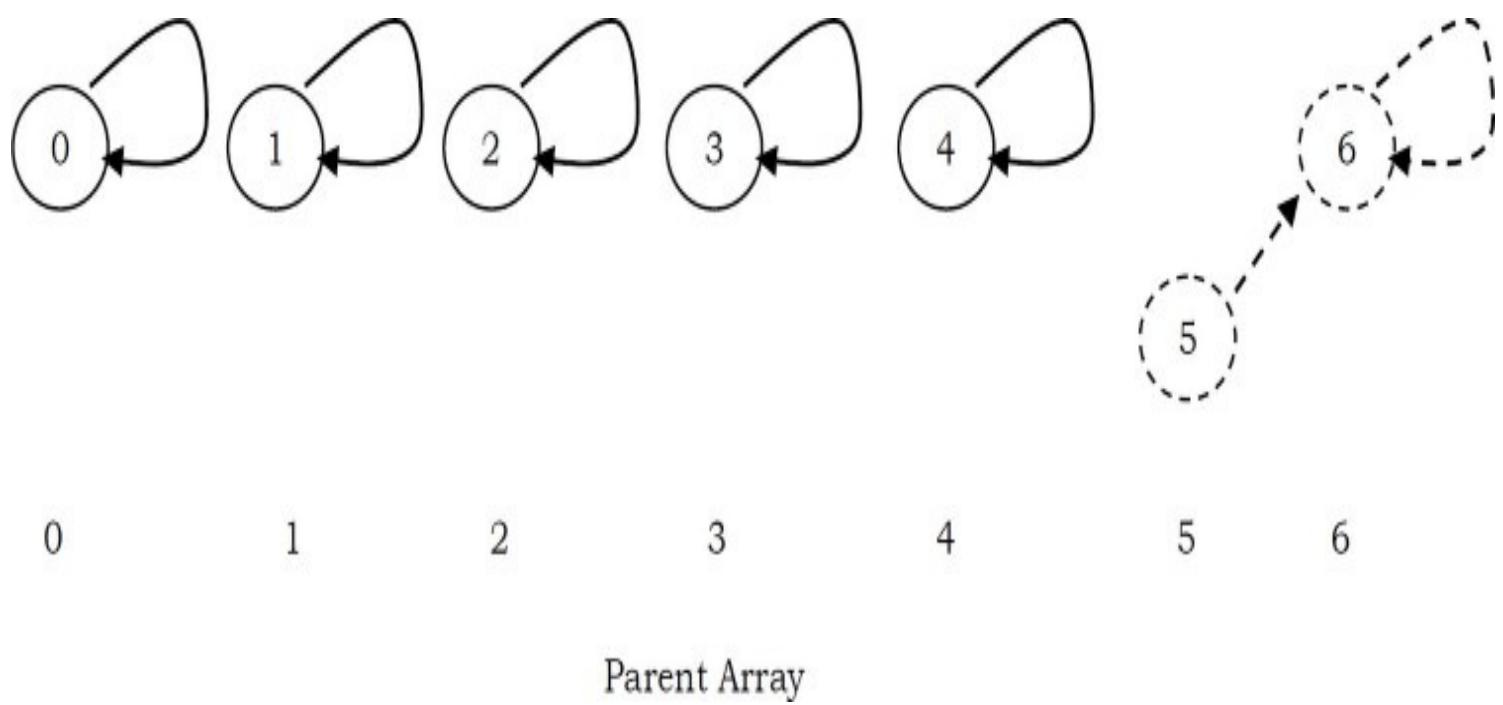
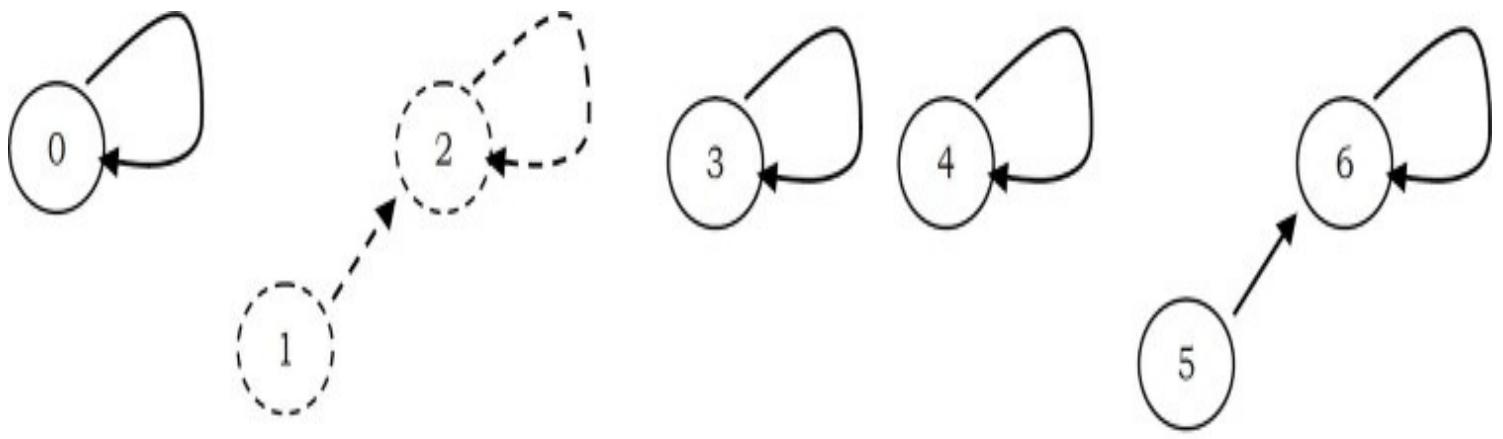


After UNION(5,6)



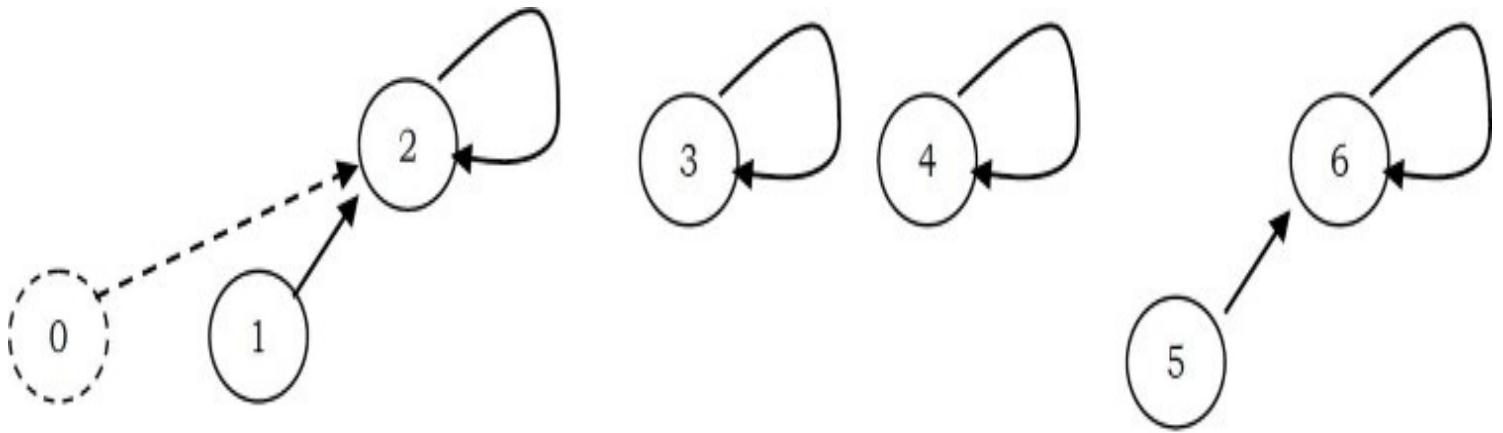
After UNION(1,2)



0 1 2 3 4 5 6

Parent Array

After UNION(0,2)



0 1 2 3 4 5 6

Parent Array

One important thing to observe here is, UNION operation is changing the root's parent only, but not for all the elements in the sets. Due to this, the time complexity of UNION operation is $O(1)$.

A FIND(X) on element X is performed by returning the root of the tree containing X. The time to perform this operation is proportional to the depth of the node representing X.

Using this method, it is possible to create a tree of depth $n - 1$ (Skew Trees). The worst-case running time of a FIND is $O(n)$ and m consecutive FIND operations take $O(mn)$ time in the worst case.

MAKESET

```
void MAKESET( int S[], int size) {  
    for(int i = size-1; i >=0; i--)  
        S[i] = i;  
}
```

FIND

```
int FIND(int S[], int size, int X) {  
    if(X >= 0 && X < size)  
        return -1;  
    if( S[X] == X )  
        return X;  
    else return FIND(S, S[X]);  
}
```

UNION

```
void UNION( int S[], int size, int root1, int root2 ) {  
    if(FIND(S, size, root1) == FIND(S, size, root2))  
        return;  
    if((root1 >= 0 && root1 < size) && (root2 >= 0 && root2 < size))  
        return;  
    S[root1] = root2;  
}
```

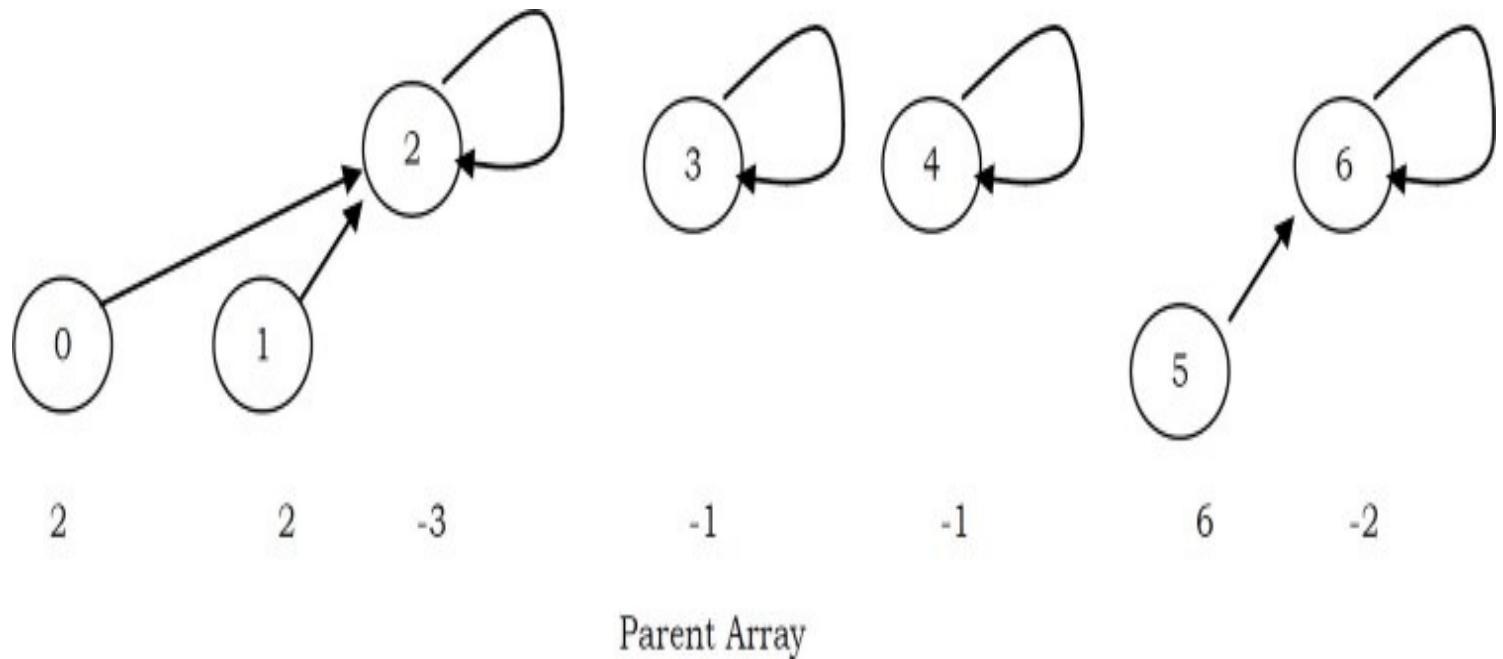
8.9 Fast UNION Implementations (Quick FIND)

The main problem with the previous approach is that, in the worst case we are getting the skew trees and as a result the FIND operation is taking $O(n)$ time complexity. There are two ways to improve it:

- UNION by Size (also called UNION by Weight): Make the smaller tree a subtree of the larger tree
- UNION by Height (also called UNION by Rank): Make the tree with less height a subtree of the tree with more height

UNION by Size

In the earlier representation, for each element i we have stored i (in the parent array) for the root element and for other elements we have stored the parent of i . But in this approach we store negative of the size of the tree (that means, if the size of the tree is 3 then store -3 in the parent array for the root element). For the previous example (after UNION(0,2)), the new representation will look like:



Assume that the size of one element set is 1 and store -1 . Other than this there is no change.

MAKESET

```
void MAKESET( int S[], int size) {  
    for(int i = size-1; i >= 0; i--)  
        S[i] = -1;  
}
```

FIND

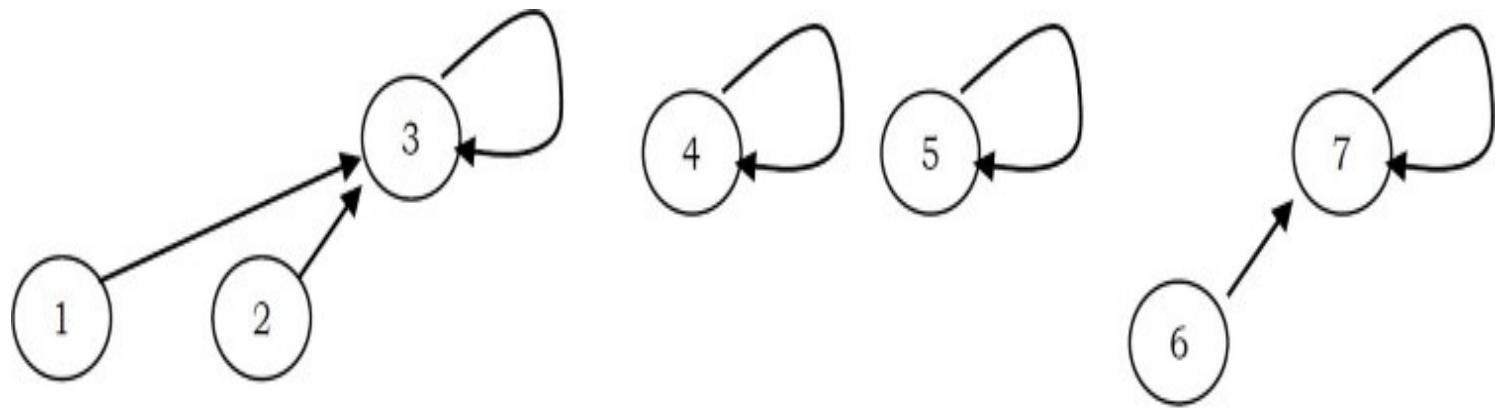
```
int FIND(int S[], int size, int X) {  
    if((X >= 0 && X < size)) )  
        return -1;  
    if( S[X] == -1 )  
        return X;  
    else return FIND(S, S[X]);  
}
```

UNION by Size

```
void UNIONBySize(int S[], int size, int root1, int root2) {  
    if((FIND(S, size, root1) == FIND(S, size, root2)) && FIND(S, size, root1) != -1)  
        return;  
    if( S[root2] < S[root1] ) {  
        S[root1] = root2;  
        S[root2] += S[root1];  
    }  
    else {  
        S[root2] = root1;  
        S[root1] += S[root2];  
    }  
}
```

Note: There is no change in FIND operation implementation.

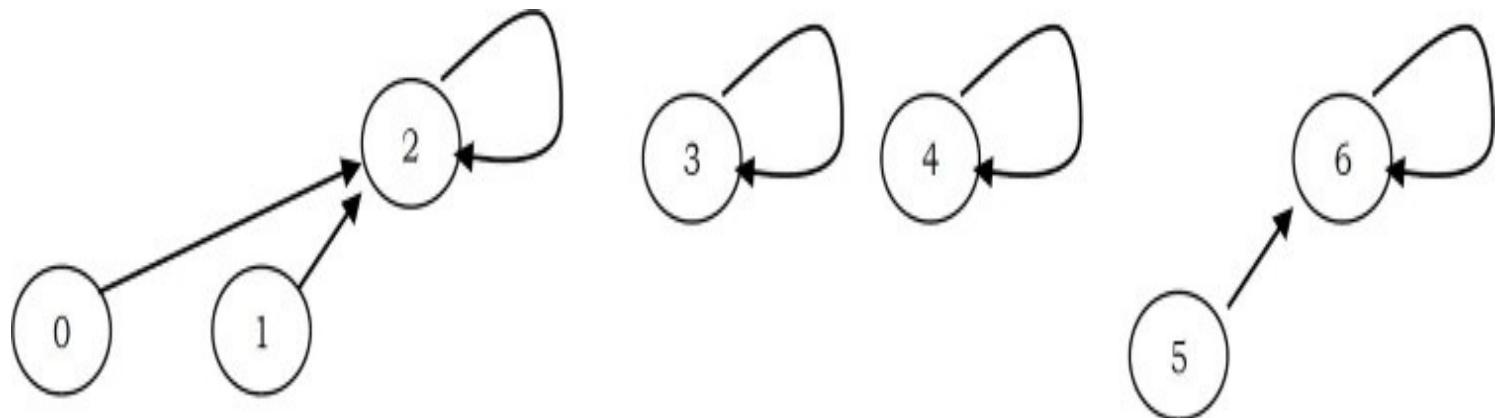
UNION by Height (UNION by Rank)



2 2 -2 -1 -1 6 -2

Parent Array

As in UNION by size, in this method we store negative of height of the tree (that means, if the height of the tree is 3 then we store -3 in the parent array for the root element). We assume the height of a tree with one element set is 1. For the previous example (after UNION(0,2)), the new representation will look like:



2 2 -2 -1 -1 6 -2

Parent Array

UNION by Height

```

void UNIONByHeight(int S[], int size, int root1, int root2) {
    if(FIND(S, size, root1) == FIND(S, size, root2)) && FIND(S, size, root1) != -1)
        return;
    if( S[root2] < S[root1] )
        S[root1] = root2;
    else {
        if( S[root2] == S[root1] ){
            S[root1]--;
            S[root2] = root1;
        }
    }
}

```

Note: For FIND operation there is no change in the implementation.

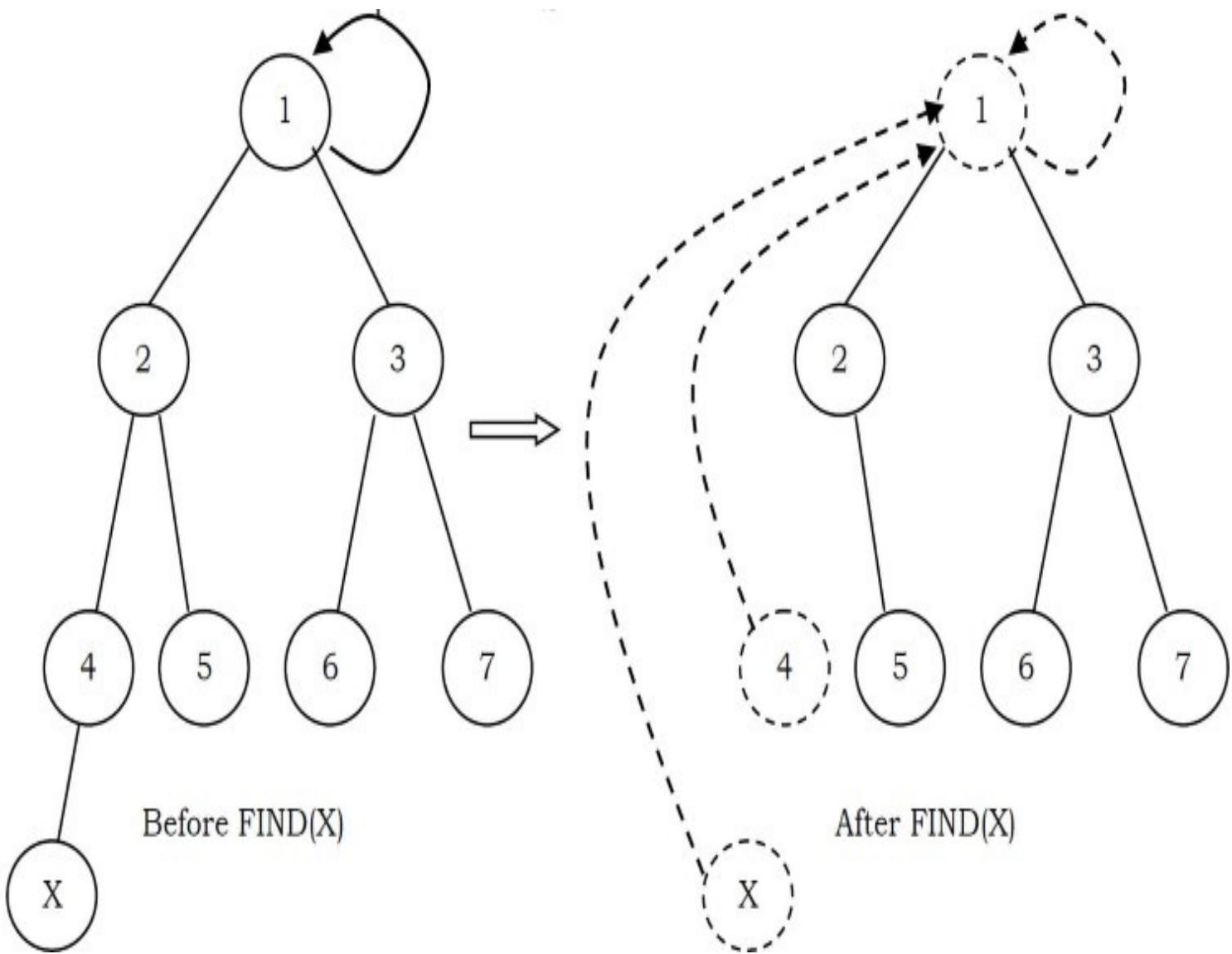
Comparing UNION by Size and UNION by Height

With UNION by size, the depth of any node is never more than $\log n$. This is because a node is initially at depth 0. When its depth increases as a result of a UNION, it is placed in a tree that is at least twice as large as before. That means its depth can be increased at most $\log n$ times. This means that the running time for a FIND operation is $O(\log n)$, and a sequence of m operations takes $O(m \log n)$.

Similarly with UNION by height, if we take the UNION of two trees of the same height, the height of the UNION is one larger than the common height, and otherwise equal to the max of the two heights. This will keep the height of tree of n nodes from growing past $O(\log n)$. A sequence of m UNIONs and FINDs can then still cost $O(m \log n)$.

Path Compression

FIND operation traverses a list of nodes on the way to the root. We can make later FIND operations efficient by making each of these vertices point directly to the root. This process is called *path compression*. For example, in the FIND(X) operation, we travel from X to the root of the tree. The effect of path compression is that every node on the path from X to the root has its parent changed to the root.



With path compression the only change to the FIND function is that $S[X]$ is made equal to the value returned by FIND. That means, after the root of the set is found recursively, X is made to point directly to it. This happen recursively to every node on the path to the root.

FIND with path compression

```
int FIND(int S[], int size, int X) {
    if!(X >= 0 && X < size))
        return;
    if( S[X] <= 0 )
        return X;
    else return(S[X] = FIND( S, S[X]));
```

}

Note: Path compression is compatible with UNION by size but not with UNION by height as

there is no efficient way to change the height of the tree.

8.10 Summary

Performing m union-find operations on a set of n objects.

Algorithm	Worst-case time
Quick-Find	mn
Quick-Union	mn
Quick-Union by Size/Height	$n + m \log n$
Path compression	$n + m \log n$
Quick-Union by Size/Height + Path Compression	$(m + n) \log n$

8.11 Disjoint Sets: Problems & Solutions

Problem-1 Consider a list of cities c_1, c_2, \dots, c_n . Assume that we have a relation R such that, for any i, j , $R(c_i, c_j)$ is 1 if cities c_i and c_j are in the same state, and 0 otherwise. If R is stored as a table, how much space does it require?

Solution: R must have an entry for every pair of cities. There are $\Theta(n^2)$ of these.

Problem-2 For [Problem-1](#), using a Disjoint sets ADT, give an algorithm that puts each city in a set such that c_i and c_j are in the same set if and only if they are in the same state.

Solution:

```
for (i = 1; i <= n; i++) {
    MAKESET(ci);
    for (j = 1; j <= i-1; j++) {
        if(R(cj, ci)) {
            UNION(cj, ci);
            break;
        }
    }
}
```

Problem-3 For [Problem-1](#), when the cities are stored in the Disjoint sets ADT, if we are given two cities c_i and c_j , how do we check if they are in the same state?

Solution: Cities c_i and c_j are in the same state if and only if $\text{FIND}(c_i) = \text{FIND}(c_j)$.

Problem-4 For [Problem-1](#), if we use linked-lists with UNION by size to implement the union-find ADT, how much space do we use to store the cities?

Solution: There is one node per city, so the space is $\Theta(n)$.

Problem-5 For [Problem-1](#), if we use trees with UNION by rank, what is the worst-case running time of the algorithm from [Problem-2](#)?

Solution: Whenever we do a UNION in the algorithm from [Problem-2](#), the second argument is a tree of size 1. Therefore, all trees have height 1, so each union takes time $O(1)$. The worst-case running time is then $\Theta(n^2)$.

Problem-6 If we use trees without union-by-rank, what is the worst-case running time of the algorithm from [Problem-2](#)? Are there more worst-case scenarios than [Problem-5](#)?

Solution: Because of the special case of the unions, union-by-rank does not make a difference for our algorithm. Hence, everything is the same as in [Problem-5](#).

Problem-7 With the quick-union algorithm we know that a sequence of n operations (*unions* and *finds*) can take slightly more than linear time in the worst case. Explain why if all the *finds* are done before all the *unions*, a sequence of n operations is guaranteed to take $O(n)$ time.

Solution: If the *find* operations are performed first, then the *find* operations take $O(1)$ time each because every item is the root of its own tree. No item has a parent, so finding the set an item is in takes a fixed number of operations. Union operations always take $O(1)$ time. Hence, a sequence of n operations with all the *finds* before the *unions* takes $O(n)$ time.

Problem-8 With reference to [Problem-7](#), explain why if all the unions are done before all the finds, a sequence of n operations is guaranteed to take $O(n)$ time.

Solution: This problem requires amortized analysis. *Find* operations can be expensive, but this expensive *find* operation is balanced out by lots of cheap *union* operations.

The accounting is as follows. *Union* operations always take $O(1)$ time, so let's say they have an actual cost of $\sqrt{2}1$. Assign each *union* operation an amortized cost of $\sqrt{2}2$, so every *union* operation puts $\sqrt{2}1$ in the account. Each *union* operation creates a new child. (Some node that was not a child of any other node before is a child now.) When all the union operations are done, there is $\$1$ in the account for every child, or in other words, for every node with a depth of one or greater. Let's say that a $\text{find}(u)$ operation costs $\sqrt{2}1$ if u is a root. For any other node, the *find* operation costs an additional $\sqrt{2}1$ for each parent pointer the *find* operation traverses. So the actual cost is $\sqrt{2}(1 + d)$, where d is the depth of u . Assign each *find* operation an amortized cost

of $\sqrt{2}^2$. This covers the case where u is a root or a child of a root. For each additional parent pointer traversed, $\sqrt{2}^1$ is withdrawn from the account to pay for it.

Fortunately, path compression changes the parent pointers of all the nodes we pay $\sqrt{2}^1$ to traverse, so these nodes become children of the root. All of the traversed nodes whose depths are 2 or greater move up, so their depths are now 1. We will never have to pay to traverse these nodes again. Say that a node is a grandchild if its depth is 2 or greater.

Every time $find(u)$ visits a grandchild, $\sqrt{2}^1$ is withdrawn from the account, but the grandchild is no longer a grandchild. So the maximum number of dollars that can ever be withdrawn from the account is the number of grandchildren. But we initially put \$1 in the bank for every child, and every grandchild is a child, so the bank balance will never drop below zero. Therefore, the amortization works out. *Union* and *find* operations both have amortized costs of $\sqrt{2}^2$, so any sequence of n operations where all the unions are done first takes $O(n)$ time.

GRAPH ALGORITHMS

CHAPTER

9



9.1 Introduction

In the real world, many problems are represented in terms of objects and connections between them. For example, in an airline route map, we might be interested in questions like: “What’s the fastest way to go from Hyderabad to New York?” or “What is the cheapest way to go from Hyderabad to New York?” To answer these questions we need information about connections (airline routes) between objects (towns). Graphs are data structures used for solving these kinds of problems.

9.2 Glossary

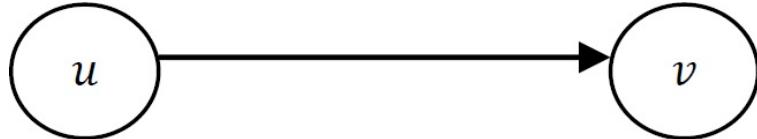
Graph: A graph is a pair (V, E) , where V is a set of nodes, called *vertices*, and E is a collection of pairs of vertices, called *edges*.

- *Vertices* and *edges* are positions and store elements

- Definitions that we use:

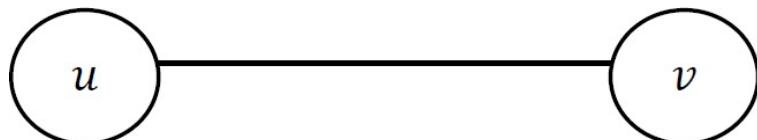
- *Directed edge:*

- ordered pair of vertices (u, v)
- first vertex u is the origin
- second vertex v is the destination
- Example: one-way road traffic



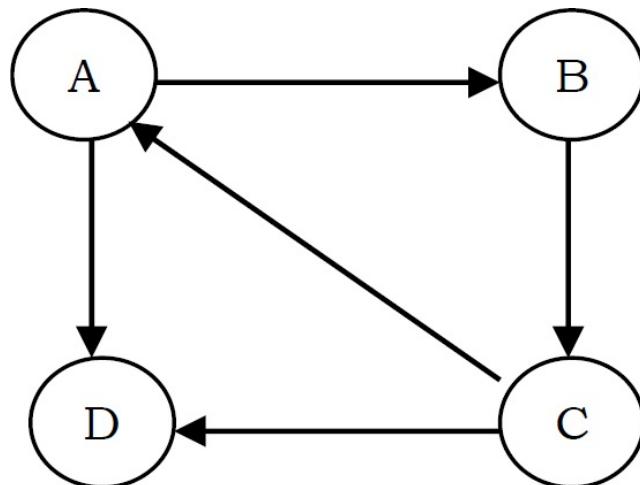
- *Undirected edge:*

- unordered pair of vertices (u, v)
- Example: railway lines



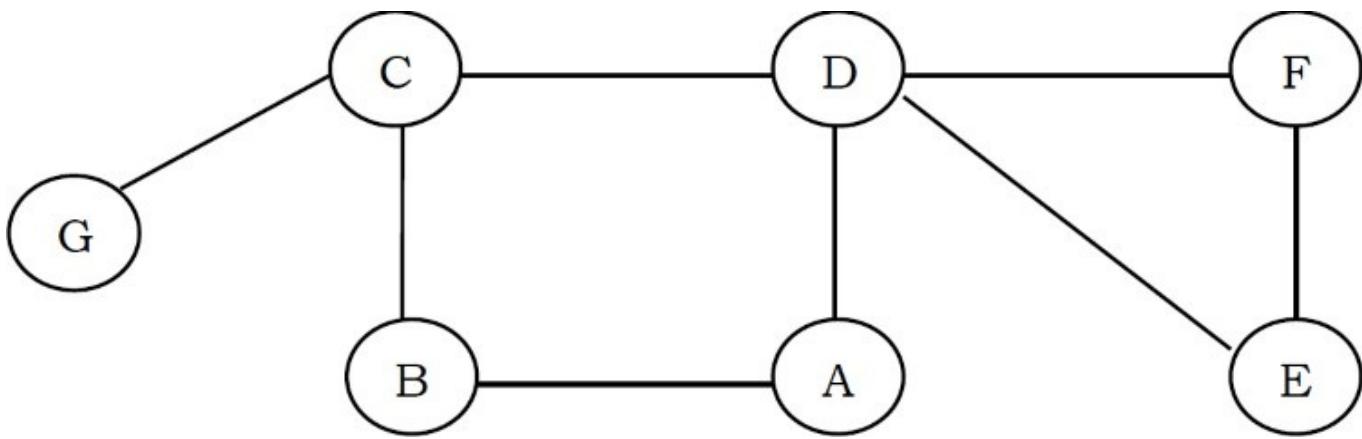
- *Directed graph:*

- all the edges are directed
- Example: route network

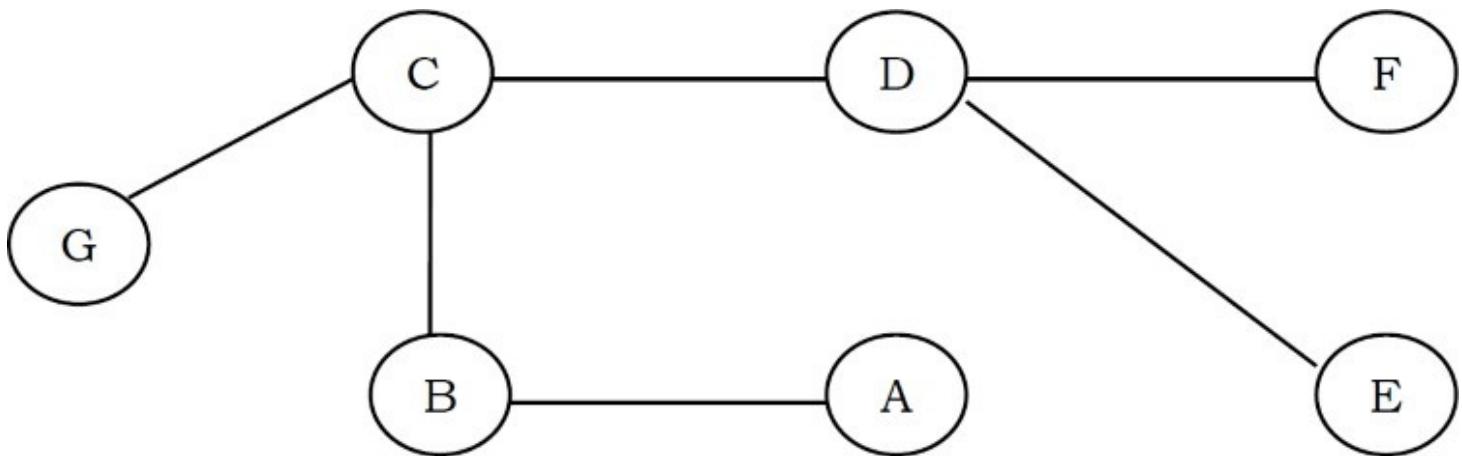


- *Undirected graph:*

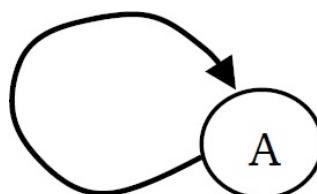
- all the edges are undirected
- Example: flight network



- When an edge connects two vertices, the vertices are said to be adjacent to each other and the edge is incident on both vertices.
- A graph with no cycles is called a *tree*. A tree is an acyclic connected graph.



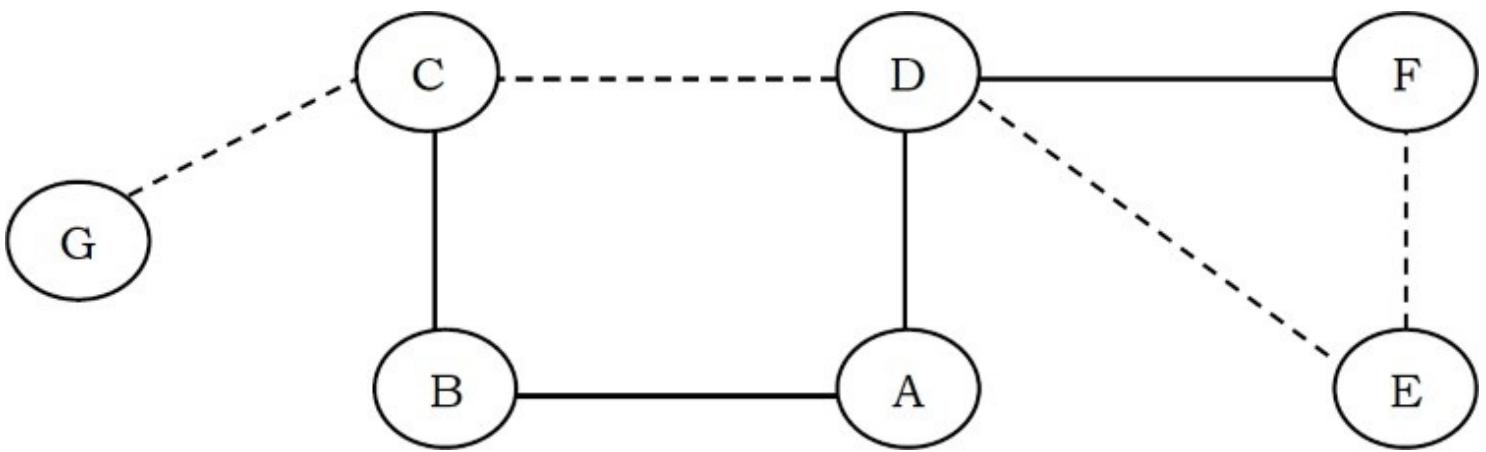
- A self loop is an edge that connects a vertex to itself.



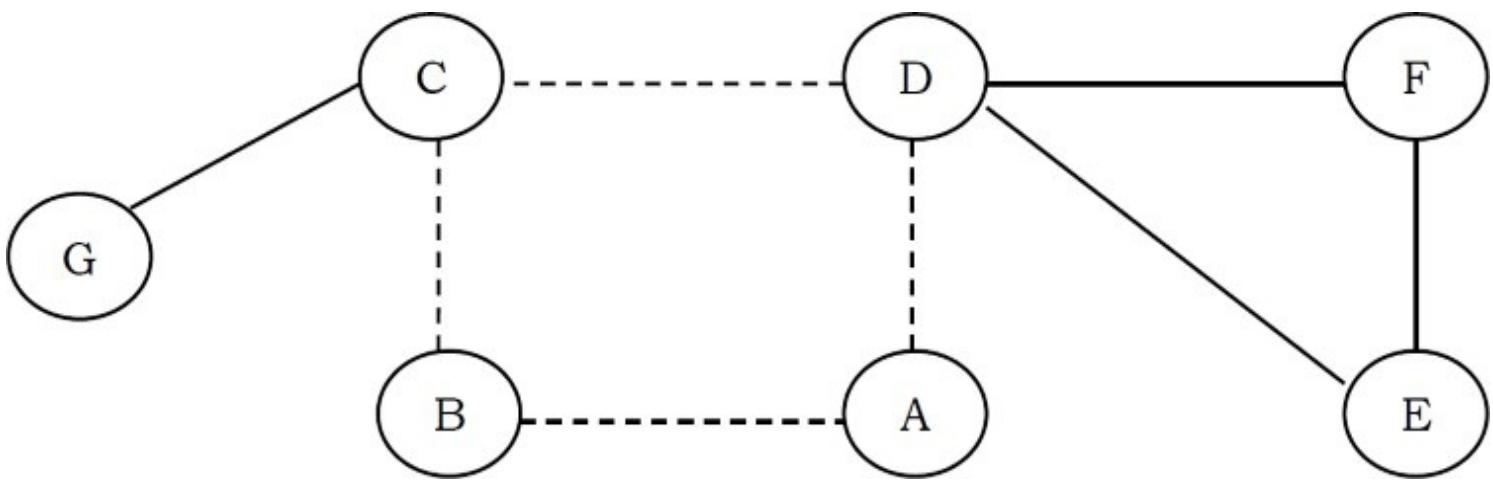
- Two edges are parallel if they connect the same pair of vertices.



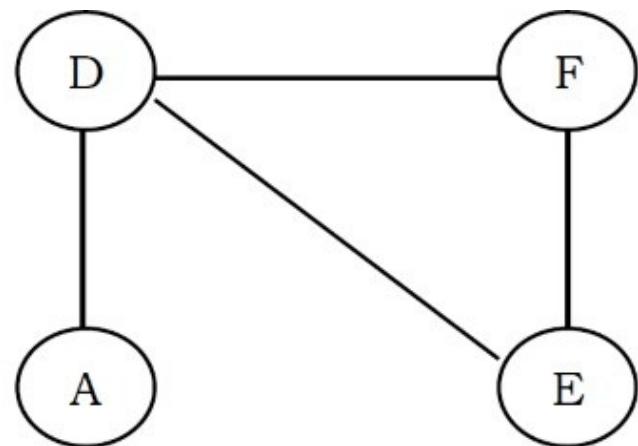
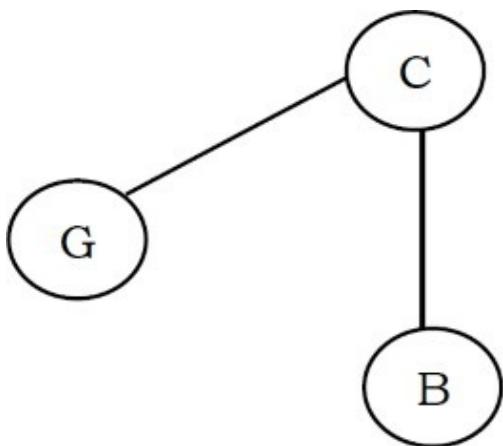
- The Degree of a vertex is the number of edges incident on it.
- A subgraph is a subset of a graph's edges (with associated vertices) that form a graph.
- A path in a graph is a sequence of adjacent vertices. Simple path is a path with no repeated vertices. In the graph below, the dotted lines represent a path from G to E.



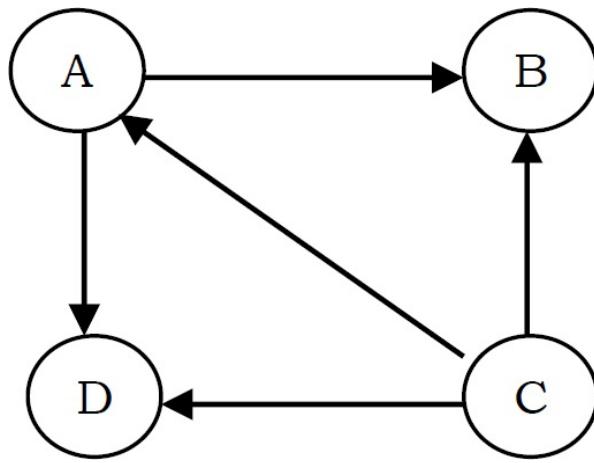
- A cycle is a path where the first and last vertices are the same. A simple cycle is a cycle with no repeated vertices or edges (except the first and last vertices).



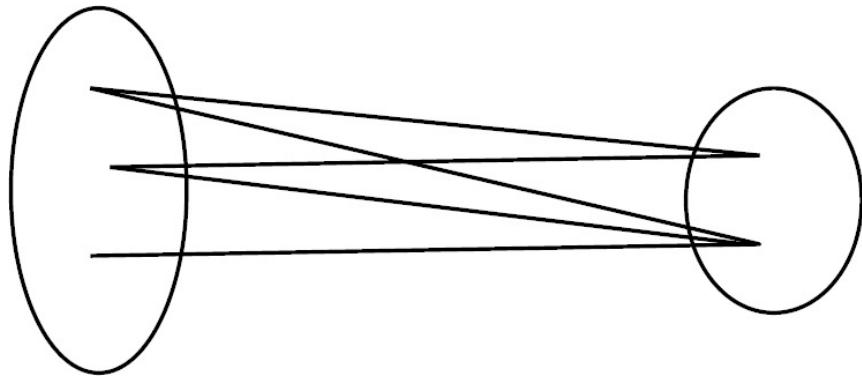
- We say that one vertex is connected to another if there is a path that contains both of them.
- A graph is connected if there is a path from *every* vertex to every other vertex.
- If a graph is not connected then it consists of a set of connected components.



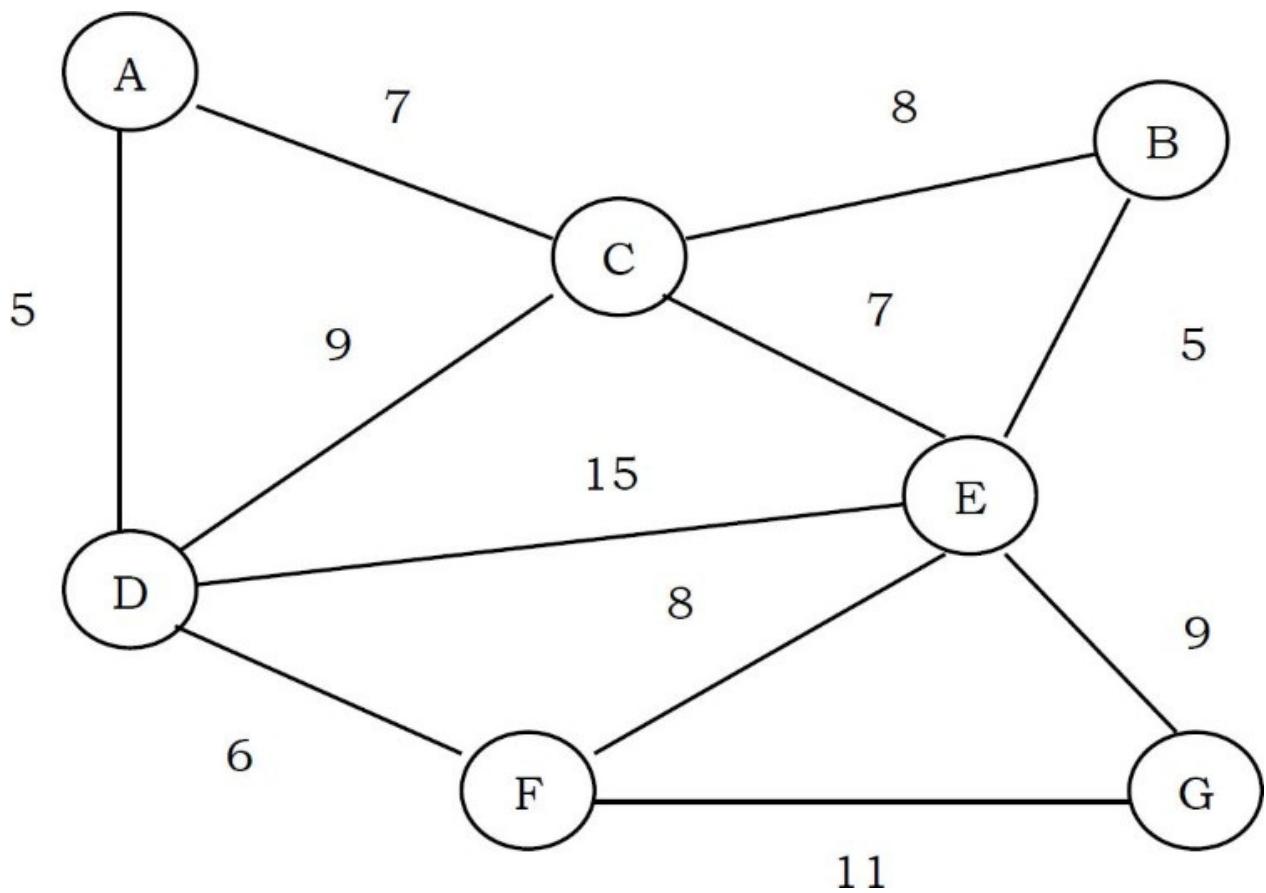
- A *directed acyclic graph* [DAG] is a directed graph with no cycles.



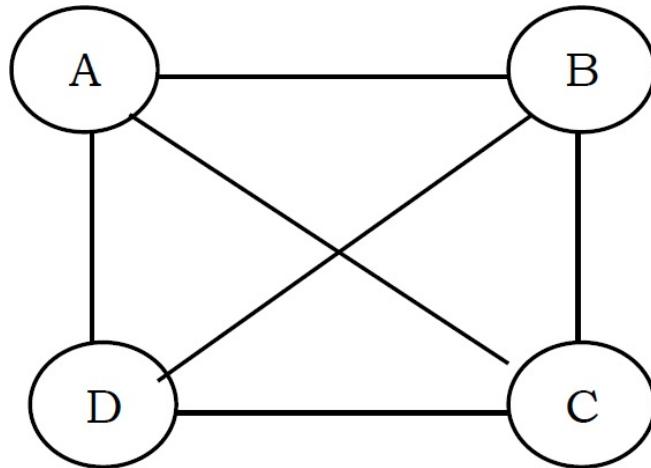
- A forest is a disjoint set of trees.
- A spanning tree of a connected graph is a subgraph that contains all of that graph's vertices and is a single tree. A spanning forest of a graph is the union of spanning trees of its connected components.
- A bipartite graph is a graph whose vertices can be divided into two sets such that all edges connect a vertex in one set with a vertex in the other set.



- In *weighted graphs* integers (*weights*) are assigned to each edge to represent (distances or costs).



- Graphs with all edges present are called *complete graphs*.



- Graphs with relatively few edges (generally if $|E| < |V| \log |V|$) are called *sparse graphs*.
- Graphs with relatively few of the possible edges missing are called *dense*.
- Directed weighted graphs are sometimes called *network*.
- We will denote the number of vertices in a given graph by $|V|$, and the number of edges by $|E|$. Note that E can range anywhere from 0 to $|V|(|V| - 1)/2$ (in undirected graph). This is because each node can connect to every other node.

9.3 Applications of Graphs

- Representing relationships between components in electronic circuits
- Transportation networks: Highway network, Flight network
- Computer networks: Local area network, Internet, Web
- Databases: For representing ER (Entity Relationship) diagrams in databases, for representing dependency of tables in databases

9.4 Graph Representation

As in other ADTs, to manipulate graphs we need to represent them in some useful form. Basically, there are three ways of doing this:

- Adjacency Matrix
- Adjacency List
- Adjacency Set

Adjacency Matrix

Graph Declaration for Adjacency Matrix

First, let us look at the components of the graph data structure. To represent graphs, we need the number of vertices, the number of edges and also their interconnections. So, the graph can be declared as:

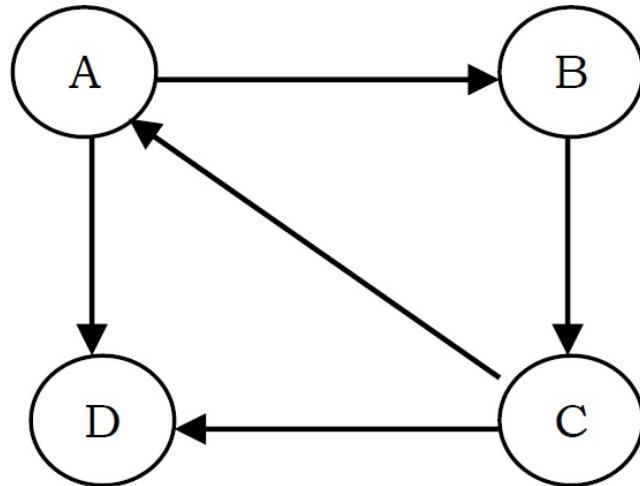
```
struct Graph {
    int V;
    int E;
    int **Adj; //Since we need two dimensional matrix
};
```

Description

In this method, we use a matrix with size $V \times V$. The values of matrix are boolean. Let us assume the matrix is Adj . The value $Adj[u, v]$ is set to 1 if there is an edge from vertex u to vertex v and 0 otherwise.

In the matrix, each edge is represented by two bits for undirected graphs. That means, an edge from **u** to **v** is represented by 1 value in both $Adj[u,v]$ and $Adj[v,u]$. To save time, we can process only half of this symmetric matrix. Also, we can assume that there is an “edge” from each vertex to itself. So, $Adj[u, u]$ is set to 1 for all vertices.

If the graph is a directed graph then we need to mark only one entry in the adjacency matrix. As an example, consider the directed graph below.



The adjacency matrix for this graph can be given as:

	A	B	C	D
A	0	1	0	1
B	0	0	1	0
C	1	0	0	1
D	0	0	0	0

Now, let us concentrate on the implementation. To read a graph, one way is to first read the vertex names and then read pairs of vertex names (edges). The code below reads an undirected graph.

```

//This code creates a graph with adj matrix representation
struct Graph *adjMatrixOfGraph() {
    int i, u, v;
    struct Graph *G = (struct Graph *) malloc(sizeof(struct Graph));
    if(!G) {
        printf("Memory Error");
        return;
    }
    scanf("Number of Vertices: %d, Number of Edges:%d", &G->V, &G->E);
    G->Adj = malloc(sizeof(G->V) * G->V);
    for(u = 0; u < G->V; u++)
        for(v = 0; v < G->V; v++)
            G->Adj[v][v] = 0;
    for(i = 0; i < G->E; i++) {
        //Read an edge
        scanf("Reading Edge: %d %d", &u, &v);
        //For undirected graphs set both the bits
        G->Adj[u][v] = 1;
        G->Adj[v][u] = 1;
    }
    return G;
}

```

The adjacency matrix representation is good if the graphs are dense. The matrix requires $O(V^2)$ bits of storage and $O(V^2)$ time for initialization. If the number of edges is proportional to V^2 , then there is no problem because V^2 steps are required to read the edges. If the graph is sparse, the initialization of the matrix dominates the running time of the algorithm as it takes takes $O(V^2)$.

Adjacency List

Graph Declaration for Adjacency List

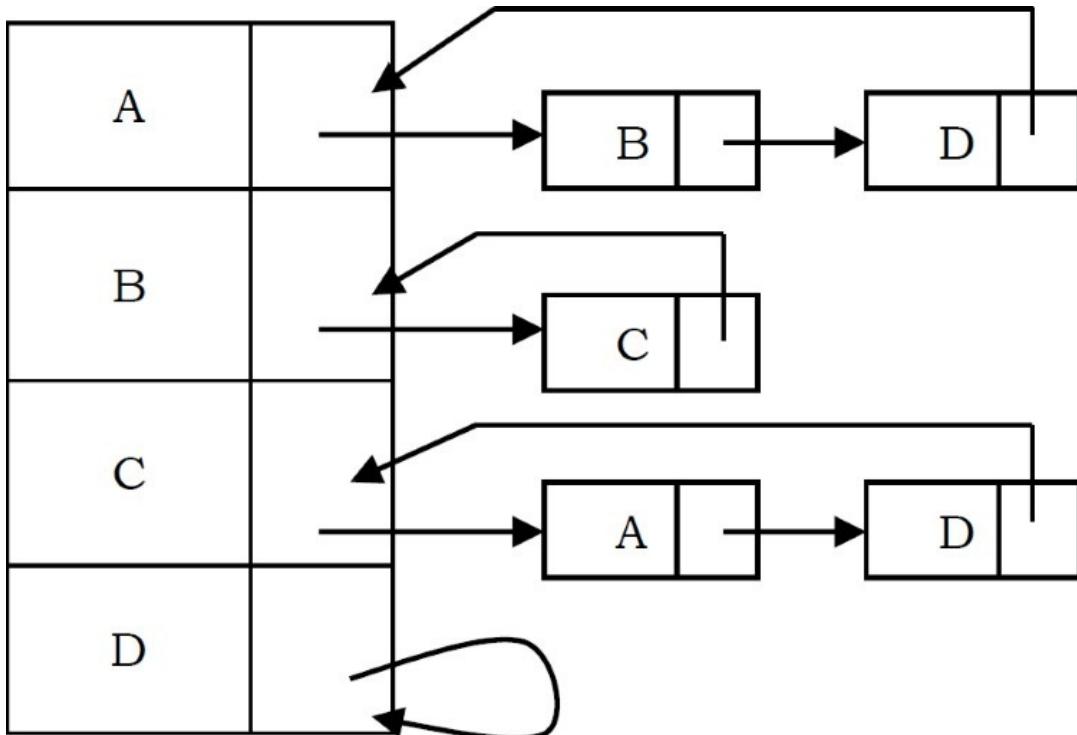
In this representation all the vertices connected to a vertex v are listed on an adjacency list for that vertex v . This can be easily implemented with linked lists. That means, for each vertex v we use a linked list and list nodes represents the connections between v and other vertices to which v has an edge.

The total number of linked lists is equal to the number of vertices in the graph. The graph ADT can be declared as:

```
struct Graph {  
    int V;  
    int E;  
    int *Adj; //head pointers to linked list  
};
```

Description

Considering the same example as that of the adjacency matrix, the adjacency list representation can be given as:



Since vertex A has an edge for B and D, we have added them in the adjacency list for A. The same is the case with other vertices as well.

```

//Nodes of the Linked List
struct ListNode {
    int vertexNumber;
    struct ListNode *next;
}

//This code creates a graph with adj list representation
struct Graph *adjListOfGraph() {
    int i, x, y;
    struct ListNode *temp;
    struct Graph *G = (struct Graph *) malloc(sizeof(struct Graph));
    if(!G) {
        printf("Memory Error");
        return;
    }
    scanf("Number of Vertices: %d, Number of Edges:%d", &G->V, &G->E);
    G->Adj = malloc(G->V * sizeof(struct ListNode));

    for(i = 0; i < G->V; i++) {
        G->Adj[i] = (struct ListNode *) malloc(sizeof(struct ListNode));
        G->Adj[i]->vertexNumber = i;
        G->Adj[i]->next = G->Adj[i];
    }
    for(i = 0; i < E; i++) {
        //Read an edge
        scanf("Reading Edge: %d %d", &x, &y);
        temp = (struct ListNode *) malloc(sizeof(struct ListNode));
        temp->vertexNumber = y;
        temp->next = G->Adj[x];
        G->Adj[x]->next = temp;
        temp = (struct ListNode *) malloc(sizeof(struct ListNode));
        temp->vertexNumber = y;
        temp->next = G->Adj[y];
        G->Adj[y]->next= temp;
    }
    return G;
}

```

For this representation, the order of edges in the input is *important*. This is because they determine the order of the vertices on the adjacency lists. The same graph can be represented in many different ways in an adjacency list. The order in which edges appear on the adjacency list affects the order in which edges are processed by algorithms.

Disadvantages of Adjacency Lists

Using adjacency list representation we cannot perform some operations efficiently. As an example, consider the case of deleting a node. In adjacency list representation, it is not enough if we simply delete a node from the list representation, if we delete a node from the adjacency list then that is enough. For each node on the adjacency list of that node specifies another vertex. We need to search other nodes linked list also for deleting it. This problem can be solved by linking the two list nodes that correspond to a particular edge and making the adjacency lists doubly linked. But all these extra links are risky to process.

Adjacency Set

It is very much similar to adjacency list but instead of using Linked lists, Disjoint Sets [Union-Find] are used. For more details refer to the [Disjoint Sets ADT](#) chapter.

Comparison of Graph Representations

Directed and undirected graphs are represented with the same structures. For directed graphs, everything is the same, except that each edge is represented just once. An edge from x to y is represented by a 1 value in $Adj[x][y]$ in the adjacency matrix, or by adding y on x 's adjacency list. For weighted graphs, everything is the same, except fill the adjacency matrix with weights instead of boolean values.

Representation	Space	Checking edge between v and w ?	Iterate over edges incident to v ?
List of edges	E	E	E
Adj Matrix	V^2	1	V
Adj List	$E + V$	$Degree(v)$	$Degree(v)$
Adj Set	$E + V$	$\log(Degree(v))$	$Degree(v)$

9.5 Graph Traversals

To solve problems on graphs, we need a mechanism for traversing the graphs. Graph traversal algorithms are also called *graph search* algorithms. Like trees traversal algorithms (Inorder, Preorder, Postorder and Level-Order traversals), graph search algorithms can be thought of as starting at some source vertex in a graph and “searching” the graph by going through the edges and marking the vertices. Now, we will discuss two such algorithms for traversing the graphs.

- Depth First Search [DFS]
- Breadth First Search [BFS]

Depth First Search [DFS]

DFS algorithm works in a manner similar to preorder traversal of the trees. Like preorder traversal, internally this algorithm also uses stack.

Let us consider the following example. Suppose a person is trapped inside a maze. To come out from that maze, the person visits each path and each intersection (in the worst case). Let us say the person uses two colors of paint to mark the intersections already passed. When discovering a new intersection, it is marked grey, and he continues to go deeper.

After reaching a “dead end” the person knows that there is no more unexplored path from the grey intersection, which now is completed, and he marks it with black. This “dead end” is either an intersection which has already been marked grey or black, or simply a path that does not lead to an intersection.

The intersections of the maze are the vertices and the paths between the intersections are the edges of the graph. The process of returning from the “dead end” is called *backtracking*. We are trying to go away from the starting vertex into the graph as deep as possible, until we have to backtrack to the preceding grey vertex. In DFS algorithm, we encounter the following types of edges.

Tree edge: encounter new vertex

Back edge: from descendent to ancestor

Forward edge: from ancestor to descendent

Cross edge: between a tree or subtrees

For most algorithms boolean classification, unvisited/visited is enough (for three color implementation refer to problems section). That means, for some problems we need to use three colors, but for our discussion two colors are enough.

false  Vertex is unvisited

true  Vertex is visited

Initially all vertices are marked unvisited (false). The DFS algorithm starts at a vertex u in the graph. By starting at vertex u it considers the edges from u to other vertices. If the edge leads to an already visited vertex, then backtrack to current vertex u . If an edge leads to an unvisited vertex, then go to that vertex and start processing from that vertex. That means the new vertex becomes the current vertex. Follow this process until we reach the dead-end. At this point start *backtracking*.

The process terminates when backtracking leads back to the start vertex. The algorithm based on this mechanism is given below: assume Visited[] is a global array.

```
int Visited[G→V];
void DFS(struct Graph *G, int u) {
    Visited[u] = 1;
    for( int v = 0; v < G→V; v++ ) {

        /* For example, if the adjacency matrix is used for representing the
           graph, then the condition to be used for finding unvisited adjacent
           vertex of u is: if( !Visited[v] && G→Adj[u][v] ) */

        for each unvisited adjacent node v of u {
            DFS(G, v);
        }
    }
}

void DFSTraversal(struct Graph *G) {
    for (int i = 0; i < G→V;i++)
        Visited[i]=0;

    //This loop is required if the graph has more than one component
    for (int i = 0; i < G→V;i++)
        if(!Visited[i])
            DFS(G, i);
}
```

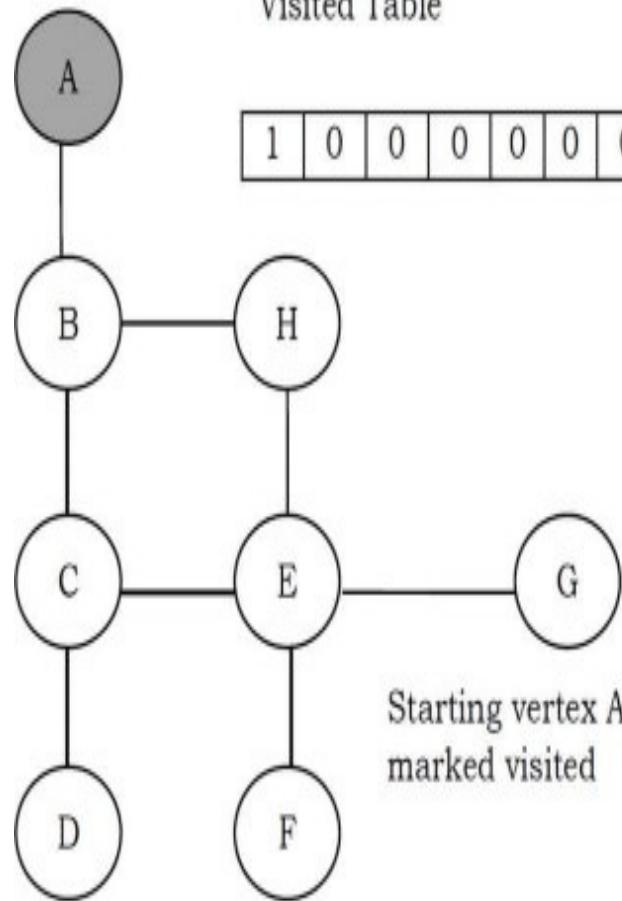
As an example, consider the following graph. We can see that sometimes an edge leads to an

already discovered vertex. These edges are called *back edges*, and the other edges are called *tree edges* because deleting the back edges from the graph generates a tree.

The final generated tree is called the DFS tree and the order in which the vertices are processed is called *DFS numbers* of the vertices. In the graph below, the gray color indicates that the vertex is visited (there is no other significance). We need to see when the Visited table is updated.

