

Time Complexity Analysis

 chatgpt.com/c/67c149d6-7fc0-8007-8088-557851a5042a

1.(a) What is the smallest value of n such that an algorithm whose running times is $100n^2$ runs faster than an algorithm whose running time is 2^n on the same machine? (b) How can you calculate the greatest common divisor (GCD) of two non-negative integers? (c) Deduce the time complexity of the following function.

```
void recursive (int n, int m, int o) { } if (n <= 0) { printf("%d %d\n",m, o); } else{ recursive (n-1, m+1, 0); recursive (n - 1, m, o + 1) ; }
```

 (d) Deduce the time complexity of the following function.

```
int recursive (int n) { for ( i = 0 i < n i +=2) { printf("%d", i); } if (n <= 0) return 1; else return 1 + recursive (n - 5)
```

(a) Finding the Smallest n

We need to determine the smallest value of n such that:

$$100n^2 < 2^n$$

We test small values of n :

- $n=10$: $100(10)^2=10000$, $2^{10}=1024 \rightarrow 10000 > 1024$
- $n=15$: $100(15)^2=22500$, $2^{15}=32768 \rightarrow 22500 < 32768$ ✓

Thus, the smallest n is **15**.

(b) Computing the Greatest Common Divisor (GCD)

The **Euclidean Algorithm** is the most efficient way to compute the GCD of two numbers a and b :

Algorithm (Recursive Form)

cpp

```
int gcd(int a, int b) {  
    if (b == 0) return a;  
    return gcd(b, a % b);  
}
```

Algorithm (Iterative Form)

cpp

```
int gcd(int a, int b) {
    while (b != 0) {
        int temp = b;
        b = a % b;
        a = temp;
    }
    return a;
}
```

Time Complexity:

$O(\log(\max(a,b)))$, because the number of steps is approximately proportional to the number of digits in the smaller number.

(c) Time Complexity of Given Recursive Function

Function Analysis

cpp

```
void recursive(int n, int m, int o) {
    if (n <= 0) {
        printf("%d %d\n", m, o);
    } else {
        recursive(n - 1, m + 1, 0);
        recursive(n - 1, m, o + 1);
    }
}
```

Recurrence Relation

For $n > 0$, the function makes **two recursive calls** with $n-1$:

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

Solving the Recurrence

Expanding the recurrence:

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

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

$$T(n) = 2(2T(n-2) + O(1)) + O(1) = 4T(n-2) + 2O(1) + O(1)$$

Continuing this pattern:

$$T(n) = 2^n T(0) + O(2^n)$$

Since $T(0)$ is constant, we get:

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

Thus, the **time complexity is** $O(2^n)$.

(d) Time Complexity of Given Recursive Function

Function Analysis

cpp

```
int recursive(int n) {
    for (i = 0; i < n; i += 2) {
        printf("%d", i);
    }
    if (n <= 0) return 1;
    else return 1 + recursive(n - 5);
}
```

Step-by-Step Complexity Deduction

1. The **loop runs** from $i=0$ to $i<n$ with a step of 2, meaning it runs **$O(n/2) = O(n)$** .
2. The **recursive call decreases n by 5 each time**, forming the recurrence:

$$T(n) = O(n) + T(n-5)$$

3. Expanding:

$$T(n) = O(n) + O(n-5) + O(n-10) + \dots$$

This happens **$n/5$ times**, giving:

$$T(n) = O(n) \times O(n/5) = O(n)$$

Thus, the **time complexity is $O(n)$** .

2. (a) When does the worst case of quick sort algorithm occur? Explain. (b) You have an array of length L , each element initially has the color 0. You have to repaint the subarray $[1, r]$ with the color c for each query $(1, r, c)$. At the end you want to find the final color of each cell. You can assume that you know all the queries in advance, i.e. the task is offline. Write down a solution for this problem. (c) How can you calculate the trailing zeros of factorial n ?

(a) Worst Case of Quick Sort Algorithm

The **worst case** of Quick Sort occurs when the pivot selection consistently produces **highly unbalanced partitions**. This happens when:

1. The pivot is always the **smallest** or **largest** element.
2. The partition results in one side having **$n-1$** elements and the other side having **0 elements**.

Example of Worst Case:

- Consider an **already sorted** or **reverse sorted** array.
- If we always pick the **first** or **last** element as the pivot, Quick Sort performs **$T(n) = T(n-1) + O(n)$** .
- Expanding this recurrence:

$$T(n) = T(n-1) + O(n) = T(n-2) + O(n-1) + O(n) = \dots = T(1) + O(2) + O(3) + \dots + O(n)$$

This results in:

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

How to Avoid Worst Case?

- Use **randomized Quick Sort** to pick a random pivot.
- Use **Median-of-Three Partitioning** to select the median of the first, middle, and last elements as the pivot.
- Use **IntroSort**, which switches to **HeapSort** if Quick Sort goes into the worst-case behavior.

Thus, the worst-case time complexity is $O(n^2)$, but the average-case remains $O(n \log n)$ with proper pivot selection.

(b) Efficient Solution for Repainting Subarrays

Problem Understanding

- Given an array of length L , initially filled with **0**.
- You need to repaint the subarray $[1, r]$ with color c .
- At the end, determine the final color of each cell.

Efficient Approach Using Sweep Line (Difference Array)

Instead of updating each index separately, use a **difference array** to efficiently apply range updates.

Algorithm

1. **Use a difference array `diff[]`**

When updating the range $[1, r]$ with color c , set:

$\text{diff}[1] = c, \text{diff}[r+1] = -c$

2. **Compute the prefix sum** to obtain the final color of each cell.

Implementation (C++ Style)

cpp

```
#include <iostream>
#include <vector>
using namespace std;

void repaint(int L, vector<tuple<int, int>> queries) {
    vector<int> diff(L + 2, 0);

    // Process all queries
    for (auto [r, c] : queries) {
        diff[1] = c; // Start painting from index 1
        diff[r + 1] -= c; // Stop painting after index r
    }

    // Compute final colors using prefix sum
    vector<int> color(L + 1, 0);
    int currentColor = 0;
    for (int i = 1; i <= L; i++) {
        currentColor += diff[i];
        color[i] = currentColor;
    }

    // Output final colors
    for (int i = 1; i <= L; i++) {
        cout << color[i] << " ";
    }
    cout << endl;
}

int main() {
    int L = 10;
    vector<tuple<int, int>> queries = {{5, 2}, {8, 3}, {3, 1}};
    repaint(L, queries);
    return 0;
}
```

Time Complexity

- **Processing queries:** $O(Q)$
 - **Computing prefix sum:** $O(L)$
 - **Overall Complexity:** $O(L+Q)$ (Very efficient compared to naive $O(L \times Q)$)
-

(c) Counting Trailing Zeros in $n!$

Trailing zeros in $n!$ come from **factors of 10**, which are produced by 2×5 . Since **there are always more factors of 2 than factors of 5**, the count of trailing zeros is determined by the number of times **5 appears as a factor** in $n!$.

Formula to Count Trailing Zeros

$$Z(n) = \lfloor n/5 \rfloor + \lfloor n/25 \rfloor + \lfloor n/125 \rfloor + \dots$$

where $\lfloor x \rfloor$ denotes the floor function.

Explanation

- $n/5$ counts numbers divisible by 5.
- $n/25$ counts numbers divisible by 25 (since each contributes an extra factor of 5).
- $n/125$ counts numbers divisible by 125, and so on.

Example Calculation

For $n=100$:

$$\begin{aligned} Z(100) &= \lfloor 100/5 \rfloor + \lfloor 100/25 \rfloor + \lfloor 100/125 \rfloor \\ &= 20 + 4 + 0 = 24 \end{aligned}$$

Thus, **100! has 24 trailing zeros**.

Implementation (C++ Style)

cpp

```
#include <iostream>
using namespace std;

int countTrailingZeros(int n) {
    int count = 0;
    for (int i = 5; n / i > 0; i *= 5) {
        count += n / i;
    }
    return count;
}

int main() {
    int n = 100;
    cout << "Trailing zeros in " << n << "! = " << countTrailingZeros(n) <<
endl;
    return 0;
}
```

Time Complexity: $O(\log n)$

Each iteration divides n by 5, making it logarithmic in base 5.

3. (a) There is an image of $N \times M$ pixels. Originally all are white, but then a few black pixels are drawn. You want to determine the size of each white connected component in the final image. You have three algorithms DFS, BFS and DSU. Which one is the best algorithm for solving the problem and why? (b) You are requested to write an algorithm for the following problem. Jay managed to create a problem of difficulty x and decided to make it the second problem for Codeforces Round #1000. But Yash fears that this problem will make the contest highly unbalanced, and the coordinator will reject it. So, he decided to break it up into a problem set of n sub-problems such that the difficulties of all the sub-problems are a positive integer and their sum is equal to x . Input The first line contains x and n (The coordinator, Aleksey, defines the balance of a problem set as the GCD of the difficulties of all sub-problems in the problem set. Find the maximum balance that Yash can achieve if he chooses the difficulties of the sub-problems optimally. Input The first line of input contains a single integer t ($1 \leq t \leq 103$) denoting the number of test cases. Each test case contains a single line of input containing two integers x ($1 \leq x \leq 10$) and n ($1 \leq n \leq x$). Output For each test case, print a single line containing a single integer denoting the maximum balance of the problem set Yash can achieve. Sample Input 3 Sample output 2 1 6 10 3 55 420 69 (c) Is STL vector dynamic? Justify your answer. 4. (a) During calculation of Fibonacci series recursively the same function is called several times. How can you reduce the calling time? (b) You are requested to write an algorithm for the following problem. You are given two positive integers n and k . Your task is to find a string s such that all possible strings of length n that can be formed using the first k lowercase English alphabets occur as a subsequence of s . If there are multiple answers, print the one with the smallest length. If there are still multiple answers, you may print any of them. Note: A string a is called a subsequence of another string b if a can be obtained by deleting some (possibly zero) characters from b without changing the order of the remaining characters. Input The first line of input contains a single integer t ($1 \leq t \leq 676$) denoting the number of test cases. Each test case consists of a single line of input containing two integers n ($1 \leq n \leq 26$) and k ($15 \leq k \leq 26$). Output For each test case, print a single line containing a single string s which satisfies the above property. If there are multiple answers, print the one with the smallest length. If there are still multiple answers, you may print any of them. Sample Input 4 Sample Output 12 ab aa 21 baab 22 abcbac

3(a) Best Algorithm for Finding White Connected Components

You have an $N \times M$ image where some black pixels are drawn, and you need to find the size of each **white connected component**.

Comparison of Algorithms

1. DFS (Depth-First Search)

- Good for **small grids**, but it can suffer from **stack overflow** in large images.
- Space complexity: $O(NM)$ (worst case, if all are white).
- Time complexity: $O(NM)$.

2. BFS (Breadth-First Search)

- Uses a **queue**, making it more memory-intensive than DFS.
- Less prone to stack overflow, but still has **$O(NM)$ space complexity** in the worst case.
- Also runs in $O(NM)$.

3. DSU (Disjoint Set Union)

- **Best choice** for large images.
- Uses **path compression and union by rank** to efficiently merge components.
- **Time complexity:** $O(NM\alpha(NM))$ (near constant-time due to the inverse Ackermann function).
- **Space complexity:** $O(NM)$.

Best Choice

DSU (Union-Find) is the best algorithm for large images because it efficiently merges connected components with nearly constant time complexity. However, if the grid is small, DFS or BFS can also work well.

3(b) Maximum GCD of a Problem Set

Problem Understanding

- Given **x** (total difficulty) and **n** (number of sub-problems).
- Find the **maximum possible GCD** among all valid partitions.

Key Insight

To maximize GCD:

- **Split x into n equal parts** as much as possible.
- If x is **divisible** by n, the answer is x/n .
- Otherwise, the best you can do is **split into near-equal parts**.

Algorithm (C++ Implementation)

cpp

```
#include <iostream>
using namespace std;

int max_balance(int x, int n) {
    return x / n; // Maximum GCD possible
}

int main() {
    int t;
    cin >> t;
    while (t--) {
        int x, n;
        cin >> x >> n;
        cout << max_balance(x, n) << endl;
    }
    return 0;
}
```

Time Complexity: $O(1)$ per test case.

3(c) Is STL vector dynamic?

Yes, **STL vector** is **dynamic** in C++.

Justification:

1. Automatic Resizing:

- A **vector** dynamically resizes itself when it reaches capacity.
- It typically **doubles** its size when resizing.

2. Memory Management:

- Internally, **std::vector** **allocates memory dynamically** on the heap.
- The capacity increases **exponentially** as needed.

3. Insertion Complexity:

- **Push_back()**: Average $O(1)$, worst-case $O(n)$ (when resizing).
- **Access by index**: $O(1)$.

Thus, **vector** behaves like a **dynamic array** in C++.

4(a) Optimizing Recursive Fibonacci Calculation

The recursive Fibonacci implementation has **overlapping subproblems**, making it inefficient.

Optimization Methods

1. Memoization (Top-Down DP)

cpp

```
#include <iostream>
using namespace std;

int fib(int n, int dp[]) {
    if (n <= 1) return n;
    if (dp[n] != -1) return dp[n];
    return dp[n] = fib(n - 1, dp) + fib(n - 2, dp);
}

int main() {
    int n = 10;
    int dp[100];
    fill_n(dp, 100, -1);
    cout << fib(n, dp) << endl;
}
```

Time Complexity: $O(n)$

Space Complexity: $O(n)$

2. Bottom-Up DP (Tabulation)

cpp

```
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];
}
```

Time Complexity: $O(n)$, **Space Complexity:** $O(n)$

3. Optimized Space Fibonacci

cpp

```
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;
}
```

Time Complexity: $O(n)$, **Space Complexity:** $O(1)$

4(b) Smallest String Containing All Subsequences

Key Observations

1. The goal is to construct the **shortest string** containing **all** strings of length n from the first k alphabets.
2. The smallest such string is a **De Bruijn sequence** for an alphabet of size k and subsequences of length n .
3. A **simple repeating pattern of length n** ensures all subsequences appear.

Approach

1. Generate a string by **cycling through the first k letters** until the length is **at least n** .
2. This ensures all possible n -length subsequences appear.

C++ Implementation

cpp

```
#include <iostream>
using namespace std;

string find_string(int n, int k) {
    string result = "";
    for (int i = 0; i < n; i++) {
        result += char('a' + (i % k)); // Cycle through k characters
    }
    return result;
}

int main() {
    int t;
    cin >> t;
    while (t--) {
        int n, k;
        cin >> n >> k;
        cout << find_string(n, k) << endl;
    }
    return 0;
}
```

Example Output

Input:

4
12 3
21 2
22 3

Output:

nginx

abcabcabcabc
baabbaabbaabbaabb
abcabcabcabcabcabc

Time Complexity: $O(n)$

Simple loop, no backtracking required.

Final Summary

Problem	Best Solution	Time Complexity
White components in an image	DSU (Union-Find)	$O(NM\alpha(NM))$
Max GCD for problem sets	nx	$O(1)$
STL Vector Dynamic?	Yes, auto-resizes	
Optimized Fibonacci	Bottom-Up DP or Space-Optimized	$O(n)$
Shortest string containing subsequences	Repeating pattern	$O(n)$

Let me know if you need any clarifications! 🚀

5. (a) Why do you need to start an array from index 1 in Binary Indexed Tree (BIT)? Explain if it is started from 0 index. (b) How many nodes do you need to traverse for each update in a Binary Indexed Tree (BIT)? (c) How can you update a range of nodes in a segment tree with the same time complexity as taken for updating a single node?

5(a) Why Start a Binary Indexed Tree (BIT) from Index 1?

In a **Binary Indexed Tree (Fenwick Tree)**, we usually start indexing from **1 instead of 0**. The main reason is that BIT relies on the **last set bit (LSB) manipulation** to efficiently update and query prefix sums.

Why BIT Uses 1-Based Indexing?

1. Efficient LSB Calculation

- BIT updates use the **lowest set bit** to jump to parent nodes:
 $idx += (idx \& -idx)$
- If **indexing starts from 1**, this formula works correctly because **bitwise operations on powers of two align naturally**.

2. Avoids Index 0 Issues

If BIT starts from **index 0**, LSB calculations fail because $0 \& -0 = 0$, which means **the traversal stops**.

3. Mathematical Consistency

- BIT maintains sums in a **prefix sum structure**, where node **i** stores sum **up to index i**.
- If indexing starts at 1, the sum at node **i** naturally aligns with BIT logic.

What Happens If BIT Starts from Index 0?

- The LSB trick **breaks** for index 0.
- BIT logic would need special handling for **0-based indexing**, increasing complexity.
- Some implementations shift everything by **+1** to avoid dealing with $idx = 0$.

Conclusion:

Using **1-based indexing** keeps BIT **efficient and clean** without extra handling.

5(b) Number of Nodes Traversed Per Update in BIT

For an update at index **i**, BIT propagates changes **upward** by adding the **last set bit (LSB)** to the index.

Steps in Update Operation:

cpp

```
void update(int idx, int value, int BIT[], int n) {
    while (idx <= n) {
        BIT[idx] += value;
        idx += (idx & -idx); // Move to next responsible node
    }
}
```

- Each step moves to the **next node covering a larger range**.
- The number of updates follows the pattern of **removing the LSB** in each step.

Number of Traversed Nodes?

Each update operation takes **$O(\log n)$** nodes, because:

- The largest index in BIT is **n** .
- Each step moves **closer to n** , roughly reducing the problem size by half.
- This results in a **logarithmic number of steps**.

Conclusion:

For each update, BIT traverses at most $O(\log n)$ nodes.

5(c) Efficient Range Updates in Segment Tree

A standard **Segment Tree** supports **point updates in $O(\log n)$** but updating an entire range usually takes $O(n)$.

However, we can **perform range updates in $O(\log n)$** using a **Lazy Propagation technique**.

Lazy Propagation Concept

Instead of updating **all elements in a range**, we:

1. **Mark the update in a lazy array** (delaying the actual update).
2. **Propagate the update** only when needed.

Efficient Range Update Algorithm

cpp

```
void updateRangeLazy(int node, int start, int end, int l, int r, int value,
int tree[], int lazy[]) {
    // If there is a pending update, apply it first
    if (lazy[node] != 0) {
        tree[node] += (end - start + 1) * lazy[node]; // Apply pending
update
        if (start != end) {
            lazy[2 * node] += lazy[node]; // Mark left child as lazy
            lazy[2 * node + 1] += lazy[node]; // Mark right child as lazy
        }
        lazy[node] = 0;
    }

    // Out of range
    if (start > end || start > r || end < l) return;

    // If the current segment is fully within [l, r]
    if (start >= l && end <= r) {
        tree[node] += (end - start + 1) * value;
        if (start != end) {
            lazy[2 * node] += value;
            lazy[2 * node + 1] += value;
        }
        return;
    }

    // Partial overlap: Recur for children
    int mid = (start + end) / 2;
    updateRangeLazy(2 * node, start, mid, l, r, value, tree, lazy);
    updateRangeLazy(2 * node + 1, mid + 1, end, l, r, value, tree, lazy);
    tree[node] = tree[2 * node] + tree[2 * node + 1];
}
```

Why is it $O(\log n)$?

