

- Better space utilization: nodes 66% full
- Fewer splits: more stable performance under heavy inserts
- Improved I/O locality: fewer disk blocks accessed
- Used in: database systems (IBM DB2), file systems (ReiserFS), B*-based caching structures

A Gentle Proof (Why It Works)

In B* Trees:

- Each non-root node contains $\geq \frac{2}{3}(2t-1)$ keys.
- Height h satisfies:

$$\left(\frac{3}{2}t\right)^h \leq n$$

Taking logs:

$$h = O(\log_t n)$$

Thus, height remains logarithmic, but nodes pack more data per level.

Fewer levels $\rightarrow$ fewer I/Os $\rightarrow$ better performance.

Try It Yourself

1. Build a B* Tree with $t = 2$.
2. Insert keys: $[5, 10, 15, 20, 25, 30, 35, 40]$.
3. Watch how redistribution occurs before splits.
4. Compare with B-Tree splits for same sequence.

Test Cases

Input Keys	t	Result	Notes
[5,10,15,20,25]	2	Root [15]	Full utilization
[5,10,15,20,25,30,35]	2	Root [20,30]	Redistribution before split
[1..15]	2	Balanced, 2/3 full nodes	High density

Complexity

Operation	Time	Space	Occupancy
Search	$O(\log n)$	$O(n)$	≥ 66
Insert	$O(\log n)$	$O(n)$	≥ 66
Delete	$O(\log n)$	$O(n)$	≥ 66

B* Trees take the elegance of B-Trees and push them closer to perfect, fewer splits, denser nodes, and smoother scaling for large datasets.

279 Adaptive Radix Tree

An Adaptive Radix Tree (ART) is a space-efficient, cache-friendly data structure that combines ideas from tries and radix trees. It dynamically adapts its node representation based on the number of children, optimizing both memory usage and lookup speed.

Unlike a fixed-size radix tree (which wastes space with sparse nodes), ART chooses a compact node type (like Node4, Node16, Node48, Node256) depending on occupancy, growing as needed.

What Problem Are We Solving?

Standard tries and radix trees are fast but memory-heavy. If keys share long prefixes, many nodes hold only one child, wasting memory.

We want a structure that:

- Keeps O(L) lookup time (L = key length)
- Adapts node size to occupancy
- Minimizes pointer overhead
- Exploits cache locality

ART achieves this by dynamically switching node types as the number of children grows.

How It Works (Plain Language)

Each internal node in ART can be one of four types:

Node Type	Capacity	Description
Node4	4 children	smallest, uses linear search
Node16	16 children	small array, vectorized search
Node48	48 children	index map, stores child pointers
Node256	256 children	direct addressing by byte value

Keys are processed byte by byte, branching at each level. When a node fills beyond its capacity, it upgrades to the next node type.

Example

Insert keys: `["A", "AB", "AC", "AD", "AE"]`

1. Start with root Node4 (can store 4 children).
2. After inserting "AE", Node4 exceeds capacity → upgrade to Node16.
3. Children remain in sorted order by key byte.

This adaptive upgrade keeps nodes dense and efficient.

Example Step by Step

Step	Operation	Node Type	Keys Stored	Note
1	Insert "A"	Node4	A	Create root
2	Insert "AB"	Node4	A, AB	Add branch
3	Insert "AC"	Node4	A, AB, AC	Still under 4
4	Insert "AD"	Node4	A, AB, AC, AD	Full
5	Insert "AE"	Upgrade to Node16	A, AB, AC, AD, AE	Adaptive growth

Visualization

```
Root (Node16)
    'A' → Node
         'B' (Leaf)
         'C' (Leaf)
         'D' (Leaf)
         'E' (Leaf)
```

Each node type adapts its layout for the best performance.

Tiny Code (Simplified Pseudocode)

```
class Node:
    def __init__(self):
        self.children = {}

def insert_art(root, key):
    node = root
    for byte in key:
        if byte not in node.children:
            node.children[byte] = Node()
        node = node.children[byte]
    node.value = True
```

(A real ART dynamically switches between Node4, Node16, Node48, Node256 representations.)

Why It Matters

- Adaptive memory use, no wasted space for sparse nodes
- Cache-friendly, contiguous memory layout

- Fast lookups, vectorized search for Node16
- Used in modern databases (e.g., HyPer, Umbra, DuckDB)

A Gentle Proof (Why It Works)

Let L = key length, b = branching factor (max 256 per byte). In a naive trie, each node allocates $O(b)$ slots, many unused.

In ART:

- Each node stores only actual children, so

$$\text{space} \approx O(n + L)$$

- Lookup remains $O(L)$ since we traverse one node per byte.
- Space improves by factor proportional to sparsity.

Thus ART maintains trie-like performance with hash table-like compactness.

Try It Yourself

1. Insert `["dog", "dot", "door", "dorm"]`
2. Observe how Node4 $\rightarrow$ Node16 transitions happen
3. Count number of nodes, compare with naive trie
4. Measure memory usage and access speed

Test Cases

Keys	Resulting Root Type	Notes
`["a", "b"]`	Node4	2 children
`["a", "b", "c", "d", "e"]`	Node16	Upgrade after 5th insert
`["aa", "ab", "ac"... "az"]`	Node48 or Node256	Dense branching

Complexity

Operation	Time	Space	Adaptive Behavior
Search	$O(L)$	$O(n + L)$	Node grows/shrinks
Insert	$O(L)$	$O(n)$	Node type upgrade
Delete	$O(L)$	$O(n)$	Downgrade if sparse

An Adaptive Radix Tree gives the best of both worlds: prefix compression of tries and space efficiency of hash maps, a modern weapon for high-performance indexing.

280 Trie Compression

A compressed trie (also called a radix tree or Patricia trie) is an optimized form of a trie where chains of single-child nodes are merged into a single edge. Instead of storing one character per node, each edge can hold an entire substring.

This reduces the height of the trie, minimizes memory usage, and accelerates searches, perfect for applications like prefix lookup, routing tables, and dictionary storage.

What Problem Are We Solving?

A naive trie wastes space when many nodes have only one child.

For example, inserting `["cat", "car", "dog"]` into a naive trie yields long, skinny paths:

```
c → a → t
c → a → r
d → o → g
```

We can compress those linear chains into edges labeled with substrings:

```
c → a → "t"
c → a → "r"
d → "og"
```

This saves memory and reduces traversal depth.

How It Works (Plain Language)

The key idea is path compression: whenever a node has a single child, merge them into one edge containing the combined substring.

Step	Operation	Result
1	Build a normal trie	One character per edge
2	Traverse each path	If node has one child, merge
3	Replace chain with a substring edge	Fewer nodes, shorter height

Compressed tries store edge labels as substrings rather than single characters.

Example

Insert `["bear", "bell", "bid", "bull", "buy"]`

1. Start with naive trie.
2. Identify single-child paths.
3. Merge paths:

```
b
    e → "ar"
        "ll"
    u → "ll"
        "y"
```

Each edge now carries a substring rather than a single letter.

Example Step by Step

Step	Insert	Action	Result
1	"bear"	Create path b-e-a-r	4 nodes
2	"bell"	Shares prefix "be"	Merge prefix
3	"bid"	New branch at "b"	Add new edge
4	Compress single-child paths	Replace edges with substrings	

Tiny Code (Simplified Pseudocode)

```
class Node:
    def __init__(self):
        self.children = {}
        self.is_end = False

def insert_trie_compressed(root, word):
    node = root
    i = 0
    while i < len(word):
        for edge, child in node.children.items():
            prefix_len = common_prefix(edge, word[i:])
            if prefix_len > 0:
```

```
                if prefix_len < len(edge):
                    # Split edge
                    remainder = edge[prefix_len:]
                    new_node = Node()
                    new_node.children[remainder] = child
                    node.children[word[i:i+prefix_len]] = new_node
                    del node.children[edge]
                node = node.children[word[i:i+prefix_len]]
                i += prefix_len
                break
        else:
            node.children[word[i:]] = Node()
            node.children[word[i:]].is_end = True
            break
    node.is_end = True
```

This simplified version merges edges whenever possible.

Why It Matters

- Saves memory by merging chains
- Faster search (fewer hops per lookup)
- Ideal for prefix-based queries
- Used in routing tables, autocomplete systems, and dictionaries

A Gentle Proof (Why It Works)

Let n be the total length of all keys and k the number of keys.

- A naive trie can have up to $O(n)$ nodes.
- A compressed trie has at most $k - 1$ internal nodes and k leaves, since each branching point corresponds to a unique prefix shared by at least two keys.

Thus, compressed tries reduce both height and node count:

$$O(n) \text{ nodes (naive)} \quad \rightarrow \quad O(k) \text{ nodes (compressed)}$$

Search and insert remain $O(L)$, where L is key length, but with fewer steps.

Try It Yourself

1. Insert `["car", "cat", "cart", "dog"]`
2. Draw both naive and compressed tries
3. Count number of nodes before and after compression
4. Verify edge labels as substrings

Test Cases

Keys	Naive Trie Nodes	Compressed Trie Nodes
`["a", "b"]`	3	3
`["apple", "app"]`	6	4
`["abc", "abd", "aef"]`	8	6
`["car", "cart", "cat"]`	9	6

Complexity

Operation	Time	Space	Notes
Search	$O(L)$	$O(k)$	L = key length
Insert	$O(L)$	$O(k)$	Split edges when needed
Delete	$O(L)$	$O(k)$	Merge edges if path shrinks

A compressed trie elegantly blends trie structure and path compression, turning long chains into compact edges, a key step toward efficient prefix trees, routing tables, and tries for text indexing.

Section 29. Persistent and Functional Data Structures

281 Persistent Stack

A persistent stack is a versioned data structure that remembers all its past states. Instead of overwriting data, every `push` or `pop` operation creates a new version of the stack while keeping access to the old ones.

This concept is part of functional data structures, where immutability and version history are first-class citizens.

What Problem Are We Solving?

In traditional stacks, each operation mutates the structure, old versions are lost.

Persistent stacks solve this by allowing:

- Access to previous states at any time
- Undo or time-travel features
- Purely functional programs where data is never mutated

Used in compilers, backtracking systems, and functional programming languages.

How It Works (Plain Language)

A stack is a linked list:

- `push(x)` adds a new head node
- `pop()` returns the next node

For persistence, we never modify nodes, instead, each operation creates a new head pointing to existing tails.

Version	Operation	Top Element	Structure
v0	empty	,	
v1	push(10)	10	10 →
v2	push(20)	20	20 → 10 →
v3	pop()	10	10 →

Each version reuses previous nodes, no data copying.

Example

Start with an empty stack `v0`:

1. `v1 = push(v0, 10)` → stack `[10]`
2. `v2 = push(v1, 20)` → stack `[20, 10]`
3. `v3 = pop(v2)` → returns 20, new stack `[10]`

Now we have three accessible versions:

```
v0:
v1: 10
v2: 20 → 10
v3: 10
```

Tiny Code (Python)

```python
class Node:
    def __init__(self, value, next_node=None):
        self.value = value
        self.next = next_node

class PersistentStack:
    def __init__(self, top=None):
        self.top = top

    def push(self, value):
        # new node points to current top
        return PersistentStack(Node(value, self.top))

    def pop(self):
        if not self.top:
            return self, None
        return PersistentStack(self.top.next), self.top.value

    def peek(self):
        return None if not self.top else self.top.value

# Example
v0 = PersistentStack()
v1 = v0.push(10)
v2 = v1.push(20)
v3, popped = v2.pop()

print(v2.peek())  # 20
print(v3.peek())  # 10
```

This approach reuses nodes, creating new versions without mutation.