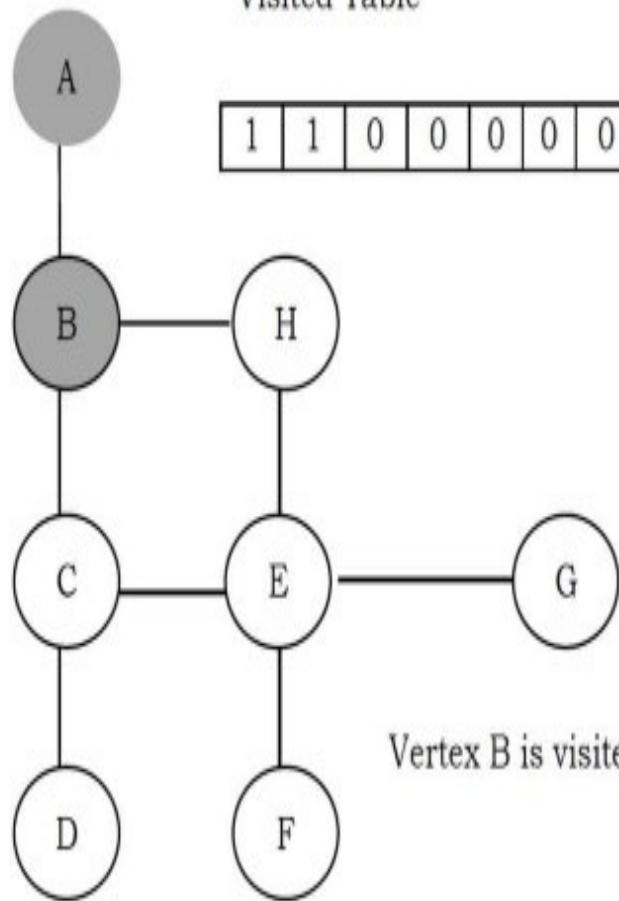
Visited Table

1	0	0	0	0	0	0	0
---	---	---	---	---	---	---	---



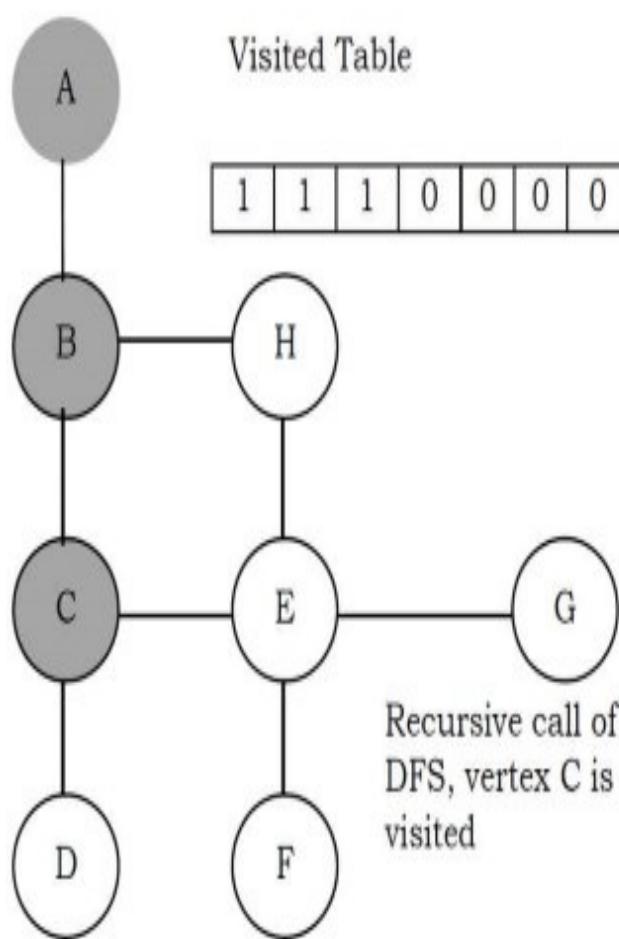
Visited Table

1	1	0	0	0	0	0	0
---	---	---	---	---	---	---	---



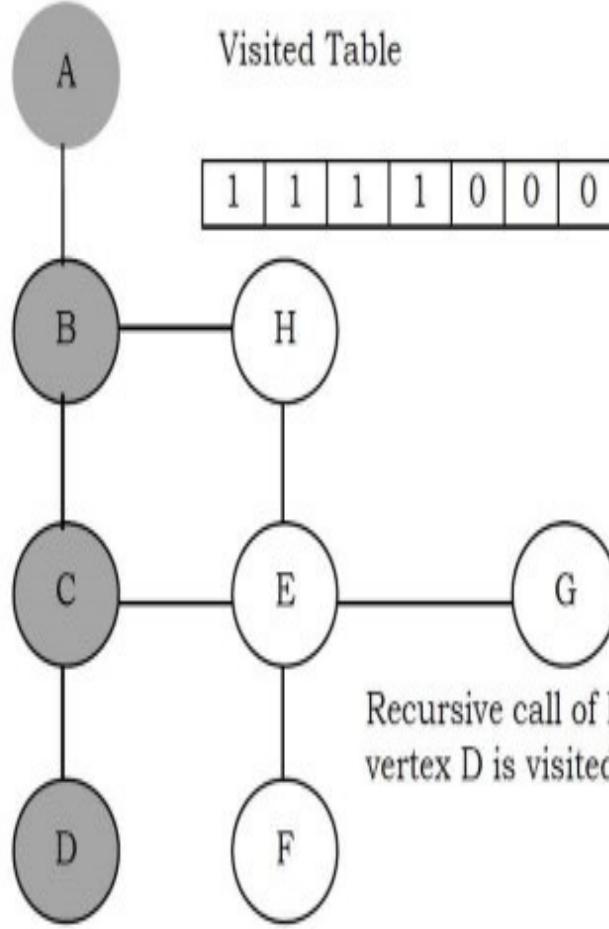
Visited Table

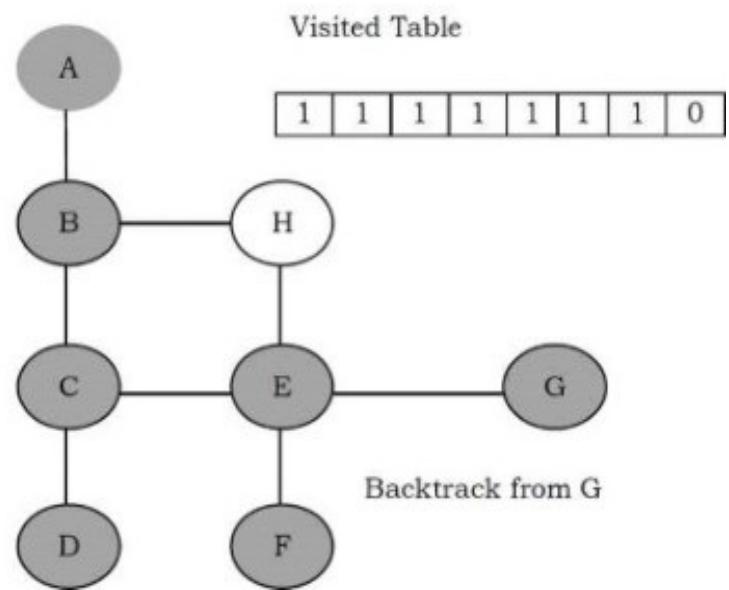
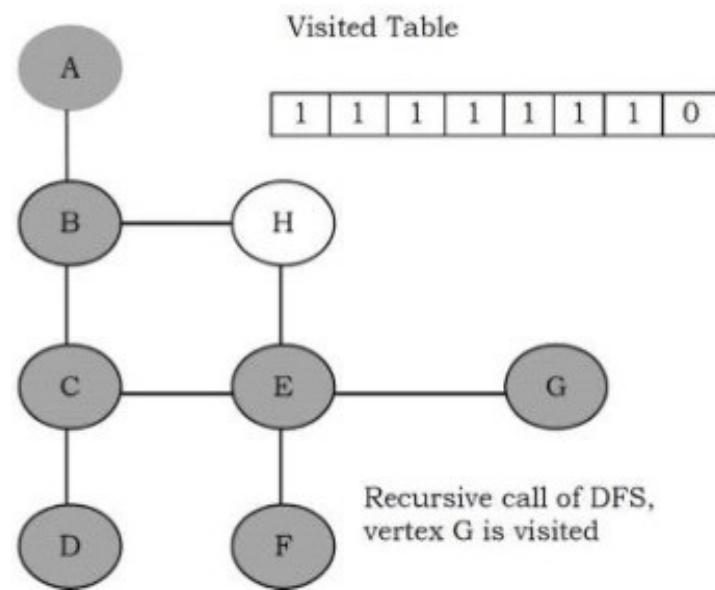
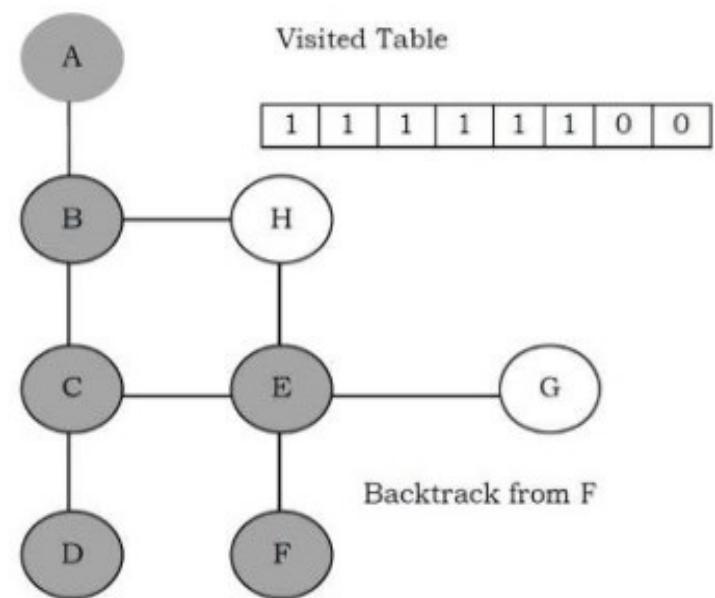
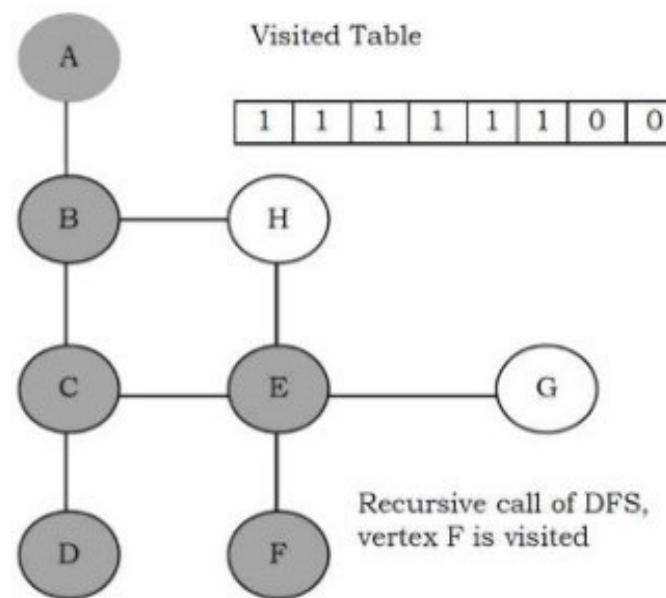
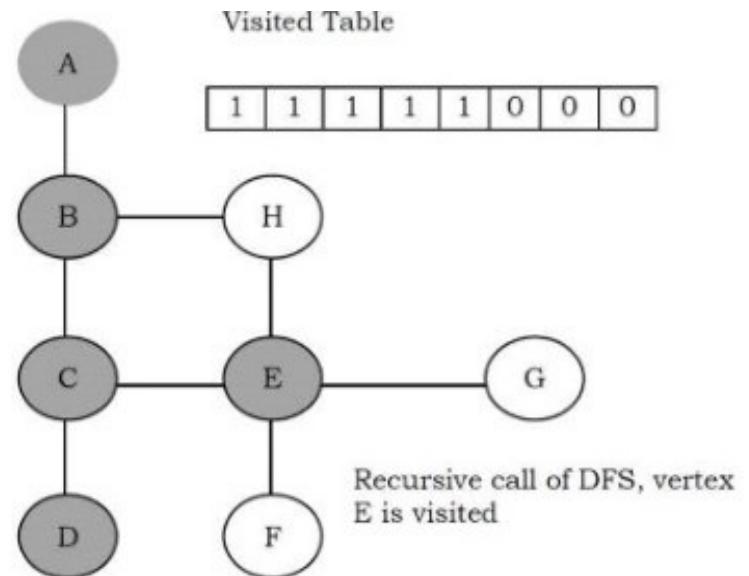
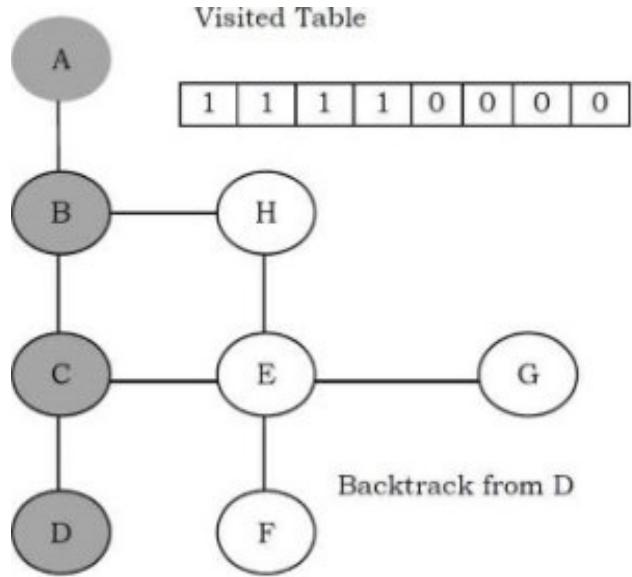
1	1	1	0	0	0	0	0
---	---	---	---	---	---	---	---

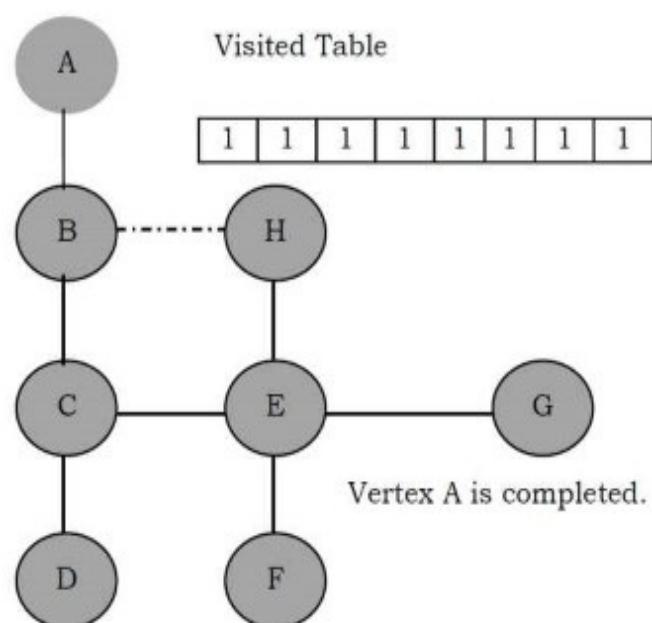
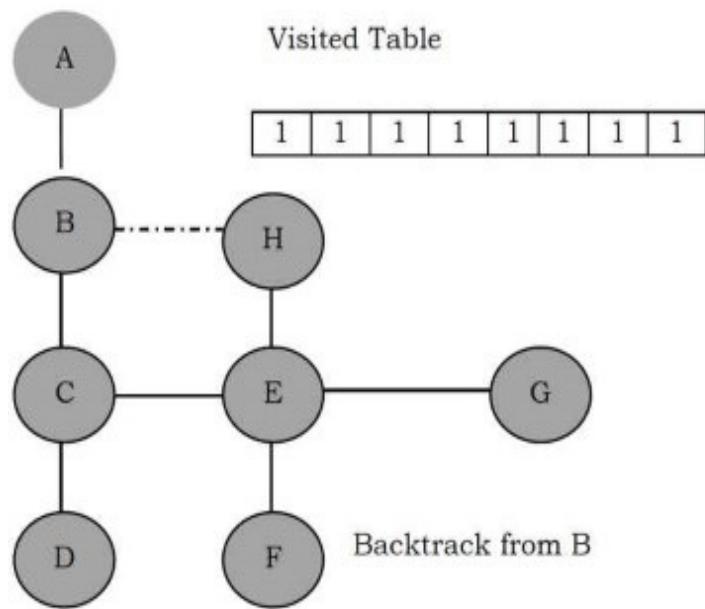
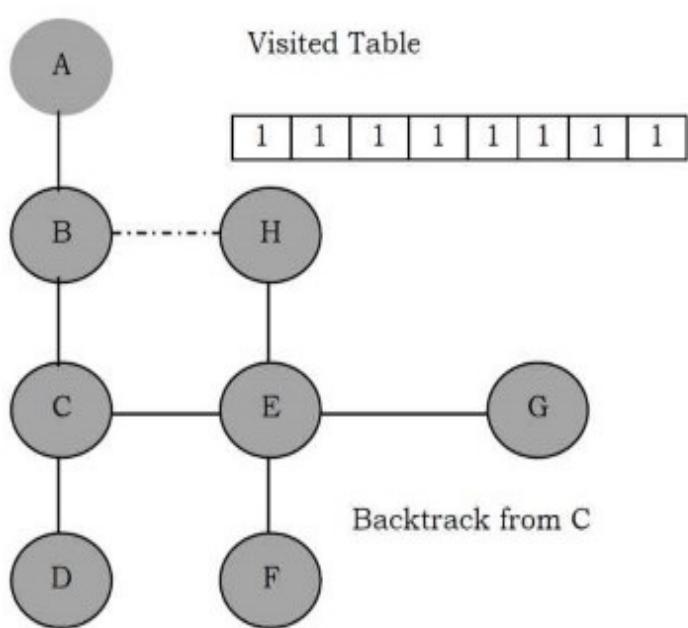
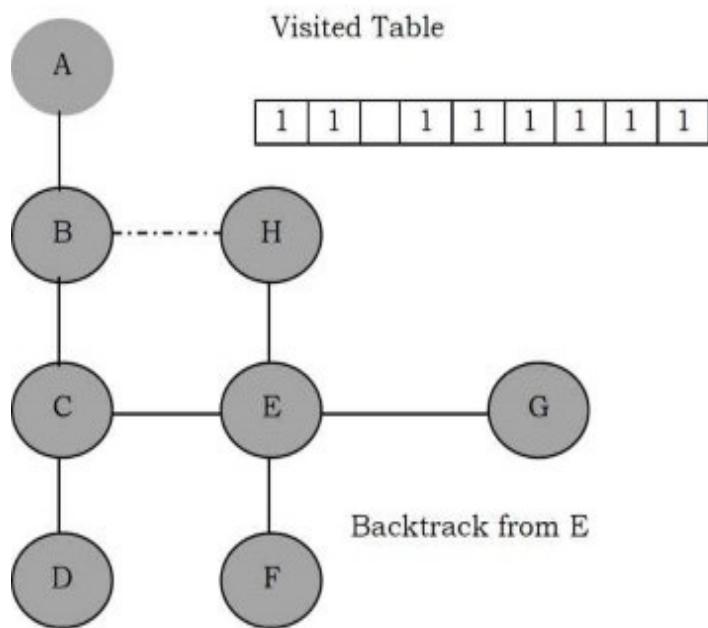
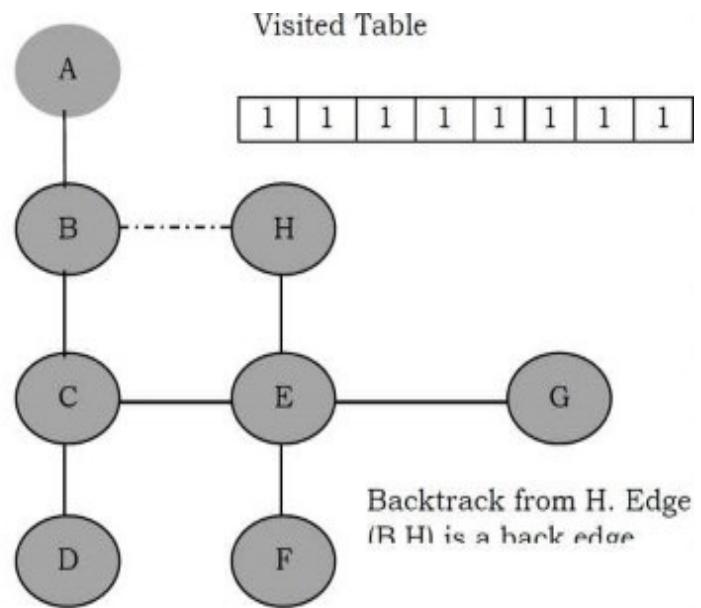
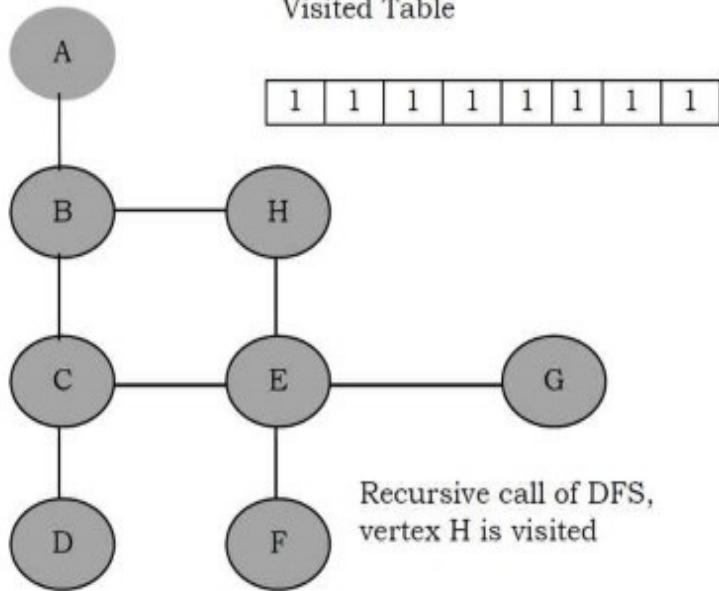


Visited Table

1	1	1	1	0	0	0	0
---	---	---	---	---	---	---	---







From the above diagrams, it can be seen that the DFS traversal creates a tree (without back edges) and we call such tree a *DFS tree*. The above algorithm works even if the given graph has connected components.

The time complexity of DFS is $O(V + E)$, if we use adjacency lists for representing the graphs. This is because we are starting at a vertex and processing the adjacent nodes only if they are not visited. Similarly, if an adjacency matrix is used for a graph representation, then all edges adjacent to a vertex can't be found efficiently, and this gives $O(V^2)$ complexity.

Applications of DFS

- Topological sorting
- Finding connected components
- Finding articulation points (cut vertices) of the graph
- Finding strongly connected components
- Solving puzzles such as mazes

For algorithms refer to *Problems Section*.

Breadth First Search [BFS]

The BFS algorithm works similar to *level – order* traversal of the trees. Like *level – order* traversal, BFS also uses queues. In fact, *level – order* traversal got inspired from BFS. BFS works level by level. Initially, BFS starts at a given vertex, which is at level 0. In the first stage it visits all vertices at level 1 (that means, vertices whose distance is 1 from the start vertex of the graph). In the second stage, it visits all vertices at the second level. These new vertices are the ones which are adjacent to level 1 vertices.

BFS continues this process until all the levels of the graph are completed. Generally *queue* data structure is used for storing the vertices of a level.

As similar to DFS, assume that initially all vertices are marked *unvisited (false)*. Vertices that have been processed and removed from the queue are marked *visited (true)*. We use a queue to represent the visited set as it will keep the vertices in the order of when they were first visited. The implementation for the above discussion can be given as:

```

void BFS(struct Graph *G, int u) {
    int v;
    struct Queue *Q = CreateQueue();
    EnQueue(Q, u);

    while(!IsEmptyQueue(Q)) {
        u = DeQueue(Q);

        Process u; //For example, print

        Visited[s]=1;

        /* For example, if the adjacency matrix is used for representing the graph,
        then the condition be used for finding unvisited adjacent vertex of u is:
        if( !Visited[v] && G->Adj[u][v] ) */

        for each unvisited adjacent node v of u {
            EnQueue(Q, v);
        }
    }
}

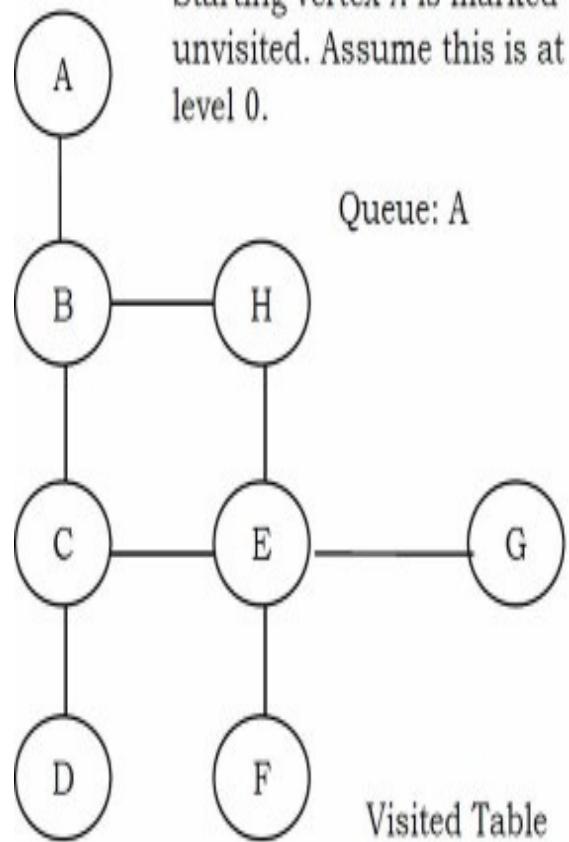
void BFSTraversal(struct Graph *G) {
    for (int i = 0; i < G->V; i++)
        Visited[i]=0;

    //This loop is required if the graph has more than one component
    for (int i = 0; i < G->V; i++)
        if(!Visited[i])
            BFS(G, i);
}

```

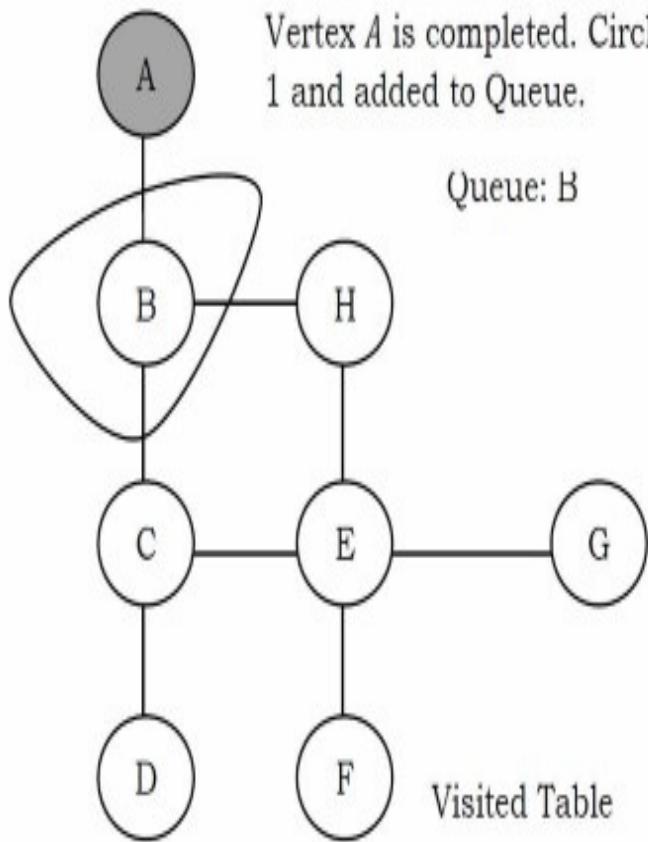
As an example, let us consider the same graph as that of the DFS example. The BFS traversal can be shown as:

Starting vertex A is marked unvisited. Assume this is at level 0.



0	0	0	0	0	0	0
---	---	---	---	---	---	---

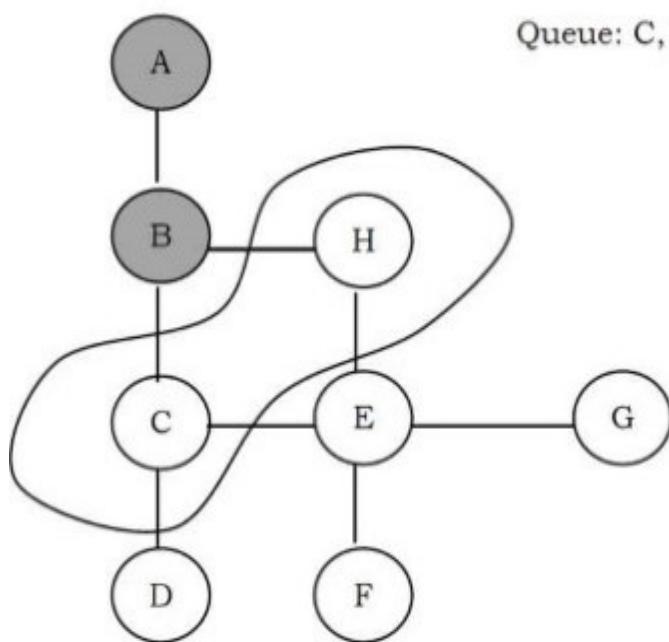
Vertex A is completed. Circled part is level 1 and added to Queue.



1	0	0	0	0	0	0
---	---	---	---	---	---	---

B is completed. Selected part is level 2 (add to Queue).

Queue: C, H

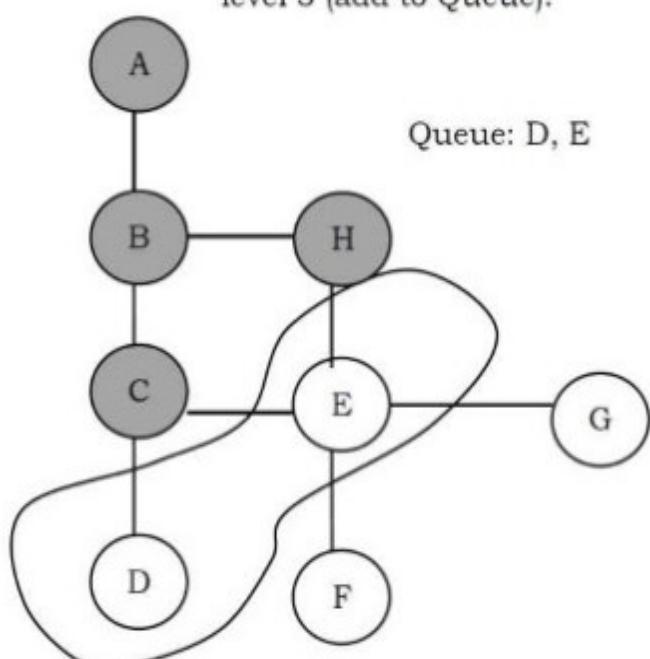


Visited Table

1	1	0	0	0	0	0
---	---	---	---	---	---	---

Vertices C and H are completed. Circled part is level 3 (add to Queue).

Queue: D, E

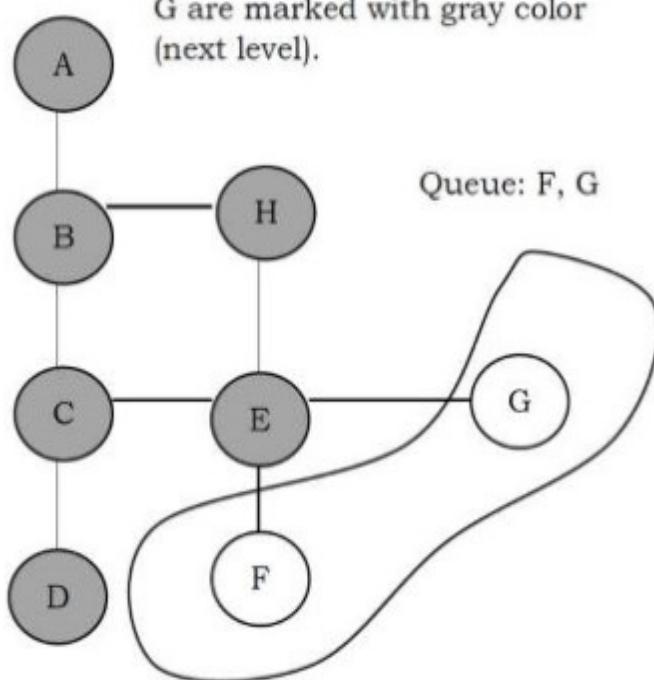


Visited Table

1	1	0	0	0	0	1
---	---	---	---	---	---	---

D and E are completed. F and G are marked with gray color (next level).

Queue: F, G

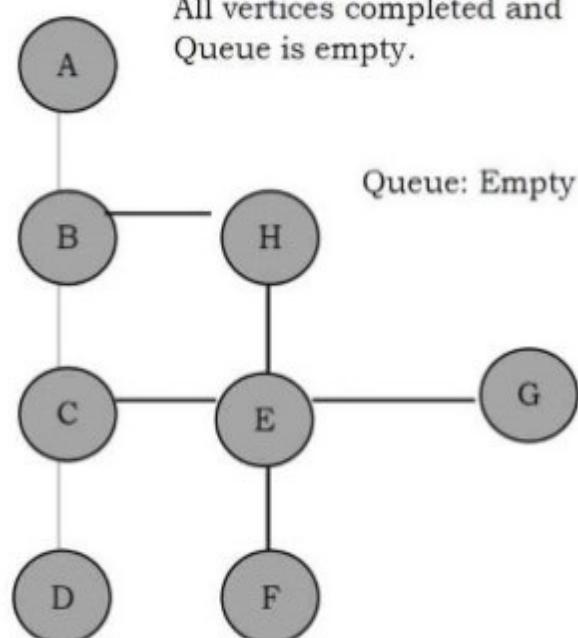


Visited Table

1	1	1	1	0	0	1
---	---	---	---	---	---	---

All vertices completed and Queue is empty.

Queue: Empty



Visited Table

1	1	1	1	1	1	1
---	---	---	---	---	---	---

Time complexity of BFS is $O(V + E)$, if we use adjacency lists for representing the graphs, and $O(V^2)$ for adjacency matrix representation.

Applications of BFS

- Finding all connected components in a graph
- Finding all nodes within one connected component
- Finding the shortest path between two nodes
- Testing a graph for bipartiteness

Comparing DFS and BFS

Comparing BFS and DFS, the big advantage of DFS is that it has much lower memory requirements than BFS because it's not required to store all of the child pointers at each level. Depending on the data and what we are looking for, either DFS or BFS can be advantageous. For example, in a family tree if we are looking for someone who's still alive and if we assume that person would be at the bottom of the tree, then DFS is a better choice. BFS would take a very long time to reach that last level.

The DFS algorithm finds the goal faster. Now, if we were looking for a family member who died a very long time ago, then that person would be closer to the top of the tree. In this case, BFS finds faster than DFS. So, the advantages of either vary depending on the data and what we are looking for.

DFS is related to preorder traversal of a tree. Like *preorder* traversal, DFS visits each node before its children. The BFS algorithm works similar to *level – order* traversal of the trees.

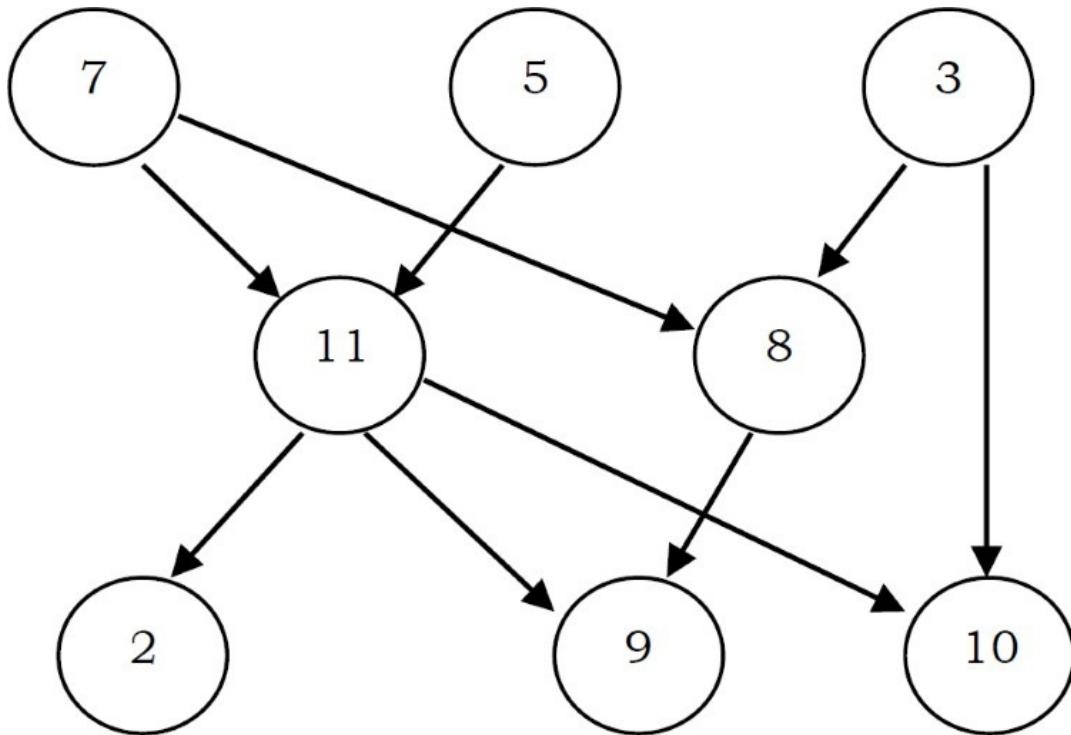
If someone asks whether DFS is better or BFS is better, the answer depends on the type of the problem that we are trying to solve. BFS visits each level one at a time, and if we know the solution we are searching for is at a low depth, then BFS is good. DFS is a better choice if the solution is at maximum depth. The below table shows the differences between DFS and BFS in terms of their applications.

Applications	DFS	BFS
Spanning forest, connected components, paths, cycles	Yes	Yes
Shortest paths		Yes
Minimal use of memory space	Yes	

9.6 Topological Sort

Topological sort is an ordering of vertices in a directed acyclic graph [DAG] in which each node comes before all nodes to which it has outgoing edges. As an example, consider the course prerequisite structure at universities. A directed edge (v,w) indicates that course v must be completed before course w . Topological ordering for this example is the sequence which does not violate the prerequisite requirement. Every DAG may have one or more topological orderings. Topological sort is not possible if the graph has a cycle, since for two vertices v and w on the cycle, v precedes w and w precedes v .

Topological sort has an interesting property. All pairs of consecutive vertices in the sorted order are connected by edges; then these edges form a directed Hamiltonian path [refer to *Problems Section*] in the DAG. If a Hamiltonian path exists, the topological sort order is unique. If a topological sort does not form a Hamiltonian path, DAG can have two or more topological orderings. In the graph below: 7, 5, 3, 11, 8, 2, 9, 10 and 3, 5, 7, 8, 11, 2, 9, 10 are both topological orderings.



Initially, *indegree* is computed for all vertices, starting with the vertices which are having indegree 0. That means consider the vertices which do not have any prerequisite. To keep track of vertices with indegree zero we can use a queue.

All vertices of indegree 0 are placed on queue. While the queue is not empty, a vertex v is removed, and all edges adjacent to v have their indegrees decremented. A vertex is put on the queue as soon as its indegree falls to 0. The topological ordering is the order in which the vertices DeQueue.

The time complexity of this algorithm is $O(|E| + |V|)$ if adjacency lists are used.

```

void TopologicalSort( struct Graph *G ) {
    struct Queue *Q;
    int counter;
    int v, w;
    Q = CreateQueue();
    counter = 0;
    for (v = 0; v < G->V; v++)
        if( indegree[v] == 0 )
            EnQueue( Q, v );
    while( !IsEmptyQueue( Q ) ) {
        v = DeQueue( Q );
        topologicalOrder[v] = ++counter;
        for each w adjacent to v
            if( --indegree[w] == 0 )
                EnQueue ( Q, w );
    }
    if( counter != G->V)
        printf("Graph has cycle");
    DeleteQueue( Q );
}

```

Total running time of topological sort is $O(V + E)$.

Note: The Topological sorting problem can be solved with DFS. Refer to the *Problems Section* for the algorithm.

Applications of Topological Sorting

- Representing course prerequisites
- Detecting deadlocks
- Pipeline of computing jobs
- Checking for symbolic link loop
- Evaluating formulae in spreadsheet

9.7 Shortest Path Algorithms

Let us consider the other important problem of a graph. Given a graph $G = (V, E)$ and a

distinguished vertex s , we need to find the shortest path from s to every other vertex in G . There are variations in the shortest path algorithms which depend on the type of the input graph and are given below.

Variations of Shortest Path Algorithms

- | |
|---|
| Shortest path in unweighted graph |
| Shortest path in weighted graph |
| Shortest path in weighted graph with negative edges |

Applications of Shortest Path Algorithms

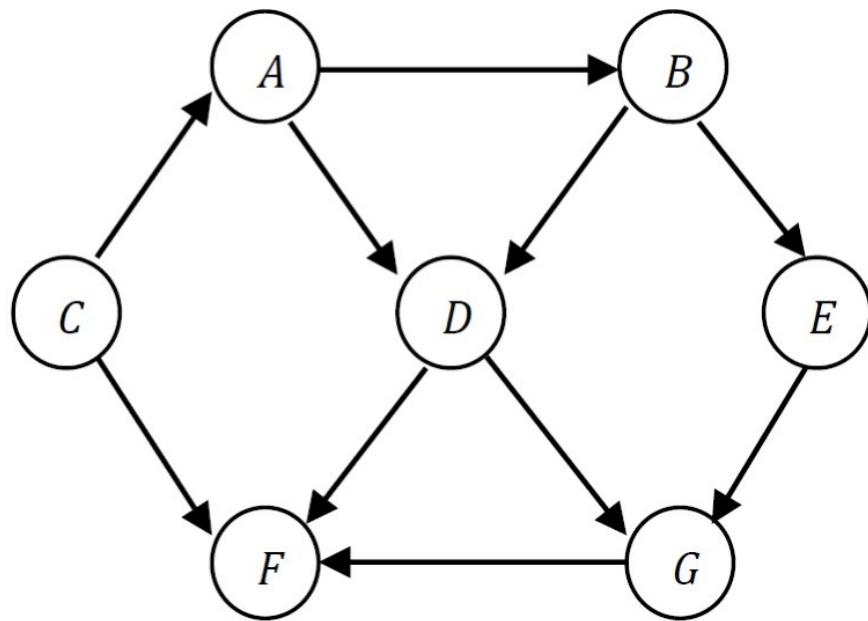
- Finding fastest way to go from one place to another
- Finding cheapest way to fly/send data from one city to another

Shortest Path in Unweighted Graph

Let s be the input vertex from which we want to find the shortest path to all other vertices. Unweighted graph is a special case of the weighted shortest-path problem, with all edges a weight of 1. The algorithm is similar to BFS and we need to use the following data structures:

- A distance table with three columns (each row corresponds to a vertex):
 - Distance from source vertex.
 - Path – contains the name of the vertex through which we get the shortest distance.
- A queue is used to implement breadth-first search. It contains vertices whose distance from the source node has been computed and their adjacent vertices are to be examined.

As an example, consider the following graph and its adjacency list representation.



The adjacency list for this graph is:

A: $B \rightarrow D$
B: $D \rightarrow E$
C: $A \rightarrow F$
D: $F \rightarrow G$
E: G
F: —
G: F

Let $s = C$. The distance from C to C is 0. Initially, distances to all other nodes are not computed, and we initialize the second column in the distance table for all vertices (except C) with -1 as below.

Vertex	Distance[v]	Previous vertex which gave Distance[v]
A	-1	-
B	-1	-
C	0	-
D	-1	-
E	-1	-
F	-1	-
G	-1	-

Algorithm

```

void UnweightedShortestPath(struct Graph *G, int s) {
    struct Queue *Q = CreateQueue();
    int v, w;
    EnQueue(Q, s);
    for (int i = 0; i < G->V; i++)
        Distance[i] = -1;
    Distance[s] = 0;
    while (!IsEmptyQueue(Q)) {
        v = DeQueue(Q);
        for each w adjacent to v
            if(Distance[w] == -1) {
                Distance[w] = Distance[v] + 1;
                Path[w] = v;
                EnQueue(Q, w); ← Each vertex EnQueue'd at most once
            }
        }
    DeleteQueue(Q);
}

```

Each vertex examined at most once

← Each vertex EnQueue'd at most once

Running time: $O(|E| + |V|)$, if adjacency lists are used. In for loop, we are checking the outgoing edges for a given vertex and the sum of all examined edges in the while loop is equal to the number of edges which gives $O(|E|)$.

If we use matrix representation the complexity is $O(|V|^2)$, because we need to read an entire row in the matrix of length $|V|$ in order to find the adjacent vertices for a given vertex.

Shortest path in Weighted Graph [Dijkstra's]

A famous solution for the shortest path problem was developed by *Dijkstra*. *Dijkstra*'s algorithm is a generalization of the BFS algorithm. The regular BFS algorithm cannot solve the shortest path problem as it cannot guarantee that the vertex at the front of the queue is the vertex closest to source s .

Before going to code let us understand how the algorithm works. As in unweighted shortest path algorithm, here too we use the distance table. The algorithm works by keeping the shortest distance of vertex v from the source in the *Distance* table. The value $Distance[v]$ holds the distance from s to v . The shortest distance of the source to itself is zero. The *Distance* table for all other vertices is set to -1 to indicate that those vertices are not already processed.

Vertex	Distance[v]	Previous vertex which gave Distance[v]
A	-1	-
B	-1	-
C	0	-
D	-1	-
E	-1	-
F	-1	-
G	-1	-

After the algorithm finishes, the *Distance* table will have the shortest distance from source s to each other vertex v. To simplify the understanding of *Dijkstra's* algorithm, let us assume that the given vertices are maintained in two sets. Initially the first set contains only the source element and the second set contains all the remaining elements. After the k^{th} iteration, the first set contains k vertices which are closest to the source. These k vertices are the ones for which we have already computed the shortest distances from source.

Notes on Dijkstra's Algorithm

- It uses greedy method: Always pick the next closest vertex to the source.
- It uses priority queue to store unvisited vertices by distance from s.
- It does not work with negative weights.

Difference between Unweighted Shortest Path and Dijkstra's Algorithm

- 1) To represent weights in the adjacency list, each vertex contains the weights of the edges (in addition to their identifier).
- 2) Instead of ordinary queue we use priority queue [distances are the priorities] and the vertex with the smallest distance is selected for processing.
- 3) The distance to a vertex is calculated by the sum of the weights of the edges on the path from the source to that vertex.
- 4) We update the distances in case the newly computed distance is smaller than the old distance which we have already computed.

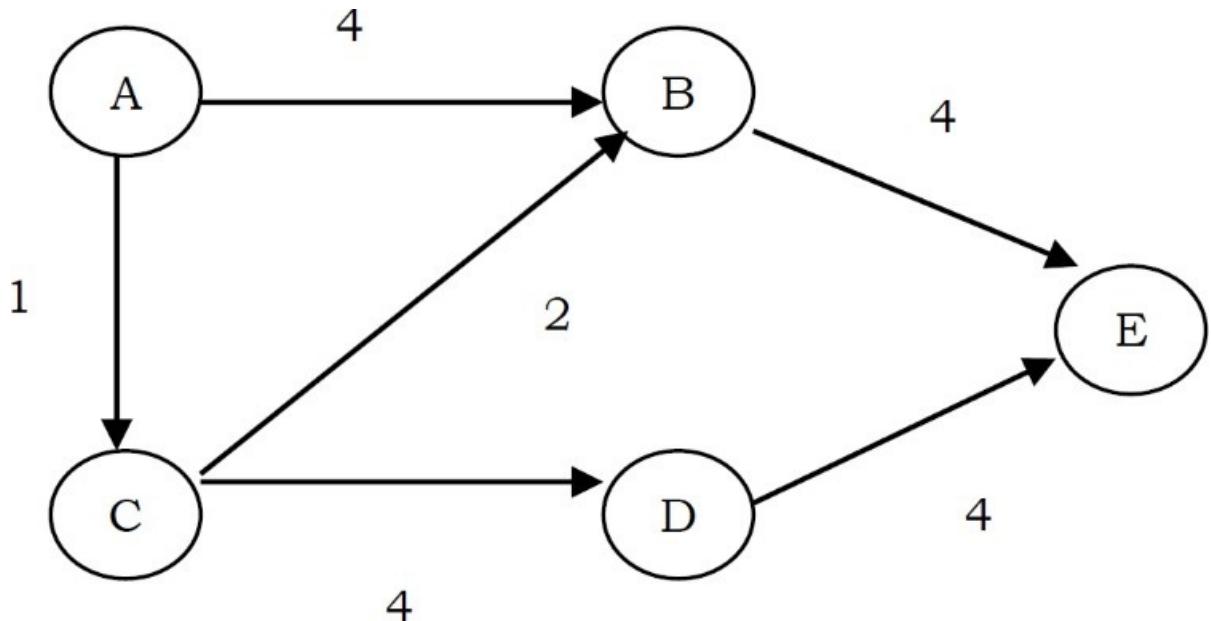
```

void Dijkstra(struct Graph *G, int s) {
    struct PriorityQueue *PQ = CreatePriorityQueue();
    int v, w;
    EnQueue(PQ, s);
    for (int i = 0; i < G->V; i++)
        Distance[i] = -1;
    Distance[s] = 0;
    while (!IsEmptyQueue(PQ)) {
        v = DeleteMin(PQ);
        for all adjacent vertices w of v {
            Compute new distance d = Distance[v] + weight[v][w];
            if(Distance[w] == -1) {
                Distance[w] = new distance d;
                Insert w in the priority queue with priority d
                Path[w] = v;
            }
            if(Distance[w] > new distance d) {
                Distance[w] = new distance d;
                Update priority of vertex w to be d;
                Path[w] = v;
            }
        }
    }
}

```

The above algorithm can be better understood through an example, which will explain each step that is taken and how *Distance* is calculated. The weighted graph below has 5 vertices from A – E.

The value between the two vertices is known as the edge cost between two vertices. For example, the edge cost between A and C is 1. Dijkstra's algorithm can be used to find the shortest path from source A to the remaining vertices in the graph.

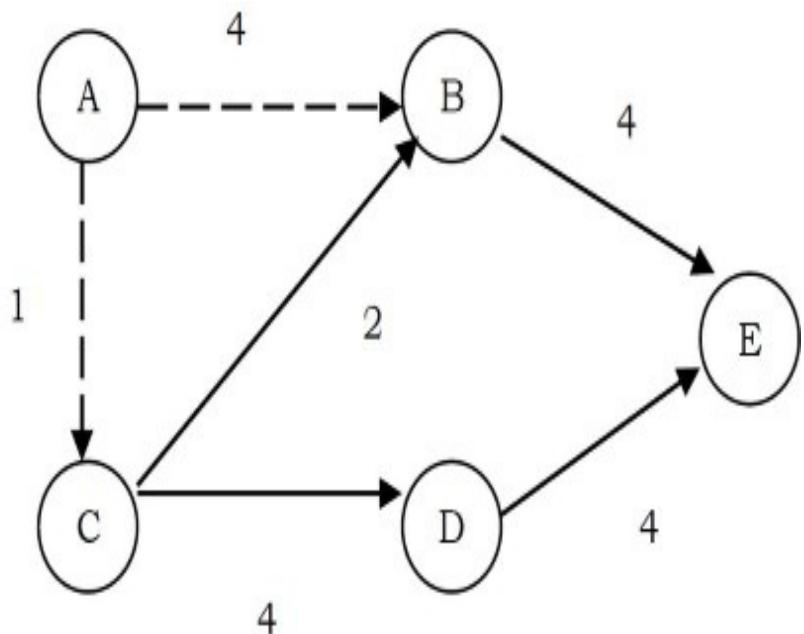


Initially the *Distance* table is:

Vertex	Distance[v]	Previous vertex which gave Distance[v]
A	0	-
B	-1	-
C	-1	-
D	-1	-
E	-1	-

After the first step, from vertex A, we can reach B and C. So, in the *Distance* table we update the reachability of B and C with their costs and the same is shown below.

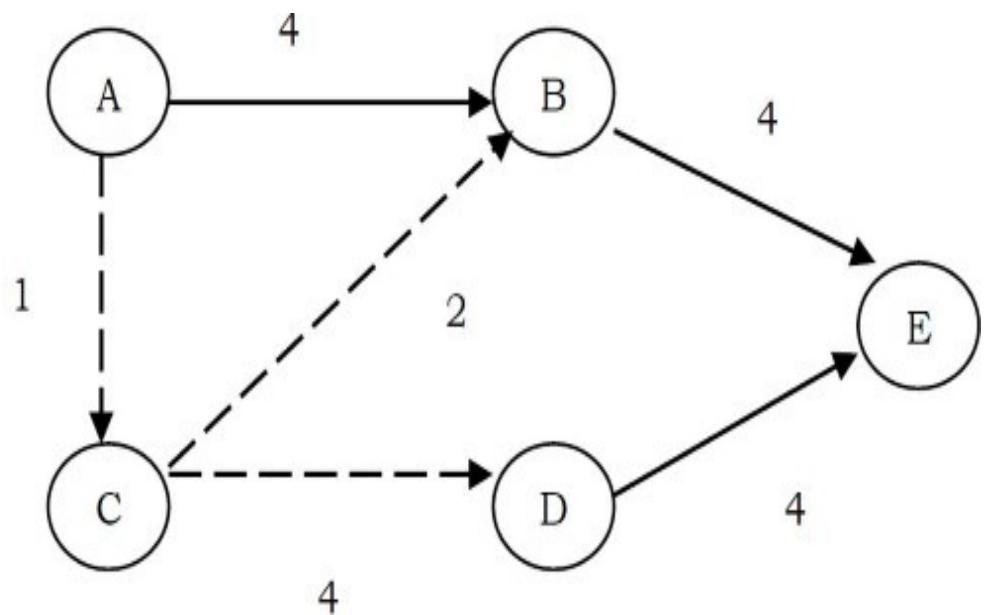
A	0	-
B	4	A
C	1	A
D	-1	-
E	-1	-



Shortest path from B,C from A

Now, let us select the minimum distance among all. The minimum distance vertex is C. That means, we have to reach other vertices from these two vertices (A and C). For example, B can be reached from A and also from C. In this case we have to select the one which gives the lowest cost. Since reaching B through C is giving the minimum cost (1 + 2), we update the *Distance* table for vertex B with cost 3 and the vertex from which we got this cost as C.

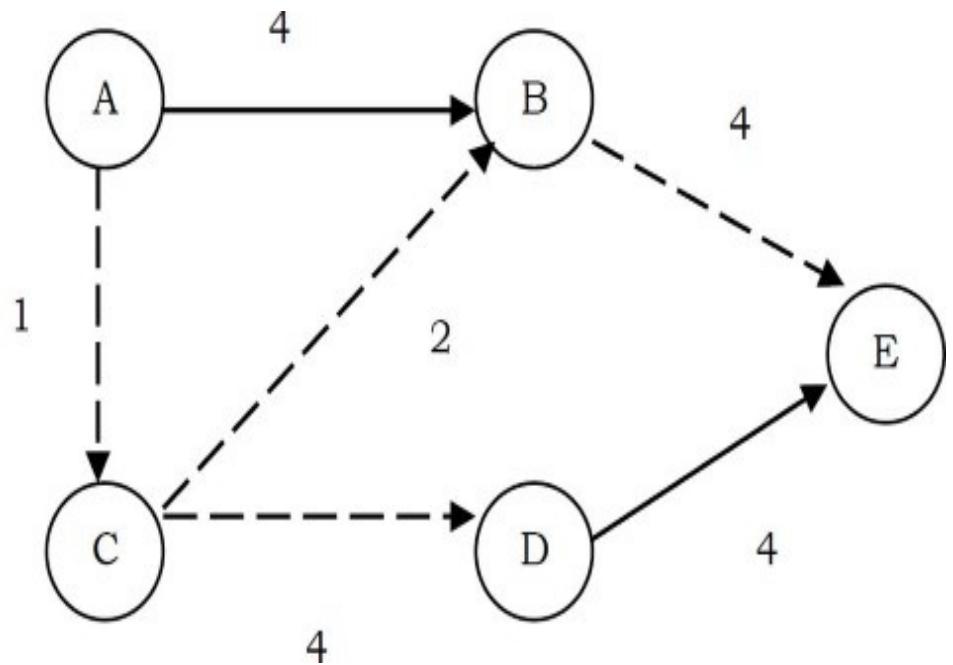
A	0	-
B	3	C
C	1	A
D	5	C
E	-1	-



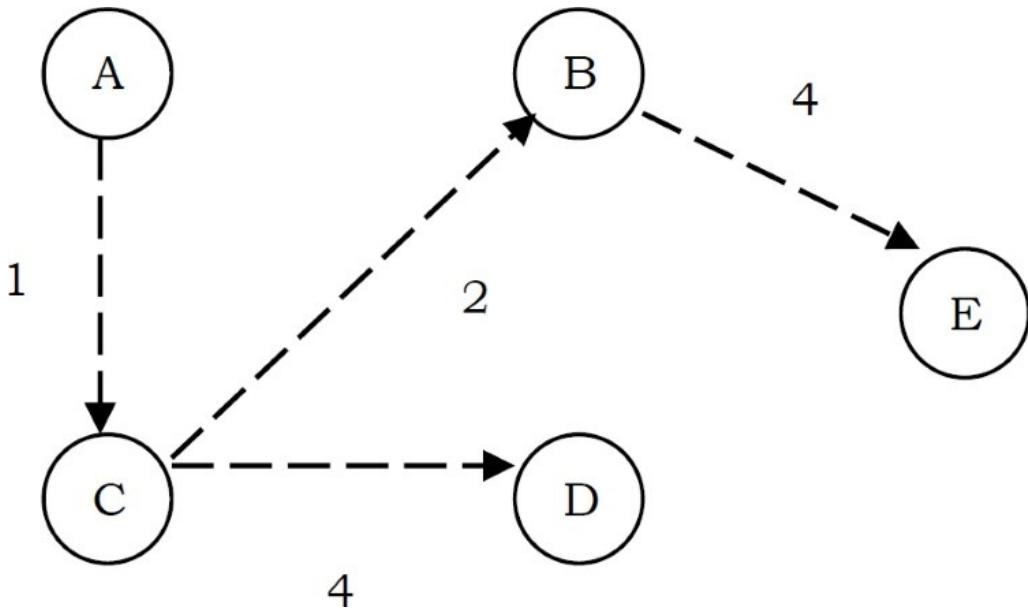
Shortest path to B,D using C as intermediate vertex

The only vertex remaining is E. To reach E, we have to see all the paths through which we can reach E and select the one which gives the minimum cost. We can see that if we use B as the intermediate vertex through C we get the minimum cost.

A	0	-
B	3	C
C	1	A
D	5	C
E	7	B



The final minimum cost tree which Dijkstra's algorithm generates is:



Performance

In Dijkstra's algorithm, the efficiency depends on the number of DeleteMins (V DeleteMins) and updates for priority queues (E updates) that are used. If a *standard binary heap* is used then the complexity is $O(E \log V)$.

The term $E \log V$ comes from E updates (each update takes $\log V$) for the standard heap. If the set used is an array then the complexity is $O(E + V^2)$.

Disadvantages of Dijkstra's Algorithm

- As discussed above, the major disadvantage of the algorithm is that it does a blind search, thereby wasting time and necessary resources.
- Another disadvantage is that it cannot handle negative edges. This leads to acyclic graphs and most often cannot obtain the right shortest path.

Relatives of Dijkstra's Algorithm

- The *Bellman-Ford* algorithm computes single-source shortest paths in a weighted digraph. It uses the same concept as that of *Dijkstra*'s algorithm but can handle negative edges as well. It has more running time than *Dijkstra*'s algorithm.
- Prim's algorithm finds a minimum spanning tree for a connected weighted graph. It implies that a subset of edges that form a tree where the total weight of all the edges in the tree is minimized.

Bellman-Ford Algorithm

If the graph has negative edge costs, then *Dijkstra*'s algorithm does not work. The problem is that once a vertex u is declared known, it is possible that from some other, unknown vertex v there is a path back to u that is very negative. In such a case, taking a path from s to v back to u is better than going from s to u without using v . A combination of *Dijkstra*'s algorithm and unweighted algorithms will solve the problem. Initialize the queue with s . Then, at each stage, we *DeQueue* a vertex v . We find all vertices W adjacent to v such that,

$$\text{distance to } v + \text{weight } (v,w) < \text{old distance to } w$$

We update w old distance and path, and place w on a queue if it is not already there. A bit can be set for each vertex to indicate presence in the queue. We repeat the process until the queue is empty.

```

void BellmanFordAlgorithm(struct Graph *G, int s) {
    struct Queue *Q = CreateQueue();
    int v, w;
    EnQueue(Q, s);
    Distance[s] = 0;           // assume the Distance table is filled with INT_MAX
    while (!IsEmptyQueue(Q)) {
        v = DeQueue(Q);
        for all adjacent vertices w of v {
            Compute new distance d= Distance[v] + weight[v][w];
            if(old distance to w > new distance d ) {
                Distance[w] = (distance to v) + weight[v][w];
                Path[w] = v;
                if(w is there in queue)
                    EnQueue(Q, w)
            }
        }
    }
}

```

This algorithm works if there are no negative-cost cycles. Each vertex can DeQueue at most $|V|$ times, so the running time is $O(|E| \cdot |V|)$ if adjacency lists are used.

Overview of Shortest Path Algorithms

Shortest path in unweighted graph [<i>Modified BFS</i>]	$O(E + V)$
Shortest path in weighted graph [<i>Dijkstra's</i>]	$O(E \log V)$
Shortest path in weighted graph with negative edges [<i>Bellman – Ford</i>]	$O(E \cdot V)$
Shortest path in weighted acyclic graph	$O(E + V)$

9.8 Minimal Spanning Tree

The *Spanning tree* of a graph is a subgraph that contains all the vertices and is also a tree. A graph may have many spanning trees. As an example, consider a graph with 4 vertices as shown below. Let us assume that the corners of the graph are vertices.



For this simple graph, we can have multiple spanning trees as shown below.



The algorithm we will discuss now is *minimum spanning tree* in an undirected graph. We assume that the given graphs are weighted graphs. If the graphs are unweighted graphs then we can still use the weighted graph algorithms by treating all weights as equal. A *minimum spanning tree* of an undirected graph G is a tree formed from graph edges that connect all the vertices of G with minimum total cost (weights). A minimum spanning tree exists only if the graph is connected. There are two famous algorithms for this problem:

- *Prim's Algorithm*
- *Kruskal's Algorithm*

Prim's Algorithm

Prim's algorithm is almost the same as Dijkstra's algorithm. As in Dijkstra's algorithm, in Prim's algorithm we keep the values *distance* and *paths* in the distance table. The only exception is that since the definition of *distance* is different, the updating statement also changes a little. The update statement is simpler than before.

```

void Prims(struct Graph *G, int s) {
    struct PriorityQueue *PQ = CreatePriorityQueue();
    int v, w;
    EnQueue(PQ, s);
    Distance[s] = 0;           // assume the Distance table is filled with -1
    while (!IsEmptyQueue(PQ)) {
        v = DeleteMin(PQ);
        for all adjacent vertices w of v {
            Compute new distance d= Distance[v] + weight[v][w];
            if(Distance[w] == -1) {
                Distance[w] = weight[v][w];
                Insert w in the priority queue with priority d
                Path[w] = v;
            }
            if(Distance[w] > new distance d) {
                Distance[w] = weight[v][w];
                Update priority of vertex w to be d;
                Path[w] = v;
            }
        }
    }
}

```

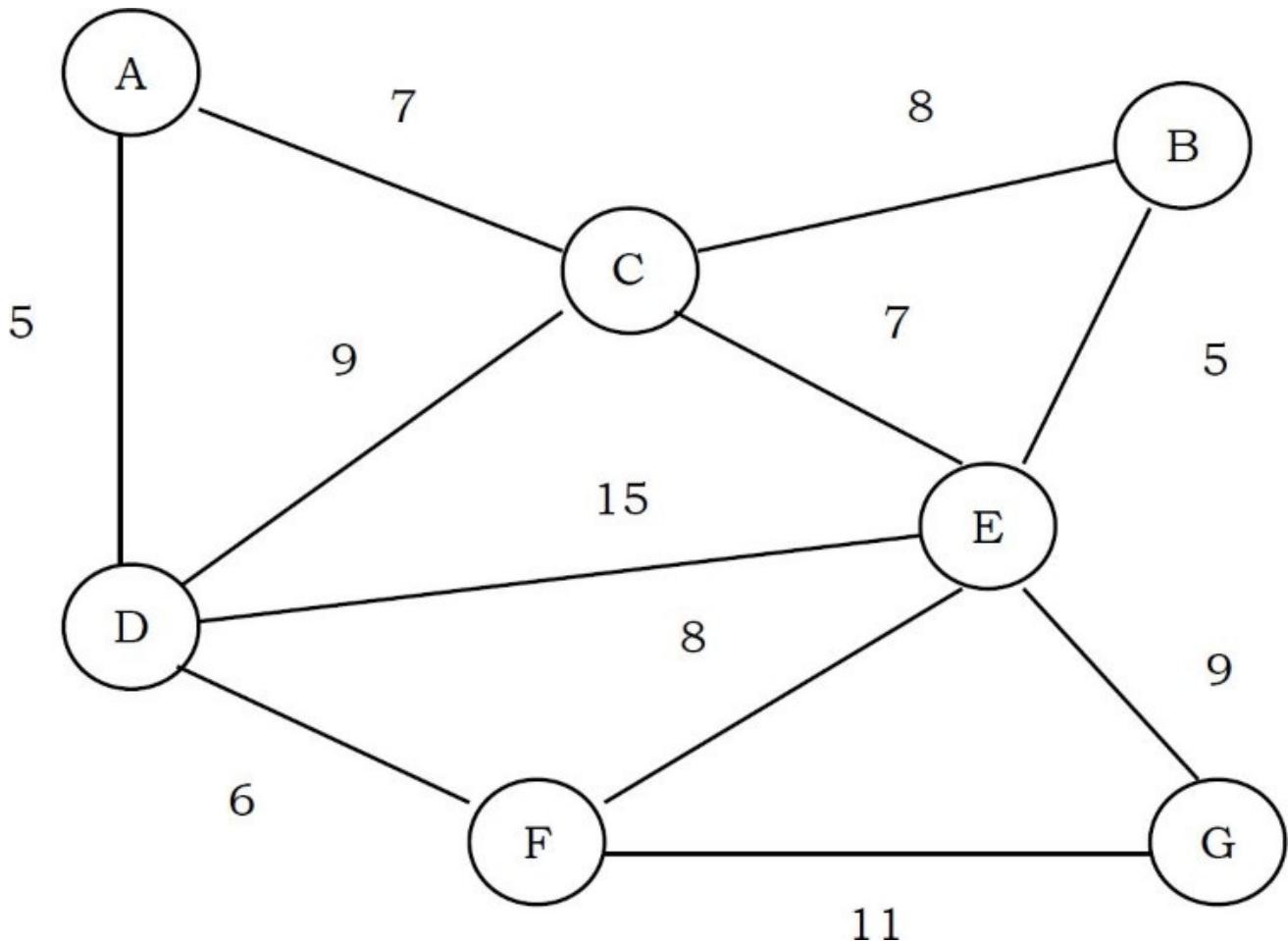
The entire implementation of this algorithm is identical to that of Dijkstra's algorithm. The running time is $O(|V|^2)$ without heaps [good for dense graphs], and $O(E \log V)$ using binary heaps [good for sparse graphs].