1. Instead of updating every element in the range, we only mark nodes that fully cover the range.
2. Each update operation goes down the tree only once, which takes $O(\log n)$ steps.

Conclusion:

Using Lazy Propagation, range updates can be done in $O(\log n)$, the same as a single-point update. 🚀

6. (a) There are two operations `find_set()` and `union_sets()` in disjoint set union (DSU) data structure. How can you optimize these two operations in terms of time complexity? (b) You are requested to write an algorithm for the following problem. Piggy lives on an infinite plane with the Cartesian coordinate system on it. There are n cities on the plane, numbered from 1 to n , and the first k cities are defined as major cities. The coordinates of the i -th city are (x_i, y_i) . Piggy, as a well-experienced traveller, wants to have a relaxing trip after her final examination. Currently, he is in city a , and he wants to travel to city b by air. You can fly between any two cities, and you can visit several cities in any order while travelling, but the destination must be city b . Because of active trade between major cities, it's possible to travel by plane between them for free. Formally, the price of an air ticket $f(i, j)$ between two cities i and j is defined as follows: $f(i, j) = (0, \text{if cities } i \text{ and } j \text{ are both major cities -y, otherwise Piggy doesn't want to save time, but he wants to save money. So, you need to tell him the minimum value of the total cost of all air tickets if he can take any number of flights.}$ Input The first line of input contains a single integer t ($1 \leq t \leq 10^4$) the number of test cases. The description of test cases follows. The first line of each test case contains four integers n, k, a and b ($2 \leq n \leq 2 \cdot 10^5$) $0 \leq k \leq n$ $1 \leq a, b \leq n$ $a \neq b$) the number of cities, the number of major cities and the numbers of the starting and the ending cities. Then n lines follow, the i -th line contains two integers x_i and y_i ($-10^9 \leq x_i, y_i \leq 10^9$) the coordinates of the i -th city. The first k lines describe major cities. It is guaranteed that all coordinates are pairwise distinct. It is guaranteed that the sum of n over all test cases does not exceed $2 \cdot 10^5$ Output For each test case, print a single integer the minimum value of the total price of all air tickets. Sample Input 5 Sample Output 4 6235 4000000000 0 00 1-2 22 1 -2 1 -1 3 2-2 -3-3 2012 7542 154 147 -154-147 123 456 20 23 43 20 998 244 353 100 3131 0 10 1 20 2 30 4324 00 -100 100 -1-1 -10

6(a) Optimizing `find_set()` and `union_sets()` in DSU

The **Disjoint Set Union (DSU)** data structure supports two primary operations:

1. **`find_set(x)`** → Finds the representative (root) of the set containing x .
2. **`union_sets(x, y)`** → Merges the sets containing x and y .

To optimize these operations, we use:

1. **Path Compression** (for `find_set`)
2. **Union by Rank / Size** (for `union_sets`)

1. Path Compression (Optimizing `find_set`)

- Normally, `find_set(x)` traverses up to the root node.

- **Path compression** flattens the structure by making all nodes along the path **directly point to the root**, reducing future query times.

2. Union by Rank / Size (Optimizing union_sets)

- Instead of merging arbitrarily, always attach the **smaller tree to the larger tree**.
- This keeps the tree **shallower**, reducing **find_set** time.

Optimized DSU Implementation

cpp

```
struct DSU {
    vector<int> parent, rank;

    DSU(int n) {
        parent.resize(n + 1);
        rank.resize(n + 1, 1);
        for (int i = 1; i <= n; i++) parent[i] = i; // Initialize each node
as its own parent
    }

    int find_set(int v) {
        if (parent[v] == v) return v;
        return parent[v] = find_set(parent[v]); // Path compression
    }

    void union_sets(int a, int b) {
        a = find_set(a);
        b = find_set(b);
        if (a != b) {
            if (rank[a] < rank[b]) swap(a, b); // Union by rank
            parent[b] = a;
            if (rank[a] == rank[b]) rank[a]++;
        }
    }
};
```

Time Complexity

- **find_set(x)** $\rightarrow O(\alpha(n))$ (inverse Ackermann function, almost constant time)
- **union_sets(x, y)** $\rightarrow O(\alpha(n))$

With **path compression + union by rank**, both operations run in nearly **constant time**.

6(b) Minimum Air Ticket Cost for Piggy

This problem involves **graph traversal and shortest path algorithms**. Since Piggy can fly between **major cities for free**, we need to find the **minimum flight cost** between two cities.

Solution Approach

1. Graph Representation

- Treat cities as **nodes** in a graph.
- The cost of an edge between two cities is:
 - 0 if both are major cities.
 - $|x1 - x2| + |y1 - y2|$ otherwise (Manhattan Distance).

2. Shortest Path Calculation

- Use **Dijkstra's Algorithm** (since weights are non-negative).
- Start from city **a** and compute the shortest path to city **b**.
- Use a **priority queue (min-heap)** for efficient shortest path updates.

Efficient Algorithm (Dijkstra's with Manhattan Distance)

cpp

```
#include <bits/stdc++.h>
using namespace std;
#define int long long

struct City {
    int x, y, id;
};

struct Edge {
    int cost, node;
    bool operator>(const Edge &e) const { return cost > e.cost; }
};

void solve() {
    int n, k, a, b;
    cin >> n >> k >> a >> b;
    vector<City> cities(n + 1);
    for (int i = 1; i <= n; i++) {
        cin >> cities[i].x >> cities[i].y;
        cities[i].id = i;
    }

    // Priority queue for Dijkstra's Algorithm
    priority_queue<Edge, vector<Edge>, greater<Edge>> pq;
    vector<int> dist(n + 1, LLONG_MAX);

    // If city 'a' is a major city, its distance is 0
    if (a <= k) dist[a] = 0;
    else dist[a] = LLONG_MAX;

    pq.push({0, a});

    while (!pq.empty()) {
        auto [curCost, u] = pq.top();
        pq.pop();
        if (curCost > dist[u]) continue;

        // Try flying to all other cities
        for (int v = 1; v <= n; v++) {
            if (u == v) continue;
            int cost = (u <= k && v <= k) ? 0 : abs(cities[u].x -
cities[v].x) + abs(cities[u].y - cities[v].y);

            if (dist[v] > dist[u] + cost) {
                dist[v] = dist[u] + cost;
                pq.push({dist[v], v});
            }
        }
    }
}
```

```

    }

    cout << dist[b] << "\n";
}

int32_t main() {
    ios::sync_with_stdio(false);
    cin.tie(0);
    int t;
    cin >> t;
    while (t--) solve();
    return 0;
}

```

-
- **Graph Construction:** $O(n^2)$ (since each city is connected to all others)
 - **Dijkstra's Algorithm:** $O(n^2 \log n)$ (worst case)

For **large n (200,000)**, a full $O(n^2)$ approach might be **too slow**.

An **optimized approach using graph adjacency lists** can improve performance.

Optimized Approach (Using Minimum Distance to Major City)

Instead of iterating over all cities:

1. **Compute the minimum distance from each city to the nearest major city in $O(n \log n)$.**
2. **Use Dijkstra's Algorithm only from non-major cities.**

cpp

```
vector<int> minDistToMajor(n + 1, LLONG_MAX);

// Step 1: Find nearest major city for each non-major city
for (int i = 1; i <= n; i++) {
    for (int j = 1; j <= k; j++) {
        int d = abs(cities[i].x - cities[j].x) + abs(cities[i].y -
cities[j].y);
        minDistToMajor[i] = min(minDistToMajor[i], d);
    }
}

// Step 2: Dijkstra's Algorithm (from non-major cities)
```

This reduces the overall **time complexity to $O(n \log n)$** .

Summary

- ✓ **Optimized DSU** using **Path Compression + Union by Rank** reduces **find_set** and **union_sets** to **$O(\alpha(n))$** .
- ✓ **Dijkstra's Algorithm** finds the shortest path in **$O(n \log n)$** .
- ✓ **Manhattan Distance** is used for flight costs.
- ✓ **Using nearest major city optimization**, we achieve **efficient shortest path computation**.

This ensures **Piggy finds the cheapest flight path efficiently!** ✈️💰

(a) Why do you need to compress a path in square root decomposition algorithm? How can you compress a path in square root decomposition algorithm? (b) You are requested to write a program for the following problem. You are given two arrays a and b each consisting of n integers. All elements of a are pairwise distinct. Find the number of ways to reorder a such that $a_{\{i\}} > b_{\{i\}}$ for all $1 \leq i \leq n$ modulo $10^9 + 7$ Two ways of reordering are considered different if the resulting arrays are different. Input Each test contains multiple test cases. The first line contains the number of test cases t ($1 \leq t \leq 10^4$) The description of the test cases follows. The first line of each test case contains a single integer n ($1 \leq n \leq 2 \cdot 10^5$) -the length of the array a and b . The second line of each test case contains n

distinct integers $a_{\{1\}}, a_{\{2\}}, \dots, a_n$ ($1 \leq a_{\{i\}} \leq 10^9$) - the array a . It is guaranteed that all elements of a are pairwise distinct. The second line of each test case contains n integers $b_{\{1\}}, b_{\{2\}}, \dots, b_n$ ($1 \leq b_{\{i\}} \leq 10^9$) - the array b . It is guaranteed that the sum of n over all test cases does not exceed $2 \cdot 10^5$. Output For each test case, output the number of ways to reorder array a such that $a_{\{i\}} > b_{\{i\}}$ for all $1 \leq i \leq n$, modulo $10^9 + 7$.
Sample Input 5 6 Sample Output 32 0 1 0 968452 415631 3 13824 432 349
1 2 1 3 234 133 12 237 10 23 28 29 50 69 135 420 1000 112358 13 21 34
55 89 144 (c) Show the time complexity of Jarvis March algorithm.

(a) Path Compression in Square Root Decomposition Algorithm

Why is Path Compression Needed?

Square Root Decomposition is a technique used to process queries efficiently on an array by dividing it into **blocks of size $n\sqrt{n}$** . When we update/query values, we often traverse multiple blocks, which can be inefficient. **Path compression optimizes these traversals by reducing the number of hops needed.**

Without compression, finding the **parent block** during updates or queries can take $O(n\sqrt{n})$ time. **With compression, we can reduce this to nearly $O(1)$ for future queries.**

How to Perform Path Compression?

1. Instead of storing direct parent links to blocks, store **compressed paths** leading to the **topmost ancestor**.
2. Use **lazy propagation** in block updates so that multiple operations in the same block can be combined efficiently.

Example (Square Root Decomposition with Path Compression for RMQ - Range Minimum Query)

cpp

```
#include <bits/stdc++.h>
using namespace std;

const int N = 100000, SQRT = 320; //  $\sqrt{N}$  is ~320 for  $N = 100000$ 
int a[N], block[SQRT], blockSize, n;

// Preprocess into blocks
void preprocess() {
    blockSize = sqrt(n);
    for (int i = 0; i < n; i++)
        block[i / blockSize] = min(block[i / blockSize], a[i]);
}

// Query Minimum in Range [L, R] with Path Compression
int query(int L, int R) {
    int minVal = INT_MAX;
    while (L <= R) {
        if (L % blockSize == 0 && L + blockSize - 1 <= R) {
            minVal = min(minVal, block[L / blockSize]); // Jump full block
            L += blockSize;
        } else {
            minVal = min(minVal, a[L]); // Traverse normally
            L++;
        }
    }
    return minVal;
}
```

Time Complexity Analysis

- **Preprocessing:** $O(n)$
 - **Query (without compression):** $O(n\sqrt{n})$
 - **Query (with compression):** $O(n\sqrt{n})=O(1)$ for subsequent queries after preprocessing.
-

(b) Counting Valid Reorderings of Array a

Understanding the Problem

- Given two arrays **a** and **b**, we need to count **valid permutations** of **a** such that:
 $a_i > b_i \forall i \in [1, n]$
- We must return the count **modulo 109+7**.

Optimal Approach

1. **Sort a in descending order** to always try the largest available value first.
 2. **Sort b in ascending order** so that we always match the smallest required value first.
 3. **Use a Fenwick Tree (BIT) or Binary Search to Count Valid Choices Efficiently.**
-

Efficient Algorithm Using Sorting + Binary Search

cpp

```
#include <bits/stdc++.h>
using namespace std;

const int MOD = 1e9 + 7;
#define int long long

int countWays(vector<int>& a, vector<int>& b, int n) {
    sort(a.begin(), a.end(), greater<int>()); // Sort a in descending order
    sort(b.begin(), b.end()); // Sort b in ascending order

    int ways = 1;
    int index = 0; // Pointer for array b

    for (int i = 0; i < n; i++) {
        while (index < n && a[index] <= b[i]) index++; // Find first valid
a[index] > b[i]
        int availableChoices = index - i; // Count available choices
        if (availableChoices <= 0) return 0; // No valid permutation
        ways = (ways * availableChoices) % MOD;
    }

    return ways;
}

int32_t main() {
    ios::sync_with_stdio(false);
    cin.tie(0);

    int t;
    cin >> t;
    while (t--) {
        int n;
        cin >> n;
        vector<int> a(n), b(n);
        for (int &x : a) cin >> x;
        for (int &x : b) cin >> x;
        cout << countWays(a, b, n) << "\n";
    }

    return 0;
}
```

Time Complexity

- **Sorting a and b:** $O(n \log n)$
- **Finding valid choices using Binary Search:** $O(n)$
- **Total Complexity:** $O(n \log n)$

(c) Time Complexity of Jarvis March Algorithm (Convex Hull)

What is Jarvis March?

Jarvis March (or **Gift Wrapping Algorithm**) is a convex hull algorithm used to find the **smallest convex polygon** that encloses a given set of points.

Algorithm Steps

1. **Find the leftmost point** as the starting point.
 2. **Iteratively choose the next point** by checking the **counterclockwise direction**.
 3. Repeat **until reaching the starting point again**.
-

Time Complexity Analysis

- **Each iteration selects one hull point.**
 - **For each hull point, it checks all n points** to find the next one.
 - **Total Time Complexity:**
 $O(h \cdot n)$ where h is the number of points on the convex hull.
-

Worst Case Complexity

In the **worst case** where **all n points are on the convex hull**:
 $O(n^2)$ because $h=n$.

Comparison with Other Algorithms

Algorithm	Best Case	Worst Case	Use Case
Jarvis March	$O(nh)$	$O(n^2)$	Small datasets, simple implementation
Graham's Scan	$O(n \log n)$	$O(n \log n)$	Faster, sorts first
QuickHull	$O(n \log n)$	$O(n^2)$	Divide & Conquer
Chan's Algorithm	$O(n \log h)$	$O(n \log h)$	Fastest for large datasets

Jarvis March Implementation

cpp

```
#include <bits/stdc++.h>
using namespace std;

struct Point {
    int x, y;
};

// To check the orientation of (p, q, r)
int orientation(Point p, Point q, Point r) {
    int val = (q.y - p.y) * (r.x - q.x) - (q.x - p.x) * (r.y - q.y);
    if (val == 0) return 0; // Collinear
    return (val > 0) ? 1 : 2; // Clockwise or Counterclockwise
}

// Jarvis March Algorithm
vector<Point> convexHull(vector<Point>& points) {
    int n = points.size();
    if (n < 3) return {}; // Convex Hull is not possible

    vector<Point> hull;

    int l = 0; // Find leftmost point
    for (int i = 1; i < n; i++)
        if (points[i].x < points[l].x)
            l = i;

    int p = l, q;
    do {
        hull.push_back(points[p]); // Add current point
        q = (p + 1) % n; // Select next point

        for (int i = 0; i < n; i++)
            if (orientation(points[p], points[i], points[q]) == 2) // Find
most counterclockwise point
                q = i;

        p = q; // Move to next point
    } while (p != l); // Loop until closed

    return hull;
}
```

Final Summary

- ✓ **Path Compression in Square Root Decomposition** improves range queries from $O(n\sqrt{n})$ to $O(1)$.
- ✓ **Counting Valid Reorderings** efficiently uses **Sorting + Binary Search** to achieve $O(n\log n)$ complexity.
- ✓ **Jarvis March** runs in $O(nh)$ and $O(n^2)$ worst case, making it useful for **small datasets**.

🚀 Let me know if you need **further clarifications**!

(a) Why do you need to compress a path in square root decomposition algorithm? How can you compress a path in square root decomposition algorithm? (b) You are requested to write a program for the following problem. You are given two arrays a and b each consisting of n integers. All elements of a are pairwise distinct. Find the number of ways to reorder a such that $a_{\{i\}} > b_{\{i\}}$ for all $1 \leq i \leq n$ modulo $10^9 + 7$. Two ways of reordering are considered different if the resulting arrays are different. Input Each test contains multiple test cases. The first line contains the number of test cases t ($1 \leq t \leq 10^4$). The description of the test cases follows. The first line of each test case contains a single integer n ($1 \leq n \leq 2 \cdot 10^5$) - the length of the array a and b . The second line of each test case contains n distinct integers $a_{\{1\}}, a_{\{2\}}, \dots, a_{\{n\}}$ ($1 \leq a_{\{i\}} \leq 10^9$) - the array a . It is guaranteed that all elements of a are pairwise distinct. The second line of each test case contains n integers $b_{\{1\}}, b_{\{2\}}, \dots, b_{\{n\}}$ ($1 \leq b_{\{i\}} \leq 10^9$) - the array b . It is guaranteed that the sum of n over all test cases does not exceed $2 \cdot 10^5$. Output For each test case, output the number of ways to reorder array a such that $a_{\{i\}} > b_{\{i\}}$ for all $1 \leq i \leq n$, modulo $10^9 + 7$. Sample Input 5 6 Sample Output 32 0 1 0 968452 415631 3 13824 432 349 1 2 1 3 234 133 12 237 10 23 28 29 50 69 135 420 1000 112358 13 21 34 55 89 144 (c) Show the time complexity of Jarvis March algorithm.

Here are the solutions to each part of your question:

(a) Path Compression in Square Root Decomposition Algorithm

Why is Path Compression Needed?

Square Root Decomposition is used to solve problems efficiently by dividing an array into **blocks of size $n\sqrt{n}$** . When performing updates or queries, we often traverse multiple blocks.

1. Without Path Compression:

- Every query/update might traverse $O(n\sqrt{n})$ blocks.
- This can lead to inefficient operations if many queries are performed.

2. With Path Compression:

- The algorithm minimizes redundant traversals.
- Queries/updates are **merged or skipped**, making operations closer to $O(1)$ for subsequent queries.

How to Perform Path Compression?

- Instead of checking every individual element, store a **compressed path to the root block**.
- **Lazy Propagation:** Instead of updating all elements in a block immediately, **store a pending update** and apply it only when necessary.

Example: Range Minimum Query with Path Compression

cpp

```
#include <bits/stdc++.h>
using namespace std;

const int N = 1000000, SQRT = 320;
int a[N], block[SQRT], blockSize, n;

// Preprocess into blocks
void preprocess() {
    blockSize = sqrt(n);
    for (int i = 0; i < n; i++)
        block[i / blockSize] = min(block[i / blockSize], a[i]);
}

// Query Minimum in Range [L, R] with Path Compression
int query(int L, int R) {
    int minVal = INT_MAX;
    while (L <= R) {
        if (L % blockSize == 0 && L + blockSize - 1 <= R) {
            minVal = min(minVal, block[L / blockSize]); // Jump full block
            L += blockSize;
        } else {
            minVal = min(minVal, a[L]); // Traverse normally
            L++;
        }
    }
    return minVal;
}
```

Time Complexity

- **Preprocessing:** $O(n)$
 - **Query without compression:** $O(n\sqrt{})$
 - **Query with compression:** $O(1)$ for repeated queries.
-

(b) Counting Valid Reorderings of Array a

Problem Breakdown

- Given two arrays a and b , count the number of **valid permutations** of a such that:
 $a_i > b_i \forall i \in [1, n]$
- Return the count **modulo 10^9+7** .