Tiny Code (C, Conceptual)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int value;
    struct Node* next;
} Node;

typedef struct {
    Node* top;
} Stack;

Stack* push(Stack* s, int value) {
    Node* node = malloc(sizeof(Node));
    node->value = value;
    node->next = s->top;
    Stack* new_stack = malloc(sizeof(Stack));
    new_stack->top = node;
    return new_stack;
}

Stack* pop(Stack* s, int* popped_value) {
    if (!s->top) return s;
    *popped_value = s->top->value;
    Stack* new_stack = malloc(sizeof(Stack));
    new_stack->top = s->top->next;
    return new_stack;
}
```

Every `push` or `pop` creates a new `Stack*` that points to the previous structure.

Why It Matters

- Immutability ensures data safety and concurrency-friendly design
- Versioning allows backtracking, undo, or branching computations
- Foundation for functional programming and persistent data stores

A Gentle Proof (Why It Works)

Each version of the stack shares unchanged nodes with previous versions. Because `push` and `pop` only modify the head reference, older versions remain intact.

If n is the total number of operations,

- Each new version adds $O(1)$ space
- Shared tails ensure total space $= O(n)$

Mathematically:

$$S_n = S_{n-1} + O(1)$$

and old versions never get overwritten, ensuring persistence.

Try It Yourself

1. Build a persistent stack with values [1, 2, 3]
2. Pop once, and confirm earlier versions still have their values
3. Compare with a mutable stack implementation
4. Visualize the shared linked nodes between versions

Test Cases

Operation	Result	Notes
`v1 = push(v0, 10)`	`[10]`	new version
`v2 = push(v1, 20)`	`[20, 10]`	shares 10-node
`v3, val = pop(v2)`	val = 20, `[10]`	old v2 intact
`v1.peek()`	`10`	unaffected by later pops

Complexity

Operation	Time	Space	Notes
Push	$O(1)$	$O(1)$	new head
Pop	$O(1)$	$O(1)$	new top pointer
Access old version	$O(1)$	,	store reference

A persistent stack elegantly combines immutability, sharing, and time-travel, a small but powerful step into the world of functional data structures.

282 Persistent Array

A persistent array is an immutable, versioned structure that allows access to all past states. Instead of overwriting elements, every update creates a new version that shares most of its structure with previous ones.

This makes it possible to "time travel", view or restore any earlier version in constant or logarithmic time, without copying the entire array.

What Problem Are We Solving?

A normal array is mutable, every `arr[i] = x` destroys the old value. If we want history, undo, or branching computation, this is unacceptable.

A persistent array keeps all versions:

Version	Operation	State
v0	`[]`	empty
v1	`set(0, 10)`	`[10]`
v2	`set(0, 20)`	`[20]` (v1 still `[10]`)

Each version reuses unmodified parts of the array, avoiding full duplication.

How It Works (Plain Language)

A persistent array can be implemented using copy-on-write or tree-based structures.

1. Copy-on-Write (Small Arrays)
    - Create a new array copy only when an element changes.
    - Simple but $O(n)$ update cost.
2. Path Copying with Trees (Large Arrays)
    - Represent the array as a balanced binary tree (like a segment tree).
    - Each update copies only the path to the changed leaf.
    - Space per update = $O(\log n)$

So, each version points to a root node. When you modify index i, a new path is created down the tree, while untouched subtrees are shared.

Example

Let's build a persistent array of size 4.

Step 1: Initial version

```
v0 = [0, 0, 0, 0]
```

Step 2: Update index 2

```
v1 = set(v0, 2, 5)  → [0, 0, 5, 0]
```

Step 3: Update index 1

```
v2 = set(v1, 1, 9)  → [0, 9, 5, 0]
```

`v0`, `v1`, and `v2` all coexist independently.

Example Step-by-Step (Tree Representation)

Each node covers a range:

```
Root: [0..3]
     Left [0..1]
           [0] → 0
           [1] → 9
     Right [2..3]
           [2] → 5
           [3] → 0
```

Updating index 1 copies only the path `[0..3] → [0..1] → [1]`, not the entire tree.

Tiny Code (Python, Tree-based)

```
class Node:
    def __init__(self, left=None, right=None, value=0):
        self.left = left
        self.right = right
        self.value = value

def build(l, r):
    if l == r:
        return Node()
    m = (l + r) // 2
    return Node(build(l, m), build(m+1, r))

def update(node, l, r, idx, val):
    if l == r:
        return Node(value=val)
    m = (l + r) // 2
    if idx <= m:
        return Node(update(node.left, l, m, idx, val), node.right)
    else:
        return Node(node.left, update(node.right, m+1, r, idx, val))

def query(node, l, r, idx):
    if l == r:
        return node.value
    m = (l + r) // 2
    return query(node.left, l, m, idx) if idx <= m else query(node.right, m+1, r, idx)

# Example
n = 4
v0 = build(0, n-1)
v1 = update(v0, 0, n-1, 2, 5)
v2 = update(v1, 0, n-1, 1, 9)

print(query(v2, 0, n-1, 2))  # 5
print(query(v1, 0, n-1, 1))  # 0
```

Each update creates a new version root.

Why It Matters

- Time-travel debugging: retrieve old states

- Undo/redo systems in editors
- Branching computations in persistent algorithms
- Functional programming without mutation

A Gentle Proof (Why It Works)

Let n be array size, u number of updates.

Each update copies $O(\log n)$ nodes. So total space:

$$O(n + u \log n)$$

Each query traverses one path $O(\log n)$. No version ever invalidates another, all roots remain accessible.

Persistence holds because we never mutate existing nodes, only allocate new ones and reuse subtrees.

Try It Yourself

1. Build an array of size 8, all zeros.
2. Create v1 = set index $4 \to 7$
3. Create v2 = set index $2 \to 9$
4. Print values from v0, v1, v2
5. Confirm that old versions remain unchanged.

Test Cases

Operation	Input	Output	Notes
build(4)	`[0,0,0,0]`	v0	base
set(v0,2,5)		`[0,0,5,0]`	new version
set(v1,1,9)		`[0,9,5,0]`	v1 reused

Operation	Time	Space	Notes

Complexity

Operation	Time	Space	Notes
Build	$O(n)$	$O(n)$	initial
Update	$O(\log n)$	$O(\log n)$	path copy
Query	$O(\log n)$	,	one path
Access Old Version	$O(1)$	,	root reference

A persistent array turns ephemeral memory into a versioned timeline, each change is a branch, every version eternal. Perfect for functional programming, debugging, and algorithmic history.

283 Persistent Segment Tree

A persistent segment tree is a versioned data structure that supports range queries and point updates, while keeping every past version accessible.

It's a powerful combination of segment trees and persistence, allowing you to query historical states, perform undo operations, and even compare past and present results efficiently.

What Problem Are We Solving?

A standard segment tree allows:

- Point updates: `arr[i] = x`
- Range queries: `sum(l, r)` or `min(l, r)`

But every update overwrites old values. A persistent segment tree solves this by creating a new version on each update, reusing unchanged nodes.

Version	Operation	State
v0	build	`[1, 2, 3, 4]`
v1	update(2, 5)	`[1, 2, 5, 4]`
v2	update(1, 7)	`[1, 7, 5, 4]`

Now you can query any version:

- `query(v0, 1, 3)` → old sum
- `query(v2, 1, 3)` → updated sum

How It Works (Plain Language)

A segment tree is a binary tree where each node stores an aggregate (sum, min, max) over a segment.

Persistence is achieved by path copying:

- When updating index `i`, only nodes on the path from root to leaf are replaced.
- All other nodes are shared between versions.

So each new version costs $O(\log n)$ nodes and space.

Step	Operation	Affected Nodes
1	Build	$O(n)$ nodes
2	Update(2, 5)	$O(\log n)$ new nodes
3	Update(1, 7)	$O(\log n)$ new nodes

Example

Let initial array be `[1, 2, 3, 4]`

1. Build tree (v0)
2. v1 = update(v0, 2 → 5)
3. v2 = update(v1, 1 → 7)

Now:

- `query(v0, 1, 4) = 10`
- `query(v1, 1, 4) = 12`
- `query(v2, 1, 4) = 17`

All versions share most nodes, saving memory.

Example Step-by-Step

Update v0 → v1 at index 2

Version	Tree Nodes Copied	Shared
v1	Path [root → left → right]	Others unchanged

So v1 differs only along one path.

Tiny Code (Python)

```
class Node:
    def __init__(self, val=0, left=None, right=None):
        self.val = val
        self.left = left
        self.right = right

def build(arr, l, r):
    if l == r:
        return Node(arr[l])
    m = (l + r) // 2
    left = build(arr, l, m)
    right = build(arr, m + 1, r)
    return Node(left.val + right.val, left, right)

def update(node, l, r, idx, val):
    if l == r:
        return Node(val)
    m = (l + r) // 2
    if idx <= m:
        left = update(node.left, l, m, idx, val)
        return Node(left.val + node.right.val, left, node.right)
    else:
        right = update(node.right, m + 1, r, idx, val)
        return Node(node.left.val + right.val, node.left, right)

def query(node, l, r, ql, qr):
    if qr < l or ql > r:
        return 0
    if ql <= l and r <= qr:
        return node.val
    m = (l + r) // 2
    return query(node.left, l, m, ql, qr) + query(node.right, m + 1, r, ql, qr)
```

```
# Example
arr = [1, 2, 3, 4]
v0 = build(arr, 0, 3)
v1 = update(v0, 0, 3, 2, 5)
v2 = update(v1, 0, 3, 1, 7)

print(query(v0, 0, 3, 0, 3))  # 10
print(query(v1, 0, 3, 0, 3))  # 12
print(query(v2, 0, 3, 0, 3))  # 17
```

Why It Matters

- Access any version instantly
- Enables time-travel queries
- Supports immutable analytics
- Used in offline queries, competitive programming, and functional databases

A Gentle Proof (Why It Works)

Each update only modifies $O(\log n)$ nodes. All other subtrees are shared, so total space:

$$S(u) = O(n + u \log n)$$

Querying any version costs $O(\log n)$ since only one path is traversed.

Persistence holds since no nodes are mutated, only replaced.

Try It Yourself

1. Build `[1, 2, 3, 4]`
2. Update index 2 $\rightarrow$ 5 (v1)
3. Update index 1 $\rightarrow$ 7 (v2)
4. Query sum(1, 4) in v0, v1, v2
5. Verify shared subtrees via visualization

Test Cases

Version	Operation	Query(0,3)	Notes
v0	`[1,2,3,4]`	10	base
v1	set(2,5)	12	changed one leaf
v2	set(1,7)	17	another update

Complexity

Operation	Time	Space	Notes
Build	$O(n)$	$O(n)$	full tree
Update	$O(\log n)$	$O(\log n)$	path copy
Query	$O(\log n)$	,	one path
Version Access	$O(1)$	,	via root

A persistent segment tree is your immutable oracle, each version a snapshot in time, forever queryable, forever intact.

284 Persistent Linked List

A persistent linked list is a versioned variant of the classic singly linked list, where every insertion or deletion produces a new version without destroying the old one.

Each version represents a distinct state of the list, and all versions coexist by sharing structure, unchanged nodes are reused, only the modified path is copied.

This technique is core to functional programming, undo systems, and immutable data structures.

What Problem Are We Solving?

A mutable linked list loses its history after every change.

With persistence, we preserve all past versions:

Version	Operation	List
v0	empty	
v1	push_front(10)	[10]
v2	push_front(20)	[20, 10]
v3	pop_front()	[10]

Each version is a first-class citizen, you can traverse, query, or compare any version at any time.

How It Works (Plain Language)

Each node in a singly linked list has:

- `value`
- `next` pointer

For persistence, we never mutate nodes. Instead, operations return a new head:

- `push_front(x)`: create a new node `n = Node(x, old_head)`
- `pop_front()`: return `old_head.next` as new head

All old nodes remain intact and shared.

Operation	New Node	Shared Structure
push_front(20)	new head	tail reused
pop_front()	new head (next)	old head still exists

Example

Step-by-step versioning

1. `v0 = []`
2. `v1 = push_front(v0, 10)` → `[10]`
3. `v2 = push_front(v1, 20)` → `[20, 10]`
4. `v3 = pop_front(v2)` → `[10]`

Versions:

```
v0:
v1: 10
v2: 20 → 10
v3: 10
```

All coexist and share structure.

Example (Graph View)

```
v0:
v1: 10 →
v2: 20 → 10 →
v3: 10 →
```

Notice: `v2.tail` is reused from `v1`.

Tiny Code (Python)

```python
class Node:
    def __init__(self, value, next_node=None):
        self.value = value
        self.next = next_node

class PersistentList:
    def __init__(self, head=None):
        self.head = head

    def push_front(self, value):
        new_node = Node(value, self.head)
        return PersistentList(new_node)

    def pop_front(self):
        if not self.head:
            return self, None
        return PersistentList(self.head.next), self.head.value

    def to_list(self):
        result, curr = [], self.head
        while curr:
            result.append(curr.value)
            curr = curr.next
        return result

# Example
v0 = PersistentList()
v1 = v0.push_front(10)
v2 = v1.push_front(20)
```

```
v3, popped = v2.pop_front()

print(v1.to_list())  # [10]
print(v2.to_list())  # [20, 10]
print(v3.to_list())  # [10]
```

Tiny Code (C, Conceptual)

```c
#include <stdio.h>
#include <stdlib.h>

typedef struct Node {
    int value;
    struct Node* next;
} Node;

typedef struct {
    Node* head;
} PList;

PList push_front(PList list, int value) {
    Node* new_node = malloc(sizeof(Node));
    new_node->value = value;
    new_node->next = list.head;
    PList new_list = { new_node };
    return new_list;
}

PList pop_front(PList list, int* popped) {
    if (!list.head) return list;
    *popped = list.head->value;
    PList new_list = { list.head->next };
    return new_list;
}
```

No mutations, only new nodes allocated.

Why It Matters

- Immutable, perfect for functional programs

- Undo / Time-travel, revisit old versions
- Safe concurrency, no data races
- Memory-efficient, tail sharing reuses old structure

A Gentle Proof (Why It Works)

Let n be number of operations. Each `push_front` or `pop_front` creates at most one new node.

Thus:

- Total space after n ops: $O(n)$
- Time per operation: $O(1)$

Persistence is guaranteed since no node is modified in place.

All versions share the unchanged suffix:

$$v_k = \text{Node}(x_k, v_{k-1})$$

Hence, structure sharing is linear and safe.

Try It Yourself

1. Start with empty list
2. Push 3 → Push 2 → Push 1
3. Pop once
4. Print all versions
5. Observe how tails are shared

Test Cases

Operation	Input	Output	Version
push_front	10	[10]	v1
push_front	20	[20, 10]	v2
pop_front	,	[10]	v3
to_list	v1	[10]	,

Complexity

Operation	Time	Space	Notes
push_front	$O(1)$	$O(1)$	new head only
pop_front	$O(1)$	$O(1)$	reuse next
access	$O(n)$	,	same as linked list

A persistent linked list is the simplest gateway to persistence, each operation is $O(1)$, each version immortal. It's the backbone of functional stacks, queues, and immutable collections.

286 Finger Tree

A finger tree is a versatile, persistent data structure that provides amortized O(1) access to both ends (front and back) and O(log n) access or updates in the middle.

It's a functional, immutable sequence structure, a balanced tree augmented with *fingers* (fast access points) to its ends. Finger trees form the foundation for many persistent data types, such as queues, deques, priority sequences, and even rope-like text editors.

What Problem Are We Solving?

Immutable lists are fast at the front but slow at the back. Immutable arrays are the opposite. Deques with persistence are hard to maintain efficiently.

We want:

- $O(1)$ front access
- $O(1)$ back access
- $O(\log n)$ middle access
- Persistence and immutability

Finger trees achieve this by combining shallow digit buffers at the edges with balanced nodes in the middle.

How It Works (Plain Language)

A finger tree is built recursively:

```
FingerTree = Empty
           | Single(a)
           | Deep(prefix, deeper_tree, suffix)
```

- prefix and suffix: small arrays (digits) with 1–4 elements
- deeper_tree: recursively holds nodes of higher rank

The *fingers* (prefix/suffix) give constant-time access to both ends. Insertions push elements into digits; when full, they roll into the deeper tree.

Example

Insert 1, 2, 3, 4, 5:

```
Deep [1,2] (Node [3,4]) [5]
```

You can:

- Push front → prepend into prefix
- Push back → append into suffix
- Access ends in O(1)
- Insert middle → recurse into deeper tree (O(log n))

Each operation returns a new version sharing unchanged subtrees.

Example State

Operation	Structure	Notes
empty	`Empty`	base
push_front(1)	`Single(1)`	one element
push_front(2)	`Deep [2] Empty [1]`	two ends
push_back(3)	`Deep [2] Empty [1,3]`	add suffix
push_back(4)	`Deep [2,4] Empty [1,3]`	balanced growth

Each version reuses most of its structure, ensuring persistence.

Tiny Code (Python – Conceptual)

This is a simplified model, not a complete implementation (real finger trees rely on more type-level machinery).

```
class Empty:
    pass

class Single:
    def __init__(self, value):
        self.value = value

class Deep:
    def __init__(self, prefix, middle, suffix):
        self.prefix = prefix
        self.middle = middle
        self.suffix = suffix

def push_front(tree, x):
    if isinstance(tree, Empty):
        return Single(x)
    if isinstance(tree, Single):
        return Deep([x], Empty(), [tree.value])
    if len(tree.prefix) < 4:
        return Deep([x] + tree.prefix, tree.middle, tree.suffix)
    else:
        # roll prefix into deeper tree
        new_middle = push_front(tree.middle, tree.prefix)
        return Deep([x], new_middle, tree.suffix)

def to_list(tree):
    if isinstance(tree, Empty):
        return []
    if isinstance(tree, Single):
        return [tree.value]
    return tree.prefix + to_list(tree.middle) + tree.suffix
```

This captures the core recursive flavor, constant-time fingers, logarithmic recursion.

Why It Matters

- Generic framework for sequences

- Amortized O(1) insertion/removal at both ends
- O(log n) concatenation, split, or search
- Basis for:
  - Functional deques
  - Priority queues
  - Ordered sequences (like RRB-trees)
  - Incremental editors

A Gentle Proof (Why It Works)

Digits store up to 4 elements, guaranteeing bounded overhead. Each recursive step reduces the size by a constant factor, ensuring depth $= O(\log n)$.

For each operation:

- Ends touched in $O(1)$
- Structural changes at depth $O(\log n)$

Thus, total cost:

$$T(n) = O(\log n), \quad \text{amortized O(1) at ends}$$

Persistence is ensured because all updates build new nodes without modifying existing ones.

Try It Yourself

1. Start with empty tree.
2. Push 1, 2, 3, 4.
3. Pop front, observe structure.
4. Push 5, inspect sharing between versions.
5. Convert each version to list, compare results.

Test Cases

Operation	Result	Notes
push_front(1)	[1]	base
push_front(2)	[2, 1]	prefix growth
push_back(3)	[2, 1, 3]	suffix add
pop_front()	[1, 3]	remove from prefix

Operation	Result	Notes

Complexity

Operation	Time	Space	Notes
push_front/back	$O(1)$ amortized	$O(1)$	uses digits
pop_front/back	$O(1)$ amortized	$O(1)$	constant fingers
random access	$O(\log n)$	$O(\log n)$	recursion
concat/split	$O(\log n)$	$O(\log n)$	efficient split

A finger tree is the Swiss Army knife of persistent sequences, fast at both ends, balanced within, and beautifully immutable. It's the blueprint behind countless functional data structures.

287 Zipper Structure

A zipper is a powerful technique that makes immutable data structures behave like mutable ones. It provides a focus—a pointer-like position—inside a persistent structure (list, tree, etc.), allowing localized updates, navigation, and edits without mutation.

Think of it as a cursor in a purely functional world. Every movement or edit yields a new version, while sharing unmodified parts.

What Problem Are We Solving?

Immutable data structures can't be "modified in place." You can't just "move a cursor" or "replace an element" without reconstructing the entire structure.

A zipper solves this by maintaining:

1. The focused element, and
2. The context (what's on the left/right or above/below).

You can then move, update, or rebuild efficiently, reusing everything else.

How It Works (Plain Language)

A zipper separates a structure into:

- Focus: current element under attention
- Context: reversible description of the path you took

When you move the focus, you update the context. When you change the focused element, you create a new node and rebuild from context.

For lists:

```
Zipper = (Left, Focus, Right)
```

For trees:

```
Zipper = (ParentContext, FocusNode)
```

You can think of it like a tape in a Turing machine—everything to the left and right is preserved.

Example (List Zipper)

We represent a list `[a, b, c, d]` with a cursor on `c`:

```
Left: [b, a]   Focus: c   Right: [d]
```

From here:

- `move_left` → focus = `b`
- `move_right` → focus = `d`
- `update(x)` → replace `c` with `x`

All in O(1), returning a new zipper version.

Operation	Result	Description

Example Operations

Operation	Result	Description
`from_list([a,b,c,d])`	([ ], a, [b,c,d])	init at head
`move_right`	([a], b, [c,d])	shift focus right
`update('X')`	([a], X, [c,d])	replace focus
`to_list`	[a,X,c,d]	rebuild full list

Tiny Code (Python – List Zipper)

```
class Zipper:
    def __init__(self, left=None, focus=None, right=None):
        self.left = left or []
        self.focus = focus
        self.right = right or []

    @staticmethod
    def from_list(lst):
        if not lst: return Zipper([], None, [])
        return Zipper([], lst[0], lst[1:])

    def move_left(self):
        if not self.left: return self
        return Zipper(self.left[:-1], self.left[-1], [self.focus] + self.right)

    def move_right(self):
        if not self.right: return self
        return Zipper(self.left + [self.focus], self.right[0], self.right[1:])

    def update(self, value):
        return Zipper(self.left, value, self.right)

    def to_list(self):
        return self.left + [self.focus] + self.right

# Example
```

```
z = Zipper.from_list(['a', 'b', 'c', 'd'])
z1 = z.move_right().move_right()   # focus on 'c'
z2 = z1.update('X')
print(z2.to_list())  # ['a', 'b', 'X', 'd']
```

Each operation returns a new zipper, persistent editing made simple.

Example (Tree Zipper – Conceptual)

A tree zipper stores the path to the root as context:

```
Zipper = (ParentPath, FocusNode)
```

Each parent in the path remembers which side you came from, so you can rebuild upward after an edit.

For example, editing a leaf `L` creates a new `L'` and rebuilds only the nodes along the path, leaving other subtrees untouched.

Why It Matters

- Enables localized updates in immutable structures
- Used in functional editors, parsers, navigation systems
- Provides O(1) local movement, O(depth) rebuilds
- Core concept in Huet's zipper, a foundational idea in functional programming

A Gentle Proof (Why It Works)

Each movement or edit affects only the local context:

- Move left/right in a list $\rightarrow O(1)$
- Move up/down in a tree $\rightarrow O(1)$
- Rebuilding full structure $\rightarrow O(\text{depth})$

No mutation occurs; each version reuses all untouched substructures.

Formally, if S is the original structure and f the focus,

$$\text{zip}(S) = (\text{context}, f)$$

and

$$\text{unzip}(\text{context}, f) = S$$

ensuring reversibility.

Try It Yourself

1. Create a zipper from `[1,2,3,4]`
2. Move focus to 3
3. Update focus to 99
4. Rebuild full list
5. Verify older zipper still has old value

Test Cases

Step	Operation	Result	Notes
1	`from_list([a,b,c,d])`	([ ], a, [b,c,d])	init
2	`move_right()`	([a], b, [c,d])	shift focus
3	`update('X')`	([a], X, [c,d])	edit
4	`to_list()`	[a, X, c, d]	rebuild

Complexity

Operation	Time	Space	Notes
Move left/right	$O(1)$	$O(1)$	shift focus
Update	$O(1)$	$O(1)$	local replacement
Rebuild	$O(n)$	$O(1)$	when unzipping
Access old version	$O(1)$	,	persistent

A zipper turns immutability into interactivity. With a zipper, you can move, focus, and edit, all without breaking persistence. It's the bridge between static structure and dynamic navigation.

289 Trie with Versioning

A Trie with Versioning is a persistent data structure that stores strings (or sequences) across multiple historical versions. Each new update—an insertion, deletion, or modification—creates a new version of the trie without mutating previous ones, using path copying for structural sharing.

This enables time-travel queries: you can look up keys as they existed at any point in history.

What Problem Are We Solving?

We want to maintain a versioned dictionary of strings or sequences, supporting:

- Fast prefix search (O(length))
- Efficient updates without mutation
- Access to past versions (e.g., snapshots, undo/redo, history)

A versioned trie achieves all three by copying only the path from the root to modified nodes while sharing all other subtrees.

Common use cases:

- Versioned symbol tables
- Historical dictionaries
- Autocomplete with rollback
- Persistent tries in functional languages

How It Works (Plain Language)

Each trie node contains:

- A mapping from character → child node
- A flag marking end of word

For persistence:

- When you insert or delete, copy only nodes on the affected path.
- Old nodes remain untouched and shared by old versions.

Thus, version v_{k+1} differs from v_k only along the modified path.

Tiny Code (Conceptual Python)

```
class TrieNode:
    def __init__(self, children=None, is_end=False):
        self.children = dict(children or {})
        self.is_end = is_end

def insert(root, word):
    def _insert(node, i):
        node = TrieNode(node.children, node.is_end)
        if i == len(word):
```

```
            node.is_end = True
            return node
        ch = word[i]
        node.children[ch] = _insert(node.children.get(ch, TrieNode()), i + 1)
        return node
    return _insert(root, 0)

def search(root, word):
    node = root
    for ch in word:
        if ch not in node.children:
            return False
        node = node.children[ch]
    return node.is_end
```

Each call to `insert` returns a new root (new version), sharing all unmodified branches.

Example

Version	Operation	Trie Content
v1	insert("cat")	{ "cat" }
v2	insert("car")	{ "cat", "car" }
v3	insert("dog")	{ "cat", "car", "dog" }
v4	delete("car")	{ "cat", "dog" }

Versions share nodes for prefix `"c"` between all earlier versions.

Why It Matters

- Immutable and Safe: No in-place mutation, perfect for functional systems
- Efficient Rollback: Access any prior version in $O(1)$ time
- Prefix Sharing: Saves memory through structural reuse
- Practical for History: Ideal for versioned dictionaries, IDEs, search indices

A Gentle Proof (Why It Works)

Each insertion copies one path of length L (word length). Total time complexity:

$$T_{\text{insert}} = O(L)$$

Each node on the new path shares all other unchanged subtrees. If N is total stored characters across all versions,

$$\text{Space} = O(N)$$

Each version root is a single pointer, enabling $O(1)$ access:

$$\text{Version}_i = \text{Root}_i$$

Old versions remain fully usable, as they never mutate.

Try It Yourself

1. Insert "cat", "car", "dog" into versioned trie
2. Delete "car" to form new version
3. Query prefix "ca" in all versions
4. Check that "car" exists only before deletion
5. Print shared node counts across versions

Test Case

Step	Operation	Version	Exists in Version	Result
1	insert("cat")	v1	cat	True
2	insert("car")	v2	car, cat	True
3	insert("dog")	v3	cat, car, dog	True
4	delete("car")	v4	car (no), cat, dog	False

Complexity

Operation	Time	Space	Notes
Insert	$O(L)$	$O(L)$	Path-copying
Delete	$O(L)$	$O(L)$	Path-copying
Lookup	$O(L)$	$O(1)$	Follows shared structure
Access old version	$O(1)$	,	Version pointer access

A Trie with Versioning blends structural sharing with prefix indexing. Each version is a frozen snapshot—compact, queryable, and immutable—perfect for versioned word histories.

290 Persistent Union-Find

A Persistent Union-Find extends the classical Disjoint Set Union (DSU) structure to support *time-travel queries*. Instead of mutating the parent and rank arrays in place, each union operation produces a new version, enabling queries like:

- "Are x and y connected at version v?"
- "What did the set look like before the last merge?"

This structure is vital for dynamic connectivity problems where the history of unions matters.

What Problem Are We Solving?

Classical DSU supports `find` and `union` efficiently in near-constant time, but only for a single evolving state. Once you merge two sets, the old version is gone.

We need a versioned DSU that keeps all previous states intact, supporting:

- Undo/rollback of operations
- Queries over past connectivity
- Offline dynamic connectivity analysis

How It Works (Plain Language)

A Persistent Union-Find uses path copying (similar to persistent arrays) to maintain multiple versions:

- Each `union` creates a new version
- Only affected parent and rank entries are updated in a new structure
- All other nodes share structure with the previous version

There are two main designs:

1. Full persistence using path copying in functional style
2. Partial persistence using rollback stack (undo operations)

We focus here on *full persistence*.

Tiny Code (Conceptual Python)

```python
class PersistentDSU:
    def __init__(self, n):
        self.versions = []
        parent = list(range(n))
        rank = [0] * n
        self.versions.append((parent, rank))

    def find(self, parent, x):
        if parent[x] == x:
            return x
        return self.find(parent, parent[x])

    def union(self, ver, x, y):
        parent, rank = [*ver[0]], [*ver[1]]  # copy arrays
        rx, ry = self.find(parent, x), self.find(parent, y)
        if rx != ry:
            if rank[rx] < rank[ry]:
                parent[rx] = ry
            elif rank[rx] > rank[ry]:
                parent[ry] = rx
            else:
                parent[ry] = rx
                rank[rx] += 1
        self.versions.append((parent, rank))
        return len(self.versions) - 1  # new version index

    def connected(self, ver, x, y):
        parent, _ = self.versions[ver]
        return self.find(parent, x) == self.find(parent, y)
```

Each union returns a new version index. You can query `connected(version, a, b)` at any time.

Example

Step	Operation	Version	Connections
1	make-set(5)	v0	0 1 2 3 4
2	union(0,1)	v1	{0,1}, 2, 3, 4
3	union(2,3)	v2	{0,1}, {2,3}, 4
4	union(1,2)	v3	{0,1,2,3}, 4

Step	Operation	Version	Connections
5	query connected(0,1)	v1	True
6	query connected(1,3)	v1	False (not yet merged)

You can check connections at any version.

Why It Matters

- Time-travel queries across historical versions
- Non-destructive updates allow safe rollback
- Crucial for offline dynamic connectivity, e.g., edge insertions over time
- Simplifies debugging, simulation, and version tracking

A Gentle Proof (Why It Works)

Let n be the number of elements and q the number of versions.

Each version differs in only a small number of parent/rank entries. If each `union` copies $O(\alpha(n))$ elements, total space after q operations is:

$$O(n + q\alpha(n))$$

Each query operates on a fixed version in:

$$O(\alpha(n))$$

Path compression is often replaced with *partial compression* or omitted to ensure persistence (full path compression breaks immutability).

Try It Yourself

1. Initialize DSU with 5 elements
2. Perform unions step by step, saving each version
3. Query connectivity across multiple versions
4. Undo merges by reverting to older versions
5. Visualize parent tree evolution

Test Cases

Version	Query	Result
v0	connected(0,1)	False
v1	connected(0,1)	True
v2	connected(2,3)	True
v3	connected(1,3)	True
v1	connected(1,3)	False

Complexity

Operation	Time	Space	Notes
Find	$O(\alpha(n))$	$O(1)$	Per version
Union	$O(\alpha(n))$	$O(n)$ copy	Copy-on-write path
Connected	$O(\alpha(n))$	$O(1)$	Versioned query
Access old version	$O(1)$	,	Version pointer lookup

A Persistent Union-Find is a historical map of connectivity. Each version captures a snapshot of relationships—immutable, queryable, and efficient—ideal for evolving graphs and rollback-capable algorithms.

Section 30. Advanced Trees and Range Queries

291 Sparse Table Build

A Sparse Table is a static data structure for answering idempotent range queries in O(1) time after O(n log n) preprocessing. It is perfect for Range Minimum/Maximum Query (RMQ), GCD, and any operation where combining overlapping answers is valid, such as `min`, `max`, `gcd`, `lcm` (with care), and bitwise `and/or`. It is not suitable for sum or other non-idempotent operations if you require O(1) queries.

What Problem Are We Solving?

Given an array `A[0..n-1]`, we want to answer queries like

- RMQ: minimum on interval `[L, R]`
- RMaxQ: maximum on interval `[L, R]` in O(1) time per query, with no updates.

How It Works (Plain Language)

Precompute answers for all ranges whose lengths are powers of two. Let `st[k][i]` store the answer on the interval of length `2^k` starting at `i`, that is `[i, i + 2^k - 1]`.

Build recurrence:

- Base layer `k = 0`: intervals of length 1 `st[0][i] = A[i]`
- Higher layers: combine two halves of length `2^{k-1} st[k][i] = op(st[k-1][i], st[k-1][i + 2^{k-1}])`

To answer a query on `[L, R]`, let `len = R - L + 1`, `k = floor(log2(len))`. For idempotent operations like `min` or `max`, we can cover the range with two overlapping blocks:

- Block 1: `[L, L + 2^k - 1]`
- Block 2: `[R - 2^k + 1, R]` Then

$$\text{ans} = \text{op}\left(\text{st}[k][L],\ \text{st}[k][R - 2^k + 1]\right)$$

Example Step by Step

Array `A = [7, 2, 3, 0, 5, 10, 3, 12, 18]`, `op = min`.

1. Build `st[0]` (length 1): `st[0] = [7, 2, 3, 0, 5, 10, 3, 12, 18]`
2. Build `st[1]` (length 2): `st[1][i] = min(st[0][i], st[0][i+1]) st[1] = [2, 2, 0, 0, 5, 3, 3, 12]`
3. Build `st[2]` (length 4): `st[2][i] = min(st[1][i], st[1][i+2]) st[2] = [0, 0, 0, 0, 3, 3]`
4. Build `st[3]` (length 8): `st[3][i] = min(st[2][i], st[2][i+4]) st[3] = [0, 0]`

Query example: RMQ on `[3, 8] len = 6`, `k = floor(log2(6)) = 2`, `2^k = 4`

- Block 1: `[3, 6]` uses `st[2][3]`
- Block 2: `[5, 8]` uses `st[2][5]` Answer

$$\min\left(\text{st}[2][3], \text{st}[2][5]\right) = \min(0, 3) = 0$$

Tiny Code (Python, RMQ with min)

```python
import math

def build_sparse_table(arr, op=min):
    n = len(arr)
    K = math.floor(math.log2(n)) + 1
    st = [[0] * n for _ in range(K)]
    for i in range(n):
        st[0][i] = arr[i]
    j = 1
    while (1 << j) <= n:
        step = 1 << (j - 1)
        for i in range(n - (1 << j) + 1):
            st[j][i] = op(st[j - 1][i], st[j - 1][i + step])
        j += 1
    # Precompute logs for O(1) queries
    lg = [0] * (n + 1)
    for i in range(2, n + 1):
        lg[i] = lg[i // 2] + 1
    return st, lg

def query(st, lg, L, R, op=min):
    length = R - L + 1
    k = lg[length]
    return op(st[k][L], st[k][R - (1 << k) + 1])