Kruskal's Algorithm

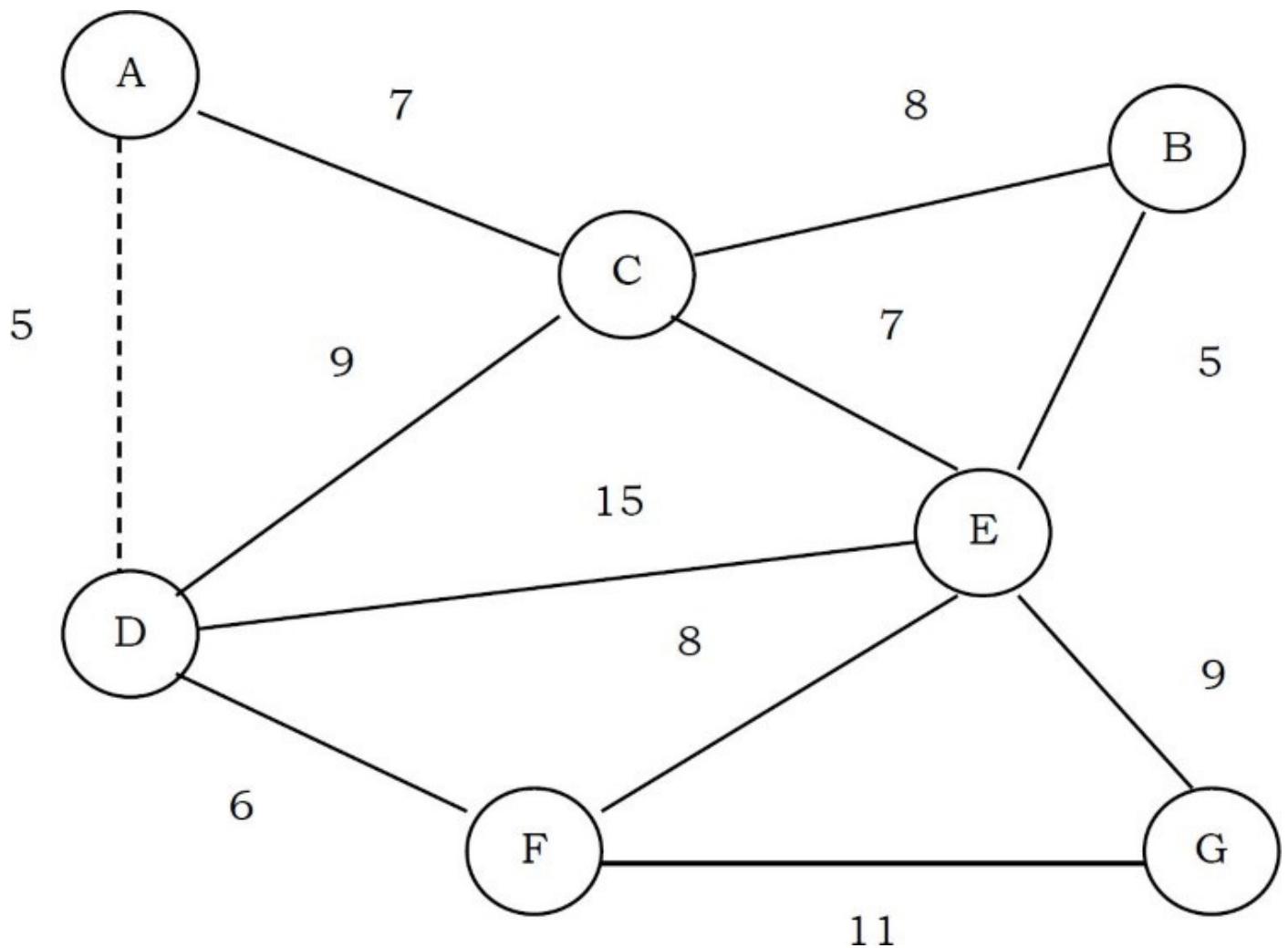
The algorithm starts with V different trees (V is the vertices in the graph). While constructing the minimum spanning tree, every time Kruskal's algorithm selects an edge that has minimum weight and then adds that edge if it doesn't create a cycle. So, initially, there are $|V|$ single-node trees in the forest. Adding an edge merges two trees into one. When the algorithm is completed, there will be only one tree, and that is the minimum spanning tree. There are two ways of implementing Kruskal's algorithm:

- By using Disjoint Sets: Using UNION and FIND operations
- By using Priority Queues: Maintains weights in priority queue

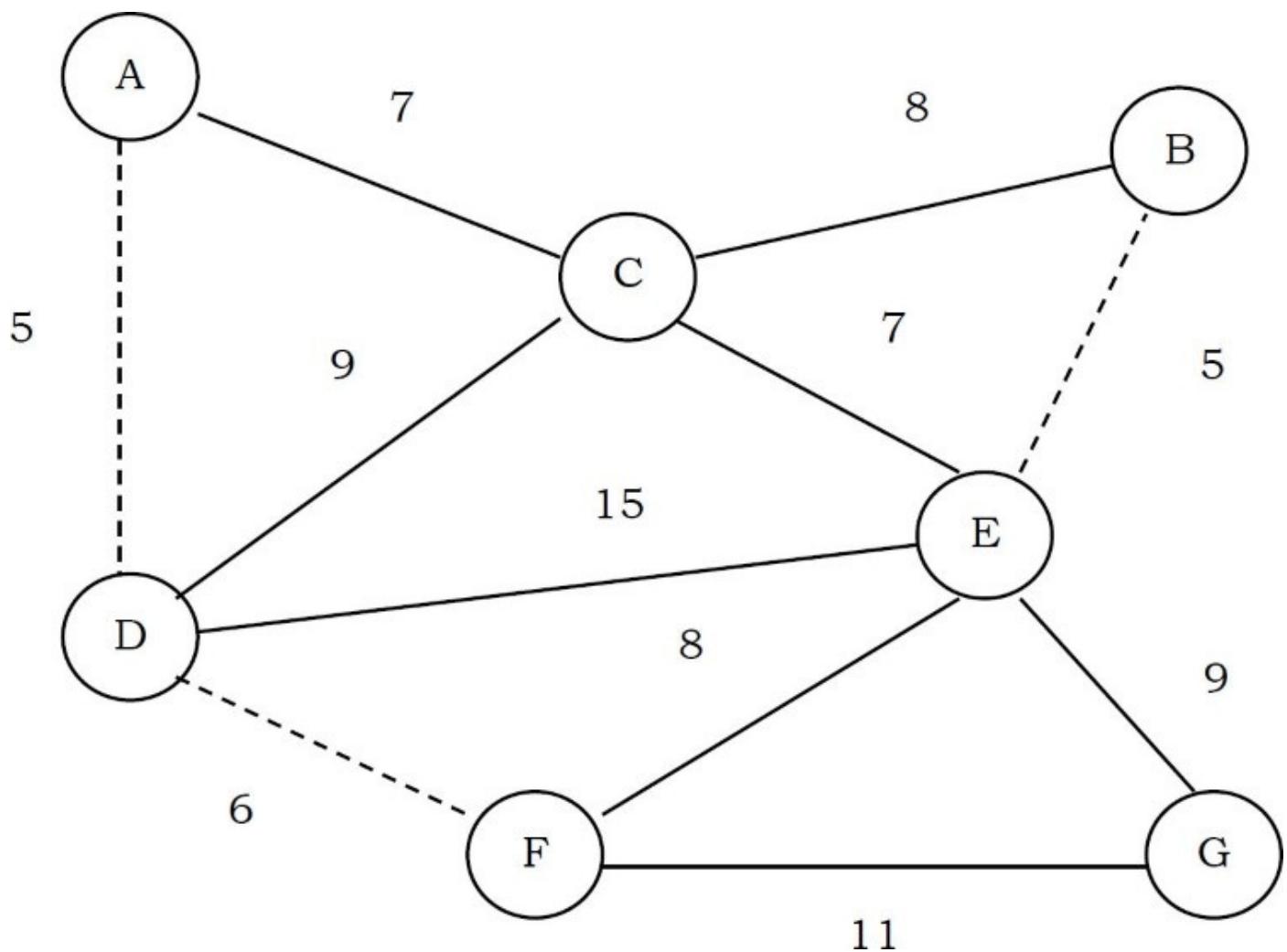
The appropriate data structure is the UNION/FIND algorithm [for implementing forests]. Two vertices belong to the same set if and only if they are connected in the current spanning forest. Each vertex is initially in its own set. If u and v are in the same set, the edge is rejected because it forms a cycle. Otherwise, the edge is accepted, and a UNION is performed on the two sets containing u and v . As an example, consider the following graph (the edges show the weights).



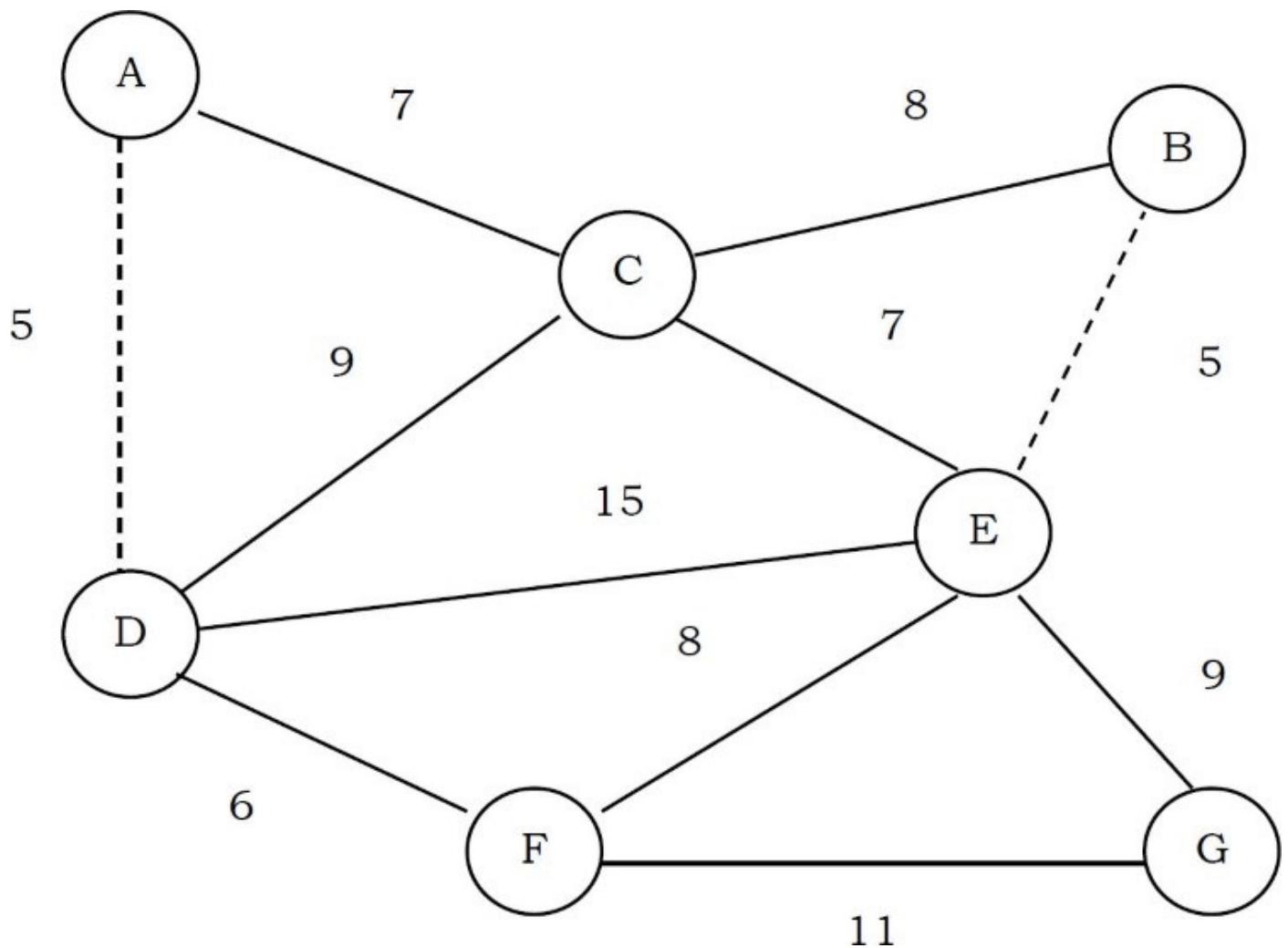
Now let us perform Kruskal's algorithm on this graph. We always select the edge which has minimum weight.



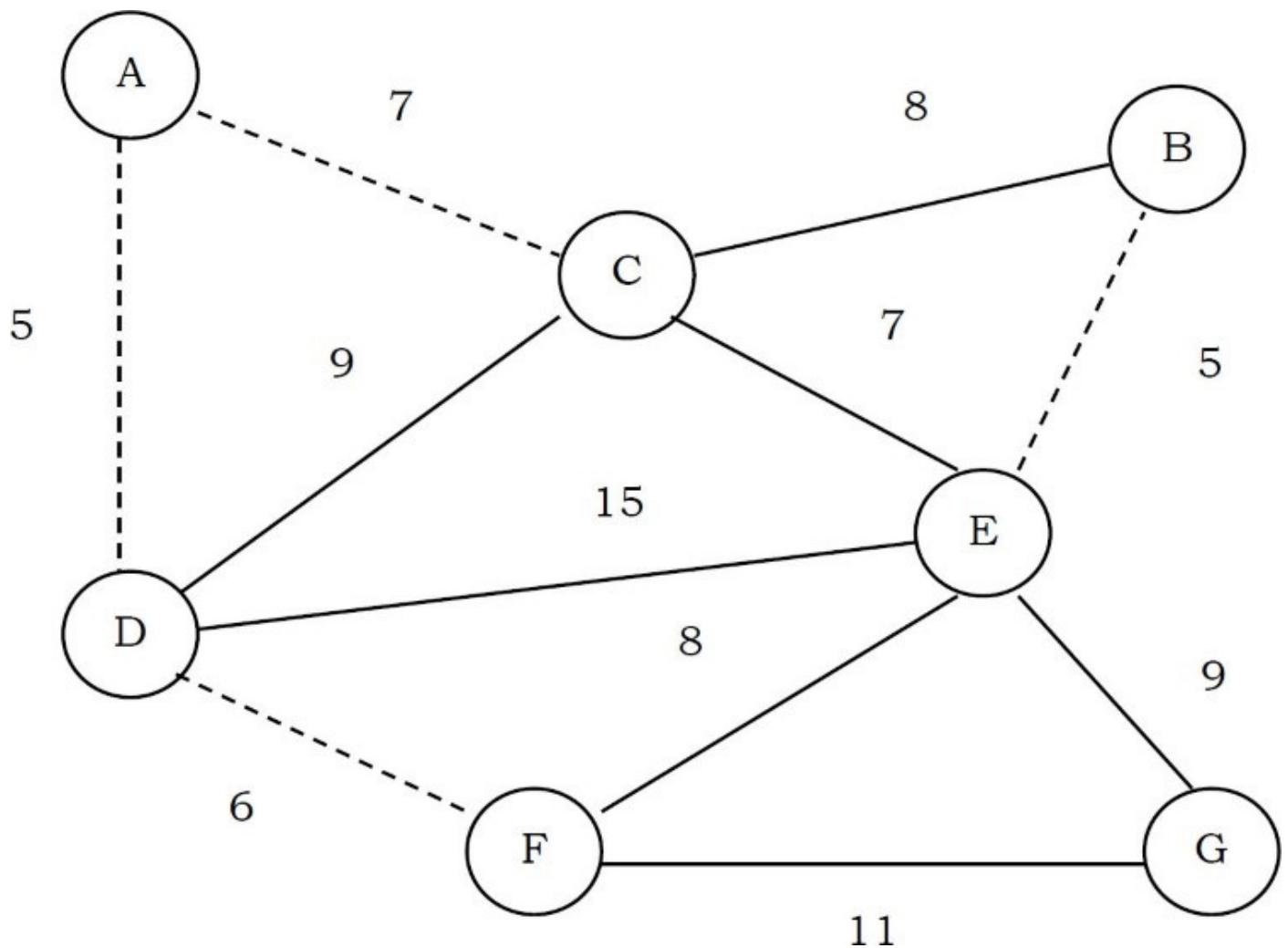
From the above graph, the edges which have minimum weight (cost) are: AD and BE. From these two we can select one of them and let us assume that we select AD (dotted line).



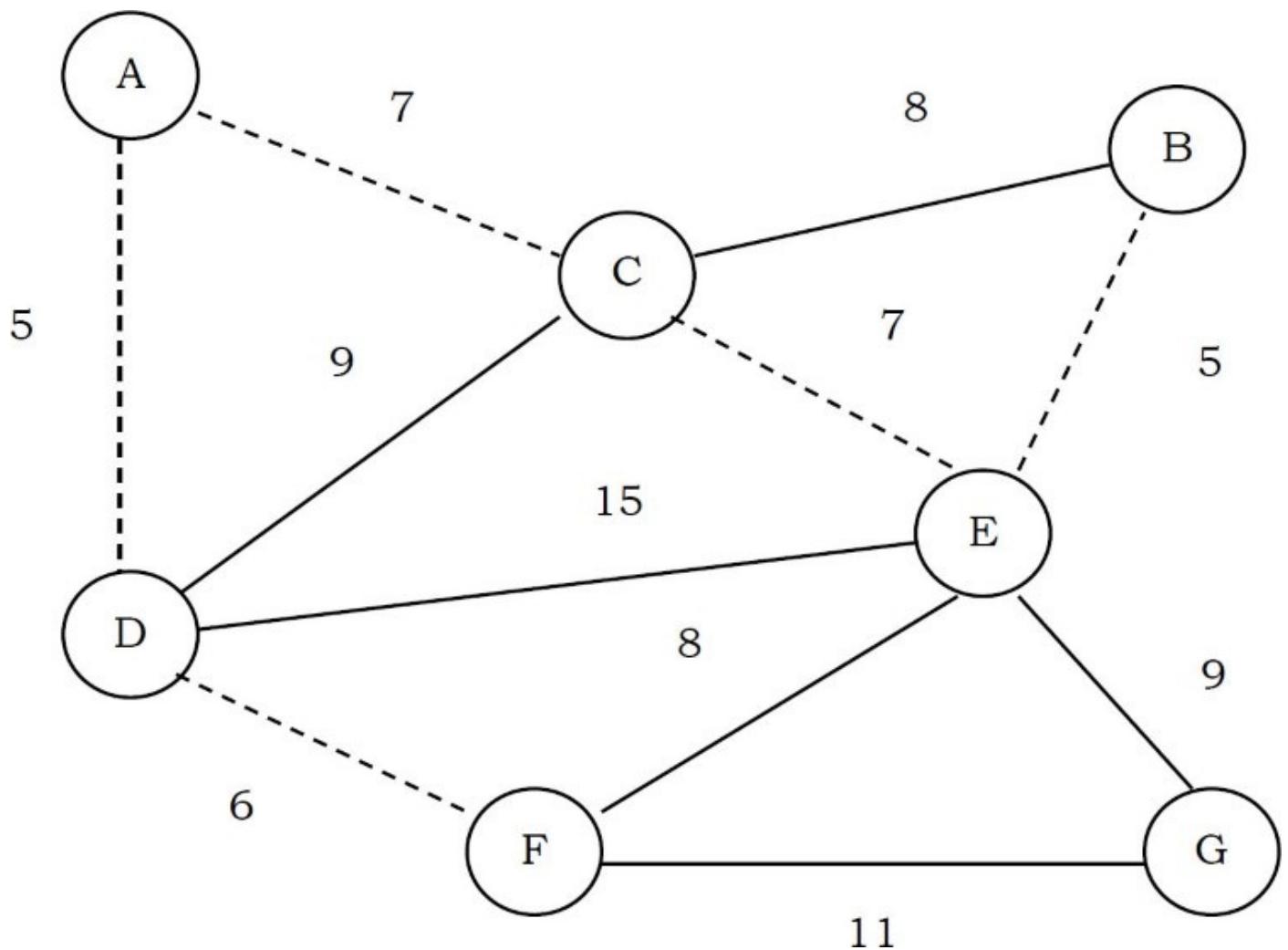
DF is the next edge that has the lowest cost (6).



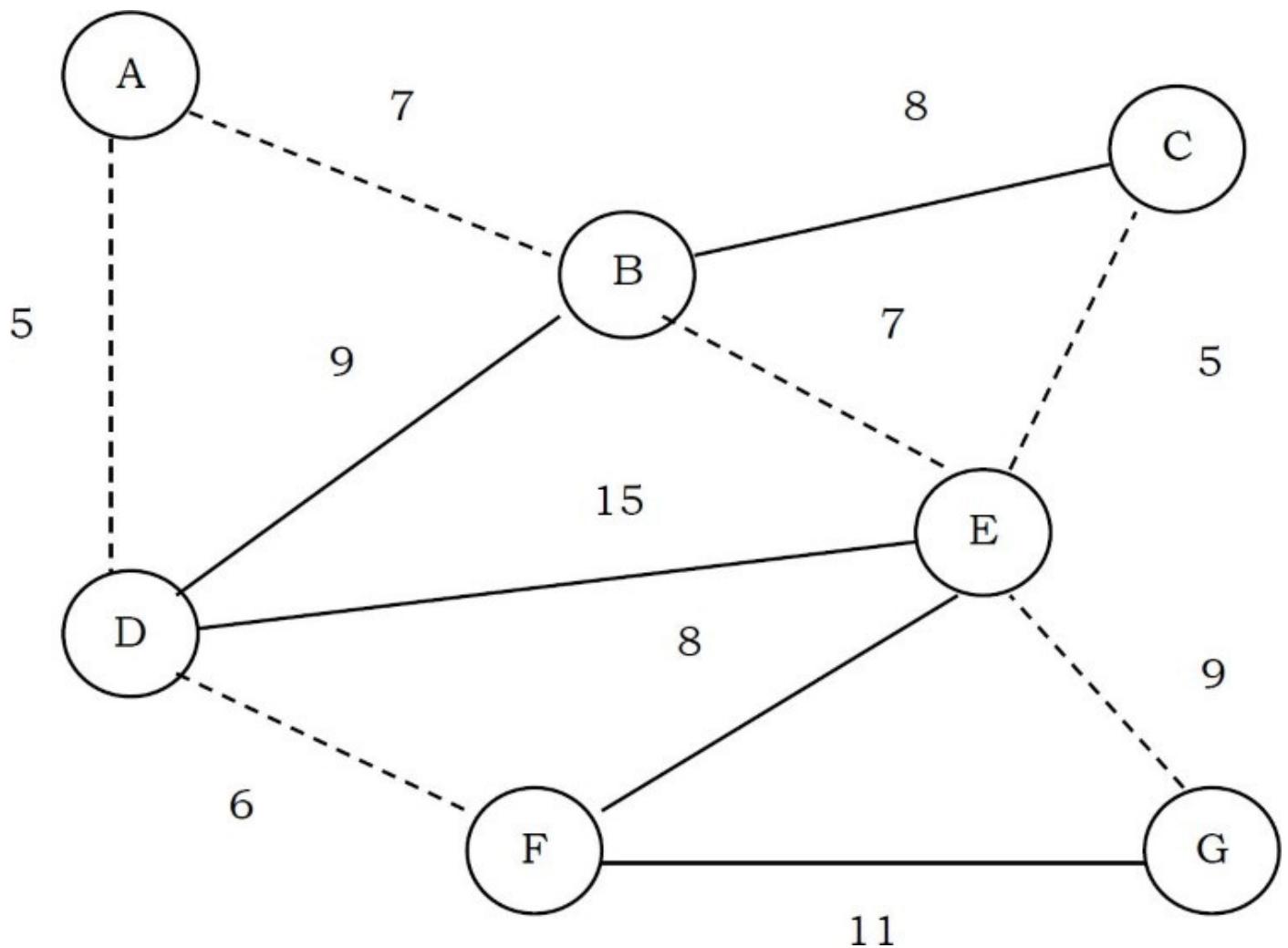
BE now has the lowest cost and we select it (dotted lines indicate selected edges).



Next, AC and CE have the low cost of 7 and we select AC.



Then we select CE as its cost is 7 and it does not form a cycle.



The next low cost edges are CB and EF. But if we select CB, then it forms a cycle. So we discard it. This is also the case with EF. So we should not select those two. And the next low cost is 9 (BD and EG). Selecting BD forms a cycle so we discard it. Adding EG will not form a cycle and therefore with this edge we complete all vertices of the graph.

```

void Kruskal(struct Graph *G) {
    S = φ; // At the end S will contains the edges of minimum spanning trees
    for (int v = 0; v < G->V; v++)
        MakeSet(v);
    Sort edges of E by increasing weights w;
    for each edge (u, v) in E { //from sorted list
        if(FIND(u) ≠ FIND(v)) {
            S = S ∪ {(u, v)};
            UNION(u, v);
        }
    }
    return S;
}

```

Note: For implementation of UNION and FIND operations, refer to the *Disjoint Sets ADT* chapter.

The worst-case running time of this algorithm is $O(E \log E)$, which is dominated by the heap operations. That means, since we are constructing the heap with E edges, we need $O(E \log E)$ time to do that.

9.9 Graph Algorithms: Problems & Solutions

Problem-1 In an undirected simple graph with n vertices, what is the maximum number of edges? Self-loops are not allowed.

Solution: Since every node can connect to all other nodes, the first node can connect to $n - 1$ nodes. The second node can connect to $n - 2$ nodes [since one edge is already there from the first node]. The total number of edges is: $1 + 2 + 3 + \dots + n - 1 = \frac{n(n-1)}{2}$ edges.

Problem-2 How many different adjacency matrices does a graph with n vertices and E edges have?

Solution: It's equal to the number of permutations of n elements, i.e., $n!$.

Problem-3 How many different adjacency lists does a graph with n vertices have?

Solution: It's equal to the number of permutations of edges, i.e., $E!$.

Problem-4 Which undirected graph representation is most appropriate for determining whether or not a vertex is isolated (is not connected to any other vertex)?

Solution: Adjacency List. If we use the adjacency matrix, then we need to check the complete row to determine whether that vertex has edges or not. By using the adjacency list, it is very easy to check, and it can be done just by checking whether that vertex has NULL for next pointer or not [NULL indicates that the vertex is not connected to any other vertex].

Problem-5 For checking whether there is a path from source s to target t , which one is best between disjoint sets and DFS?

Solution: The table below shows the comparison between disjoint sets and DFS. The entries in the table represent the case for any pair of nodes (for s and t).

Method	Processing Time	Query Time	Space
Union-Find	$V + E \log V$	$\log V$	V
DFS	$E + V$	1	$E + V$

Problem-6 What is the maximum number of edges a directed graph with n vertices can have and still not contain a directed cycle?

Solution: The number is $V(V - 1)/2$. Any directed graph can have at most n^2 edges. However, since the graph has no cycles it cannot contain a self loop, and for any pair x,y of vertices, at most one edge from (x,y) and (y,x) can be included. Therefore the number of edges can be at most $(V^2 - V)/2$ as desired. It is possible to achieve $V(V - 1)/2$ edges. Label n nodes 1,2,..., n and add an edge (x, y) if and only if $x < y$. This graph has the appropriate number of edges and cannot contain a cycle (any path visits an increasing sequence of nodes).

Problem-7 How many simple directed graphs with no parallel edges and self-loops are possible in terms of V ?

Solution: $(V) \times (V - 1)$. Since, each vertex can connect to $V - 1$ vertices without self-loops.

Problem-8 What are the differences between DFS and BFS?

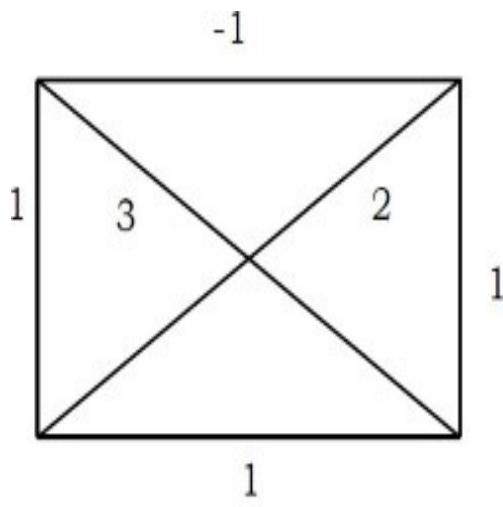
Solution:

DFS	BFS
Backtracking is possible from a dead end.	Backtracking is not possible.
Vertices from which exploration is incomplete are processed in a LIFO order	The vertices to be explored are organized as a FIFO queue.
The search is done in one particular direction	The vertices at the same level are maintained in parallel.

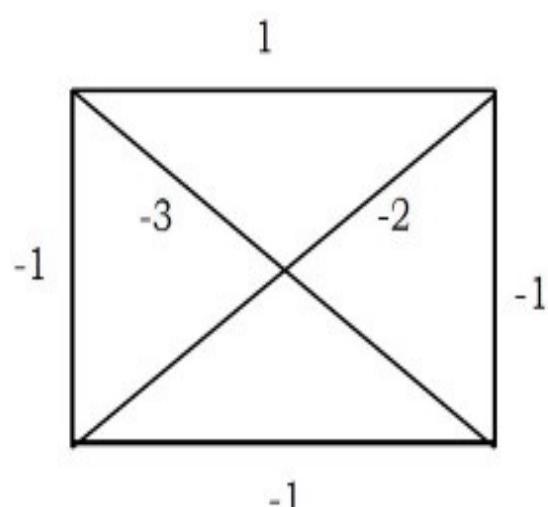
Problem-9 Earlier in this chapter, we discussed minimum spanning tree algorithms. Now,

give an algorithm for finding the maximum-weight spanning tree in a graph.

Solution:



Given graph



Transformed graph with negative edge weights

Using the given graph, construct a new graph with the same nodes and edges. But instead of using the same weights, take the negative of their weights. That means, weight of an edge = negative of weight of the corresponding edge in the given graph. Now, we can use existing *minimum spanning tree* algorithms on this new graph. As a result, we will get the maximum-weight spanning tree in the original one.

Problem-10 Give an algorithm for checking whether a given graph G has simple path from source s to destination d . Assume the graph G is represented using the adjacent matrix.

Solution: Let us assume that the structure for the graph is:

```
struct Graph {  
    int V;           //Number of vertices  
    int E;           //Number of edges  
    int ** adjMatrix; //Two dimensional array for storing the connections  
};
```

For each vertex call *DFS* and check whether the current vertex is the same as the destination vertex or not. If they are the same, then return 1. Otherwise, call the *DFS* on its unvisited neighbors. One important thing to note here is that, we are calling the *DFS* algorithm on vertices which are not yet visited.

```

void HasSimplePath(struct Graph *G, int s, int d) {
    int t;
    Viisited[s] = 1;
    if(s == d)
        return 1;
    for(t = 0; t < G->V; t++) {
        if(G->adjMatrix[s][t] && !Viisited[t])
            if(DFS(G, t, d))
                return 1;
    }
    return 0;
}

```

Time Complexity: $O(E)$. In the above algorithm, for each node, since we are not calling *DFS* on all of its neighbors (discarding through *if* condition), Space Complexity: $O(V)$.

Problem-11 Count simple paths for a given graph G has simple path from source s to destination d ? Assume the graph is represented using the adjacent matrix.

Solution: Similar to the discussion in [Problem-10](#), start at one node and call DFS on that node. As a result of this call, it visits all the nodes that it can reach in the given graph. That means it visits all the nodes of the connected component of that node. If there are any nodes that have not been visited, then again start at one of those nodes and call DFS.

Before the first DFS in each connected component, increment the connected components *count*. Continue this process until all of the graph nodes are visited. As a result, at the end we will get the total number of connected components. The implementation based on this logic is given below:

```

void CountSimplePaths(struct Graph * G, int s, int d) {
    int t;
    Viisited[s] = 1;
    if(s == d) {
        count++;
        Visited[s] = 0;
        return;
    }
    for(t = 0; t < G->V; t++) {
        if(G->adjMatrix[s][t] && !Viisited[t]) {
            DFS(G, t, d);
            Visited[t] = 0;
        }
    }
}

```

Problem-12 All pairs shortest path problem: Find the shortest graph distances between every pair of vertices in a given graph. Let us assume that the given graph does not have negative edges.

Solution: The problem can be solved using n applications of *Dijkstra's algorithm*. That means we apply *Dijkstra's algorithm* on each vertex of the given graph. This algorithm does not work if the graph has edges with negative weights.

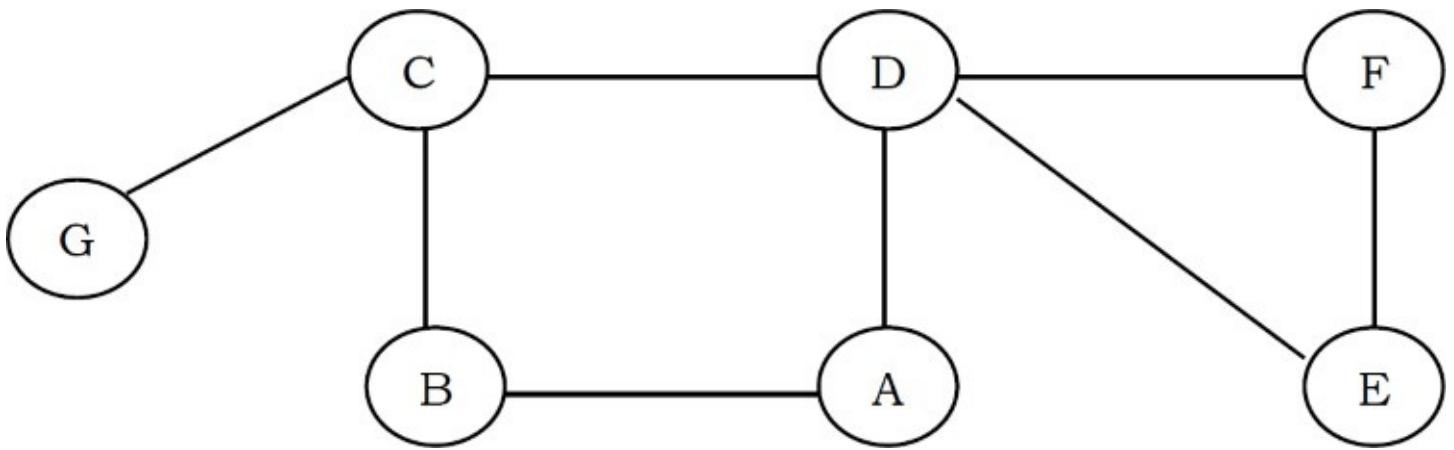
Problem-13 In [Problem-12](#), how do we solve the all pairs shortest path problem if the graph has edges with negative weights?

Solution: This can be solved by using the *Floyd – Warshall algorithm*. This algorithm also works in the case of a weighted graph where the edges have negative weights. This algorithm is an example of Dynamic Programming -refer to the *Dynamic Programming* chapter.

Problem-14 DFS Application: Cut Vertex or Articulation Points

Solution: In an undirected graph, a *cut vertex* (or articulation point) is a vertex, and if we remove it, then the graph splits into two disconnected components. As an example, consider the following figure. Removal of the “D” vertex divides the graph into two connected components ($\{E,F\}$ and $\{A,B, C, G\}$).

Similarly, removal of the “C” vertex divides the graph into ($\{G\}$ and $\{A, B,D,E,F\}$). For this graph, A and C are the cut vertices.

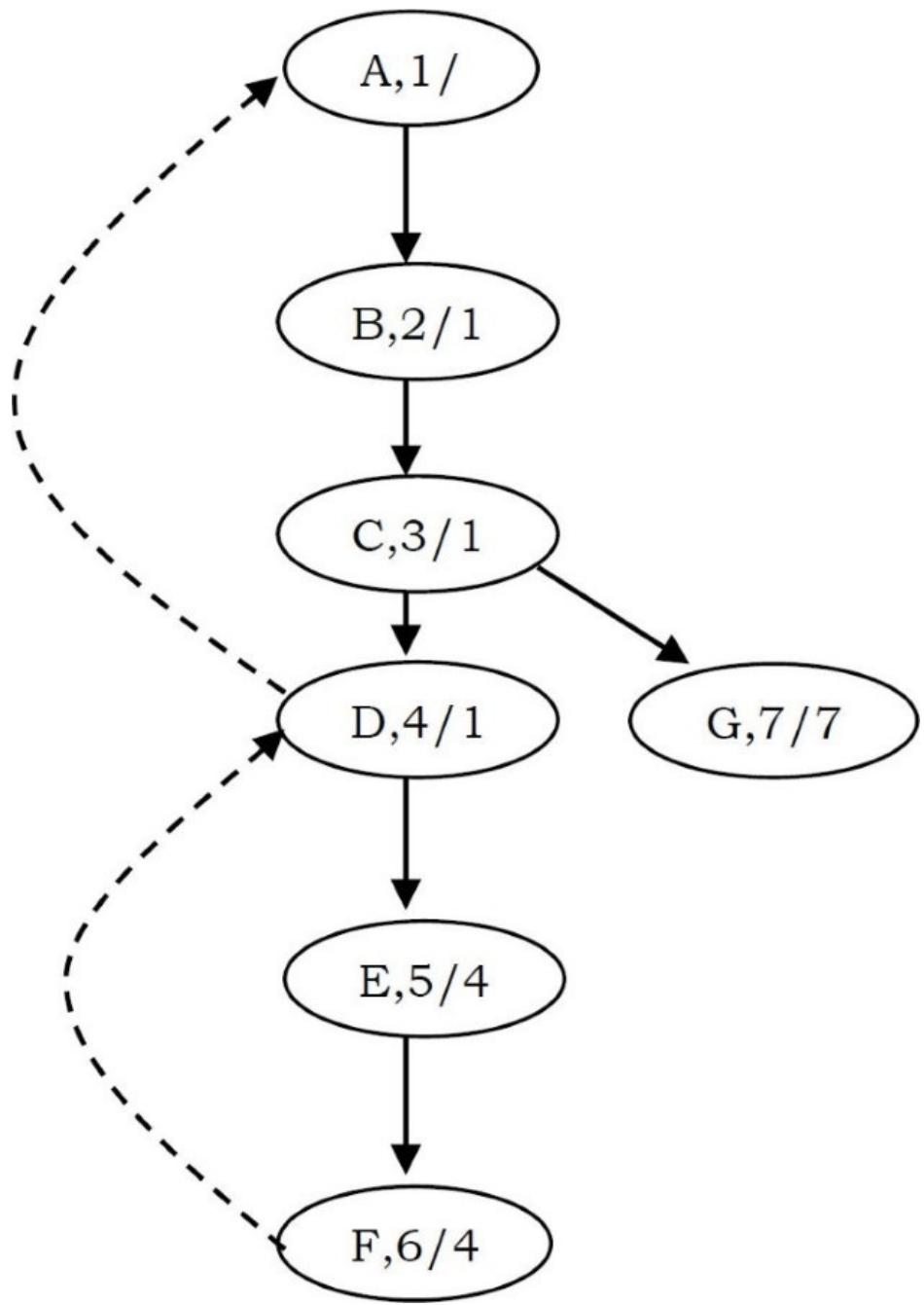


Note: A connected, undirected graph is called *bi-connected* if the graph is still connected after removing any vertex.

DFS provides a linear-time algorithm ($O(n)$) to find all cut vertices in a connected graph. Starting at any vertex, call a *DFS* and number the nodes as they are visited. For each vertex v , we call this *DFS* number $dfsnum(v)$. The tree generated with *DFS* traversal is called *DFS spanning tree*. Then, for every vertex v in the *DFS* spanning tree, we compute the lowest-numbered vertex, which we call $low(v)$, that is reachable from v by taking zero or more tree edges and then possibly one back edge (in that order).

Based on the above discussion, we need the following information for this algorithm: the *dfsnum* of each vertex in the *DFS* tree (once it gets visited), and for each vertex v , the lowest depth of neighbors of all descendants of v in the *DFS* tree, called the *low*.

The *dfsnum* can be computed during *DFS*. The *low* of v can be computed after visiting all descendants of v (i.e., just before v gets popped off the *DFS* stack) as the minimum of the *dfsnum* of all neighbors of v (other than the parent of v in the *DFS* tree) and the *low* of all children of v in the *DFS* tree.



The root vertex is a cut vertex if and only if it has at least two children. A non-root vertex u is a cut vertex if and only if there is a son v of u such that $\text{low}(v) \geq \text{dfsnum}(u)$. This property can be tested once the DFS is returned from every child of u (that means, just before u gets popped off the DFS stack), and if true, u separates the graph into different bi-connected components. This can be represented by computing one bi-connected component out of every such v (a component which contains v will contain the sub-tree of v , plus u), and then erasing the sub-tree of v from the tree.

For the given graph, the DFS tree with dfsnum/low can be given as shown in the figure below. The implementation for the above discussion is:

```

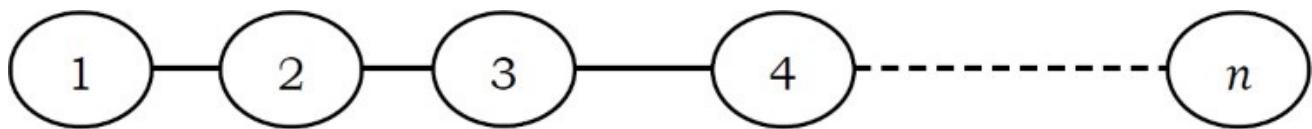
int adjMatrix [256] [256] ;
int dfsnum [256], num = 0, low [256];
void CutVertices( int u ) {
    low[u] = dfsnum[u] = num++;

    for (int v = 0 ; v < 256; ++v ) {
        if(adjMatrix[u][v] && dfsnum[v] == -1) {
            CutVertices( v );
            if(low[v] > dfsnum[u])
                printf("Cut Vertex:%d",u);
            low[u] = min ( low[u] , low[v] ) ;
        }
        else // (u,v) is a back edge
            low[u] = min(low[u] , dfsnum[v]) ;
    }
}

```

Problem-15 Let G be a connected graph of order n . What is the maximum number of cut-vertices that G can contain?

Solution: $n - 2$. As an example, consider the following graph. In the graph below, except for the vertices 1 and n , all the remaining vertices are cut vertices. This is because removing 1 and n vertices does not split the graph into two. This is a case where we can get the maximum number of cut vertices.

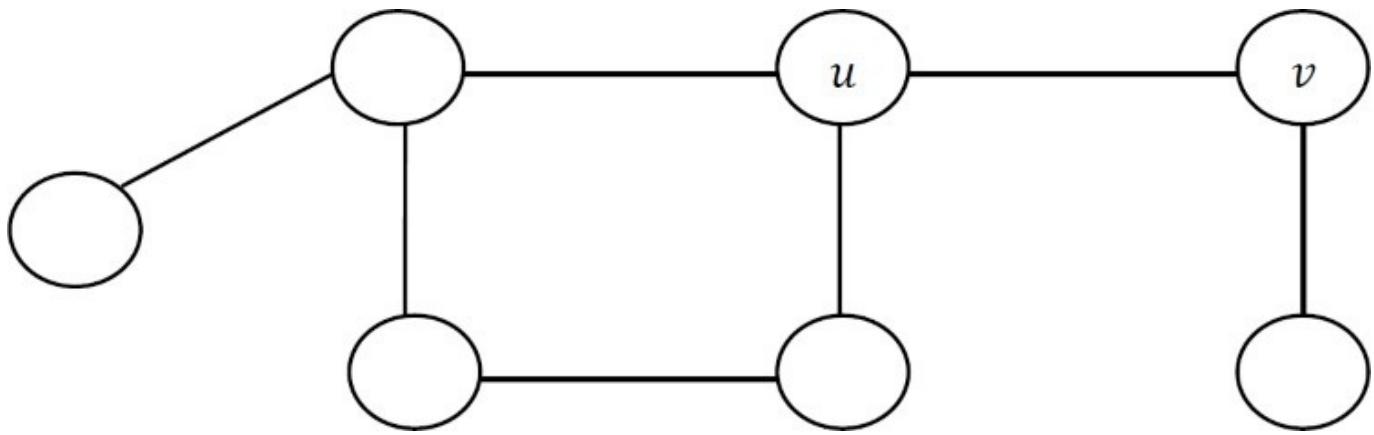


Problem-16 DFS Application: Cut Bridges or Cut Edges

Solution:

Definition: Let G be a connected graph. An edge uv in G is called a *bridge* of G if $G - uv$ is disconnected.

As an example, consider the following graph.



In the above graph, if we remove the edge uv then the graph splits into two components. For this graph, uv is a bridge. The discussion we had for cut vertices holds good for bridges also. The only change is, instead of printing the vertex, we give the edge. The main observation is that an edge (u, v) cannot be a bridge if it is part of a cycle. If (u, v) is not part of a cycle, then it is a bridge.

We can detect cycles in *DFS* by the presence of back edges, (u, v) is a bridge if and only if none of v or v 's children has a back edge to u or any of u 's ancestors. To detect whether any of v 's children has a back edge to u 's parent, we can use a similar idea as above to see what is the smallest *dfsnum* reachable from the subtree rooted at v .

```

int dfsnum[256], num = 0, low [256];
void Bridges( struct Graph *G, int u ) {
    low[u] = dfsnum[u] = num++;
    for (int v = 0 ; G->V; ++v ) {
        if(G->adjMatrix[u][v] && dfsnum[v] == -1) {
            cutVertices( v );
            if(low[v] > dfsnum[u])
                print (u,v) as a bridge
            low[u] = min ( low[u] , low[v] );
        }
        else // (u,v) is a back edge
            low[u] = min(low[u] , dfsnum[v]);
    }
}

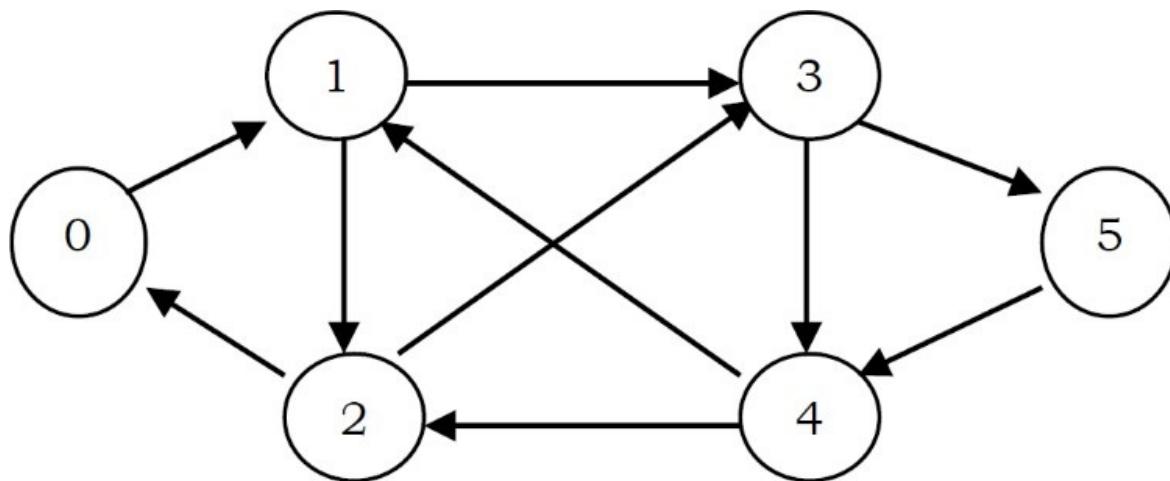
```

Solution: Before discussing this problem let us see the terminology:

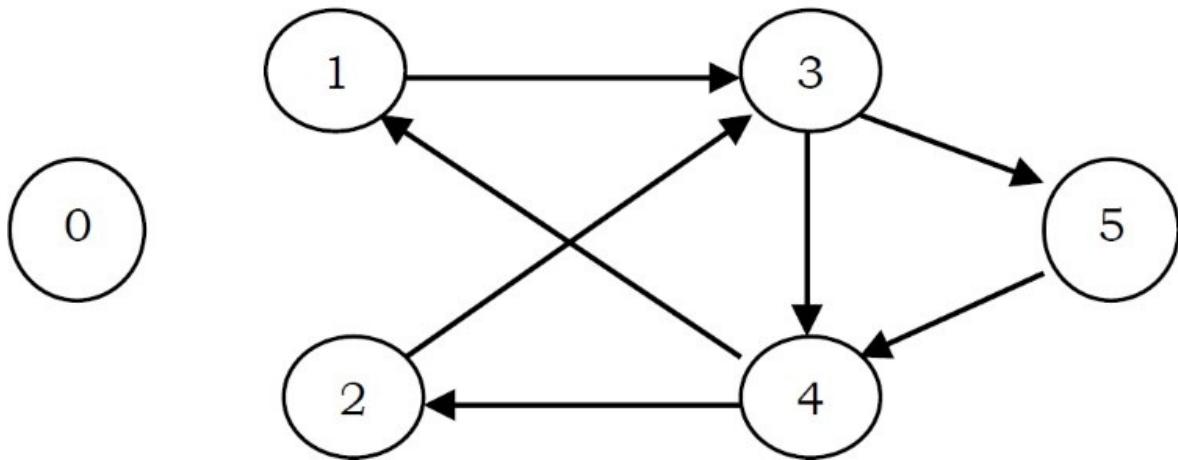
- *Eulerian tour*- a path that contains all edges without repetition.
- *Eulerian circuit* – a path that contains all edges without repetition and starts and ends in the same vertex.
- *Eulerian graph* – a graph that contains an Eulerian circuit.
- *Even vertex*: a vertex that has an even number of incident edges.
- *Odd vertex*: a vertex that has an odd number of incident edges.

Euler circuit: For a given graph we have to reconstruct the circuits using a pen, drawing each line exactly once. We should not lift the pen from the paper while drawing. That means, we must find a path in the graph that visits every edge exactly once and this problem is called an *Euler path* (also called *Euler tour*) or *Euler circuit problem*. This puzzle has a simple solution based on DFS.

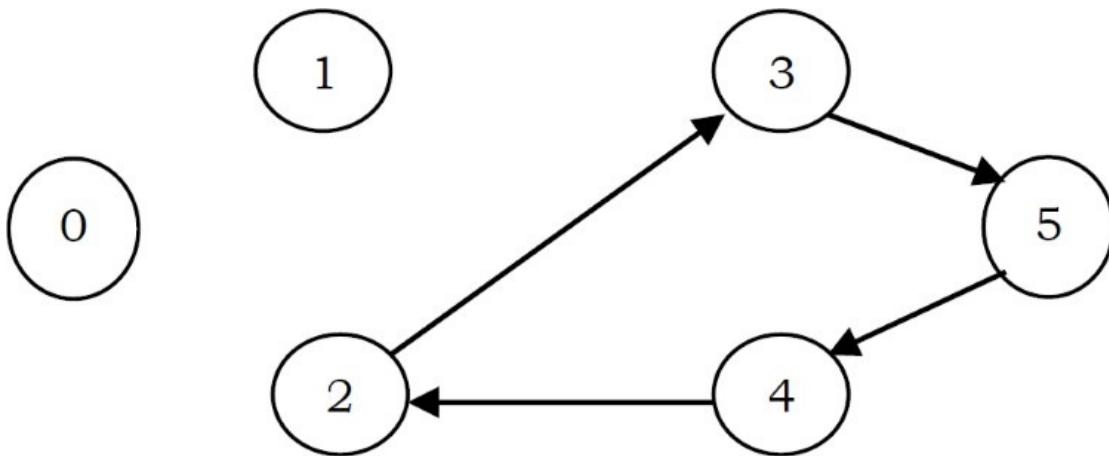
An *Euler* circuit exists if and only if the graph is connected and the number of neighbors of each vertex is even. Start with any node, select any untraversed outgoing edge, and follow it. Repeat until there are no more remaining unselected outgoing edges. For example, consider the following graph: A legal Euler Circuit of this graph is 0 1 3 4 1 2 3 5 4 2 0.



If we start at vertex 0, we can select the edge to vertex 1, then select the edge to vertex 2, then select the edge to vertex 0. There are now no remaining unchosen edges from vertex 0:



We now have a circuit $0,1,2,0$ that does not traverse every edge. So, we pick some other vertex that is on that circuit, say vertex 1. We then do another depth first search of the remaining edges. Say we choose the edge to node 3, then 4, then 1. Again we are stuck. There are no more unchosen edges from node 1. We now splice this path $1,3,4,1$ into the old path $0,1,2,0$ to get: $0,1,3,4,1,2,0$. The unchosen edges now look like this:



We can pick yet another vertex to start another DFS. If we pick vertex 2, and splice the path $2,3,5,4,2$, then we get the final circuit $0,1,3,4,1,2,3,5,4,2,0$.

A similar problem is to find a simple cycle in an undirected graph that visits every vertex. This is known as the *Hamiltonian cycle problem*. Although it seems almost identical to the *Euler* circuit problem, no efficient algorithm for it is known.

Notes:

- A connected undirected graph is *Eulerian* if and only if every graph vertex has an even degree, or exactly two vertices with an odd degree.
- A directed graph is *Eulerian* if it is strongly connected and every vertex has an equal *in* and *out* degree.

Application: A postman has to visit a set of streets in order to deliver mails and packages. He needs to find a path that starts and ends at the post-office, and that passes through each street

(edge) exactly once. This way the postman will deliver mails and packages to all the necessary streets, and at the same time will spend minimum time/effort on the road.

Problem-18 DFS Application: Finding Strongly Connected Components.

Solution: This is another application of DFS. In a directed graph, two vertices u and v are strongly connected if and only if there exists a path from u to v and there exists a path from v to u . The strong connectedness is an equivalence relation.

- A vertex is strongly connected with itself
- If a vertex u is strongly connected to a vertex v , then v is strongly connected to u
- If a vertex u is strongly connected to a vertex v , and v is strongly connected to a vertex x , then u is strongly connected to x

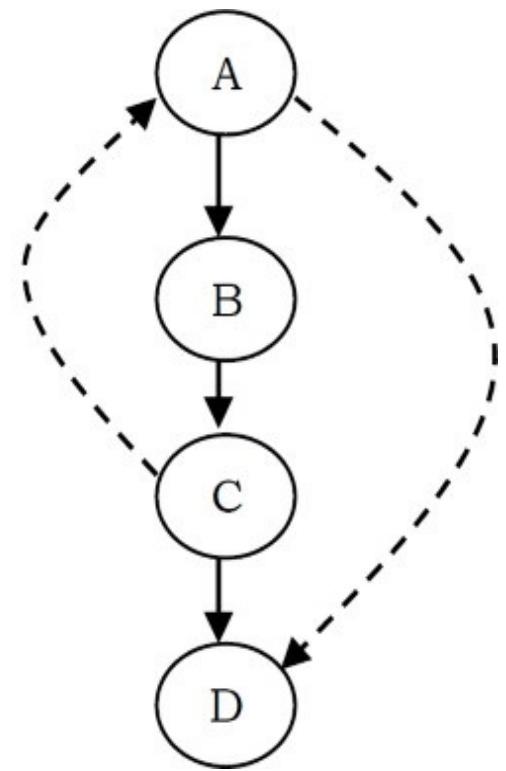
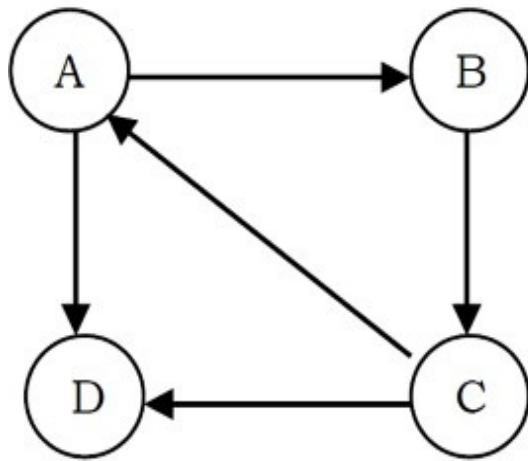
What this says is, for a given directed graph we can divide it into strongly connected components. This problem can be solved by performing two depth-first searches. With two DFS searches we can test whether a given directed graph is strongly connected or not. We can also produce the subsets of vertices that are strongly connected.

Algorithm

- Perform DFS on given graph G .
- Number vertices of given graph G according to a post-order traversal of depth-first spanning forest.
- Construct graph G_r by reversing all edges in G .
- Perform DFS on G_r : Always start a new DFS (initial call to Visit) at the highest-numbered vertex.
- Each tree in the resulting depth-first spanning forest corresponds to a strongly-connected component.

Why this algorithm works?

Let us consider two vertices, v and w . If they are in the same strongly connected component, then there are paths from v to w and from w to v in the original graph G , and hence also in G_r . If two vertices v and w are not in the same depth-first spanning tree of G_r , clearly they cannot be in the same strongly connected component. As an example, consider the graph shown below on the left. Let us assume this graph is G .

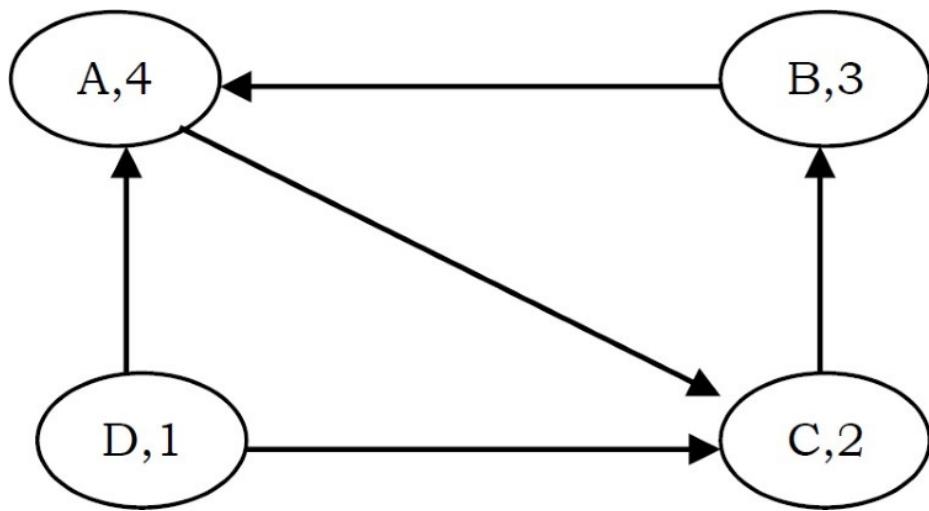


Now, as per the algorithm, performing *DFS* on this G graph gives the following diagram. The dotted line from C to A indicates a back edge.

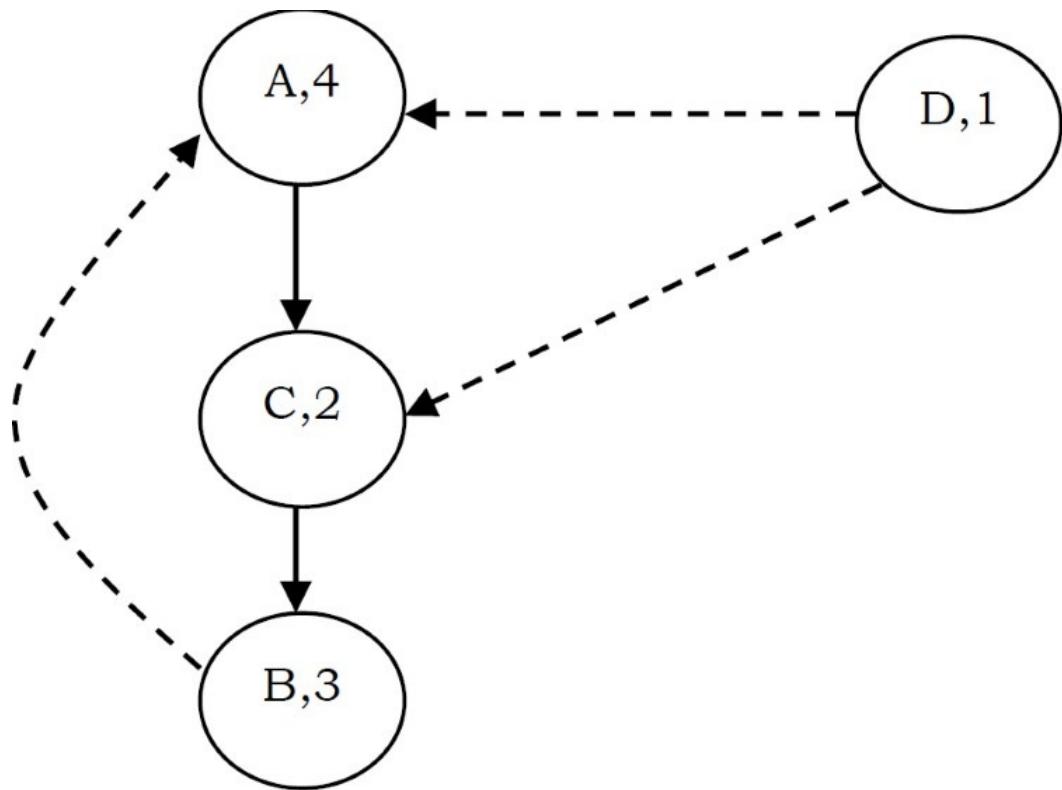
Now, performing post order traversal on this tree gives: D,C,B and A .

Vertex	Post Order Number
A	4
B	3
C	2
D	1

Now reverse the given graph G and call it G_r and at the same time assign postorder numbers to the vertices. The reversed graph G_r will look like:



The last step is performing DFS on this reversed graph G_r . While doing DFS , we need to consider the vertex which has the largest DFS number. So, first we start at A and with DFS we go to C and then B . At B , we cannot move further. This says that $\{A, B, C\}$ is a strongly connected component. Now the only remaining element is D and we end our second DFS at D . So the connected components are: $\{A, B, C\}$ and $\{D\}$.



The implementation based on this discussion can be shown as:

```

//Graph represented in adj matrix.
int adjMatrix [256][256], table[256];
vector <int> st ;
int counter = 0 ;
//This table contains the DFS Search number
int dfsnum [256], num = 0, low[256] ;
void StronglyConnectedComponents( int u ) {
    low[u] = dfsnum[ u ] = num++;
    Push(st, u) ;
    for( int v = 0 ; v < 256; ++v ) {
        if(graph[u][v] && table[v] == -1) {
            if( dfsnum[v] == -1)
                StronglyConnectedComponents(v) ;
            low[u] = min(low[u] , low[v]) ;
        }
    }
    if(low[u] == dfsnum[u]) {
        while( table[u] != counter) {
            table[st.back()] = counter;
            Push(st) ;
        }
        ++ counter;
    }
}

```

Problem-19 Count the number of connected components of Graph G which is represented in the adjacent matrix.

Solution: This problem can be solved with one extra counter in *DFS*.

```

//Visited[] is a global array.
int Visited[G→V];
void DFS(struct Graph *G, int u) {
    Visited[u] = 1;
    for( int v = 0; v < G→V; v++ ) {
        /* For example, if the adjacency matrix is used for representing the
           graph, then the condition to be used for finding unvisited adjacent
           vertex of u is: if( !Visited[v] && G→Adj[u][v] ) */
        for each unvisited adjacent node v of u {
            DFS(G, v);
        }
    }
}
void DFSTraversal(struct Graph *G) {
    int count = 0;
    for (int i = 0; i < G→V;i++)
        Visited[i]=0;
    //This loop is required if the graph has more than one component
    for (int i = 0; i < G→V;i++)
        if(!Visited[i]) {
            DFS(G, i);
            count++;
        }
    return count;
}

```

Time Complexity: Same as that of DFS and it depends on implementation. With adjacency matrix the complexity is $O(|E| + |V|)$ and with adjacency matrix the complexity is $O(|V|^2)$.

Problem-20 Can we solve the [Problem-19](#), using BFS?

Solution: **Yes.** This problem can be solved with one extra counter in BFS.

```

void BFS(struct Graph *G, int u) {
    int v,
    Queue Q = CreateQueue();
    EnQueue(Q, u);
    while(!IsEmptyQueue(Q)) {
        u = DeQueue(Q);
        Process u; //For example, print
        Visited[s]=1;
        /* For example, if the adjacency matrix is used for representing the
           graph, then the condition be used for finding unvisited adjacent
           vertex of u is: if( !Visited[v] && G->Adj[u][v] ) */
        for each unvisited adjacent node v of u {
            EnQueue(Q, v);
        }
    }
}

void BFSTraversal(struct Graph *G) {
    for (int i = 0; i < G->V; i++)
        Visited[i]=0;
    //This loop is required if the graph has more than one component
    for (int i = 0; i < G->V; i++)
        if(!Visited[i])
            BFS(G, i);
}

```

Time Complexity: Same as that of *BFS* and it depends on implementation. With adjacency matrix the complexity is $O(|E| + |V|)$ and with adjacency matrix the complexity is $O(|V|^2)$.

Problem-21 Let us assume that $G(V,E)$ is an undirected graph. Give an algorithm for finding a spanning tree which takes $O(|E|)$ time complexity (not necessarily a minimum spanning tree).

Solution: The test for a cycle can be done in constant time, by marking vertices that have been added to the set S . An edge will introduce a cycle, if both its vertices have already been marked.

Algorithm:

```

S = {};
for each edge e ∈ E {
    if(add e to S doesn't form a cycle) {
        add e to S;
        mark e;
    }
}

```

Problem-22 Is there any other way of solving 0?

Solution: Yes. We can run *BFS* and find the *BFS* tree for the graph (level order tree of the graph). Then start at the root element and keep moving to the next levels and at the same time we have to consider the nodes in the next level only once. That means, if we have a node with multiple input edges then we should consider only one of them; otherwise they will form a cycle.

Problem-23 Detecting a cycle in an undirected graph

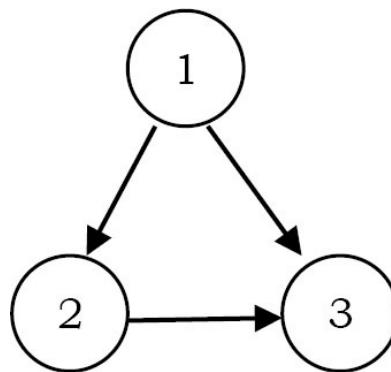
Solution: An undirected graph is acyclic if and only if a *DFS* yields no back edges, edges (u, v) where v has already been discovered and is an ancestor of u .

- Execute *DFS* on the graph.
- If there is a back edge – the graph has a cycle.

If the graph does not contain a cycle, then $|E| < |V|$ and *DFS* cost $O(|V|)$. If the graph contains a cycle, then a back edge is discovered after $2|V|$ steps at most.

Problem-24 Detecting a cycle in DAG

Solution:



Cycle detection on a graph is different than on a tree. This is because in a graph, a node can have multiple parents. In a tree, the algorithm for detecting a cycle is to do a depth first search, marking nodes as they are encountered. If a previously marked node is seen again, then a cycle exists. This won't work on a graph. Let us consider the graph shown in the figure below. If we use a tree cycle detection algorithm, then it will report the wrong result. That means that this graph has a cycle in it. But the given graph does not have a cycle in it. This is because node 3 will be seen twice in a *DFS* starting at node 1.

The cycle detection algorithm for trees can easily be modified to work for graphs. The key is that in a *DFS* of an acyclic graph, a node whose descendants have all been visited can be seen again without implying a cycle. But, if a node is seen for the second time before all its descendants have been visited, then there must be a cycle. Can you see why this is? Suppose there is a cycle containing node A. This means that A must be reachable from one of its descendants. So when the *DFS* is visiting that descendant, it will see A again, before it has finished visiting all of A's descendants. So there is a cycle. In order to detect cycles, we can modify the depth first search.

```

int DetectCycle(struct Graph *G) {
    for (int i = 0; i < G->V; i++) {
        Visited[s]=0;
        Predecessor[i] = 0;
    }
    for (int i = 0; i < G->V; i++) {
        if(!Visited[i] && HasCycle(G, i))
            return 1;
    }
    return false;
}

int HasCycle(struct Graph *G, int u) {
    Visited[u]=1;
    for (int i = 0; i < G->V; i++) {
        if(G->Adj[s][i]) {
            if(Predecessor[i] != u && Visited[i])
                return 1;
            else {
                Predecessor[i] = u;
                return HasCycle(G, i);
            }
        }
    }
    return 0;
}

```

Time Complexity: $O(V + E)$.

Problem-25 Given a directed acyclic graph, give an algorithm for finding its depth.

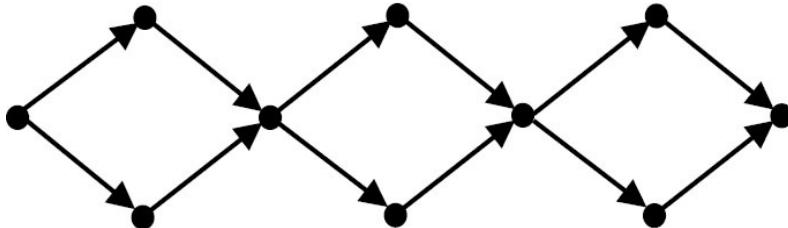
Solution: If it is an undirected graph, we can use the simple unweighted shortest path algorithm (check *Shortest Path Algorithms* section). We just need to return the highest number among all distances. For directed acyclic graph, we can solve by following the similar approach which we used for finding the depth in trees. In trees, we have solved this problem using level order

traversal (with one extra special symbol to indicate the end of the level).

```
//Assuming the given graph is a DAG
int DepthInDAG( struct Graph *G ) {
    struct Queue *Q;
    int counter;
    int v, w;
    Q = CreateQueue();
    counter = 0;
    for (v = 0; v < G->V; v++)
        if( indegree[v] == 0 )
            EnQueue( Q , v );
    EnQueue( Q, '$' );
    while( !IsEmptyQueue( Q ) ) {
        v = DeQueue( Q );
        if(v == '$') {
            counter++;
            if(!IsEmptyQueue( Q ))
                EnQueue( Q , '$' );
        }
        for each w adjacent to v
            if( --indegree[w] == 0 )
                EnQueue ( Q , w );
    }
    DeleteQueue( Q );
    return counter;
}
```

Total running time is $O(V + E)$.

Problem-26 How many topological sorts of the following dag are there?



Solution: If we observe the above graph there are three stages with 2 vertices. In the early

discussion of this chapter, we saw that topological sort picks the elements with zero indegree at any point of time. At each of the two vertices stages, we can first process either the top vertex or the bottom vertex. As a result, at each of these stages we have two possibilities. So the total number of possibilities is the multiplication of possibilities at each stage and that is, $2 \times 2 \times 2 = 8$.

Problem-27 Unique topological ordering: Design an algorithm to determine whether a directed graph has a unique topological ordering.

Solution: A directed graph has a unique topological ordering if and only if there is a directed edge between each pair of consecutive vertices in the topological order. This can also be defined as: a directed graph has a unique topological ordering if and only if it has a Hamiltonian path. If the digraph has multiple topological orderings, then a second topological order can be obtained by swapping a pair of consecutive vertices.

Problem-28 Let us consider the prerequisites for courses at *IIT Bombay*. Suppose that all prerequisites are mandatory, every course is offered every semester, and there is no limit to the number of courses we can take in one semester. We would like to know the minimum number of semesters required to complete the major. Describe the data structure we would use to represent this problem, and outline a linear time algorithm for solving it.

Solution: Use a directed acyclic graph (DAG). The vertices represent courses and the edges represent the prerequisite relation between courses at *IIT Bombay*. It is a DAG, because the prerequisite relation has no cycles.

The number of semesters required to complete the major is one more than the longest path in the dag. This can be calculated on the DFS tree recursively in linear time. The longest path out of a vertex x is 0 if x has outdegree 0, otherwise it is $1 + \max \{ \text{longest path out of } y \mid (x,y) \text{ is an edge of } G \}$.

Problem-29 At a university let's say *IIT Bombay*), there is a list of courses along with their prerequisites. That means, two lists are given:

A – Courses list

B – Prerequisites: B contains couples (x,y) where $x,y \in A$ indicating that course x can't be taken before course y .