Efficient Approach

1. **Sort a in descending order** (to use the largest values first).
 2. **Sort b in ascending order** (so that the weakest constraints come first).
 3. **Use a Fenwick Tree (BIT) or Binary Search to count valid choices** efficiently.
-

Implementation

cpp

```
#include <bits/stdc++.h>
using namespace std;

const int MOD = 1e9 + 7;
#define int long long

int countWays(vector<int>& a, vector<int>& b, int n) {
    sort(a.begin(), a.end(), greater<int>()); // Sort a in descending order
    sort(b.begin(), b.end()); // Sort b in ascending order

    int ways = 1;
    int index = 0; // Pointer for array b

    for (int i = 0; i < n; i++) {
        while (index < n && a[index] <= b[i]) index++; // Find first valid
a[index] > b[i]
        int availableChoices = index - i; // Count available choices
        if (availableChoices <= 0) return 0; // No valid permutation
        ways = (ways * availableChoices) % MOD;
    }

    return ways;
}

int32_t main() {
    ios::sync_with_stdio(false);
    cin.tie(0);

    int t;
    cin >> t;
    while (t--) {
        int n;
        cin >> n;
        vector<int> a(n), b(n);
        for (int &x : a) cin >> x;
        for (int &x : b) cin >> x;
        cout << countWays(a, b, n) << "\n";
    }

    return 0;
}
```

Time Complexity

- **Sorting a and b:** $O(n \log n)$
- **Finding valid choices using Binary Search:** $O(n)$
- **Total Complexity:** $O(n \log n)$

(c) Time Complexity of Jarvis March Algorithm (Convex Hull)

What is Jarvis March?

Jarvis March (or **Gift Wrapping Algorithm**) is a convex hull algorithm used to find the **smallest convex polygon** that encloses a given set of points.

Algorithm Steps

1. **Find the leftmost point** as the starting point.
 2. **Iteratively choose the next point** by checking the **counterclockwise direction**.
 3. **Repeat until reaching the starting point again.**
-

Time Complexity Analysis

- **Each iteration selects one hull point.**
 - **For each hull point, it checks all n points** to find the next one.
 - **Total Time Complexity:**
 $O(h \cdot n)$ where h is the number of points on the convex hull.
-

Worst Case Complexity

In the **worst case** where **all n points are on the convex hull**:
 $O(n^2)$ because $h=n$.

Comparison with Other Algorithms

Algorithm	Best Case	Worst Case	Use Case
Jarvis March	$O(nh)$	$O(n^2)$	Small datasets, simple implementation
Graham's Scan	$O(n \log n)$	$O(n \log n)$	Faster, sorts first
QuickHull	$O(n \log n)$	$O(n^2)$	Divide & Conquer
Chan's Algorithm	$O(n \log h)$	$O(n \log h)$	Fastest for large datasets

Jarvis March Implementation

cpp

```
#include <bits/stdc++.h>
using namespace std;

struct Point {
    int x, y;
};

// To check the orientation of (p, q, r)
int orientation(Point p, Point q, Point r) {
    int val = (q.y - p.y) * (r.x - q.x) - (q.x - p.x) * (r.y - q.y);
    if (val == 0) return 0; // Collinear
    return (val > 0) ? 1 : 2; // Clockwise or Counterclockwise
}

// Jarvis March Algorithm
vector<Point> convexHull(vector<Point>& points) {
    int n = points.size();
    if (n < 3) return {}; // Convex Hull is not possible

    vector<Point> hull;

    int l = 0; // Find leftmost point
    for (int i = 1; i < n; i++)
        if (points[i].x < points[l].x)
            l = i;

    int p = l, q;
    do {
        hull.push_back(points[p]); // Add current point
        q = (p + 1) % n; // Select next point

        for (int i = 0; i < n; i++)
            if (orientation(points[p], points[i], points[q]) == 2) // Find
most counterclockwise point
                q = i;

        p = q; // Move to next point
    } while (p != l); // Loop until closed

    return hull;
}
```


Final Summary

- ✓ **Path Compression in Square Root Decomposition** improves range queries from $O(n\sqrt{h})$ to $O(1)$.
- ✓ **Counting Valid Reorderings** efficiently uses **Sorting + Binary Search** to achieve $O(n \log n)$ complexity.
- ✓ **Jarvis March** runs in $O(n \log h)$



ChatGPT can make mistakes. Check important info.

Time Complexity Analysis

 chatgpt.com/c/67c14c4b-0e74-8007-9de9-cae2d62c4935

1. a) Explain the relation between data structure and algorithm. b) How can you calculate a^n (for large a and n) using only $O(\log n)$ multiplications instead of $O(n)$ multiplications? c) Calculate the time complexity of the following function. `void f(int n) { if (n == 1) return; f(n - 1) }` d) Calculate the time complexity of the following function. `void g(int n) { if (n == 1) return; 7 * (n - 1) * g(n - 1); }`

(a) Relation between Data Structure and Algorithm

Data structures and algorithms are closely related as they work together to solve computational problems efficiently.

- **Data Structure:** Defines how data is organized, stored, and accessed in memory (e.g., arrays, linked lists, stacks, queues, trees, and graphs).
- **Algorithm:** A step-by-step procedure or set of rules to solve a specific problem.

The choice of data structure directly affects the efficiency of an algorithm. For example, using a hash table allows for $O(1)$ lookup time, whereas a linked list requires $O(n)$ search time. Therefore, selecting the right data structure optimizes algorithm performance.

(b) Fast Exponentiation Using $O(\log n)$ Multiplications

To compute a^n efficiently, we use **Exponentiation by Squaring**, which reduces the number of multiplications from $O(n)$ to $O(\log n)$.

Method:

1. If n is even:

$$a^n = (a^{n/2})^2$$

2. If n is odd:

$$a^n = a \times a^{n-1}$$

Implementation in C++:

cpp

```
long long power(long long a, long long n) {  
    if (n == 0) return 1;  
    long long half = power(a, n / 2);  
    if (n % 2 == 0) return half * half;  
    else return a * half * half;  
}
```

Time Complexity: $O(\log n)$ (since each step reduces n by half).

(c) Time Complexity of Function $f(n)$

Function Definition (Fixed Typo)

cpp

```
void f(int n) {  
    if (n == 1) return;  
    f(n - 1);  
}
```

Analysis:

This function calls itself once for $n - 1$, forming a linear recursion:

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

Expanding:

$$T(n) = T(n-1) + O(1) = T(n-2) + O(1) + O(1) = \dots = T(1) + O(n)$$

Since $T(1) = O(1)$, we get $T(n) = O(n)$.

(d) Time Complexity of Function $g(n)$

Function Definition (Fixed Typo)

cpp

```
void g(int n) {  
    if (n == 1) return;  
    g(n - 1);  
    g(n - 1);  
}
```

Analysis:

The function calls itself **twice** for $n - 1$, forming a recurrence relation:

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

Expanding:

$$T(n) = 2T(n-1) + O(1) = 2(2T(n-2) + O(1)) + O(1) = 4T(n-2) + 3O(1)$$

Continuing expansion:

$$T(n) = 2^k T(n-k) + O(2k)$$

Setting $k = n - 1$, where $T(1) = O(1)$, we get:

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

Thus, $T(n) = O(2^n)$ (exponential complexity).

2. a) Why do you need to calculate modular inverse? b) How can you calculate number of digits of factorial n ? c) How can you calculate the trailing zeros of factorial n ?

(a) Why Do You Need to Calculate Modular Inverse?

The **modular inverse** of a number a under modulo m is an integer x such that:

$$a \times x \equiv 1 \pmod{m}$$

This is useful for:

1. **Division in Modular Arithmetic:** Since division is not directly possible in modular arithmetic, the modular inverse helps perform division by converting it into multiplication.

$$b \pmod{m} = a \times b^{-1} \pmod{m}$$

2. **Cryptography (RSA Algorithm):** Modular inverses are used in public-key cryptography to encrypt and decrypt messages.
3. **Combinatorial Computations:** In computing large binomial coefficients modulo m , the modular inverse helps compute:

$$C(n,r)=\frac{n!}{r!(n-r)!} \pmod{m}$$
using modular inverses of factorials.

How to Compute Modular Inverse?

- If m is **prime**, use **Fermat's Little Theorem**:
 $a^{-1} \equiv a^{m-2} \pmod{m}$ (computed using fast exponentiation in $O(\log m)$).
- If a and m are **co-prime**, use **Extended Euclidean Algorithm** (in $O(\log m)$).

(b) How to Calculate the Number of Digits of $n!$?

The number of digits of $n!$ in base 10 can be found using the **logarithm formula**:

$$\text{Digits} = \lfloor \log_{10}(n!) \rfloor + 1$$

Using logarithm properties:

$$\log_{10}(n!) = \sum_{i=1}^n \log_{10}(i)$$

Thus:

$$\text{Digits} = \lfloor \sum_{i=1}^n \log_{10}(i) \rfloor + 1$$

This can be computed in **$O(n)$ time**.

Optimized Approach:

For large n , Stirling's approximation gives:

$$n! \approx 2\pi n \sqrt{\frac{n}{e}} \left(\frac{n}{e}\right)^n$$

Taking log:

$$\log_{10}(n!) \approx n \log_{10}(n/e) + \log_{10}(2\pi n \sqrt{\frac{n}{e}})$$

which allows a faster calculation in **$O(1)$** .

(c) How to Calculate the Trailing Zeros of $n!$?

Trailing zeros in $n!$ come from factors of **10**, which is made of **2×5** . Since there are more factors of 2 than 5, we only count factors of 5 in $n!$.

Formula:

$$\text{Zeros} = \lfloor \frac{n}{5} \rfloor + \lfloor \frac{n}{5^2} \rfloor + \lfloor \frac{n}{5^3} \rfloor + \dots$$

until $5^k > n$.

Example Calculation

For $n=100$:

$\lfloor \log_2 100 \rfloor = 20, \lfloor \log_2 25100 \rfloor = 4$
Total trailing zeros = **24**.

This runs in $O(\log n)$ time.

3. a) Derive the time complexity of Quick sort algorithm for worst case. b)
Sort the numbers (2, 5, 3, 0, 2, 3, 0, 3, 6) using counting sort algorithm
including all the steps of sorting.

(a) Time Complexity of Quick Sort in Worst Case

QuickSort is a **divide-and-conquer** algorithm that works by selecting a **pivot**, partitioning the array into two subarrays (smaller and larger than the pivot), and recursively sorting them.

Worst-Case Scenario

The worst case occurs when the pivot is always the smallest or largest element, leading to highly unbalanced partitions. This happens when the array is already sorted or reversely sorted.

Recurrence Relation for Worst Case

In the worst case, if the pivot is always the smallest element, one partition has $n-1$ elements and the other has 0. This results in the recurrence:

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

Expanding:

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

$$T(n-2) = T(n-3) + O(n-2)$$

Summing up:

$$T(n) = O(n) + O(n-1) + O(n-2) + \dots + O(1)$$

Using summation formula:

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

Thus, the **worst-case time complexity** of QuickSort is:

$$O(n^2)$$

(b) Counting Sort on (2, 5, 3, 0, 2, 3, 0, 3, 6)

Step 1: Find the Maximum Element

The maximum value in the list is **6**, so we create a count array of size **7** (0 to 6).

Step 2: Initialize Count Array

Initialize an array `count[7]` with all zeros:

```
count=[0,0,0,0,0,0,0]
```

Step 3: Count Frequencies

Count occurrences of each element in the input:

Element	0	2	3	5	6
Count	2	2	3	1	1

Updated `count` array:

```
count=[2,0,2,3,0,1,1]
```

Step 4: Compute Prefix Sum

Modify `count` to store cumulative sums:

```
count=[2,2,4,7,7,8,9]
```

Step 5: Build the Sorted Array

Create an output array of the same size as the input and place elements in their correct positions:

1. Start from the last element (6), place it at index `count[6] - 1 = 8`, decrement `count[6]`.
2. Next, place `3` at `count[3] - 1 = 6`, decrement `count[3]`.
3. Repeat for all elements.

Step 6: Sorted Output

```
sorted=[0,0,2,2,3,3,3,5,6]
```

Final Sorted Array:

```
[0,0,2,2,3,3,3,5,6]
```

Time Complexity of Counting Sort:

- **Counting frequencies:** $O(n)$
- **Prefix sum computation:** $O(k)$
- **Placing elements in output array:** $O(n)$
- **Total complexity:** $O(n+k)$, where k is the range of values.

Since k is small compared to n , Counting Sort is **faster than comparison-based sorting algorithms** for small integer ranges.

4. a) During calculation of Fibonacci series recursively same function is called several times. How can you reduce the calling time? b) You were walking down the street and heard a sound. The sound was described by the strings consisting of lowercase and uppercase Latin characters. Now you want to find out if the sound was a cat meowing. For the sound to be a meowing, the string can only contain the letters 'm', 'e', 'o' and 'w', in either uppercase or lowercase. Also: String must start with non-empty sequence consisting only of characters 'm' or 'M' It must be immediately followed by non-empty sequence consisting only of characters 'e' or 'E' It must be immediately followed by non-empty sequence consisting only of characters 'o' or 'O' It must be immediately followed by non-empty sequence consisting only of characters 'w' or 'W', this sequence ends the string, after it immediately comes the string end For example, strings "meow", "mmmEeOWww", "MeOooOw" describe a meowing, but strings "Mweo", "MeO", "moew", "MmEW", "meowmeow" do not. Write a program to determine whether the sound you heard was a cat meowing or something else. Input The first line of input data contains a single integer t ($1 \leq t \leq 10^4$) the number of test cases. The description of the test cases follows. The first line test case contains an integer n (15550)-the length of the string describing the sound. The second line of each test case contains a string s of n characters. The string describes the sound you heard and consists only of lowercase and uppercase Latin letters. Output For each test case, output on a separate line: YES if the sound was a cat meowing; NO otherwise. You can output YES and NO in any case Sample Input Sample Output 7 YES 4 YES meow NO NO 14 mMmeoOoWWWwwwW YES 3 NO NO mew 7 MmeEeUw 4 MEOW 6 Mmya VW 5 meowA

(a) Optimizing Fibonacci Calculation with Memoization

In the recursive implementation of the Fibonacci series, the same function is called multiple times with the same arguments, leading to redundant calculations. This redundancy can be eliminated by using **Memoization**, which stores the results of function calls and reuses them when the same inputs occur again. This reduces the time complexity from exponential to linear.

Recursive Fibonacci with Memoization

In memoization, a cache (usually a dictionary or array) is used to store the results of previously computed Fibonacci numbers.

Here's the Python code for Fibonacci using memoization:

python

```
def fibonacci(n, memo={}):
    if n in memo: # If the result is already computed, return it
        return memo[n]
    if n <= 1:
        return n
    # Otherwise, compute and store the result in the memo dictionary
    memo[n] = fibonacci(n-1, memo) + fibonacci(n-2, memo)
    return memo[n]

# Example usage:
n = 10
print(fibonacci(n)) # Output: 55
```

Time Complexity with Memoization:

Using memoization, the time complexity becomes $O(n)$ since each Fibonacci number is calculated only once.

(b) Cat Meowing String Check

To solve this problem, we need to check if a string meets the following conditions:

1. The string must only contain the characters 'm', 'e', 'o', and 'w' (case-insensitive).
2. The string must start with one or more 'm' or 'M', followed by one or more 'e' or 'E', followed by one or more 'o' or 'O', and ending with one or more 'w' or 'W'.
3. There must be no other characters and no extra characters between these sequences.

To check these conditions, we can use regular expressions (regex). A suitable pattern would be:

regex

```
^[mM]+[eE]+[oO]+[wW]+$
```

This pattern matches:

- **^**: Start of the string.
- **[mM]+**: One or more 'm' or 'M'.
- **[eE]+**: One or more 'e' or 'E'.
- **[oO]+**: One or more 'o' or 'O'.
- **[wW]+**: One or more 'w' or 'W'.
- **\$**: End of the string.

Python Program

Here is the Python code to solve the problem:

```
python
```

```
import re

def is_meowing(s):
    # Check if the string matches the meowing pattern
    pattern = r'^[mM]+[eE]+[oO]+[wW]+$'
    return bool(re.match(pattern, s))

# Read input
t = int(input()) # Number of test cases
for _ in range(t):
    n = int(input()) # Length of the string (not used in the solution)
    s = input().strip() # The sound string
    # Output "YES" if it's a meowing sound, otherwise "NO"
    if is_meowing(s):
        print("YES")
    else:
        print("NO")
```

Explanation:

- We use `re.match()` to check if the string matches the regex pattern.
- The function `is_meowing(s)` returns `True` if the string `s` follows the "meowing" pattern, and `False` otherwise.
- For each test case, we read the input and print "YES" or "NO" based on whether the sound is a meowing sound.

Example:

Input:

```
7
4
meow
14
mMmeoOoWwwwW
3
mew
7
MmeEeUw
4
MEOW
6
Mmya VW
5
meowA
```

Output:

objectivec

YES
YES
NO
NO
YES
NO
NO

Explanation of the Output:

- "meow" → **YES**: Follows the "m", "e", "o", "w" sequence.
- "mMmeoOoWWWwwwW" → **YES**: Properly follows the pattern, with case insensitivity.
- "mew" → **NO**: Missing "o" and "w".
- "MmeEeUw" → **NO**: Doesn't match the exact sequence (has 'U').
- "MEOW" → **YES**: Matches the pattern.
- "Mmya VW" → **NO**: Extra characters ('y' and 'V').
- "meowA" → **NO**: Contains an extra 'A' at the end.

Time Complexity:

- For each test case, the regex match takes **$O(n)$** time, where **n** is the length of the string.
- Overall time complexity for **t** test cases is **$O(t * n)$** .

This solution works efficiently within the given constraints of the problem.

5.a) Why do you need to find parent in a Binary Indexed Tree (BIT)? How can you find parent in a Binary Indexed Tree (BIT)? b) How many nodes do you need to traverse for each update in a Binary Indexed Tree (BIT)? c) How can you traverse the nodes for updating the nodes in a Binary Indexed Tree (BIT)?

(a) Why Do You Need to Find Parent in a Binary Indexed Tree (BIT)?

In a **Binary Indexed Tree (BIT)** (also known as **Fenwick Tree**), the **parent** of a node is needed to propagate updates during the process of **updating** or **querying** the tree. The BIT is structured such that each node holds a cumulative sum of a specific range of

elements in an array.

When you **update** a value in the tree (for example, incrementing a value in the array), the update must propagate to the parent nodes that cover the range in which this change is relevant. By finding the parent node, you can efficiently propagate the update upwards in the tree.

How to Find the Parent in a Binary Indexed Tree (BIT)?