# Example
A = [7, 2, 3, 0, 5, 10, 3, 12, 18]
st, lg = build_sparse_table(A, op=min)
print(query(st, lg, 3, 8, op=min))  # 0
print(query(st, lg, 0, 2, op=min))  # 2
```

For `max`, just pass `op=max`. For `gcd`, pass `math.gcd`.

Why It Matters

- O(1) query time for static arrays
- O(n log n) preprocessing with simple transitions
- Excellent for RMQ style tasks, LCA via RMQ on Euler tours, and many competitive programming problems
- Cache friendly and implementation simple compared to segment trees when no updates are needed

A Gentle Proof (Why It Works)

The table stores answers for all intervals of length `2^k`. Any interval `[L, R]` can be covered by two overlapping power of two blocks of equal length `2^k`, where `k = floor(log2(R - L + 1))`. For idempotent operations `op`, overlap does not affect correctness, so

$$\text{op}([L, R]) = \text{op}([L, L + 2^k - 1],\ [R - 2^k + 1, R])$$

Both blocks are precomputed, so the query is constant time.

Try It Yourself

1. Build a table for `A = [5, 4, 3, 6, 1, 2]` with `op = min`.
2. Answer RMQ on `[1, 4]` and `[0, 5]`.
3. Swap `op` to `max` and recheck.
4. Use `op = gcd` and verify results on several ranges.

Test Cases

Array	op	Query	Expected
[7, 2, 3, 0, 5, 10, 3]	min	[0, 2]	2
[7, 2, 3, 0, 5, 10, 3]	min	[3, 6]	0
[1, 5, 2, 4, 6, 1, 3]	max	[2, 5]	6
[12, 18, 6, 9, 3]	gcd	[1, 4]	3

Complexity

Phase	Time	Space
Preprocess	$O(n \log n)$	$O(n \log n)$
Query	$O(1)$	,

Note Sparse Table supports static data. If you need updates, consider a segment tree or Fenwick tree. Sparse Table excels when the array is fixed and you need very fast queries.

292 Cartesian Tree

A Cartesian Tree is a binary tree built from an array such that:

1. In-order traversal of the tree reproduces the array, and
2. The tree satisfies the heap property with respect to the array values (min-heap or max-heap).

This structure elegantly bridges arrays and binary trees, and plays a key role in algorithms for Range Minimum Query (RMQ), Lowest Common Ancestor (LCA), and sequence decomposition.

What Problem Are We Solving?

We want to represent an array $A[0..n-1]$ as a tree that encodes range relationships. For RMQ, if the tree is a min-heap Cartesian Tree, then the LCA of nodes i and j corresponds to the index of the minimum element in the range $[i, j]$.

Thus, building a Cartesian Tree gives us an elegant path from RMQ to LCA in $O(1)$ after $O(n)$ preprocessing.

How It Works (Plain Language)

A Cartesian Tree is built recursively:

- The root is the smallest element (for min-heap) or largest (for max-heap).
- The left subtree is built from elements to the left of the root.
- The right subtree is built from elements to the right of the root.

A more efficient linear-time construction uses a stack:

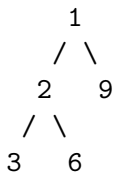
1. Traverse the array from left to right.
2. Maintain a stack of nodes in increasing order.
3. For each new element, pop while the top is greater, then attach the new node as the right child of the last popped node or the left child of the current top.

Example

Let $A = [3, 2, 6, 1, 9]$

1. Start with empty stack
2. Insert 3 → stack = [3]
3. Insert 2 → pop 3 (since $3 > 2$)
   - 2 becomes parent of 3
   - stack = [2]
4. Insert 6 → $6 > 2$ → right child
   - stack = [2, 6]
5. Insert 1 → pop 6, pop 2 → 1 is new root
   - 2 becomes right child of 1
6. Insert 9 → right child of 6

Tree structure (min-heap):



In-order traversal: `[3, 2, 6, 1, 9]` Heap property: every parent is smaller than its children

Tiny Code (Python, Min-Heap Cartesian Tree)

```
class Node:
    def __init__(self, val):
        self.val = val
        self.left = None
        self.right = None

def build_cartesian_tree(arr):
```

```
    stack = []
    root = None
    for val in arr:
        node = Node(val)
        last = None
        while stack and stack[-1].val > val:
            last = stack.pop()
        node.left = last
        if stack:
            stack[-1].right = node
        else:
            root = node
        stack.append(node)
    return root

def inorder(node):
    return inorder(node.left) + [node.val] + inorder(node.right) if node else []
```

Example usage:

```
A = [3, 2, 6, 1, 9]
root = build_cartesian_tree(A)
print(inorder(root))  # [3, 2, 6, 1, 9]
```

Why It Matters

- RMQ in O(1): RMQ becomes LCA in Cartesian Tree (after Euler Tour + Sparse Table).
- Monotonic Stack Connection: Linear construction mirrors the logic of stack-based range problems (Next Greater Element, Histogram).
- Divide-and-Conquer Decomposition: Represents array's recursive structure.
- Efficient Building: Linear time with stack.

A Gentle Proof (Why It Works)

Each element is pushed and popped at most once, so total operations $= O(n)$. Heap property ensures RMQ correctness:

- In min-heap tree, root of any subtree is the minimum of that segment.
- Thus, LCA(i, j) gives the index of $\min(A[i..j])$.

So by reducing RMQ to LCA, we achieve:

$$\text{RMQ}(i, j) = \text{index}(\text{LCA}(i, j))$$

Try It Yourself

1. Build a Cartesian Tree for $A = [4, 5, 2, 3, 1]$ (min-heap).
2. Verify in-order traversal equals original array.
3. Mark parents smaller than children.
4. Identify RMQ(1, 3) from the tree using LCA.

Test Cases

Array	Tree Type	Root	RMQ(1, 3)	Inorder Matches
[3, 2, 6, 1, 9]	min-heap	1	2	
[5, 4, 3, 2, 1]	min-heap	1	2	
[1, 2, 3, 4, 5]	min-heap	1	2	
[2, 7, 5, 9]	min-heap	2	5	

Complexity

Operation	Time	Space	Notes
Build	$O(n)$	$O(n)$	Stack-based construction
Query (RMQ)	$O(1)$	,	After Euler + Sparse Table
LCA Preprocess	$O(n \log n)$	$O(n \log n)$	Sparse Table method

A Cartesian Tree weaves together order and hierarchy: in-order for sequence, heap for dominance, a silent bridge between arrays and trees.

293 Segment Tree Beats

Segment Tree Beats is an advanced variant of the classical segment tree that can handle non-trivial range queries and updates beyond sum, min, or max. It's designed for problems where the operation is *not linear* or *not invertible*, such as range chmin/chmax, range add with min tracking, or range second-min queries.

It "beats" the limitation of classical lazy propagation by storing extra state (like second minimum, second maximum) to decide when updates can stop early.

What Problem Are We Solving?

Standard segment trees can't efficiently handle complex updates like:

- "Set all $A[i]$ in $[L, R]$ to `min(A[i], x)`"
- "Set all $A[i]$ in $[L, R]$ to `max(A[i], x)`"

Because different elements in a segment may behave differently depending on their value relative to `x`.

Segment Tree Beats solves this by maintaining extra constraints in each node so we can "beat" recursion and skip branches early when conditions are met.

How It Works (Plain Language)

Each node stores not just an aggregate but *enough info to know when an operation can be fully applied.*

For Range Chmin (A[i] = min(A[i], x)):

- If `max <= x`: nothing changes
- If `second_max < x < max`: only elements with `max` are updated
- If `x < second_max`: recurse to children

Each node stores:

- `max` (maximum value in range)
- `second_max` (second largest value)
- `count_max` (number of times `max` appears)
- `sum` (sum over range)

This lets us decide update logic without touching all elements.

Example (Range Chmin)

Let $A = [4, 7, 6, 3]$

We apply `chmin(L=0, R=3, x=5)` $\rightarrow$ every element > 5 is set to 5.

Step:

1. Node `[0, 3]`: `max = 7`, `second_max = 6`
2. Since `x = 5 < second_max = 6`, recurse
3. Update left child `[0,1]`: has `7` $\rightarrow$ `7` becomes `5`
4. Update right `[2,3]`: `max = 6` $\rightarrow$ `6` becomes `5`

New array: `[4, 5, 5, 3]`

Tiny Code (Simplified Range Chmin)

```
class Node:
    def __init__(self):
        self.sum = 0
        self.max = 0
        self.smax = -float('inf')
        self.cnt = 0
        self.l = None
        self.r = None

def merge(a, b):
    node = Node()
    node.sum = a.sum + b.sum
    if a.max == b.max:
        node.max = a.max
        node.smax = max(a.smax, b.smax)
        node.cnt = a.cnt + b.cnt
    elif a.max > b.max:
        node.max = a.max
        node.smax = max(a.smax, b.max)
        node.cnt = a.cnt
    else:
        node.max = b.max
        node.smax = max(a.max, b.smax)
        node.cnt = b.cnt
    return node

def push_chmin(node, x, length):
    if node.max <= x:
        return
    node.sum -= (node.max - x) * node.cnt
    node.max = x

def update_chmin(node, l, r, ql, qr, x):
    if r < ql or qr < l or node.max <= x:
        return
    if ql <= l and r <= qr and node.smax < x:
        push_chmin(node, x, r - l + 1)
```

```
        return
    m = (l + r) // 2
    update_chmin(node.l, l, m, ql, qr, x)
    update_chmin(node.r, m+1, r, ql, qr, x)
    new = merge(node.l, node.r)
    node.max, node.smax, node.cnt, node.sum = new.max, new.smax, new.cnt, new.sum
```

This is the essence: skip updates when possible, split when necessary.

Why It Matters

- Handles non-linear updates efficiently
- Preserves logarithmic complexity by reducing unnecessary recursion
- Used in many competitive programming RMQ-like challenges with range cap operations
- Generalizes segment tree to "hard" problems (range `min` caps, range `max` caps, conditional sums)

A Gentle Proof (Why It Works)

The trick: by storing max, second max, and count, we can stop descending if the operation affects only elements equal to max. At most O(log n) nodes per update because:

- Each update lowers some max values
- Each element's value decreases logarithmically before stabilizing

Thus total complexity amortizes to:

$$O((n+q)\log n)$$

Try It Yourself

1. Build a Segment Tree Beats for $A = [4, 7, 6, 3]$.
2. Apply `chmin(0,3,5)` $\rightarrow$ verify `[4,5,5,3]`.
3. Apply `chmin(0,3,4)` $\rightarrow$ verify `[4,4,4,3]`.
4. Track `sum` after each operation.

Test Cases

Array	Operation	Result
[4,7,6,3]	chmin(0,3,5)	[4,5,5,3]
[4,5,5,3]	chmin(1,2,4)	[4,4,4,3]
[1,10,5,2]	chmin(0,3,6)	[1,6,5,2]
[5,5,5]	chmin(0,2,4)	[4,4,4]

Complexity

Operation	Time (Amortized)	Space	Notes
Build	$O(n)$	$O(n)$	Same as normal segment tree
Range Chmin	$O(\log n)$	$O(n)$	Amortized over operations
Query (Sum)	$O(\log n)$	,	Combine like usual

Segment Tree Beats lives at the intersection of elegance and power, retaining $O(\log n)$ intuition while tackling the kinds of operations classical segment trees can't touch.

294 Merge Sort Tree

A Merge Sort Tree is a segment tree where each node stores a sorted list of the elements in its range. It allows efficient queries that depend on order statistics, such as counting how many elements fall within a range or finding the k-th smallest element in a subarray.

It's called "Merge Sort Tree" because it is built exactly like merge sort: divide, conquer, and merge sorted halves.

What Problem Are We Solving?

Classical segment trees handle sum, min, or max, but not *value-based* queries. Merge Sort Trees enable operations like:

- Count how many numbers in $A[L..R]$ are $\leq x$
- Count elements in a value range $[a, b]$
- Find the k-th smallest element in $A[L..R]$

These problems often arise in range frequency queries, inversions counting, and offline queries.

How It Works (Plain Language)

Each node of the tree covers a segment `[l, r]` of the array. Instead of storing a single number, it stores a sorted list of all elements in that segment.

Building:

1. If `l == r`, store `[A[l]]`.
2. Otherwise, recursively build left and right children.
3. Merge the two sorted lists to form this node's list.

Querying: To count numbers $\leq x$ in range `[L, R]`:

- Visit all segment tree nodes that fully or partially overlap `[L, R]`.
- In each node, binary search for position of `x` in the node's sorted list.

Example

Let $A = [2, 5, 1, 4, 3]$

Step 1: Build Tree

Each leaf stores one value:

Node Range	Stored List
[0,0]	[2]
[1,1]	[5]
[2,2]	[1]
[3,3]	[4]
[4,4]	[3]

Now merge:

Node Range	Stored List
[0,1]	[2,5]
[2,3]	[1,4]
[2,4]	[1,3,4]
[0,4]	[1,2,3,4,5]

Step 2: Query Example

Count elements ≤ 3 in range `[1, 4]`.

We query nodes that cover `[1,4]`: `[1,1]`, `[2,3]`, `[4,4]`.

- `[1,1]` → list = `[5]` → count = 0
- `[2,3]` → list = `[1,4]` → count = 1
- `[4,4]` → list = `[3]` → count = 1

Total = 2 elements 3.

Tiny Code (Python, Count x)