Let us consider a student who wants to take only one course in a semester. Design a schedule for this student.

Example: $A = \{\text{C-Lang, Data Structures, OS, CO, Algorithms, Design Patterns, Programming}\}$. $B = \{(\text{C-Lang, CO}), (\text{OS, CO}), (\text{Data Structures, Algorithms}), (\text{Design Patterns, Programming})\}$. One possible schedule could be:

Semester 1:	Data Structures
Semester 2:	Algorithms
Semester 3:	C-Lang

Semester 4:	OS
Semester 5:	CO
Semester 6:	Design Patterns
Semester 7:	Programming

Solution: The solution to this problem is exactly the same as that of topological sort. Assume that the courses names are integers in the range $[1..n]$, n is known (n is not constant). The relations between the courses will be represented by a directed graph $G = (V,E)$, where V are the set of courses and if course i is prerequisite of course j , E will contain the edge (i,j) . Let us assume that the graph will be represented as an Adjacency list.

First, let's observe another algorithm to topologically sort a DAG in $O(|V| + |E|)$.

- Find in-degree of all the vertices - $O(|V| + |E|)$
- Repeat:
 - Find a vertex v with in-degree=0 - $O(|V|)$
 - Output v and remove it from G , along with its edges - $O(|V|)$
 - Reduce the in-degree of each node u such as (v, u) was an edge in G and keep a list of vertices with in-degree=0 – $O(\text{degree}(v))$
 - Repeat the process until all the vertices are removed

The time complexity of this algorithm is also the same as that of the topological sort and it is $O(|V| + |E|)$.

Problem-30 In [Problem-29](#), a student wants to take all the courses in A , in the minimal number of semesters. That means the student is ready to take any number of courses in a semester. Design a schedule for this scenario. *One possible schedule is:*

Semester 1: C-Lang, OS, Design Patterns

Semester 2: Data Structures, CO, Programming

Semester 3: Algorithms

Solution: A variation of the above topological sort algorithm with a slight change: In each semester, instead of taking one subject, take all the subjects with zero indegree. That means, execute the algorithm on all the nodes with degree 0 (instead of dealing with one source in each stage, all the sources will be dealt and printed).

Time Complexity: $O(|V| + |E|)$.

Problem-31 LCA of a DAG: Given a DAG and two vertices v and w , find the *lowest common ancestor* (LCA) of v and w . The LCA of v and w is an ancestor of v and w that has no descendants that are also ancestors of v and w .

Hint: Define the height of a vertex v in a DAG to be the length of the longest path from *root* to v . Among the vertices that are ancestors of both v and w , the one with the greatest height is an LCA

of v and w .

Problem-32 Shortest ancestral path: Given a DAG and two vertices v and w , find the *shortest ancestral path* between v and w . An ancestral path between v and w is a common ancestor x along with a shortest path from v to x and a shortest path from w to x . The shortest ancestral path is the ancestral path whose total length is minimized.

Hint: Run BFS two times. First run from v and second time from w . Find a DAG where the shortest ancestral path goes to a common ancestor x that is not an LCA.

Problem-33 Let us assume that we have two graphs G_1 and G_2 . How do we check whether they are isomorphic or not?

Solution: There are many ways of representing the same graph. As an example, consider the following simple graph. It can be seen that all the representations below have the same number of vertices and the same number of edges.



Definition: Graphs $G_1 = \{V_1, E_1\}$ and $G_2 = \{V_2, E_2\}$ are isomorphic if

- 1) There is a one-to-one correspondence from V_1 to V_2 and
- 2) There is a one-to-one correspondence from E_1 to E_2 that map each edge of G_1 to G_2 .

Now, for the given graphs how do we check whether they are isomorphic or not?

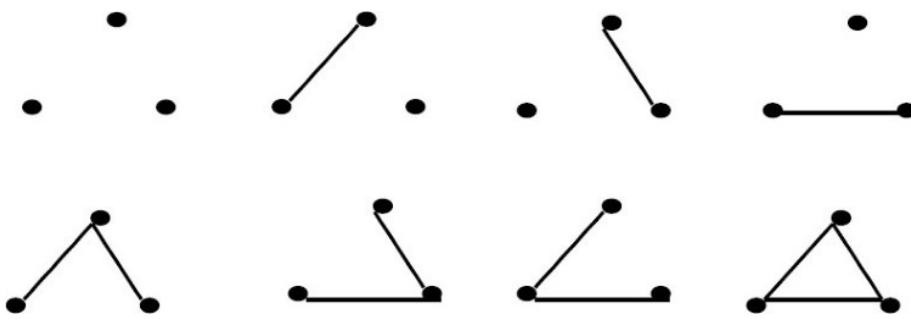
In general, it is not a simple task to prove that two graphs are isomorphic. For that reason we must consider some properties of isomorphic graphs. That means those properties must be satisfied if the graphs are isomorphic. If the given graph does not satisfy these properties then we say they are not isomorphic graphs.

Property: Two graphs are isomorphic if and only if for some ordering of their vertices their adjacency matrices are equal.

Based on the above property we decide whether the given graphs are isomorphic or not. In order to check the property, we need to do some matrix transformation operations.

Problem-34 How many simple undirected non-isomorphic graphs are there with n vertices?

Solution: We will try to answer this question in two steps. First, we count all labeled graphs. Assume all the representations below are labeled with $\{1,2,3\}$ as vertices. The set of all such graphs for $n = 3$ are:



There are only two choices for each edge: it either exists or it does not. Therefore, since the maximum number of edges is $\binom{n}{2}$ (and since the maximum number of edges in an undirected graph with n vertices is $\frac{n(n-1)}{2} = n_{c_2} = \binom{n}{2}$), the total number of undirected labeled graphs is $2^{\binom{n}{2}}$.

Problem-35 Hamiltonian path in DAGs: Given a DAG, design a linear time algorithm to determine whether there is a path that visits each vertex exactly once.

Solution: The *Hamiltonian* path problem is an NP-Complete problem (for more details ref *Complexity Classes* chapter). To solve this problem, we will try to give the approximation algorithm (which solves the problem, but it may not always produce the optimal solution).

Let us consider the topological sort algorithm for solving this problem. Topological sort has an interesting property: that if all pairs of consecutive vertices in the sorted order are connected by edges, then these edges form a directed *Hamiltonian* path in the DAG. If a *Hamiltonian* path exists, the topological sort order is unique. Also, if a topological sort does not form a *Hamiltonian* path, the DAG will have two or more topological orderings.

Approximation Algorithm: Compute a topological sort and check if there is an edge between each consecutive pair of vertices in the topological order.

In an unweighted graph, find a path from s to t that visits each vertex exactly once. The basic solution based on backtracking is, we start at s and try all of its neighbors recursively, making sure we never visit the same vertex twice. The algorithm based on this implementation can be given as:

```

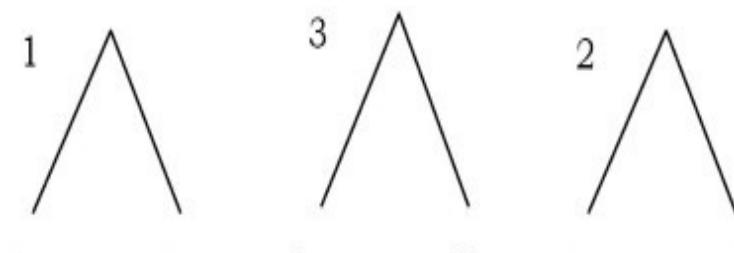
bool seenTable[32];
void HamiltonianPath( struct Graph *G, int u ) {
    if( u == t )
        /* Check that we have seen all vertices. */
    else {
        for( int v = 0; v < n; v++ )
            if( !seenTable[v] && G->Adj[u][v] ) {
                seenTable[v] = true;
                HamiltonianPath( v );
                seenTable[v] = false;
            }
    }
}

```

Note that if we have a partial path from s to u using vertices $s = v_1, v_2, \dots, v_k = u$, then we don't care about the order in which we visited these vertices so as to figure out which vertex to visit next. All that we need to know is the set of vertices we have seen (the `seenTable[]` array) and which vertex we are at right now (u). There are 2^n possible sets of vertices and n choices for u . In other words, there are 2^n possible `seenTable[]` arrays and n different parameters to `Hamiltonian_path()`. What `Hamiltonian_path()` does during any particular recursive call is completely determined by the `seenTable[]` array and the parameter u .

Problem-36 For a given graph G with n vertices how many trees we can construct?

Solution: There is a simple formula for this problem and it is named after Arthur Cayley. For a given graph with n labeled vertices the formula for finding number of trees on is n^{n-2} . Below, the number of trees with different n values is shown.

n value	Formula value: n^{n-2}	Number of Trees
2	1	1 ————— 2
3	3	

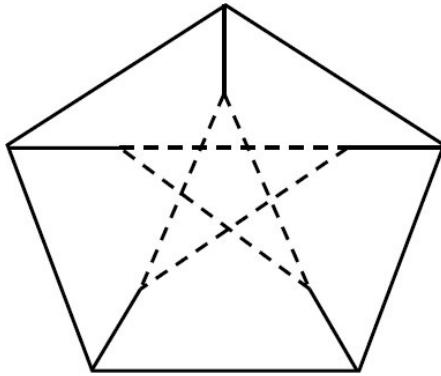
Problem-37 For a given graph G with n vertices how many spanning trees can we construct?

Solution: The solution to this problem is the same as that of [Problem-36](#). It is just another way of asking the same question. Because the number of edges in both regular tree and spanning tree are the same.

Problem-38 The *Hamiltonian cycle* problem: Is it possible to traverse each of the vertices of a graph exactly once, starting and ending at the same vertex?

Solution: Since the *Hamiltonian* path problem is an NP-Complete problem, the *Hamiltonian* cycle problem is an NP-Complete problem. A *Hamiltonian* cycle is a cycle that traverses every vertex of a graph exactly once. There are no known conditions in which are both necessary and sufficient, but there are a few sufficient conditions.

- For a graph to have a *Hamiltonian* cycle the degree of each vertex must be two or more.
- The Petersen graph does not have a *Hamiltonian* cycle and the graph is given below.



- In general, the more edges a graph has, the more likely it is to have a *Hamiltonian* cycle.
- Let G be a simple graph with $n \geq 3$ vertices. If every vertex has a degree of at least $\frac{n}{2}$, then G has a *Hamiltonian* cycle.
- The best known algorithm for finding a *Hamiltonian* cycle has an exponential worst-case complexity.

Note: For the approximation algorithm of *Hamiltonian* path, refer to the [Dynamic Programming](#) chapter.

Problem-39 What is the difference between *Dijkstra's* and *Prim's* algorithm?

Solution: *Dijkstra's* algorithm is almost identical to that of *Prim's*. The algorithm begins at a specific vertex and extends outward within the graph until all vertices have been reached. The only distinction is that *Prim's* algorithm stores a minimum cost edge whereas *Dijkstra's* algorithm stores the total cost from a source vertex to the current vertex. More simply, *Dijkstra's* algorithm stores a summation of minimum cost edges whereas *Prim's* algorithm stores at most one minimum cost edge.

Problem-40 Reversing Graph: : Give an algorithm that returns the reverse of the directed graph (each edge from v to w is replaced by an edge from w to v).

Solution: In graph theory, the reverse (also called *transpose*) of a directed graph G is another directed graph on the same set of vertices with all the edges reversed. That means, if G contains an edge (u, v) then the reverse of G contains an edge (v, u) and vice versa.

Algorithm:

```
Graph ReverseTheDirectedGraph(struct Graph *G) {
    Create new graph with name ReversedGraph and
        let us assume that this will contain the reversed graph.
    //The reversed graph also will contain same number of vertices and edges.
    for each vertex of given graph G {
        for each vertex w adjacent to v {
            Add the w to v edge in ReversedGraph;
            //That means we just need to reverse the bits in adjacency matrix.
        }
    }
    return ReversedGraph;
}
```

Problem-41 Travelling Sales Person Problem: Find the shortest path in a graph that visits each vertex at least once, starting and ending at the same vertex?

Solution: The Traveling Salesman Problem (*TSP*) is related to finding a Hamiltonian cycle. Given a weighted graph G , we want to find the shortest cycle (may be non-simple) that visits all the vertices.

Approximation algorithm: This algorithm does not solve the problem but gives a solution which is within a factor of 2 of optimal (in the worst-case).

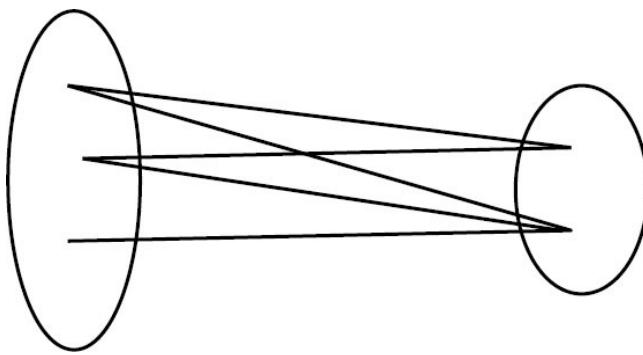
- 1) Find a Minimal Spanning Tree (MST).
- 2) Do a DFS of the MST.

For details, refer to the chapter on [Complexity Classes](#).

Problem-42 Discuss Bipartite matchings?

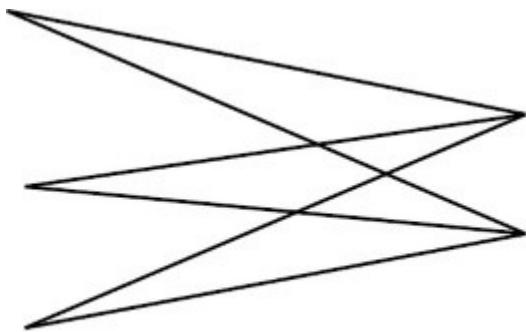
Solution: In Bipartite graphs, we divide the graphs in to two disjoint sets, and each edge connects a vertex from one set to a vertex in another subset (as shown in figure).

Definition: A simple graph $G = (V, E)$ is called a *bipartite graph* if its vertices can be divided into two disjoint sets $V = V_1 \cup V_2$, such that every edge has the form $e = (a, b)$ where $a \in V_1$ and $b \in V_2$. One important condition is that no vertices both in V_1 or both in V_2 are connected.

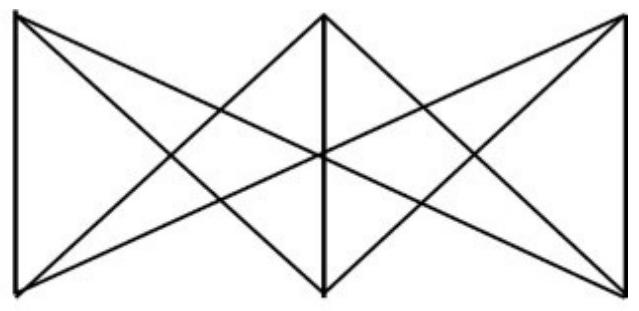


Properties of Bipartite Graphs

- A graph is called bipartite if and only if the given graph does not have an odd length cycle.
- A *complete bipartite graph* $K_{m,n}$ is a bipartite graph that has each vertex from one set adjacent to each vertex from another set.

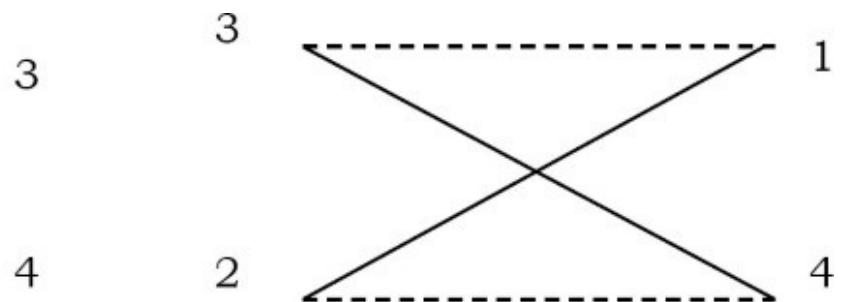
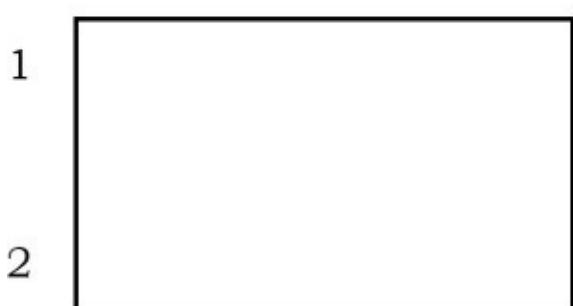


$K_{2,3}$



$K_{3,3}$

- A subset of edges $M \subset E$ is a *matching* if no two edges have a common vertex. As an example, matching sets of edges are represented with dotted lines. A matching M is called *maximum* if it has the largest number of possible edges. In the graphs, the dotted edges represent the alternative matching for the given graph.



- A matching M is *perfect* if it matches all vertices. We must have $V_1 = V_2$ in order to have perfect matching.
- An *alternating path* is a path whose edges alternate between matched and unmatched edges. If we find an alternating path, then we can improve the matching. This is because an alternating path consists of matched and unmatched edges. The number of unmatched edges exceeds the number of matched edges by one.

Therefore, an alternating path always increases the matching by one.

The next question is, how do we find a perfect matching? Based on the above theory and definition, we can find the perfect matching with the following approximation algorithm.

Matching Algorithm (Hungarian algorithm)

- 1) Start at unmatched vertex.
- 2) Find an alternating path.
- 3) If it exists, change matching edges to no matching edges and conversely. If it does not exist, choose another unmatched vertex.
- 4) If the number of edges equals $V/2$, stop. Otherwise proceed to step 1 and repeat, as long as all vertices have been examined without finding any alternating paths.

Time Complexity of the Matching Algorithm: The number of iterations is in $O(V)$. The complexity of finding an alternating path using BFS is $O(E)$. Therefore, the total time complexity is $O(V \times E)$.

Problem-43 Marriage and Personnel Problem?

Marriage Problem: There are X men and Y women who desire to get married. Participants indicate who among the opposite sex could be a potential spouse for them. Every woman can be married to at most one man, and every man to at most one woman. How can we marry everybody to someone they like?

Personnel Problem: You are the boss of a company. The company has M workers and N jobs. Each worker is qualified to do some jobs, but not others. How will you assign jobs to each worker?

Solution: These two cases are just another way of asking about bipartite graphs, and the solution is the same as that of [Problem-42](#).

Problem-44 How many edges will be there in complete bipartite graph $K_{m,n}$?

Solution: $m \times n$. This is because each vertex in the first set can connect all vertices in the second set.

Problem-45 A graph is called a regular graph if it has no loops and multiple edges where each vertex has the same number of neighbors; i.e., every vertex has the same degree. Now, if $K_{m,n}$ is a regular graph, what is the relation between m and n ?

Solution: Since each vertex should have the same degree, the relation should be $m = n$.

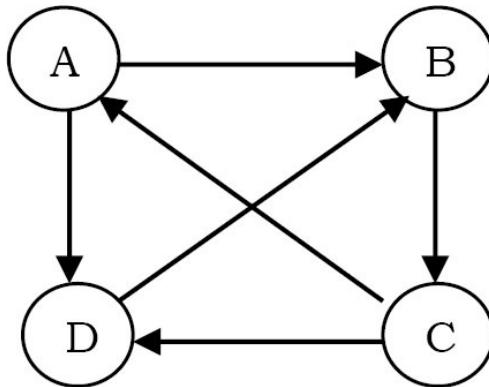
Problem-46 What is the maximum number of edges in the maximum matching of a bipartite graph with n vertices?

Solution: From the definition of *matching*, we should not have edges with common vertices. So

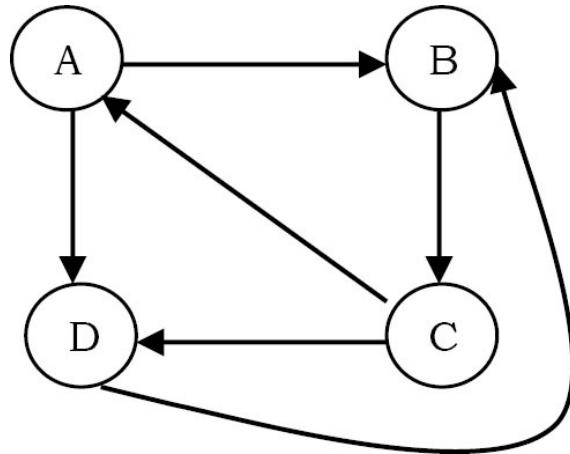
in a bipartite graph, each vertex can connect to only one vertex. Since we divide the total vertices into two sets, we can get the maximum number of edges if we divide them in half. Finally the answer is $\frac{n}{2}$.

Problem-47 Discuss Planar Graphs. *Planar graph:* Is it possible to draw the edges of a graph in such a way that the edges do not cross?

Solution: A graph G is said to be planar if it can be drawn in the plane in such a way that no two edges meet each other except at a vertex to which they are incident. Any such drawing is called a plane drawing of G . As an example consider the below graph:



This graph we can easily convert to a planar graph as below (without any crossed edges).



How do we decide whether a given graph is planar or not?

The solution to this problem is not simple, but researchers have found some interesting properties that we can use to decide whether the given graph is a planar graph or not.

Properties of Planar Graphs

- If a graph G is a connected planar simple graph with V vertices, where $V = 3$ and E edges, then $E = 3V - 6$.
- K_5 is non-planar. [K_5 stands for complete graph with 5 vertices].
- If a graph G is a connected planar simple graph with V vertices and E edges, and no

triangles, then $E = 2V - 4$.

- $K_{3,3}$ is non-planar. [$K_{3,3}$ stands for bipartite graph with 3 vertices on one side and the other 3 vertices on the other side. $K_{3,3}$ contains 6 vertices].
- If a graph G is a connected planar simple graph, then G contains at least one vertex of 5 degrees or less.
- A graph is planar if and only if it does not contain a subgraph that has K_5 and $K_{3,3}$ as a contraction.
- If a graph G contains a nonplanar graph as a subgraph, then G is non-planar.
- If a graph G is a planar graph, then every subgraph of G is planar.
- For any connected planar graph $G = (V,E)$, the following formula should hold: $V + F - E = 2$, where F stands for the number of faces.
- For any planar graph $G = (V,E)$ with K components, the following formula holds: $V + F - E = 1 + K$.

In order to test the planarity of a given graph, we use these properties and decide whether it is a planar graph or not. Note that all the above properties are only the necessary conditions but not sufficient.

Problem-48 How many faces does $K_{2,3}$ have?

Solution: From the above discussion, we know that $V + F - E = 2$, and from an earlier problem we know that $E = m \times n = 2 \times 3 = 6$ and $V = m + n = 5$. $\therefore 5 + F - 6 = 2 \Rightarrow F = 3$.

Problem-49 Discuss Graph Coloring

Solution: A k –coloring of a graph G is an assignment of one color to each vertex of G such that no more than k colors are used and no two adjacent vertices receive the same color. A graph is called k –colorable if and only if it has a k –coloring.

Applications of Graph Coloring: The graph coloring problem has many applications such as scheduling, register allocation in compilers, frequency assignment in mobile radios, etc.

Clique: A *clique* in a graph G is the maximum complete subgraph and is denoted by $\omega(G)$.

Chromatic number: The chromatic number of a graph G is the smallest number k such that G is k –colorable, and it is denoted by $X(G)$.

The lower bound for $X(G)$ is $\omega(G)$, and that means $\omega(G) \leq X(G)$.

Properties of Chromatic number: Let G be a graph with n vertices and G' is its complement. Then,

- $X(G) \leq \Delta(G) + 1$, where $\Delta(G)$ is the maximum degree of G .
- $X(G) \omega(G') \geq n$
- $X(G) + \omega(G') \leq n + 1$

- $X(G) + (G') \leq n + 1$

K-colorability problem: Given a graph $G = (V, E)$ and a positive integer $k \leq V$. Check whether G is k -colorable?

This problem is NP-complete and will be discussed in detail in the chapter on *Complexity Classes*.

Graph coloring algorithm: As discussed earlier, this problem is NP-Complete. So we do not have a polynomial time algorithm to determine $X(G)$. Let us consider the following approximation (no efficient) algorithm.

- Consider a graph G with two non-adjacent vertices a and b . The connection G_1 is obtained by joining the two non-adjacent vertices a and b with an edge. The contraction G_2 is obtained by shrinking $\{a, b\}$ into a single vertex $c(a, b)$ and by joining it to each neighbor in G of vertex a and of vertex b (and eliminating multiple edges).
- A coloring of G in which a and b have the same color yields a coloring of G_1 . A coloring of G in which a and b have different colors yields a coloring of G_2 .
- Repeat the operations of connection and contraction in each graph generated, until the resulting graphs are all cliques. If the smallest resulting clique is a K -clique, then $(G) = K$.

Important notes on Graph Coloring

- Any simple planar graph G can be colored with 6 colors.
- Every simple planar graph can be colored with less than or equal to 5 colors.

Problem-50 What is the four coloring problem?

Solution: A graph can be constructed from any map. The regions of the map are represented by the vertices of the graph, and two vertices are joined by an edge if the regions corresponding to the vertices are adjacent. The resulting graph is planar. That means it can be drawn in the plane without any edges crossing.

The *Four Color Problem* is whether the vertices of a planar graph can be colored with at most four colors so that no two adjacent vertices use the same color.

History: The *Four Color Problem* was first given by *Francis Guthrie*. He was a student at *University College London* where he studied under *Augustus De Morgan*. After graduating from London he studied law, but some years later his brother *Frederick Guthrie* had become a student of *De Morgan*. One day Francis asked his brother to discuss this problem with *De Morgan*.

Problem-51 When an adjacency-matrix representation is used, most graph algorithms require time $O(V^2)$. Show that determining whether a directed graph, represented in an adjacency-

matrix that contains a sink can be done in time $O(V)$. A sink is a vertex with in-degree $|V| - 1$ and out-degree 0 (Only one can exist in a graph).

Solution: A vertex i is a sink if and only if $M[i,j] = 0$ for all j and $M[j, i] = 1$ for all $j \neq i$. For any pair of vertices i and j :

$$M[i,j] = 1 \rightarrow \text{vertex } i \text{ can't be a sink}$$
$$M[i,j] = 0 \rightarrow \text{vertex } j \text{ can't be a sink}$$

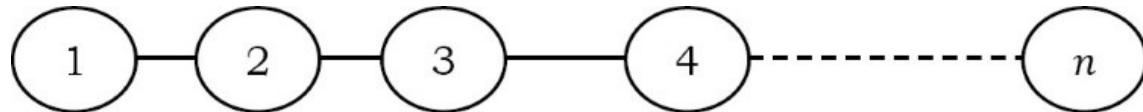
Algorithm:

- Start at $i = 1, j = 1$
- If $M[i,j] = 0 \rightarrow i$ wins, $j++$
- If $M[i,j] = 1 \rightarrow j$ wins, $i++$
- Proceed with this process until $j = n$ or $i = n + 1$
- If $i == n + 1$, the graph does not contain a sink
- Otherwise, check row i – it should be all zeros; and check column i – it should be all but $M[i, i]$ ones; – if so, i is a sink.

Time Complexity: $O(V)$, because at most $2|V|$ cells in the matrix are examined.

Problem-52 What is the worst – case memory usage of DFS?

Solution: It occurs when the $O(|V|)$, which happens if the graph is actually a list. So the algorithm is memory efficient on graphs with small diameter.



Problem-53 Does DFS find the shortest path from start node to some node w ?

Solution: No. In DFS it is not compulsory to select the smallest weight edge.

Problem-54 True or False: Dijkstra's algorithm does not compute the “all pairs” shortest paths in a directed graph with positive edge weights because, running the algorithm a single time, starting from some single vertex x , it will compute only the min distance from x to y for all nodes y in the graph.

Solution: True.

Problem-55 True or False: Prim's and Kruskal's algorithms may compute different minimum spanning trees when run on the same graph.

Solution: True.

SORTING

CHAPTER 10



10.1 What is Sorting?

Sorting is an algorithm that arranges the elements of a list in a certain order [either *ascending* or *descending*]. The output is a permutation or reordering of the input.

10.2 Why is Sorting Necessary?

Sorting is one of the important categories of algorithms in computer science and a lot of research has gone into this category. Sorting can significantly reduce the complexity of a problem, and is often used for database algorithms and searches.

10.3 Classification of Sorting Algorithms

Sorting algorithms are generally categorized based on the following parameters.

By Number of Comparisons

In this method, sorting algorithms are classified based on the number of comparisons. For comparison based sorting algorithms, best case behavior is $O(n \log n)$ and worst case behavior is $O(n^2)$. Comparison-based sorting algorithms evaluate the elements of the list by key comparison operation and need at least $O(n \log n)$ comparisons for most inputs.

Later in this chapter we will discuss a few *non – comparison (linear)* sorting algorithms like Counting sort, Bucket sort, Radix sort, etc. Linear Sorting algorithms impose few restrictions on the inputs to improve the complexity.

By Number of Swaps

In this method, sorting algorithms are categorized by the number of swaps (also called inversions).

By Memory Usage

Some sorting algorithms are “*in place*” and they need $O(1)$ or $O(\log n)$ memory to create auxiliary locations for sorting the data temporarily.

By Recursion

Sorting algorithms are either recursive [quick sort] or non-recursive [selection sort, and insertion sort], and there are some algorithms which use both (merge sort).

By Stability

Sorting algorithm is *stable* if for all indices i and j such that the key $A[i]$ equals key $A[j]$, if record $R[i]$ precedes record $R[j]$ in the original file, record $R[i]$ precedes record $R[j]$ in the sorted list. Few sorting algorithms maintain the relative order of elements with equal keys (equivalent elements retain their relative positions even after sorting).

By Adaptability

With a few sorting algorithms, the complexity changes based on pre-sortedness [quick sort]: pre-sortedness of the input affects the running time. Algorithms that take this into account are known to be adaptive.

10.4 Other Classifications

Another method of classifying sorting algorithms is:

- Internal Sort
- External Sort

Internal Sort

Sort algorithms that use main memory exclusively during the sort are called *internal* sorting algorithms. This kind of algorithm assumes high-speed random access to all memory.

External Sort

Sorting algorithms that use external memory, such as tape or disk, during the sort come under this category.

10.5 Bubble Sort

Bubble sort is the simplest sorting algorithm. It works by iterating the input array from the first element to the last, comparing each pair of elements and swapping them if needed. Bubble sort continues its iterations until no more swaps are needed. The algorithm gets its name from the way smaller elements “bubble” to the top of the list. Generally, insertion sort has better performance than bubble sort. Some researchers suggest that we should not teach bubble sort because of its simplicity and high time complexity.

The only significant advantage that bubble sort has over other implementations is that it can detect whether the input list is already sorted or not.

Implementation

```

void BubbleSort(int A[], int n) {
    for (int pass = n - 1; pass >= 0; pass--) {
        for (int i = 0; i <= pass - 1 ; i++) {
            if(A[i] > A[i+1]) {
                // swap elements
                int temp = A[i];
                A[i] = A[i+1];
                A[i+1] = temp;
            }
        }
    }
}

```

Algorithm takes $O(n^2)$ (even in best case). We can improve it by using one extra flag. No more swaps indicate the completion of sorting. If the list is already sorted, we can use this flag to skip the remaining passes.

```

void BubbleSortImproved(int A[], int n) {
    int pass, i, temp, swapped = 1;
    for (pass = n - 1; pass >= 0 && swapped; pass--) {
        swapped = 0;
        for (i = 0; i <= pass - 1 ; i++) {
            if(A[i] > A[i+1]) {
                // swap elements
                temp = A[i];
                A[i] = A[i+1];
                A[i+1] = temp;
                swapped = 1;
            }
        }
    }
}

```

This modified version improves the best case of bubble sort to $O(n)$.

Performance

Worst case complexity : $O(n^2)$
Best case complexity (Improved version) : $O(n)$

Average case complexity (Basic version) : $O(n^2)$

Worst case space complexity : $O(1)$ auxiliary

10.6 Selection Sort

Selection sort is an in-place sorting algorithm. Selection sort works well for small files. It is used for sorting the files with very large values and small keys. This is because selection is made based on keys and swaps are made only when required.

Advantages

- Easy to implement
- In-place sort (requires no additional storage space)

Disadvantages

- Doesn't scale well: $O(n^2)$

Algorithm

1. Find the minimum value in the list
2. Swap it with the value in the current position
3. Repeat this process for all the elements until the entire array is sorted

This algorithm is called *selection sort* since it repeatedly *selects* the smallest element.

Implementation

```

void Selection(int A [], int n) {
    int i, j, min, temp;
    for (i = 0; i < n - 1; i++) {
        min = i;
        for (j = i+1; j < n; j++) {
            if(A [j] < A [min])
                min = j;
        }
        // swap elements
        temp = A[min];
        A[min] = A[i];
        A[i] = temp;
    }
}

```

Performance

Worst case complexity : $O(n^2)$

Best case complexity : $O(n^2)$

Average case complexity : $O(n^2)$

Worst case space complexity: $O(1)$ auxiliary

10.7 Insertion Sort

Insertion sort is a simple and efficient comparison sort. In this algorithm, each iteration removes an element from the input data and inserts it into the correct position in the list being sorted. The choice of the element being removed from the input is random and this process is repeated until all input elements have gone through.

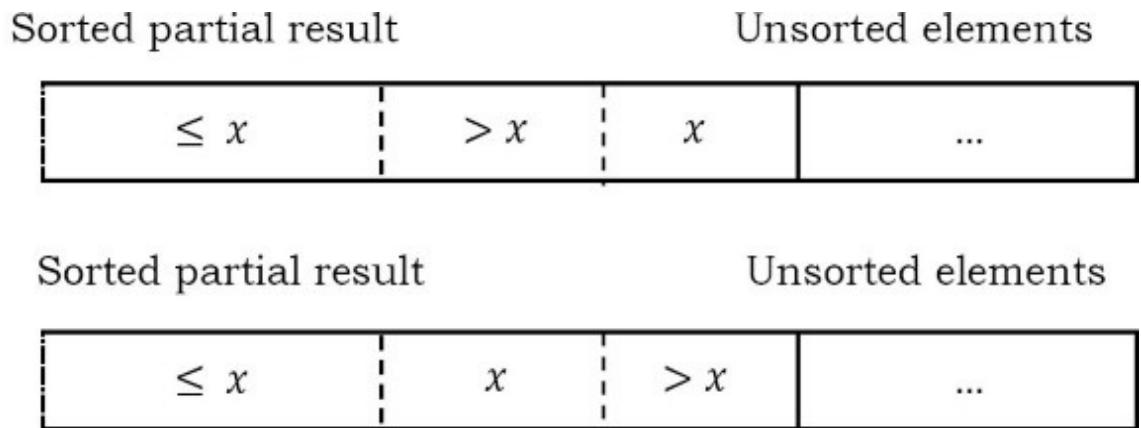
Advantages

- Simple implementation
- Efficient for small data
- Adaptive: If the input list is presorted [may not be completely] then insertions sort takes $O(n + d)$, where d is the number of inversions
- Practically more efficient than selection and bubble sorts, even though all of them have $O(n^2)$ worst case complexity

- Stable: Maintains relative order of input data if the keys are same
- In-place: It requires only a constant amount $O(1)$ of additional memory space
- Online: Insertion sort can sort the list as it receives it

Algorithm

Every repetition of insertion sort removes an element from the input data, and inserts it into the correct position in the already-sorted list until no input elements remain. Sorting is typically done in-place. The resulting array after k iterations has the property where the first $k + 1$ entries are sorted.



Each element greater than x is copied to the right as it is compared against x .

Implementation

```
void InsertionSort(int A[], int n) {
    int i, j, v;
    for (i = 1; i <= n - 1; i++) {
        v = A[i];
        j = i;
        while (A[j-1] > v && j >= 1) {
            A[j] = A[j-1];
            j--;
        }
        A[j] = v;
    }
}
```

Example

Given an array: 6 8 1 4 5 3 7 2 and the goal is to put them in ascending order.

6 8 1 4 5 3 7 2 (Consider index 0)

6 8 1 4 5 3 7 2 (Consider indices 0 - 1)

1 6 8 4 5 3 7 2 (Consider indices 0 - 2: insertion places 1 in front of 6 and 8)

1 4 6 8 5 3 7 2 (Process same as above is repeated until array is sorted)

1 4 5 6 8 3 7 2

1 3 4 5 6 7 8 2

1 2 3 4 5 6 7 8 (The array is sorted!)

Analysis

Worst case analysis

Worst case occurs when for every i the inner loop has to move all elements $A[1], \dots, A[i - 1]$ (which happens when $A[i] = \text{key}$ is smaller than all of them), that takes $\Theta(i - 1)$ time.

$$\begin{aligned} T(n) &= \Theta(1) + \Theta(2) + \Theta(2) + \dots + \Theta(n - 1) \\ &= \Theta(1 + 2 + 3 + \dots + n - 1) = \Theta\left(\frac{n(n - 1)}{2}\right) \approx \Theta(n^2) \end{aligned}$$

Average case analysis

For the average case, the inner loop will insert $A[i]$ in the middle of $A[1], \dots, A[i - 1]$. This takes $\Theta(i/2)$ time.

$$T(n) = \sum_{i=1}^n \Theta(i/2) \approx \Theta(n^2)$$

Performance

If every element is greater than or equal to every element to its left, the running time of insertion sort is $\Theta(n)$. This situation occurs if the array starts out already sorted, and so an already-sorted array is the best case for insertion sort.

Worst case complexity: $\Theta(n^2)$

Best case complexity: $\Theta(n)$

Average case complexity: $\Theta(n^2)$

Worst case space complexity: $O(n^2)$ total, $O(1)$ auxiliary

Comparisons to Other Sorting Algorithms

Insertion sort is one of the elementary sorting algorithms with $O(n^2)$ worst-case time. Insertion sort is used when the data is nearly sorted (due to its adaptiveness) or when the input size is small (due to its low overhead). For these reasons and due to its stability, insertion sort is used as the recursive base case (when the problem size is small) for higher overhead divide-and-conquer sorting algorithms, such as merge sort or quick sort.

Notes:

- Bubble sort takes $\frac{n^2}{2}$ comparisons and $\frac{n^2}{2}$ swaps (inversions) in both average case and in worst case.
- Selection sort takes $\frac{n^2}{2}$ comparisons and n swaps.
- Insertion sort takes $\frac{n^2}{4}$ comparisons and $\frac{n^2}{8}$ swaps in average case and in the worst case they are double.
- Insertion sort is almost linear for partially sorted input.
- Selection sort is best suited for elements with bigger values and small keys.

10.8 Shell Sort

Shell sort (also called *diminishing increment sort*) was invented by *Donald Shell*. This sorting algorithm is a generalization of insertion sort. Insertion sort works efficiently on input that is already almost sorted. Shell sort is also known as n-gap insertion sort. Instead of comparing only the adjacent pair, shell sort makes several passes and uses various gaps between adjacent elements (ending with the gap of 1 or classical insertion sort).

In insertion sort, comparisons are made between the adjacent elements. At most 1 inversion is eliminated for each comparison done with insertion sort. The variation used in shell sort is to avoid comparing adjacent elements until the last step of the algorithm. So, the last step of shell sort is effectively the insertion sort algorithm. It improves insertion sort by allowing the comparison and exchange of elements that are far away. This is the first algorithm which got less than quadratic complexity among comparison sort algorithms.

Shellsort is actually a simple extension for insertion sort. The primary difference is its capability of exchanging elements that are far apart, making it considerably faster for elements to get to where they should be. For example, if the smallest element happens to be at the end of an array, with insertion sort it will require the full array of steps to put this element at the beginning of the array. However, with shell sort, this element can jump more than one step a time and reach the

proper destination in fewer exchanges.

The basic idea in shellsort is to exchange every h th element in the array. Now this can be confusing so we'll talk more about this, h determines how far apart element exchange can happen, say for example take h as 13, the first element (index-0) is exchanged with the 14th element (index-13) if necessary (of course). The second element with the 15th element, and so on. Now if we take has 1, it is exactly the same as a regular insertion sort.

Shellsort works by starting with big enough (but not larger than the array size) h so as to allow eligible element exchanges that are far apart. Once a sort is complete with a particular h , the array can be said as h -sorted. The next step is to reduce h by a certain sequence, and again perform another complete h -sort. Once h is 1 and h -sorted, the array is completely sorted. Notice that the last sequence for ft is 1 so the last sort is always an insertion sort, except by this time the array is already well-formed and easier to sort.

Shell sort uses a sequence h_1, h_2, \dots, h_t called the *increment sequence*. Any increment sequence is fine as long as $h_1 = 1$, and some choices are better than others. Shell sort makes multiple passes through the input list and sorts a number of equally sized sets using the insertion sort. Shell sort improves the efficiency of insertion sort by *quickly* shifting values to their destination.

Implementation

```
void ShellSort(int A[], int array_size) {
    int i, j, h, v;
    for (h = 1; h = array_size/9; h = 3*h+1);
    for ( ; h > 0; h = h/3) {
        for (i = h+1; i = array_size; i += 1) {
            v = A[i];
            j = i;
            while (j > h && A[j-h] > v) {
                A[j] = A[j-h];
                j -= h;
            }
            A[j] = v;
        }
    }
}
```

Note that when $h == 1$, the algorithm makes a pass over the entire list, comparing adjacent elements, but doing very few element exchanges. For $h == 1$, shell sort works just like insertion sort, except the number of inversions that have to be eliminated is greatly reduced by the previous

steps of the algorithm with $h > 1$.

Analysis

Shell sort is efficient for medium size lists. For bigger lists, the algorithm is not the best choice. It is the fastest of all $O(n^2)$ sorting algorithms.

The disadvantage of Shell sort is that it is a complex algorithm and not nearly as efficient as the merge, heap, and quick sorts. Shell sort is significantly slower than the merge, heap, and quick sorts, but is a relatively simple algorithm, which makes it a good choice for sorting lists of less than 5000 items unless speed is important. It is also a good choice for repetitive sorting of smaller lists.

The best case in Shell sort is when the array is already sorted in the right order. The number of comparisons is less. The running time of Shell sort depends on the choice of increment sequence.

Performance

Worst case complexity depends on gap sequence. Best known: $O(n \log^2 n)$

Best case complexity: $O(n)$

Average case complexity depends on gap sequence

Worst case space complexity: $O(n)$

10.9 Merge Sort

Merge sort is an example of the divide and conquer strategy.

Important Notes

- *Merging* is the process of combining two sorted files to make one bigger sorted file.
- *Selection* is the process of dividing a file into two parts: k smallest elements and $n - k$ largest elements.
- Selection and merging are opposite operations
 - selection splits a list into two lists
 - merging joins two files to make one file
- Merge sort is Quick sort's complement
- Merge sort accesses the data in a sequential manner
- This algorithm is used for sorting a linked list

- Merge sort is insensitive to the initial order of its input
- In Quick sort most of the work is done before the recursive calls. Quick sort starts with the largest subfile and finishes with the small ones and as a result it needs stack. Moreover, this algorithm is not stable. Merge sort divides the list into two parts; then each part is conquered individually. Merge sort starts with the small subfiles and finishes with the largest one. As a result it doesn't need stack. This algorithm is stable.

Implementation

```
void Mergesort(int A[], int temp[], int left, int right) {
    int mid;
    if(right > left) {
        mid = (right + left) / 2;
        Mergesort(A, temp, left, mid);
        Mergesort(A, temp, mid+1, right);
        Merge(A, temp, left, mid+1, right);
    }
}

void Merge(int A[], int temp[], int left, int mid, int right) {
    int i, left_end, size, temp_pos;
    left_end = mid - 1;
    temp_pos = left;
    size = right - left + 1;
    while ((left <= left_end) && (mid <= right)) {
        if(A[left] <= A[mid]) {
            temp[temp_pos] = A[left];
            temp_pos = temp_pos + 1;
            left = left + 1;
        }
        else {
            temp[temp_pos] = A[mid];
            temp_pos = temp_pos + 1;
            mid = mid + 1;
        }
    }
    while (left <= left_end) {
        temp[temp_pos] = A[left];
        left = left + 1;
        temp_pos = temp_pos + 1;
    }
    while (mid <= right) {
        temp[temp_pos] = A[mid];
        mid = mid + 1;
        temp_pos = temp_pos + 1;
    }
    for (i = 0; i <= size; i++) {
        A[right] = temp[right];
        right = right - 1;
    }
}
```

Analysis

In Merge sort the input list is divided into two parts and these are solved recursively. After solving the sub problems, they are merged by scanning the resultant sub problems. Let us assume $T(n)$ is the complexity of Merge sort with n elements. The recurrence for the Merge Sort can be defined as:

Recurrence for Mergesort is $T(n) = 2T\left(\frac{n}{2}\right) + \Theta(n)$.

Using Master theorem, we get, $T(n) = \Theta(n \log n)$.

Note: For more details, refer to [Divide and Conquer](#) chapter.

Performance

Worst case complexity : $\Theta(n \log n)$

Best case complexity : $\Theta(n \log n)$

Average case complexity : $\Theta(n \log n)$

Worst case space complexity: $\Theta(n)$ auxiliary

10.10 Heap Sort

Heapsort is a comparison-based sorting algorithm and is part of the selection sort family. Although somewhat slower in practice on most machines than a good implementation of Quick sort, it has the advantage of a more favorable worst-case $\Theta(n \log n)$ runtime. Heapsort is an in-place algorithm but is not a stable sort.

Performance

Worst case performance: $\Theta(n \log n)$

Best case performance: $\Theta(n \log n)$

Average case performance: $\Theta(n \log n)$

Worst case space complexity: $\Theta(n)$ total, $\Theta(1)$ auxiliary

For other details on Heapsort refer to the [Priority Queues](#) chapter.

10.11 Quicksort

Quick sort is an example of a divide-and-conquer algorithmic technique. It is also called *partition exchange sort*. It uses recursive calls for sorting the elements, and it is one of the famous algorithms among comparison-based sorting algorithms.

Divide: The array $A[low \dots high]$ is partitioned into two non-empty sub arrays $A[low \dots q]$ and $A[q + 1 \dots high]$, such that each element of $A[low \dots high]$ is less than or equal to each element of $A[q + 1 \dots high]$. The index q is computed as part of this partitioning procedure.

Conquer: The two sub arrays $A[low \dots q]$ and $A[q + 1 \dots high]$ are sorted by recursive calls to Quick sort.

Algorithm

The recursive algorithm consists of four steps:

- 1) If there are one or no elements in the array to be sorted, return.
- 2) Pick an element in the array to serve as the “pivot” point. (Usually the left-most element in the array is used.)
- 3) Split the array into two parts – one with elements larger than the pivot and the other with elements smaller than the pivot.
- 4) Recursively repeat the algorithm for both halves of the original array.

Implementation

```

void Quicksort( int A[], int low, int high ) {
    int pivot;
    /* Termination condition! */
    if( high > low ) {
        pivot = Partition( A, low, high );
        Quicksort( A, low, pivot-1 );
        Quicksort( A, pivot+1, high );
    }
}

int Partition( int A, int low, int high ) {
    int left, right, pivot_item = A[low];
    left = low;
    right = high;
    while ( left < right ) {
        /* Move left while item < pivot */
        while( A[left] <= pivot_item )
            left++;
        /* Move right while item > pivot */
        while( A[right] > pivot_item )
            right--;
        if( left < right )
            swap(A,left,right);
    }
    /* right is final position for the pivot */
    A[low] = A[right];
    A[right] = pivot_item;
    return right;
}

```

Analysis

Let us assume that $T(n)$ be the complexity of Quick sort and also assume that all elements are distinct. Recurrence for $T(n)$ depends on two subproblem sizes which depend on partition element. If pivot is i^{th} smallest element then exactly $(i - 1)$ items will be in left part and $(n - i)$ in right part. Let us call it as i -split. Since each element has equal probability of selecting it as pivot the probability of selecting i^{th} element is $\frac{1}{n}$.

Best Case: Each partition splits array in halves and gives

$$T(n) = 2T(n/2) + \Theta(n) = \Theta(n\log n), [\text{using Divide and Conquer master theorem}]$$

Worst Case: Each partition gives unbalanced splits and we get

$$T(n) = T(n - 1) + \Theta(n) = \Theta(n^2) [\text{using Subtraction and Conquer master theorem}]$$

The worst-case occurs when the list is already sorted and last element chosen as pivot.

Average Case: In the average case of Quick sort, we do not know where the split happens. For this reason, we take all possible values of split locations, add all their complexities and divide with n to get the average case complexity.

$$\begin{aligned} T(n) &= \sum_{i=1}^n \frac{1}{n} (\text{runtime with } i\text{-split}) + n + 1 \\ &= \frac{1}{n} \sum_{i=1}^n (T(i-1) + T(n-i)) + n + 1 \\ &\quad // \text{since we are dealing with best case we can assume } T(n-i) \text{ and } T(i-1) \text{ are equal} \\ &= \frac{2}{n} \sum_{i=1}^n T(i-1) + n + 1 \\ &= \frac{2}{n} \sum_{i=0}^{n-1} T(i) + n + 1 \end{aligned}$$

Multiply both sides by n .

$$nT(n) = 2 \sum_{i=0}^{n-1} T(i) + n^2 + n$$

Same formula for $n - 1$.

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

Subtract the $n - 1$ formula from n .

$$nT(n) - (n-1)T(n-1) = 2 \sum_{i=0}^{n-1} T(i) + n^2 + n - (2 \sum_{i=0}^{n-2} T(i) + (n-1)^2 + (n-1))$$

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

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

Divide with $n(n+1)$.

$$\begin{aligned} \frac{T(n)}{n+1} &= \frac{T(n-1)}{\frac{n}{n-1}} + \frac{2}{\frac{n+1}{n}} \\ &= \frac{T(n-2)}{\frac{n-1}{n-2}} + \frac{2}{\frac{n}{n-1}} + \frac{2}{\frac{n+1}{n}} \\ &\quad \vdots \\ &= O(1) + 2 \sum_{i=3}^n \frac{1}{i} \\ &= O(1) + O(2 \log n) \\ \frac{T(n)}{n+1} &= O(\log n) \\ \frac{T(n)}{T(n)} &= O((n+1) \log n) = O(n \log n) \end{aligned}$$

Time Complexity, $T(n) = O(n \log n)$.

Performance

Worst case Complexity: $O(n^2)$

Best case Complexity: $O(n \log n)$

Average case Complexity: $O(n \log n)$

Worst case space Complexity: $O(1)$

Randomized Quick sort

In average-case behavior of Quick sort, we assume that all permutations of the input numbers are equally likely. However, we cannot always expect it to hold. We can add randomization to an algorithm in order to reduce the probability of getting worst case in Quick sort.

There are two ways of adding randomization in Quick sort: either by randomly placing the input data in the array or by randomly choosing an element in the input data for pivot. The second choice is easier to analyze and implement. The change will only be done at the *partition* algorithm.

In normal Quick sort, *pivot* element was always the leftmost element in the list to be sorted. Instead of always using $A[low]$ as *pivot*, we will use a randomly chosen element from the subarray $A[low..high]$ in the randomized version of Quick sort. It is done by exchanging element $A[low]$ with an element chosen at random from $A[low..high]$. This ensures that the *pivot* element is equally likely to be any of the $high - low + 1$ elements in the subarray.

Since the pivot element is randomly chosen, we can expect the split of the input array to be reasonably well balanced on average. This can help in preventing the worst-case behavior of quick sort which occurs in unbalanced partitioning. Even though the randomized version improves the worst case complexity, its worst case complexity is still $O(n^2)$. One way to improve *Randomized – Quick sort* is to choose the pivot for partitioning more carefully than by picking a random element from the array. One common approach is to choose the pivot as the median of a set of 3 elements randomly selected from the array.

10.12 Tree Sort

Tree sort uses a binary search tree. It involves scanning each element of the input and placing it into its proper position in a binary search tree. This has two phases:

- First phase is creating a binary search tree using the given array elements.
- Second phase is traversing the given binary search tree in inorder, thus resulting in a sorted array.

Performance

The average number of comparisons for this method is $O(n \log n)$. But in worst case, the number of comparisons is reduced by $O(n^2)$, a case which arises when the sort tree is skew tree.

10.13 Comparison of Sorting Algorithms

Name	Average Case	Worst Case	Auxiliary Memory	Is Stable?	Other Notes
Bubble	$O(n^2)$	$O(n^2)$	1	yes	Small code
Selection	$O(n^2)$	$O(n^2)$	1	no	Stability depends on the implementation.
Insertion	$O(n^2)$	$O(n^2)$	1	yes	Average case is also $O(n + d)$, where d is the number of inversions.
Shell	-	$O(n \log^2 n)$	1	no	
Merge sort	$O(n \log n)$	$O(n \log n)$	depends	yes	
Heap sort	$O(n \log n)$	$O(n \log n)$	1	no	
Quick sort	$O(n \log n)$	$O(n^2)$	$O(\log n)$	depends	Can be implemented as a stable sort depending on how the pivot is handled.
Tree sort	$O(n \log n)$	$O(n^2)$	$O(n)$	depends	Can be implemented as a stable sort.

Note: n denotes the number of elements in the input.

10.14 Linear Sorting Algorithms

In earlier sections, we have seen many examples of comparison-based sorting algorithms. Among them, the best comparison-based sorting has the complexity $O(n \log n)$. In this section, we will discuss other types of algorithms: Linear Sorting Algorithms. To improve the time complexity of sorting these algorithms, we make some assumptions about the input. A few examples of Linear Sorting Algorithms are:

- Counting Sort
- Bucket Sort
- Radix Sort

10.15 Counting Sort

Counting sort is not a comparison sort algorithm and gives $O(n)$ complexity for sorting. To achieve $O(n)$ complexity, *counting* sort assumes that each of the elements is an integer in the range 1 to K , for some integer K . When $i = O(n)$, the *counting* sort runs in $O(n)$ time. The basic idea of Counting sort is to determine, for each input element X , the number of elements less than X . This information can be used to place it directly into its correct position. For example, if 10 elements are less than X , then X belongs to position 11 in the output.

In the code below, $A[0 .. n - 1]$ is the input array with length n . In Counting sort we need two more arrays: let us assume array $B[0 .. n - 1]$ contains the sorted output and the array $C[0 .. K - 1]$ provides temporary storage.

```

void CountingSort (int A[], int n, int B[], int K) {
    int C[K], i, j;
    //Complexity: O(K)
    for (i =0 ; i<K; i++)
        C[i] = 0;
    //Complexity: O(n)
    for (j =0 ; j<n; j++)
        C[A[j]] = C[A[j]] + 1;
    //C[i] now contains the number of elements equal to i
    //Complexity: O(K)
    for (i =1 ; i<K; i++)
        C[i] = C[i] + C[i-1];
    // C[i] now contains the number of elements ≤ i
    //Complexity: O(n)
    for (j = n-1; j>=0; j--) {
        B[C[A[j]]] = A[j];
        C[A[j]] = C[A[j]] - 1;
    }
}

```

Total Complexity: $O(K) + O(n) + O(K) + O(n) = O(n)$ if $K = O(n)$. Space Complexity: $O(n)$ if $K = O(n)$.

Note: Counting works well if $K = O(n)$. Otherwise, the complexity will be greater.

10.16 Bucket Sort (or Bin Sort)

Like *Counting* sort, *Bucket* sort also imposes restrictions on the input to improve the performance. In other words, Bucket sort works well if the input is drawn from fixed set. *Bucket* sort is the generalization of *Counting* Sort. For example, assume that all the input elements from $\{0, 1, \dots, K - 1\}$, i.e., the set of integers in the interval $[0, K - 1]$. That means, K is the number of distinct elements in the input. *Bucket* sort uses K counters. The i^{th} counter keeps track of the number of occurrences of the i^{th} element. Bucket sort with two buckets is effectively a version of Quick sort with two buckets.

For bucket sort, the hash function that is used to partition the elements need to be very good and must produce ordered hash: if $i < k$ then $\text{hash}(i) < \text{hash}(k)$. Second, the elements to be sorted must be uniformly distributed.

The aforementioned aside, bucket sort is actually very good considering that counting sort is reasonably speaking its upper bound. And counting sort is very fast. The particular distinction for bucket sort is that it uses a hash function to partition the keys of the input array, so that multiple keys may hash to the same bucket. Hence each bucket must effectively be a growable list; similar to radix sort.

In the below code insertionsort is used to sort each bucket. This is to inculcate that the bucket sort algorithm does not specify which sorting technique to use on the buckets. A programmer may choose to continuously use bucket sort on each bucket until the collection is sorted (in the manner of the radix sort program below). Whichever sorting method is used on the , bucket sort still tends toward $O(n)$.

```
#define BUCKETS 10
void BucketSort(int A[], int array_size) {
    int i, j, k;
    int buckets[BUCKETS];
    for(j = 0; j < BUCKETS; j++)
        buckets[j] = 0;
    for(i = 0; i < array_size; i++)
        ++ buckets[A[i]];
    for(i = 0, j = 0; j < BUCKETS; j++)
        for(k = buckets[j]; k > 0; --k)
            A[i++] = j;
}
```

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

10.17 Radix Sort

Similar to *Counting* sort and *Bucket* sort, this sorting algorithm also assumes some kind of information about the input elements. Suppose that the input values to be sorted are from base d . That means all numbers are d -digit numbers.

In Radix sort, first sort the elements based on the last digit [the least significant digit]. These results are again sorted by second digit [the next to least significant digit]. Continue this process for all digits until we reach the most significant digits. Use some stable sort to sort them by last digit. Then stable sort them by the second least significant digit, then by the third, etc. If we use Counting sort as the stable sort, the total time is $O(nd) \approx O(n)$.

Algorithm:

- 1) Take the least significant digit of each element.

- 2) Sort the list of elements based on that digit, but keep the order of elements with the same digit (this is the definition of a stable sort).
- 3) Repeat the sort with each more significant digit.

The speed of Radix sort depends on the inner basic operations. If the operations are not efficient enough, Radix sort can be slower than other algorithms such as Quick sort and Merge sort. These operations include the insert and delete functions of the sub-lists and the process of isolating the digit we want. If the numbers are not of equal length then a test is needed to check for additional digits that need sorting. This can be one of the slowest parts of Radix sort and also one of the hardest to make efficient.

Since Radix sort depends on the digits or letters, it is less flexible than other sorts. For every different type of data, Radix sort needs to be rewritten, and if the sorting order changes, the sort needs to be rewritten again. In short, Radix sort takes more time to write, and it is very difficult to write a general purpose Radix sort that can handle all kinds of data.

For many programs that need a fast sort, Radix sort is a good choice. Still, there are faster sorts, which is one reason why Radix sort is not used as much as some other sorts.

Time Complexity: $O(nd) \approx O(n)$, if d is small.

10.18 Topological Sort

Refer to [Graph Algorithms](#) Chapter.

10.19 External Sorting

External sorting is a generic term for a class of sorting algorithms that can handle massive amounts of data. These external sorting algorithms are useful when the files are too big and cannot fit into main memory.

As with internal sorting algorithms, there are a number of algorithms for external sorting. One such algorithm is External Mergesort. In practice, these external sorting algorithms are being supplemented by internal sorts.

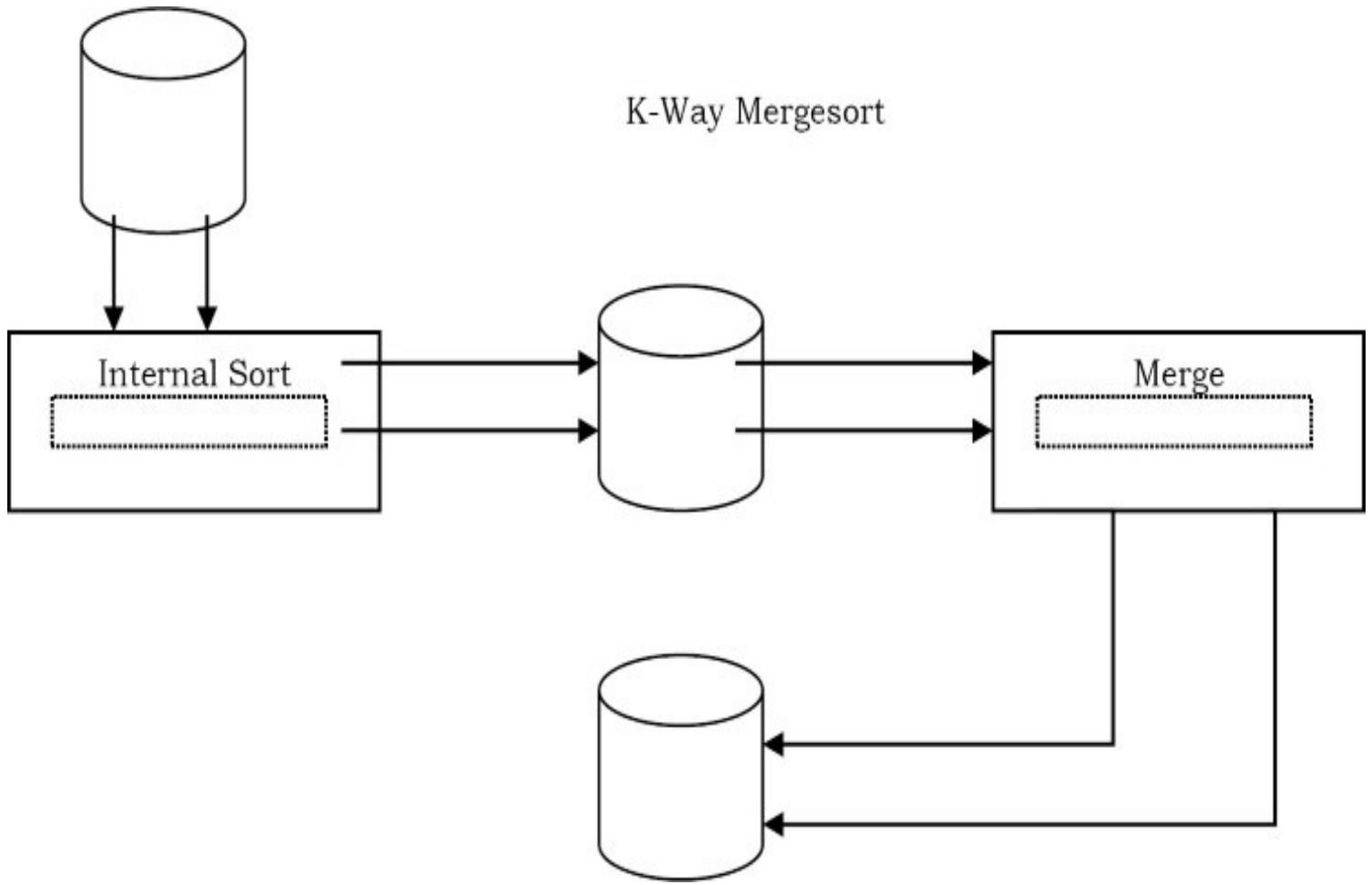
Simple External Mergesort

A number of records from each tape are read into main memory, sorted using an internal sort, and then output to the tape. For the sake of clarity, let us assume that 900 megabytes of data needs to be sorted using only 100 megabytes of RAM.

- 1) Read 100MB of the data into main memory and sort by some conventional method

(let us say Quick sort).

- 2) Write the sorted data to disk.
- 3) Repeat steps 1 and 2 until all of the data is sorted in chunks of 100MB. Now we need to merge them into one single sorted output file.
- 4) Read the first 10MB of each sorted chunk (call them input buffers) in main memory (90MB total) and allocate the remaining 10MB for output buffer.
- 5) Perform a 9-way Mergesort and store the result in the output buffer. If the output buffer is full, write it to the final sorted file. If any of the 9 input buffers gets empty, fill it with the next 10MB of its associated 100MB sorted chunk; or if there is no more data in the sorted chunk, mark it as exhausted and do not use it for merging.



The above algorithm can be generalized by assuming that the amount of data to be sorted exceeds the available memory by a factor of K . Then, K chunks of data need to be sorted and a K -way merge has to be completed.

If X is the amount of main memory available, there will be K input buffers and 1 output buffer of size $X/(K + 1)$ each. Depending on various factors (how fast is the hard drive?) better performance can be achieved if the output buffer is made larger (for example, twice as large as one input buffer).

Complexity of the 2-way External Merge sort: In each pass we read + write each page in file. Let

us assume that there are n pages in file. That means we need $\lceil \log n \rceil + 1$ number of passes. The total cost is $2n(\lceil \log n \rceil + 1)$.

10.20 Sorting: Problems & Solutions

Problem-1 Given an array $A[0...n-1]$ of n numbers containing the repetition of some number.

Give an algorithm for checking whether there are repeated elements or not. Assume that we are not allowed to use additional space (i.e., we can use a few temporary variables, $O(1)$ storage).

Solution: Since we are not allowed to use extra space, one simple way is to scan the elements one-by-one and for each element check whether that element appears in the remaining elements. If we find a match we return true.

```
int CheckDuplicatesInArray(in A[], int n) {
    for (int i = 0; i < n; i++)
        for (int j = i + 1; j < n; j++)
            if(A[i]==A[j])
                return true;
    return false;
}
```

Each iteration of the inner, j -indexed loop uses $O(1)$ space, and for a fixed value of i , the j loop executes $n - i$ times. The outer loop executes $n - 1$ times, so the entire function uses time proportional to

$$\sum_{i=1}^{n-1} n - i = n(n - 1) - \sum_{i=1}^{n-1} i = n(n - 1) - \frac{n(n-1)}{2} = \frac{n(n-1)}{2} = O(n^2)$$

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-2 Can we improve the time complexity of [Problem-1](#)?

Solution: Yes, using sorting technique.

```

int CheckDuplicatesInArray(in A[], int n) {
    //for heap sort algorithm refer Priority Queues chapter
    Heapsort( A, n );
    for (int i = 0; i < n-1; i++)
        if(A[i]==A[i+1])
            return true;
    return false;
}

```

Heapsort function takes $O(n\log n)$ time, and requires $O(1)$ space. The scan clearly takes $n - 1$ iterations, each iteration using $O(1)$ time. The overall time is $O(n\log n + n) = O(n\log n)$.

Time Complexity: $O(n\log n)$. Space Complexity: $O(1)$.

Note: For variations of this problem, refer [Searching](#) chapter.

Problem-3 Given an array $A[0 \dots n - 1]$, where each element of the array represents a vote in the election. Assume that each vote is given as an integer representing the ID of the chosen candidate. Give an algorithm for determining who wins the election.

Solution: This problem is nothing but finding the element which repeated the maximum number of times. The solution is similar to the [Problem-1](#) solution: keep track of counter.

```

int CheckWhoWinsTheElection(in A[], int n) {
    int i, j, counter = 0, maxCounter = 0, candidate;
    candidate = A[0];
    for (i = 0; i < n; i++) {
        candidate = A[i];
        counter = 0;
        for (j = i + 1; j < n; j++) {
            if(A[i]==A[j]) counter++;
        }
        if(counter > maxCounter) {
            maxCounter = counter;
            candidate = A[i];
        }
    }
    return candidate;
}

```

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Note: For variations of this problem, refer to [Searching](#) chapter.

Problem-4 Can we improve the time complexity of [Problem-3](#)? Assume we don't have any extra space.

Solution: Yes. The approach is to sort the votes based on candidate ID, then scan the sorted array and count up which candidate so far has the most votes. We only have to remember the winner, so we don't need a clever data structure. We can use Heapsort as it is an in-place sorting algorithm.

```
int CheckWhoWinsTheElection(in A[], int n) {
    int i, j, currentCounter = 1, maxCounter = 1;
    int currentCandidate, maxCandidate;
    currentCandidate = maxCandidate= A[0];
    //for heap sort algorithm refer Priority Queues Chapter
    Heapsort( A, n );
    for (int i = 1; i <= n; i++) {
        if( A[i] == currentCandidate)
            currentCounter++;
        else {
            currentCandidate = A[i];
            currentCounter = 1;
        }
        if(currentCounter > maxCounter)
            maxCounter = currentCounter;
        else {
            maxCandidate = currentCandidate;
            maxCounter = currentCounter;
        }
    }
    return candidate;
}
```

Since Heapsort time complexity is $O(n \log n)$ and in-place, it only uses an additional $O(1)$ of storage in addition to the input array. The scan of the sorted array does a constant-time conditional $n - 1$ times, thus using $O(n)$ time. The overall time bound is $O(n \log n)$.