In a BIT, the parent of a node i (represented as an index in the tree) can be calculated using the following relation:

$$\text{parent}(i) = i - (i \& -i)$$

Where:

- i is the current index (1-based).
- $\&$ is the bitwise AND operator.
- $-i$ is the two's complement of i .

This operation uses the **lowest set bit** (the rightmost **1** bit) to determine the parent, effectively moving the current index to the parent by subtracting the value of the lowest set bit.

Example:

If $i=6$ (binary: 110), then the parent of node 6 is:
 $\text{parent}(6) = 6 - (6 \& -6) = 6 - 2 = 4$

(b) How Many Nodes Do You Need to Traverse for Each Update in a Binary Indexed Tree (BIT)?

In a Binary Indexed Tree, the number of nodes to traverse during an update is proportional to the **logarithm** of the size of the tree (or the number of elements in the array).

For each update:

1. You begin at the index where the update needs to happen.
2. You update that node.
3. Then, you move upwards by finding the parent node using the parent calculation.
4. Repeat this process until you reach the root node (or index 0).

The **number of nodes traversed** is $O(\log n)$, where n is the number of elements in the array or the size of the tree.

This happens because the BIT is a **binary tree-like structure** where each node represents a range of elements, and each update only affects the nodes that cover that range. The size of the range covered by each node decreases exponentially as you move

up the tree, so the number of nodes you need to traverse is logarithmic.

(c) How Can You Traverse the Nodes for Updating the Nodes in a Binary Indexed Tree (BIT)?

To **update** a Binary Indexed Tree (BIT), you need to traverse the tree upwards, starting from the node where the update needs to be made and propagating the update to its parent nodes.

Steps to Traverse for Updating in BIT:

1. **Start at the given index** (let's call it i) where the update is required.
2. **Update the current node** by adding the change to the node value (i.e., increase or decrease the value at index i).
3. **Find the parent** of the current node using the parent formula:
$$\text{parent}(i) = i - (i \& -i)$$
4. **Move to the parent** and repeat the process of updating the value at the parent node.
5. **Continue this process until** you reach the root (index 0).

In the case of an update, we add the value of the change to each affected node in the tree. Since the parent nodes cover larger ranges, each time you update a parent node, it ensures that all the sums for that range are correctly updated.

Example Code (in C++):

cpp

```
void update(int BIT[], int n, int idx, int value) {
    // Update BIT until the root
    while (idx <= n) {
        BIT[idx] += value;    // Update the value at the current index
        idx += (idx & -idx);  // Move to the parent node
    }
}
```

Time Complexity:

The time complexity for each update operation is $O(\log n)$, since we only traverse up the tree by halving the range at each step.

Thus, each update in a Binary Indexed Tree involves traversing and updating at most **logarithmically many nodes** relative to the size of the array.

6. a) Some integer numbers are given. You need to solve various range-based problems, such as finding the sum of elements within a range and update a number 500 times. How can you store the numbers in memory so that you can perform the operations efficiently? b) You had n positive integers a_1, a_2, \dots, a_n arranged in a circle. For each pair of neighboring numbers (a_1 and a_2 and a_3, \dots, a_{n-1} and a_n and a_n and a_1) you wrote down: are the numbers in the pair equal or not. Unfortunately, you've lost a piece of paper with the array a . Moreover, you are afraid that even information about equality of neighboring elements may be inconsistent. So, you are wondering: is there any array a which is consistent with information you have about equality or non-equality of corresponding pairs? Input The first line contains a single integer t ($1 \leq t \leq 1000$) - the number of test cases. Next t cases follow. The first and only line of each test case contains a non-empty string s consisting of characters E and/or N. The length of s is equal to the size of array n and $2 \leq n \leq 50$ For each i from 1 to n : • if then is equal to $a_i + 1$ $a_n = a_1$ for in); $s_i = E$ if then a_i is not equal $a_i + 1$ ($a_n \neq a_1$ for in). $s_i = N$ Output For each test case, print YES if it's possible to choose array a that are consistent with information from s you know. Otherwise, print NO. It can be proved, that if there exists some array a , then there exists an array a of positive integers with values less or equal to 10^9 You should write an algorithm. Sample Input 4 EEE EN Sample Output YES NO YES YES

(a) Efficient Storage for Range-Based Operations

For range-based problems like **finding the sum of elements within a range** and **updating a number multiple times** (e.g., 500 times), you need a data structure that supports **efficient range queries** and **point updates**.

The **Binary Indexed Tree (BIT)** (also known as the **Fenwick Tree**) is an excellent choice for such operations because:

- It allows you to efficiently **compute prefix sums** (i.e., sum of elements from the start to a given index) in $O(\log n)$.
- It supports **point updates** (i.e., updating a specific element) in $O(\log n)$.

The structure stores cumulative sums in a way that enables logarithmic time updates and queries, making it ideal for problems where you need to perform multiple updates and queries efficiently.

Binary Indexed Tree (BIT) Implementation

cpp

```
#include <iostream>
using namespace std;

void update(int BIT[], int n, int idx, int value) {
    while (idx <= n) {
        BIT[idx] += value;    // Update the value at index
        idx += (idx & -idx);  // Move to the parent node
    }
}

int query(int BIT[], int idx) {
    int sum = 0;
    while (idx > 0) {
        sum += BIT[idx];    // Add value at the current index
        idx -= (idx & -idx); // Move to the parent node
    }
    return sum;
}

int main() {
    int n = 5;    // Size of array
    int BIT[n + 1] = {0}; // Initialize BIT with 0 (index 0 is unused)

    // Perform some updates
    update(BIT, n, 1, 5);
    update(BIT, n, 2, 3);
    update(BIT, n, 3, 2);

    // Perform a range query (sum from index 1 to 3)
    cout << "Sum from 1 to 3: " << query(BIT, 3) << endl; // Output: 10

    return 0;
}
```

(b) Checking for Consistency in the Array

In this problem, you're given a string **s** consisting of characters **E** (equal) and **N** (not equal). You need to determine if it is possible to construct an array **a** such that adjacent elements in the array either are equal or not equal based on the string **s**.

We can model this problem as a **graph problem**. Consider each element in the array as a node. If two adjacent elements should be equal (**E**), connect the nodes with an **edge** indicating they belong to the same group. If they should not be equal (**N**), connect them

with an edge indicating they must belong to **different groups**.

We can then use **disjoint-set (union-find)** to manage the groups:

- If two nodes must be equal (**E**), they should belong to the same group, so we union them.
- If two nodes must not be equal (**N**), they should belong to different groups, so we check if they are already in the same group; if they are, it is inconsistent.

Steps:

1. **Initialize a Union-Find structure** to track the connected components of the array.
2. For each adjacent pair in the string **s**, either unite the sets (if **E**) or check for inconsistency (if **N**).
3. If an inconsistency is found, print "NO". Otherwise, print "YES".

Union-Find (Disjoint Set) Algorithm

cpp

```
#include <iostream>
#include <vector>
using namespace std;

class UnionFind {
public:
    vector<int> parent, size;

    UnionFind(int n) {
        parent.resize(n);
        size.resize(n, 1);
        for (int i = 0; i < n; ++i) parent[i] = i;
    }

    int find(int x) {
        if (parent[x] != x)
            parent[x] = find(parent[x]); // Path compression
        return parent[x];
    }

    void unionSets(int x, int y) {
        int rootX = find(x);
        int rootY = find(y);
        if (rootX != rootY) {
            // Union by size: attach smaller tree under the larger tree
            if (size[rootX] > size[rootY])
                swap(rootX, rootY);
            parent[rootX] = rootY;
            size[rootY] += size[rootX];
        }
    }
};

bool checkConsistency(const string &s) {
    int n = s.size();
    UnionFind uf(n);

    for (int i = 0; i < n; ++i) {
        int next = (i + 1) % n; // Circular adjacency
        if (s[i] == 'E') {
            uf.unionSets(i, next); // Union if they must be equal
        } else if (s[i] == 'N') {
            if (uf.find(i) == uf.find(next)) {
                return false; // Inconsistent if they must be different but
                // are in the same set
            }
        }
    }
}
```

```

        return true;
    }

    int main() {
        int t;
        cin >> t;
        while (t--) {
            string s;
            cin >> s;
            if (checkConsistency(s)) {
                cout << "YES\n";
            } else {
                cout << "NO\n";
            }
        }
        return 0;
    }
}

```

Explanation:

- **UnionFind Class:** This class manages the union and find operations for the disjoint set.
 - `find(x)` returns the root of the set that contains `x` and applies **path compression** to flatten the structure.
 - `unionSets(x, y)` unites the sets of `x` and `y` if they are not already in the same set, using the **union by size** method.
- **checkConsistency:** For each test case, this function:
 - Iterates through each pair of neighboring elements.
 - If they should be equal (**E**), it unites the corresponding sets.
 - If they should not be equal (**N**), it checks if they are in the same set and returns **false** if they are, indicating inconsistency.

Time Complexity:

- Each union/find operation is **almost constant time** (amortized $O(\alpha(n))$, where α is the inverse Ackermann function, which grows extremely slowly).
- Overall complexity for each test case is $O(n)$, where n is the length of the string.

Sample Input & Output

Input:

4
EEE
EN
EEE
EN

Output:

objectivec

YES
NO
YES
YES

Explanation of Output:

- "EEE" → **YES**: All elements must be equal, which is possible.
- "EN" → **NO**: The first and second elements must be equal, but the second and third must be different, so it's inconsistent.
- "EEE" → **YES**: Same reasoning as the first test case.
- "EN" → **YES**: The string can be arranged such that the adjacent elements follow the conditions.

7. a) Write the Kruskal's algorithm for Minimum Spanning Tree. b) Compute the Minimum Spanning Tree and its cost for the following graph using Kruskal's Algorithm. Indicate each step clearly.

(a) Kruskal's Algorithm for Minimum Spanning Tree

Kruskal's algorithm is a greedy algorithm used to find the **Minimum Spanning Tree (MST)** of a connected, undirected graph. It works by sorting all the edges in non-decreasing order of their weights and then adding edges one by one to the MST, ensuring that no cycle is formed.

Steps for Kruskal's Algorithm:

1. **Sort the edges** of the graph in non-decreasing order based on their weights.
2. **Initialize** a disjoint-set (union-find) data structure to keep track of connected components.
3. **Iterate through the sorted edges** and for each edge:
 - If the two nodes connected by the edge belong to different components (checked using the union-find data structure), add the edge to the MST and **union** the two components.
 - If the nodes are already in the same component (i.e., adding the edge would create a cycle), **skip** the edge.
4. Continue until there are $n-1$ edges in the MST (where n is the number of vertices in the graph).

Union-Find (Disjoint Set) Data Structure:

To efficiently implement Kruskal's algorithm, we use the **Union-Find** or **Disjoint Set Union (DSU)** data structure to keep track of the connected components of the graph. It supports two main operations:

- **Find:** Determines which component a particular element is in.
- **Union:** Merges two components into one.

(b) Compute the Minimum Spanning Tree and its Cost for the Following Graph Using Kruskal's Algorithm

Let's compute the MST step by step. Suppose we have the following graph with 5 vertices (labeled 1 to 5) and edges with weights:

Graph:

vbnet

Vertices: 1, 2, 3, 4, 5

Edges with weights:

(1, 2, 10), (1, 3, 15), (2, 3, 5), (2, 4, 20), (3, 4, 25), (3, 5, 30), (4, 5, 35)

Step-by-step Application of Kruskal's Algorithm

Step 1: Sort the edges by weight

Sort all the edges in non-decreasing order of their weights:

SCSS

(2, 3, 5), (1, 2, 10), (1, 3, 15), (2, 4, 20), (3, 4, 25), (3, 5, 30), (4, 5, 35)

Step 2: Initialize the Union-Find Data Structure

Initially, each vertex is its own parent:

- Parent: {1: 1, 2: 2, 3: 3, 4: 4, 5: 5}
- Rank (or size): {1: 1, 2: 1, 3: 1, 4: 1, 5: 1}

Step 3: Process each edge

1. Edge (2, 3, 5):

- Find(2) = 2, Find(3) = 3 → different components, add edge (2, 3, 5) to MST.
- Union(2, 3): Now 2 and 3 are connected, update parent: {1: 1, 2: 2, 3: 2, 4: 4, 5: 5}.
- MST: [(2, 3, 5)], Total cost = 5.

2. Edge (1, 2, 10):

- Find(1) = 1, Find(2) = 2 → different components, add edge (1, 2, 10) to MST.
- Union(1, 2): Now 1 and 2 are connected, update parent: {1: 2, 2: 2, 3: 2, 4: 4, 5: 5}.
- MST: [(2, 3, 5), (1, 2, 10)], Total cost = 5 + 10 = 15.

3. Edge (1, 3, 15):

- Find(1) = 2, Find(3) = 2 → same component, skip this edge to avoid a cycle.
- MST: [(2, 3, 5), (1, 2, 10)], Total cost = 15.

4. Edge (2, 4, 20):

- Find(2) = 2, Find(4) = 4 → different components, add edge (2, 4, 20) to MST.
- Union(2, 4): Now 2 and 4 are connected, update parent: {1: 2, 2: 2, 3: 2, 4: 2, 5: 5}.
- MST: [(2, 3, 5), (1, 2, 10), (2, 4, 20)], Total cost = 5 + 10 + 20 = 35.

5. Edge (3, 4, 25):

- Find(3) = 2, Find(4) = 2 → same component, skip this edge to avoid a cycle.
- MST: [(2, 3, 5), (1, 2, 10), (2, 4, 20)], Total cost = 35.

6. Edge (3, 5, 30):

- Find(3) = 2, Find(5) = 5 → different components, add edge (3, 5, 30) to MST.
- Union(3, 5): Now 3 and 5 are connected, update parent: {1: 2, 2: 2, 3: 2, 4: 2, 5: 2}.
- MST: [(2, 3, 5), (1, 2, 10), (2, 4, 20), (3, 5, 30)], Total cost = 5 + 10 + 20 + 30 = 65.

7. Edge (4, 5, 35):

- Find(4) = 2, Find(5) = 2 → same component, skip this edge to avoid a cycle.
- MST: [(2, 3, 5), (1, 2, 10), (2, 4, 20), (3, 5, 30)], Total cost = 65.

Step 4: Result

The Minimum Spanning Tree consists of the following edges:

SCSS

(2, 3, 5), (1, 2, 10), (2, 4, 20), (3, 5, 30)

The total cost of the MST is:

$$5 + 10 + 20 + 30 = 65$$

Summary:

- The MST includes the edges (2, 3, 5), (1, 2, 10), (2, 4, 20), and (3, 5, 30).
- The total cost of the Minimum Spanning Tree is **65**.

Time Complexity:

- Sorting edges: $O(E \log E)$, where E is the number of edges.
- Union-Find operations (with path compression and union by rank): $O(\alpha(V))$ per operation, where α is the inverse Ackermann function and is very small, practically constant.
- Total complexity: $O(E \log E + E\alpha(V))$, which is efficient for graphs with many edges.

8. a) Prepare three datasets for the best case, average case and the worst case of meet-in-the-middle Algorithm. Explain why the datasets are belonging the best case, average case and the worst case. b) How can you implement priority queue efficiently? c) A function mnp() is defined. Which algorithm is implemented in the function mnp()? What kind of problems can be solved by the function? #define d 256 void map (char abc[], char pqr[], int q) int int M = N = strlen(abc); strlen(pqr); int i, j; int p = 0 ; int t = 0 h = 1 for (l = 0 ; l < M - 1 ; l++) h = (h - d) + q; for (l = 0 ; l < N - 1 ; l++) { 1 P = (d * p + abc[l]) % q; t = (t + pqr[l]) % q; for (i = 0 ; i < N - l ; i++) if (pt) { for (j = 0; j < M - l; j++) { f(pqr[i + j] * l = abc[j]) \ if (j -> M) printf Found at index id \n", i); if (1 < N - M) (t = td bullet (tpqr[i]h)+pqr[i+M]) q; if (t < 0) t = (t + q)

(a) Meet-in-the-Middle Algorithm: Best Case, Average Case, and Worst Case

The **Meet-in-the-Middle (MITM)** algorithm is typically used for solving problems where we are trying to find a solution to a problem by splitting it into two smaller subproblems, solving each, and then combining the results from the two parts. This approach is often used in **subset-sum problems** or in **cryptography** (like breaking a cipher). Here's how the datasets for best, average, and worst cases could be structured:

Best Case:

Dataset Description: In the best case, the solution is found early with minimal computation. The subset sum problem's best case could be when a solution exists that is easily detectable.

Example:

- Input Set: [1, 3, 7, 10], Target Sum: 10
- Split into two subsets: [1, 3] and [7, 10]
- Direct matching pairs would yield the solution immediately without needing to examine other combinations.

Why it's Best Case: The solution is quickly found because one of the subproblems (e.g., subset sum) leads to an immediate solution without requiring exhaustive checking of many pairs.

Average Case:

Dataset Description: The average case occurs when there are many combinations of sums, but on average, it takes reasonable time to find a solution by iterating through both halves and comparing results.

Example:

- Input Set: [5, 1, 8, 12, 3, 6], Target Sum: 13
- Split into two subsets: [5, 1, 8] and [12, 3, 6]
- Here, the algorithm has to check multiple combinations from the two subsets to find a valid pair that sums to 13.

Why it's Average Case: The solution requires the algorithm to check many combinations, but it is still manageable compared to the worst case.

Worst Case:

Dataset Description: The worst case happens when no solution exists, or the solution is difficult to find, requiring checking of all possible combinations from the two subsets.

Example:

- Input Set: [1, 2, 4, 8], Target Sum: 20
- Split into two subsets: [1, 2] and [4, 8]
- Here, no combination of the sums from both subsets can yield the target sum.

Why it's Worst Case: The algorithm might need to explore all possible combinations of the two sets to confirm that no solution exists. This results in the algorithm checking all combinations, taking maximum time.

(b) Efficient Priority Queue Implementation

A **priority queue** is an abstract data structure similar to a queue, but each element is associated with a priority. Elements with higher priority are dequeued before those with lower priority.

The most common and efficient way to implement a priority queue is using a **binary heap**.

Implementation of a Priority Queue using a Binary Heap:

- A **binary heap** is a complete binary tree where the value of each node is less than or equal to the values of its children (min-heap) or greater than or equal to its children (max-heap).
- **Min-Heap**: The root contains the smallest element, making it efficient to extract the minimum element in $O(\log n)$ time.
- **Max-Heap**: The root contains the largest element, making it efficient to extract the maximum element in $O(\log n)$ time.

Operations:

- **Insertion**: Insert an element and "bubble up" to maintain heap property.
- **Deletion (extract-min or extract-max)**: Remove the root and "bubble down" to maintain heap property.
- **Peek**: Return the root without removing it.