```
import bisect

class MergeSortTree:
    def __init__(self, arr):
        self.n = len(arr)
        self.tree = [[] for _ in range(4 * self.n)]
        self._build(arr, 1, 0, self.n - 1)

    def _build(self, arr, node, l, r):
        if l == r:
            self.tree[node] = [arr[l]]
            return
        m = (l + r) // 2
        self._build(arr, node * 2, l, m)
        self._build(arr, node * 2 + 1, m + 1, r)
        self.tree[node] = sorted(self.tree[node * 2] + self.tree[node * 2 + 1])

    def query_leq(self, node, l, r, ql, qr, x):
        if r < ql or qr < l:
            return 0
        if ql <= l and r <= qr:
            return bisect.bisect_right(self.tree[node], x)
        m = (l + r) // 2
        return (self.query_leq(node * 2, l, m, ql, qr, x) +
                self.query_leq(node * 2 + 1, m + 1, r, ql, qr, x))

# Example
A = [2, 5, 1, 4, 3]
```

```
mst = MergeSortTree(A)
print(mst.query_leq(1, 0, 4, 1, 4, 3))  # count  3 in [1,4] = 2
```

Why It Matters

- Enables order-based queries (, , count, rank)
- Useful for offline range counting, kth-smallest, and inversion queries
- Combines divide-and-conquer sorting with range decomposition

A Gentle Proof (Why It Works)

Each level of the tree merges sorted lists from children.

- Each element appears in $O(\log n)$ nodes.
- Each merge is linear in subarray size.

Thus, total build time:

$$O(n \log n)$$

Each query visits $O(\log n)$ nodes, each with $O(\log n)$ binary search:

$$O(\log^2 n)$$

Try It Yourself

1. Build tree for $A = [5, 1, 4, 2, 3]$.
2. Query count 3 in `[0, 4]`.
3. Query count 2 in `[1, 3]`.
4. Implement query for "count between $[a, b]$" using two `query_leq` calls.

Test Cases

Array	Query	Condition	Answer
[2,5,1,4,3]	[1,4], 3	count	2
[2,5,1,4,3]	[0,2], 2	count	2
[1,2,3,4,5]	[2,4], 4	count	3
[5,4,3,2,1]	[0,4], 3	count	3

Complexity

Operation	Time	Space
Build	$O(n \log n)$	$O(n \log n)$
Query (x)	$O(\log^2 n)$	,
Query (range count)	$O(\log^2 n)$	,

Merge Sort Trees elegantly bridge sorting and segmentation, empowering range queries that depend not on aggregates, but on the distribution of values themselves.

295 Wavelet Tree

A Wavelet Tree is a compact, indexable structure over a sequence that supports rank, select, and range queries by value in O(log) time with O(n log) space, where ( ) is the alphabet size. Think of it as a value-aware segment tree built on bitvectors that let you jump between levels using rank counts.

What Problem Are We Solving?

Given an array $A[1..n]$ over values in $[1..\sigma]$, define the following queries:

- rank(x, r): number of occurrences of value x in $A[1..r]$
- select(x, k): position of the k-th occurrence of x in A
- kth(l, r, k): the k-th smallest value in the subarray $A[l..r]$
- range_count(l, r, a, b): number of values in $A[l..r]$ that lie in $[a, b]$

How It Works

1. Value partitioning by halves
   Recursively partition the value domain $[v_{\min}, v_{\max}]$ into two halves at midpoint m.
   - Left child stores all elements $\leq m$
   - Right child stores all elements $> m$
2. Stable partition plus bitvector
   At each node, keep the original order and record a bitvector B of length equal to the number of elements that arrive at the node:

- $B[i] = 0$ if the i-th element goes to the left child
- $B[i] = 1$ if it goes to the right child

Support fast ranks on B: $\text{rank}_0(B, i)$ and $\text{rank}_1(B, i)$.

3. Navigating queries
   - Position based descent: translate positions using prefix counts from B.
     If a query interval at this node is $[l, r]$, then the corresponding interval in the left child is $[\text{rank}_0(B, l-1) + 1,\ \text{rank}_0(B, r)]$ and in the right child is $[\text{rank}_1(B, l-1) + 1,\ \text{rank}_1(B, r)]$.
   - Value based descent: choose left or right child by comparing the value with m.

Height is $O(\log \sigma)$. Each step uses $O(1)$ bitvector rank operations.

Example

Array: $A = [3, 1, 4, 1, 5, 9, 2, 6]$, values in [1..9]

Root split by midpoint $m = 5$

- Left child receives elements ≤ 5: $\{3, 1, 4, 1, 5, 2\}$
- Right child receives elements > 5: $\{9, 6\}$

Root bitvector marks routing left (0) or right (1), preserving order:

- A by node: [3, 1, 4, 1, 5, 9, 2, 6]
- B: [0, 0, 0, 0, 0, 1, 0, 1]

Left child split on [1..5] by $m = 3$

- Left-left (values ≤ 3): positions where $B = 0$ at root, then route by $m = 3$
  Sequence arriving: [3, 1, 4, 1, 5, 2]
  Bitvector at this node B_L: [0, 0, 1, 0, 1, 0]
  Children:
  - ≤ 3: [3, 1, 1, 2]
  - > 3: [4, 5]
- Right-right subtree of root contains [9, 6] (no further split shown)

Rank translation example at the root

For an interval $[l, r]$ at the root, the corresponding intervals are: - Left child: $[\,\mathrm{rank}_0(B, l-1)+1,\ \mathrm{rank}_0(B, r)\,]$ - Right child: $[\,\mathrm{rank}_1(B, l-1)+1,\ \mathrm{rank}_1(B, r)\,]$

Example: take $[l, r] = [2, 7]$ at the root with $B = [0, 0, 0, 0, 0, 1, 0, 1]$ - $\mathrm{rank}_0(B, 1) = 1$, $\mathrm{rank}_0(B, 7) = 6 \rightarrow$ left interval $[2, 6]$ - $\mathrm{rank}_1(B, 1) = 0$, $\mathrm{rank}_1(B, 7) = 1 \rightarrow$ right interval $[1, 1]$

Height is $O(\log \sigma)$, each descent step uses $O(1)$ rank operations on the local bitvector.

Core Operations

1. rank(x, r)
   Walk top down. At a node with split value m:
   - If $x \leq m$, set $r \leftarrow \mathrm{rank}_0(B, r)$ and go left
   - Otherwise set $r \leftarrow \mathrm{rank}_1(B, r)$ and go right

   When you reach the leaf for value x, the current r is the answer.
2. select(x, k)
   Start at the leaf for value x with local index k.
   Move upward to the root, inverting the position mapping at each parent:
   - If you came from the left child, set $k \leftarrow \mathrm{select\_pos\_0}(B, k)$
   - If you came from the right child, set $k \leftarrow \mathrm{select\_pos\_1}(B, k)$
     The final k at the root is the global position of the k-th x.
3. kth(l, r, k)
   At a node with split value m, let

   $$c \;=\; \mathrm{rank}_0(B, r) \;-\; \mathrm{rank}_0(B, l-1)$$

   which is the number of items routed left within $[l, r]$.
   - If $k \leq c$, map the interval to the left child via

     $$l' \;=\; \mathrm{rank}_0(B, l-1)+1, \quad r' \;=\; \mathrm{rank}_0(B, r)$$

     and recurse on (l', r', k).
   - Otherwise go right with

     $$k \leftarrow k - c, \quad l' \;=\; \mathrm{rank}_1(B, l-1)+1, \quad r' \;=\; \mathrm{rank}_1(B, r)$$

     and recurse on (l', r', k).

4. range_count(l, r, a, b)
   Recurse only into value intervals that intersect $[a, b]$.
   At each visited node, map the position interval using B:

   - Left child interval
     $$[\,\mathrm{rank}_0(B, l-1)+1,\ \mathrm{rank}_0(B, r)\,]$$
   - Right child interval
     $$[\,\mathrm{rank}_1(B, l-1)+1,\ \mathrm{rank}_1(B, r)\,]$$

   Stop when a node's value range is fully inside or outside $[a, b]$:
   - Fully inside: add its interval length
   - Disjoint: add 0

Tiny Code Sketch in Python

This sketch shows the structure and kth query. A production version needs succinct rank structures for (B) to guarantee (O(1)) ranks.