Problem-5 Can we further improve the time complexity of [Problem-3](#)?

Solution: In the given problem, the number of candidates is less but the number of votes is significantly large. For this problem we can use counting sort.

Time Complexity: $O(n)$, n is the number of votes (elements) in the array. Space Complexity: $O(k)$,

k is the number of candidates participating in the election.

Problem-6 Given an array A of n elements, each of which is an integer in the range $[1, n^2]$, how do we sort the array in $O(n)$ time?

Solution: If we subtract each number by 1 then we get the range $[0, n^2 - 1]$. If we consider all numbers as 2-digit base n . Each digit ranges from 0 to $n^2 - 1$. Sort this using radix sort. This uses only two calls to counting sort. Finally, add 1 to all the numbers. Since there are 2 calls, the complexity is $O(2n) \approx O(n)$.

Problem-7 For [Problem-6](#), what if the range is $[1 \dots n^3]$?

Solution: If we subtract each number by 1 then we get the range $[0, n^3 - 1]$. Considering all numbers as 3-digit base n : each digit ranges from 0 to $n^3 - 1$. Sort this using radix sort. This uses only three calls to counting sort. Finally, add 1 to all the numbers. Since there are 3 calls, the complexity is $O(3n) \approx O(n)$.

Problem-8 Given an array with n integers, each of value less than n^{100} , can it be sorted in linear time?

Solution: Yes. The reasoning is same as in of [Problem-6](#) and [Problem-7](#).

Problem-9 Let A and B be two arrays of n elements each. Given a number K , give an $O(n \log n)$ time algorithm for determining whether there exists $a \in A$ and $b \in B$ such that $a + b = K$.

Solution: Since we need $O(n \log n)$, it gives us a pointer that we need to sort. So, we will do that.

```
int Find( int A[], int B[], int n, K ) {
    int i, c;
    Heapsort( A, n );           // O(n log n)
    for (i = 0; i < n; i++) {    // O(n)
        c = k - B[i];          // O(1)
        if(BinarySearch(A, c))  // O(log n)
            return 1;
    }
    return 0;
}
```

Note: For variations of this problem, refer to [Searching](#) chapter.

Problem-10 Let A, B and C be three arrays of n elements each. Given a number K , give an $O(n \log n)$ time algorithm for determining whether there exists $a \in A$, $b \in B$ and $c \in C$ such that $a + b + c = K$.

Solution: Refer to [Searching](#) chapter.

Problem-11 Given an array of n elements, can we output in sorted order the K elements following the median in sorted order in time $O(n + K \log K)$.

Solution: Yes. Find the median and partition the median. With this we can find all the elements greater than it. Now find the K^{th} largest element in this set and partition it; and get all the elements less than it. Output the sorted list of the final set of elements. Clearly, this operation takes $O(n + K \log K)$ time.

Problem-12 Consider the sorting algorithms: Bubble sort, Insertion sort, Selection sort, Merge sort, Heap sort, and Quick sort. Which of these are stable?

Solution: Let us assume that A is the array to be sorted. Also, let us say R and S have the same key and R appears earlier in the array than S . That means, R is at $A[i]$ and S is at $A[j]$, with $i < j$. To show any stable algorithm, in the sorted output R must precede S .

Bubble sort: Yes. Elements change order only when a smaller record follows a larger. Since S is not smaller than R it cannot precede it.

Selection sort: No. It divides the array into sorted and unsorted portions and iteratively finds the minimum values in the unsorted portion. After finding a minimum x , if the algorithm moves x into the sorted portion of the array by means of a swap, then the element swapped could be R which then could be moved behind S . This would invert the positions of R and S , so in general it is not stable. If swapping is avoided, it could be made stable but the cost in time would probably be very significant.

Insertion sort: Yes. As presented, when S is to be inserted into sorted subarray $A[1..j - 1]$, only records larger than S are shifted. Thus R would not be shifted during S 's insertion and hence would always precede it.

Merge sort: Yes, In the case of records with equal keys, the record in the left subarray gets preference. Those are the records that came first in the unsorted array. As a result, they will precede later records with the same key.

Heap sort: No. Suppose $i = 1$ and R and S happen to be the two records with the largest keys in the input. Then R will remain in location 1 after the array is heapified, and will be placed in location n in the first iteration of Heapsort. Thus S will precede R in the output.

Quick sort: No. The partitioning step can swap the location of records many times, and thus two records with equal keys could swap position in the final output.

Problem-13 Consider the same sorting algorithms as that of [Problem-12](#). Which of them are in-place?

Solution:

Bubble sort: Yes, because only two integers are required.

Insertion sort: Yes, since we need to store two integers and a record.

Selection sort: Yes. This algorithm would likely need space for two integers and one record.

Merge sort: No. Arrays need to perform the merge. (If the data is in the form of a linked list, the sorting can be done in-place, but this is a nontrivial modification.)

Heap sort: Yes, since the heap and partially-sorted array occupy opposite ends of the input array.

Quicksort: No, since it is recursive and stores $O(\log n)$ activation records on the stack. Modifying it to be non-recursive is feasible but nontrivial.

Problem-14 Among Quick sort, Insertion sort, Selection sort, and Heap sort algorithms, which one needs the minimum number of swaps?

Solution: Selection sort – it needs n swaps only (refer to theory section).

Problem-15 What is the minimum number of comparisons required to determine if an integer appears more than $n/2$ times in a sorted array of n integers?

Solution: Refer to [Searching](#) chapter.

Problem-16 Sort an array of 0's, 1's and 2's: Given an array $A[]$ consisting of 0's, 1's and 2's, give an algorithm for sorting $A[]$. The algorithm should put all 0's first, then all 1's and all 2's last.

Example: Input = {0,1,1,0,1,2,1,2,0,0,0,1}, Output = {0,0,0,0,0,1,1,1,1,2,2}

Solution: Use Counting sort. Since there are only three elements and the maximum value is 2, we need a temporary array with 3 elements.

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

Note: For variations of this problem, refer to [Searching](#) chapter.

Problem-17 Is there any other way of solving [Problem-16](#)?

Solution: Using Quick sort. Since we know that there are only 3 elements, 0,1 and 2 in the array, we can select 1 as a pivot element for Quick sort. Quick sort finds the correct place for 1 by moving all 0's to the left of 1 and all 2's to the right of 1. For doing this it uses only one scan.

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

Note: For efficient algorithm, refer to [Searching](#) chapter.

Problem-18 How do we find the number that appeared the maximum number of times in an array?

Solution: One simple approach is to sort the given array and scan the sorted array. While scanning, keep track of the elements that occur the maximum number of times.

Algorithm:

```
QuickSort(A, n);
int i, j, count=1, Number=A[0], j=0;
for(i=0;i<n;i++) {
    if(A[j]==A) {
        count++;
        Number=A[j];
    }
    j=i;
}
printf("Number:%d, count:%d", Number, count);
```

Time Complexity = Time for Sorting + Time for Scan = $O(n \log n)$ + $O(n)$ = $O(n \log n)$. Space Complexity: $O(1)$.

Note: For variations of this problem, refer to [Searching](#) chapter.

Problem-19 Is there any other way of solving [Problem-18](#)?

Solution: Using Binary Tree. Create a binary tree with an extra field *count* which indicates the number of times an element appeared in the input. Let us say we have created a Binary Search Tree [BST]. Now, do the In-Order traversal of the tree. The In-Order traversal of BST produces the sorted list. While doing the In-Order traversal keep track of the maximum element.

Time Complexity: $O(n) + O(n) \approx O(n)$. The first parameter is for constructing the BST and the second parameter is for Inorder Traversal. Space Complexity: $O(2n) \approx O(n)$, since every node in BST needs two extra pointers.

Problem-20 Is there yet another way of solving [Problem-18](#)?

Solution: Using Hash Table. For each element of the given array we use a counter, and for each occurrence of the element we increment the corresponding counter. At the end we can just return the element which has the maximum counter.

Time Complexity: $O(n)$. Space Complexity: $O(n)$. For constructing the hash table we need $O(n)$.

Note: For the efficient algorithm, refer to the [Searching](#) chapter.

Problem-21 Given a 2 GB file with one string per line, which sorting algorithm would we use to sort the file and why?

Solution: When we have a size limit of 2GB, it means that we cannot bring all the data into the main memory.

Algorithm: How much memory do we have available? Let's assume we have X MB of memory available. Divide the file into K chunks, where $X * K \sim 2\text{ GB}$.

- Bring each chunk into memory and sort the lines as usual (any $O(n \log n)$ algorithm).
- Save the lines back to the file.
- Now bring the next chunk into memory and sort.
- Once we're done, merge them one by one; in the case of one set finishing, bring more data from the particular chunk.

The above algorithm is also known as *external sort*. Step 3 – 4 is known as K-way merge. The idea behind going for an external sort is the size of data. Since the data is huge and we can't bring it to the memory, we need to go for a disk-based sorting algorithm.

Problem-22 Nearly sorted: Given an array of n elements, each which is at most K positions from its target position, devise an algorithm that sorts in $O(n \log K)$ time.

Solution: Divide the elements into n/K groups of size K , and sort each piece in $O(K \log K)$ time, let's say using Mergesort. This preserves the property that no element is more than K elements out of position. Now, merge each block of K elements with the block to its left.

Problem-23 Is there any other way of solving [Problem-22](#)?

Solution: Insert the first K elements into a binary heap. Insert the next element from the array into the heap, and delete the minimum element from the heap. Repeat.

Problem-24 Merging K sorted lists: Given K sorted lists with a total of n elements, give an $O(n \log K)$ algorithm to produce a sorted list of all n elements.

Solution: Simple Algorithm for merging K sorted lists: Consider groups each having $\frac{n}{K}$ elements. Take the first list and merge it with the second list using a linear-time algorithm for merging two sorted lists, such as the merging algorithm used in merge sort. Then, merge the resulting list of $\frac{2n}{K}$ elements with the third list, and then merge the resulting list of $\frac{3n}{K}$ elements with the fourth list. Repeat this until we end up with a single sorted list of all n elements.

Time Complexity: In each iteration we are merging K elements.

$$T(n) = \frac{2n}{K} + \frac{3n}{K} + \frac{4n}{K} + \dots + \frac{Kn}{K}(n) = \frac{n}{K} \sum_{i=2}^K i$$

$$T(n) = \frac{n}{K} \left[\frac{K(K+1)}{2} \right] \approx O(nK)$$

Problem-25 Can we improve the time complexity of [Problem-24](#)?

Solution: One method is to repeatedly pair up the lists and then merge each pair. This method can also be seen as a tail component of the execution merge sort, where the analysis is clear. This is called the Tournament Method. The maximum depth of the Tournament Method is $\log K$ and in each iteration we are scanning all the n elements.

Time Complexity; $O(n \log K)$.

Problem-26 Is there any other way of solving [Problem-24](#)?

Solution: The other method is to use a *rain* priority queue for the minimum elements of each of the K lists. At each step, we output the extracted minimum of the priority queue, determine from which of the K lists it came, and insert the next element from that list into the priority queue. Since we are using priority queue, that maximum depth of priority queue is $\log K$.

Time Complexity; $O(n \log K)$.

Problem-27 Which sorting method is better for Linked Lists?

Solution: Merge Sort is a better choice. At first appearance, merge sort may not be a good selection since the middle node is required to subdivide the given list into two sub-lists of equal length. We can easily solve this problem by moving the nodes alternatively to two lists (refer to [Linked Lists](#) chapter). Then, sorting these two lists recursively and merging the results into a single list will sort the given one.

```

typedef struct ListNode {
    int data;
    struct ListNode *next;
};

struct ListNode * LinkedListMergeSort(struct ListNode * first) {
    struct ListNode * list1HEAD = NULL;
    struct ListNode * list1TAIL = NULL;
    struct ListNode * list2HEAD = NULL;
    struct ListNode * list2TAIL = NULL;
    if(first==NULL || first->next==NULL)
        return first;
    while (first != NULL) {
        Append(first, list1HEAD, list1TAIL);
        if(first != NULL)
            Append(first, list2HEAD, list2TAIL);
    }
    list1HEAD = LinkedListMergeSort(list1HEAD);
    list2HEAD = LinkedListMergeSort(list2HEAD);
    return Merge(list1HEAD, list2HEAD);
}

```

Note: Append() appends the first argument to the tail of a singly linked list whose head and tail are defined by the second and third arguments.

All external sorting algorithms can be used for sorting linked lists since each involved file can be considered as a linked list that can only be accessed sequentially. We can sort a doubly linked list using its next fields as if it was a singly linked one and reconstruct the prev fields after sorting with an additional scan.

Problem-28 Can we implement Linked Lists Sorting with Quick Sort?

Solution: The original Quick Sort cannot be used for sorting Singly Linked Lists. This is because we cannot move backward in Singly Linked Lists. But we can modify the original Quick Sort and make it work for Singly Linked Lists.

Let us consider the following modified Quick Sort implementation. The first node of the input list is considered a *pivot* and is moved to *equal*. The value of each node is compared with the *pivot* and moved to *less* (respectively, *equal* or *larger*) if the nodes value is smaller than (respectively, *equal* to or *larger* than) the *pivot*. Then, *less* and *larger* are sorted recursively. Finally, joining *less*, *equal* and *larger* into a single list yields a sorted one.

Append() appends the first argument to the tail of a singly linked list whose head and tail are defined by the second and third arguments. On return, the first argument will be modified so that it

points to the next node of the list. *Join()* appends the list whose head and tail are defined by the third and fourth arguments to the list whose head and tail are defined by the first and second arguments. For simplicity, the first and fourth arguments become the head and tail of the resulting list.

```
typedef struct ListNode {
    int data;
    struct ListNode *next;
};

void Qsort(struct ListNode *first, struct ListNode * last) {
    struct ListNode *lesHEAD=NULL, lesTAIL=NULL;
    struct ListNode *equHEAD=NULL, equTAIL=NULL;
    struct ListNode *larHEAD=NULL, larTAIL=NULL;
    struct ListNode *current = *first;
    int pivot, info;
    if(current == NULL) return;
    pivot = current->data;
    Append(current, equHEAD, equTAIL);
    while (current != NULL) {
        info = current->data;
        if(info < pivot)
            Append(current, lesHEAD, lesTAIL)
        else if(info > pivot)
            Append(current, larHEAD, larTAIL)
        else
            Append(current, equHEAD, equTAIL);
    }
    Quicksort(&lesHEAD, &lesTAIL);
    Quicksort(&larHEAD, &larTAIL);
    Join(lesHEAD, lesTAIL, equHEAD, equTAIL);
    Join(lesHEAD, equTAIL, larHEAD, larTAIL);
    *first = lesHEAD;
    *last = larTAIL;
}
```

Problem-29 Given an array of 100,000 pixel color values, each of which is an integer in the range [0,255]. Which sorting algorithm is preferable for sorting them?

Solution: Counting Sort. There are only 256 key values, so the auxiliary array would only be of size 256, and there would be only two passes through the data, which would be very efficient in both time and space.

Problem-30 Similar to [Problem-29](#), if we have a telephone directory with 10 million entries,

which sorting algorithm is best?

Solution: Bucket Sort. In Bucket Sort the buckets are defined by the last 7 digits. This requires an auxiliary array of size 10 million and has the advantage of requiring only one pass through the data on disk. Each bucket contains all telephone numbers with the same last 7 digits but with different area codes. The buckets can then be sorted by area code with selection or insertion sort; there are only a handful of area codes.

Problem-31 Give an algorithm for merging K -sorted lists.

Solution: Refer to [Priority Queues](#) chapter.

Problem-32 Given a big file containing billions of numbers. Find maximum 10 numbers from this file.

Solution: Refer to [Priority Queues](#) chapter.

Problem-33 There are two sorted arrays A and B . The first one is of size $m + n$ containing only m elements. Another one is of size n and contains n elements. Merge these two arrays into the first array of size $m + n$ such that the output is sorted.

Solution: The trick for this problem is to start filling the destination array from the back with the largest elements. We will end up with a merged and sorted destination array.

```
void Merge(int[] A[], int m, int B[], int n) {
    int count = m;
    int i = n - 1, j = count - 1, k = m - 1;
    for(;k>=0;k--) {
        if(B[i] > A[j] || j < 0) {
            A[k] = B[i];
            i--;
            if(i<0)
                break;
        }
        else {
            A[k] = A[j];
            j--;
        }
    }
}
```

Time Complexity: $O(m + n)$. Space Complexity: $O(1)$.

Problem-34 Nuts and Bolts Problem: Given a set of n nuts of different sizes and n bolts such that there is a one-to-one correspondence between the nuts and the bolts, find for each nut its corresponding bolt. Assume that we can only compare nuts to bolts: we cannot

compare nuts to nuts and bolts to bolts.

Alternative way of framing the question: We are given a box which contains bolts and nuts. Assume there are n nuts and n bolts and that each nut matches exactly one bolt (and vice versa). By trying to match a bolt and a nut we can see which one is bigger, but we cannot compare two bolts or two nuts directly. Design an efficient algorithm for matching the nuts and bolts.

Solution: Brute Force Approach: Start with the first bolt and compare it with each nut until we find a match. In the worst case, we require n comparisons. Repeat this for successive bolts on all remaining gives $O(n^2)$ complexity.

Problem-35 For [Problem-34](#), can we improve the complexity?

Solution: In [Problem-34](#), we got $O(n^2)$ complexity in the worst case (if bolts are in ascending order and nuts are in descending order). Its analysis is the same as that of Quick Sort. The improvement is also along the same lines. To reduce the worst case complexity, instead of selecting the first bolt every time, we can select a random bolt and match it with nuts. This randomized selection reduces the probability of getting the worst case, but still the worst case is $O(n^2)$.

Problem-36 For [Problem-34](#), can we further improve the complexity?

Solution: We can use a divide-and-conquer technique for solving this problem and the solution is very similar to randomized Quick Sort. For simplicity let us assume that bolts and nuts are represented in two arrays B and N .

The algorithm first performs a partition operation as follows: pick a random bolt $B[t]$. Using this bolt, rearrange the array of nuts into three groups of elements:

- First the nuts smaller than $B[i]$
- Then the nut that matches $B[i]$, and
- Finally, the nuts larger than $B[i]$.

Next, using the nut that matches $B[i]$, perform a similar partition on the array of bolts. This pair of partitioning operations can easily be implemented in $O(n)$ time, and it leaves the bolts and nuts nicely partitioned so that the “pivot” bolt and nut are aligned with each other and all other bolts and nuts are on the correct side of these pivots – smaller nuts and bolts precede the pivots, and larger nuts and bolts follow the pivots. Our algorithm then completes by recursively applying itself to the subarray to the left and right of the pivot position to match these remaining bolts and nuts. We can assume by induction on n that these recursive calls will properly match the remaining bolts.

To analyze the running time of our algorithm, we can use the same analysis as that of randomized Quick Sort. Therefore, applying the analysis from Quick Sort, the time complexity of our algorithm is $O(n \log n)$.

Alternative Analysis: We can solve this problem by making a small change to Quick Sort. Let us assume that we pick the last element as the pivot, say it is a nut. Compare the nut with only bolts as we walk down the array. This will partition the array for the bolts. Every bolt less than the partition nut will be on the left. And every bolt greater than the partition nut will be on the right.

While traversing down the list, find the matching bolt for the partition nut. Now we do the partition again using the matching bolt. As a result, all the nuts less than the matching bolt will be on the left side and all the nuts greater than the matching bolt will be on the right side. Recursively call on the left and right arrays.

The time complexity is $O(2n\log n) \approx O(n\log n)$.

Problem-37 Given a binary tree, can we print its elements in sorted order in $O(n)$ time by performing an In-order tree traversal?

Solution: Yes, if the tree is a Binary Search Tree [BST]. For more details refer to [Trees](#) chapter.

Problem-38 Given an array of elements, convert it into an array such that $A < B > C < D > E < F$ and so on.

Solution: Sort the array, then swap every adjacent element to get the final result.

```
#include<algorithm>
convertArraytoSawToothWave(){
    int A[] = {0,-6,9,13,10,-1,8,12,54,14,-5};
    int n = sizeof(A)/sizeof(A[0]), i = 1, temp;
    sort(A, A+n);
    for(i=1; i < n; i+=2){
        if(i+1 < n){
            temp = A[i]; A[i] = A[i+1]; A[i+1] = temp;
        }
    }
    for(i=0; i < n; i++){
        printf("%d ", A[i]);
    }
}
```

The time complexity is $O(n\log n + n) \approx O(n\log n)$, for sorting and a scan.

Problem-39 Can we do [Problem-38](#) with $O(n)$ time?

Solution: Make sure all even positioned elements are greater than their adjacent odd elements, and we don't need to worry about odd positioned elements. Traverse all even positioned elements of input array, and do the following:

- If the current element is smaller than the previous odd element, swap previous and

- current.
- If the current element is smaller than the next odd element, swap next and current.

```

convertArraytoSawToothWave(){
    int A[] = {0,-6,9,13,10,-1,8,12,54,14,-5};
    int n = sizeof(A)/sizeof(A[0]), i = 1, temp;
    sort(A, A+n);
    for(i=1; i < n; i+=2){
        if (i>0 && A[i-1] > A[i] ){
            temp = A[i]; A[i] = A[i-1]; A[i-1] = temp;
        }
        if (i<n-1 && A[i] < A[i+1] ){
            temp = A[i]; A[i] = A[i+1]; A[i+1] = temp;
        }
    }
    for(i=0; i < n; i++){
        cout<<A[i]<< " ";
    }
}

```

The time complexity is $O(n)$.

Problem-40 Merge sort uses

- Divide and conquer strategy
- Backtracking approach
- Heuristic search
- Greedy approach

Solution: (a). Refer theory section.

Problem-41 Which of the following algorithm design techniques is used in the quicksort algorithm?

- Dynamic programming
- Backtracking
- Divide and conquer
- Greedy method

Solution: (c). Refer theory section.

Problem-42 For merging two sorted lists of sizes m and n into a sorted list of size $m+n$, we required comparisons of

- $O(m)$
- $O(n)$
- $O(m + n)$

(d) $O(\log m + \log n)$

Solution: (c). We can use merge sort logic. Refer theory section.

Problem-43 Quick-sort is run on two inputs shown below to sort in ascending order

- (i) 1, 2, 3n
- (ii) n, n-1, n-2, 2, 1

Let C1 and C2 be the number of comparisons made for the inputs (i) and (ii) respectively. Then,

- (a) $C_1 < C_2$
- (b) $C_1 > C_2$
- (c) $C_1 = C_2$
- (d) we cannot say anything for arbitrary n .

Solution: (b). Since the given problems needs the output in ascending order, Quicksort on already sorted order gives the worst case ($O(n^2)$). So, (i) generates worst case and (ii) needs fewer comparisons.

Problem-44 Give the correct matching for the following pairs:

- | | |
|-----|---------------------------|
| (A) | $O(\log n)$ |
| (B) | $O(n)$ |
| (C) | $O(n \log n)$ |
| (D) | $O(n^2)$ |
| (P) | Selection |
| (Q) | Insertion sort |
| (R) | Binary search |
| (S) | Merge sort |
| (a) | A – R B – P C – Q – D – S |
| (b) | A – R B – P C – S D – Q |
| (c) | A – P B – R C – S D – Q |
| (d) | A – P B – S C – R D – Q |

Solution: (b). Refer theory section.

Problem-45 Let s be a sorted array of n integers. Let $t(n)$ denote the time taken for the most efficient algorithm to determine if there are two elements with sum less than 1000 in s. which of the following statements is true?

- a) $t(n)$ is $O(1)$
- b) $n < t(n) < n \log_2^n$
- c) $n \log_2^n < t(n) < \binom{n}{2}$
- d) $t(n) = \binom{n}{2}$

Solution: (a). Since the given array is already sorted it is enough if we check the first two elements of the array.

Problem-46 The usual $\Theta(n^2)$ implementation of Insertion Sort to sort an array uses linear search to identify the position where an element is to be inserted into the already sorted part of the array. If, instead, we use binary search to identify the position, the worst case running time will

- (a) remain $\Theta(n^2)$
- (b) become $\Theta(n(\log n)^2)$
- (c) become $\Theta(n \log n)$
- (d) become $\Theta(n)$

Solution: (a). If we use binary search then there will be $\log_2 n!$ comparisons in the worst case, which is $\Theta(n \log n)$. But the algorithm as a whole will still have a running time of $\Theta(n^2)$ on average because of the series of swaps required for each insertion.

Problem-47 In quick sort, for sorting n elements, the $n/4^{th}$ smallest element is selected as pivot using an $O(n)$ time algorithm. What is the worst case time complexity of the quick sort?

- (A) $\Theta(n)$
- (B) $\Theta(n \log n)$
- (C) $\Theta(n^2)$
- (D) $\Theta(n^2 \log n)$

Solution: The recursion expression becomes: $T(n) = T(n/4) + T(3n/4) + en$. Solving the recursion using *variant* of master theorem, we get $\Theta(n \log n)$.

Problem-48 Consider the Quicksort algorithm. Suppose there is a procedure for finding a pivot element which splits the list into two sub-lists each of which contains at least one-fifth of the elements. Let $T(n)$ be the number of comparisons required to sort n elements. Then

- A) $T(n) \leq 2T(n/5) + n$
- B) $T(n) \leq T(n/5) + T(4n/5) + n$
- C) $T(n) \leq 2T(4n/5) + n$
- D) $T(n) \leq 2T(n/2) + n$

Solution: (C). For the case where $n/5$ elements are in one subset, $T(n/5)$ comparisons are needed for the first subset with $n/5$ elements, $T(4n/5)$ is for the rest $4n/5$ elements, and n is for finding the pivot. If there are more than $n/5$ elements in one set then other set will have less than $4n/5$ elements and time complexity will be less than $T(n/5) + T(4n/5) + n$.

Problem-49 Which of the following sorting algorithms has the lowest worst-case complexity?

- (A) Merge sort
- (B) Bubble sort
- (C) Quick sort
- (D) Selection sort

Solution: (A). Refer theory section.

Problem-50 Which one of the following in place sorting algorithms needs the minimum number of swaps?

- (A) Quick sort
- (B) Insertion sort
- (C) Selection sort
- (D) Heap sort

Solution: (C). Refer theory section.

Problem-51 You have an array of n elements. Suppose you implement quicksort by always choosing the central element of the array as the pivot. Then the tightest upper bound for the worst case performance is

- (A) $O(n^2)$
- (B) $O(n \log n)$
- (C) $\Theta(n \log n)$
- (D) $O(n^3)$

Solution: (A). When we choose the first element as the pivot, the worst case of quick sort comes if the input is sorted- either in ascending or descending order.

Problem-52 Let P be a Quicksort Program to sort numbers in ascending order using the first element as pivot. Let t_1 and t_2 be the number of comparisons made by P for the inputs $\{1, 2, 3, 4, 5\}$ and $\{4, 1, 5, 3, 2\}$ respectively. Which one of the following holds?

- (A) $t_1 = 5$
- (B) $t_1 < t_2$
- (C) $t_1 > t_2$
- (D) $t_1 = t_2$

Solution: (C). Quick Sort's worst case occurs when first (or last) element is chosen as pivot with sorted arrays.

Problem-53 The minimum number of comparisons required to find the minimum and the maximum of 100 numbers is ____

Solution: 147 (Formula for the minimum number of comparisons required is $3n/2 - 3$ with n numbers).

Problem-54 The number of elements that can be sorted in $T(\log n)$ time using heap sort is

- (A) $\Theta(1)$
- (B) $\Theta(\sqrt{\log n})$
- (C) $\Theta(\log n / (\log \log n))$
- (D) $\Theta(\log n)$

Solution: (D). Sorting an array with k elements takes time $\Theta(k \log k)$ as k grows. We want to choose k such that $\Theta(k \log k) = \Theta(\log n)$. Choosing $k = \Theta(\log n)$ doesn't necessarily work, since

$\Theta(k \log k) = \Theta(\log n \log \log n) \neq \Theta(\log n)$. On the other hand, if you choose $k = T(\log n / \log \log n)$, then the runtime of the sort will be

$$\begin{aligned} &= \Theta((\log n / \log \log n) \log (\log n / \log \log n)) \\ &= \Theta((\log n / \log \log n) (\log \log n - \log \log \log n)) \\ &= \Theta(\log n - \log n \log \log \log n / \log \log n) \\ &= \Theta(\log n (1 - \log \log \log n / \log \log n)) \end{aligned}$$

Notice that $1 - \log \log \log n / \log \log n$ tends toward 1 as n goes to infinity, so the above expression actually is $\Theta(\log n)$, as required. Therefore, if you try to sort an array of size $\Theta(\log n / \log \log n)$ using heap sort, as a function of n , the runtime is $\Theta(\log n)$.

Problem-55 Which one of the following is the tightest upper bound that represents the number of swaps required to sort n numbers using selection sort?

- (A) $O(\log n)$
- (B) $O(n)$
- (C) $O(n \log n)$
- (D) $O(n^2)$

Solution: (B). Selection sort requires only $O(n)$ swaps.

Problem-56 Which one of the following is the recurrence equation for the worst case time complexity of the Quicksort algorithm for sorting $n (\geq 2)$ numbers? In the recurrence equations given in the options below, c is a constant.

- (A) $T(n) = 2T(n/2) + cn$
- (B) $T(n) = T(n-1) + T(0) + cn$
- (C) $T(n) = 2T(n-2) + cn$
- (D) $T(n) = T(n/2) + cn$

Solution: (B). When the pivot is the smallest (or largest) element at partitioning on a block of size n the result yields one empty sub-block, one element (pivot) in the correct place and sub block of size $n-1$.

Problem-57 True or False. In randomized quicksort, each key is involved in the same number of comparisons.

Solution: False.

Problem-58 True or False: If Quicksort is written so that the partition algorithm always uses the median value of the segment as the pivot, then the worst-case performance is $O(n \log n)$.

Soution: True.

SEARCHING

CHAPTER

11



11.1 What is Searching?

In computer science, *searching* is the process of finding an item with specified properties from a collection of items. The items may be stored as records in a database, simple data elements in arrays, text in files, nodes in trees, vertices and edges in graphs, or they may be elements of other search spaces.

11.2 Why do we need Searching?

Searching is one of the core computer science algorithms. We know that today's computers store a lot of information. To retrieve this information proficiently we need very efficient searching algorithms. There are certain ways of organizing the data that improves the searching process. That means, if we keep the data in proper order, it is easy to search the required element. Sorting is one of the techniques for making the elements ordered. In this chapter we will see different searching algorithms.

11.3 Types of Searching

Following are the types of searches which we will be discussing in this book.

- Unordered Linear Search
- Sorted/Ordered Linear Search
- Binary Search
- Interpolation search
- Binary Search Trees (operates on trees and refer [Trees](#) chapter)
- Symbol Tables and Hashing
- String Searching Algorithms: Tries, Ternary Search and Suffix Trees

11.4 Unordered Linear Search

Let us assume we are given an array where the order of the elements is not known. That means the elements of the array are not sorted. In this case, to search for an element we have to scan the complete array and see if the element is there in the given list or not.

```
int UnOrderedLinearSearch (int A[], int n, int data) {  
    for (int i = 0; i < n; i++) {  
        if(A[i] == data)  
            return i;  
    }  
    return -1;  
}
```

Time complexity: $O(n)$, in the worst case we need to scan the complete array. Space complexity: $O(1)$.

11.5 Sorted/Ordered Linear Search

If the elements of the array are already sorted, then in many cases we don't have to scan the complete array to see if the element is there in the given array or not. In the algorithm below, it can be seen that, at any point if the value at $A[i]$ is greater than the $data$ to be searched, then we just return -1 without searching the remaining array.

```

int OrderedLinearSearch(int A[], int n, int data) {
    for (int i = 0; i < n; i++) {
        if(A[i] == data)
            return i;
        else if(A[i] > data)
            return -1;
    }
    return -1;
}

```

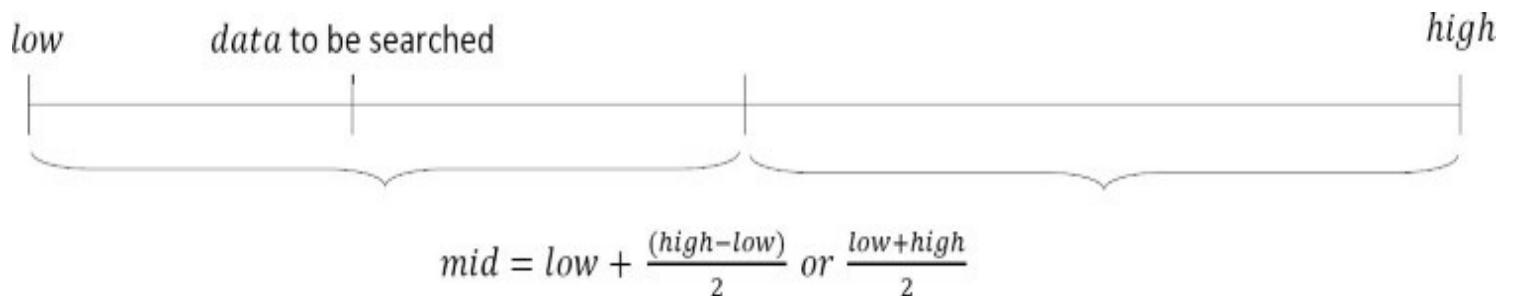
Time complexity of this algorithm is $O(n)$. This is because in the worst case we need to scan the complete array. But in the average case it reduces the complexity even though the growth rate is the same.

Space complexity: $O(1)$.

Note: For the above algorithm we can make further improvement by incrementing the index at a faster rate (say, 2). This will reduce the number of comparisons for searching in the sorted list.

11.6 Binary Search

Let us consider the problem of searching a word in a dictionary. Typically, we directly go to some approximate page [say, middle page] and start searching from that point. If the *name* that we are searching is the same then the search is complete. If the page is before the selected pages then apply the same process for the first half; otherwise apply the same process to the second half. Binary search also works in the same way. The algorithm applying such a strategy is referred to as *binary search algorithm*.



```

//Iterative Binary Search Algorithm
int BinarySearchIterative(int A[], int n, int data) {
    int low = 0;
    int high = n-1;
    while (low <= high) {
        mid = low + (high-low)/2; //To avoid overflow
        if(A[mid] == data)
            return mid;
        else if(A[mid] < data)
            low = mid + 1;
        else high = mid - 1;
    }
    return -1;
}

//Recursive Binary Search Algorithm
int BinarySearchRecursive(int A[], int low, int high, int data) {
    int mid = low + (high-low)/2; //To avoid overflow
    if (low>high)
        return -1;
    if(A[mid] == data)
        return mid;
    else if(A[mid] < data)
        return BinarySearchRecursive (A, mid + 1, high, data);
    else return BinarySearchRecursive (A, low, mid - 1 , data);
    return -1;
}

```

Recurrence for binary search is $T(n) = T(\frac{n}{2}) + \Theta(1)$. This is because we are always considering only half of the input list and throwing out the other half. Using *Divide and Conquer* master theorem, we get, $T(n) = O(\log n)$.

Time Complexity: $O(\log n)$. Space Complexity: $O(1)$ [for iterative algorithm].

11.7 Interpolation Search

Undoubtedly binary search is a great algorithm for searching with average running time complexity of $\log n$. It always chooses the middle of the remaining search space, discarding one half or the other, again depending on the comparison between the key value found at the estimated (middle) position and the key value sought. The remaining search space is reduced to the part

before or after the estimated position.

In the mathematics, interpolation is a process of constructing new data points within the range of a discrete set of known data points. In computer science, one often has a number of data points which represent the values of a function for a limited number of values of the independent variable. It is often required to interpolate (i.e. estimate) the value of that function for an intermediate value of the independent variable.

For example, suppose we have a table like this, which gives some values of an unknown function f . Interpolation provides a means of estimating the function at intermediate points, such as $x = 55$.

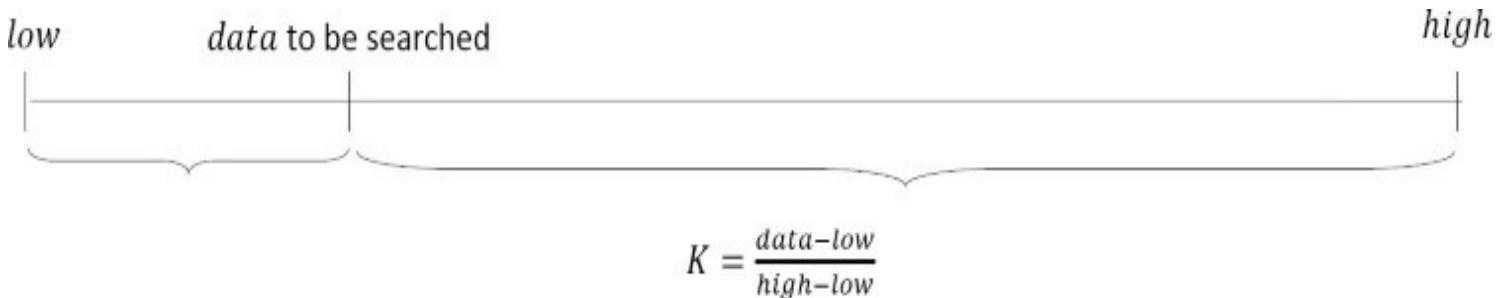
x	$f(x)$
1	10
2	20
3	30
4	40
5	50
6	60
7	70

There are many different interpolation methods, and one of the simplest methods is linear interpolation. Since 55 is midway between 50 and 60, it is reasonable to take $f(55)$ midway between $f(5) = 50$ and $f(6) = 60$, which yields 55.

Linear interpolation takes two data points, say (x_1, y_1) and (x_2, y_2) , and the interpolant is given by:

$$y = y_1 + (y_2 - y_1) \frac{x - x_1}{x_2 - x_1} \text{ at point } (x, y)$$

With above inputs, what will happen if we don't use the constant $\frac{1}{2}$, but another more accurate constant "K", that can lead us closer to the searched item.



This algorithm tries to follow the way we search a name in a phone book, or a word in the dictionary. We, humans, know in advance that in case the name we're searching starts with a "m",

like “monk” for instance, we should start searching near the middle of the phone book. Thus if we’re searching the word “career” in the dictionary, you know that it should be placed somewhere at the beginning. This is because we know the order of the letters, we know the interval (a-z), and somehow we intuitively know that the words are dispersed equally. These facts are enough to realize that the binary search can be a bad choice. Indeed the binary search algorithm divides the list in two equal sub-lists, which is useless if we know in advance that the searched item is somewhere in the beginning or the end of the list. Yes, we can use also jump search if the item is at the beginning, but not if it is at the end, in that case this algorithm is not so effective.

The interpolation search algorithm tries to improve the binary search. The question is how to find this value? Well, we know bounds of the interval and looking closer to the image above we can define the following formula.

$$K = \frac{\text{data} - \text{low}}{\text{high} - \text{low}}$$

This constant K is used to narrow down the search space. For binary search, this constant K is $(\text{low} + \text{high})/2$.

Now we can be sure that we’re closer to the searched value. On average the interpolation search makes about $\log(\log n)$ comparisons (if the elements are uniformly distributed), where n is the number of elements to be searched. In the worst case (for instance where the numerical values of the keys increase exponentially) it can make up to $O(n)$ comparisons. In interpolation-sequential search, interpolation is used to find an item near the one being searched for, then linear search is used to find the exact item. For this algorithm to give best results, the dataset should be ordered and uniformly distributed.

```
int InterpolationSearch(int A[], int data){
    int low = 0, mid, high = sizeof(A) - 1;
    while (low <= high) {
        mid = low + (((data - A[low]) * (high - low)) / (A[high] - A[low]));
        if (data == A[mid])
            return mid + 1;
        if (data < A[mid])
            high = mid - 1;
        else
            low = mid + 1;
    }
    return -1;
}
```

11.8 Comparing Basic Searching Algorithms

Implementation	Search-Worst Case	Search-Average Case
Unordered Array	n	$n/2$
Ordered Array (Binary Search)	$\log n$	$\log n$
Unordered List	n	$n/2$
Ordered List	n	$n/2$
Binary Search Trees (for skew trees)	n	$\log n$
Interpolation search	n	$\log(\log n)$

Note: For discussion on binary search trees refer [Trees](#) chapter.

11.9 Symbol Tables and Hashing

Refer to [Symbol Tables](#) and [Hashing](#) chapters.

11.10 String Searching Algorithms

Refer to [String Algorithms](#) chapter.

11.11 Searching: Problems & Solutions

Problem-1 Given an array of n numbers, give an algorithm for checking whether there are any duplicate elements in the array or no?

Solution: This is one of the simplest problems. One obvious answer to this is exhaustively searching for duplicates in the array. That means, for each input element check whether there is any element with the same value. This we can solve just by using two simple *for* loops. The code for this solution can be given as:

```

void CheckDuplicatesBruteForce(int A[], int n) {
    for(int i = 0; i < n; i++) {
        for(int j = i+1; j < n; j++) {
            if(A[i] == A[j]) {
                printf("Duplicates exist: %d", A[i]);
                return;
            }
        }
    }
    printf("No duplicates in given array.");
}

```

Time Complexity: $O(n^2)$, for two nested *for* loops. Space Complexity: $O(1)$.

Problem-2 Can we improve the complexity of [Problem-1](#)'s solution?

Solution: Yes. Sort the given array. After sorting, all the elements with equal values will be adjacent. Now, do another scan on this sorted array and see if there are elements with the same value and adjacent.

```

void CheckDuplicatesSorting(int A[], int n) {
    Sort(A, n); //sort the array

    for(int i = 0; i < n-1; i++) {
        if(A[i] == A[i+1]) {
            printf("Duplicates exist: %d", A[i]);
            return;
        }
    }
    printf("No duplicates in given array.");
}

```

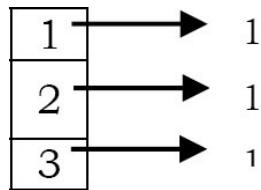
Time Complexity: $O(n \log n)$, for sorting (assuming $n \log n$ sorting algorithm). Space Complexity: $O(1)$.

Problem-3 Is there any alternative way of solving *Problem-1*?

Solution: Yes, using hash table. Hash tables are a simple and effective method used to implement dictionaries. *Average* time to search for an element is $O(1)$, while worst-case time is $O(n)$. Refer to [Hashing](#) chapter for more details on hashing algorithms. As an example, consider the array, $A = \{3,2,1,2,2,3\}$.

Scan the input array and insert the elements into the hash. For each inserted element, keep the

counter as 1 (assume initially all entries are filled with zeros). This indicates that the corresponding element has occurred already. For the given array, the hash table will look like (after inserting the first three elements 3,2 and 1):



Now if we try inserting 2, since the counter value of 2 is already 1, we can say the element has appeared twice.

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

Problem-4 Can we further improve the complexity of [Problem-1](#) solution?

Solution: Let us assume that the array elements are positive numbers and all the elements are in the range 0 to $n - 1$. For each element $A[i]$, go to the array element whose index is $A[i]$. That means select $A[A[i]]$ and mark $-A[A[i]]$ (negate the value at $A[A[i]]$). Continue this process until we encounter the element whose value is already negated. If one such element exists then we say duplicate elements exist in the given array. As an example, consider the array, $A = \{3,2,1,2,2,3\}$.

Initially,

3	2	1	2	2	3
0	1	2	3	4	5

At step-1, negate $A[\text{abs}(A[0])]$,

3	2	1	-2	2	3
0	1	2	3	4	5

At step-2, negate $A[\text{abs}(A[1])]$,

3	2	-1	-2	2	3
0	1	2	3	4	5

At step-3, negate $A[\text{abs}(A[2])]$,

3	-2	- 1	-2	2	3
0	1	2	3	4	5

At step-4, negate $A[abs(A[3])]$,

3	-2	- 1	-2	2	3
0	1	2	3	4	5

At step-4, observe that $A[abs(A[3])]$ is already negative. That means we have encountered the same value twice.

```
void CheckDuplicates(int A[], int n) {
    for(int i = 0; i < n; i++) {
        if(A[abs(A[i])] < 0) {
            printf("Duplicates exist:%d", A[i]);
            return;
        }
        else A[A[i]] = - A[A[i]];
    }
    printf("No duplicates in given array.");
}
```

Time Complexity: $O(n)$. Since only one scan is required. Space Complexity: $O(1)$.

Notes:

- This solution does not work if the given array is read only.
- This solution will work only if all the array elements are positive.
- If the elements range is not in 0 to $n - 1$ then it may give exceptions.

Problem-5 Given an array of n numbers. Give an algorithm for finding the element which appears the maximum number of times in the array?

Brute Force Solution: One simple solution to this is, for each input element check whether there is any element with the same value, and for each such occurrence, increment the counter. Each time, check the current counter with the max counter and update it if this value is greater than max counter. This we can solve just by using two simple *for* loops.

```

int MaxRepititionsBruteForce(int A[], int n) {
    int counter = 0, max=0;
    for(int i = 0; i < n; i++) {
        counter=0;
        for(int j = 0; j < n; j++) {
            if(A[i] == A[j])
                counter++;
        }
        if(counter > max) max = counter;
    }
    return max;
}

```

Time Complexity: $O(n^2)$, for two nested *for* loops. Space Complexity: $O(1)$.

Problem-6 Can we improve the complexity of [Problem-5](#) solution?

Solution: Yes. Sort the given array. After sorting, all the elements with equal values come adjacent. Now, just do another scan on this sorted array and see which element is appearing the maximum number of times.

Time Complexity: $O(n \log n)$. (for sorting). Space Complexity: $O(1)$.

Problem-7 Is there any other way of solving [Problem-5](#)?

Solution: Yes, using hash table. For each element of the input, keep track of how many times that element appeared in the input. That means the counter value represents the number of occurrences for that element.

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

Problem-8 or [Problem-5](#), can we improve the time complexity? Assume that the elements' range is 1 to n . That means all the elements are within this range only.

Solution: Yes. We can solve this problem in two scans. We *cannot* use the negation technique of [Problem-3](#) for this problem because of the number of repetitions. In the first scan, instead of negating, add the value n . That means for each occurrence of an element add the array size to that element. In the second scan, check the element value by dividing it by n and return the element which gives the maximum value. The code based on this method is given below.

```

void MaxRepetitions(int A[], int n) {
    int i = 0, max = 0, maxIndex;
    for(i = 0; i < n; i++)
        A[A[i] % n] += n;
    for(i = 0; i < n; i++)
        if(A[i]/n > max) {
            max = A[i]/n;
            maxIndex = i;
        }
    return maxIndex;
}

```

Notes:

- This solution does not work if the given array is read only.
- This solution will work only if the array elements are positive.
- If the elements range is not in 1 to n then it may give exceptions.

Time Complexity: $O(n)$. Since no nested *for* loops are required. Space Complexity: $O(1)$.

Problem-9 Given an array of n numbers, give an algorithm for finding the first element in the array which is repeated. For example, in the array $A = \{3,2,1,2,2,3\}$, the first repeated number is 3 (not 2). That means, we need to return the first element among the repeated elements.

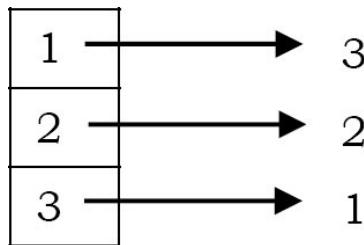
Solution: We can use the brute force solution that we used for [Problem-1](#). For each element, since it checks whether there is a duplicate for that element or not, whichever element duplicates first will be returned.

Problem-10 For [Problem-9](#), can we use the sorting technique?

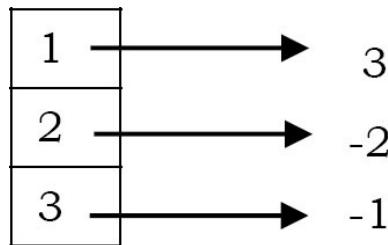
Solution: No. For proving the failed case, let us consider the following array. For example, $A = \{3, 2, 1, 2, 2, 3\}$. After sorting we get $A = \{1,2,2,2,3,3\}$. In this sorted array the first repeated element is 2 but the actual answer is 3.

Problem-11 For [Problem-9](#), can we use hashing technique?

Solution: Yes. But the simple hashing technique which we used for [Problem-3](#) will not work. For example, if we consider the input array as $A = \{3,2,1,2,3\}$, then the first repeated element is 3, but using our simple hashing technique we get the answer as 2. This is because 2 is coming twice before 3. Now let us change the hashing table behavior so that we get the first repeated element. Let us say, instead of storing 1 value, initially we store the position of the element in the array. As a result the hash table will look like (after inserting 3,2 and 1):



Now, if we see 2 again, we just negate the current value of 2 in the hash table. That means, we make its counter value as -2 . The negative value in the hash table indicates that we have seen the same element two times. Similarly, for 3 (the next element in the input) also, we negate the current value of the hash table and finally the hash table will look like:



After processing the complete input array, scan the hash table and return the highest negative indexed value from it (i.e., -1 in our case). The highest negative value indicates that we have seen that element first (among repeated elements) and also repeating.

What if the element is repeated more than twice? In this case, just skip the element if the corresponding value i is already negative.

Problem-12 For [Problem-9](#), can we use the technique that we used for [Problem-3](#) (negation technique)?

Solution: No. As an example of contradiction, for the array $A = \{3,2,1,2,2,3\}$ the first repeated element is 3. But with negation technique the result is 2.

Problem-13 Finding the Missing Number: We are given a list of $n - 1$ integers and these integers are in the range of 1 to n . There are no duplicates in the list. One of the integers is missing in the list. Given an algorithm to find the missing integer. **Example:** I/P: [1,2,4,6,3,7,8] O/P: 5

Brute Force Solution: One simple solution to this is, for each number in 1 to n , check whether that number is in the given array or not.

```

int FindMissingNumber(int A[], int n) {
    int i, j, found=0;
    for (i = 1; i <=n; i++) {
        found = 0;
        for (j = 0; j < n; j++)
            if(A[j]==i)
                found = 1;
        if(!found) return i;
    }
    return -1;
}

```

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-14 For [Problem-13](#), can we use sorting technique?

Solution: Yes. Sorting the list will give the elements in increasing order and with another scan we can find the missing number.

Time Complexity: $O(n \log n)$, for sorting. Space Complexity: $O(1)$.

Problem-15 For [Problem-13](#), can we use hashing technique?

Solution: Yes. Scan the input array and insert elements into the hash. For inserted elements, keep *counter* as 1 (assume initially all entries are filled with zeros). This indicates that the corresponding element has occurred already. Now, scan the hash table and return the element which has counter value zero.

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

Problem-16 For [Problem-13](#), can we improve the complexity?

Solution: Yes. We can use summation formula.

- 1) Get the sum of numbers, $sum = n \times (n + 1)/2$.
- 2) Subtract all the numbers from sum and you will get the missing number.

Time Complexity: $O(n)$, for scanning the complete array.

Problem-17 In [Problem-13](#), if the sum of the numbers goes beyond the maximum allowed integer, then there can be integer overflow and we may not get the correct answer. Can we solve this problem?

Solution:

- 1) XOR all the array elements, let the result of XOR be X .

- 2) XOR all numbers from 1 to n , let XOR be Y.
- 3) XOR of X and Y gives the missing number.

```
int FindMissingNumber(int A[], int n) {
    int i, X, Y;
    for (i = 0; i < n; i++)
        X ^= A[i];
    for (i = 1; i <= n; i++)
        Y ^= i;
    //In fact, one variable is enough.
    return X ^ Y;
}
```

Time Complexity: $O(n)$, for scanning the complete array. Space Complexity: $O(1)$.

Problem-18 Find the Number Occurring an Odd Number of Times: Given an array of positive integers, all numbers occur an even number of times except one number which occurs an odd number of times. Find the number in $O(n)$ time & constant space. **Example :** I/P = [1,2,3,2,3,1,3] O/P = 3

Solution: Do a bitwise XOR of all the elements. We get the number which has odd occurrences. This is because, $A \text{ XOR } A = 0$.

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

Problem-19 Find the two repeating elements in a given array: Given an array with size, all elements of the array are in range 1 to n and also all elements occur only once except two numbers which occur twice. Find those two repeating numbers. For example: if the array is 4,2,4,5,2,3,1 with size = 7 and $n = 5$. This input has $n + 2 = 7$ elements with all elements occurring once except 2 and 4 which occur twice. So the output should be 4 2.

Solution: One simple way is to scan the complete array for each element of the input elements. That means use two loops. In the outer loop, select elements one by one and count the number of occurrences of the selected element in the inner loop. For the code below, assume that *PrintRepeatedElements* is called with $n + 2$ to indicate the size.

```
void PrintRepeatedElements(int A[], int size) {
    for(int i = 0; i < size; i++)
        for(int j = i+1; j < size; j++)
            if(A[i] == A[j])
                printf("%d", A[i]);
}
```

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-20 For [Problem-19](#), can we improve the time complexity?

Solution: Sort the array using any comparison sorting algorithm and see if there are any elements which are contiguous with the same value.

Time Complexity: $O(n \log n)$. Space Complexity: $O(1)$.

Problem-21 For [Problem-19](#), can we improve the time complexity?

Solution: Use Count Array. This solution is like using a hash table. For simplicity we can use array for storing the counts. Traverse the array once and keep track of the count of all elements in the array using a temp array $count[]$ of size n . When we see an element whose count is already set, print it as duplicate. For the code below assume that $PrintRepeatedElements$ is called with $n + 2$ to indicate the size.

```
void PrintRepeatedElements(int A[], int size) {
    int *count = (int *)calloc(sizeof(int), (size - 2));
    for(int i = 0; i < size; i++) {
        count[A[i]]++;
        if(count[A[i]] == 2)
            printf("%d", A[i]);
    }
}
```

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

Problem-22 Consider [Problem-19](#). Let us assume that the numbers are in the range 1 to n . Is there any other way of solving the problem?

Solution: Yes, by using XOR Operation. Let the repeating numbers be X and Y , if we XOR all the elements in the array and also all integers from 1 to n , then the result will be $X \text{ XOR } Y$. The 1's in binary representation of $X \text{ XOR } Y$ correspond to the different bits between X and Y . If the k^{th} bit of $X \text{ XOR } Y$ is 1, we can XOR all the elements in the array and also all integers from 1 to n whose k^{th} bits are 1. The result will be one of X and Y .

```

void PrintRepeatedElements (int A[], int size) {
    int XOR = A[0];
    int i, right_most_set_bit_no, X= 0, Y = 0;
    for(i = 0; i < size; i++)           /* Compute XOR of all elements in A[]*/
        XOR ^= A[i];
    for(i = 1; i <= n; i++)           /* Compute XOR of all elements {1, 2 ..n} */
        XOR ^= i;
    right_most_set_bit_no = XOR & ~(XOR -1); // Get the rightmost set bit in right_most_set_bit_no
    /* Now divide elements in two sets by comparing rightmost set */
    for(i = 0; i < size; i++) {
        if(A[i] & right_most_set_bit_no)
            X = X ^ A[i];      /*XOR of first set in A[] */
        else
            Y = Y ^ A[i];      /*XOR of second set in A[] */
    }
    for(i = 1; i <= n; i++) {
        if(i & right_most_set_bit_no)
            X = X ^ i;        /*XOR of first set in A[] and {1, 2, ...n }*/
        else
            Y = Y ^ i;        /*XOR of second set in A[] and {1, 2, ...n }*/
    }
    printf("%d and %d",X, Y);
}

```

Time Complexity: O(n). Space Complexity: O(1).

Problem-23 Consider [Problem-19](#). Let us assume that the numbers are in the range 1 to n . Is there yet other way of solving the problem?

Solution: We can solve this by creating two simple mathematical equations. Let us assume that two numbers we are going to find are X and Y . We know the sum of n numbers is $n(n + 1)/2$ and the product is $n!$. Make two equations using these sum and product formulae, and get values of two unknowns using the two equations. Let the summation of all numbers in array be S and product be P and the numbers which are being repeated are X and Y .

$$X + Y = S - \frac{n(n + 1)}{2}$$

$$XY = P/n!$$

Using the above two equations, we can find out X and Y . There can be an addition and multiplication overflow problem with this approach.

Time Complexity: O(n). Space Complexity: O(1).

Problem-24 Similar to [Problem-19](#), let us assume that the numbers are in the range 1 to n. Also, $n - 1$ elements are repeating thrice and remaining element repeated twice. Find the element which repeated twice.

Solution: If we *XOR* all the elements in the array and all integers from 1 to n, then all the elements which are repeated thrice will become zero. This is because, since the element is repeating thrice and *XOR* another time from range makes that element appear four times. As a result, the output of $a \text{ XOR } a \text{ XOR } a \text{ XOR } a = 0$. It is the same case with all elements that are repeated three times.

With the same logic, for the element which repeated twice, if we *XOR* the input elements and also the range, then the total number of appearances for that element is 3. As a result, the output of $a \text{ XOR } a \text{ XOR } a = a$. Finally, we get the element which repeated twice.

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

Problem-25 Given an array of n elements. Find two elements in the array such that their sum is equal to given element K .

Brute Force Solution: One simple solution to this is, for each input element, check whether there is any element whose sum is K . This we can solve just by using two simple for loops. The code for this solution can be given as:

```
void BruteForceSearch[int A[], int n, int K) {
    for (int i = 0; i < n; i++) {
        for(int j = i; j < n; j++) {
            if(A[i]+A[j] == K) {
                printf("Items Found:%d %d", i, j);
                return;
            }
        }
    }
    printf("Items not found: No such elements");
}
```

Time Complexity: $O(n^2)$. This is because of two nested *for* loops. Space Complexity: $O(1)$.

Problem-26 For [Problem-25](#), can we improve the time complexity?

Solution: Yes. Let us assume that we have sorted the given array. This operation takes $O(n \log n)$. On the sorted array, maintain indices $loIndex = 0$ and $hiIndex = n - 1$ and compute $A[loIndex] + A[hiIndex]$. If the sum equals K , then we are done with the solution. If the sum is less than K , decrement $hiIndex$, if the sum is greater than K , increment $loIndex$.

```

void Search(int A[], int n, int K) {
    int loIndex, hiIndex, sum;
    Sort(A, n);
    for(loIndex = 0, hiIndex = n-1; loIndex < hiIndex) {
        sum = A[loIndex] + A[hiIndex];
        if(sum == K) {
            printf("Elements Found: %d %d", loIndex, hiIndex);
            return;
        }
        else if(sum < K)
            loIndex = loIndex + 1;
        else
            hiIndex = hiIndex - 1;
    }
    return;
}

```

Time Complexity: $O(n \log n)$. If the given array is already sorted then the complexity is $O(n)$.

Space Complexity: $O(1)$.

Problem-27 Does the solution of [Problem-25](#) work even if the array is not sorted?

Solution: Yes. Since we are checking all possibilities, the algorithm ensures that we get the pair of numbers if they exist.

Problem-28 Is there any other way of solving [Problem-25](#)?

Solution: Yes, using hash table. Since our objective is to find two indexes of the array whose sum is K . Let us say those indexes are X and Y . That means, $A[X] + A[Y] = K$. What we need is, for each element of the input array $A[X]$, check whether $K - A[X]$ also exists in the input array. Now, let us simplify that searching with hash table.

Algorithm:

- For each element of the input array, insert it into the hash table. Let us say the current element is $A[X]$.
- Before proceeding to the next element we check whether $K - A[X]$ also exists in the hash table or not.
- The existence of such number indicates that we are able to find the indexes.
- Otherwise proceed to the next input element.

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

Problem-29 Given an array A of n elements. Find three indices, i, j & k such that $A[i]^2 + A[j]^2 + A[k]^2$

$$= A[k]^2?$$

Solution:

Algorithm:

- Sort the given array in-place.
- For each array index i compute $A[i]^2$ and store in array.
- Search for 2 numbers in array from 0 to $i - 1$ which adds to $A[i]$ similar to [Problem-25](#). This will give us the result in $O(n)$ time. If we find such a sum, return true, otherwise continue.

```
Sort(A); // Sort the input array
for (int i=0; i < n; i++)
    A[i] = A[i]*A[i];
for (i=n; i > 0; i--) {
    res = false;
    if(res) {
        //Problem-11/12 Solution
    }
}
```

Time Complexity: Time for sorting + $n \times$ (Time for finding the sum) = $O(n \log n) + n \times O(n) = n^2$.

Space Complexity: $O(1)$.

Problem-30 Two elements whose sum is closest to zero. Given an array with both positive and negative numbers, find the two elements such that their sum is closest to zero. For the below array, algorithm should give -80 and 85. Example: 1 60 -10 70 -80 85

Brute Force Solution: For each element, find the *sum* with every other element in the array and compare sums. Finally, return the minimum *sum*.

```

void TwoElementsWithMinSum(int A[], int n) {
    int i, j, min_sum, sum, min_i, min_j, inv_count = 0;
    if(n < 2) {
        printf("Invalid Input");
        return;
    }
    /* Initialization of values */
    min_i = 0;
    min_j = 1;
    min_sum = A[0] + A[1];
    for(i= 0; i < n - 1; i++) {
        for(j = i + 1; j < n; j++) {
            sum = A[i] + A[j];
            if(abs(min_sum) > abs(sum)) {
                min_sum = sum;
                min_i = i;
                min_j = j;
            }
        }
    }
    printf(" The two elements are %d and %d", arr[min_i], arr[min_j]);
}

```

Time complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-31 Can we improve the time complexity of [Problem-30](#)?

Solution: Use Sorting.

Algorithm:

1. Sort all the elements of the given input array.
2. Maintain two indexes, one at the beginning ($i = 0$) and the other at the ending ($j = n - 1$). Also, maintain two variables to keep track of the smallest positive sum closest to zero and the smallest negative sum closest to zero.
3. While $i < j$:
 - a. If the current pair sum is $>$ zero and $<$ *positiveClosest* then update the *positiveClosest*. Decrement *j*.
 - b. If the current pair sum is $<$ zero and $>$ *negativeClosest* then update the *negativeClosest*. Increment *i*.
 - c. Else, print the pair

```

void TwoElementsWithMinSum(int A[], int n) {
    int i = 0, j = n-1, temp, positiveClosest = INT_MAX, negativeClosest = INT_MIN;
    Sort(A, n);
    while(i < j) {
        temp = A[i] + A[j];
        if(temp > 0) {
            if (temp < positiveClosest)
                positiveClosest = temp;
            j--;
        }
        else if (temp < 0) {
            if (temp > negativeClosest)
                negativeClosest = temp;
            i++;
        }
        else printf("Closest Sum: %d ", A[i] + A[j]);
    }
    return (abs(negativeClosest)> positiveClosest: positiveClosest: negativeClosest);
}

```

Time Complexity: $O(n \log n)$, for sorting. Space Complexity: $O(1)$.

Problem-32 Given an array of n elements. Find three elements in the array such that their sum is equal to given element K ?

Brute Force Solution: The default solution to this is, for each pair of input elements check whether there is any element whose sum is K . This we can solve just by using three simple for loops. The code for this solution can be given as:

```

void BruteForceSearch[int A[], int n, int data) {
    for (int i = 0; i < n; i++) {
        for(int j = i+1; j < n; j++) {
            for(int k = j+1; k < n; k++) {
                if(A[i] + A[j] + A[k]== data) {
                    printf("Items Found:%d %d %d", i, j, k);
                    return;
                }
            }
        }
    }
    printf("Items not found: No such elements");
}

```

Time Complexity: $O(n^3)$, for three nested *for* loops. Space Complexity: $O(1)$.

Problem-33 Does the solution of [Problem-32](#) work even if the array is not sorted?

Solution: Yes. Since we are checking all possibilities, the algorithm ensures that we can find three numbers whose sum is K if they exist.

Problem-34 Can we use sorting technique for solving [Problem-32](#)?

Solution: Yes.

```
void Search(int A[], int n, int data) {  
    Sort(A, n);  
    for(int k = 0; k < n; k++) {  
        for(int i = k + 1, j = n-1; i < j; ) {  
            if(A[k] + A[i] + A[j] == data) {  
                printf("Items Found:%d %d %d", i, j, k);  
                return;  
            }  
            else if(A[k] + A[i] + A[j] < data)  
                i = i + 1;  
            else  
                j = j - 1;  
        }  
    }  
    return;  
}
```

Time Complexity: Time for sorting + Time for searching in sorted list = $O(n \log n) + O(n^2) \approx O(n^2)$. This is because of two nested *for* loops. Space Complexity: $O(1)$.

Problem-35 Can we use hashing technique for solving [Problem-32](#)?

Solution: Yes. Since our objective is to find three indexes of the array whose sum is K . Let us say those indexes are X, Y and Z . That means, $A[X] + A[Y] + A[Z] = K$.

Let us assume that we have kept all possible sums along with their pairs in hash table. That means the key to hash table is $K - A[X]$ and values for $K - A[X]$ are all possible pairs of input whose sum is if – $A[X]$.

Algorithm:

- Before starting the search, insert all possible sums with pairs of elements into the hash table.

- For each element of the input array, insert into the hash table. Let us say the current element is $A[X]$.
- Check whether there exists a hash entry in the table with key: $K - A[X]$.
- If such element exists then scan the element pairs of $K - A[X]$ and return all possible pairs by including $A[X]$ also.
- If no such element exists (with $K - A[X]$ as key) then go to next element.

Time Complexity: The time for storing all possible pairs in Hash table + searching = $O(n^2)$ + $O(n^2) \approx O(n^2)$. Space Complexity: $O(n)$.

Problem-36 Given an array of n integers, the *3 – sum problem* is to find three integers whose sum is closest to zero.

Solution: This is the same as that of [Problem-32](#) with K value is zero.

Problem-37 Let A be an array of n distinct integers. Suppose A has the following property: there exists an index $1 \leq k \leq n$ such that $A[1], \dots, A[k]$ is an increasing sequence and $A[k + 1], \dots, A[n]$ is a decreasing sequence. Design and analyze an efficient algorithm for finding k .

Similar question: Let us assume that the given array is sorted but starts with negative numbers and ends with positive numbers [such functions are called monotonically increasing functions]. In this array find the starting index of the positive numbers. Assume that we know the length of the input array. Design a $O(\log n)$ algorithm.

Solution: Let us use a variant of the binary search.

```

int Search (int A[], int n, int first, int last) {
    int mid, first = 0, last = n-1;
    while(first <= last) {
        // if the current array has size 1
        if(first == last)
            return A[first];
        // if the current array has size 2
        else if(first == last-1)
            return max(A[first], A[last]);
        // if the current array has size 3 or more
        else {
            mid = first + (last-first)/2;
            if(A[mid-1] < A[mid] && A[mid] > A[mid+1])
                return A[mid];
            else if(A[mid-1] < A[mid] && A[mid] < A[mid+1])
                first = mid+1;
            else if(A[mid-1] > A[mid] && A[mid] > A[mid+1])
                last = mid-1;
            else
                return INT_MIN ;
        } // end of else
    } // end of while
}

```

The recursion equation is $T(n) = 2T(n/2) + c$. Using master theorem, we get $O(\log n)$.

Problem-38 If we don't know n , how do we solve the [Problem-37](#)?

Solution: Repeatedly compute $A[1], A[2], A[4], A[8], A[16]$ and so on, until we find a value of n such that $A[n] > 0$.

Time Complexity: $O(\log n)$, since we are moving at the rate of 2. Refer to *Introduction to Analysis of Algorithms* chapter for details on this.

Problem-39 Given an input array of size unknown with all 1's in the beginning and 0's in the end. Find the index in the array from where 0's start. Consider there are millions of 1's and 0's in the array. E.g. array contents 1111111.....1100000.....0000000.

Solution: This problem is almost similar to [Problem-38](#). Check the bits at the rate of 2^k where $k = 0, 1, 2, \dots$. Since we are moving at the rate of 2, the complexity is $O(\log n)$.

Problem-40 Given a sorted array of n integers that has been rotated an unknown number of times, give a $O(\log n)$ algorithm that finds an element in the array.

Example: Find 5 in array (15 16 19 20 25 1 3 4 5 7 10 14) **Output:** 8 (the index of 5 in the array)

Solution: Let us assume that the given array is $A[]$ and use the solution of [Problem-37](#) with an extension. The function below *FindPivot* returns the k value (let us assume that this function returns the index instead of the value). Find the pivot point, divide the array into two sub-arrays and call binary search.

The main idea for finding the pivot point is – for a sorted (in increasing order) and pivoted array, the pivot element is the only element for which the next element to it is smaller than it. Using the above criteria and the binary search methodology we can get pivot element in $O(\log n)$ time.