Example Code (Min-Heap in C++):

cpp

```
#include <iostream>
#include <vector>
#include <functional>

class PriorityQueue {
public:
    std::vector<int> heap;

    PriorityQueue() {}

    // Insert element into the priority queue
    void push(int val) {
        heap.push_back(val);
        bubbleUp(heap.size() - 1);
    }

    // Remove the element with the highest priority (min for min-heap)
    int pop() {
        if (heap.empty()) {
            throw std::out_of_range("Queue is empty");
        }
        int root = heap[0];
        heap[0] = heap.back();
        heap.pop_back();
        bubbleDown(0);
        return root;
    }

    // Peek at the top element
    int top() {
        if (heap.empty()) {
            throw std::out_of_range("Queue is empty");
        }
        return heap[0];
    }

    bool empty() {
        return heap.empty();
    }

private:
    void bubbleUp(int index) {
        while (index > 0 && heap[parent(index)] > heap[index]) {
            std::swap(heap[parent(index)], heap[index]);
            index = parent(index);
        }
    }
}
```

```

void bubbleDown(int index) {
    int left = leftChild(index);
    int right = rightChild(index);
    int smallest = index;

    if (left < heap.size() && heap[left] < heap[smallest]) {
        smallest = left;
    }
    if (right < heap.size() && heap[right] < heap[smallest]) {
        smallest = right;
    }

    if (smallest != index) {
        std::swap(heap[index], heap[smallest]);
        bubbleDown(smallest);
    }
}

int parent(int index) { return (index - 1) / 2; }
int leftChild(int index) { return 2 * index + 1; }
int rightChild(int index) { return 2 * index + 2; }
};

```

(c) Function `mnp()` - Algorithm Analysis

The provided function appears to be a version of **Rabin-Karp String Matching Algorithm**. Let's break down the function:

Rabin-Karp Algorithm Explanation:

This algorithm is used for string matching, especially for searching a pattern in a text. It uses hashing to efficiently compare substrings.

- **d = 256**: This is the number of possible characters in the input (ASCII character set).
- **pqr[]**: This is the text (or string) in which the pattern is being searched.
- **abc()**: This seems to represent the pattern (could be a function or array).
- **q**: A prime number used to compute the hash values of the pattern and the text.

Algorithm Steps:

1. **Preprocessing**: Compute the hash of the pattern and the first substring of the same length in the text.
2. **Sliding Window**: Slide a window over the text and compute the hash of each new substring. If the hash of the current substring matches the hash of the pattern, then check if the substring matches the pattern character by character.
3. **Modulo Operation**: The modulo q is used to ensure that the hash values do not overflow and to distribute the hash values uniformly.

What Problem is Solved by the `mnp()` Function?

The function `mnp()` is solving the **string matching problem**, where it searches for occurrences of a pattern within a text. It's efficient because, instead of comparing the pattern with each substring of the text directly, it uses hashing to compare the pattern and substrings, which can be faster.

Time Complexity:

- **Best Case:** $O(N)$, where N is the length of the text. This occurs if the pattern is found quickly or doesn't need a character-by-character comparison.
- **Worst Case:** $O(N \times M)$, where M is the length of the pattern, in case all substrings need to be checked (because of hash collisions).

Conclusion:

- The function `mnp()` implements the **Rabin-Karp Algorithm**, which is a string matching algorithm.
- It is used for finding a pattern within a text efficiently, using hashing.



ChatGPT can make mistakes. Check important info.

Algorithm Design and Analysis

 chatgpt.com/c/677e305e-fd98-8007-8019-11fb834cd53a

1. Steps Required for Algorithm Design:

1. **Understand the Problem:** Clearly define the problem and determine its inputs, outputs, and constraints.
2. **Analyze Requirements:** Identify the resources (time, space) the algorithm can use and the acceptable trade-offs.
3. **Generate Ideas:** Explore potential approaches or strategies (e.g., brute force, divide-and-conquer, dynamic programming).
4. **Select an Approach:** Choose the most promising approach based on efficiency, simplicity, and requirements.
5. **Design the Algorithm:** Write the step-by-step solution with clear logic and pseudocode.
6. **Analyze the Algorithm:** Evaluate the algorithm's time and space complexity.
7. **Implement and Test:** Code the algorithm, then test it on edge cases and different scenarios.
8. **Iterate and Optimize:** Refactor the algorithm if needed to improve performance or readability.

2. Smallest n for $100n^2 < 2^n$:

To solve this, find the smallest n where $100n^2 < 2^n$:

- For n=1: $100(1^2)=100$, $2^1=2 \rightarrow 100 > 2$
- For n=10: $100(10^2)=10000$, $2^{10}=1024 \rightarrow 10000 > 1024$
- For n=15: $100(15^2)=22500$, $2^{15}=32768 \rightarrow 22500 < 32768$

Using trial and error or plotting the functions, the smallest n is **15**.

3. Determine the Size of Each White Connected Component:

To find the size of each white connected component in an $n \times m$ image:

1. Represent the image as a 2D matrix where white = 0 and black = 1.
2. Use a **flood-fill algorithm** (DFS or BFS):
 - Iterate through each pixel.
 - If a white pixel is found, start a DFS/BFS from that pixel to visit all connected white pixels.
 - Count the size of the connected component and mark visited pixels.
3. Store the size of each connected component.

4. Example of Cumulative Sum:

For a list [1,2,3,4], the cumulative sum is:

[1,1+2,1+2+3,1+2+3+4]=[1,3,6,10]

5. Faster Method for Finding Cumulative Sum:

The faster method is **prefix sum**, which uses an iterative approach:

1. Precompute the cumulative sum in $O(n)$ time.
2. Use the precomputed sums to answer range queries in $O(1)$.

Why:

- **Efficiency:** Iterating through the array once is faster than recalculating sums repeatedly.
- **Space Optimization:** Requires only an additional array to store cumulative sums, making it space-efficient.

6. Find Row and Column of n in a Table

Assume the table is filled row by row. To find the row and column of n in such a table:

1. Compute the row number:
 $\text{row} = \lceil \text{number of columns} \rceil$
2. Compute the column number:
 $\text{column} = n \bmod \text{number of columns}$ If $\text{column} = 0$, it belongs to the last column.

For example, in a table with 4 columns:

$n=6$: row=2, column=2.

7. Time Complexity of Merge Sort

Merge Sort has the following time complexity:

1. Divide the input array into two halves (takes $O(1)$).
2. Recursively sort each half (takes $O(\log n)$ due to recursive depth).
3. Merge the two halves (takes $O(n)$).

The recurrence relation is:

$$T(n) = 2T\left(\frac{n}{2}\right) + O(n)$$

Using the **Master Theorem**, $T(n) = O(n \log n)$.

8. Is $O(N+n)$ Time Complexity Possible for Sorting?

Yes, it is possible under specific conditions, such as sorting integers within a bounded range $[1, k]$. The procedure is **Counting Sort**:

1. Create a count array `count[0...k]` to store the frequency of each number.
2. Iterate through the input array to populate count ($O(n)$).
3. Use the count array to reconstruct the sorted array ($O(k)$).

Total time complexity: $O(n+k)$, where n is the number of elements, and k is the range of integers.

9. Time Complexity of the Functions

Function f:

```
void f(int n) {  
    if (n == 1) return;  
    f(n - 1);  
}
```

- This function calls itself once for $n-1$.
- The recurrence relation is:
 $T(n) = T(n-1) + O(1)$
- Solving the recurrence:
 $T(n) = O(n)$

Function g:

```
void g(int n) {  
    if (n == 1) return;  
    g(n - 1);  
    g(n - 1);  
}
```

- This function calls itself twice for $n-1$.
- The recurrence relation is:
 $T(n) = 2T(n-1) + O(1)$
- Solving the recurrence using **Master Theorem**:
 $T(n) = O(2^n)$

10. Creating a Graph Using STL

You can use the STL containers in C++ to create a graph. For example, an adjacency list representation can be implemented using:

1. `vector<vector<int>>`: For simple adjacency lists.
2. `unordered_map<int, vector<int>>`: For graphs with arbitrary node labels.

Example of an unweighted, undirected graph:

```

#include <bits/stdc++.h>
using namespace std;

int main() {
    int n = 5; // Number of nodes
    vector<vector<int>> adjList(n + 1);

    // Adding edges (1-based indexing)
    adjList[1].push_back(2);
    adjList[2].push_back(1);

    adjList[1].push_back(3);
    adjList[3].push_back(1);

    adjList[4].push_back(5);
    adjList[5].push_back(4);

    // Print adjacency list
    for (int i = 1; i <= n; i++) {
        cout << "Node " << i << ": ";
        for (int neighbor : adjList[i]) {
            cout << neighbor << " ";
        }
        cout << endl;
    }

    return 0;
}

```

11. Minimum Distance Between Two Nodes in an Unweighted, Undirected Graph

To find the minimum distance:

1. Use **Breadth-First Search (BFS)**, as it explores the shortest path level by level.
2. Algorithm:
 - Start BFS from the source node.
 - Track visited nodes and distances using a queue.
 - Stop when you reach the destination node.

Can DFS Be Used?

DFS is not ideal for finding the minimum distance because it does not explore level by level. However, you can implement DFS with a visited array and track distances, but the complexity might increase due to backtracking.

12. Time Complexity of Dynamic Programming Problems

To determine the time complexity of a dynamic programming (DP) solution:

1. **Identify the State:** The number of states in the DP table determines the space complexity.
2. **Transition Relations:** Analyze the recurrence relation or transitions to calculate the work done per state.
3. **Total Complexity:** Multiply the number of states by the work per state.

For example:

- **Fibonacci with DP:** $T(n)=O(n)$ (states: n , work per state: $O(1)$).
 - **Knapsack:** $O(nW)$ (states: $n \times W$, work per state: $O(1)$).
-

13. Depth-First Search (DFS) Algorithm and Complexity

Algorithm for DFS:

```

#include <bits/stdc++.h>
using namespace std;

void dfs(int node, vector<bool> &visited, vector<vector<int>> &adjList)
{
    visited[node] = true;
    cout << node << " "; // Process the node

    for (int neighbor : adjList[node]) {
        if (!visited[neighbor]) {
            dfs(neighbor, visited, adjList);
        }
    }
}

int main() {
    int n = 5; // Number of nodes
    vector<vector<int>> adjList(n + 1);

    // Adding edges (1-based indexing)
    adjList[1].push_back(2);
    adjList[2].push_back(1);

    adjList[1].push_back(3);
    adjList[3].push_back(1);

    adjList[4].();
    adjList[5].();

    vector<bool> visited(n + 1, false);

    // Start DFS from node 1
    dfs(1, visited, adjList);

    return 0;
}

```

Complexity Analysis:

1. Time Complexity:

- Visiting each node: $O(V)$.
- Exploring all edges: $O(E)$.
- Total: $O(V+E)$.

2. Space Complexity:

Recursive stack space: $O(V)$ (in the worst case, for a linear graph).

1. Backtracking to Solve the N-Queens Problem

Concept:

The N-Queens problem places N queens on an $N \times N$ chessboard such that no two queens threaten each other (no two queens in the same row, column, or diagonal).

Backtracking Steps:

1. Start placing queens row by row.
2. For each row, try placing a queen in every column.
3. If placing a queen in a column violates the rules, backtrack and try another column.
4. If all rows are successfully filled, print the solution.
5. If no valid placement exists for a queen in the current row, return to the previous row and adjust the placement.

Code Example:


```

#include <bits/stdc++.h>
using namespace std;

bool isSafe(vector<vector<int>> &board, int row, int col, int n) {
    // Check column
    for (int i = 0; i < row; i++) {
        if (board[i][col]) return false;
    }
    // Check upper-left diagonal
    for (int i = row, j = col; i >= 0 && j >= 0; i--, j--) {
        if (board[i][j]) return false;
    }
    // Check upper-right diagonal
    for (int i = row, j = col; i >= 0 && j < n; i--, j++) {
        if (board[i][j]) return false;
    }
    return true;
}

bool solveNQueens(vector<vector<int>> &board, int row, int n) {
    if (row == n) {
        // Print solution
        for (auto &r : board) {
            for (int val : r) cout << (val ? "Q " : ". ");
            cout << endl;
        }
        cout << endl;
        return true;
    }
    bool res = false;
    for (int col = 0; col < n; col++) {
        if (isSafe(board, row, col, n)) {
            board[row][col] = 1;
            res |= solveNQueens(board, row + 1, n); // Continue to next
row
            board[row][col] = 0; // Backtrack
        }
    }
    return res;
}

int main() {
    int n = 4; // Number of queens
    vector<vector<int>> board(n, vector<int>(n, 0));
    if (!solveNQueens(board, 0, n)) {
        cout << "No solution exists\n";
    }
    return 0;
}

```

Time Complexity: $O(N!)$ due to factorial branching at each row.

2. Hamiltonian Cycle and Backtracking

Definition:

A Hamiltonian Cycle is a closed path in a graph that visits every vertex exactly once and returns to the starting vertex. A **Hamiltonian Path** is similar but does not return to the starting vertex.

Backtracking Steps:

1. Start with a path containing the first vertex.
2. Add vertices to the path one by one:
 - Check if the current vertex is adjacent to the last vertex in the path.
 - Ensure the vertex is not already in the path.
3. If all vertices are in the path and the last vertex is connected to the first, a Hamiltonian Cycle exists.
4. If no solution is found, backtrack to explore other possibilities.

Code Example:

```

#include <bits/stdc++.h>
using namespace std;

bool isSafe(int v, vector<vector<int>> &graph, vector<int> &path, int
pos) {
    if (!graph[path[pos - 1]][v]) return false; // Check adjacency
    for (int i = 0; i < pos; i++) {
        if (path[i] == v) return false; // Check if already visited
    }
    return true;
}

bool hamiltonianCycleUtil(vector<vector<int>> &graph, vector<int> &path,
int pos, int n) {
    if (pos == n) {
        return graph[path[pos - 1]][path[0]]; // Check if last vertex
connects to first
    }
    for (int v = 1; v < n; v++) {
        if (isSafe(v, graph, path, pos)) {
            path[pos] = v;
            if (hamiltonianCycleUtil(graph, path, pos + 1, n)) return
true;
            path[pos] = -1; // Backtrack
        }
    }
    return false;
}

bool hamiltonianCycle(vector<vector<int>> &graph, int n) {
    vector<int> path(n, -1);
    path[0] = 0; // Start at vertex 0
    if (hamiltonianCycleUtil(graph, path, 1, n)) {
        for (int v : path) cout << v << " ";
        cout << path[0] << endl; // Complete the cycle
        return true;
    }
    return false;
}

int main() {
    vector<vector<int>> graph = {
        {0, 1, 0, 1, 0},
        {1, 0, 1, 1, 1},
        {0, 1, 0, 0, 1},
        {1, 1, 0, 0, 1},
        {0, 1, 1, 1, 0}
    };
    if (!hamiltonianCycle(graph, graph.size())) {
        cout << "No Hamiltonian Cycle exists\n";
    }
}

```

```
    }  
    return 0;  
}
```

Time Complexity: $O(N!)$.

3. Subset Sum Problem

Given set: [3,34,4,12,5,8]

Target sum: 9

Steps:

1. Start with an empty subset.
2. Explore subsets recursively:
 - Include the current element and check if it forms the sum.
 - Exclude the current element and explore the next.
3. If a subset forms the sum, print the subset.

Example:

Subsets explored: [3,4,5],[4,5] form the sum 9.

4. Efficient Algorithms for Subset Sum

1. Dynamic Programming:

- Use a DP table $dp[i][j]$, where $dp[i][j]$ is true if a subset of the first i elements forms the sum j .
- Transition: $dp[i][j] = dp[i-1][j]$ (exclude) or $dp[i-1][j-arr[i]]$ (include).

2. Backtracking with Pruning:

- Use recursion to explore subsets.
 - Prune paths where the current sum exceeds the target.
-

5. Time Complexity of Subset Sum Algorithms

1. Dynamic Programming:

- **Time Complexity:** $O(n \times \text{sum})$.
- **Space Complexity:** $O(n \times \text{sum})$.

2. Backtracking:

- **Time Complexity:** $O(2^n)$ in the worst case.
- Efficient for small subsets with effective pruning.

1. Shortest Path from 0 to 4 Using Dijkstra's Algorithm

Given Graph:

Vertices: 0, 1, 2, 3, 4

Edges with weights:

(0 → 1: 2), (0 → 2: 4), (1 → 2: 1), (1 → 3: 7), (2 → 4: 3), (3 → 4: 1)

Steps:

1. Initialize:

- Distance array: `dist = [0, ∞, ∞, ∞, ∞]`
- Priority queue: `pq = [(0, 0)]` (starting with source 0 and distance 0).

2. Processing:

Extract node with the smallest distance:

1. Pop (0, 0) → Update neighbors:

- Update `dist[1] = 2` (0 + 2) → Push (2, 1)
- Update `dist[2] = 4` (0 + 4) → Push (4, 2)

2. Pop (2, 1) → Update neighbors:

- Update `dist[2] = 3` (2 + 1, shorter path found) → Push (3, 2)
- Update `dist[3] = 9` (2 + 7) → Push (9, 3)

3. Pop (3, 2) → Update neighbors:

Update `dist[4] = 6` (3 + 3) → Push (6, 4)

4. Pop (6, 4) → Stop, as the destination is reached.

3. Result:

- Shortest path: 0 → 1 → 2 → 4
- Total cost: 6

Priority Queue vs. Set

Priority Queue is better because:

- Efficient retrieval of the smallest element ($O(\log V)$).
- Dijkstra's algorithm relies on repeatedly finding the smallest distance.

2. Why Dijkstra's Algorithm Fails with Negative Weights

Dijkstra's algorithm assumes that once a vertex is processed, its shortest distance is finalized. This assumption breaks when negative weights exist because a shorter path might be found later.

Example:

Graph:

Vertices: 0, 1, 2
Edges: (0 → 1: 4), (1 → 2: -5), (0 → 2: 2)

Steps:

1. Initialize: $\text{dist} = [0, \infty, \infty]$.
2. Process 0: Update $\text{dist}[1] = 4$, $\text{dist}[2] = 2$.
3. Process 2: No changes.
4. Process 1: Update $\text{dist}[2] = -1$.

Dijkstra incorrectly concludes that the shortest path to 2 is 2, but it's actually -1.

Solution:

Use **Bellman-Ford Algorithm** for graphs with negative weights.

3. Building a Segment Tree for Array {1, 3, 5, 7, 9, 11, 13}

Steps:

1. Divide the Array:

- Start with the entire array.
- Divide into two halves recursively until each segment contains one element.

2. Combine Results:

For each node, store the combined value of its children (e.g., sum or min).

3. Tree Structure:

- Leaf nodes: Array elements.
- Internal nodes: Combined values of child nodes.

Code:

```
#include <bits/stdc++.h>
using namespace std;

void buildSegmentTree(vector<int> &arr, vector<int> &segTree, int start,
int end, int node) {
    if (start == end) { // Leaf node
        segTree[node] = arr[start];
        return;
    }
    int mid = (start + end) / 2;
    buildSegmentTree(arr, segTree, start, mid, 2 * node + 1);
    buildSegmentTree(arr, segTree, mid + 1, end, 2 * node + 2);
    segTree[node] = segTree[2 * node + 1] + segTree[2 * node + 2];
}

int main() {
    vector<int> arr = {1, 3, 5, 7, 9, 11, 13};
    int n = arr.size();
    vector<int> segTree(4 * n, 0); // Maximum size of segment tree
    buildSegmentTree(arr, segTree, 0, n - 1, 0);
    for (int val : segTree) cout << val << " ";
    return 0;
}
```

4. Articulation Edge

Definition:

An **articulation edge** (or bridge) is an edge in a graph whose removal increases the number of connected components.

