The Little Book of Algorithms

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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.

```
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 Book

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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:

```c
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:

```c
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:

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

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

But if we allocate an array:

```c
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

```c
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.

```
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

```
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: (O$\log n$)- Reporting results: (O(k)) where (k) = number of elements in range $\rightarrow$ Total: (O$\log n + k$)

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:

```c
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.

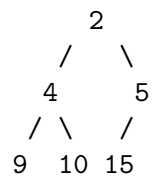
1. The Heap Property

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:

```c
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 = $(\text{Olog}\, n)$

C. Operations

Operation	Time	Space	Notes
Search	$(\text{Olog}\, n)$	O(n)	Randomized balance
Insert	$(\text{Olog}\, n)$	O(n)	Rebuild towers
Delete	$(\text{Olog}\, n)$	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	$O(\log^2 n + k)$	$O(\log^2 n)$	Multi-dim
KD-Tree	Spatial	$O(\sqrt{n})$ avg	O(log n)	Nearest neighbor
Merge Sort Tree	Offline rank	$O(\log^2 n)$	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

```cpp
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 $\rightarrow$ 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:

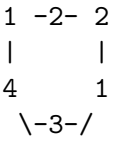
- $O((V + E) \log V)$ with binary heap

Used when:

- Graph is dense
- Easier to grow tree than sort all edges

C. Example

Graph:



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

```cpp
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:

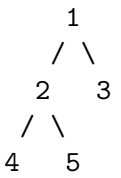
```
const int LOG = 20;
vector<int> adj[MAX];
int up[MAX][LOG], depth[MAX];

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:



- 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):

```
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:

```
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:

$$dp[t] = \min_{c_i \le t}(dp[t-c_i] + 1)$$

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

```
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

```
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: (On^3) time, (On^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 · 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

```c
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 (O$n \log n$) 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 (Olog 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: ($On \log n$)

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.

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

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 $f(n) \rightarrow$ 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 → 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 $O(n) \to$ 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 $n = 5$:

```
        F(5)
       /    \
    F(4)    F(3)
   /   \    /   \
 F(3) F(2) F(2) F(1)
 / \
F(2) F(1)
```

Repeated nodes: `F(3)`, `F(2)` Memoization would store these results and reuse them.

With Memoization (Tree Collapsed):

```
      F(5)
     /   \
  F(4)  F(3)
```

Each node computed once, repeated calls replaced by cache lookups.

Tiny Code (Python)

```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	$O(2^{}) \rightarrow O(n)$
fib(10)	177	11	$O(2^{}) \rightarrow O(n)$
fib(20)	21891	21	$O(2^{}) \rightarrow O(n)$

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.).

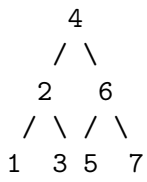
This structure reveals not just correctness but also efficiency and complexity.

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.

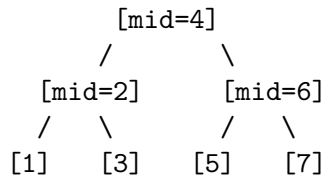
This model abstracts away details and focuses purely on information flow.

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:
   - $1 \quad 2$ (ok)
   - $2 \quad 4$ (ok)
   - $4 > 3$ (disorder)
   - $3 \quad 5$ (ok)
   - $5 \quad 6$ (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:

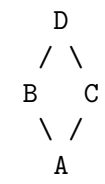
```
A  B, A  C, B  D, C  D
```

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?
- Is the given parent–child relation a valid hierarchy?
- Does this undirected graph contain cycles or disconnected parts?

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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

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 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):

```
1 → 2 → 3
↑   ↓
4 ← 5
```

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:

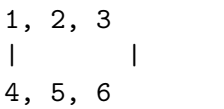
- Use two traversals:

    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.

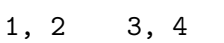
Example (Undirected)

Graph 1:



All nodes reachable → Connected.

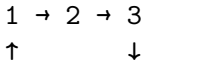
Graph 2:



Two separate parts → Not connected.

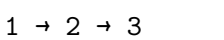
Example (Directed)

Graph:



Every node reachable from every other → Strongly connected

Graph:



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.