Algorithm:

- 1) Find out the pivot point and divide the array into two sub-arrays.
- 2) Now call binary search for one of the two sub-arrays.
 - a. if the element is greater than the first element then search in left subarray.
 - b. else search in right subarray.
- 3) If element is found in selected sub-array, then return index *else* return -1.

```

int FindPivot(int A[], int start, int finish) {
    if(finish - start == 0)
        return start;
    else if(start == finish - 1) {
        if(A[start] >= A[finish])
            return start;
        else    return finish;
    }
    else {
        mid = start + (finish-start)/2;
        if(A[start] >= A[mid])
            return FindPivot(A, start, mid);
        else    return FindPivot(A, mid, finish);
    }
}
int Search(int A[], int n, int x) {
    int pivot = FindPivot(A, 0, n-1);
    if(A[pivot] == x)
        return pivot;
    if(A[pivot] <= x)
        return BinarySearch(A, 0, pivot-1, x);
    else return BinarySearch(A, pivot+1, n-1, x);
}
int BinarySearch(int A[], int low, int high, int x) {
    if(high >= low)  {
        int mid = low + (high - low)/2;
        if(x == A[mid])
            return mid;
        if(x > A[mid])
            return BinarySearch(A, (mid + 1), high, x);
        else    return BinarySearch(A, low, (mid - 1), x);
    }
    return -1;      // -1 if element is not found
}

```

Time complexity: $O(\log n)$.

Problem-41 For [Problem-40](#), can we solve with recursion?

Solution: Yes.

```

int BinarySearchRotated(int A[], int start, int finish, int data) {
    int mid = start + (finish - start) / 2;
    if(start > finish)
        return -1;
    if(data == A[mid])
        return mid;
    else if(A[start] <= A[mid]) {      // start half is in sorted order.
        if(data >= A[start] && data < A[mid])
            return BinarySearchRotated(A, start, mid - 1, data);
        else    return BinarySearchRotated(A, mid + 1, finish, data);
    }
    else { // A[mid] <= A[finish], finish half is in sorted order.
        if(data > A[mid] && data <= A[finish])
            return BinarySearchRotated(A, mid + 1, finish, data);
        else    return BinarySearchRotated(A, start, mid - 1, data);
    }
}

```

Time complexity: $O(\log n)$.

Problem-42 Bitonic search: An array is *bitonic* if it is comprised of an increasing sequence of integers followed immediately by a decreasing sequence of integers. Given a bitonic array A of n distinct integers, describe how to determine whether a given integer is in the array in $O(\log n)$ steps.

Solution: The solution is the same as that for [Problem-37](#).

Problem-43 Yet, other way of framing [Problem-37](#).

Let $A[]$ be an array that starts out increasing, reaches a maximum, and then decreases. Design an $O(\log n)$ algorithm to find the index of the maximum value.

Problem-44 Give an $O(n \log n)$ algorithm for computing the median of a sequence of n integers.

Solution: Sort and return element at $\frac{n}{2}$.

Problem-45 Given two sorted lists of size m and n , find median of all elements in $O(\log(m + n))$ time.

Solution: Refer to [Divide and Conquer](#) chapter.

Problem-46 Given a sorted array A of n elements, possibly with duplicates, find the index of the first occurrence of a number in $O(\log n)$ time.

Solution: To find the first occurrence of a number we need to check for the following condition.

Return the position if any one of the following is true:

```
mid == low && A[mid] == data || A[mid] == data && A[mid-1] < data
```

```
int BinarySearchFirstOccurrence(int A[], int low, int high, int data) {  
    int mid;  
    if(high >= low) {  
        mid = low + (high-low) / 2;  
        if((mid == low && A[mid] == data) || (A[mid] == data && A[mid - 1] < data))  
            return mid;  
        // Give preference to left half of the array  
        else if(A[mid] >= data)  
            return BinarySearchFirstOccurrence (A, low, mid - 1, data);  
        else    return BinarySearchFirstOccurrence (A, mid + 1, high, data);  
    }  
    return -1;  
}
```

Time Complexity: $O(\log n)$.

Problem-47 Given a sorted array A of n elements, possibly with duplicates. Find the index of the last occurrence of a number in $O(\log n)$ time.

Solution: To find the last occurrence of a number we need to check for the following condition. Return the position if any one of the following is true:

```
mid == high && A[mid] == data || A[mid] == data && A[mid+1] > data
```

```
int BinarySearchLastOccurrence(int A[], int low, int high, int data) {  
    int mid;  
    if(high >= low) {  
        mid = low + (high-low) / 2;  
        if((mid == high && A[mid] == data) || (A[mid] == data && A[mid + 1] > data))  
            return mid;  
        // Give preference to right half of the array  
        else if(A[mid] <= data)  
            return BinarySearchLastOccurrence (A, mid + 1, high, data);  
        else    return BinarySearchLastOccurrence (A, low, mod - 1, data);  
    }  
    return -1;  
}
```

Time Complexity: $O(\log n)$.

Problem-48 Given a sorted array of n elements, possibly with duplicates. Find the number of occurrences of a number.

Brute Force Solution: Do a linear search of the array and increment count as and when we find the element data in the array.

```
int LinearSearchCount(int A[], int n, int data) {  
    int count = 0;  
    for (int i = 0; i < n; i++)  
        if(A[i] == data)  
            count++;  
    return count;  
}
```

Time Complexity: $O(n)$.

Problem-49 Can we improve the time complexity of [Problem-48](#)?

Solution: Yes. We can solve this by using one binary search call followed by another small scan.

Algorithm:

- Do a binary search for the *data* in the array. Let us assume its position is K .
- Now traverse towards the left from K and count the number of occurrences of *data*. Let this count be *leftCount*.
- Similarly, traverse towards right and count the number of occurrences of *data*. Let this count be *rightCount*.
- Total number of occurrences = *leftCount* + 1 + *rightCount*

Time Complexity – $O(\log n + S)$ where S is the number of occurrences of *data*.

Problem-50 Is there any alternative way of solving [Problem-48](#)?

Solution:

Algorithm:

- Find first occurrence of *data* and call its index as *firstOccurrence* (for algorithm refer to [Problem-46](#))
- Find last occurrence of *data* and call its index as *lastOccurrence* (for algorithm refer to [Problem-47](#))
- Return *lastOccurrence* – *firstOccurrence* + 1

Time Complexity = $O(\log n + \log n) = O(\log n)$.

Problem-51 What is the next number in the sequence 1,11,21 and why?

Solution: Read the given number loudly. This is just a fun problem.

One One
Two Ones
One two, one one → 1211

So the answer is: the next number is the representation of the previous number by reading it loudly.

Problem-52 Finding second smallest number efficiently.

Solution: We can construct a heap of the given elements using up just less than n comparisons (Refer to the [Priority Queues](#) chapter for the algorithm). Then we find the second smallest using $\log n$ comparisons for the GetMax() operation. Overall, we get $n + \log n + \text{constant}$.

Problem-53 Is there any other solution for [Problem-52](#)?

Solution: Alternatively, split the n numbers into groups of 2, perform $n/2$ comparisons successively to find the largest, using a tournament-like method. The first round will yield the maximum in $n - 1$ comparisons. The second round will be performed on the winners of the first round and the ones that the maximum popped. This will yield $\log n - 1$ comparison for a total of $n + \log n - 2$. The above solution is called the *tournament problem*.

Problem-54 An element is a majority if it appears more than $n/2$ times. Give an algorithm takes an array of n element as argument and identifies a majority (if it exists).

Solution: The basic solution is to have two loops and keep track of the maximum count for all different elements. If the maximum count becomes greater than $n/2$, then break the loops and return the element having maximum count. If maximum count doesn't become more than $n/2$, then the majority element doesn't exist.

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-55 Can we improve [Problem-54](#) time complexity to $O(n \log n)$?

Solution: Using binary search we can achieve this. Node of the Binary Search Tree (used in this approach) will be as follows.

```
struct TreeNode {  
    int element;  
    int count;  
    struct TreeNode *left;  
    struct TreeNode *right;  
} BST;
```

Insert elements in BST one by one and if an element is already present then increment the count of the node. At any stage, if the count of a node becomes more than $n/2$, then return. This method works well for the cases where $n/2 + 1$ occurrences of the majority element are present at the start of the array, for example {1,1,1,1,1,2,3, and 4}.

Time Complexity: If a binary search tree is used then worst time complexity will be $O(n^2)$. If a balanced-binary-search tree is used then $O(n \log n)$. Space Complexity: $O(n)$.

Problem-56 Is there any other of achieving $O(n \log n)$ complexity for [Problem-54](#)?

Solution: Sort the input array and scan the sorted array to find the majority element.

Time Complexity: $O(n \log n)$. Space Complexity: $O(1)$.

Problem-57 Can we improve the complexity for [Problem-54](#)?

Solution: If an element occurs more than $n/2$ times in A then it must be the median of A . But, the reverse is not true, so once the median is found, we must check to see how many times it occurs in A . We can use linear selection which takes $O(n)$ time (for algorithm, refer to [Selection Algorithms](#) chapter).

```
int CheckMajority(int A[], int n) {
    1) Use linear selection to find the median m of A.
    2) Do one more pass through A and count the number of occurrences of m.
        a. If m occurs more than n/2 times then return true;
        b. Otherwise return false.
}
```

Problem-58 Is there any other way of solving [Problem-54](#)?

Solution: Since only one element is repeating, we can use a simple scan of the input array by keeping track of the count for the elements. If the count is 0, then we can assume that the element visited for the first time otherwise that the resultant element.

```

int MajorityNum(int[] A, int n) {
    int count = 0, element = -1;
    for(int i = 0; i < n; i++) {
        // If the counter is 0 then set the current candidate to majority num and set the counter to 1.
        if(count == 0) {
            element = A[i];
            count = 1;
        }
        else if(element == A[i]) {
            // Increment counter If the counter is not 0 and element is same as current candidate.
            count++;
        }
        else {
            // Decrement counter If the counter is not 0 and element is different from current candidate.
            count--;
        }
    }
    return element;
}

```

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

Problem-59 Given an array of $2n$ elements of which n elements are the same and the remaining n elements are all different. Find the majority element.

Solution: The repeated elements will occupy half the array. No matter what arrangement it is, only one of the below will be true:

- All duplicate elements will be at a relative distance of 2 from each other. Ex:**n, 1, n, 100, n, 54, n...**
- At least two duplicate elements will be next to each other.
Ex: **n,n, 1,100, n, 54, n,...**
n, 1,n,n,n,54,100...
1,100,54, n.n.n.n....

In worst case, we will need two passes over the array:

- First Pass: compare $A[i]$ and $A[i + 1]$
- Second Pass: compare $A[i]$ and $A[i + 2]$

Something will match and that's your element. This will cost $O(n)$ in time and $O(1)$ in space.

Problem-60 Given an array with $2n + 1$ integer elements, n elements appear twice in arbitrary places in the array and a single integer appears only once somewhere inside.

Find the lonely integer with $O(n)$ operations and $O(1)$ extra memory.

Solution: Except for one element, all elements are repeated. We know that $A \text{ XOR } A = 0$. Based on this if we XOR all the input elements then we get the remaining element.

```
int Solution(int* A) {
    int i, res;
    for (i = res = 0; i < 2n+1; i++)
        res = res ^ A[i];
    return res;
}
```

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

Problem-61 Throwing eggs from an n-story building: Suppose we have an n story building and a number of eggs. Also assume that an egg breaks if it is thrown from floor F or higher, and will not break otherwise. Devise a strategy to determine floor F , while breaking $O(\log n)$ eggs.

Solution: Refer to [Divide and Conquer](#) chapter.

Problem-62 Local minimum of an array: Given an array A of n distinct integers, design an $O(\log n)$ algorithm to find a *local minimum*: an index i such that $A[i - 1] < A[i] < A[i + 1]$.

Solution: Check the middle value $A[n/2]$, and two neighbors $A[n/2 - 1]$ and $A[n/2 + 1]$. If $A[n/2]$ is local minimum, stop; otherwise search in half with smaller neighbor.

Problem-63 Give an $n \times n$ array of elements such that each row is in ascending order and each column is in ascending order, devise an $O(n)$ algorithm to determine if a given element x is in the array. You may assume all elements in the $n \times n$ array are distinct.

Solution: Let us assume that the given matrix is $A[n][n]$. Start with the last row, first column [or first row, last column]. If the element we are searching for is greater than the element at $A[1][n]$, then the first column can be eliminated. If the search element is less than the element at $A[1][n]$, then the last row can be completely eliminated. Once the first column or the last row is eliminated, start the process again with the left-bottom end of the remaining array. In this algorithm, there would be maximum n elements that the search element would be compared with.

Time Complexity: $O(n)$. This is because we will traverse at most $2n$ points. Space Complexity: $O(1)$.

Problem-64 Given an $n \times n$ array a of n^2 numbers, give an $O(n)$ algorithm to find a pair of indices i and j such that $A[i][j] < A[i + 1][j], A[i][j] < A[i][j + 1], A[i][j] < A[i - 1][j]$, and $A[i][j] < A[i][j - 1]$.

Solution: This problem is the same as [Problem-63](#).

Problem-65 Given $n \times n$ matrix, and in each row all 1's are followed by 0's. Find the row with the maximum number of 0's.

Solution: Start with first row, last column. If the element is 0 then move to the previous column in the same row and at the same time increase the counter to indicate the maximum number of 0's. If the element is 1 then move to the next row in the same column. Repeat this process until you reach last row, first column.

Time Complexity: $O(2n) \approx O(n)$ (similar to [Problem-63](#)).

Problem-66 Given an input array of size unknown, with all numbers in the beginning and special symbols in the end. Find the index in the array from where the special symbols start.

Solution: Refer to [Divide and Conquer](#) chapter.

Problem-67 Separate even and odd numbers: Given an array $A[]$, write a function that segregates even and odd numbers. The functions should put all even numbers first, and then odd numbers. **Example:** Input = {12,34,45,9,8,90,3} Output = {12,34,90,8,9,45,3}

Note: In the output, the order of numbers can be changed, i.e., in the above example 34 can come before 12, and 3 can come before 9.

Solution: The problem is very similar to *Separate 0's and 1's* (Problem-68) in an array, and both problems are variations of the famous *Dutch national flag problem*.

Algorithm: The logic is similar to Quick sort.

- 1) Initialize two index variables left and right: $left = 0$, $right = n - 1$
- 2) Keep incrementing the left index until you see an odd number.
- 3) Keep decrementing the right index until you see an even number.
- 4) If $left < right$ then swap $A[left]$ and $A[right]$

```

void DutchNationalFlag(int A[], int n) {
    int left = 0, right = n-1;
    while(left < right) {
        // Increment left index while we see 0 at left
        while(A[left]%2 == 0 && left < right)
            left++;
        // Decrement right index while we see 1 at right
        while(A[right]%2 == 1 && left < right)
            right--;
        if(left < right) {
            // Swap A[left] and A[right]
            swap(&A[left], &A[right]);
            left++;
            right--;
        }
    }
}

```

Time Complexity: $O(n)$.

Problem-68 The following is another way of structuring [Problem-67](#), but with a slight difference.

Separate 0's and 1's in an array: We are given an array of 0's and 1's in random order. Separate 0's on the left side and 1's on the right side of the array. Traverse the array only once.

Input array = [0,1,0,1,0,0,1,1,1,0] **Output array** = [0,0,0,0,0,1,1,1,1]

Solution: Counting 0's or 1's

1. Count the number of 0's. Let the count be C .
2. Once we have the count, put C 0's at the beginning and 1's at the remaining $n - C$ positions in the array.

Time Complexity: $O(n)$. This solution scans the array two times.

Problem-69 Can we solve [Problem-68](#) in one scan?

Solution: Yes. Use two indexes to traverse: Maintain two indexes. Initialize the first index left as 0 and the second index right as $n - 1$. Do the following while $left < right$:

- 1) Keep the incrementing index left while there are Os in it
- 2) Keep the decrementing index right while there are Is in it
- 3) If $left < right$ then exchange $A[left]$ and $A[right]$

```

//Function to put all 0s on left and all 1s on right
void Separate0and1(int A[], int n) {
    /* Initialize left and right indexes */
    int left = 0, right = n-1;
    while(left < right) {
        /* Increment left index while we see 0 at left */
        while(A[left] == 0 && left < right)
            left++;
        /* Decrement right index while we see 1 at right */
        while(A[right] == 1 && left < right)
            right--;
        /* If left is smaller than right then there is a 1 at left
        and a 0 at right. Swap A[left] and A[right]*/
        if(left < right) {
            A[left] = 0;
            A[right] = 1;
            left++;
            right--;
        }
    }
}

```

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

Problem-70 Sort an array of 0's, 1's and 2's [or R's, G's and B's]: Given an array $A[]$ consisting of 0's, 1's and 2's, give an algorithm for sorting $A[]$. The algorithm should put all 0's first, then all 1's and finally all 2's at the end. **Example Input** = {0,1,1,0,1,2,1,2,0,0,0,1}, **Output** = {0,0,0,0,0,1,1,1,1,2,2}

Solution:

```

void Sorting012sDutchFlagProblem(int A[],int n){
    int low=0,mid=0,high=n-1;
    while(mid <=high){
        switch(A[mid]){
            case 0:
                swap(A[low],A[mid]);
                low++;mid++;
                break;
            case 1:
                mid++;
                break;
            case 2:
                swap(A[mid],A[high]);
                high--;
                break;
        }
    }
}

```

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

Problem-71 Maximum difference between two elements: Given an array $A[]$ of integers, find out the difference between any two elements such that the larger element appears after the smaller number in $A[]$.

Examples: If array is [2,3,10,6,4,8,1] then returned value should be 8 (Difference between 10 and 2). If array is [7,9,5,6,3,2] then the returned value should be 2 (Difference between 7 and 9)

Solution: Refer to *Divide and Conquer* chapter.

Problem-72 Given an array of 101 elements. Out of 101 elements, 25 elements are repeated twice, 12 elements are repeated 4 times, and one element is repeated 3 times. Find the element which repeated 3 times in $O(1)$.

Solution: Before solving this problem, let us consider the following *XOR* operation property: $a \text{ XOR } a = 0$. That means, if we apply the *XOR* on the same elements then the result is 0.

Algorithm:

- *XOR* all the elements of the given array and assume the result is A .
- After this operation, 2 occurrences of the number which appeared 3 times becomes 0 and one occurrence remains the same.
- The 12 elements that are appearing 4 times become 0.
- The 25 elements that are appearing 2 times become 0.

- So just *XOR'ing* all the elements gives the result.

Time Complexity: $O(n)$, because we are doing only one scan. Space Complexity: $O(1)$.

Problem-73 Given a number n , give an algorithm for finding the number of trailing zeros in $n!$.

Solution:

```
int NumberOfTrailingZerosInNumber(int n) {
    int i, count = 0;
    if(n < 0) return -1;
    for (i = 5; n / i > 0; i *= 5)
        count += n / i;
    return count;
}
```

Time Complexity: $O(\log n)$.

Problem-74 Given an array of $2n$ integers in the following format $a_1 \ a_2 \ a_3 \ ... \ a_n \ b_1 \ b_2 \ b_3 \ ... \ b_n$. Shuffle the array to $a_1 \ b_1 \ a_2 \ b_2 \ a_3 \ b_3 \ ... \ a_n \ b_n$ without any extra memory.

Solution: A brute force solution involves two nested loops to rotate the elements in the second half of the array to the left. The first loop runs n times to cover all elements in the second half of the array. The second loop rotates the elements to the left. Note that the start index in the second loop depends on which element we are rotating and the end index depends on how many positions we need to move to the left.

```
void ShuffleArray() {
    int n = 4;
    int A[] = {1,3,5,7,2,4,6,8};
    for (int i = 0, q = 1, k = n; i < n; i++, k++, q++) {
        for (int j = k; j > i + q; j--) {
            int tmp = A[j-1];
            A[j-1] = A[j];
            A[j] = tmp;
        }
    }
    for (int i = 0; i < 2*n; i++)
        printf("%d", A[i]);
}
```

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

Problem-75 Can we improve [Problem-74](#) solution?

Solution: Refer to the *Divide and Conquer* chapter. A better solution of time complexity $O(n \log n)$ can be achieved using the *Divide and Concur* technique. Let us look at an example

1. Start with the array: $a_1 \ a_2 \ a_3 \ a_4 \ b_1 \ b_2 \ b_3 \ b_4$
2. Split the array into two halves: $a_1 \ a_2 \ a_3 \ a_4 : b_1 \ b_2 \ b_3 \ b_4$
3. Exchange elements around the center: exchange $a_3 \ a_4$ with $b_1 \ b_2$ and you get: $a_1 \ a_2 \ b_1 \ b_2 \ a_3 \ a_4 \ b_3 \ b_4$
4. Split $a_1 \ a_2 \ b_1 \ b_2$ into $a_1 \ a_2 : b_1 \ b_2$. Then split $a_3 \ a_4 \ b_3 \ b_4$ into $a_3 \ a_4 : b_3 \ b_4$
5. Exchange elements around the center for each subarray you get: $a_1 \ b_1 \ a_2 \ b_2$ and $a_3 \ b_3 \ a_4 \ b_4$

Note that this solution only handles the case when $n = 2^i$ where $i = 0, 1, 2, 3$, etc. In our example $n = 2^2 = 4$ which makes it easy to recursively split the array into two halves. The basic idea behind swapping elements around the center before calling the recursive function is to produce smaller size problems. A solution with linear time complexity may be achieved if the elements are of a specific nature. For example, if you can calculate the new position of the element using the value of the element itself. This is nothing but a hashing technique.

Problem-76 Given an array $A[]$, find the maximum $j - i$ such that $A[j] > A[i]$. For example, Input: {34, 8, 10, 3, 2, 80, 30, 33, 1} and Output: 6 ($j = 7, i = 1$).

Solution: Brute Force Approach: Run two loops. In the outer loop, pick elements one by one from the left. In the inner loop, compare the picked element with the elements starting from the right side. Stop the inner loop when you see an element greater than the picked element and keep updating the maximum $j - i$ so far.

```
int maxIndexDiff(int A[], int n){  
    int maxDiff = -1;  
    int i, j;  
    for (i = 0; i < n; ++i){  
        for (j = n-1; j > i; --j){  
            if(A[j] > A[i] && maxDiff < (j - i))  
                maxDiff = j - i;  
        }  
    }  
    return maxDiff;  
}
```

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-77 Can we improve the complexity of [Problem-76](#)?

Solution: To solve this problem, we need to get two optimum indexes of $A[]$: left index i and

right index j . For an element $A[i]$, we do not need to consider $A[i]$ for the left index if there is an element smaller than $A[i]$ on the left side of $A[i]$. Similarly, if there is a greater element on the right side of $A[j]$ then we do not need to consider this j for the right index.

So we construct two auxiliary Arrays $\text{LeftMins}[]$ and $\text{RightMaxs}[]$ such that $\text{LeftMins}[i]$ holds the smallest element on the left side of $A[i]$ including $A[i]$, and $\text{RightMaxs}[j]$ holds the greatest element on the right side of $A[j]$ including $A[j]$. After constructing these two auxiliary arrays, we traverse both these arrays from left to right.

While traversing $\text{LeftMins}[]$ and $\text{RightMaxs}[]$, if we see that $\text{LeftMins}[i]$ is greater than $\text{RightMaxs}[j]$, then we must move ahead in $\text{LeftMins}[]$ (or do $i++$) because all elements on the left of $\text{LeftMins}[i]$ are greater than or equal to $\text{LeftMins}[i]$. Otherwise we must move ahead in $\text{RightMaxs}[j]$ to look for a greater $y - i$ value.

```
int maxIndexDiff(int A[], int n){  
    int maxDiff, i, j;  
    int *LeftMins = (int *)malloc(sizeof(int)*n);  
    int *RightMaxs = (int *)malloc(sizeof(int)*n);  
    LeftMins[0] = A[0];  
    for (i = 1; i < n; ++i)  
        LeftMins[i] = min(A[i], LeftMins[i-1]);  
    RightMaxs[n-1] = A[n-1];  
    for (j = n-2; j >= 0; --j)  
        RightMaxs[j] = max(A[j], RightMaxs[j+1]);  
    i = 0, j = 0, maxDiff = -1;  
    while (j < n && i < n){  
        if (LeftMins[i] < RightMaxs[j]){  
            maxDiff = max(maxDiff, j-i);  
            j = j + 1;  
        }  
        else  
            i = i+1;  
    }  
    return maxDiff;  
}
```

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

Problem-78 Given an array of elements, how do you check whether the list is pairwise sorted or not? A list is considered pairwise sorted if each successive pair of numbers is in sorted (non-decreasing) order.

Solution:

```

int checkPairwiseSorted(int A[], int n) {
    if (n == 0 || n == 1)
        return 1;
    for (int i = 0; i < n - 1; i += 2){
        if (A[i] > A[i+1])
            return 0;
    }
    return 1;
}

```

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

Problem-79 Given an array of n elements, how do you print the frequencies of elements without using extra space. Assume all elements are positive, editable and less than n .

Solution: Use *negation* technique.

```

void frequencyCounter(int A[],int n){
    int pos = 0;
    while(pos < n){
        int expectedPos = A[pos] - 1;
        if(A[pos] > 0 && A[expectedPos] > 0){
            swap(A[pos], A[expectedPos]);
            A[expectedPos] = -1;
        }
        else if(A[pos] > 0){
            A[expectedPos]--;
            A[pos + 1] = 0;
        }
        else{
            pos++;
        }
    }
    for(int i = 0; i < n; ++i){
        printf("%d frequency is %d\n", i + 1 ,abs(A[i]));
    }
}

int main(int argc, char* argv[]){
    int A[] = {10, 10, 9, 4, 7, 6, 5, 2, 3, 2, 1};
    frequencyCounter(A, sizeof(A)/ sizeof(A[0]));
    return 0;
}

```

Array should have numbers in the range $[1, n]$ (where n is the size of the array). The if condition

$(A[pos] > 0 \ \&\& A[expectedPos] > 0)$ means that both the numbers at indices pos and $expectedPos$ are actual numbers in the array but not their frequencies. So we will swap them so that the number at the index pos will go to the position where it should have been if the numbers $1, 2, 3, \dots, n$ are kept in $0, 1, 2, \dots, n - 1$ indices. In the above example input array, initially $pos = 0$, so 10 at index 0 will go to index 9 after the swap. As this is the first occurrence of 10, make it to -1. Note that we are storing the frequencies as negative numbers to differentiate between actual numbers and frequencies.

The else if condition ($A[pos] > 0$) means $A[pos]$ is a number and $A[expectedPos]$ is its frequency without including the occurrence of $A[pos]$. So increment the frequency by 1 (that is decrement by 1 in terms of negative numbers). As we count its occurrence we need to move to next pos, so $pos++$, but before moving to that next position we should make the frequency of the number $pos + 1$ which corresponds to index pos of zero, since such a number has not yet occurred.

The final else part means the current index pos already has the frequency of the number $pos + 1$, so move to the next pos , hence $pos++$.

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

Problem-80 Which is faster and by how much, a linear search of only 1000 elements on a 5-GHz computer or a binary search of 1 million elements on a 1-GHz computer. Assume that the execution of each instruction on the 5-GHz computer is five times faster than on the 1-GHz computer and that each iteration of the linear search algorithm is twice as fast as each iteration of the binary search algorithm.

Solution: A binary search of 1 million elements would require $\log_2^{1,000,000}$ or about 20 iterations at most (i.e., worst case). A linear search of 1000 elements would require 500 iterations on the average (i.e., going halfway through the array). Therefore, binary search would be $\frac{500}{20} = 25$ faster (in terms of iterations) than linear search. However, since linear search iterations are twice as fast, binary search would be $\frac{25}{2}$ or about 12 times faster than linear search overall, on the same machine. Since we run them on different machines, where an instruction on the 5-GHz machine is 5 times faster than an instruction on a 1-GHz machine, binary search would be $\frac{12}{5}$ or about 2 times faster than linear search! The key idea is that software improvements can make an algorithm run much faster without having to use more powerful software.

SELECTION ALGORITHMS [MEDIAN]

CHAPTER

12



12.1 What are Selection Algorithms?

Selection algorithm is an algorithm for finding the k^{th} smallest/largest number in a list (also called as k^{th} order statistic). This includes finding the minimum, maximum, and median elements. For finding the k^{th} order statistic, there are multiple solutions which provide different complexities, and in this chapter we will enumerate those possibilities.

12.2 Selection by Sorting

A selection problem can be converted to a sorting problem. In this method, we first sort the input elements and then get the desired element. It is efficient if we want to perform many selections.

For example, let us say we want to get the minimum element. After sorting the input elements we can simply return the first element (assuming the array is sorted in ascending order). Now, if we want to find the second smallest element, we can simply return the second element from the sorted list.

That means, for the second smallest element we are not performing the sorting again. The same is also the case with subsequent queries. Even if we want to get k^{th} smallest element, just one scan of the sorted list is enough to find the element (or we can return the k^{th} -indexed value if the elements are in the array).

From the above discussion what we can say is, with the initial sorting we can answer any query in one scan, $O(n)$. In general, this method requires $O(n \log n)$ time (for *sorting*), where n is the length of the input list. Suppose we are performing n queries, then the average cost per operation is just $\frac{n \log n}{n} \approx O(\log n)$. This kind of analysis is called *amortized* analysis.

12.3 Partition-based Selection Algorithm

For the algorithm check [Problem-6](#). This algorithm is similar to Quick sort.

12.4 Linear Selection Algorithm - Median of Medians Algorithm

Worst-case performance	$O(n)$
Best-case performance	$O(n)$
Worst-case space complexity	$O(1)$ auxiliary

Refer to [Problem-11](#).

12.5 Finding the K Smallest Elements in Sorted Order

For the algorithm check [Problem-6](#). This algorithm is similar to Quick sort.

12.6 Selection Algorithms: Problems & Solutions

Problem-1 Find the largest element in an array A of size n .

Solution: Scan the complete array and return the largest element.

```

void FindLargestInArray(int n, const int A[]) {
    int large = A[0];
    for (int i = 1; i <= n-1; i++)
        if(A[i] > large)
            large = A[i];
    printf("Largest:%d", large);
}

```

Time Complexity - $O(n)$. Space Complexity - $O(1)$.

Note: Any deterministic algorithm that can find the largest of n keys by comparison of keys takes at least $n - 1$ comparisons.

Problem-2 Find the smallest and largest elements in an array A of size n .

Solution:

```

void FindSmallestAndLargestInArray (int A[], int n) {
    int small = A[0];
    int large = A[0];
    for (int i = 1; i <= n-1; i++)
        if(A[i] < small)
            small = A[i];
        else if(A[i] > large)
            large = A[i];
    printf("Smallest:%d, Largest:%d", small, large);
}

```

Time Complexity - $O(n)$. Space Complexity - $O(1)$. The worst-case number of comparisons is $2(n - 1)$.

Problem-3 Can we improve the previous algorithms?

Solution: Yes. We can do this by comparing in pairs.

```

// n is assumed to be even. Compare in pairs.
void FindWithPairComparison (int A[], int n) {
    int large = small = -1;
    for (int i = 0; i <= n - 1; i = i + 2) {           // Increment i by 2.
        if(A[i] < A[i + 1]) {
            if(A[i] < small)
                small = A[i];
            if(A[i + 1] > large)
                large = A[i + 1];
        }
        else {
            if(A[i + 1] < small)
                small = A[i + 1];
            if(A[i] > large)
                large = A[i];
        }
    }
    printf("Smallest:%d, Largest:%d", small, large);
}

```

Time Complexity - O(n). Space Complexity - O(1).

$$\text{Number of comparisons: } \begin{cases} \frac{3n}{2} - 2, & \text{if } n \text{ is even} \\ \frac{3n}{2} - \frac{3}{2}, & \text{if } n \text{ is odd} \end{cases}$$

Summary:

Straightforward comparison – $2(n - 1)$ comparisons

Compare for min only if comparison for max fails
--

Best case: increasing order – $n - 1$ comparisons

Worst case: decreasing order – $2(n - 1)$ comparisons

Average case: $3n/2 - 1$ comparisons

Note: For divide and conquer techniques refer to [Divide and Conquer](#) chapter.

Problem-4 Give an algorithm for finding the second largest element in the given input list of elements.

Solution: Brute Force Method

Algorithm:

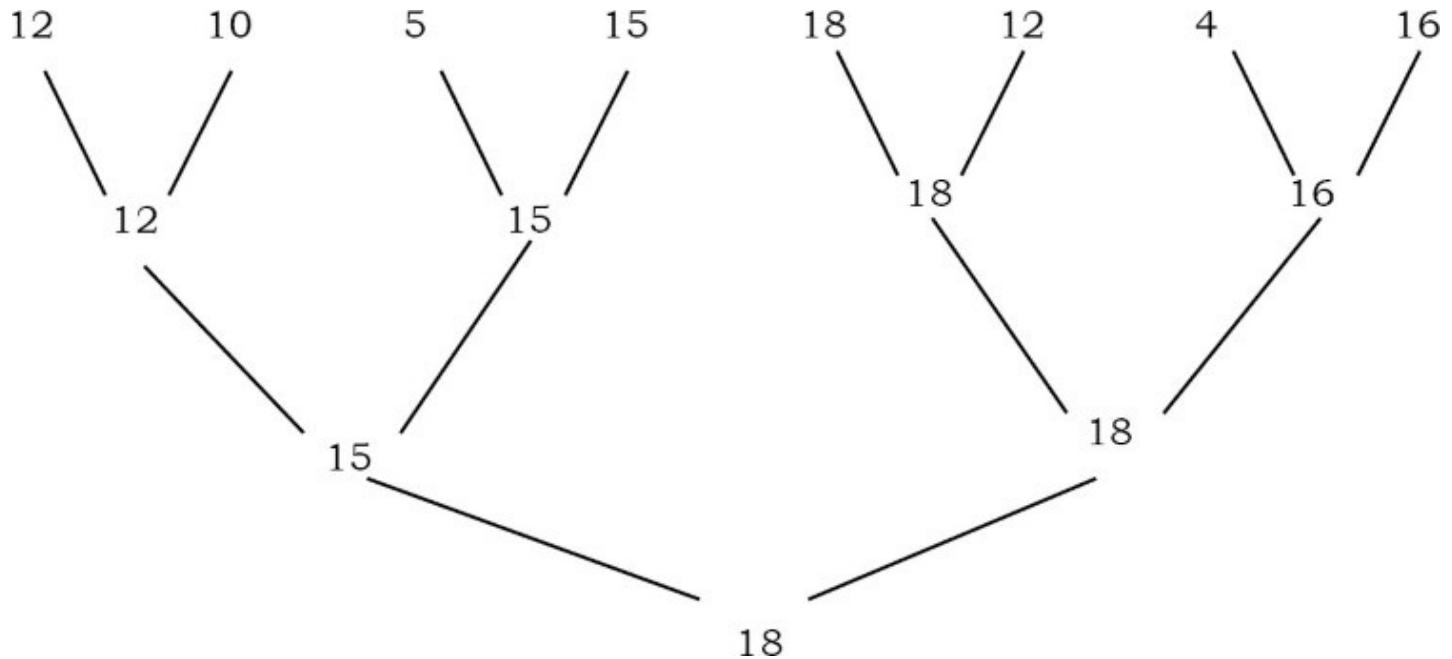
- Find largest element: needs $n - 1$ comparisons
- Delete (discard) the largest element
- Again find largest element: needs $n - 2$ comparisons

Total number of comparisons: $n - 1 + n - 2 = 2n - 3$

Problem-5 Can we reduce the number of comparisons in [Problem-4](#) solution?

Solution: The Tournament method: For simplicity, assume that the numbers are distinct and that n is a power of 2. We pair the keys and compare the pairs in rounds until only one round remains. If the input has eight keys, there are four comparisons in the first round, two in the second, and one in the last. The winner of the last round is the largest key. The figure below shows the method.

The tournament method directly applies only when n is a power of 2. When this is not the case, we can add enough items to the end of the array to make the array size a power of 2. If the tree is complete then the maximum height of the tree is $\log n$. If we construct the complete binary tree, we need $n - 1$ comparisons to find the largest. The second largest key has to be among the ones that were lost in a comparison with the largest one. That means, the second largest element should be one of the opponents of the largest element. The number of keys that are lost to the largest key is the height of the tree, i.e. $\log n$ [if the tree is a complete binary tree]. Then using the selection algorithm to find the largest among them, take $\log n - 1$ comparisons. Thus the total number of comparisons to find the largest and second largest keys is $n + \log n - 2$.



Problem-6 Find the k -smallest elements in an array S of n elements using partitioning method.

Solution: Brute Force Approach: Scan through the numbers k times to have the desired element. This method is the one used in bubble sort (and selection sort), every time we find out the smallest element in the whole sequence by comparing every element. In this method, the sequence has to be traversed k times. So the complexity is $O(n \times k)$.

Problem-7 Can we use the sorting technique for solving [Problem-6](#)?

Solution: Yes. Sort and take the first k elements.

1. Sort the numbers.
2. Pick the first k elements.

The time complexity calculation is trivial. Sorting of n numbers is of $O(n \log n)$ and picking k elements is of $O(k)$. The total complexity is $O(n \log n + k) = O(n \log n)$.

Problem-8 Can we use the *tree sorting* technique for solving [Problem-6](#)?

Solution: Yes.

1. Insert all the elements in a binary search tree.
2. Do an InOrder traversal and print k elements which will be the smallest ones. So, we have the k smallest elements.

The cost of creation of a binary search tree with n elements is $O(n \log n)$ and the traversal up to k elements is $O(k)$. Hence the complexity is $O(n \log n + k) = O(n \log n)$.

Disadvantage: If the numbers are sorted in descending order, we will be getting a tree which will be skewed towards the left. In that case, the construction of the tree will be $0 + 1 + 2 + \dots + (n-1) = \frac{n(n-1)}{2}$ which is $O(n^2)$. To escape from this, we can keep the tree balanced, so that the cost of constructing the tree will be only $n \log n$.

Problem-9 Can we improve the *tree sorting* technique for solving [Problem-6](#)?

Solution: Yes. Use a smaller tree to give the same result.

1. Take the first k elements of the sequence to create a balanced tree of k nodes (this will cost $k \log k$).
2. Take the remaining numbers one by one, and
 - a. If the number is larger than the largest element of the tree, return.
 - b. If the number is smaller than the largest element of the tree, remove the largest element of the tree and add the new element. This step is to make sure that a smaller element replaces a larger element from the tree. And of course the cost of this operation is $\log k$ since the tree is a balanced tree of k elements.

Once Step 2 is over, the balanced tree with k elements will have the smallest k elements. The only

remaining task is to print out the largest element of the tree.

Time Complexity:

1. For the first k elements, we make the tree. Hence the cost is $k \log k$.
2. For the rest $n - k$ elements, the complexity is $O(\log k)$.

Step 2 has a complexity of $(n - k) \log k$. The total cost is $k \log k + (n - k) \log k = n \log k$ which is $O(n \log k)$. This bound is actually better than the ones provided earlier.

Problem-10 Can we use the partitioning technique for solving [Problem-6](#)?

Solution: Yes.

Algorithm

1. Choose a pivot from the array.
2. Partition the array so that: $A[\text{low}..\text{pivotpoint} - 1] \leq \text{pivotpoint} \leq A[\text{pivotpoint} + 1..\text{high}]$.
3. if $k < \text{pivotpoint}$ then it must be on the left of the pivot, so do the same method recursively on the left part.
4. if $k = \text{pivotpoint}$ then it must be the pivot and print all the elements from low to pivotpoint .
5. if $k > \text{pivotpoint}$ then it must be on the right of pivot, so do the same method recursively on the right part.

The top-level call would be $\text{kthSmallest} = \text{Selection}(1, n, k)$.

```

int Selection (int low, int high, int k) {
    int pivotpoint;
    if(low == high)
        return S[low];
    else {
        pivotpoint = Partition(low, high);
        if(k == pivotpoint)
            return S[pivotpoint]; //we can print all the elements from low to pivotpoint.
        else if(k < pivotpoint)
            return Selection (low, pivotpoint - 1, k);
        else return Selection (pivotpoint + 1, high, k);
    }
}

void Partition (int low, int high) {
    int i, j, pivotitem;
    pivotitem = S[low];
    j = low;
    for (i = low + 1; i <= high; i++)
        if(S[i] < pivotitem) {
            j++;
            Swap S[i] and S[j];
        }
    pivotpoint = j;
    Swap S[low] and S[pivotpoint];
    return pivotpoint;
}

```

Time Complexity: $O(n^2)$ in worst case as similar to Quicksort. Although the worst case is the same as that of Quicksort, this performs much better on the average [$O(n \log k)$ – Average case].

Problem-11 Find the k^{th} -smallest element in an array S of n elements in best possible way.

Solution: This problem is similar to [Problem-6](#) and all the solutions discussed for [Problem-6](#) are valid for this problem. The only difference is that instead of printing all the k elements, we print only the k^{th} element. We can improve the solution by using the *median of medians* algorithm. Median is a special case of the selection algorithm. The algorithm $\text{Selection}(A, k)$ to find the k^{th} smallest element from set A of n elements is as follows:

Algorithm: $\text{Selection}(A, k)$

1. Partition A into $\lceil \frac{\text{length}(A)}{5} \rceil$ groups, with each group having five items (the last group may have fewer items).

2. Sort each group separately (e.g., insertion sort).
3. Find the median of each of the $\frac{n}{5}$ groups and store them in some array (let us say A').
4. Use *Selection* recursively to find the median of A' (median of medians). Let us assume the median of medians is m .

$$m = \text{Selection}(A', \frac{\frac{\text{length}(A)}{5}}{2});$$

5. Let $q = \#$ elements of A smaller than m ;
6. If($k == q + 1$)

return m ;

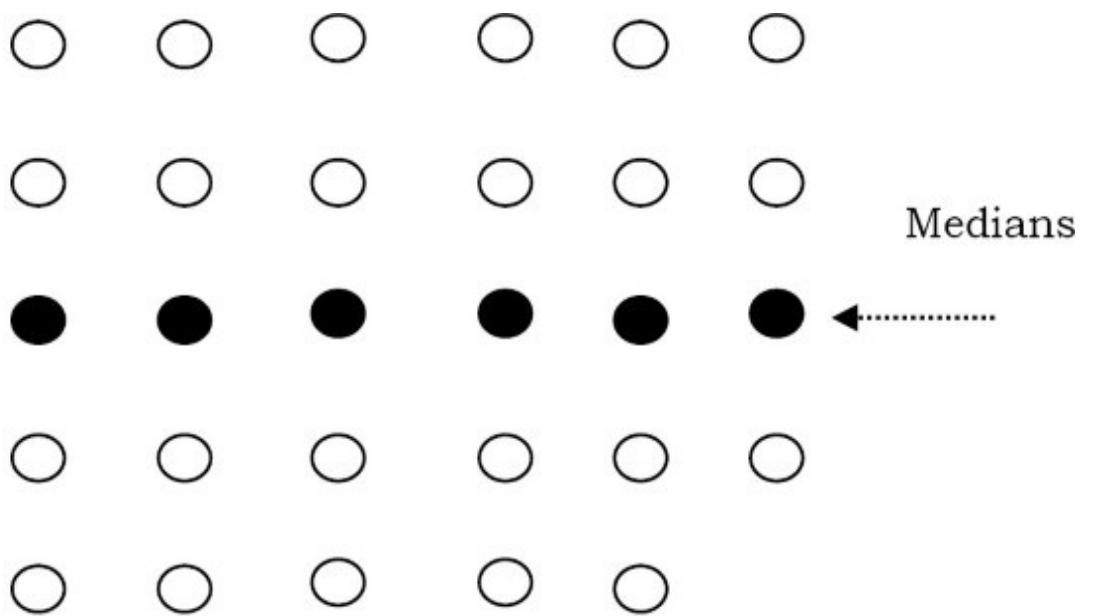
/ Partition with pivot */*

7. Else partition A into X and Y
 - $X = \{ \text{items smaller than } m \}$
 - $Y = \{ \text{items larger than } m \}$

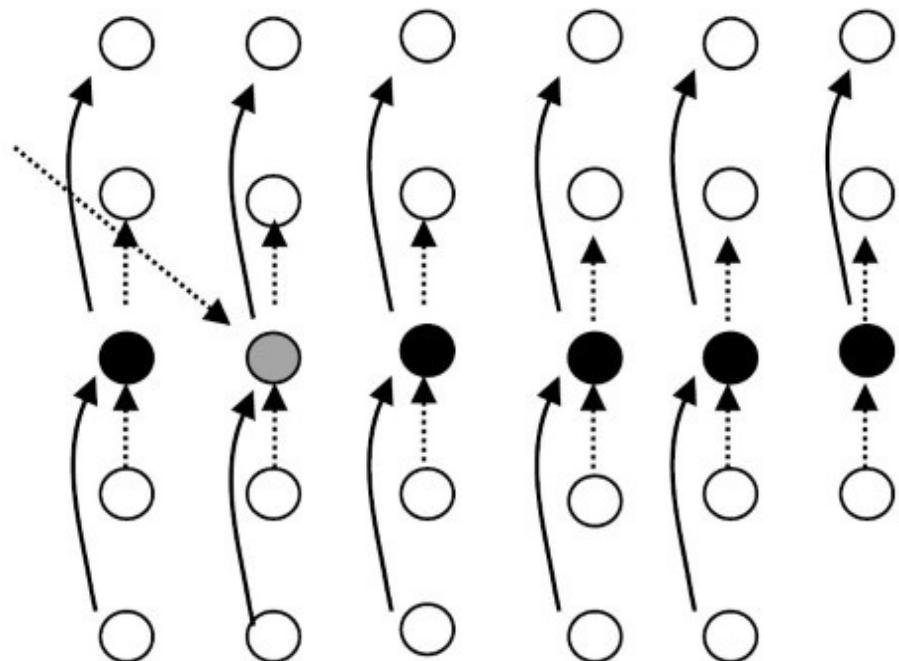
/ Next, form a subproblem */*

8. If($k < q + 1$)
 - return $\text{Selection}(X, k)$;
9. Else
 - return $\text{Selection}(Y, k - (q+1))$;

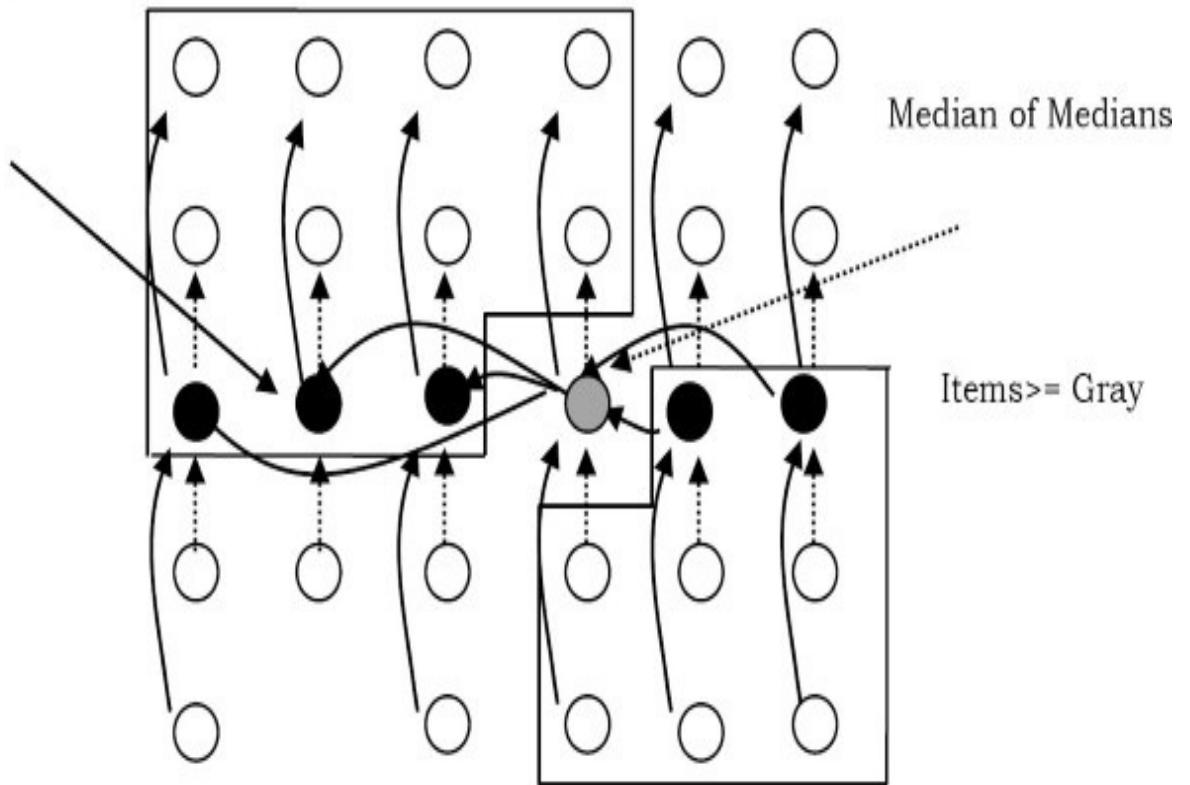
Before developing recurrence, let us consider the representation of the input below. In the figure, each circle is an element and each column is grouped with 5 elements. The black circles indicate the median in each group of 5 elements. As discussed, sort each column using constant time insertion sort.



Median of
Medians



After sorting rearrange the medians so that all medians will be in ascending order



In the figure above the gray circled item is the median of medians (let us call this m). It can be seen that at least $1/2$ of 5 element group medians $\leq m$. Also, these $1/2$ of 5 element groups contribute 3 elements that are $\leq m$ except 2 groups [last group which may contain fewer than 5 elements, and other group which contains m]. Similarly, at least $1/2$ of 5 element groups contribute 3 elements that are $\geq m$ as shown above. $1/2$ of 5 element groups contribute 3 elements, except 2 groups gives: $3(\lceil \frac{1}{2} \lceil \frac{n}{5} \rceil \rceil - 2) \approx \frac{3n}{10} - 6$. The remaining are $n - \frac{3n}{10} - 6 \approx \frac{7n}{10} + 6$. Since $\frac{7n}{10} + 6$ is greater than $\frac{3n}{10} - 6$ we need to consider $\frac{7n}{10} + 6$ for worst.

Components in recurrence:

- In our selection algorithm, we choose m , which is the median of medians, to be a pivot, and partition A into two sets X and Y . We need to select the set which gives maximum size (to get the worst case).
- The time in function *Selection* when called from procedure *partition*. The number of keys in the input to this call to *Selection* is $\frac{n}{5}$.
- The number of comparisons required to partition the array. This number is $\text{length}(S)$, let us say n .

We have established the following recurrence:
 $T(n) = T\left(\frac{n}{5}\right) + \Theta(n) + \text{Max}\{T(X), T(Y)\}$

From the above discussion we have seen that, if we select median of medians m as pivot, the partition sizes are: $\frac{3n}{10} - 6$ and $\frac{7n}{10} + 6$. If we select the maximum of these, then we get:

$$\begin{aligned} T(n) &= T\left(\frac{n}{5}\right) + \Theta(n) + T\left(\frac{7n}{10} + 6\right) \\ &\approx T\left(\frac{n}{5}\right) + \Theta(n) + T\left(\frac{7n}{10}\right) + O(1) \\ &\leq c\frac{7n}{10} + c\frac{n}{5} + \Theta(n) + O(1) \end{aligned}$$

Finally, $T(n) = \Theta(n)$.

Problem-12 In [Problem-11](#), we divided the input array into groups of 5 elements. The constant 5 play an important part in the analysis. Can we divide in groups of 3 which work in linear time?

Solution: In this case the modification causes the routine to take more than linear time. In the worst case, at least half of the $\lceil \frac{n}{3} \rceil$ medians found in the grouping step are greater than the median of medians m , but two of those groups contribute less than two elements larger than m . So as an upper bound, the number of elements larger than the pivotpoint is at least:

$$2\left(\lceil \frac{1}{2} \lceil \frac{n}{3} \rceil \rceil - 2\right) \geq \frac{n}{3} - 4$$

Likewise this is a lower bound. Thus up to $n - (\frac{n}{3} - 4) = \frac{2n}{3} + 4$ elements are fed into the recursive call to *Select*. The recursive step that finds the median of medians runs on a problem of size $\lceil \frac{n}{3} \rceil$, and consequently the time recurrence is:

$$T(n) = T\left(\lceil \frac{n}{3} \rceil\right) + T\left(\frac{2n}{3} + 4\right) + \Theta(n).$$

Assuming that $T(n)$ is monotonically increasing, we may conclude that $T\left(\frac{2n}{3} + 4\right) \geq T\left(\frac{2n}{3}\right) \geq 2T\left(\frac{n}{3}\right)$, and we can say the upper bound for this as $T(n) \geq 3T\left(\frac{n}{3}\right) + \Theta(n)$, which is $O(n \log n)$. Therefore, we cannot select 3 as the group size.

Problem-13 As in [Problem-12](#), can we use groups of size 7?

Solution: Following a similar reasoning, we once more modify the routine, now using groups of 7 instead of 5. In the worst case, at least half the $\lceil \frac{n}{7} \rceil$ medians found in the grouping step are greater than the median of medians m , but two of those groups contribute less than four elements larger than m . So as an upper bound, the number of elements larger than the pivotpoint is at least:

$$4\left(\lceil \frac{1}{2} \lceil \frac{n}{7} \rceil \rceil - 2\right) \geq \frac{2n}{7} - 8.$$

Likewise this is a lower bound. Thus up to $n - (\frac{2n}{7} - 8) = \frac{5n}{7} + 8$ elements are fed into the recursive call to Select. The recursive step that finds the median of medians runs on a problem of size $\lceil \frac{n}{7} \rceil$, and consequently the time recurrence is

$$\begin{aligned}
T(n) &= T(\lceil \frac{n}{7} \rceil) + T(\frac{5n}{7} + 8) + O(n) \\
T(n) &\leq c \lceil \frac{n}{7} \rceil + c(\frac{5n}{7} + 8) + O(n) \\
&\leq c \frac{n}{7} + c \frac{5n}{7} + 8c + an, a \text{ is a constant} \\
&= cn - c \frac{n}{7} + an + 9c \\
&= (a + c)n - (c \frac{n}{7} - 9c).
\end{aligned}$$

This is bounded above by $(a + c)n$ provided that $c \frac{n}{7} - 9c \geq 0$. Therefore, we can select 7 as the group size.

Problem-14 Given two arrays each containing n sorted elements, give an $O(\log n)$ -time algorithm to find the median of all $2n$ elements.

Solution: The simple solution to this problem is to merge the two lists and then take the average of the middle two elements (note the union always contains an even number of values). But, the merge would be $\Theta(n)$, so that doesn't satisfy the problem statement. To get $\log n$ complexity, let $medianA$ and $medianB$ be the medians of the respective lists (which can be easily found since both lists are sorted). If $medianA == medianB$, then that is the overall median of the union and we are done. Otherwise, the median of the union must be between $medianA$ and $medianB$. Suppose that $medianA < medianB$ (the opposite case is entirely similar). Then we need to find the median of the union of the following two sets:

$$\{x \in A \mid x \geq medianA\} \cup \{x \in B \mid x \leq medianB\}$$

So, we can do this recursively by resetting the *boundaries* of the two arrays. The algorithm tracks both arrays (which are sorted) using two indices. These indices are used to access and compare the median of both arrays to find where the overall median lies.

```

void FindMedian(int A[], int alo, int ahi, int B[], int blo, int bhi) {
    amid = alo + (ahi - alo)/2;
    amed = a[amid];
    bmid = blo + (bhi - blo)/2;
    bmed = b[bmid];
    if( ahi - alo + bhi - blo < 4 ) {
        Handle the boundary cases and solve it smaller problem in O(1) time.
        return;
    }
    else if(amed < bmed)
        FindMedian(A, amid, ahi, B, blo, bmid+1);
    else
        FindMedian(A, alo, amid+1, B, bmid+1, bhi);
}

```

Time Complexity: $O(\log n)$, since we are reducing the problem size by half every time.

Problem-15 Let A and B be two sorted arrays of n elements each. We can easily find the k^{th} smallest element in A in $O(1)$ time by just outputting $A[k]$. Similarly, we can easily find the k^{th} smallest element in B . Give an $O(\log k)$ time algorithm to find the k^{th} smallest element overall {i.e., the k^{th} smallest in the union of A and B }.

Solution: It's just another way of asking [Problem-14](#).

Problem-16 **Find the k smallest elements in sorted order:** Given a set of n elements from a totally-ordered domain, find the k smallest elements, and list them in sorted order. Analyze the worst-case running time of the best implementation of the approach.

Solution: Sort the numbers, and list the k smallest.

$T(n) = \text{Time complexity of sort} + \text{listing } k \text{ smallest elements} = \Theta(n \log n) + \Theta(n) = \Theta(n \log n)$.

Problem-17 For [Problem-16](#), if we follow the approach below, then what is the complexity?

Solution: Using the priority queue data structure from heap sort, construct a min-heap over the set, and perform extract-min k times. Refer to the [Priority Queues \(Heaps\)](#) chapter for more details.

Problem-18 For [Problem-16](#), if we follow the approach below then what is the complexity?

Find the k^{th} -smallest element of the set, partition around this pivot element, and sort the k smallest elements.

Solution:

$$\begin{aligned}
T(n) &= \text{Time complexity of } k^{th} - \text{smallest} + \text{Finding pivot} + \text{Sorting prefix} \\
&= \Theta(n) + \Theta(n) + \Theta(k \log k) = \Theta(n + k \log k)
\end{aligned}$$

Since, $k \leq n$, this approach is better than [Problem-16](#) and [Problem-17](#).

Problem-19 Find k nearest neighbors to the median of n distinct numbers in $O(n)$ time.

Solution: Let us assume that the array elements are sorted. Now find the median of n numbers and call its index as X (since array is sorted, median will be at $\frac{n}{2}$ location). All we need to do is select k elements with the smallest absolute differences from the median, moving from $X - 1$ to 0, and $X + 1$ to $n - 1$ when the median is at index m .

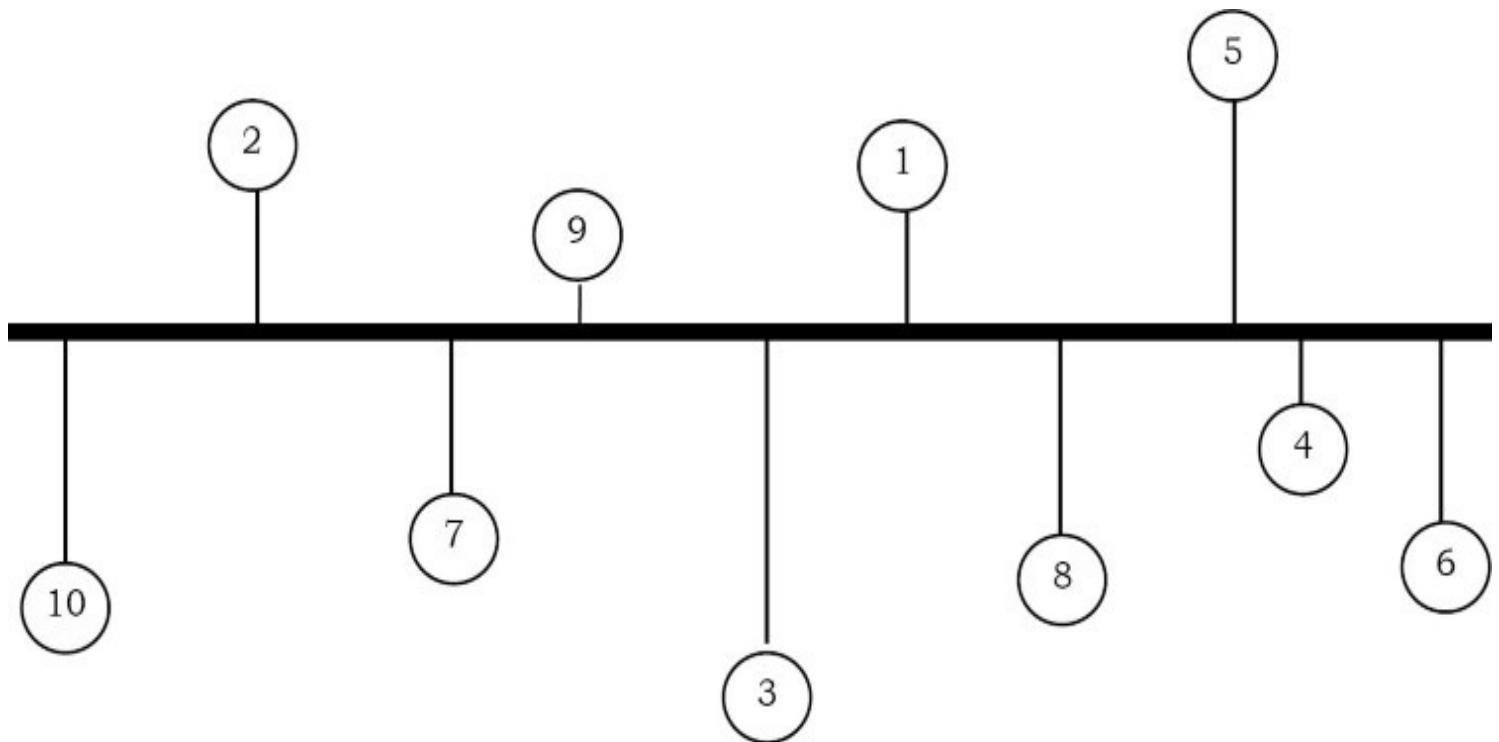
Time Complexity: Each step takes $\Theta(n)$. So the total time complexity of the algorithm is $\Theta(n)$.

Problem-20 Is there any other way of solving [Problem-19](#)?

Solution: Assume for simplicity that n is odd and k is even. If set A is in sorted order, the median is in position $n/2$ and the k numbers in A that are closest to the median are in positions $(n - k)/2$ through $(n + k)/2$.

We first use linear time selection to find the $(n - k)/2$, $n/2$, and $(n + k)/2$ elements and then pass through set A to find the numbers less than the $(n + k)/2$ element, greater than the $(n - k)/2$ element, and not equal to the $n/2$ element. The algorithm takes $O(n)$ time as we use linear time selection exactly three times and traverse the n numbers in A once.

Problem-21 Given (x,y) coordinates of n houses, where should you build a road parallel to x-axis to minimize the construction cost of building driveways?



Solution: The road costs nothing to build. It is the driveways that cost money. The driveway cost is proportional to its distance from the road. Obviously, they will be perpendicular. The solution is to put the street at the median of the y coordinates.

Problem-22 Given a big file containing billions of numbers, find the maximum 10 numbers from that file.

Solution: Refer to the [*Priority Queues*](#) chapter.

Problem-23 Suppose there is a milk company. The company collects milk every day from all its agents. The agents are located at different places. To collect the milk, what is the best place to start so that the least amount of total distance is travelled?

Solution: Starting at the median reduces the total distance travelled because it is the place which is at the center of all the places.

SYMBOL TABLES

CHAPTER

13



13.1 Introduction

Since childhood, we all have used a dictionary, and many of us have a word processor (say, Microsoft Word) which comes with a spell checker. The spell checker is also a dictionary but limited in scope. There are many real time examples for dictionaries and a few of them are:

- Spell checker
- The data dictionary found in database management applications
- Symbol tables generated by loaders, assemblers, and compilers
- Routing tables in networking components (DNS lookup)

In computer science, we generally use the term ‘symbol table’ rather than ‘dictionary’ when referring to the abstract data type (ADT).

13.2 What are Symbol Tables?

We can define the *symbol table* as a data structure that associates a *value* with a *key*. It supports the following operations:

- Search whether a particular name is in the table
- Get the attributes of that name
- Modify the attributes of that name
- Insert a new name and its attributes
- Delete a name and its attributes

There are only three basic operations on symbol tables: searching, inserting, and deleting.

Example: DNS lookup. Let us assume that the key in this case is the URL and the value is an IP address.

- Insert URL with specified IP address
- Given URL, find corresponding IP address

Key[Website]	Value [IP Address]
www.CareerMonks.com	128.112.136.11
www.AuthorsInn.com	128.112.128.15
www.AuthInn.com	130.132.143.21
www.klm.com	128.103.060.55
www.CareerMonk.com	209.052.165.60

13.3 Symbol Table Implementations

Before implementing symbol tables, let us enumerate the possible implementations. Symbol tables can be implemented in many ways and some of them are listed below.

Unordered Array Implementation

With this method, just maintaining an array is enough. It needs $O(n)$ time for searching, insertion and deletion in the worst case.

Ordered [Sorted] Array Implementation

In this we maintain a sorted array of keys and values.

- Store in sorted order by key
- $\text{keys}[i] = i^{\text{th}}$ largest key
- $\text{values}[i] = \text{value associated with } i^{\text{th}}$ largest key

Since the elements are sorted and stored in arrays, we can use a simple binary search for finding an element. It takes $O(\log n)$ time for searching and $O(n)$ time for insertion and deletion in the worst case.

Unordered Linked List Implementation

Just maintaining a linked list with two data values is enough for this method. It needs $O(n)$ time for searching, insertion and deletion in the worst case.

Ordered Linked List Implementation

In this method, while inserting the keys, maintain the order of keys in the linked list. Even if the list is sorted, in the worst case it needs $O(n)$ time for searching, insertion and deletion.

Binary Search Trees Implementation

Refer to [Trees](#) chapter. The advantages of this method are: it does not need much code and it has a fast search [$O(\log n)$ on average].

Balanced Binary Search Trees Implementation

Refer to [Trees](#) chapter. It is an extension of binary search trees implementation and takes $O(\log n)$ in worst case for search, insert and delete operations.

Ternary Search Implementation

Refer to [String Algorithms](#) chapter. This is one of the important methods used for implementing dictionaries.

Hashing Implementation

This method is important. For a complete discussion, refer to the [Hashing](#) chapter.

13.4 Comparison Table of Symbols for Implementations

Let us consider the following comparison table for all the implementations.

Implementation	Search	Insert	Delete
Unordered Array	n	n	n
Ordered Array (can be implemented with array binary search)	$\log n$	n	n
Unordered List	n	n	n
Ordered List	n	n	n
Binary Search Trees ($O(\log n)$ on average)	$\log n$	$\log n$	$\log n$
Balanced Binary Search Trees ($O(\log n)$ in worst case)	$\log n$	$\log n$	$\log n$
Ternary Search (only change is in logarithms base)	$\log n$	$\log n$	$\log n$
Hashing ($O(1)$ on average)	1	1	1

Notes:

- In the above table, n is the input size.
- Table indicates the possible implementations discussed in this book. But, there could be other implementations.

HASHING

CHAPTER

14



14.1 What is Hashing?

Hashing is a technique used for storing and retrieving information as quickly as possible. It is used to perform optimal searches and is useful in implementing symbol tables.

14.2 Why Hashing?

In the *Trees* chapter we saw that balanced binary search trees support operations such as *insert*, *delete* and *search* in $O(\log n)$ time. In applications, if we need these operations in $O(1)$, then hashing provides a way. Remember that worst case complexity of hashing is still $O(n)$, but it gives $O(1)$ on the average.

14.3 HashTable ADT

The common operations for hash table are:

- CreatHashTable: Creates a new hash table
- HashSearch: Searches the key in hash table
- HashInsert: Inserts a new key into hash table
- HashDelete: Deletes a key from hash table
- DeleteHashTable: Deletes the hash table

14.4 Understanding Hashing

In simple terms we can treat *array* as a hash table. For understanding the use of hash tables, let us consider the following example: Give an algorithm for printing the first repeated character if there are duplicated elements in it. Let us think about the possible solutions. The simple and brute force way of solving is: given a string, for each character check whether that character is repeated or not. The time complexity of this approach is $O(n^2)$ with $O(1)$ space complexity.

Now, let us find a better solution for this problem. Since our objective is to find the first repeated character, what if we remember the previous characters in some array?