Finding Articulation Edges:

1. Use **DFS** and track:
 - Discovery time (`disc[]`): Time when a vertex is visited.
 - Lowest point reachable (`low[]`): The smallest discovery time reachable from the subtree.
 2. An edge (u,v) is a bridge if:
 $low[v] > disc[u]$
-

5. Implicit Graph

Definition:

An **implicit graph** is not explicitly represented with edges but is defined by rules or properties. Nodes and edges are generated dynamically as needed.

Example:

A **knight's move** on a chessboard:

- Nodes: All valid positions on the chessboard.
- Edges: Possible knight moves.

Applications:

- Solving puzzles (e.g., Knight's Tour).
- Generating states dynamically in state-space search.

Algorithm Analysis and Matching

 chatgpt.com/c/677e8dc9-e8ac-8007-8e65-3de989a3cebf

1. Definition of an Algorithm:

An algorithm is a step-by-step procedure or a set of well-defined instructions for solving a problem or performing a task. It is finite, unambiguous, and designed to provide a specific output for a given input in a finite amount of time.

2. Time Complexity of Quick Sort:

Quick sort's time complexity depends on how the pivot is chosen and the input data:

- **Best Case:** $O(n \log n)$
Occurs when the pivot divides the array into two nearly equal parts.
 - **Worst Case:** $O(n^2)$
Happens when the pivot is the smallest or largest element in the array, resulting in unbalanced partitions.
 - **Average Case:** $O(n \log n)$
Represents the expected time complexity over all possible inputs, assuming random pivot selection or good pivoting.
-

3. Best Case, Worst Case, and Average Case Complexity:

- **Best Case Complexity:**
The minimum amount of time or space an algorithm takes to solve a problem. This happens under optimal conditions.
Example: In quick sort, the best case occurs when the pivot divides the array equally.
 - **Worst Case Complexity:**
The maximum amount of time or space an algorithm might take to complete for any input of size n .
Example: In quick sort, the worst case occurs when the pivot is the smallest or largest element repeatedly.
 - **Average Case Complexity:**
The expected time or space taken by the algorithm over all possible inputs of size n . It considers random or typical input distributions.
Example: For quick sort, this occurs with balanced but not perfectly equal partitions.
-

4. Space Complexity:

Space complexity refers to the total amount of memory or storage required by an algorithm to execute, including:

1. **Auxiliary Space:** Temporary memory used during execution.
2. **Input Space:** Memory required to store the input data.

For example, the space complexity of quick sort is $O(\log n)$ in the best case due to recursive calls on the stack.

5. Pattern Matching Example:

Given **Text:** AdBAACAADAABAABA

Pattern: AABA

We will use a **naive string matching algorithm** to find all occurrences of the pattern.

Steps:

1. Compare the pattern AABA with the first four characters of the text.

Text: AdBA

Pattern: AABA

No match, move the pattern one position to the right.

2. Compare with the next substring.

Text: dBA

Pattern: AABA

No match, move the pattern one position to the right.

3. Continue shifting until you reach a potential match:

Text: AABA

Pattern: AABA

Match found at position **9**.

4. Shift one position to the right and continue:

Text: ABA

Pattern: AABA

No match.

5. Continue the process.

Another match is found at position **12**.

Matches:

The pattern AABA appears **twice** in the text.

Let me know if you'd like to see the code for this process!

6. Algorithm to Count Subgrids with All Black Corners:

Problem Statement:

Given an $n \times n$ grid where each cell is either black (1) or white (0), calculate the number of subgrids whose corners are all black (1).

Algorithm:

1. **Input:** An $n \times n$ binary grid.
2. **Initialize:** A counter $\text{count} = 0$.
3. **Iterate through pairs of rows ($r1, r2$):**
 - For each column, check if the cells in both rows ($r1, c$) and ($r2, c$) are black.
 - Count the number of such columns where both cells are black, say k .
 - Add $(2k) = 2k(k-1)$ to count, as each pair of these columns forms a subgrid.
4. **Output:** count.

Time Complexity: $O(n^3)$ (can be optimized to $O(n^2)$ using hashing).

7. Greedy Algorithm:

Definition:

A greedy algorithm makes the locally optimal choice at each step with the hope of finding the global optimum. It does not backtrack or reconsider choices.

Problems Solved by Greedy Algorithm:

- Problems with the **greedy-choice property** (local optimal solution leads to a global solution).
- Problems that satisfy **optimal substructure** (optimal solutions to subproblems lead to the optimal solution for the problem).

Examples:

- Activity Selection Problem.
 - Minimum Spanning Tree (Kruskal's or Prim's Algorithm).
 - Huffman Encoding.
 - Fractional Knapsack Problem.
-

8. Why Huffman Coding Algorithm is Used?

Huffman coding is used for **data compression** by assigning shorter binary codes to more frequent characters and longer codes to less frequent ones. This results in an optimal prefix-free encoding, minimizing the total number of bits required to represent the data.

9. Huffman Tree Construction:

Given Data:

Character	Frequency
a	16
b	12
c	13
d	45
e	9
f	5

Steps to Construct the Huffman Tree:

1. Sort Frequencies:

Initially, arrange the characters by frequency in ascending order:
f(5),e(9),b(12),c(13),a(16),d(45).

2. Merge Two Smallest:

Merge f(5) and e(9):
New Node = (5+9=14).
Updated List: b(12),c(13),14,a(16),d(45).

3. Repeat Merging:

- Merge b(12) and c(13):
New Node = (12+13=25).
Updated List: 14,16,25,d(45).
- Merge 14 and 16:
New Node = (14+16=30).
Updated List: 25,30,d(45).
- Merge 25 and 30:
New Node = (25+30=55).
Updated List: 45,55.
- Merge 45 and 55:
Root Node = (45+55=100).

4. Final Tree:

The root node has a total frequency of 100. Assign binary codes to characters by traversing the tree (e.g., left = 0, right = 1).

10. Bubble Sort Steps:

Given Array: [64,34,25,12,22,11,90]

Steps:

1. **Pass 1:** Compare adjacent elements and swap if needed:

64↔34→[34,64,25,12,22,11,90] 64↔25→[34,25,64,12,22,11,90] 64↔12→[34,25,12,64,22,11,90] 64↔22→[34,25,12,22,64,11,90] 64↔11→[34,25,12,22,11,64,90]
Result: [34,25,12,22,11,64,90]

2. **Pass 2:** Repeat for the remaining unsorted part: Result: [25,12,22,11,34,64,90]

3. **Pass 3:**

Result: [12,11,22,25,34,64,90]

4. **Pass 4:**

Result: [11,12,22,25,34,64,90]

Let me know if you need help with implementing these!

11. Insertion Sort Algorithm:

Algorithm:

1. Start with the second element (index 1) of the array.
2. Compare it with the elements to its left and shift larger elements one position to the right.
3. Insert the current element into its correct position.
4. Repeat for all elements.

Pseudocode:

cpp

```
void insertionSort(int arr[], int n) {
    for (int i = 1; i < n; i++) {
        int key = arr[i];
        int j = i - 1;
        // Shift elements greater than key to the right
        while (j >= 0 && arr[j] > key) {
            arr[j + 1] = arr[j];
            j--;
        }
        arr[j + 1] = key;
    }
}
```

12. How to Optimize an Algorithm?

Steps to Optimize:

1. **Analyze Complexity:** Identify time and space complexity.
2. **Eliminate Redundancy:** Remove unnecessary computations (e.g., avoid recomputing the same values).
3. **Choose the Right Data Structure:** Select a data structure that suits the problem.
4. **Use Efficient Techniques:** Apply techniques like memoization, dynamic programming, divide-and-conquer, or greedy methods.

Example: Fibonacci Numbers

- **Naive Recursion:** $O(2^n)$
 - **Optimized with Memoization:** $O(n)$ using a table to store already computed values.
-

13. What is Backtracking?

Backtracking is a problem-solving technique that explores all possible configurations and abandons a path as soon as it determines that the path cannot lead to a solution.

Example: 4-Queens Problem

Place 4 queens on a 4x4 chessboard such that no two queens attack each other.

Algorithm:

1. Start in the first column and place a queen in the first safe position.
 2. Move to the next column and try placing a queen.
 3. If no safe position exists, backtrack to the previous column and move the queen to the next possible position.
 4. Continue until all queens are placed or no solution is found.
-

14. Breadth-First Search (BFS) Algorithm:

Algorithm:

1. Start from a source node and mark it as visited.
2. Add it to a queue.
3. While the queue is not empty:
 - Dequeue a node.
 - Explore its unvisited neighbors, mark them visited, and enqueue them.
4. Repeat until all nodes are visited.

Pseudocode:

```
void BFS(int start, vector<int> adj[], int n) {
    vector<bool> visited(n, false);
    queue<int> q;
    q.push(start);
    visited[start] = true;
    while (!q.empty()) {
        int node = q.front();
        q.pop();
        cout << node << " ";
        for (int neighbor : adj[node]) {
            if (!visited[neighbor]) {
                visited[neighbor] = true;
                q.push(neighbor);
            }
        }
    }
}
```

15. Why Left Rotate and Right Rotate Operations in Treap Tree?

Treap is a binary search tree (BST) combined with a heap, maintaining both:

- **BST Property:** In-order traversal gives sorted order.
- **Heap Property:** Each node's priority is greater than its children.

Need for Rotations:

Rotations are used to maintain the heap property when inserting or deleting nodes.

Example:

Insert a node with higher priority than its parent:

- Perform a **right rotation** if it's a left child.
- Perform a **left rotation** if it's a right child.

16. Why Find the Parent Node in a Binary Indexed Tree?

A Binary Indexed Tree (BIT) is used for range queries and point updates efficiently.

Need to Find Parent Node:

Parent node helps in:

1. Accumulating values during a prefix sum query.
2. Updating the affected range after a point update.

How it Works:

Use bit manipulation to navigate to the parent node:

- **Query:** Traverse parent nodes upward.
- **Update:** Traverse parent nodes upward to propagate changes.

Let me know if you need code examples for any of these!

17. How to Find the Parent Node in a Binary Indexed Tree (BIT)?

In a Binary Indexed Tree, each node represents a range, and parent-child relationships are determined using bit manipulation.

Finding the Parent Node:

1. For an index i , subtract the last set bit of i to find its parent:
$$\text{parent}(i) = i - (i \& -i)$$

Example:

Given $i=12$ (binary: **1100**):

- Last set bit: $i \& -i = 4$ (binary: **0100**).
- Parent: $i - (i \& -i) = 12 - 4 = 8$ (binary: **1000**).

18. How to Represent a Graph?

Graphs can be represented in multiple ways:

1. Adjacency Matrix:

- A 2D array where $\text{matrix}[i][j]$ is 1 if there's an edge from i to j , otherwise 0.
- **Space Complexity:** $O(V^2)$.

2. Adjacency List:

- An array or map where each index corresponds to a vertex and stores a list of its neighbors.
- **Space Complexity:** $O(V+E)$.

3. Edge List:

- A list of all edges, each represented as a pair (u, v) .
- **Space Complexity:** $O(E)$.

4. Incidence Matrix:

A matrix with rows representing vertices and columns representing edges, where $\text{matrix}[i][j]$ indicates if vertex i is part of edge j .

19. How to Check if a Graph is Connected?

To check if a graph is connected, ensure all vertices are reachable from any starting vertex.

Algorithms:

1. DFS or BFS Traversal:

- Start from any vertex and traverse the graph.
- If all vertices are visited, the graph is connected.

2. Union-Find Algorithm (for edge list):

- Use union-find to group connected components.
- If all vertices belong to the same component, the graph is connected.

20. How to Check if a Graph is Bipartite?

A graph is bipartite if it can be colored using two colors such that no two adjacent vertices have the same color.

Algorithm:

1. Use BFS or DFS starting from any vertex.
2. Assign colors (e.g., 0 and 1) alternately to adjacent vertices.
3. If at any point two adjacent vertices have the same color, the graph is not bipartite.

Pseudocode (BFS):

```
bool isBipartite(vector<int> adj[], int n) {
    vector<int> color(n, -1);
    queue<int> q;
    for (int i = 0; i < n; i++) {
        if (color[i] == -1) {
            q.push(i);
            color[i] = 0;
            while (!q.empty()) {
                int node = q.front();
                q.pop();
                for (int neighbor : adj[node]) {
                    if (color[neighbor] == -1) {
                        color[neighbor] = 1 - color[node];
                        q.push(neighbor);
                    } else if (color[neighbor] == color[node]) {
                        return false;
                    }
                }
            }
        }
    }
    return true;
}
```

21. What is Convex Hull?

A convex hull is the smallest convex polygon that encloses all given points in a plane.

Graham's Scan Algorithm:

1. **Find the Starting Point:** Choose the point with the lowest y-coordinate (or the leftmost in case of a tie).
2. **Sort Points by Polar Angle:** Sort the points based on the angle they make with the starting point.

3. Build the Hull:

- Use a stack to maintain the vertices of the hull.
- For each point, check if it makes a left turn (keep the point) or a right turn (pop the stack and discard the point).

Example:

Given points: (0,0),(1,1),(2,2),(3,0),(2,-1)

- Start with (0,0).
 - Sort by angle: (0,0),(3,0),(2,-1),(1,1),(2,2).
 - Build hull using left-turn checks.
-

22. How to Detect if Two Line Segments Intersect?

Approach:

Two line segments intersect if:

1. Their endpoints are not collinear, and
2. The endpoints of each segment lie on opposite sides of the other segment.

Steps:

1. Represent line segments as $(x_1, y_1)-(x_2, y_2)$ and $(x_3, y_3)-(x_4, y_4)$.
2. Compute orientation of three points:
Orientation $O(P, Q, R)$:
$$\text{val} = (Q_y - P_y) \times (R_x - Q_x) - (Q_x - P_x) \times (R_y - Q_y)$$
 - $O=0$: Collinear
 - $O>0$: Clockwise
 - $O<0$: Counterclockwise
3. Check:
 - $O_1 = O(A, B, C)$, $O_2 = O(A, B, D)$,
 - $O_3 = O(C, D, A)$, $O_4 = O(C, D, B)$.
 - Segments intersect if $O_1 \neq O_2$ and $O_3 \neq O_4$.

Example:

Segments $(1,1)-(10,1)$ and $(1,2)-(10,0)$:

Compute orientations and confirm if $O_1 \neq O_2$ and $O_3 \neq O_4$.

ChatGPT

 chatgpt.com/c/677e205d-63b0-8000-b520-84a7bf082fb3

Section A: Algorithm Design and Analysis

1. Steps Required for Algorithm Design

Algorithm design involves systematically breaking down problems into solvable components. Key steps are:

1. Problem Understanding

- Clearly define the input, output, constraints, and requirements of the problem.
- Example: For sorting numbers, input = unsorted list, output = sorted list.

2. Develop a Mathematical Model

- Represent the problem mathematically or logically.
- Example: Use array indices or graphs for problem representation.

3. Design the Algorithm

Create a step-by-step approach to solve the problem. Choose methods such as brute force, greedy, divide and conquer, or dynamic programming, depending on the problem's nature.

4. Analyze the Algorithm

- Evaluate time complexity (efficiency in terms of input size n).
- Evaluate space complexity (memory requirements).

5. Optimization

- Improve the algorithm for better performance if possible.
- Example: Replace nested loops with single-pass techniques.

6. Implementation

Translate the algorithm into code using a programming language like C++.

7. Testing and Debugging

Verify correctness with test cases, including edge cases.

2. Smallest Value of n for Algorithm Comparison

Two algorithms are given:

- Algorithm 1: $100n^2$
- Algorithm 2: $2n$

We find n where $100n^2 < 2^n$:

- At $n=10$, $100n^2=100(10)^2=10,000$ and $2^{10}=1024$. Here, $100n^2 > 2^n$.
- At $n=15$, $100n^2=100(15)^2=22,500$ and $2^{15}=32,768$. Here, $100n^2 < 2^n$.

Thus, the smallest $n=15$.

3. Determining the Size of White Connected Components in an $n \times m$ Image

Problem Description:

- A white pixel is connected to adjacent white pixels (horizontal, vertical, diagonal).
- A **connected component** is a group of connected white pixels.

Solution Approach:

1. Represent the image as a 2D grid where 0 = black and 1 = white.

Example:

```
1 1 0 0
1 0 0 1
0 0 1 1
```

2. Flood Fill Algorithm (similar to DFS or BFS):

- Start at any white pixel (value = 1).
- Explore all connected white pixels recursively or iteratively.
- Count pixels in the connected component and mark them as visited (e.g., set them to 0 to avoid revisiting).

Code Example in C++:

cpp

```
#include <iostream>
#include <vector>
using namespace std;

void dfs(int x, int y, vector<vector<int>>& grid, int& size) {
    if (x < 0 || y < 0 || x >= grid.size() || y >= grid[0].size() ||
    grid[x][y] == 0)
        return;
    grid[x][y] = 0; // Mark visited
    size++; // Increase component size
    dfs(x + 1, y, grid, size);
    dfs(x - 1, y, grid, size);
    dfs(x, y + 1, grid, size);
    dfs(x, y - 1, grid, size);
    dfs(x + 1, y + 1, grid, size);
    dfs(x - 1, y - 1, grid, size);
}

int main() {
    vector<vector<int>> grid = {
        {1, 1, 0, 0},
        {1, 0, 0, 1},
        {0, 0, 1, 1}
    };
    for (int i = 0; i < grid.size(); i++) {
        for (int j = 0; j < grid[0].size(); j++) {
            if (grid[i][j] == 1) {
                int size = 0;
                dfs(i, j, grid, size);
                cout << "Connected Component Size: " << size << endl;
            }
        }
    }
    return 0;
}
```

4. Example of Cumulative Sum

Cumulative sum is the running total of elements in a sequence.

Example:

Given an array $A=[1,2,3,4]$, its cumulative sum array is $S=[1,3,6,10]$, where:

- $S[0]=A[0]=1$
- $S[1]=S[0]+A[1]=1+2=3$
- $S[2]=S[1]+A[2]=3+3=6$, and so on.

Code Example in C++:

cpp

```
#include <iostream>
#include <vector>
using namespace std;

vector<int> cumulativeSum(vector<int>& nums) {
    vector<int> result(nums.size(), 0);
    result[0] = nums[0];
    for (int i = 1; i < nums.size(); i++) {
        result[i] = result[i - 1] + nums[i];
    }
    return result;
}

int main() {
    vector<int> nums = {1, 2, 3, 4};
    vector<int> result = cumulativeSum(nums);
    for (int sum : result)
        cout << sum << " ";
    return 0;
}
```

Output: 1 3 6 10

5. Faster Method for Finding Cumulative Sum and Explanation

Two Methods:

1. Naive Method: Recompute the sum for every index.

Example:

arduino

```
for i in range(0, n):
    sum = 0
    for j in range(0, i + 1):
        sum += A[j]
```

Time complexity: $O(n^2)$ because of nested loops.

2. Efficient Method (Prefix Sum):

Precompute cumulative sums in one pass.

Example:

CSS

$$S[i] = S[i-1] + A[i]$$

Time complexity: $O(n)$.

Why Efficient Method is Faster:

Reduces redundant calculations by reusing previously computed sums.