```
import bisect

class WaveletTree:
    def __init__(self, arr, lo=None, hi=None):
        self.lo = min(arr) if lo is None else lo
        self.hi = max(arr) if hi is None else hi
        self.b = []          # bitvector as 0-1 list
        self.pref = [0]      # prefix sums of ones for O(1) rank1
        if self.lo == self.hi or not arr:
            self.left = self.right = None
            return
        mid = (self.lo + self.hi) // 2
        left_part, right_part = [], []
        for x in arr:
            go_right = 1 if x > mid else 0
            self.b.append(go_right)
            self.pref.append(self.pref[-1] + go_right)
            if go_right:
                right_part.append(x)
            else:
                left_part.append(x)
        self.left = WaveletTree(left_part, self.lo, mid)
        self.right = WaveletTree(right_part, mid + 1, self.hi)
```

```
    def rank1(self, idx):  # ones in b[1..idx]
        return self.pref[idx]

    def rank0(self, idx):  # zeros in b[1..idx]
        return idx - self.rank1(idx)

    def kth(self, l, r, k):
        # 1-indexed positions
        if self.lo == self.hi:
            return self.lo
        mid = (self.lo + self.hi) // 2
        cnt_left = self.rank0(r) - self.rank0(l - 1)
        if k <= cnt_left:
            nl = self.rank0(l - 1) + 1
            nr = self.rank0(r)
            return self.left.kth(nl, nr, k)
        else:
            nl = self.rank1(l - 1) + 1
            nr = self.rank1(r)
            return self.right.kth(nl, nr, k - cnt_left)
```

Usage example:

```
A = [3,1,4,1,5,9,2,6]
wt = WaveletTree(A)
print(wt.kth(1, 8, 3))  # 3rd smallest in the whole array
```

Why It Matters

- Combines value partitioning with positional stability, enabling order statistics on subranges
- Underpins succinct indexes, FM indexes, rank select dictionaries, and fast offline range queries
- Efficient when ( ) is moderate or compressible

A Gentle Proof of Bounds

The tree has height $O(\log \sigma)$ since each level halves the value domain. Each query descends one level and performs $O(1)$ rank operations on a bitvector. Therefore

$$T_{\text{query}} = O(\log \sigma)$$

Space stores one bit per element per level on average, so

$$S = O(n \log \sigma)$$

With compressed bitvectors supporting constant time rank and select, these bounds hold in practice.

Try It Yourself

1. Build a wavelet tree for $A = [2, 7, 1, 8, 2, 8, 1]$.
2. Compute kth$(2, 6, 2)$.
3. Compute range_count$(2, 7, 2, 8)$.
4. Compare against a naive sort on $A[l..r]$.

Test Cases

Array	Query	Answer
[3,1,4,1,5,9,2,6]	kth(1,8,3)	3
[3,1,4,1,5,9,2,6]	range_count(3,7,2,5)	3
[1,1,1,1,1]	rank(1,5)	5
[5,4,3,2,1]	kth(2,5,2)	3

Complexity

Operation	Time	Space
Build	$O(n \log \sigma)$	$O(n \log \sigma)$
rank, select	$O(\log \sigma)$	–
kth, range_count	$O(\log \sigma)$	–

Wavelet trees are a sharp tool for order aware range queries. By weaving bitvectors with stable partitions, they deliver succinct, logarithmic time answers on top of the original sequence.

296 KD-Tree

A KD-Tree (k-dimensional tree) is a binary space partitioning data structure for organizing points in a k-dimensional space. It enables fast range searches, nearest neighbor queries, and spatial indexing, often used in geometry, graphics, and machine learning (like k-NN).

What Problem Are We Solving?

We need to store and query n points in k-dimensional space such that:

- Nearest neighbor query: find the point closest to a query q.
- Range query: find all points within a given region (rectangle or hypersphere).
- k-NN query: find the k closest points to q.

A naive search checks all n points, which takes $O(n)$ time.
A KD-Tree reduces this to $O(\log n)$ expected query time for balanced trees.

How It Works

1. Recursive Partitioning by Dimension

At each level, the KD-Tree splits the set of points along one dimension, cycling through all dimensions.

If the current depth is d, use the axis $a = d \bmod k$:

- Sort points by their a-th coordinate.
- Choose the median point as the root to maintain balance.
- Left child: points with smaller a-th coordinate.
- Right child: points with larger a-th coordinate.

2. Search (Nearest Neighbor)

To find nearest neighbor of query q:

1. Descend tree following split planes (like BST).
2. Track current best (closest point found so far).
3. Backtrack if potential closer point exists across split plane (distance to plane $<$ current best).

This ensures pruning of subtrees that cannot contain closer points.

Example

Suppose 2D points:

$$P = (2,3), (5,4), (9,6), (4,7), (8,1), (7,2)$$

Step 1: Root splits by (x)-axis (axis 0). Sorted by (x): ((2,3), (4,7), (5,4), (7,2), (8,1), (9,6)). Median = ((7,2)). Root = (7,2).

Step 2:

- Left subtree (points with (x < 7)) split by (y)-axis.
- Right subtree (points with (x > 7)) split by (y)-axis.

This creates alternating partitions by x and y, forming axis-aligned rectangles.

Tiny Code (Python)

```
class Node:
    def __init__(self, point, axis):
        self.point = point
        self.axis = axis
        self.left = None
        self.right = None

def build_kdtree(points, depth=0):
    if not points:
        return None
    k = len(points[0])
    axis = depth % k
    points.sort(key=lambda p: p[axis])
    median = len(points) // 2
    node = Node(points[median], axis)
    node.left = build_kdtree(points[:median], depth + 1)
    node.right = build_kdtree(points[median + 1:], depth + 1)
    return node
```

How Nearest Neighbor Works

Given query (q), maintain best distance (d_{best}). For each visited node:

- Compute distance (d = |q - p|)

- If (d < d_{best}), update best
- Check opposite branch only if (|q[a] - p[a]| < d_{best})

Example Table

Step	Node Visited	Axis	Current Best	Distance to Plane	Search Next
1	(7,2)	x	(7,2), 0.0	0.0	Left
2	(5,4)	y	(5,4), 2.8	2.0	Left
3	(2,3)	x	(5,4), 2.8	3.0	Stop

Why It Matters

- Efficient spatial querying in multidimensional data.
- Common in k-NN classification, computer graphics, and robotics pathfinding.
- Basis for libraries like `scipy.spatial.KDTree`.

A Gentle Proof (Why It Works)

Each level splits points into halves, forming $O(\log n)$ height. Each query visits a bounded number of nodes (dependent on dimension). Expected nearest neighbor cost:

$$T_{\text{query}} = O(\log n)$$

Building sorts points at each level:

$$T_{\text{build}} = O(n \log n)$$

Try It Yourself

1. Build KD-Tree for 2D points ([(2,3),(5,4),(9,6),(4,7),(8,1),(7,2)]).
2. Query nearest neighbor of (q = (9,2)).
3. Trace visited nodes, prune subtrees when possible.

Test Cases

Points	Query	Nearest	Expected Path
[(2,3),(5,4),(9,6),(4,7),(8,1),(7,2)]	(9,2)	(8,1)	Root → Right → Leaf
[(1,1),(2,2),(3,3)]	(2,3)	(2,2)	Root → Right
[(0,0),(10,10)]	(5,5)	(10,10)	Root → Right

Complexity

Operation	Time	Space
Build	$O(n \log n)$	$O(n)$
Nearest Neighbor	$O(\log n)$ (expected)	$O(\log n)$
Range Query	$O(n^{1-1/k} + m)$	–

KD-Trees blend geometry with binary search, cutting space by dimensions to answer questions faster than brute force.

297 Range Tree

A Range Tree is a multi-level search structure for answering orthogonal range queries in multidimensional space, such as finding all points inside an axis-aligned rectangle. It extends 1D balanced search trees to higher dimensions using recursive trees on projections.

What Problem Are We Solving?

Given a set of n points in k-dimensional space, we want to efficiently answer queries like:

> "List all points (x, y) such that $x_1 \leq x \leq x_2$ and $y_1 \leq y \leq y_2$."

A naive scan is $O(n)$ per query. Range Trees reduce this to $O(\log^k n + m)$, where m is the number of reported points.

How It Works

1. 1D Case (Baseline)

A simple balanced BST (e.g. AVL) on x coordinates supports range queries by traversing paths and collecting nodes in range.

2. 2D Case (Extension)

- Build a primary tree on x coordinates.
- At each node, store a secondary tree built on y coordinates of the points in its subtree.

Each level recursively maintains sorted views along other axes.

3. Range Query

1. Search primary tree for split node s, where paths to x_1 and x_2 diverge.
2. For nodes fully in $[x_1, x_2]$, query their associated y-tree for $[y_1, y_2]$.
3. Combine results.

Example

Given points:

$$P = (2,3), (4,7), (5,1), (7,2), (8,5)$$

Query: $[3,7] \times [1,5]$

- Primary tree on x: median $(5,1)$ as root.
- Secondary trees at each node on y.

Search path:

- Split node $(5,1)$ covers $x \in [3,7]$.
- Visit subtrees with $x \in [4,7]$.
- Query y in $[1,5]$ inside secondary trees.

Returned points: $(5,1), (7,2), (4,7) \rightarrow$ filter $y \leq 5 \rightarrow (5,1), (7,2)$.

Tiny Code (Python-like Pseudocode)

```
class RangeTree:
    def __init__(self, points, depth=0):
        if not points:
            self.node = None
            return
        axis = depth % 2
```

```
        points.sort(key=lambda p: p[axis])
        mid = len(points) // 2
        self.node = points[mid]
        self.left = RangeTree(points[:mid], depth + 1)
        self.right = RangeTree(points[mid + 1:], depth + 1)
        self.sorted_y = sorted(points, key=lambda p: p[1])
```

Query recursively:

- Filter nodes by x.
- Binary search on y-lists.

Step-by-Step Table (2D Query)

Step	Operation	Axis	Condition	Action
1	Split at (5,1)	x	$3 \leq 5 \leq 7$	Recurse both sides
2	Left (2,3),(4,7)	x	$x < 5$	Visit (4,7) subtree
3	Right (7,2),(8,5)	x	$x \leq 7$	Visit (7,2) subtree
4	Filter by y	y	$1 \leq y \leq 5$	Keep (5,1),(7,2)

Why It Matters

Range Trees provide deterministic performance for multidimensional queries, unlike kd-trees (which may degrade). They're ideal for:

- Orthogonal range counting
- Database indexing
- Computational geometry problems

They are static structures, suited when data doesn't change often.

A Gentle Proof (Why It Works)

Each dimension adds a logarithmic factor. In 2D, build time:

$$T(n) = O(n \log n)$$

Query visits $O(\log n)$ nodes in primary tree, each querying $O(\log n)$ secondary trees:

$$Q(n) = O(\log^2 n + m)$$

Space is $O(n \log n)$ due to secondary trees.

Try It Yourself

1. Build a 2D Range Tree for $P = (1, 2), (2, 3), (3, 4), (4, 5), (5, 6)$
2. Query rectangle $[2, 4] \times [3, 5]$.
3. Trace visited nodes and verify output.

Test Cases

Points	Query Rectangle	Result
[(2,3),(4,7),(5,1),(7,2),(8,5)]	[3,7] × [1,5]	(5,1),(7,2)
[(1,2),(2,4),(3,6),(4,8),(5,10)]	[2,4] × [4,8]	(2,4),(3,6),(4,8)
[(1,1),(2,2),(3,3)]	[1,2] × [1,3]	(1,1),(2,2)

Complexity

Operation	Time	Space
Build	$O(n \log n)$	$O(n \log n)$
Query (2D)	$O(\log^2 n + m)$	,
Update	, (rebuild needed)	,

Range Trees are precise geometric indexes: each axis divides the space, and nested trees give fast access to all points in any axis-aligned box.

298 Fenwick 2D Tree

A 2D Fenwick Tree (also known as 2D Binary Indexed Tree) extends the 1D Fenwick Tree to handle range queries and point updates on 2D grids such as matrices. It efficiently computes prefix sums and supports dynamic updates in $O(\log^2 n)$ time.

What Problem Are We Solving?

Given an $n \times m$ matrix A, we want to support two operations efficiently:

1. Update: Add a value v to element $A[x][y]$.
2. Query: Compute the sum of all elements in submatrix $[1..x][1..y]$.

A naive approach takes $O(nm)$ per query. The 2D Fenwick Tree reduces both update and query to $O(\log n \cdot \log m)$.

How It Works

Each node (i, j) in the tree stores the sum of a submatrix region determined by the binary representation of its indices:

$$T[i][j] = \sum_{x=i-2^{r_i}+1}^{i} \sum_{y=j-2^{r_j}+1}^{j} A[x][y]$$

where r_i and r_j denote the least significant bit (LSB) of i and j.

Update Rule

When updating (x, y) by v:

```
for i in range(x, n+1, i & -i):
    for j in range(y, m+1, j & -j):
        tree[i][j] += v
```

Query Rule

To compute prefix sum $(1, 1)$ to (x, y):