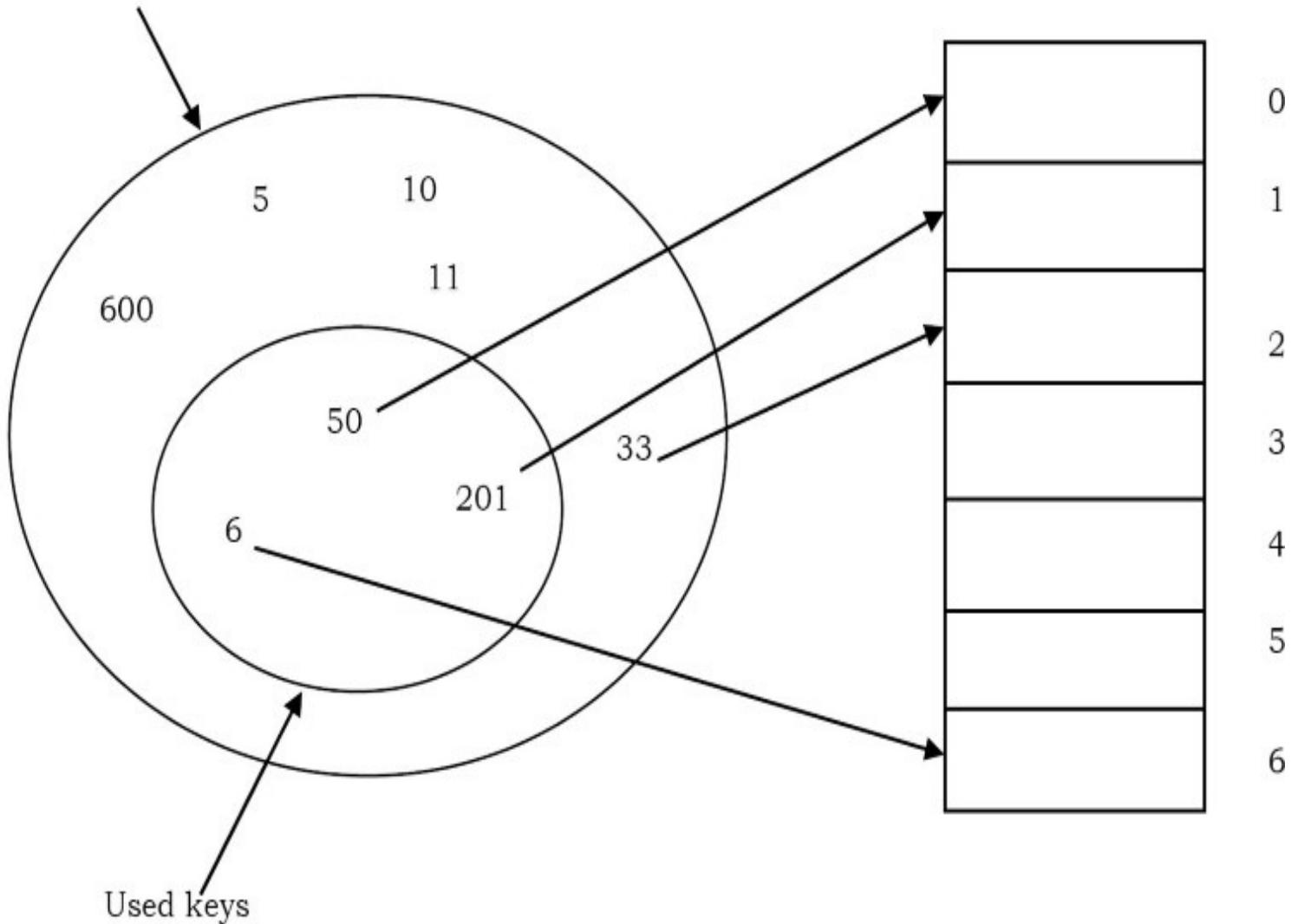
We know that the number of possible characters is 256 (for simplicity assume *ASCII* characters only). Create an array of size 256 and initialize it with all zeros. For each of the input characters go to the corresponding position and increment its count. Since we are using arrays, it takes constant time for reaching any location. While scanning the input, if we get a character whose counter is already 1 then we can say that the character is the one which is repeating for the first time.

```
char FirstRepeatedChar ( char *str ) {
    int i, len=strlen(str);
    int count[256]; //additional array
    for(i=0; i<256; ++i)
        count[i] = 0;
    for(i=0; i<len; ++i) {
        if(count[str[i]]==1) {
            printf("%c", str[i]);
            break;
        }
        else  count[str[i]]++;
    }
    if(i==len)
        printf("No Repeated Characters");
    return 0;
}
```

Why not Arrays?

In the previous problem, we have used an array of size 256 because we know the number of different possible characters [256] in advance. Now, let us consider a slight variant of the same problem. Suppose the given array has numbers instead of characters, then how do we solve the problem?

Universe of possible keys



In this case the set of possible values is infinity (or at least very big). Creating a huge array and storing the counters is not possible. That means there are a set of universal keys and limited locations in the memory. If we want to solve this problem we need to somehow map all these possible keys to the possible memory locations. From the above discussion and diagram it can be seen that we need a mapping of possible keys to one of the available locations. As a result using simple arrays is not the correct choice for solving the problems where the possible keys are very big. The process of mapping the keys to locations is called *hashing*.

Note: For now, do not worry about how the keys are mapped to locations. That depends on the function used for conversions. One such simple function is *key % table size*.

14.5 Components of Hashing

Hashing has four key components:

- 1) Hash Table
- 2) Hash Functions
- 3) Collisions
- 4) Collision Resolution Techniques

14.6 Hash Table

Hash table is a generalization of array. With an array, we store the element whose key is k at a position k of the array. That means, given a key k , we find the element whose key is k by just looking in the k^{th} position of the array. This is called *direct addressing*.

Direct addressing is applicable when we can afford to allocate an array with one position for every possible key. But if we do not have enough space to allocate a location for each possible key, then we need a mechanism to handle this case. Another way of defining the scenario is: if we have less locations and more possible keys, then simple array implementation is not enough.

In these cases one option is to use hash tables. Hash table or hash map is a data structure that stores the keys and their associated values, and hash table uses a hash function to map keys to their associated values. The general convention is that we use a hash table when the number of keys actually stored is small relative to the number of possible keys.

14.7 Hash Function

The hash function is used to transform the key into the index. Ideally, the hash function should map each possible key to a unique slot index, but it is difficult to achieve in practice.

Given a collection of elements, a hash function that maps each item into a unique slot is referred to as a *perfect hash function*. If we know the elements and the collection will never change, then it is possible to construct a perfect hash function. Unfortunately, given an arbitrary collection of elements, there is no systematic way to construct a perfect hash function. Luckily, we do not need the hash function to be perfect to still gain performance efficiency.

One way to always have a perfect hash function is to increase the size of the hash table so that each possible value in the element range can be accommodated. This guarantees that each element will have a unique slot. Although this is practical for small numbers of elements, it is not feasible when the number of possible elements is large. For example, if the elements were nine-digit Social Security numbers, this method would require almost one billion slots. If we only want to store data for a class of 25 students, we will be wasting an enormous amount of memory.

Our goal is to create a hash function that minimizes the number of collisions, is easy to compute, and evenly distributes the elements in the hash table. There are a number of common ways to extend the simple remainder method. We will consider a few of them here.

The *folding method* for constructing hash functions begins by dividing the elements into equal-size pieces (the last piece may not be of equal size). These pieces are then added together to give the resulting hash value. For example, if our element was the phone number 436-555-4601, we would take the digits and divide them into groups of 2 (43,65,55,46,01). After the addition, $43+65+55+46+01$, we get 210. If we assume our hash table has 11 slots, then we need to perform the extra step of dividing by 11 and keeping the remainder. In this case $210 \% 11$ is 1, so the phone number 436-555-4601 hashes to slot 1. Some folding methods go one step further and reverse every other piece before the addition. For the above example, we get $43+56+55+64+01=219$ which gives $219 \% 11 = 10$.

How to Choose Hash Function?

The basic problems associated with the creation of hash tables are:

- An efficient hash function should be designed so that it distributes the index values of inserted objects uniformly across the table.
- An efficient collision resolution algorithm should be designed so that it computes an alternative index for a key whose hash index corresponds to a location previously inserted in the hash table.
- We must choose a hash function which can be calculated quickly, returns values within the range of locations in our table, and minimizes collisionsns.

Characteristics of Good Hash Functions

A good hash function should have the following characteristics:

- Minimize collision
- Be easy and quick to compute
- Distribute key values evenly in the hash table
- Use all the information provided in the key
- Have a high load factor for a given set of keys

14.8 Load Factor

The load factor of a non-empty hash table is the number of items stored in the table divided by the size of the table. This is the decision parameter used when we want to rehash or expand the existing hash table entries. This also helps us in determining the efficiency of the hashing function. That means, it tells whether the hash function is distributing the keys uniformly or not.

$$\text{Load factor} = \frac{\text{Number of elements in hash table}}{\text{Hash Table size}}$$

14.9 Collisions

Hash functions are used to map each key to a different address space, but practically it is not possible to create such a hash function and the problem is called *collision*. Collision is the condition where two records are stored in the same location.

14.10 Collision Resolution Techniques

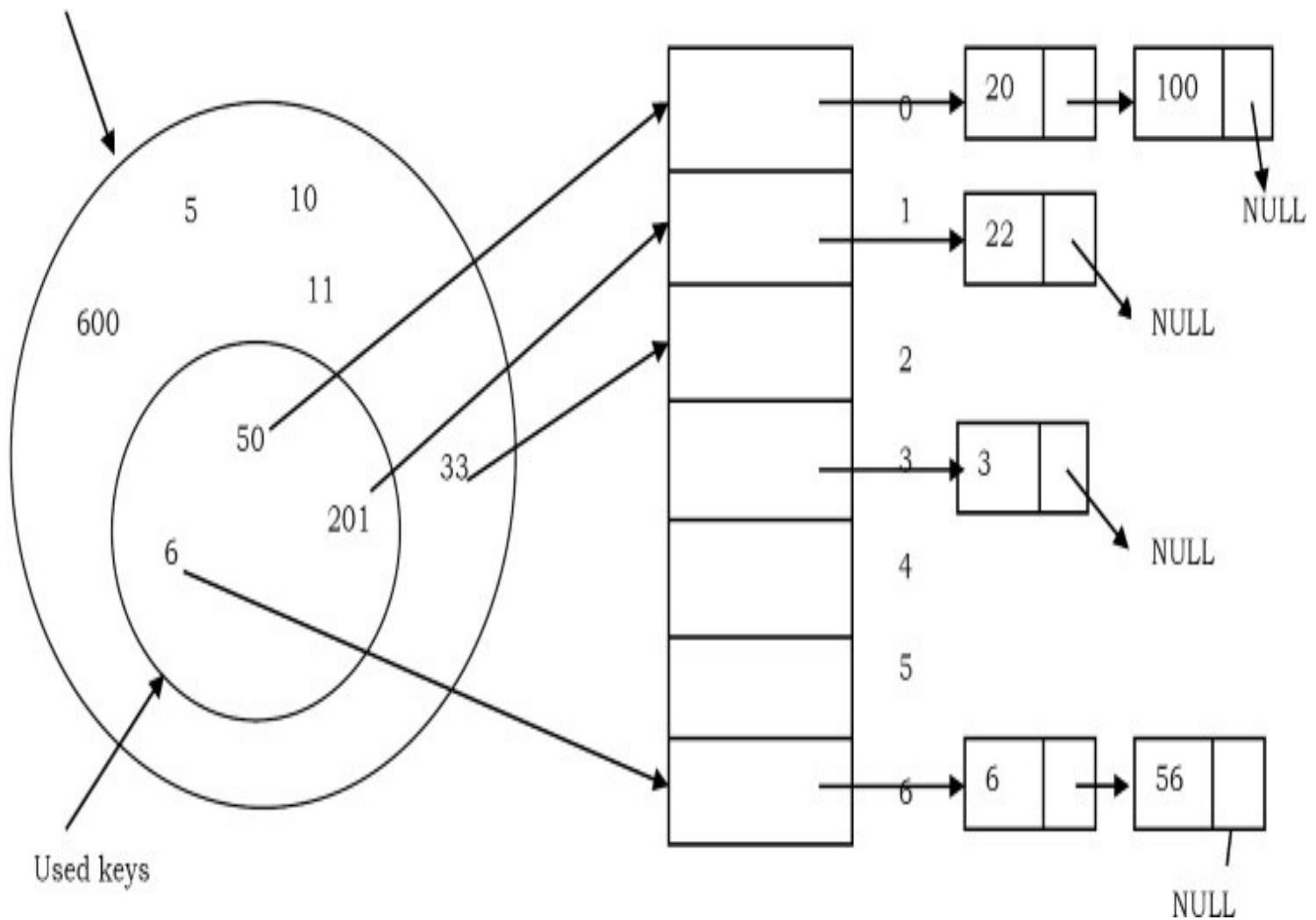
The process of finding an alternate location is called *collision resolution*. Even though hash tables have collision problems, they are more efficient in many cases compared to all other data structures, like search trees. There are a number of collision resolution techniques, and the most popular are direct chaining and open addressing.

- **Direct Chaining:** An array of linked list application
 - Separate chaining
- **Open Addressing:** Array-based implementation
 - Linear probing (linear search)
 - Quadratic probing (*nonlinear search*)
 - Double hashing (use two hash functions)

14.11 Separate Chaining

Collision resolution by chaining combines linked representation with hash table. When two or more records hash to the same location, these records are constituted into a singly-linked list called a *chain*.

Universe of possible keys



14.12 Open Addressing

In open addressing all keys are stored in the hash table itself. This approach is also known as *closed hashing*. This procedure is based on probing. A collision is resolved by probing.

Linear Probing

The interval between probes is fixed at 1. In linear probing, we search the hash table sequentially, starting from the original hash location. If a location is occupied, we check the next location. We wrap around from the last table location to the first table location if necessary. The function for rehashing is the following:

$$\text{rehash}(\text{key}) = (n + 1) \% \text{tablesize}$$

One of the problems with linear probing is that table items tend to cluster together in the hash table. This means that the table contains groups of consecutively occupied locations that are

called *clustering*.

Clusters can get close to one another, and merge into a larger cluster. Thus, the one part of the table might be quite dense, even though another part has relatively few items. Clustering causes long probe searches and therefore decreases the overall efficiency.

The next location to be probed is determined by the step-size, where other step-sizes (more than one) are possible. The step-size should be relatively prime to the table size, i.e. their greatest common divisor should be equal to 1. If we choose the table size to be a prime number, then any step-size is relatively prime to the table size. Clustering cannot be avoided by larger step-sizes.

Quadratic Probing

The interval between probes increases proportionally to the hash value (the interval thus increasing linearly, and the indices are described by a quadratic function). The problem of Clustering can be eliminated if we use the quadratic probing method.

In quadratic probing, we start from the original hash location i . If a location is occupied, we check the locations $i + 1^2, i + 2^2, i + 3^2, i + 4^2\dots$ We wrap around from the last table location to the first table location if necessary. The function for rehashing is the following:

$$\text{rehash}(\text{key}) = (n + k^2) \% \text{tablesize}$$

Example: Let us assume that the table size is 11 (0..10)

Hash Function: $h(\text{key}) = \text{key mod } 11$

0	
1	
2	2
3	13
4	25
5	5
6	24
7	9
8	19
9	31
10	21

Insert keys

$$31 \bmod 11 = 9$$

$$19 \bmod 11 = 8$$

$$2 \bmod 11 = 2$$

$$13 \bmod 11 = 2 \rightarrow 2 + 1^2 = 3$$

$$25 \bmod 11 = 3 \rightarrow 3 + 1^2 = 4$$

$$24 \bmod 11 = 2 \rightarrow 2 + 1^2, 2 + 2^2 = 6$$

$$21 \bmod 11 = 10$$

$$9 \bmod 11 = 9 \rightarrow 9 + 1^2, 9 + 2^2 \bmod 11, 9 + 3^2 \bmod 11 = 7$$

Even though clustering is avoided by quadratic probing, still there are chances of clustering. Clustering is caused by multiple search keys mapped to the same hash key. Thus, the probing sequence for such search keys is prolonged by repeated conflicts along the probing sequence. Both linear and quadratic probing use a probing sequence that is independent of the search key.

Double Hashing

The interval between probes is computed by another hash function. Double hashing reduces clustering in a better way. The increments for the probing sequence are computed by using a second hash function. The second hash function $h2$ should be:

$$h2(key) \neq 0 \text{ and } h2 \neq h1$$

We first probe the location $h1(key)$. If the location is occupied, we probe the location $h1(key) + h2(key)$, $h1(key) + 2 * h2(key)$, ...

Example:

Table size is 11 (0..10)

Hash Function: assume $h1(key) = key \bmod 11$ and $h2(key) = 7 - (key \bmod 7)$

0	
1	
2	
3	58
4	25
5	
6	91
7	
8	
9	25
10	14

Insert keys:

$$58 \bmod 11 = 3$$

$$14 \bmod 11 = 3 \rightarrow 3 + 7 = 10$$

$$91 \bmod 11 = 3 \rightarrow 3 + 7, 3 + 2 * 7 \bmod 11 = 6$$

$$25 \bmod 11 = 3 \rightarrow 3 + 3, 3 + 2 * 3 = 9$$

14.13 Comparison of Collision Resolution Techniques

Comparisons: Linear Probing vs. Double Hashing

The choice between linear probing and double hashing depends on the cost of computing the hash function and on the load factor [number of elements per slot] of the table. Both use few probes but double hashing take more time because it hashes to compare two hash functions for long keys.

Comparisons: Open Addressing vs. Separate Chaining

It is somewhat complicated because we have to account for the memory usage. Separate chaining uses extra memory for links. Open addressing needs extra memory implicitly within the table to terminate the probe sequence. Open-addressed hash tables cannot be used if the data does not have unique keys. An alternative is to use separate chained hash tables.

Comparisons: Open Addressing methods

Linear Probing	Quadratic Probing	Double hashing
Fastest among three	Easiest to implement and deploy	Makes more efficient use of memory
Uses few probes	Uses extra memory for links and it does not probe all locations in the table	Uses few probes but takes more time
A problem occurs known as primary clustering	A problem occurs known as secondary clustering	More complicated to implement
Interval between probes is fixed - often at 1.	Interval between probes increases proportional to the hash value	Interval between probes is computed by another hash function

14.14 How Hashing Gets O(1) Complexity

From the previous discussion, one doubts how hashing gets O(1) if multiple elements map to the same location...

The answer to this problem is simple. By using the load factor we make sure that each block (for example, linked list in separate chaining approach) on the average stores the maximum number of elements less than the *load factor*. Also, in practice this load factor is a constant (generally, 10 or 20). As a result, searching in 20 elements or 10 elements becomes constant.

If the average number of elements in a block is greater than the load factor, we rehash the elements with a bigger hash table size. One thing we should remember is that we consider average occupancy (total number of elements in the hash table divided by table size) when deciding the rehash.

The access time of the table depends on the load factor which in turn depends on the hash function. This is because hash function distributes the elements to the hash table. For this reason, we say hash table gives O(1) complexity on average. Also, we generally use hash tables in cases

where searches are more than insertion and deletion operations.

14.15 Hashing Techniques

There are two types of hashing techniques: static hashing and dynamic hashing

Static Hashing

If the data is fixed then static hashing is useful. In static hashing, the set of keys is kept fixed and given in advance, and the number of primary pages in the directory are kept fixed.

Dynamic Hashing

If the data is not fixed, static hashing can give bad performance, in which case dynamic hashing is the alternative, in which case the set of keys can change dynamically.

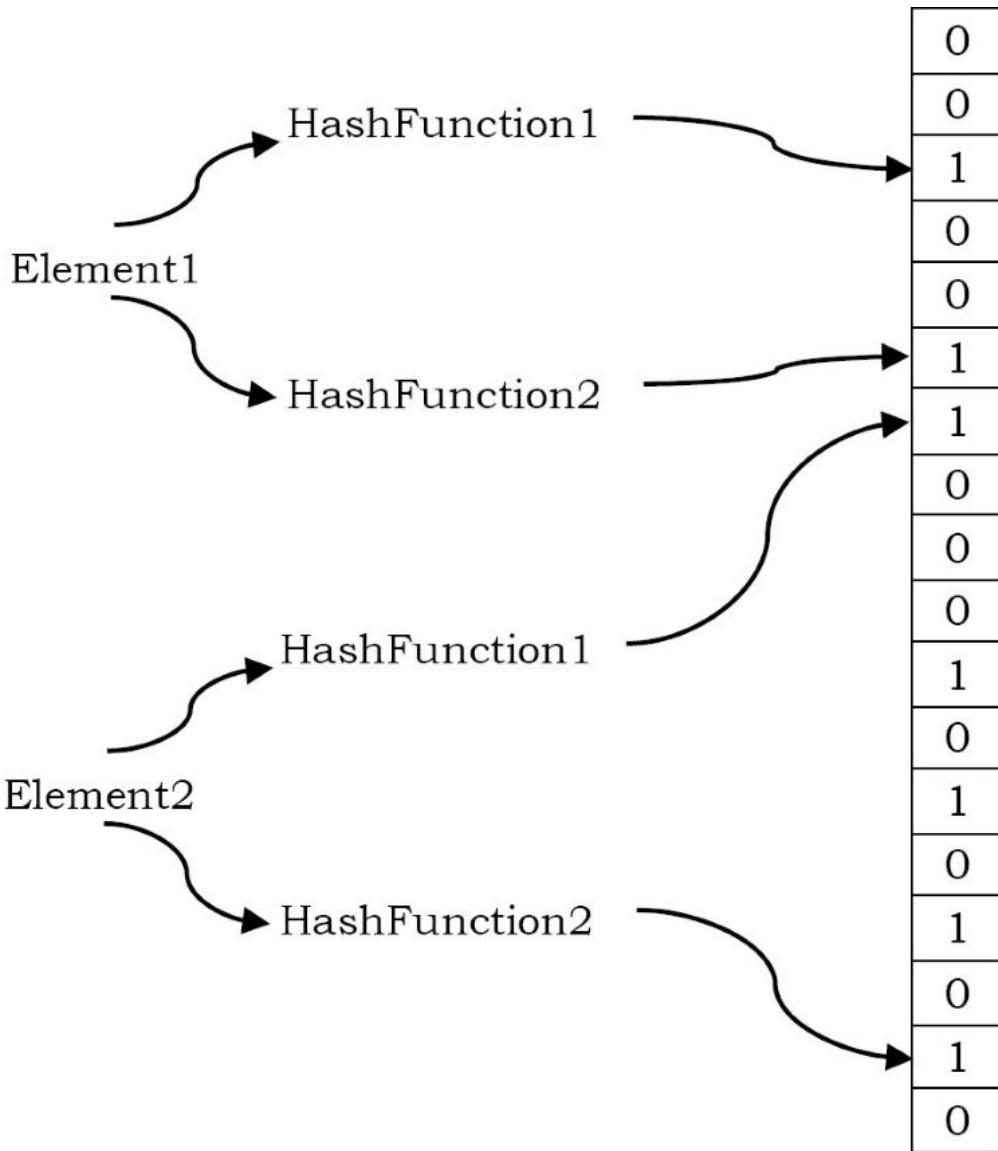
14.16 Problems for which Hash Tables are not suitable

- Problems for which data ordering is required
- Problems having multidimensional data
- Prefix searching, especially if the keys are long and of variable-lengths
- Problems that have dynamic data
- Problems in which the data does not have unique keys.

14.17 Bloom Filters

A Bloom filter is a probabilistic data structure which was designed to check whether an element is present in a set with memory and time efficiency. It tells us that the element either definitely is *not* in the set or *may* be in the set. The base data structure of a Bloom filter is a *Bit Vector*. The algorithm was invented in 1970 by Burton Bloom and it relies on the use of a number of different hash functions.

How it works?



Now that the bits in the bit vector have been set for *Element1* and *Element2*; we can query the bloom filter to tell us if something has been seen before.

The element is hashed but instead of setting the bits, this time a check is done and if the bits that would have been set are already set the bloom filter will return true that the element has been seen before.

A Bloom filter starts off with a bit array initialized to zero. To store a data value, we simply apply k different hash functions and treat the resulting k values as indices in the array, and we set each of the k array elements to 1. We repeat this for every element that we encounter.

Now suppose an element turns up and we want to know if we have seen it before. What we do is apply the k hash functions and look up the indicated array elements. If any of them are 0 we can be 100% sure that we have never encountered the element before - if we had, the bit would have been set to 1. However, even if all of them are one, we still can't conclude that we have seen the element before because all of the bits could have been set by the k hash functions applied to multiple other elements. All we can conclude is that it is *likely* that we have encountered the

element before.

Note that it is not possible to remove an element from a Bloom filter. The reason is simply that we can't unset a bit that appears to belong to an element because it might also be set by another element.

If the bit array is mostly empty, i.e., set to zero, and the k hash functions are independent of one another, then the probability of a false positive (i.e., concluding that we have seen a data item when we actually haven't) is low. For example, if there are only k bits set, we can conclude that the probability of a false positive is very close to zero as the only possibility of error is that we entered a data item that produced the same k hash values - which is unlikely as long as the 'has' functions are independent.

As the bit array fills up, the probability of a false positive slowly increases. Of course when the bit array is full, every element queried is identified as having been seen before. So clearly we can trade space for accuracy as well as for time.

One-time removal of an element from a Bloom filter can be simulated by having a second Bloom filter that contains elements that have been removed. However, false positives in the second filter become false negatives in the composite filter, which may be undesirable. In this approach, re-adding a previously removed item is not possible, as one would have to remove it from the *removed* filter.

Selecting hash functions

The requirement of designing k different independent hash functions can be prohibitive for large k . For a good hash function with a wide output, there should be little if any correlation between different bit-fields of such a hash, so this type of hash can be used to generate multiple *different* hash functions by slicing its output into multiple bit fields. Alternatively, one can pass k different initial values (such as 0, 1, ..., $k - 1$) to a hash function that takes an initial value – or add (or append) these values to the key. For larger m and/or k , independence among the hash functions can be relaxed with negligible increase in the false positive rate.

Selecting size of bit vector

A Bloom filter with 1% error and an optimal value of k , in contrast, requires only about 9.6 bits per element – regardless of the size of the elements. This advantage comes partly from its compactness, inherited from arrays, and partly from its probabilistic nature. The 1% false-positive rate can be reduced by a factor of ten by adding only about 4.8 bits per element.

Space Advantages

While risking false positives, Bloom filters have a strong space advantage over other data structures for representing sets, such as self-balancing binary search trees, tries, hash tables, or simple arrays or linked lists of the entries. Most of these require storing at least the data items themselves, which can require anywhere from a small number of bits, for small integers, to an arbitrary number of bits, such as for strings (tries are an exception, since they can share storage between elements with equal prefixes). Linked structures incur an additional linear space overhead for pointers.

However, if the number of potential values is small and many of them can be in the set, the Bloom filter is easily surpassed by the deterministic bit array, which requires only one bit for each potential element.

Time Advantages

Bloom filters also have the unusual property that the time needed either to add items or to check whether an item is in the set is a fixed constant, $O(k)$, completely independent of the number of items already in the set. No other constant-space set data structure has this property, but the average access time of sparse hash tables can make them faster in practice than some Bloom filters. In a hardware implementation, however, the Bloom filter shines because its k lookups are independent and can be parallelized.

Implementation

Refer to *Problems Section*.

14.18 Hashing: Problems & Solutions

Problem-1 Implement a separate chaining collision resolution technique. Also, discuss time complexities of each function.

Solution: To create a hashtable of given size, say n , we allocate an array of n/L (whose value is usually between 5 and 20) pointers to list, initialized to NULL. To perform *Search/Insert/Delete* operations, we first compute the index of the table from the given key by using *hashfunction* and then do the corresponding operation in the linear list maintained at that location. To get uniform distribution of keys over a hashtable, maintain table size as the prime number.

```

#define LOAD_FACTOR 20
struct ListNode {
    int key;
    int data;
    struct ListNode *next;
};
struct HashTableNode {
    int bcount;           //Number of elements in block
    struct ListNode *next;
};
struct HashTable {
    int tsize;
    int count;           //Number of elements in table
    struct HashTableNode **Table;
};
struct HashTable *CreatHashTable(int size) {
    struct HashTable *h;
    h = (struct HashTable *)malloc(sizeof(struct HashTable));
    if(!h)
        return NULL;
    h->tsize = size / LOAD_FACTOR;
    h->count = 0;
    h->Table = (struct HashTableNode **) malloc( sizeof(struct HashTableNode *) * h->tsize);
    if(!h->Table) {
        printf("Memory Error");
        return NULL;
    }
    for(int i=0; i < h->tsize; i++) {
        h->Table[i]->next = NULL;
        h->Table[i]->bcount = 0;
    }
    return h;
}
int HashSearch(Struct HashTable *h, int data) {
    struct ListNode *temp;
    temp = h->Table[Hash(data, h->tsize)]->next;           //Assume Hash is a built-in function
    while(temp) {
        if(temp->data == data)
            return 1;
        temp = temp->next;
    }
    return 0;
}
int HashInsert(Struct HashTable *h, int data) {
    int index;
    struct ListNode *temp, *newNode;
    if(HashSearch(h, data))
        return 0;
    index = Hash(data, h->tsize);           //Assume Hash is a built-in function
    temp = h->Table[index]->next;
    newNode = (struct ListNode *) malloc(sizeof(struct ListNode));
    if(!newNode) {
        printf("Out of Space");
        return -1;
    }
    newNode->key = index;
    newNode->data = data;
    newNode->next = h->Table[index]->next;
}

```



```

h->Table[index]->next = newNode;
h->Table[index]->bcount++;
h->count++;
if(h->count / h->tsize > LOAD_FACTOR)
    Rehash(h);
return 1;
}
int HashDelete(Struct HashTable *h, int data) {
    int index;
    struct ListNode *temp, *prev;
    index = Hash(data, h->tsize);
    for(temp = h->Table[index]->next, prev = NULL; temp; prev = temp, temp = temp->next) {
        if(temp->data == data) {
            if(prev != NULL)
                prev->next = temp->next;
            free(temp);
            h->Table[index]->bcount--;
            h->count--;
            return 1;
        }
    }
    return 0;
}
void Rehash(Struct HashTable *h) {
    int oldsize, i, index;
    struct ListNode *p, * temp, *temp2;
    struct HashTableNode **oldTable;
    oldsize = h->tsize;
    oldTable = h->Table;
    h->tsize = h->tsize * 2;
    h->Table = (struct HashTableNode **) malloc(h->tsize * sizeof(struct HashTableNode *));
    if(!h->Table) {
        printf("Allocation Failed");
        return;
    }
    for(i = 0; i < oldsize; i++) {
        for(temp = oldTable[i]->next; temp; temp = temp->next) {
            index = Hash(temp->data, h->tsize);
            temp2 = temp; temp = temp->next;
            temp2->next = h->Table[index]->next;
            h->Table[index]->next = temp2;
        }
    }
}

```

CreatHashTable – O(n). HashSearch - O(1) average. HashInsert - O(1) average. HashDelete - O(1) average.

Problem-2 Given an array of characters, give an algorithm for removing the duplicates.

Solution: Start with the first character and check whether it appears in the remaining part of the string using a simple linear search. If it repeats, bring the last character to that position and decrement the size of the string by one. Continue this process for each distinct character of the given string.

```
int elem(int *A, size_t n, int e){  
    for (int i = 0; i < n; ++i)  
        if (A[i] == e)  
            return 1;  
    return 0;  
}  
  
int RemoveDuplicates(int *A, int n){  
    int m = 0;  
    for (int i = 0; i < n; ++i)  
        if (!elem(A, m, A[i]))  
            A[m++] = A[i];  
    return m;  
}
```

Time Complexity: O(n^2). Space Complexity: O(1).

Problem-3 Can we find any other idea to solve this problem in better time than O(n^2)?
Observe that the order of characters in solutions do not matter.

Solution: Use sorting to bring the repeated characters together. Finally scan through the array to remove duplicates in consecutive positions.

```

int Compare(const void* a, const void *b) {
    return *(char*)a - *(char*)b;
}
void RemoveDuplicates(char s[]) {
    int last, current;
    QuickSort(s, strlen(s), sizeof(char), Compare);
    current = 0, last = 0;
    for(; s[current]; i++) {
        if(s[last] != s[current])
            s[++last] = s[current];
    }
    s[last] = '\0';
}

```

Time Complexity: $\Theta(n \log n)$. Space Complexity: O(1).

Problem-4 Can we solve this problem in a single pass over given array?

Solution: We can use hash table to check whether a character is repeating in the given string or not. If the current character is not available in hash table, then insert it into hash table and keep that character in the given string also. If the current character exists in the hash table then skip that character.

```

void RemoveDuplicates(char s[]) {
    int src, dst;
    struct HastTable *h;
    h = CreatHashTable();
    current = last = 0;
    for(; s[current]; current++) {
        if( !HashSearch(h, s[current])) {
            s[last++] = s[current];
            HashInsert(h, s[current]);
        }
    }
    s[last] = '\0';
}

```

Time Complexity: $\Theta(n)$ on average. Space Complexity: O(n).

Problem-5 Given two arrays of unordered numbers, check whether both arrays have the same set of numbers?

Solution: Let us assume that two given arrays are A and B. A simple solution to the given

problem is: for each element of A, check whether that element is in B or not. A problem arises with this approach if there are duplicates. For example consider the following inputs:

$$A = \{2,5,6,8,10,2,2\}$$
$$B = \{2,5,5,8,10,5,6\}$$

The above algorithm gives the wrong result because for each element of A there is an element in B also. But if we look at the number of occurrences, they are not the same. This problem we can solve by moving the elements which are already compared to the end of the list. That means, if we find an element in B, then we move that element to the end of B, and in the next searching we will not find those elements. But the disadvantage of this is it needs extra swaps. Time Complexity of this approach is $O(n^2)$, since for each element of A we have to scan B.

Problem-6 Can we improve the time complexity of [Problem-5](#)?

Solution: Yes. To improve the time complexity, let us assume that we have sorted both the lists. Since the sizes of both arrays are n , we need $O(n \log n)$ time for sorting them. After sorting, we just need to scan both the arrays with two pointers and see whether they point to the same element every time, and keep moving the pointers until we reach the end of the arrays.

Time Complexity of this approach is $O(n \log n)$. This is because we need $O(n \log n)$ for sorting the arrays. After sorting, we need $O(n)$ time for scanning but it is less compared to $O(n \log n)$.

Problem-7 Can we further improve the time complexity of [Problem-5](#)?

Solution: Yes, by using a hash table. For this, consider the following algorithm.

Algorithm:

- Construct the hash table with array A elements as keys.
- While inserting the elements, keep track of the number frequency for each number. That means, if there are duplicates, then increment the counter of that corresponding key.
- After constructing the hash table for A's elements, now scan the array B.
- For each occurrence of B's elements reduce the corresponding counter values.
- At the end, check whether all counters are zero or not.
- If all counters are zero, then both arrays are the same otherwise the arrays are different.

Time Complexity; $O(n)$ for scanning the arrays. Space Complexity; $O(n)$ for hash table.

Problem-8 Given a list of number pairs; if $pair(i,j)$ exists, and $pair(j,i)$ exists, report all such pairs. For example, in $\{\{1,3\},\{2,6\},\{3,5\},\{7,4\},\{5,3\},\{8,7\}\}$, we see that $\{3,5\}$ and $\{5,3\}$ are present. Report this pair when you encounter $\{5,3\}$. We call such pairs 'symmetric pairs'. So, give an efficient algorithm for finding all such pairs.

Solution: By using hashing, we can solve this problem in just one scan. Consider the following algorithm.

Algorithm:

- Read the pairs of elements one by one and insert them into the hash table. For each pair, consider the first element as key and the second element as value.
- While inserting the elements, check if the hashing of the second element of the current pair is the same as the first number of the current pair.
- If they are the same, then that indicates a symmetric pair exists and output that pair.
- Otherwise, insert that element into that. That means, use the first number of the current pair as key and the second number as value and insert them into the hash table.
- By the time we complete the scanning of all pairs, we have output all the symmetric pairs.

Time Complexity; $O(n)$ for scanning the arrays. Note that we are doing a scan only of the input.

Space Complexity; $O(n)$ for hash table.

Problem-9 Given a singly linked list, check whether it has a loop in it or not.

Solution: Using Hash Tables

Algorithm:

- Traverse the linked list nodes one by one.
- Check if the node's address is there in the hash table or not.
- If it is already there in the hash table, that indicates we are visiting a node which was already visited. This is possible only if the given linked list has a loop in it.
- If the address of the node is not there in the hash table, then insert that node's address into the hash table.
- Continue this process until we reach the end of the linked list or we find the loop.

Time Complexity; $O(n)$ for scanning the linked list. Note that we are doing a scan only of the input. Space Complexity; $O(n)$ for hash table.

Note: for an efficient solution, refer to the [Linked Lists](#) chapter.

Problem-10 Given an array of 101 elements. Out of them 50 elements are distinct, 24 elements are repeated 2 times, and one element is repeated 3 times. Find the element that is repeated 3 times in $O(1)$.

Solution: Using Hash Tables

Algorithm:

- Scan the input array one by one.
- Check if the element is already there in the hash table or not.
- If it is already there in the hash table, increment its counter value [this indicates the number of occurrences of the element].
- If the element is not there in the hash table, insert that node into the hash table with counter value 1.
- Continue this process until reaching the end of the array.

Time Complexity: $O(n)$, because we are doing two scans. Space Complexity: $O(n)$, for hash table.

Note: For an efficient solution refer to the [Searching](#) chapter.

Problem-11 Given m sets of integers that have n elements in them, provide an algorithm to find an element which appeared in the maximum number of sets?

Solution: Using Hash Tables

Algorithm:

- Scan the input sets one by one.
- For each element keep track of the counter. The counter indicates the frequency of occurrences in all the sets.
- After completing the scan of all the sets, select the one which has the maximum counter value.

Time Complexity: $O(mn)$, because we need to scan all the sets. Space Complexity: $O(mn)$, for hash table. Because, in the worst case all the elements may be different.

Problem-12 Given two sets A and B , and a number K , Give an algorithm for finding whether there exists a pair of elements, one from A and one from B , that add up to K .

Solution: For simplicity, let us assume that the size of A is m and the size of B is n .

Algorithm:

- Select the set which has minimum elements.
- For the selected set create a hash table. We can use both key and value as the same.
- Now scan the second array and check whether (*K-selected element*) exists in the hash table or not.
- If it exists then return the pair of elements.
- Otherwise continue until we reach the end of the set.

Time Complexity: $O(\text{Max}(m,n))$, because we are doing two scans. Space Complexity: $O(\text{Min}(m,n))$, for hash table. We can select the small set for creating the hash table.

Problem-13 Give an algorithm to remove the specified characters from a given string which are given in another string?

Solution: For simplicity, let us assume that the maximum number of different characters is 256. First we create an auxiliary array initialized to 0. Scan the characters to be removed, and for each of those characters we set the value to 1, which indicates that we need to remove that character.

After initialization, scan the input string, and for each of the characters, we check whether that character needs to be deleted or not. If the flag is set then we simply skip to the next character, otherwise we keep the character in the input string. Continue this process until we reach the end of the input string. All these operations we can do in-place as given below.

```
void RemoveChars(char str[], char removeTheseChars[]) {
    int srcInd, destInd;
    int auxi[256]; //additional array
    for(srcInd = 0; srcInd < 256; srcIndex++)
        auxi[srcInd]=0;
    //set true for all characters to be removed
    srcIndex=0;
    while(removeTheseChars[srcInd]) {
        auxi[removeTheseChars[srcInd]]=1;
        srcInd++;
    }
    //copy chars unless it must be removed
    srcInd=destInd=0;
    while(str[srcInd++]) {
        if(!auxi[str[srcInd]])
            str[destInd++]=str[srcInd];
    }
}
```

Time Complexity: Time for scanning the characters to be removed + Time for scanning the input array= $O(n) + O(m) \approx O(n)$. Where m is the length of the characters to be removed and n is the length of the input string.

Space Complexity: $O(m)$, length of the characters to be removed. But since we are assuming the maximum number of different characters is 256, we can treat this as a constant. But we should keep in mind that when we are dealing with multi-byte characters, the total number of different characters is much more than 256.

Problem-14 Give an algorithm for finding the first non-repeated character in a string. For example, the first non-repeated character in the string “abzddab” is ‘z’.

Solution: The solution to this problem is trivial. For each character in the given string, we can scan the remaining string if that character appears in it. If it does not appear then we are done with the solution and we return that character. If the character appears in the remaining string, then go to the next character.

```
char FirstNonRepeatedChar( char *str ) {  
    int i, j, repeated = 0;  
    int len = strlen(str);  
    for(i = 0; i < len; i++ ) {  
        repeated = 0;  
        for(j = 0; j < len; j++ ) {  
            if( i != j && str[i] == str[j] ) {  
                repeated = 1;  
                break;  
            }  
        }  
        if( repeated == 0 ) // Found the first non-repeated character  
            return str[i];  
    }  
    return " ";  
}
```

Time Complexity: $O(n^2)$, for two for loops. Space Complexity: $O(1)$.

Problem-15 Can we improve the time complexity of [Problem-13](#)?

Solution: Yes. By using hash tables we can reduce the time complexity. Create a hash table by reading all the characters in the input string and keeping count of the number of times each character appears. After creating the hash table, we can read the hash table entries to see which element has a count equal to 1. This approach takes $O(n)$ space but reduces the time complexity also to $O(n)$.

```

char FirstNonRepeatedCharUsinghash( char * str ) {
    int i, len=strlen(str);
    int count[256]; // additional array
    for(i=0;i<len;++i)
        count[i] = 0;
    for(i=0;i<len;++i)
        count[str[i]]++;
    for(i=0; i<len; ++i) {
        if(count[str[i]]==1) {
            printf("%c",str[i]);
            break;
        }
    }
    if(i==len)
        printf("No Non-repeated Characters");
    return 0;
}

```

Time Complexity: We have $O(n)$ to create the hash table and another $O(n)$ to read the entries of hash table. So the total time is $O(n) + O(n) = O(2n) \approx O(n)$. Space Complexity: $O(n)$ for keeping the count values.

Problem-16 Given a string, give an algorithm for finding the first repeating letter in a string?

Solution: The solution to this problem is somewhat similar to [Problem-13](#) and [Problem-15](#). The only difference is, instead of scanning the hash table twice we can give the answer in just one scan. This is because while inserting into the hash table we can see whether that element already exists or not. If it already exists then we just need to return that character.

```

char FirstRepeatedCharUsinghash( char * str ) {
    int i, len=strlen(str);
    int count[256]; //additional array
    for(i=0;i<len;++i)
        count[i] = 0;
    for(i=0; i<len; ++i) {
        if(count[str[i]]==1) {
            printf("%c",str[i]);
            break;
        }
        else count[str[i]]++;
    }
    if(i==len)
        printf("No Repeated Characters");
    return 0;
}

```

Time Complexity: We have $O(n)$ for scanning and creating the hash table. Note that we need only one scan for this problem. So the total time is $O(n)$. **Space Complexity:** $O(n)$ for keeping the count values.

Problem-17 Given an array of n numbers, create an algorithm which displays all pairs whose sum is S .

Solution: This problem is similar to [Problem-12](#). But instead of using two sets we use only one set.

Algorithm:

- Scan the elements of the input array one by one and create a hash table. Both key and value can be the same.
- After creating the hash table, again scan the input array and check whether ($S - selected\ element$) exists in the hash table or not.
- If it exists then return the pair of elements.
- Otherwise continue and read all the elements of the array.

Time Complexity: We have $O(n)$ to create the hash table and another $O(n)$ to read the entries of the hash table. So the total time is $O(n) + O(n) = O(2n) \approx O(n)$. **Space Complexity:** $O(n)$ for keeping the count values.

Problem-18 Is there any other way of solving [Problem-17](#)?

Solution: Yes. The alternative solution to this problem involves sorting. First sort the input array. After sorting, use two pointers, one at the starting and another at the ending. Each time add the

values of both the indexes and see if their sum is equal to S . If they are equal then print that pair. Otherwise increase the left pointer if the sum is less than S and decrease the right pointer if the sum is greater than S .

Time Complexity: Time for sorting + Time for scanning = $O(n \log n)$ + $O(n) \approx O(n \log n)$.

Space Complexity: $O(1)$.

Problem-19 We have a file with millions of lines of data. Only two lines are identical; the rest are unique. Each line is so long that it may not even fit in the memory. What is the most efficient solution for finding the identical lines?

Solution: Since a complete line may not fit into the main memory, read the line partially and compute the hash from that partial line. Then read the next part of the line and compute the hash. This time use the previous hash also while computing the new hash value. Continue this process until we find the hash for the complete line. Do this for each line and store all the hash values in a file [or maintain a hash table of these hashes]. If at any point you get same hash value, read the corresponding lines part by part and compare.

Note: Refer to [Searching](#) chapter for related problems.

Problem-20 If h is the hashing function and is used to hash n keys into a table of size s , where $n \leq s$, the expected number of collisions involving a particular key X is :

- (A) less than 1.
- (B) less than n .
- (C) less than s .
- (D) less than $\frac{n}{2}$.

Solution: A.

Problem-21 Implement Bloom Filters

Solution: A Bloom Filter is a data structure designed to tell, rapidly and memory-efficiently, whether an element is present in a set. It is based on a probabilistic mechanism where false positive retrieval results are possible, but false negatives are not. At the end we will see how to tune the parameters in order to minimize the number of false positive results.

Let's begin with a little bit of theory. The idea behind the Bloom filter is to allocate a bit vector of length m , initially all set to 0, and then choose k independent hash functions, h_1, h_2, \dots, h_k , each with range $[1..m]$. When an element a is added to the set then the bits at positions $h_1(a), h_2(a), \dots, h_k(a)$ in the bit vector are set to 1. Given a query element q we can test whether it is in the set using the bits at positions $h_1(q), h_2(q), \dots, h_k(q)$ in the vector. If any of these bits is 0 we report that q is not in the set otherwise we report that q is. The thing we have to care about is that in the first case there remains some probability that q is not in the set which could lead us to a false positive response.

```

typedef unsigned int (*hashFunctionPointer)(const char *);

struct Bloom{
    int bloomArraySize;
    unsigned char *bloomArray;
    int nHashFunctions;
    hashFunctionPointer *funcsArray;
};

#define SETBLOOMBIT(a, n) (a[n/CHAR_BIT] |= (1<<(n%CHAR_BIT)))
#define GETBLOOMBIT(a, n) (a[n/CHAR_BIT] & (1<<(n%CHAR_BIT)))

struct Bloom *createBloom(int size, int nHashFunctions, ...){
    struct Bloom *blm;
    va_list l;
    int n;
    if(!(blm=malloc(sizeof(struct Bloom))))
        return NULL;
    if(!(blm->bloomArray=calloc((size+CHAR_BIT-1)/CHAR_BIT, sizeof(char)))) {
        free(blm);
        return NULL;
    }
    if(!(blm->funcsArray=(hashFunctionPointer*)malloc(nHashFunctions*sizeof(hashFunctionPointer)))) {
        free(blm->bloomArray);
        free(blm);
        return NULL;
    }
    va_start(l, nHashFunctions);
    for(n=0; n<nHashFunctions; ++n) {
        blm->funcsArray[n]=va_arg(l, hashFunctionPointer);
    }
    va_end(l);
    blm->nHashFunctions=nHashFunctions;
    blm->bloomArraySize=size;
    return blm;
}

int deleteBloom(struct Bloom *blm){
    free(blm->bloomArray);
    free(blm->funcsArray);
    free(blm);
    return 0;
}

int addElementBloom(struct Bloom *blm, const char *s){
    for(int n=0; n<blm->nHashFunctions; ++n) {
        SETBLOOMBIT(blm->bloomArray, blm->funcsArray[n](s)%blm->bloomArraySize);
    }
    return 0;
}

int checkElementBloom(struct Bloom *blm, const char *s){
    for(int n=0; n<blm->nHashFunctions; ++n) {
        if(!(GETBLOOMBIT(blm->bloomArray, blm->funcsArray[n](s)%blm->bloomArraySize))) return 0;
    }
    return 1;
}

unsigned int shiftAddXORHash(const char *key){
    unsigned int h=0;
    while(*key) h^=(h<<5)+(h>>2)+(unsigned char)*key++;
    return h;
}

unsigned int XORHash(const char *key){
    unsigned int h=0;
    hash_t h=0;
    while(*key) h^=*key++;
    return h;
}

```

```
}

int test(){
    FILE *fp;
    char line[1024];
    char *p;
    struct Bloom *blm;
    if(!(blm=createBloom(1500000, 2, shiftAddXORHash, XORHash))) {
        fprintf(stderr, "ERROR: Could not create Bloom filter\n");
        return -1;
    }
    if(!(fp=fopen("path", "r"))) {
        fprintf(stderr, "ERROR: Could not open file %s\n", argv[1]);
        return -1;
    }
    while(fgets(line, 1024, fp)) {
        if((p=strchr(line, '\r')))*p='\0';
        if((p=strchr(line, '\n')))*p='\0';
        addElementBloom(blm, line);
    }
    fclose(fp);
    while(fgets(line, 1024, stdin)) {
        if((p=strchr(line, '\r')))*p='\0';
        if((p=strchr(line, '\n')))*p='\0';
        p=strtok(line, "\t,.;\r\n?/-/");
        while(p) {
            if(!checkBloom(blm, p)) {
                printf("No match for word \"%s\"\n", p);
            }
            p=strtok(NULL, "\t,.;\r\n?/-/");
        }
    }
    deleteBloom(blm);
    return 1;
}
```

STRING ALGORITHMS

CHAPTER 15



15.1 Introduction

To understand the importance of string algorithms let us consider the case of entering the URL (Uniform Resource Locator) in any browser (say, Internet Explorer, Firefox, or Google Chrome). You will observe that after typing the prefix of the URL, a list of all possible URLs is displayed. That means, the browsers are doing some internal processing and giving us the list of matching URLs. This technique is sometimes called *auto – completion*.

Similarly, consider the case of entering the directory name in the command line interface (in both Windows and UNIX). After typing the prefix of the directory name, if we press the *tab* button, we get a list of all matched directory names available. This is another example of auto completion.

In order to support these kinds of operations, we need a data structure which stores the string data efficiently. In this chapter, we will look at the data structures that are useful for implementing string algorithms.

We start our discussion with the basic problem of strings: given a string, how do we search a

substring (pattern)? This is called a *string matching* problem. After discussing various string matching algorithms, we will look at different data structures for storing strings.

15.2 String Matching Algorithms

In this section, we concentrate on checking whether a pattern P is a substring of another string T (T stands for text) or not. Since we are trying to check a fixed string P , sometimes these algorithms are called *exact string matching* algorithms. To simplify our discussion, let us assume that the length of given text T is n and the length of the pattern P which we are trying to match has the length m . That means, T has the characters from 0 to $n - 1$ ($T[0 \dots n - 1]$) and P has the characters from 0 to $m - 1$ ($P[0 \dots m - 1]$). This algorithm is implemented in C ++ as `strstr()`.

In the subsequent sections, we start with the brute force method and gradually move towards better algorithms.

- Brute Force Method
- Rabin-Karp String Matching Algorithm
- String Matching with Finite Automata
- KMP Algorithm
- Boyer-Moore Algorithm
- Suffix Trees

15.3 Brute Force Method

In this method, for each possible position in the text T we check whether the pattern P matches or not. Since the length of T is n , we have $n - m + 1$ possible choices for comparisons. This is because we do not need to check the last $m - 1$ locations of T as the pattern length is m . The following algorithm searches for the first occurrence of a pattern string P in a text string T .

Algorithm

```
int BruteForceStringMatch (int T[], int n, int P[], int m) {
    for (int i = 0; i <= n - m; i++) {
        int j = 0;
        while (j < m && P[j] == T[i + j])
            j = j + 1;
        if(j == m)
            return i;
    }
    return -1;
}
```

Time Complexity: $O((n - m + 1) \times m) \approx O(n \times m)$. Space Complexity: $O(1)$.

15.4 Rabin-Karp String Matching Algorithm

In this method, we will use the hashing technique and instead of checking for each possible position in T , we check only if the hashing of P and the hashing of m characters of T give the same result.

Initially, apply the hash function to the first m characters of T and check whether this result and P 's hashing result is the same or not. If they are not the same, then go to the next character of T and again apply the hash function to m characters (by starting at the second character). If they are the same then we compare those m characters of T with P .

Selecting Hash Function

At each step, since we are finding the hash of m characters of T , we need an efficient hash function. If the hash function takes $O(m)$ complexity in every step, then the total complexity is $O(n \times m)$. This is worse than the brute force method because first we are applying the hash function and also comparing.

Our objective is to select a hash function which takes $O(1)$ complexity for finding the hash of m characters of T every time. Only then can we reduce the total complexity of the algorithm. If the hash function is not good (worst case), the complexity of the Rabin-Karp algorithm is $O(n - m + 1) \times m) \approx O(n \times m)$. If we select a good hash function, the complexity of the Rabin-Karp algorithm complexity is $O(m + n)$. Now let us see how to select a hash function which can compute the hash of m characters of T at each step in $O(1)$.

For simplicity, let's assume that the characters used in string T are only integers. That means, all characters in $T \in \{0,1,2,\dots,9\}$. Since all of them are integers, we can view a string of m consecutive characters as decimal numbers. For example, string '61815' corresponds to the number 61815. With the above assumption, the pattern P is also a decimal value, and let us assume that the decimal value of P is p . For the given text $T[0..n - 1]$, let $t(i)$ denote the decimal value of length- m substring $T[i..i + m - 1]$ for $i = 0, 1, \dots, n - m - 1$. So, $t(i) == p$ if and only if $T[i..i + m - 1] == P[0..m - 1]$.

We can compute p in $O(m)$ time using Horner's Rule as:

$$p = P[m - 1] + 10(P[m - 2] + 10(P[m - 3] + \dots + 10(P[1] + 10P[0])\dots))$$

The code for the above assumption is:

```

value = 0;
for (int i = 0; i < m-1; i++) {
    value = value * 10;
    value = value + P[i];
}

```

We can compute all $t(i)$, for $i = 0, 1, \dots, n - m - 1$ values in a total of $O(n)$ time. The value of $t(0)$ can be similarly computed from $T[0.. m - 1]$ in $O(m)$ time. To compute the remaining values $t(0), t(1), \dots, t(n - m - 1)$, understand that $t(i + 1)$ can be computed from $t(i)$ in constant time.

$$t(i + 1) = 10 * (t(i) - 10^{m-1} * T[i]) + T[i + m - 1]$$

For example, if $T = "123456"$ and $m = 3$

$$\begin{aligned} t(0) &= 123 \\ t(1) &= 10 * (123 - 100 * 1) + 4 = 234 \end{aligned}$$

Step by Step explanation

First : remove the first digit : $123 - 100 * 1 = 23$

Second: Multiply by 10 to shift it : $23 * 10 = 230$

Third: Add last digit : $230 + 4 = 234$

The algorithm runs by comparing, $t(i)$ with p . When $t(i) == p$, then we have found the substring P in T , starting from position i .

15.5 String Matching with Finite Automata

In this method we use the finite automata which is the concept of the Theory of Computation (ToC). Before looking at the algorithm, first let us look at the definition of finite automata.

Finite Automata

A finite automaton F is a 5-tuple $(Q, q_0, A, \Sigma, \delta)$, where

- Q is a finite set of states
- $q_0 \in Q$ is the start state
- $A \subseteq Q$ is a set of accepting states
- Σ is a finite input alphabet
- δ is the transition function that gives the next state for a given current state and input

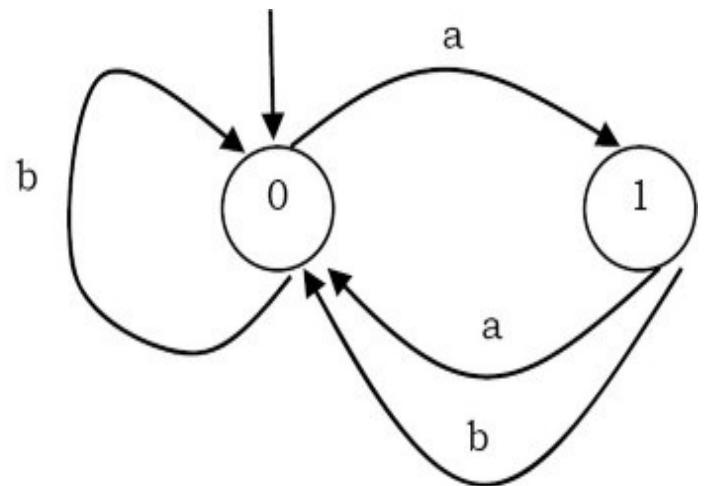
How does Finite Automata Work?

- The finite automaton F begins in state q_0
- Reads characters from Σ one at a time
- If F is in state q and reads input character a , F moves to state $\delta(q,a)$
- At the end, if its state is in A , then we say, F accepted the input string read so far
- If the input string is not accepted it is called the rejected string

Example: Let us assume that $Q = \{0,1\}, q_0 = 0, A = \{1\}, \Sigma = \{a, b\}$. $\delta(q,d)$ as shown in the transition table/diagram. This accepts strings that end in an odd number of a 's; e.g., $abbaaa$ is accepted, aa is rejected.

Input		
State	a	b
0	1	0
1	0	0

Transition Function/Table



Important Notes for Constructing the Finite Automata

For building the automata, first we start with the initial state. The FA will be in state k if k characters of the pattern have been matched. If the next text character is equal to the pattern character c , we have matched $k + 1$ characters and the FA enters state $k + 1$. If the next text character is not equal to the pattern character, then the FA go to a state $0,1,2,\dots$ or k , depending on how many initial pattern characters match the text characters ending with c .

Matching Algorithm

Now, let us concentrate on the matching algorithm.

- For a given pattern $P[0.. m - 1]$, first we need to build a finite automaton F
 - The state set is $Q = \{0,1,2, \dots, m\}$
 - The start state is 0
 - The only accepting state is m
 - Time to build F can be large if Σ is large
- Scan the text string $T[0.. n - 1]$ to find all occurrences of the pattern $P[0.. m - 1]$

- String matching is efficient: $\Theta(n)$
 - Each character is examined exactly once
 - Constant time for each character
 - But the time to compute δ (transition function) is $O(m|\Sigma|)$. This is because δ has $O(m|\Sigma|)$ entries. If we assume $|\Sigma|$ is constant then the complexity becomes $O(m)$.

Algorithm:

```
//Input: Pattern string P[0..m-1], δ and F
//Goal: All valid shifts displayed
FiniteAutomataStringMatcher(int P[], int m, F, δ) {
    q = 0;
    for (int i = 0; i < m; i++)
        q = δ(q, T[i]);
    if(q == m)
        printf("Pattern occurs with shift: %d", i-m);
}
```

Time Complexity: $O(m)$.

15.6 KMP Algorithm

As before, let us assume that T is the string to be searched and P is the pattern to be matched. This algorithm was presented by Knuth, Morris and Pratt. It takes $O(n)$ time complexity for searching a pattern. To get $O(n)$ time complexity, it avoids the comparisons with elements of T that were previously involved in comparison with some element of the pattern P .

The algorithm uses a table and in general we call it *prefix function* or *prefix table* or *fail function* F . First we will see how to fill this table and later how to search for a pattern using this table. The prefix function F for a pattern stores the knowledge about how the pattern matches against shifts of itself. This information can be used to avoid useless shifts of the pattern P . It means that this table can be used for avoiding backtracking on the string T .

Prefix Table

```

int F[]; //assume F is a global array
void Prefix-Table(int P[], int m) {
    int i=1,j=0, F[0]=0;
    while(i<m) {
        if(P[i]==P[j]) {
            F[i]=j+1;
            i++;
            j++;
        }
        else if(j>0)
            j=F[j-1];
        else {
            F[i]=0;
            i++;
        }
    }
}

```

As an example, assume that $P = a\ b\ a\ b\ a\ c\ a$. For this pattern, let us follow the step-by-step instructions for filling the prefix table F. Initially: $m = \text{length}[P] = 7, F[0] = 0$ and $F[1] = 0$.

Step 1: $i = 1, j = 0, F[1] = 0$

	0	1	2	3	4	5	6
P	a	b	a	b	a	c	a
F	0	0					

Step 2: $i = 2, j = 0, F[2] = 1$

	0	1	2	3	4	5	6
P	a	b	a	b	a	c	a
F	0	0	1				

Step 3: $i = 3, j = 1, F[3] = 2$

	0	1	2	3	4	5	6
P	a	b	a	b	a	c	a
F	0	0	1	2			

Step 4: $i = 4, j = 2, F[4] = 3$

	0	1	2	3	4	5	6
P	a	b	a	b	a	c	a
F	0	0	1	2	3		

Step 5: $i = 5, j = 3, F[5] = 1$

	0	1	2	3	4	5	6
P	a	b	a	b	a	c	a
F	0	0	1	2	3	0	

Step 6: $i = 6, j = 1, F[6] = 1$

	0	1	2	3	4	5	6
P	a	b	a	b	a	c	a
F	0	0	1	2	3	0	1

At this step the filling of the prefix table is complete.

Matching Algorithm

The KMP algorithm takes pattern P , string T and prefix function F as input, and finds a match of P in T .

```

int KMP(char T[], int n, int P[], int m) {
    int i=0,j=0;
    Prefix-Table(P,m);
    while(i<n) {
        if(T[i]==P[j]) {
            if(j==m-1)
                return i-j;
            else {
                i++;
                j++;
            }
        }
        else if(j>0)
            j=F[j-1];
        else
            i++;
    }
    return -1;
}

```

Time Complexity: $O(m + n)$, where m is the length of the pattern and n is the length of the text to be searched. Space Complexity: $O(m)$.

Now, to understand the process let us go through an example. Assume that $T = b \ a \ c \ b \ a \ b \ a \ b \ a \ c \ a \ c \ a \ c \ a$ & $P = a \ b \ a \ b \ a \ c \ a$. Since we have already filled the prefix table, let us use it and go to the matching algorithm. Initially: $n = \text{size of } T = 15$; $m = \text{size of } P = 7$.

Step 1: $i = 0, j = 0$, comparing $P[0]$ with $T[0]$. $P[0]$ does not match with $T[0]$. P will be shifted one position to the right.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P	a	b	a	b	a	c	a								

Step 2 : $i = 1, j = 0$, comparing $P[0]$ with $T[1]$. $P[0]$ matches with $T[1]$. Since there is a match, P is not shifted.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P		a	b	a	b	a	c	a							

Step 3: $i = 2, j = 1$, comparing $P[1]$ with $T[2]$. $P[1]$ does not match with $T[2]$. Backtracking on P ,

comparing $P[0]$ and $T[2]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P		a	b	a	b	a	c	a							

Step 4: $i = 3, j = 0$, comparing $P[0]$ with $T[3]$. $P[0]$ does not match with $T[3]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P				a	b	a	b	a	c	a					

Step 5: $i = 4, j = 0$, comparing $P[0]$ with $T[4]$. $P[0]$ matches with $T[4]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P				a	b	a	b	a	c	a					

Step 6: $i = 5, j = 1$, comparing $P[1]$ with $T[5]$. $P[1]$ matches with $T[5]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P				a	b	a	b	a	c	a					

Step 7: $i = 6, j = 2$, comparing $P[2]$ with $T[6]$. $P[2]$ matches with $T[6]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P				a	b	a	b	a	c	a					

Step 8: $i = 7, j = 3$, comparing $P[3]$ with $T[7]$. $P[3]$ matches with $T[7]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P				a	b	a	b	a	c	a					

Step 9: $i = 8, j = 4$, comparing $P[4]$ with $T[8]$. $P[4]$ matches with $T[8]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P				a	b	a	b	a	c	a					

Step 10: $i = 9, j = 5$, comparing $P[5]$ with $T[9]$. $P[5]$ does not match with $T[9]$. Backtracking on P , comparing $P[4]$ with $T[9]$ because after mismatch $\text{F}[4] = 3$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P					a	b	a	b	a	c	a				

Comparing $P[3]$ with $T[9]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P						a	b	a	b	a	c	a	c	a	

Step 11: $i = 10, j = 4$, comparing $P[4]$ with $T[10]$. $P[4]$ matches with $T[10]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P						a	b	a	b	a	c	a	c	a	

Step 12: $i = 11, j = 5$, comparing $P[5]$ with $T[11]$. $P[5]$ matches with $T[11]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P						a	b	a	b	a	c	a	c	a	

Step 13: $i = 12, j = 6$, comparing $P[6]$ with $T[12]$. $P[6]$ matches with $T[12]$.

T	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a
P						a	b	a	b	a	c	a	c	a	

Pattern P has been found to completely occur in string T . The total number of shifts that took place for the match to be found are: $i - m = 13 - 7 = 6$ shifts.

Notes:

- KMP performs the comparisons from left to right
- KMP algorithm needs a preprocessing (prefix function) which takes $O(m)$ space and time complexity
- Searching takes $O(n + m)$ time complexity (does not depend on alphabet size)

15.7 Boyer-Moore Algorithm

Like the KMP algorithm, this also does some pre-processing and we call it *last function*. The algorithm scans the characters of the pattern from right to left beginning with the rightmost character. During the testing of a possible placement of pattern P in T , a mismatch is handled as follows: Let us assume that the current character being matched is $T[i] = c$ and the corresponding pattern character is $P[j]$. If c is not contained anywhere in P , then shift the pattern P completely past $T[i]$. Otherwise, shift P until an occurrence of character c in P gets aligned with $T[i]$. This technique avoids needless comparisons by shifting the pattern relative to the text.

The *last* function takes $O(m + |\Sigma|)$ time and the actual search takes $O(nm)$ time. Therefore the worst case running time of the Boyer-Moore algorithm is $O(nm + |\Sigma|)$. This indicates that the worst-case running time is quadratic, in the case of $n == m$, the same as the brute force algorithm.

- The Boyer-Moore algorithm is very fast on the large alphabet (relative to the length of the pattern).
- For the small alphabet, Boyer-Moore is not preferable.
- For binary strings, the KMP algorithm is recommended.
- For the very shortest patterns, the brute force algorithm is better.

15.8 Data Structures for Storing Strings

If we have a set of strings (for example, all the words in the dictionary) and a word which we want to search in that set, in order to perform the search operation faster, we need an efficient way of storing the strings. To store sets of strings we can use any of the following data structures.

- Hashing Tables
- Binary Search Trees
- Tries
- Ternary Search Trees

15.9 Hash Tables for Strings

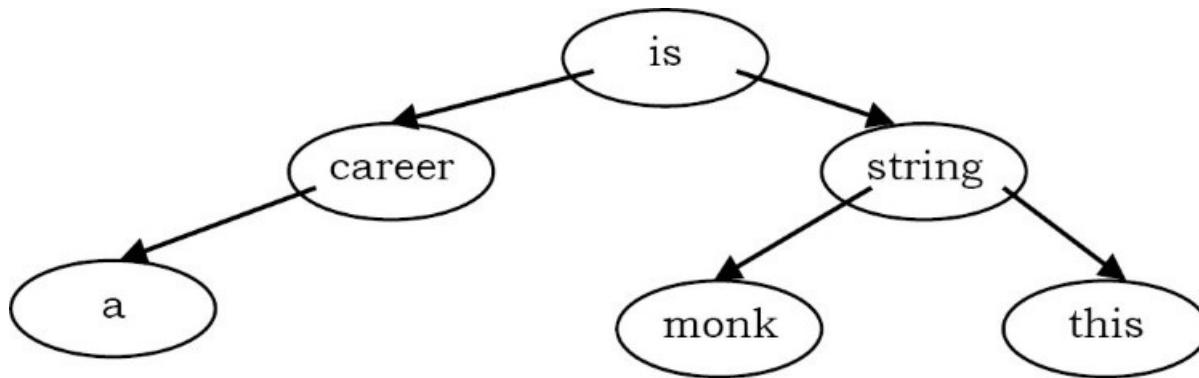
As seen in the *Hashing* chapter, we can use hash tables for storing the integers or strings. In this case, the keys are nothing but the strings. The problem with hash table implementation is that we lose the ordering information – after applying the hash function, we do not know where it will map to. As a result, some queries take more time. For example, to find all the words starting with the letter “K”, with hash table representation we need to scan the complete hash table. This is because the hash function takes the complete key, performs hash on it, and we do not know the location of each word.