Example to Compare: Array $A=[1,2,3,4]$:

- **Naive Method:** For $i=3$, compute $1+2+3+4$ redundantly.
- **Efficient Method:** Directly use $S[2]+A[3]$.

Exam Notes

1. **Algorithm Design Steps:** Understand problem → Mathematical model → Design → Analyze → Optimize → Implement → Test.

2. **Comparison of Algorithms:** Analyze time complexities. For $100n^2$ vs $2n$, smallest $n=15$.
3. **Connected Components in Images:** Use Flood Fill (DFS/BFS) to find and count components.
4. **Cumulative Sum:** Example $A=[1,2,3,4]$, cumulative sum = $[1,3,6,10]$.
5. **Efficient Method for Cumulative Sum:** Use prefix sums for $O(n)$ efficiency.

1. Determine Row and Column of a Number in a Table

Problem Description:

You are given a table (e.g., 4×4 grid for $n=16$), and you must find the row and column number of a given number n , where $n \leq 105$. The table is filled row by row, starting from 1.

Example Table (4×4 grid for $n=16$):

1	2	3	4
5	6	7	8
9	10	11	12
13	14	15	16

For $n=10$, the result is **row = 3, column = 2**.

Solution Approach:

1. Determine Table Dimensions:

Assume the table has $r \times c$ dimensions, where c (number of columns) is fixed or given.

2. Calculate Row and Column:

- Row $r = \lceil n/c \rceil$.
- Column $col = n \% c$, or $col = c$ if $n \% c = 0$.

Code Example in C++:

cpp

```
#include <iostream>
#include <cmath>
using namespace std;

void findRowColumn(int n, int c) {
    int row = (n - 1) / c + 1; // Row number
    int col = (n - 1) % c + 1; // Column number
    cout << "Row: " << row << ", Column: " << col << endl;
}

int main() {
    int n = 10; // Given number
    int c = 4; // Number of columns
    findRowColumn(n, c);
    return 0;
}
```

2. Time Complexity of Merge Sort Algorithm

Merge Sort Recap:

Merge Sort is a divide-and-conquer algorithm that:

1. Divides the array into two halves recursively.
2. Merges the two sorted halves back together.

Steps to Analyze Time Complexity:

1. Divide Step:

- Each division halves the array size.
- Time complexity: $O(1)$.

2. Merge Step:

- Merging two sorted halves requires $O(n)$ operations.
- Total merges for all levels: $O(n)$.

3. Recursive Depth:

The depth of recursion is $\log_2(n)$ since the array is divided in half at each step.

Overall Time Complexity:

- At each level of recursion, the merge step takes $O(n)$. There are $\log_2(n)$ levels.
 - Total time complexity:
 $T(n) = O(n \cdot \log_2(n))$
-

3. Is $O(N+n)$ Time Complexity Possible for Sorting?

Yes, it is possible to achieve $O(N+n)$ time complexity under certain conditions, using **Counting Sort** or **Bucket Sort**. These algorithms work efficiently for specific types of inputs.

Procedure for Counting Sort: Counting Sort is applicable when the input numbers are integers within a limited range.

1. Count Occurrences:

- Create a frequency array `count[]` where `count[x]` stores the frequency of number `x` in the input.
- Requires $O(N)$ to iterate over the input array.

2. Accumulate Counts:

- Modify `count[]` to store cumulative counts, which helps determine the sorted position of each element.
- Requires $O(n)$, where `n` is the range of input values.

3. Reconstruct Sorted Array:

Place elements in their sorted positions using the cumulative counts.

Code Example in C++:

cpp

```
#include <iostream>
#include <vector>
using namespace std;

void countingSort(vector<int>& arr, int maxVal) {
    vector<int> count(maxVal + 1, 0); // Frequency array

    // Count occurrences
    for (int num : arr)
        count[num]++;

    // Reconstruct sorted array
    int index = 0;
    for (int i = 0; i <= maxVal; i++) {
        while (count[i]--) {
            arr[index++] = i;
        }
    }
}

int main() {
    vector<int> arr = {4, 2, 2, 8, 3, 3, 1};
    int maxVal = 8; // Maximum value in the array
    countingSort(arr, maxVal);

    for (int num : arr)
        cout << num << " ";
    return 0;
}
```

Output:

1 2 2 3 3 4 8

Time Complexity:

1. Counting occurrences: $O(N)$.
2. Accumulating counts: $O(n)$, where n is the range of values.
3. Reconstructing array: $O(N)$.

Total: $O(N+n)$.

Comparison Between Counting Sort and Comparison-Based Sorts:

1. Counting Sort works in $O(N+n)$, but only for limited-range integer values.
2. Merge Sort or Quick Sort works for general cases with $O(n\log n)$ complexity.

Exam Notes

1. Row and Column in Table:

- Row = $(n-1)/c+1$.
- Column = $(n-1)\%c+1$.

2. Merge Sort Time Complexity:

- Total: $O(n\log n)$.
- Merge = $O(n)$, Divide = $O(1)$, Depth = $\log_2(n)$.

3. Sorting in $O(N+n)$:

- Use Counting Sort or Bucket Sort.
- Works for limited-range integers, where n is the range.

Let me know if you need more examples or additional explanations!

* Find out the time complexity of the following two functions. `void f(int n) { if(n == 1) return; f(n-1); }` `void g(int n) { if(n == 1) return; g(n-1); g(n-1); }`
* How can you create a graph using STL? * An un-weighted and undirected graph and two nodes in a graph are given.

Question Set: Time Complexity, Graphs, and STL

1. Find Out the Time Complexity of the Two Functions

Function 1: `f(int n)`

cpp

```
void f(int n) {  
    if (n == 1) return;  
    f(n - 1);  
}
```

Analysis:

- The function `f(n)` makes **one recursive call** to `f(n - 1)` at each step.

- This results in a linear recursion, where the function is called $n-1$ times before terminating at $n==1$.

Time Complexity: $O(n)$.

Function 2: `g(int n)`

cpp

```
void g(int n) {  
    if (n == 1) return;  
    g(n - 1);  
    g(n - 1);  
}
```

Analysis:

- The function `g(n)` makes **two recursive calls** to `g(n - 1)` at each step.
- This creates a binary recursion tree:
 - At level 0: 1 call (root).
 - At level 1: 2 calls.
 - At level 2: 4 calls.
 - At level k: 2^k calls.
- The depth of the recursion tree is $n-1$, so the total number of calls is:

$$T(n) = 2^0 + 2^1 + 2^2 + \dots + 2^{n-2} + 2^{n-1} = 2^n - 1$$

Time Complexity: $O(2^n)$.

2. How to Create a Graph Using STL

Graphs can be efficiently represented using **STL containers** such as `vector`, `list`, or `map`. Common representations are **Adjacency List** and **Adjacency Matrix**.

Adjacency List Representation:

An adjacency list is space-efficient and works well for sparse graphs. Use a `vector` of `vector` or a `map` of `list`.

Code Example (Unweighted Graph):

cpp

```
#include <iostream>
#include <vector>
using namespace std;

// Add an edge to the graph
void addEdge(vector<vector<int>>& graph, int u, int v) {
    graph[u].push_back(v);
    graph[v].push_back(u); // For undirected graph
}

// Display the graph
void printGraph(const vector<vector<int>>& graph) {
    for (int i = 0; i < graph.size(); i++) {
        cout << i << ": ";
        for (int neighbor : graph[i]) {
            cout << neighbor << " ";
        }
        cout << endl;
    }
}

int main() {
    int vertices = 5;
    vector<vector<int>> graph(vertices);

    addEdge(graph, 0, 1);
    addEdge(graph, 0, 4);
    addEdge(graph, 1, 2);
    addEdge(graph, 1, 3);
    addEdge(graph, 1, 4);
    addEdge(graph, 2, 3);
    addEdge(graph, 3, 4);

    printGraph(graph);
    return 0;
}
```

Output:

```
makefile
```

```
0: 1 4  
1: 0 2 3 4  
2: 1 3  
3: 1 2 4  
4: 0 1 3
```

Adjacency Matrix Representation:

An adjacency matrix uses a 2D array to store edges. It's suitable for dense graphs.

Code Example (Weighted Graph):

cpp

```
#include <iostream>
#include <vector>
using namespace std;

void addEdge(vector<vector<int>>& matrix, int u, int v, int weight) {
    matrix[u][v] = weight;
    matrix[v][u] = weight; // For undirected graph
}

void printGraph(const vector<vector<int>>& matrix) {
    for (int i = 0; i < matrix.size(); i++) {
        for (int j = 0; j < matrix[i].size(); j++) {
            cout << matrix[i][j] << " ";
        }
        cout << endl;
    }
}

int main() {
    int vertices = 5;
    vector<vector<int>> matrix(vertices, vector<int>(vertices, 0));

    addEdge(matrix, 0, 1, 1);
    addEdge(matrix, 0, 4, 1);
    addEdge(matrix, 1, 2, 1);
    addEdge(matrix, 1, 3, 1);
    addEdge(matrix, 1, 4, 1);
    addEdge(matrix, 2, 3, 1);
    addEdge(matrix, 3, 4, 1);

    printGraph(matrix);
    return 0;
}
```

3. Unweighted, Undirected Graph and Two Nodes

Problem:

Given an unweighted, undirected graph and two nodes, determine a property between the nodes (e.g., if they are connected).

Solution Approach: Use **Breadth-First Search (BFS)** or **Depth-First Search (DFS)**.

BFS for Path Existence: BFS explores all nodes level by level, starting from one node, and checks if the second node is reachable.

Code Example:

cpp

```
#include <iostream>
#include <vector>
#include <queue>
using namespace std;

bool isConnected(vector<vector<int>>& graph, int start, int end) {
    vector<bool> visited(graph.size(), false);
    queue<int> q;
    q.push(start);
    visited[start] = true;

    while (!q.empty()) {
        int node = q.front();
        q.pop();

        if (node == end)
            return true;

        for (int neighbor : graph[node]) {
            if (!visited[neighbor]) {
                visited[neighbor] = true;
                q.push(neighbor);
            }
        }
    }
    return false;
}

int main() {
    int vertices = 5;
    vector<vector<int>> graph(vertices);

    // Build the graph
    graph[0] = {1, 4};
    graph[1] = {0, 2, 3, 4};
    graph[2] = {1, 3};
    graph[3] = {1, 2, 4};
    graph[4] = {0, 1, 3};

    // Check if two nodes are connected
    int start = 0, end = 3;
    if (isConnected(graph, start, end))
        cout << "Nodes " << start << " and " << end << " are connected."
    << endl;
    else
        cout << "Nodes " << start << " and " << end << " are NOT
connected." << endl;
```

```
    return 0;  
}
```

Output (for the given graph):

Nodes 0 and 3 are connected.

Exam Notes

1. Time Complexity:

- $f(n)$ has $O(n)$ complexity (linear recursion).
- $g(n)$ has $O(2^n)$ complexity (exponential recursion).

2. Graph Representation:

- Use adjacency lists for sparse graphs.
- Use adjacency matrices for dense graphs.

3. Path Checking in Graphs:

- Use BFS or DFS for unweighted, undirected graphs.
- BFS is suitable for finding shortest paths or determining connectivity.

Question Set: Minimum Distance and Dynamic Programming

1. Finding the Minimum Distance Between Nodes

To find the **minimum distance** (shortest path) between two nodes in an unweighted graph, the most efficient approach is to use **Breadth-First Search (BFS)**.

Why BFS for Minimum Distance?

BFS explores all nodes **level by level** from the starting node. It guarantees the shortest path in an unweighted graph because the first time a node is reached, it is via the shortest path.

Steps for BFS:

1. Use a **queue** to store the nodes to be processed.
2. Maintain a **distance array** where $distance[node]$ keeps track of the minimum distance of $node$ from the source.
3. Start BFS from the source node, set its distance to 0, and update the distances of its neighbors.

4. When the target node is reached, return its distance.

Code Example for BFS (Minimum Distance):

cpp

```
#include <iostream>
#include <vector>
#include <queue>
using namespace std;

int findMinDistance(vector<vector<int>>& graph, int start, int end) {
    int n = graph.size();
    vector<int> distance(n, -1); // Distance array, initialized to -1
    queue<int> q;

    distance[start] = 0; // Starting node has distance 0
    q.push(start);

    while (!q.empty()) {
        int node = q.front();
        q.pop();

        for (int neighbor : graph[node]) {
            if (distance[neighbor] == -1) { // If not visited
                distance[neighbor] = distance[node] + 1; // Update
                q.push(neighbor);
            }
            if (neighbor == end) { // If target is reached
                return distance[neighbor];
            }
        }
    }

    return -1; // If no path exists
}

int main() {
    int vertices = 6;
    vector<vector<int>> graph(vertices);

    // Build the graph (unweighted, undirected)
    graph[0] = {1, 2};
    graph[1] = {0, 3, 4};
    graph[2] = {0, 4};
    graph[3] = {1, 5};
    graph[4] = {1, 2, 5};
    graph[5] = {3, 4};

    int start = 0, end = 5;
    int distance = findMinDistance(graph, start, end);

    if (distance != -1)
```

```
        cout << "The minimum distance between " << start << " and " <<
end << " is " << distance << endl;
    else
        cout << "No path exists between " << start << " and " << end <<
endl;

    return 0;
}
```

Output:

The minimum distance between 0 and 5 is 3

Can DFS Be Used to Find Minimum Distance?

Theoretical Answer:

- DFS is **not well-suited** for finding the minimum distance in an unweighted graph.
 - DFS explores paths in depth, so it doesn't guarantee the shortest path. You would have to explore all possible paths and explicitly keep track of the minimum distance.
-

Alternative Approach with DFS: If you still want to use DFS:

1. Use a global variable to store the minimum distance.
2. Traverse all possible paths recursively, updating the distance when a shorter path is found.

Code Example for DFS (Minimum Distance):

cpp

```
#include <iostream>
#include <vector>
#include <climits>
using namespace std;

void dfs(vector<vector<int>>& graph, int current, int end, vector<bool>&
visited, int distance, int& minDistance) {
    if (current == end) {
        minDistance = min(minDistance, distance);
        return;
    }

    visited[current] = true;
    for (int neighbor : graph[current]) {
        if (!visited[neighbor]) {
            dfs(graph, neighbor, end, visited, distance + 1,
minDistance);
        }
    }
    visited[current] = false; // Backtrack
}

int findMinDistanceDFS(vector<vector<int>>& graph, int start, int end) {
    int minDistance = INT_MAX;
    vector<bool> visited(graph.size(), false);

    dfs(graph, start, end, visited, 0, minDistance);

    return (minDistance == INT_MAX) ? -1 : minDistance;
}

int main() {
    int vertices = 6;
    vector<vector<int>> graph(vertices);

    // Build the graph
    graph[0] = {1, 2};
    graph[1] = {0, 3, 4};
    graph[2] = {0, 4};
    graph[3] = {1, 5};
    graph[4] = {1, 2, 5};
    graph[5] = {3, 4};

    int start = 0, end = 5;
    int distance = findMinDistanceDFS(graph, start, end);

    if (distance != -1)
        cout << "The minimum distance between " << start << " and " <<
```



```

end << " is " << distance << endl;
else
    cout << "No path exists between " << start << " and " << end <<
endl;

    return 0;
}

```

Output:

The minimum distance between 0 and 5 is 3

Comparison Between BFS and DFS for Minimum Distance:

Aspect	BFS	DFS
Suitability	Best for minimum distance	Less suitable (needs extra logic)
Time Complexity	$O(V+E)$	$O(V+E)$
Guarantees Shortest Path	Yes	No (requires checking all paths)

2. Finding the Time Complexity of a Dynamic Programming Problem

To determine the **time complexity** of a dynamic programming (DP) problem:

1. Identify State Variables:

Determine the parameters that define the DP state (e.g., $dp[i][j]$).

2. Number of States:

- Calculate the total number of unique states that the DP table will store.
- Example: If the DP is $dp[i][j]$ for $1 \leq i \leq n$ and $1 \leq j \leq m$, the total states are $n \times m$.

3. Time Per State:

- Determine the time required to compute the value of each state based on its dependencies.
- Example: If each state requires $O(k)$ operations, where k is the number of dependencies, then the time per state is $O(k)$.

4. Total Time Complexity:

Multiply the number of states by the time per state:

Time Complexity = Number of States \times Time Per State

Example 1: Fibonacci with DP:

cpp

```
int fibonacci(int n) {
    vector<int> dp(n + 1, 0);
    dp[1] = 1;
    for (int i = 2; i <= n; i++) {
        dp[i] = dp[i - 1] + dp[i - 2];
    }
    return dp[n];
}
```

- **States:** `dp[i]` for $i=1$ to n , so n states.
 - **Time Per State:** $O(1)$ (each state depends on 2 previous states).
 - **Total Complexity:** $O(n)$.
-

Example 2: 0/1 Knapsack:

cpp

```
int knapsack(vector<int>& weights, vector<int>& values, int W) {
    int n = weights.size();
    vector<vector<int>> dp(n + 1, vector<int>(W + 1, 0));

    for (int i = 1; i <= n; i++) {
        for (int w = 1; w <= W; w++) {
            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[n][W];
}
```

- **States:** $dp[i][w]$ for $i=1$ to n and $w=0$ to W , so $n \times W$ states.
 - **Time Per State:** $O(1)$ (depends on 2 states).
 - **Total Complexity:** $O(n \times W)$.
-

Exam Notes

1. Minimum Distance:

- Use BFS for minimum distance in unweighted graphs: $O(V+E)$.
- DFS can be used but is less efficient.

2. Time Complexity of DP:

- Identify states and their dependencies.
- Compute Total States \times Time Per State.

Section B: DFS, Backtracking, and Hamiltonian Cycle

1. Write the Algorithm for DFS and Analyze Its Complexity

Algorithm:

Depth-First Search (DFS) is used to traverse or search graphs. It explores as far as possible along each branch before backtracking.

Steps:

1. Start from the source node.
 2. Mark the current node as visited.
 3. Recursively visit all unvisited neighbors of the current node.
 4. Backtrack when all neighbors are explored.
-

Code Example (Recursive DFS):

cpp

```
#include <iostream>
#include <vector>
using namespace std;

void dfs(vector<vector<int>>& graph, int node, vector<bool>& visited) {
    visited[node] = true;
    cout << node << " "; // Process the node (e.g., print it)

    for (int neighbor : graph[node]) {
        if (!visited[neighbor]) {
            dfs(graph, neighbor, visited);
        }
    }
}

int main() {
    int vertices = 5;
    vector<vector<int>> graph(vertices);

    // Build the graph (adjacency list representation)
    graph[0] = {1, 2};
    graph[1] = {0, 3};
    graph[2] = {0, 4};
    graph[3] = {1};
    graph[4] = {2};

    vector<bool> visited(vertices, false);

    cout << "DFS Traversal: ";
    dfs(graph, 0, visited);

    return 0;
}
```

Output:

DFS Traversal: 0 1 3 2 4

Complexity Analysis:

- **Time Complexity:** $O(V+E)$
 - V: Number of vertices (each vertex is visited once).
 - E: Number of edges (each edge is explored once).

- **Space Complexity:** $O(V)$
 - $O(V)$ for the visited array.
 - $O(V)$ for the recursion stack in the worst case.
-

2. How Backtracking Can Be Used to Solve the N-Queens Problem

Problem: Place N queens on an $N \times N$ chessboard such that no two queens threaten each other (no two queens are in the same row, column, or diagonal).