```
res = 0
for i in range(x, 0, -i & -i):
    for j in range(y, 0, -j & -j):
        res += tree[i][j]
return res
```

Range Query

Sum of submatrix $[(x_1, y_1), (x_2, y_2)]$:

$$S = Q(x_2, y_2) - Q(x_1 - 1, y_2) - Q(x_2, y_1 - 1) + Q(x_1 - 1, y_1 - 1)$$

Example

Given a 4×4 matrix:

x/y	1	2	3	4
1	2	1	0	3
2	1	2	3	1
3	0	1	2	0
4	4	0	1	2

Build Fenwick 2D Tree, then query sum in submatrix $[2, 2]$ to $[3, 3]$.

Expected result:

$$A[2][2] + A[2][3] + A[3][2] + A[3][3] = 2 + 3 + 1 + 2 = 8$$

Step-by-Step Update Example

Suppose we add $v = 5$ at $(2, 3)$:

Step	(i, j) Updated	Added Value	Reason
1	$(2, 3)$	$+5$	Base position
2	$(2, 4)$	$+5$	Next by $j \mathrel{+}= j\&-j$
3	$(4, 3)$	$+5$	Next by $i \mathrel{+}= i\&-i$
4	$(4, 4)$	$+5$	Both indices propagate upward

Tiny Code (Python-like Pseudocode)

```python
class Fenwick2D:
    def __init__(self, n, m):
        self.n, self.m = n, m
        self.tree = [[0]*(m+1) for _ in range(n+1)]

    def update(self, x, y, val):
        i = x
        while i <= self.n:
            j = y
            while j <= self.m:
                self.tree[i][j] += val
                j += j & -j
            i += i & -i

    def query(self, x, y):
        res = 0
        i = x
        while i > 0:
            j = y
            while j > 0:
                res += self.tree[i][j]
                j -= j & -j
            i -= i & -i
        return res

    def range_sum(self, x1, y1, x2, y2):
        return (self.query(x2, y2) - self.query(x1-1, y2)
                - self.query(x2, y1-1) + self.query(x1-1, y1-1))
```

Why It Matters

2D Fenwick Trees are lightweight, dynamic structures for prefix sums and submatrix queries. They're widely used in:

- Image processing (integral image updates)
- Grid-based dynamic programming
- Competitive programming for 2D range queries

They trade slightly higher code complexity for excellent update-query efficiency.

A Gentle Proof (Why It Works)

Each update/query operation performs $\log n$ steps on x and $\log m$ on y:

$$T(n, m) = O(\log n \cdot \log m)$$

Each level adds contributions from subregions determined by LSB decomposition, ensuring every cell contributes exactly once to the query sum.

Try It Yourself

1. Initialize 4×4 Fenwick 2D.
2. Add 5 to $(2, 3)$.
3. Query sum $(1, 1)$ to $(2, 3)$.
4. Verify it matches manual computation.

Test Cases

Matrix (Partial)	Update	Query Rectangle	Result
$[[2, 1, 0], [1, 2, 3], [0, 1, 2]]$	$(2, 3) + 5$	$[1, 1]$–$[2, 3]$	14
$[[1, 1, 1], [1, 1, 1], [1, 1, 1]]$	$(3, 3) + 2$	$[2, 2]$–$[3, 3]$	5
$[[4, 0], [0, 4]]$	,	$[1, 1]$–$[2, 2]$	8

Complexity

Operation	Time	Space
Update	$O(\log n \cdot \log m)$	$O(nm)$
Query	$O(\log n \cdot \log m)$	,

The 2D Fenwick Tree is an elegant bridge between prefix sums and spatial queries, simple, powerful, and efficient for dynamic 2D grids.

299 Treap Split/Merge

A Treap Split/Merge algorithm allows you to divide and combine treaps (randomized balanced binary search trees) efficiently, using priority-based rotations and key-based ordering. This is the foundation for range operations like splits, merges, range updates, and segment queries on implicit treaps.

What Problem Are We Solving?

We often need to:

1. Split a treap into two parts:
    - All keys $\leq k$ go to the left treap
    - All keys $> k$ go to the right treap
2. Merge two treaps T_1 and T_2 where all keys in $T_1 < T_2$

These operations enable efficient range queries, persistent edits, and order-statistics while maintaining balanced height.

How It Works (Plain Language)

Treaps combine two properties:

- BST Property: Left $<$ Root $<$ Right
- Heap Property: Node priority $>$ children priorities

Split and merge rely on recursive descent guided by key and priority.

Split Operation

Split treap T by key k:

- If $T.key \leq k$, split $T.right$ into $(t2a, t2b)$ and set $T.right = t2a$
- Else, split $T.left$ into $(t1a, t1b)$ and set $T.left = t1b$

Return $(T.left, T.right)$

Merge Operation

Merge T_1 and T_2:

- If $T_1.priority > T_2.priority$, set $T_1.right = \text{merge}(T_1.right, T_2)$
- Else, set $T_2.left = \text{merge}(T_1, T_2.left)$

Return new root.

Example

Suppose we have treap with keys:

$$[1, 2, 3, 4, 5, 6, 7]$$

Split by $k = 4$:

Left Treap: $[1, 2, 3, 4]$ Right Treap: $[5, 6, 7]$

Now, merge them back restores original order.

Step-by-Step Split Example

Step	Node Key	Compare to $k = 4$	Action
1	4	≤ 4	Go right
2	5	> 4	Split left subtree
3	5.left= \$	return (null,5)	Combine back

Result: left $= [1, 2, 3, 4]$, right $= [5, 6, 7]$

Tiny Code (Python-like Pseudocode)

```
import random

class Node:
    def __init__(self, key):
        self.key = key
        self.priority = random.random()
        self.left = None
```

```
        self.right = None

def split(root, key):
    if not root:
        return (None, None)
    if root.key <= key:
        left, right = split(root.right, key)
        root.right = left
        return (root, right)
    else:
        left, right = split(root.left, key)
        root.left = right
        return (left, root)

def merge(t1, t2):
    if not t1 or not t2:
        return t1 or t2
    if t1.priority > t2.priority:
        t1.right = merge(t1.right, t2)
        return t1
    else:
        t2.left = merge(t1, t2.left)
        return t2
```

Why It Matters

Treap split/merge unlocks flexible sequence manipulation and range-based operations:

- Range sum / min / max queries
- Insert or delete in $O(\log n)$
- Persistent or implicit treaps for lists
- Lazy propagation for intervals

It's a key building block in functional and competitive programming data structures.

A Gentle Proof (Why It Works)

Each split or merge operation traverses down the height of the treap. Since treaps are expected balanced, height is $O(\log n)$.

- Split correctness: Each recursive call preserves BST ordering.
- Merge correctness: Maintains heap property since highest priority becomes root.

Thus, both return valid treaps.

Try It Yourself

1. Build treap with keys [1..7].
2. Split by $k = 4$.
3. Print inorder traversals of both sub-treaps.
4. Merge back. Confirm structure matches original.

Test Cases

Input Keys	Split Key	Left Treap Keys	Right Treap Keys
[1,2,3,4,5,6,7]	4	[1,2,3,4]	[5,6,7]
[10,20,30,40]	25	[10,20]	[30,40]
[5,10,15,20]	5	[5]	[10,15,20]

Complexity

Operation	Time	Space
Split	$O(\log n)$	$O(1)$
Merge	$O(\log n)$	$O(1)$

Treap Split/Merge is the elegant heart of many dynamic set and sequence structures, one key, one random priority, two simple operations, infinite flexibility.

300 Mo's Algorithm on Tree

Mo's Algorithm on Tree is an extension of the classical Mo's algorithm used on arrays. It allows efficient processing of offline queries on trees, especially those involving subtrees or paths, by converting them into a linear order (Euler tour) and then applying a square root decomposition strategy.

What Problem Are We Solving?

When you need to answer multiple queries like:

- "How many distinct values are in the subtree of node u?"
- "What is the sum over the path from u to v?"

A naive approach may require $O(n)$ traversal per query, leading to $O(nq)$ total complexity. Mo's algorithm on trees reduces this to approximately $O((n+q)\sqrt{n})$, by reusing results from nearby queries.

How It Works (Plain Language)

1. Euler Tour Flattening Transform the tree into a linear array using an Euler tour. Each node's first appearance marks its position in the linearized sequence.
2. Query Transformation
    - For subtree queries, a subtree becomes a continuous range in the Euler array.
    - For path queries, break into two subranges and handle Least Common Ancestor (LCA) separately.
3. Mo's Ordering Sort queries by:
    - Block of left endpoint (using block = $\lfloor L/\sqrt{N} \rfloor$)
    - Right endpoint (ascending or alternating per block)
4. Add/Remove Function Maintain a frequency map or running result as the window moves.

Example

Given a tree:

```
1
  2
     4
     5
  3
```

Euler Tour: `[1, 2, 4, 4, 5, 5, 2, 3, 3, 1]`

Subtree(2): Range covering `[2, 4, 4, 5, 5, 2]`

Each subtree query becomes a range query over the Euler array. Mo's algorithm processes ranges efficiently in sorted order.

Step-by-Step Example

Step	Query (L,R)	Current Range	Add/Remove	Result
1	(2,6)	[2,6]	+4,+5	Count=2
2	(2,8)	[2,8]	+3	Count=3
3	(1,6)	[1,6]	-3,+1	Count=3

Each query is answered by incremental adjustment, not recomputation.

Tiny Code (Python-like Pseudocode)

```
import math

# Preprocessing
def euler_tour(u, p, g, order):
    order.append(u)
    for v in g[u]:
        if v != p:
            euler_tour(v, u, g, order)
            order.append(u)

# Mo's structure
class Query:
    def __init__(self, l, r, idx):
        self.l, self.r, self.idx = l, r, idx

def mo_on_tree(n, queries, order, value):
    block = int(math.sqrt(len(order)))
    queries.sort(key=lambda q: (q.l // block, q.r))

    freq = [0]*(n+1)
    answer = [0]*len(queries)
    cur = 0
    L, R = 0, -1

    def add(pos):
        nonlocal cur
        node = order[pos]
        freq[node] += 1
```

```
        if freq[node] == 1:
            cur += value[node]

    def remove(pos):
        nonlocal cur
        node = order[pos]
        freq[node] -= 1
        if freq[node] == 0:
            cur -= value[node]

    for q in queries:
        while L > q.l:
            L -= 1
            add(L)
        while R < q.r:
            R += 1
            add(R)
        while L < q.l:
            remove(L)
            L += 1
        while R > q.r:
            remove(R)
            R -= 1
        answer[q.idx] = cur
    return answer
```

Why It Matters

- Converts tree queries into range queries efficiently
- Reuses computation by sliding window technique
- Useful for frequency, sum, or distinct count queries
- Supports subtree queries, path queries (with LCA handling), and color-based queries

A Gentle Proof (Why It Works)

1. Euler Tour guarantees every subtree is a contiguous range.
2. Mo's algorithm ensures total number of add/remove operations is $O((n+q)\sqrt{n})$.
3. Combining them, each query is handled incrementally within logarithmic amortized cost.

Thus, offline complexity is sublinear per query.

Try It Yourself

1. Build Euler tour for tree of 7 nodes.
2. Write subtree queries for nodes $2, 3, 4$.
3. Sort queries by block order.
4. Implement add/remove logic to count distinct colors or sums.
5. Compare performance with naive DFS per query.

Test Cases

Nodes	Query	Expected Result
[1-2-3-4-5]	Subtree(2)	Sum or count over nodes 2–5
[1: {2,3}, 2:{4,5}]	Subtree(1)	All nodes
[1-2,1-3]	Path(2,3)	LCA=1 handled separately

Complexity

Operation	Time	Space
Preprocessing (Euler)	$O(n)$	$O(n)$
Query Sorting	$O(q \log q)$	$O(q)$
Processing	$O((n+q)\sqrt{n})$	$O(n)$

Mo's Algorithm on Tree is the elegant meeting point of graph traversal, offline range query, and amortized optimization, bringing sublinear query handling to complex hierarchical data.