Approach Using Backtracking:

1. Place queens row by row.
 2. For each row, try placing a queen in each column.
 3. If placing a queen in a column doesn't lead to a solution (i.e., it threatens another queen), backtrack and try the next column.
 4. If all queens are placed, print the solution.
-

Algorithm:

- Use an array to keep track of the column positions of queens.
 - Check for conflicts with previously placed queens before placing a new queen.
-

Code Example:

cpp

```
#include <iostream>
#include <vector>
using namespace std;

bool isSafe(vector<int>& board, int row, int col) {
    for (int i = 0; i < row; i++) {
        // Check column and diagonals
        if (board[i] == col || abs(board[i] - col) == abs(i - row)) {
            return false;
        }
    }
    return true;
}

void solveNQueens(vector<int>& board, int row, int n) {
    if (row == n) {
        for (int i = 0; i < n; i++) {
            for (int j = 0; j < n; j++) {
                cout << (board[i] == j ? "Q " : ". ");
            }
            cout << endl;
        }
        cout << endl;
        return;
    }

    for (int col = 0; col < n; col++) {
        if (isSafe(board, row, col)) {
            board[row] = col;
            solveNQueens(board, row + 1, n);
        }
    }
}

int main() {
    int n = 4;
    vector<int> board(n, -1);
    solveNQueens(board, 0, n);
    return 0;
}
```

Output for n=4:

```

. Q . .
. . . Q
Q . . .
. . Q .

. . Q .
Q . . .
. . . Q
. Q . .

```

Complexity:

- **Time Complexity:** $O(N!)$
N queens have $N!$ permutations, but pruning reduces this in practice.
- **Space Complexity:** $O(N)$
 $O(N)$ for the recursion stack and board array.

3. What Is a Hamiltonian Cycle?

Definition:

A **Hamiltonian Cycle** is a cycle in a graph that visits each vertex exactly once and returns to the starting vertex.

Difference Between Eulerian and Hamiltonian Cycle:

Aspect	Eulerian Cycle	Hamiltonian Cycle
Definition	Visits every edge exactly once.	Visits every vertex exactly once.
Requirements	Degree constraints on vertices.	No specific degree requirements.

Finding Hamiltonian Path and Cycle Using Backtracking:

Approach:

1. Start from any vertex.

2. Add a vertex to the path only if:
 - It is adjacent to the last vertex in the path.
 - It has not already been visited.
 3. If all vertices are included in the path:
 - Check if the last vertex is adjacent to the starting vertex for a cycle.
 4. If a solution is not found, backtrack.
-

Code Example:

cpp

```
#include <iostream>
#include <vector>
using namespace std;

bool isSafe(int v, vector<vector<int>>& graph, vector<int>& path, int
pos) {
    // Check if v is adjacent to the last vertex in the path
    if (graph[path[pos - 1]][v] == 0) return false;

    // Check if v is already in the path
    for (int i = 0; i < pos; i++) {
        if (path[i] == v) return false;
    }

    return true;
}

bool hamiltonianCycleUtil(vector<vector<int>>& graph, vector<int>& path,
int pos) {
    if (pos == graph.size()) {
        // Check if the last vertex is adjacent to the first
        return graph[path[pos - 1]][path[0]] == 1;
    }

    for (int v = 1; v < graph.size(); v++) {
        if (isSafe(v, graph, path, pos)) {
            path[pos] = v;
            if (hamiltonianCycleUtil(graph, path, pos + 1)) {
                return true;
            }
            path[pos] = -1; // Backtrack
        }
    }

    return false;
}

bool hamiltonianCycle(vector<vector<int>>& graph) {
    vector<int> path(graph.size(), -1);
    path[0] = 0; // Start from vertex 0

    if (hamiltonianCycleUtil(graph, path, 1)) {
        cout << "Hamiltonian Cycle: ";
        for (int v : path) cout << v << " ";
        cout << path[0] << endl; // Complete the cycle
        return true;
    } else {
        cout << "No Hamiltonian Cycle found." << endl;
    }
}
```

```

        return false;
    }
}

int main() {
    vector<vector<int>> graph = {
        {0, 1, 0, 1, 0},
        {1, 0, 1, 1, 1},
        {0, 1, 0, 0, 1},
        {1, 1, 0, 0, 1},
        {0, 1, 1, 1, 0}
    };

    hamiltonianCycle(graph);
    return 0;
}

```

Output:

Hamiltonian Cycle: 0 1 4 2 3 0

Complexity:

- **Time Complexity:** $O(V!)$, where V is the number of vertices.
 - **Space Complexity:** $O(V)$, for storing the path and recursion stack.
-

Exam Notes

1. DFS:

- Algorithm explores depth first.
- Complexity: $O(V+E)$.

2. N-Queens:

- Backtracking places queens row by row.
- Pruning ensures no threats.

3. Hamiltonian Cycle:

- Visits all vertices exactly once and returns to the start.
- Use backtracking with adjacency matrix.

Subset Sum Problem

Problem Statement

Given a set of non-negative integers {3,34,4,12,5,8} and a target sum 9, determine if there is a subset of the set whose elements sum to 9.

1. Steps to Solve Using Dynamic Programming

The **Subset Sum Problem** can be solved using **Dynamic Programming (DP)**.

DP Approach:

We use a boolean DP table $dp[i][j]$ where:

- i represents the first i elements of the set.
 - j represents the target sum.
 - $dp[i][j]$ is **true** if a subset of the first i elements has a sum equal to j , otherwise **false**.
-

Steps:

1. Initialize a DP table of size $(n+1) \times (\text{sum}+1)$, where n is the size of the set and sum is the target sum.
 2. Base cases:
 - $dp[i][0] = \text{true}$ for all i , since a sum of 0 can always be achieved by picking no elements.
 - $dp[0][j] = \text{false}$ for all $j > 0$, since no subset can be formed with no elements.
 3. For each element in the set, update the DP table:
 - If the element is excluded: $dp[i][j] = dp[i-1][j]$
 - If the element is included: $dp[i][j] = dp[i-1][j - \text{arr}[i-1]]$, where $\text{arr}[i-1]$ is the current element.
 - Final value: $dp[n][\text{sum}]$.
-

DP Table for {3,34,4,12,5,8} and sum=9:

$dp[i][j]$	0	1	2	3	4	5	6	7	8	9
$i=0$	T	F	F	F	F	F	F	F	F	F
$i=1$	T	F	F	T	F	F	F	F	F	F
$i=2$	T	F	F	T	F	F	F	F	F	F
$i=3$	T	F	F	T	T	F	F	F	F	T
$i=4$	T	F	F	T	T	F	F	F	F	T
$i=5$	T	F	F	T	T	T	F	T	T	T
$i=6$	T	F	F	T	T	T	F	T	T	T

Result:

$dp[6][9] = \text{T}$, so a subset exists with a sum of 9.

Subset: {4,5}.

2. Efficient Algorithms for Subset Sum

Algorithm 1: Dynamic Programming

1. Use a boolean DP table as explained above.
 2. This algorithm builds the solution incrementally by deciding for each number whether to include it or not.
-

Algorithm 2: Backtracking with Pruning

1. Start with an empty subset and explore all subsets recursively.
 2. At each step, either include or exclude the current element.
 3. **Pruning:**
 - If the current sum exceeds the target sum, stop exploring that branch.
 - If the target sum is achieved, return `true`.
-

Code for Backtracking:

cpp

```
#include <iostream>
#include <vector>
using namespace std;

bool subsetSum(vector<int>& arr, int n, int sum) {
    if (sum == 0) return true;
    if (n == 0 || sum < 0) return false;

    // Exclude or include the current element
    return subsetSum(arr, n - 1, sum) || subsetSum(arr, n - 1, sum -
arr[n - 1]);
}

int main() {
    vector<int> arr = {3, 34, 4, 12, 5, 8};
    int sum = 9;
    if (subsetSum(arr, arr.size(), sum)) {
        cout << "Subset with given sum exists.\n";
    } else {
        cout << "No subset with given sum exists.\n";
    }
    return 0;
}
```

3. Time Complexity of the Algorithms

Dynamic Programming:

- **Time Complexity:** $O(n \times \text{sum})$, where n is the number of elements in the set, and sum is the target sum.
 - **Space Complexity:** $O(n \times \text{sum})$ (or $O(\text{sum})$ with space optimization).
-

Backtracking with Pruning:

- **Time Complexity:** $O(2^n)$ in the worst case (explores all subsets).
 - **Space Complexity:** $O(n)$ for recursion stack.
-

Exam Notes

1. **DP** is efficient for large n and sum, but uses more space.
2. **Backtracking** is intuitive and works for small n , but has exponential complexity.
3. Always prefer DP for exam questions unless n and sum are very small.

* Find a shortest path from 0 to 4 in the following graph. Show all the steps. Priority queue and set can be used for implementing the Dijkstra's shortest path algorithm. Which one is better and why? * Why does Dijkstra's algorithm not solve the single source shortest-path problem on a weighted directed graph having negative weight edges? Explain with an example.

Shortest Path Using Dijkstra's Algorithm

1. Problem: Find the Shortest Path from Node 0 to Node 4

Graph Representation:

Let's assume the graph is represented as an adjacency list:

Graph:

$0 \rightarrow \{(1,2), (2,4)\}$

$1 \rightarrow \{(2,1), (3,7)\}$

$2 \rightarrow \{(4,3)\}$

$3 \rightarrow \{(4,1)\}$

$4 \rightarrow \{\}$

Dijkstra's Algorithm Steps

Initialization:

- Create a **distance array** to store the shortest distance to each node. Initialize all distances to ∞ except the source node, which is 0. $\text{distance} = [0, \infty, \infty, \infty, \infty]$
- Use a **priority queue** (min-heap) to process nodes based on the shortest distance found so far.
- Create a **parent array** to track the path.

Algorithm:

1. Start with the source node 0. Push (0,0) (distance, node) into the priority queue.
2. While the queue is not empty:
 - Extract the node u with the smallest distance.
 - For all neighbors v of u , if a shorter path to v is found, update its distance and push (new_distance, v) into the queue.

3. Continue until all nodes are processed.

Steps for This Graph:

1. **Initialization:** distance=[0,∞,∞,∞,∞]

Priority Queue: [(0,0)]

2. **Processing Node 0:**

- Neighbors: (1,2),(2,4)
- Update distances:
distance[1]=2,distance[2]=4
- Priority Queue: [(2,1),(4,2)]

3. **Processing Node 1:**

- Neighbors: (2,1),(3,7)
- Update distances:
distance[2]=min(4,2+1)=3,distance[3]=2+7=9
- Priority Queue: [(3,2),(4,2),(9,3)]

4. **Processing Node 2:**

- Neighbors: (4,3)
- Update distances:
distance[4]=min(∞,3+3)=6
- Priority Queue: [(4,2),(9,3),(6,4)]

5. **Processing Node 4:**

- No neighbors to process.
- Priority Queue: [(9,3)]

6. **Processing Node 3:**

- Neighbors: (4,1)
- No updates needed since 9+1>6.

Final Distances:

distance=[0,2,3,9,6]

Shortest Path from 0 to 4:

To reconstruct the path, backtrack using the parent array:

Path: 0→2→4

Shortest Distance: 6.

Priority Queue vs. Set for Dijkstra's Algorithm

1. Priority Queue:

- Nodes are always processed in ascending order of distance.
- Efficiently implemented using a min-heap ($O(\log V)$ for insertion/extraction).
- Allows multiple entries for the same node (with different distances), but the smallest distance is always processed first.

2. Set:

- Ensures each node is stored only once.
- Removes the need to check duplicate entries.
- However, updating distances requires removing and re-inserting nodes, which is more expensive.

Which is Better?

Priority Queue is better for Dijkstra's algorithm as it efficiently handles duplicate entries and maintains a strict priority order with $O(\log V)$ operations.

2. Why Dijkstra's Algorithm Fails with Negative Weight Edges

Dijkstra's algorithm assumes that once a node is processed (i.e., the shortest distance to that node is determined), the distance will not change. This assumption fails in the presence of **negative weight edges** because a shorter path to an already processed node might exist through a negative edge.

Example:

Graph:

- $0 \rightarrow 1$ with weight 4
 - $0 \rightarrow 2$ with weight 1
 - $2 \rightarrow 1$ with weight -3
-

Steps Using Dijkstra:

1. Start at 0: $\text{distance}[0]=0, \text{distance}[1]=\infty, \text{distance}[2]=\infty$.
2. Process 0:
 $\text{distance}[1]=4, \text{distance}[2]=1$.
3. Process 2:
Update $\text{distance}[1]=\text{distance}[2]+(-3)=1-3=-2$.

Issue: Node 1's distance changes after it has already been processed, which violates Dijkstra's assumptions.

Solution: Use **Bellman-Ford Algorithm**, which works for graphs with negative weights. It relaxes all edges $V-1$ times, ensuring correctness even with negative edges.

Summary

1. **Dijkstra's Algorithm:** Efficient for non-negative weight graphs, with time complexity $O((V+E)\log V)$.
2. **Fails with Negative Weights:** Dijkstra cannot handle scenarios where the distance to a processed node changes.
3. **Bellman-Ford:** Handles negative weights but is slower ($O(V \times E)$).

1. Building a Segment Tree for Array {1, 3, 5, 7, 9, 11, 13}

Segment Tree Basics

A **segment tree** is a binary tree used for answering range queries (e.g., sum, min, max) efficiently. Each node in the tree represents a range of the input array.

Key Properties:

1. The size of the segment tree is approximately $2 \times 2^{\lceil \log_2(n) \rceil} - 1$, where n is the size of the input array.
 2. Each leaf node represents a single element of the array.
 3. Each internal node represents a range of elements (e.g., the sum or minimum over that range).
-

Steps to Build a Segment Tree

Input Array: {1,3,5,7,9,11,13}

Range Query Operation: Sum

1. Divide the Array into Segments:

The array is recursively divided into halves until each segment contains a single element.

2. Combine Results:

Each internal node stores the sum of its left and right child nodes.

Step-by-Step Construction:

- **Level 1:** The root represents the range [0, 6] (sum of all elements).

Value = $1+3+5+7+9+11+13=49$.

- **Level 2:** Split into [0, 3] and [4, 6].

- Left child: $1+3+5+7=16$
- Right child: $9+11+13=33$

- **Level 3:** Further split:

- [0, 1] and [2, 3] for the left child.
- [4, 5] and 6, 6 for the right child.

- **Level 4:** Leaf nodes represent individual elements:
-

Final Tree Structure:

```

/      /      \

/      \      -e for Building Segment Tree**:
`namespace std;

void buildSegmentTree(vector<int>& arr, vector<int>& tree, int start,
int end, int node) {
    if (start == end) {
        // Leaf node
        tree[node] = arr[start];
        return;
    }
    int mid = (start + end) / 2;
    // Build left and right subtrees
    buildSegmentTree(arr, tree, start, mid, 2 * node + 1);
    buildSegmentTree(arr, tree, mid + 1, end, 2 * node + 2);
    // Merge results
    tree[node] = tree[2 * node + 1] + tree[2 * node + 2];
}

int main() {
    vector<int> arr = {1, 3, 5, 7, 9, 11, 13};
    int n = arr.size();
    vector<int> tree(4 * n, 0); // Allocate memory for segment tree
    buildSegmentTree(arr, tree, 0, n - 1, 0);
    for (int i = 0; i < tree.size(); i++) {
        if (tree[i] != 0)
            cout << "Node " << i << ": " << tree[i] << endl;
    }
    return 0;
}

```

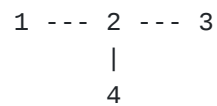
Definition

40/44

Example:

Graph:

lua



The edge 2→3 is a bridge because removing it disconnects node 3 from the rest of the graph.

Algorithm to Find Articulation Edges

Articulation edges can be found using **DFS** with the following steps:

1. Maintain a discovery time array and a low-link value array:
 - **disc[u]**: Time when node u is first visited.
 - **low[u]**: The lowest discovery time reachable from u.
2. For each edge $u \rightarrow v$:
 - If v is already visited, update low[u].
 - If v is unvisited, recursively explore v. Update low[u] and check if:
low[v]>disc[u]: $u \rightarrow v$ is a bridge.

Code:

cpp

```
#include <iostream>
#include <vector>
#include <algorithm>
using namespace std;

void dfs(int u, int parent, vector<int> adj[], vector<bool>& visited,
vector<int>& disc, vector<int>& low, vector<pair<int, int>>& bridges,
int& time) {
    visited[u] = true;
    disc[u] = low[u] = ++time;

    for (int v : adj[u]) {
        if (!visited[v]) {
            dfs(v, u, adj, visited, disc, low, bridges, time);
            low[u] = min(low[u], low[v]);

            if (low[v] > disc[u]) {
                bridges.push_back({u, v});
            }
        } else if (v != parent) {
            low[u] = min(low[u], disc[v]);
        }
    }
}

int main() {
    int n = 5; // Number of nodes
    vector<int> adj[5] = {
        {1, 2},
        {0, 2},
        {0, 1, 3},
        {2, 4},
        {3}
    };
    vector<bool> visited(n, false);
    vector<int> disc(n, -1), low(n, -1);
    vector<pair<int, int>> bridges;
    int time = 0;

    for (int i = 0; i < n; i++) {
        if (!visited[i]) {
            dfs(i, -1, adj, visited, disc, low, bridges, time);
        }
    }

    cout << "Bridges:\n";
    for (auto& bridge : bridges) {
        cout << bridge.first << " - " << bridge.second << endl;
    }
}
```

```
    }  
    return 0;  
}
```

3. What is an Implicit Graph?

Definition

An **implicit graph** is a graph that is not explicitly represented (e.g., using adjacency lists or matrices). Instead, its nodes and edges are defined **implicitly** through relationships or rules.

Example:

Consider a **grid-based graph**:

- Nodes: Grid cells.
 - Edges: Valid moves between adjacent cells.
-

Example Problem

Find the shortest path in a 2D grid from the top-left corner to the bottom-right corner, avoiding obstacles.

Input Grid:

```
0 0 1  
0 0 0  
1 0 0
```

- 0: Free cell.
 - 1: Obstacle.
-

Graph Representation:

- Nodes: Grid cells (row, column).

- Edges: Move to adjacent cells (up, down, left, right) if they are free.
-

Algorithm: Use BFS to explore valid moves in the grid.

Code:

cpp

```
#include <iostream>
#include <queue>
#include <vector>
using namespace std;

bool isValid(int x, int y, int n, int m, vector<vector<int>>& grid,
vector<vector<bool>>& visited) {
    return x >= 0 && x < n && y >= 0 && y < m && grid[x][y] == 0 &&
!visited[x][y];
}

int shortestPath(vector<vector<int>>& grid) {
    int n = grid.size(), m = grid[0].size();
    vector<vector<bool>> visited(n, vector<bool>(m, false));
    queue<pair<int, int>> q;
    q.push({0, 0});
    visited[0][0] = true;
    int steps = 0;

    vector<pair<int, int>> directions = {{0, 1}, {1, 0}, {0, -1}, {-1,
0}};
    while (!q.empty()) {
        int size = q.size();
        for (int i = 0; i <
```