15.10 Binary Search Trees for Strings

In this representation, every node is used for sorting the strings alphabetically. This is possible because the strings have a natural ordering: A comes before B, which comes before C, and so on. This is because words can be ordered and we can use a Binary Search Tree (BST) to store and retrieve them. For example, let us assume that we want to store the following strings using BSTs:

this is a career monk string

For the given string there are many ways of representing them in BST. One such possibility is shown in the tree below.



Issues with Binary Search Tree Representation

This method is good in terms of storage efficiency. But the disadvantage of this representation is that, at every node, the search operation performs the complete match of the given key with the node data, and as a result the time complexity of the search operation increases. So, from this we can say that BST representation of strings is good in terms of storage but not in terms of time.

15.11 Tries

Now, let us see the alternative representation that reduces the time complexity of the search operation. The name *trie* is taken from the word re”trie”.

What is a Trie?

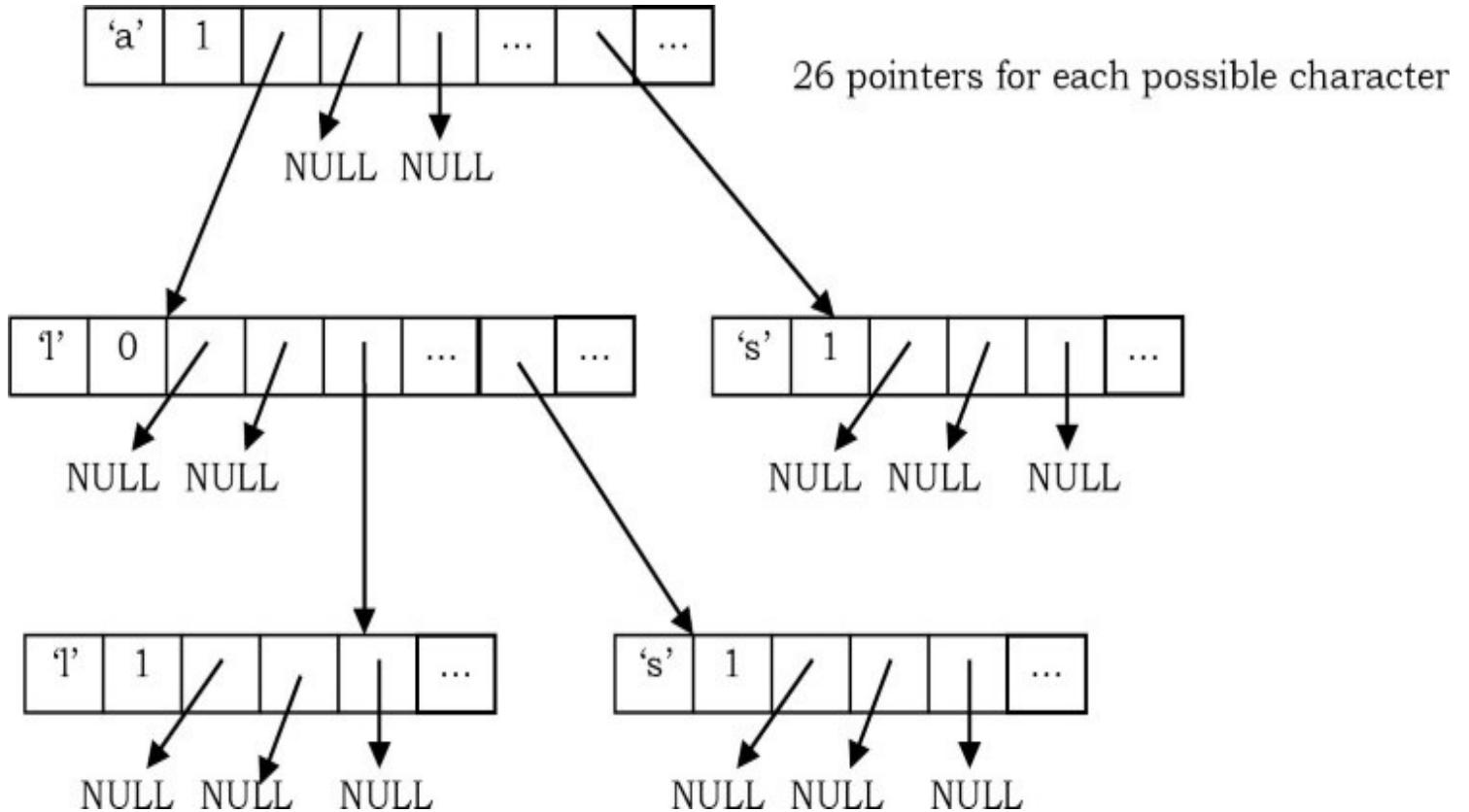
A *trie* is a tree and each node in it contains the number of pointers equal to the number of characters of the alphabet. For example, if we assume that all the strings are formed with English alphabet characters “a” to “z” then each node of the trie contains 26 pointers. A trie data structure can be declared as:

```

struct TrieNode {
    char data;           // Contains the current node character.
    int is_End_Of_String; // Indicates whether the string formed from root to
                          // current node is a string or not
    struct TrieNode *child[26]; // Pointers to other tri nodes
};


```

Suppose we want to store the strings “a”, “all”, “als”, and “as”“: trie for these strings will look like:



Why Tries?

The tries can insert and find strings in $O(L)$ time (where L represents the length of a single word). This is much faster than hash table and binary search tree representations.

Trie Declaration

The structure of the TrieNode has data (char), is_End_Of_String (boolean), and has a collection of child nodes (Collection of TrieNodes). It also has one more method called subNode(char). This method takes a character as argument and will return the child node of that character type if that is present. The basic element - TrieNode of a TRIE data structure looks like this:

```

struct TrieNode {
    char data;
    int is_End_Of_String;
    struct TrieNode *child[26];
};

struct TrieNode *TrieNode subNode(struct TrieNode *root, char c){
    if(root == NULL){
        for(int i=0; i < 26; i++){
            if(root.child[i]→data == c)
                return root.child[i];
        }
    }
    return NULL;
}

```

Now that we have defined our TrieNode, let's go ahead and look at the other operations of TRIE. Fortunately, the TRIE data structure is simple to implement since it has two major methods: insert() and search(). Let's look at the elementary implementation of both these methods.

Inserting a String in Trie

To insert a string, we just need to start at the root node and follow the corresponding path (path from root indicates the prefix of the given string). Once we reach the NULL pointer, we just need to create a skew of tail nodes for the remaining characters of the given string.

```

void InsertInTrie(struct TrieNode *root, char *word) {
    if(!*word) return;
    if(!root) {
        struct TrieNode *newNode = (struct TrieNode *) malloc (sizeof(struct TrieNode *));
        newNode→data=*word;
        for(int i =0; i<26; i++)
            newNode→child[i]=NULL;
        if(!*(word+1))
            newNode→is_End_Of_String = 1;
        else newNode→child[*word] = InsertInTrie(newNode→child[*word], word+1);
        return newNode;
    }
    root→child[*word] = InsertInTrie(root→child[*word], word+1);
    return root;
}

```

Time Complexity: $O(L)$, where L is the length of the string to be inserted.

Note: For real dictionary implementation, we may need a few more checks such as checking whether the given string is already there in the dictionary or not.

Searching a String in Trie

The same is the case with the search operation: we just need to start at the root and follow the pointers. The time complexity of the search operation is equal to the length of the given string that want to search.

```
int SearchInTrie(struct TrieNode *root, char *word) {
    if(!root)
        return -1;
    if(!*word) {
        if(root->is_End_Of_String)
            return 1;
        else return -1;
    }
    if(root->data == *word)
        return SearchInTrie(root->child[*word], word+1);
    else return -1;
}
```

Time Complexity: $O(L)$, where L is the length of the string to be searched.

Issues with Tries Representation

The main disadvantage of tries is that they need lot of memory for storing the strings. As we have seen above, for each node we have too many node pointers. In many cases, the occupancy of each node is less. The final conclusion regarding tries data structure is that they are faster but require huge memory for storing the strings.

Note: There are some improved tries representations called *trie compression techniques*. But, even with those techniques we can reduce the memory only at the leaves and not at the internal nodes.

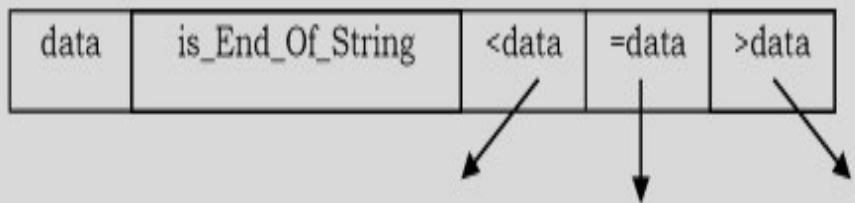
15.12 Ternary Search Trees

This representation was initially provided by Jon Bentley and Sedgewick. A ternary search tree takes the advantages of binary search trees and tries. That means it combines the memory

efficiency of BSTs and the time efficiency of tries.

Ternary Search Trees Declaration

```
struct TSTNode {  
    char data;  
    int is_End_Of_String;  
    struct TSTNode *left;  
    struct TSTNode *eq;  
    struct TSTNode *right;  
};
```

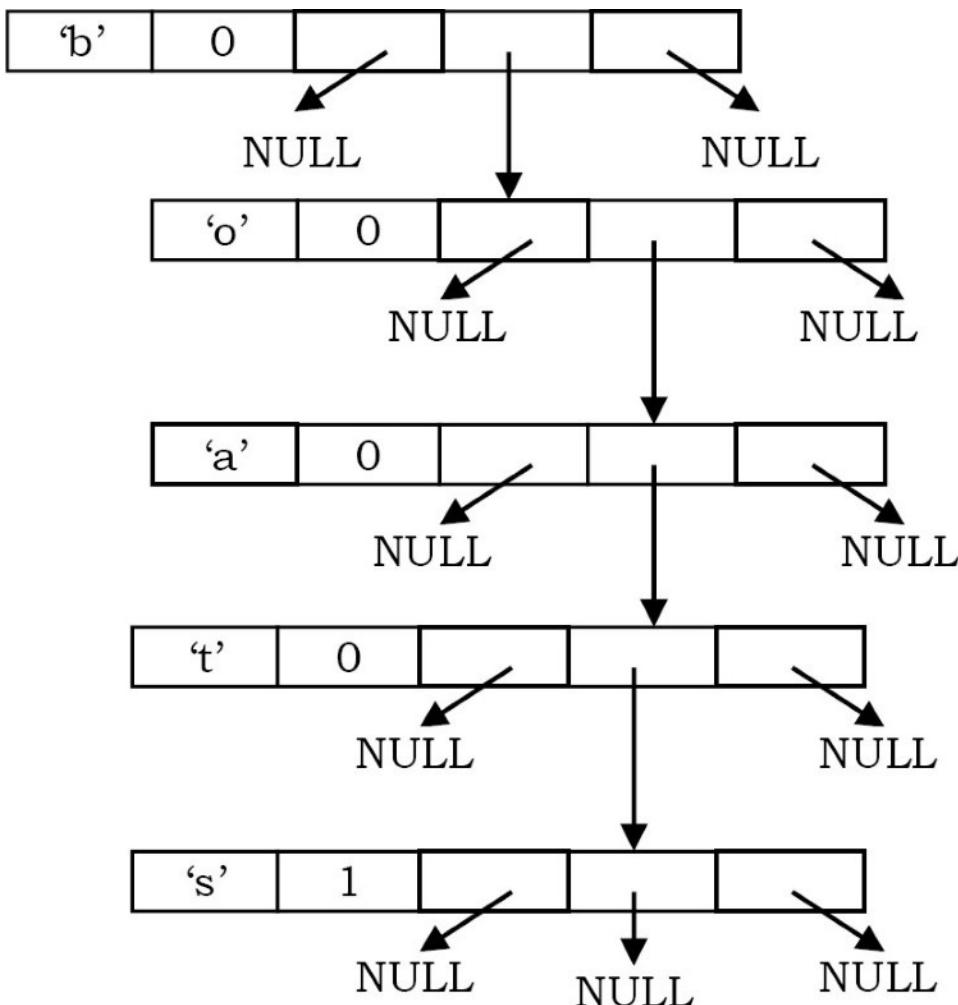


The Ternary Search Tree (TST) uses three pointers:

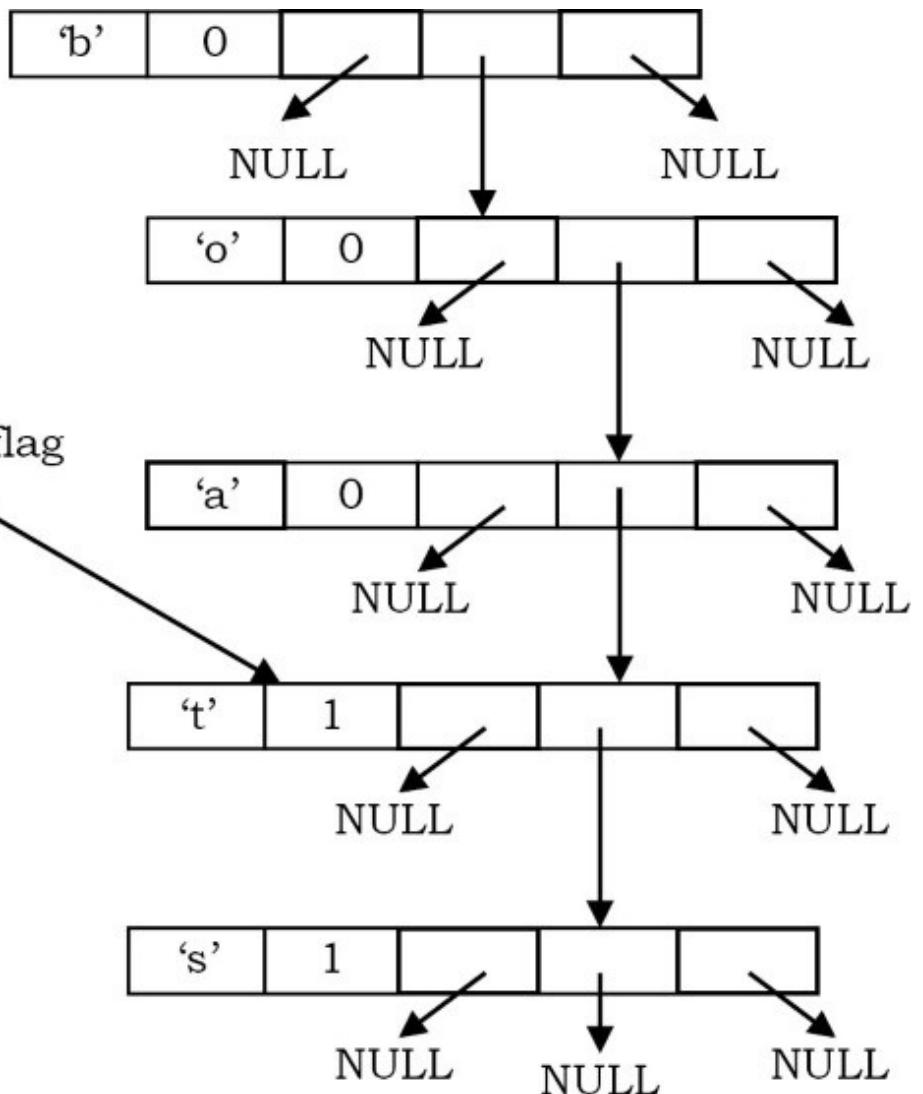
- The *left* pointer points to the TST containing all the strings which are alphabetically less than *data*.
- The *right* pointer points to the TST containing all the strings which are alphabetically greater than *data*.
- The *eq* pointer points to the TST containing all the strings which are alphabetically equal to *data*. That means, if we want to search for a string, and if the current character of the input string and the *data* of current node in TST are the same, then we need to proceed to the next character in the input string and search it in the subtree which is pointed by *eq*.

Inserting strings in Ternary Search Tree

For simplicity let us assume that we want to store the following words in TST (also assume the same order): *boats*, *boat*, *bat* and *bats*. Initially, let us start with the *boats* string.

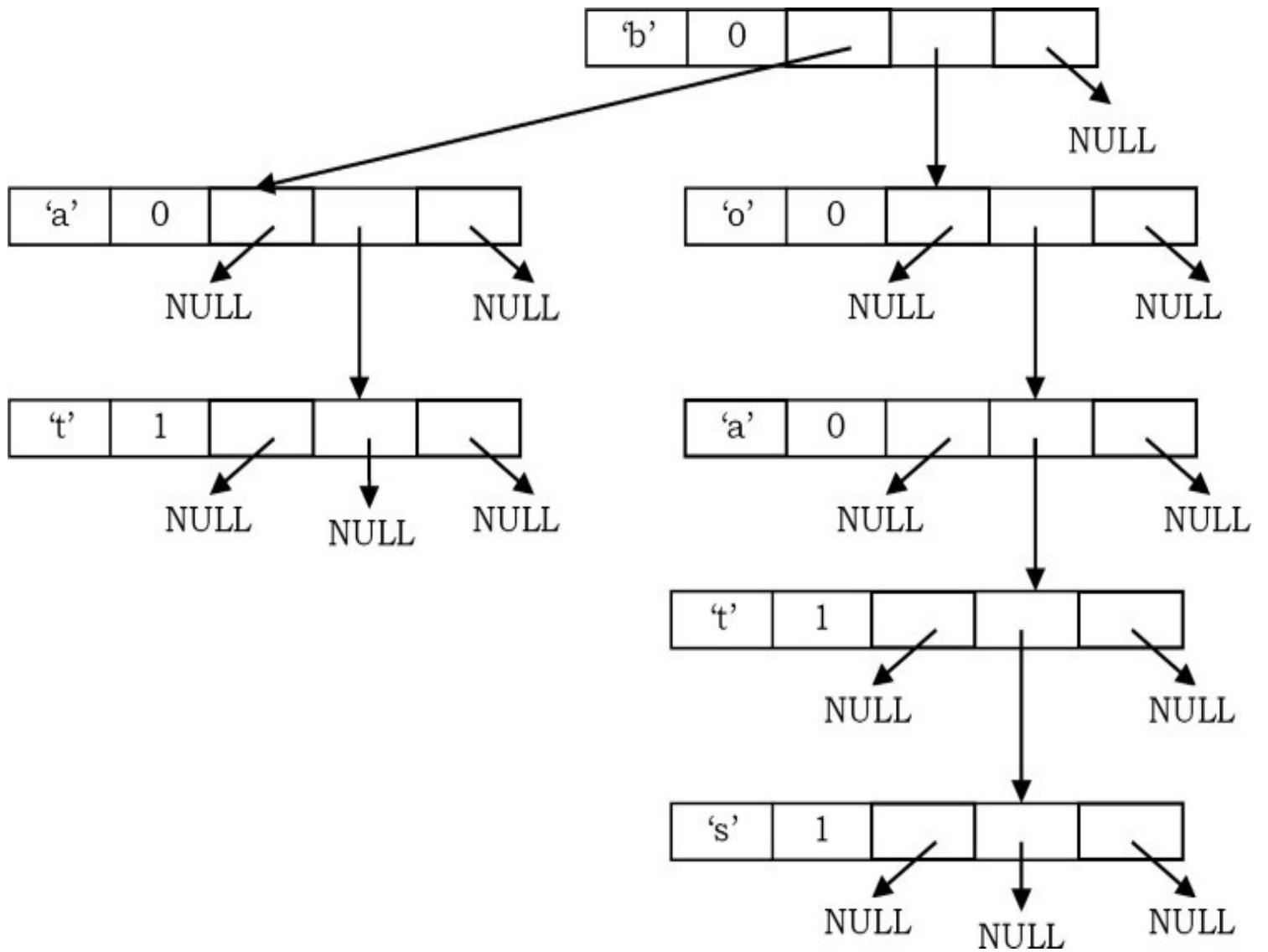


Now if we want to insert the string *boat*, then the TST becomes [the only change is setting the *is_End_Of_String* flag of “*t*” node to 1]:

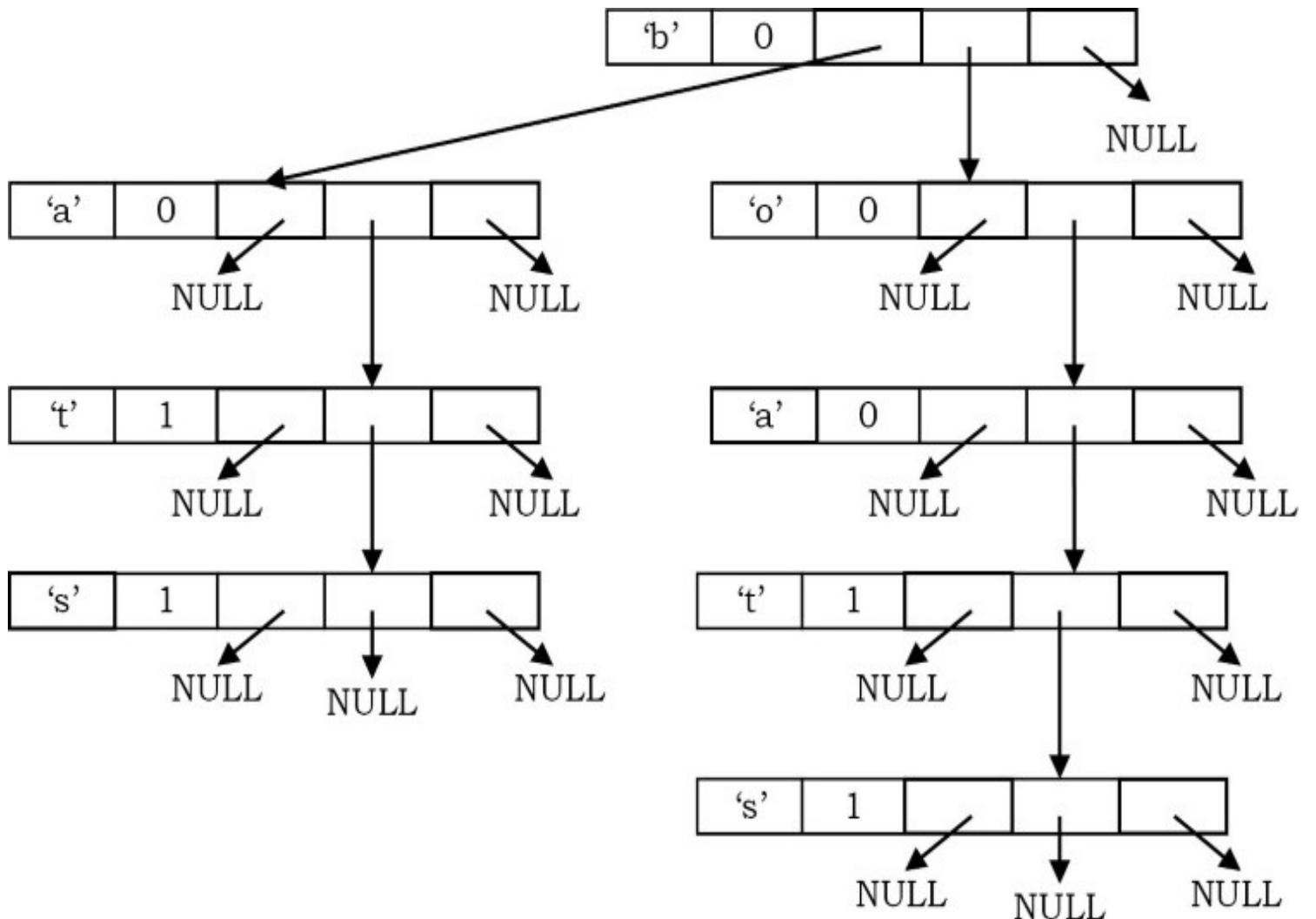


Set the *is_EndOfString* flag to 1.

Now, let us insert the next string: *bat*



Now, let us insert the final word: *bats*.



Based on these examples, we can write the insertion algorithm as below. We will combine the insertion operation of BST and tries.

```

struct TSTNode *InsertInTST(struct TSTNode *root, char *word) {
    if(root == NULL) {
        root = (struct TSTNode *) malloc(sizeof(struct TSTNode));
        root->data = *word;
        root->is_End_Of_String = 1;
        root->left = root->eq = root->right = NULL;
    }
    if(*word < root->data)
        root->left = InsertInTST (root->left, word);
    else if(*word == root->data) {
        if(*(word+1))
            root->eq = InsertInTST (root->eq, word+1);
        else root->is_End_Of_String = 1;
    }
    else  root->right = InsertInTST (root->right, word);
    return root;
}

```

Time Complexity: $O(L)$, where L is the length of the string to be inserted.

Searching in Ternary Search Tree

If after inserting the words we want to search for them, then we have to follow the same rules as that of binary search. The only difference is, in case of match we should check for the remaining characters (in *eq* subtree) instead of return. Also, like BSTs we will see both recursive and non-recursive versions of the search method.

```

int SearchInTSTRecursive(struct TSTNode *root, char *word) {
    if(!root)
        return -1;
    if(*word < root->data)
        return SearchInTSTRecursive(root->left, word);
    else if(*word > root->data)
        return SearchInTSTRecursive(root->right, word);
    else {
        if(root->is_End_Of_String && *(word+1)==0)
            return 1;
        return SearchInTSTRecursive(root->eq, ++word);
    }
}

int SearchInTSTNon-Recursive(struct TSTNode *root, char *word) {
    while (root) {
        if(*word < root->data)
            root = root->left;
        else if(*word == root->data) {
            if(root->is_End_Of_String && *(word+1) == 0)
                return 1;
            word++;
            root = root->eq;
        }
        else root = root->right;
    }
    return -1;
}

```

Time Complexity: $O(L)$, where L is the length of the string to be searched.

Displaying All Words of Ternary Search Tree

If we want to print all the strings of TST we can use the following algorithm. If we want to print them in sorted order, we need to follow the inorder traversal of TST.

```

char word[1024];
void DisplayAllWords(struct TSTNode *root) {
    if(!root)
        return;
    DisplayAllWords(root→left);
    word[i] = root→data;
    if(root→is_End_Of_String) {
        word[i] = '\0';
        printf("%c", word);
    }
    i++;
    DisplayAllWords(root→eq);
}

i--;
DisplayAllWords(root→right);
}

```

Finding the Length of the Largest Word in TST

This is similar to finding the height of the BST and can be found as:

```

int MaxLengthOfLargestWordInTST(struct TSTNode *root) {
    if(!root)
        return 0;
    return Max(MaxLengthOfLargestWordInTST(root→left),
               MaxLengthOfLargestWordInTST(root→eq)+1,
               MaxLengthOfLargestWordInTST(root→right)));
}

```

15.13 Comparing BSTs, Tries and TSTs

- Hash table and BST implementation stores complete the string at each node. As a result they take more time for searching. But they are memory efficient.
- TSTs can grow and shrink dynamically but hash tables resize only based on load factor.
- TSTs allow partial search whereas BSTs and hash tables do not support it.
- TSTs can display the words in sorted order, but in hash tables we cannot get the sorted order.
- Tries perform search operations very fast but they take huge memory for storing the string.

- TSTs combine the advantages of BSTs and Tries. That means they combine the memory efficiency of BSTs and the time efficiency of tries

15.14 Suffix Trees

Suffix trees are an important data structure for strings. With suffix trees we can answer the queries very fast. But this requires some preprocessing and construction of a suffix tree. Even though the construction of a suffix tree is complicated, it solves many other string-related problems in linear time.

Note: Suffix trees use a tree (suffix tree) for one string, whereas Hash tables, BSTs, Tries and TSTs store a set of strings. That means, a suffix tree answers the queries related to one string.

Let us see the terminology we use for this representation.

Prefix and Suffix

Given a string $T = T_1T_2 \dots T_n$, the *prefix* of T is a string $T_1 \dots T_i$ where i can take values from 1 to n . For example, if $T = \text{banana}$, then the prefixes of T are: $b, ba, ban, bana, banan, banana$.

Similarly, given a string $T = T_1T_2 \dots T_n$, the *suffix* of T is a string $T_i \dots T_n$ where i can take values from n to 1. For example, if $T = \text{banana}$, then the suffixes of T are: $a, na, ana, nana, anana, banana$.

Observation

From the above example, we can easily see that for a given text T and pattern P , the exact string matching problem can also be defined as:

- Find a suffix of T such that P is a prefix of this suffix or
- Find a prefix of T such that P is a suffix of this prefix.

Example: Let the text to be searched be $T = \text{acebkkbac}$ and the pattern be $P = \text{kkb}$. For this example, P is a prefix of the suffix kkbac and also a suffix of the prefix acebkkb .

What is a Suffix Tree?

In simple terms, the suffix tree for text T is a Trie-like data structure that represents the suffixes of T . The definition of suffix trees can be given as: A suffix tree for a n character string $T[1 \dots n]$ is a rooted tree with the following properties.

- A suffix tree will contain n leaves which are numbered from 1 to n

- Each internal node (except root) should have at least 2 children
- Each edge in a tree is labeled by a nonempty substring of T
- No two edges of a node (children edges) begin with the same character
- The paths from the root to the leaves represent all the suffixes of T

The Construction of Suffix Trees

Algorithm

1. Let S be the set of all suffixes of T . Append $\$$ to each of the suffixes.
2. Sort the suffixes in S based on their first character.
3. For each group S_c ($c \in \Sigma$):
 - (i) If S_c group has only one element, then create a leaf node.
 - (ii) Otherwise, find the longest common prefix of the suffixes in S_c group, create an internal node, and recursively continue with Step 2, S being the set of remaining suffixes from S_c after splitting off the longest common prefix.

For better understanding, let us go through an example. Let the given text be $T = tata\$$. For this string, give a number to each of the suffixes.

Index	Suffix
1	$\$$
2	$t\$$
3	$at\$$
4	$tat\$$
5	$atat\$$
6	$tata\$$

Now, sort the suffixes based on their initial characters.

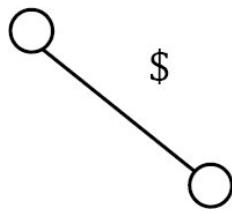
Index	Suffix
1	$\$$
3	$at\$$
5	$atat\$$
2	$t\$$
4	$tat\$$
6	$tata\$$

The suffixes are grouped into three sets based on their first character:

- Group S_1 based on a : $at\$$, $atat\$$
- Group S_2 based on a : $\$$
- Group S_3 based on t : $t\$$, $tat\$$, $tata\$$

In the three groups, the first group has only one element. So, as per the algorithm, create a leaf

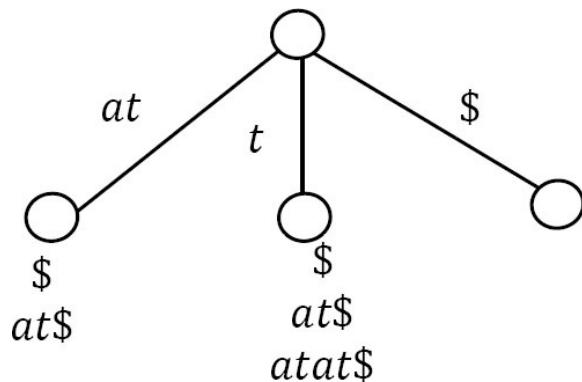
node for it, as shown below.



Now, for S_2 and S_3 (as they have more than one element), let us find the longest prefix in the group, and the result is shown below.

Group	Indexes for this group	Longest Prefix of Group Suffixes
S_2	3, 5	<i>at</i>
S_3	2, 4, 6	<i>t</i>

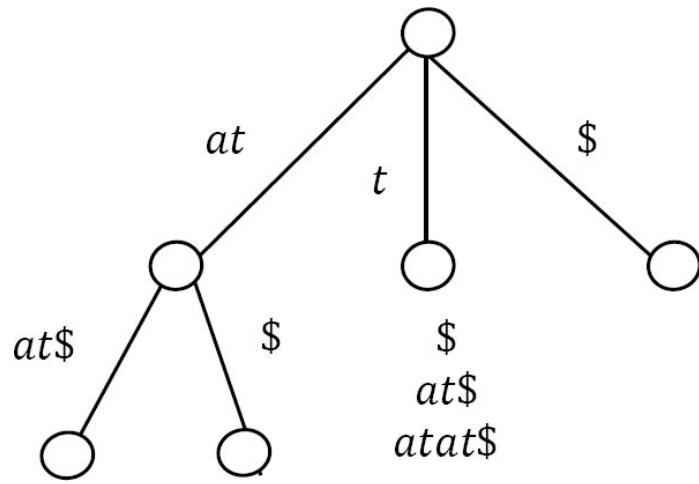
For S_2 and S_3 , create internal nodes, and the edge contains the longest common prefix of those groups.



Now we have to remove the longest common prefix from the S_2 and S_3 group elements.

Group	Indexes for this group	Longest Prefix of Group Suffixes	Resultant Suffixes
S_2	3, 5	<i>at</i>	\$, <i>at\$</i>
S_3	2, 4, 6	<i>t</i>	\$, <i>at\$</i> , <i>atat\$</i>

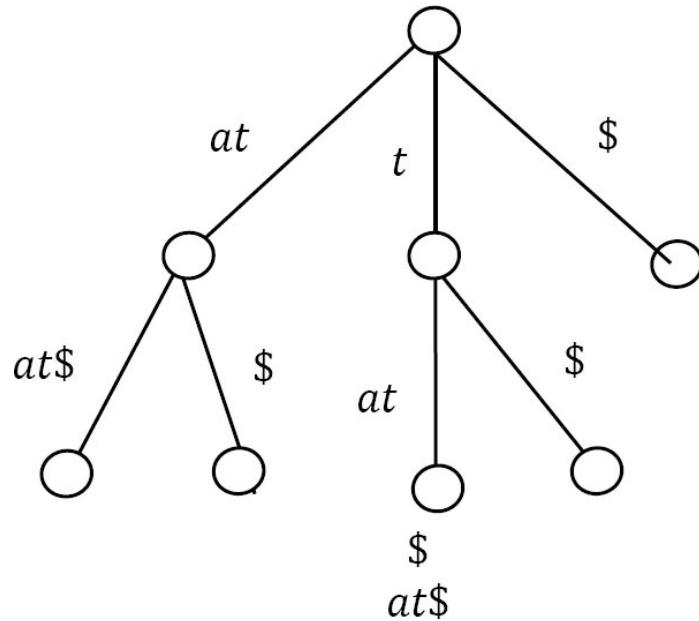
Our next step is solving S_2 and S_3 recursively. First let us take S_2 . In this group, if we sort them based on their first character, it is easy to see that the first group contains only one element \$, and the second group also contains only one element, *at\$*. Since both groups have only one element, we can directly create leaf nodes for them.



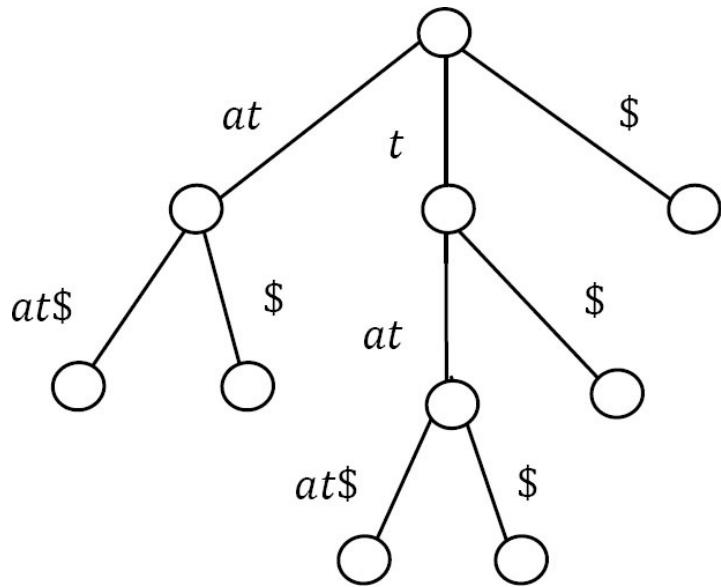
At this step, both S_1 and S_2 elements are done and the only remaining group is S_3 . As similar to earlier steps, in the S_3 group, if we sort them based on their first character, it is easy to see that there is only one element in the first group and it is $\$$. For S_3 remaining elements, remove the longest common prefix.

Group	Indexes for this group	Longest Prefix of Group Suffixes	Resultant Suffixes
S_3	4, 6	at	$\$, at\$$

In the S_3 second group, there are two elements: $\$$ and $at\$$. We can directly add the leaf nodes for the first group element $\$$. Let us add S_3 subtree as shown below.



Now, S_3 contains two elements. If we sort them based on their first character, it is easy to see that there are only two elements and among them one is $\$$ and other is $at\$$. We can directly add the leaf nodes for them. Let us add S_3 subtree as shown below.



Since there are no more elements, this is the completion of the construction of the suffix tree for string $T = \text{tatat}$. The time-complexity of the construction of a suffix tree using the above algorithm is $O(n^2)$ where n is the length of the input string because there are n distinct suffixes. The longest has length n , the second longest has length $n - 1$, and so on.

Note:

- There are $O(n)$ algorithms for constructing suffix trees.
- To improve the complexity, we can use indices instead of string for branches.

Applications of Suffix Trees

All the problems below (but not limited to these) on strings can be solved with suffix trees very efficiently (for algorithms refer to *Problems* section).

- **Exact String Matching:** Given a text T and a pattern P , how do we check whether P appears in T or not?
- **Longest Repeated Substring:** Given a text T how do we find the substring of T that is the maximum repeated substring?
- **Longest Palindrome:** Given a text T how do we find the substring of T that is the longest palindrome of T ?
- **Longest Common Substring:** Given two strings, how do we find the longest common substring?
- **Longest Common Prefix:** Given two strings $X[i \dots n]$ and $Y[j \dots m]$, how do we find the longest common prefix?
- How do we search for a regular expression in given text T ?
- Given a text T and a pattern P , how do we find the first occurrence of P in T ?

15.15 String Algorithms: Problems & Solutions

Problem-1 Given a paragraph of words, give an algorithm for finding the word which appears the maximum number of times. If the paragraph is scrolled down (some words disappear from the first frame, some words still appear, and some are new words), give the maximum occurring word. Thus, it should be dynamic.

Solution: For this problem we can use a combination of priority queues and tries. We start by creating a trie in which we insert a word as it appears, and at every leaf of trie. Its node contains that word along with a pointer that points to the node in the heap [priority queue] which we also create. This heap contains nodes whose structure contains a *counter*. This is its frequency and also a pointer to that leaf of trie, which contains that word so that there is no need to store the word twice.

Whenever a new word comes up, we find it in trie. If it is already there, we increase the frequency of that node in the heap corresponding to that word, and we call it heapify. This is done so that at any point of time we can get the word of maximum frequency. While scrolling, when a word goes out of scope, we decrement the counter in heap. If the new frequency is still greater than zero, heapify the heap to incorporate the modification. If the new frequency is zero, delete the node from heap and delete it from trie.

Problem-2 Given two strings, how can we find the longest common substring?

Solution: Let us assume that the given two strings are T_1 and T_2 . The longest common substring of two strings, T_1 and T_2 , can be found by building a generalized suffix tree for T_1 and T_2 . That means we need to build a single suffix tree for both the strings. Each node is marked to indicate if it represents a suffix of T_1 or T_2 or both. This indicates that we need to use different marker symbols for both the strings (for example, we can use \$ for the first string and # for the second symbol). After constructing the common suffix tree, the deepest node marked for both T_1 and T_2 represents the longest common substring.

Another way of doing this is: We can build a suffix tree for the string $T_1\$T_2\#$. This is equivalent to building a common suffix tree for both the strings.

Time Complexity: $O(m + n)$, where m and n are the lengths of input strings T_1 and T_2 .

Problem-3 Longest Palindrome: Given a text T how do we find the substring of T which is the longest palindrome of T ?

Solution: The longest palindrome of $T[1..n]$ can be found in $O(n)$ time. The algorithm is: first build a suffix tree for $T\$reverse(T)\#$ or build a generalized suffix tree for T and $reverse(T)$. After building the suffix tree, find the deepest node marked with both \$ and #. Basically it means find the longest common substring.

Problem-4 Given a string (word), give an algorithm for finding the next word in the dictionary.

Solution: Let us assume that we are using Trie for storing the dictionary words. To find the next

word in Tries we can follow a simple approach as shown below. Starting from the rightmost character, increment the characters one by one. Once we reach Z, move to the next character on the left side.

Whenever we increment, check if the word with the incremented character exists in the dictionary or not. If it exists, then return the word, otherwise increment again. If we use *TST*, then we can find the inorder successor for the current word.

Problem-5 Give an algorithm for reversing a string.

Solution:

```
//If the str is editable
char *ReversingString(char str[]) {
    char temp, start, end;
    if(str == NULL || *str == '\0')
        return str;
    for (end = 0; str[end]; end++);
    end--;
    for (start = 0; start < end; start++, end--) {
        temp = str[start]; str[start] = str[end]; str[end] = temp;
    }
    return str;
}
```

Time Complexity: $O(n)$, where n is the length of the given string. Space Complexity: $O(n)$.

Problem-6 If the string is not editable, how do we create a string that is the reverse of the given string?

Solution: If the string is not editable, then we need to create an array and return the pointer of that.

```

//If str is a const string (not editable)
char* ReversingString(char* str) {
    int start, end, len;
    char temp, *ptr=NULL;
    len=strlen(str);
    ptr=malloc(sizeof(char)*(len+1));
    ptr=strcpy(ptr,str);
    for (start=0, end=len-1; start<=end; start++, end--) {      //Swapping
        temp=ptr[start]; ptr[start]=ptr[end]; ptr[end]=temp;
    }
    return ptr;
}

```

Time Complexity: $O\left(\frac{n}{2}\right) \approx O(n)$, where n is the length of the given string. Space Complexity: $O(1)$.

Problem-7 Can we reverse the string without using any temporary variable?

Solution: Yes, we can use XOR logic for swapping the variables.

```

char* ReversingString(char *str) {
    int start = 0, end= strlen(str)-1;
    while( start<end ) {
        str[start] ^= str[end];    str[end] ^= str[start];    str[start] ^= str[end];
        ++start;
        --end;
    }
    return str;
}

```

Time Complexity: $O\left(\frac{n}{2}\right) \approx O(n)$, where n is the length of the given string. Space Complexity: $O(1)$.

Problem-8 Given a text and a pattern, give an algorithm for matching the pattern in the text. Assume ? (single character matcher) and * (multi character matcher) are the wild card characters.

Solution: Brute Force Method. For efficient method, refer to the theory section.

```

int PatternMatching(char *text, char *pattern) {
    if(*pattern == 0)
        return 1;
    if(*text == 0)
        return *p == 0;
    if('? == *pattern)
        return PatternMatching(text+1,pattern+1) || PatternMatching(text,pattern+1);
    if('* == *pattern)
        return PatternMatching(text+1,pattern) || PatternMatching(text,pattern+1);
    if(*text == *pattern)
        return PatternMatching(text+1,pattern+1);
    return -1;
}

```

Time Complexity: $O(mn)$, where m is the length of the text and n is the length of the pattern.

Space Complexity: $O(1)$.

Problem-9 Give an algorithm for reversing words in a sentence.

Example: Input: “This is a Career Monk String”, Output: “String Monk Career a is This”

Solution: Start from the beginning and keep on reversing the words. The below implementation assumes that ‘ ’ (space) is the delimiter for words in given sentence.

```

void ReverseWordsInSentences(char *text) {
    int wordStart, wordEnd, length;
    length = strlen(text);
    ReversingString(text, 0, length-1);
    for(wordStart = wordEnd = 0; wordEnd < length; wordEnd++) {
        if(text[wordEnd] != ' ') {
            wordStart = wordEnd;
            while (text[wordEnd] != ' ' && wordEnd < length)
                wordEnd++;
            wordEnd--;
            ReversingString(text, wordStart, wordEnd); //Found current word, reverse it now.
        }
    }
}

void ReversingString(char text[], int start, int end) {
    for (char temp; start < end; start++, end--) {
        temp = str[end];
        str[end] = str[start];
        str[start] = temp;
    }
}

```

Time Complexity: $O(2n) \approx O(n)$, where n is the length of the string. Space Complexity: $O(1)$.

Problem-10 Permutations of a string [anagrams]: Give an algorithm for printing all possible permutations of the characters in a string. Unlike combinations, two permutations are considered distinct if they contain the same characters but in a different order. For simplicity assume that each occurrence of a repeated character is a distinct character. That is, if the input is “aaa”, the output should be six repetitions of “aaa”. The permutations may be output in any order.

Solution: The solution is reached by generating $n!$ strings, each of length n , where n is the length of the input string.

```

void Permutations(int depth, char *permutation, int *used, char *original) {
    int length = strlen(original);
    if(depth == length)
        printf("%s", permutation);
    else {
        for (int i = 0; i < length; i++) {
            if(!used[i]) {
                used[i] = 1;
                permutation[depth] = original[i];
                Permutations(depth + 1, permutation, used, original);
                used[i] = 0;
            }
        }
    }
}

```

Problem-11 Combinations of a String: Unlike permutations, two combinations are considered to be the same if they contain the same characters, but may be in a different order. Give an algorithm that prints all possible combinations of the characters in a string. For example, “ac” and “ab” are different combinations from the input string “abc”, but “ab” is the same as “ba”.

Solution: The solution is achieved by generating $n!/r! (n - r)!$ strings, each of length between 1 and n where n is the length of the given input string.

Algorithm:

For each of the input characters

- Put the current character in output string and print it.
- If there are any remaining characters, generate combinations with those remaining characters.

```

void Combinations(int depth, char *combination, int start, char *original) {
    int length = strlen(original);
    for (int i = start; i < length; i++) {
        combination[depth] = original[i];
        combination[depth + 1] = '\0';
        printf("%s", combination);
        if(i < length - 1)
            Combinations(depth + 1, combination, start + 1, original);
    }
}

```

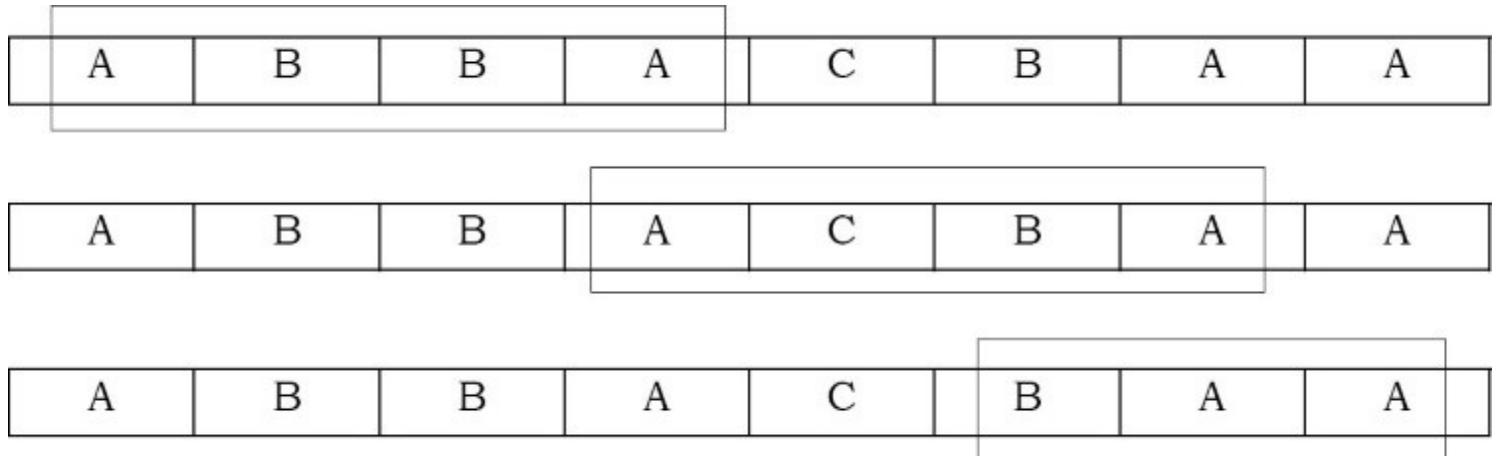
Problem-12 Given a string “ABCCBCBA”, give an algorithm for recursively removing the adjacent characters if they are the same. For example, ABCCBCBA nnnnnn> ABBCBA->ACBA

Solution: First we need to check if we have a character pair; if yes, then cancel it. Now check for next character and previous element. Keep canceling the characters until we either reach the start of the array, reach the end of the array, or don't find a pair.

```
void RremoveAdjacentPairs(char* str) {  
    int len = strlen(str), i, j = 0;  
    for (i=1; i <= len; i++) {  
        while ((str[i] == str[j]) && (j >= 0)){ //Cancel pairs  
            i++;  
            j--;  
        }  
        str[++j] = str[i];  
    }  
    return;  
}
```

Problem-13 Given a set of characters *CHARS* and a input string *INPUT*, find the minimum window in *str* which will contain all the characters in *CHARS* in complexity O(*n*). For example, *INPUT* = *ABBACBAA* and *CHARS* = *AAB* has the minimum window *BAA*.

Solution: This algorithm is based on the sliding window approach. In this approach, we start from the beginning of the array and move to the right. As soon as we have a window which has all the required elements, try sliding the window as far right as possible with all the required elements. If the current window length is less than the minimum length found until now, update the minimum length. For example, if the input array is *ABBACBAA* and the minimum window should cover characters *AAB*, then the sliding window will move like this:



Algorithm: The input is the given array and chars is the array of characters that need to be found.

- 1 Make an integer array `shouldfind[]` of len 256. The i^{th} element of this array will have the count of how many times we need to find the element of ASCII value i .
- 2 Make another array `hasfound` of 256 elements, which will have the count of the required elements found until now.
- 3 Count ≤ 0
- 4 While `input[i]`
 - a. If `input[i]` element is not to be found → continue
 - b. If `input[i]` element is required \Rightarrow increase count by 1.
 - c. If count is length of `chars[]` array, slide the window as much right as possible.
 - d. If current window length is less than min length found until now, update min length.

```
#define MAX 256
void MinLengthWindow(char input[], char chars[]) {
    int shouldfind[MAX] = {0}, hasfound[MAX] = {0};
    int j=0, cnt = 0, start=0, finish, minwindow = INT_MAX;
    int charlen = strlen(chars), iplen = strlen(input);
    for (int i=0; i< charlen; i++)
        shouldfind[chars[i]] += 1;
    finish = iplen;
    for (int i=0; i< iplen; i++) {
        if(!shouldfind[input[i]])
            continue;
        hasfound[input[i]] += 1;
        if(shouldfind[input[i]] >= hasfound[input[i]])
            cnt++;
        if(cnt == charlen) {
            while (shouldfind[input[j]] == 0 || hasfound[input[j]] > shouldfind[input[j]]) {
                if(hasfound[input[j]] > shouldfind[input[j]])
                    hasfound[input[j]]--;
                j++;
            }
            if(minwindow > (i - j +1)) {
                minwindow = i - j +1;
                finish = i;
                start = j;
            }
        }
    }
    printf("Start:%d and Finish: %d", start, finish);
}
```

Complexity: If we walk through the code, i and j can traverse at most n steps (where n is the input

size) in the worst case, adding to a total of $2n$ times. Therefore, time complexity is $O(n)$.

Problem-14 We are given a 2D array of characters and a character pattern. Give an algorithm to find if the pattern is present in the 2D array. The pattern can be in any order (all 8 neighbors to be considered) but we can't use the same character twice while matching. Return 1 if match is found, 0 if not. For example: Find “MICROSOFT” in the below matrix.

A	C	P	R	C
X	S	O	P	C
V	O	V	N	I
W	G	F	M	N
Q	A	T	I	T

Solution: Manually finding the solution of this problem is relatively intuitive; we just need to describe an algorithm for it. Ironically, describing the algorithm is not the easy part.

How do we do it manually? First we match the first element, and when it is matched we match the second element in the 8 neighbors of the first match. We do this process recursively, and when the last character of the input pattern matches, return true.

During the above process, take care not to use any cell in the 2D array twice. For this purpose, you mark every visited cell with some sign. If your pattern matching fails at some point, start matching from the beginning (of the pattern) in the remaining cells. When returning, you unmark the visited cells.

Let's convert the above intuitive method into an algorithm. Since we are doing similar checks for pattern matching every time, a recursive solution is what we need. In a recursive solution, we need to check if the substring passed is matched in the given matrix or not. The condition is not to use the already used cell, and to find the already used cell, we need to add another 2D array to the function (or we can use an unused bit in the input array itself.) Also, we need the current position of the input matrix from where we need to start. Since we need to pass a lot more information than is actually given, we should be having a wrapper function to initialize the extra information to be passed.

Algorithm:

If we are past the last character in the pattern

 Return true

If we get a used cell again

 Return false if we got past the 2D matrix

 Return false

If searching for first element and cell doesn't match

 FindMatch with next cell in row-first order (or column-first order)

Otherwise if character matches
mark this cell as used
res = FindMatch with next position of pattern in 8 neighbors
mark this cell as unused
Return res

Otherwise
Return false

```

#define MAX 100
boolean FindMatch_wrapper(char mat[MAX][MAX], char *pat, int nrow, int ncol) {
    if(strlen(pat) > nrow*ncol) return false;
    int used[MAX][MAX] = {{0,},};
    return FindMatch(mat, pat, used, 0, 0, nrow, ncol, 0);
}
//level: index till which pattern is matched & x, y: current position in 2D array
boolean FindMatch(char mat[MAX][MAX], char *pat, int used[MAX][MAX],
                  int x, int y, int nrow, int ncol, int level) {
    if(level == strlen(pat)) //pattern matched
        return true;
    if(nrow == x || ncol == y) return false;
    if(used[x][y]) return false;
    if(mat[x][y] != pat[level] && level == 0) {
        if(x < (nrow - 1))
            return FindMatch(mat, pat, used, x+1, y, nrow, ncol, level); //next element in same row
        else if(y < (ncol - 1))
            return FindMatch(mat, pat, used, 0, y+1, nrow, ncol, level); //first element from same column
        else return false;
    }
    else if(mat[x][y] == pat[level]) {
        boolean res;
        used[x][y] = 1; //marking this cell as used
        //finding subpattern in 8 neighbors
        res = (x > 0 ? FindMatch(mat, pat, used, x-1, y, nrow, ncol, level+1) : false) ||
              (res = x < (nrow - 1) ? FindMatch(mat, pat, used, x+1, y, nrow, ncol, level+1) : false) ||
              (res = y > 0 ? FindMatch(mat, pat, used, x, y-1, nrow, ncol, level+1) : false) ||
              (res = y < (ncol - 1) ? FindMatch(mat, pat, used, x, y+1, nrow, ncol, level+1) : false) ||
              (res = x < (nrow - 1)&&(y < ncol - 1)?FindMatch(mat, pat, used, x+1, y+1, nrow, ncol, level+1) : false) ||
              (res = x < (nrow - 1) && y > 0 ? FindMatch(mat, pat, used, x+1, y-1, nrow, ncol, level+1) : false) ||
              (res = x > 0 && y < (ncol - 1) ? FindMatch(mat, pat, used, x-1, y+1, nrow, ncol, level+1) : false) ||
              (res = x > 0 && y > 0 ? FindMatch(mat, pat, used, x-1, y-1, nrow, ncol, level+1) : false);
        used[x][y] = 0; //marking this cell as unused
        return res;
    }
    else return false;
}

```

Problem-15 Given two strings $str1$ and $str2$, write a function that prints all interleavings of the given two strings. We may assume that all characters in both strings are different.
Example: Input: $str1 = "AB"$, $str2 = "CD"$ and Output: ABCD ACBD ACDB CABD

CADB CDAB. An interleaved string of given two strings preserves the order of characters in individual strings. For example, in all the interleavings of above first example, ‘A’ comes before ‘B’ and ‘C’ comes before ‘D’.

Solution: Let the length of $str1$ be m and the length of $str2$ be n . Let us assume that all characters in $str1$ and $str2$ are different. Let $Count(m,n)$ be the count of all interleaved strings in such strings. The value of $Count(m,n)$ can be written as following.

$$Count(m, n) = Count(m-1, n) + Count(m, n-1)$$

$$Count(1, 0) = 1 \text{ and } Count(0, 1) = 1$$

To print all interleavings, we can first fix the first character of $str1[0..m-1]$ in output string, and recursively call for $str1[1..m-1]$ and $str2[0..n-1]$. And then we can fix the first character of $str2[0..n-1]$ and recursively call for $str1[0..m-1]$ and $str2[1..n-1]$.

```

void PrintInterleavings(char *str1, char *str2, char *iStr, int m, int n, int i){
    // Base case: If all characters of str1 & str2 have been included in output string,
    // then print the output string
    if ( m==0 && n ==0 )
        printf("%s\n", iStr);

    // If some characters of str1 are left to be included, then include the
    // first character from the remaining characters and recur for rest
    if ( m != 0 ) {
        iStr[i] = str1[0];
        PrintInterleavings(str1 + 1, str2, iStr, m-1, n, i+1);
    }

    // If some characters of str2 are left to be included, then include the
    // first character from the remaining characters and recur for rest
    if ( n != 0 ) {
        iStr[i] = str2[0];
        PrintInterleavings(str1, str2+1, iStr, m, n-1, i+1);
    }
}

// Allocates memory for output string and uses PrintInterleavings() for printing all interleaving's
void Print(char *str1, char *str2, int m, int n){
    // allocate memory for the output string
    char *iStr= (char*)malloc((m+n+1)*sizeof(char));
    // Set the terminator for the output string
    iStr[m+n] = '\0';
    // print all interleaving's using PrintInterleavings()
    PrintInterleavings(str1, str2, iStr, m, n, 0);
    free(iStr);
}

```

Problem-16 Given a matrix with size $n \times n$ containing random integers. Give an algorithm which checks whether rows match with a column(s) or not. For example, if i^{th} row matches with j^{th} column, and i^{th} row contains the elements - [2,6,5,8,9]. Then; 1^{st} column would also contain the elements - [2,6,5,8,9].

Solution: We can build a trie for the data in the columns (rows would also work). Then we can compare the rows with the trie. This would allow us to exit as soon as the beginning of a row does not match any column (backtracking). Also this would let us check a row against all columns in one pass.

If we do not want to waste memory for empty pointers then we can further improve the solution by constructing a suffix tree.

Problem-17 Write a method to replace all spaces in a string with ‘%20’. Assume string has sufficient space at end of string to hold additional characters.

Solution: Find the number of spaces. Then, starting from end (assuming string has enough space), replace the characters. Starting from end reduces the overwrites.

```
void encodeSpaceWithString(char* A){  
    char *space = "%20";  
    int stringLength = strlen(A);  
    if(stringLength == 0){  
        return;  
    }  
    int i, numberOfSpaces = 0;  
    for(i = 0; i < stringLength; i++){  
        if(A[i] == ' ' || A[i] == '\t'){  
            numberOfSpaces++;  
        }  
    }  
    if(!numberOfSpaces)  
        return;  
    int newLength = len + numberOfSpaces * 2;  
    A[newLength] = '\0';  
    for(i = stringLength-1; i >= 0; i--){  
        if(A[i] == ' ' || A[i] == '\t'){  
            A[newLength--] = '0';  
            A[newLength--] = '2';  
            A[newLength--] = '%';  
        }  
        else{  
            A[newLength--] = A[i];  
        }  
    }  
}
```

Time Complexity: $O(n)$. Space Complexity: $O(1)$. Here, we do not have to worry about the space needed for extra characters.

Problem-18 Running length encoding: Write an algorithm to compress the given string by using the count of repeated characters and if new compressed string length is not smaller than the original string then return the original string.

Solution:

With extra space of O(2):

```
string CompressString(string inputStr){  
    char last = inputStr.at(0);  
    int size = 0, count = 1;  
    char temp[2];  
    string str;  
    for (int i = 1; i < inputStr.length(); i++){  
        if(last == inputStr.at(i))  
            count++;  
        else{  
            itoa(count, temp, 10);  
            str += last;  
            str += temp;  
            last = inputStr.at(i);  
            count = 1;  
        }  
    }  
    str = str + last + temp;  
    // If the compressed string size is greater than input string, return input string  
    if(str.length() >= inputStr.length())  
        return inputStr;  
    else return str;  
}
```

Time Complexity: $O(n)$. Space Complexity: $O(1)$, but it uses a temporary array of size two.

Without extra space (inplace):

```
char CompressString(char *inputStr, char currentChar, int lengthIndex, int& countChar, int& index){  
    if(lengthIndex == -1)  
        return currentChar;  
    char lastChar = CompressString(inputStr, inputStr[lengthIndex], lengthIndex-1, countChar, index);  
    if(lastChar == currentChar)  
        countChar++;  
    else {  
        inputStr[index++] = lastChar;  
        for(int i = 0; i < NumToString(countChar).length(); i++)  
            inputStr[index++] = NumToString(countChar).at(i);  
        countChar = 1;  
    }  
    return currentChar;  
}
```

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

ALGORITHMS DESIGN TECHNIQUES

CHAPTER

16



16.1 Introduction

In the previous chapters, we have seen many algorithms for solving different kinds of problems. Before solving a new problem, the general tendency is to look for the similarity of the current problem to other problems for which we have solutions. This helps us in getting the solution easily.

In this chapter, we will see different ways of classifying the algorithms and in subsequent chapters we will focus on a few of them (Greedy, Divide and Conquer, Dynamic Programming).

16.2 Classification

There are many ways of classifying algorithms and a few of them are shown below:

- Implementation Method
- Design Method
- Other Classifications

16.3 Classification by Implementation Method

Recursion or Iteration

A *recursive* algorithm is one that calls itself repeatedly until a base condition is satisfied. It is a common method used in functional programming languages like C,C++, etc.

Iterative algorithms use constructs like loops and sometimes other data structures like stacks and queues to solve the problems.

Some problems are suited for recursive and others are suited for iterative. For example, the *Towers of Hanoi* problem can be easily understood in recursive implementation. Every recursive version has an iterative version, and vice versa.

Procedural or Declarative (non-Procedural)

In *declarative* programming languages, we say what we want without having to say how to do it. With *procedural* programming, we have to specify the exact steps to get the result. For example, SQL is more declarative than procedural, because the queries don't specify the steps to produce the result. Examples of procedural languages include: C, PHP, and PERL.

Serial or Parallel or Distributed

In general, while discussing the algorithms we assume that computers execute one instruction at a time. These are called *serial* algorithms.

Parallel algorithms take advantage of computer architectures to process several instructions at a time. They divide the problem into subproblems and serve them to several processors or threads. Iterative algorithms are generally parallelizable.

If the parallel algorithms are distributed on to different machines then we call such algorithms *distributed* algorithms.

Deterministic or Non-Deterministic

Deterministic algorithms solve the problem with a predefined process, whereas *non-deterministic* algorithms guess the best solution at each step through the use of heuristics.

Exact or Approximate

As we have seen, for many problems we are not able to find the optimal solutions. That means, the algorithms for which we are able to find the optimal solutions are called *exact* algorithms. In computer science, if we do not have the optimal solution, we give approximation algorithms.

Approximation algorithms are generally associated with NP-hard problems (refer to the [Complexity Classes](#) chapter for more details).

16.4 Classification by Design Method

Another way of classifying algorithms is by their design method.

Greedy Method

Greedy algorithms work in stages. In each stage, a decision is made that is good at that point, without bothering about the future consequences. Generally, this means that some *local best* is chosen. It assumes that the local best selection also makes for the *global* optimal solution.

Divide and Conquer

The D & C strategy solves a problem by:

- 1) Divide: Breaking the problem into sub problems that are themselves smaller instances of the same type of problem.
- 2) Recursion: Recursively solving these sub problems.
- 3) Conquer: Appropriately combining their answers.

Examples: merge sort and binary search algorithms.

Dynamic Programming

Dynamic programming (DP) and memoization work together. The difference between DP and divide and conquer is that in the case of the latter there is no dependency among the sub problems, whereas in DP there will be an overlap of sub-problems. By using memoization [maintaining a table for already solved sub problems], DP reduces the exponential complexity to polynomial complexity ($O(n^2)$, $O(n^3)$, etc.) for many problems.

The difference between dynamic programming and recursion is in the memoization of recursive calls. When sub problems are independent and if there is no repetition, memoization does not help, hence dynamic programming is not a solution for all problems.

By using memoization [maintaining a table of sub problems already solved], dynamic

programming reduces the complexity from exponential to polynomial.

Linear Programming

In linear programming, there are inequalities in terms of inputs and *maximizing* (or *minimizing*) some linear function of the inputs. Many problems (example: maximum flow for directed graphs) can be discussed using linear programming.

Reduction [Transform and Conquer]

In this method we solve a difficult problem by transforming it into a known problem for which we have asymptotically optimal algorithms. In this method, the goal is to find a reducing algorithm whose complexity is not dominated by the resulting reduced algorithms. For example, the selection algorithm for finding the median in a list involves first sorting the list and then finding out the middle element in the sorted list. These techniques are also called *transform and conquer*.

16.5 Other Classifications

Classification by Research Area

In computer science each field has its own problems and needs efficient algorithms. Examples: search algorithms, sorting algorithms, merge algorithms, numerical algorithms, graph algorithms, string algorithms, geometric algorithms, combinatorial algorithms, machine learning, cryptography, parallel algorithms, data compression algorithms, parsing techniques, and more.

Classification by Complexity

In this classification, algorithms are classified by the time they take to find a solution based on their input size. Some algorithms take linear time complexity ($O(n)$) and others take exponential time, and some never halt. Note that some problems may have multiple algorithms with different complexities.

Randomized Algorithms

A few algorithms make choices randomly. For some problems, the fastest solutions must involve randomness. Example: Quick Sort.

Branch and Bound Enumeration and Backtracking

These were used in Artificial Intelligence and we do not need to explore these fully. For the Backtracking method refer to the *Recusion and Backtracking* chapter.

Note: In the next few chapters we discuss the Greedy, Divide and Conquer, and Dynamic Programming] design methods. These methods are emphasized because they are used more often than other methods to solve problems.

GREEDY ALGORITHMS

CHAPTER 17



17.1 Introduction

Let us start our discussion with simple theory that will give us an understanding of the Greedy technique. In the game of *Chess*, every time we make a decision about a move, we have to also think about the future consequences. Whereas, in the game of *Tennis* (or *Volleyball*), our action is based on the immediate situation.

This means that in some cases making a decision that looks right at that moment gives the best solution (*Greedy*), but in other cases it doesn't. The Greedy technique is best suited for looking at the immediate situation.

17.2 Greedy Strategy

Greedy algorithms work in stages. In each stage, a decision is made that is good at that point, without bothering about the future. This means that some *local best* is chosen. It assumes that a local good selection makes for a global optimal solution.

17.3 Elements of Greedy Algorithms

The two basic properties of optimal Greedy algorithms are:

- 1) Greedy choice property
- 2) Optimal substructure

Greedy choice property

This property says that the globally optimal solution can be obtained by making a locally optimal solution (Greedy). The choice made by a Greedy algorithm may depend on earlier choices but not on the future. It iteratively makes one Greedy choice after another and reduces the given problem to a smaller one.

Optimal substructure

A problem exhibits optimal substructure if an optimal solution to the problem contains optimal solutions to the subproblems. That means we can solve subproblems and build up the solutions to solve larger problems.

17.4 Does Greedy Always Work?

Making locally optimal choices does not always work. Hence, Greedy algorithms will not always give the best solutions. We will see particular examples in the *Problems* section and in the *Dynamic Programming* chapter.

17.5 Advantages and Disadvantages of Greedy Method

The main advantage of the Greedy method is that it is straightforward, easy to understand and easy to code. In Greedy algorithms, once we make a decision, we do not have to spend time re-examining the already computed values. Its main disadvantage is that for many problems there is no greedy algorithm. That means, in many cases there is no guarantee that making locally optimal improvements in a locally optimal solution gives the optimal global solution.

17.6 Greedy Applications

- Sorting: Selection sort, Topological sort
- Priority Queues: Heap sort
- Huffman coding compression algorithm

- Prim's and Kruskal's algorithms
- Shortest path in Weighted Graph [Dijkstra's]
- Coin change problem
- Fractional Knapsack problem
- Disjoint sets-UNION by size and UNION by height (or rank)
- Job scheduling algorithm
- Greedy techniques can be used as an approximation algorithm for complex problems

17.7 Understanding Greedy Technique

For better understanding let us go through an example.

Huffman Coding Algorithm

Definition

Given a set of n characters from the alphabet A [each character $c \in A$] and their associated frequency $\text{freq}(c)$, find a binary code for each character $c \in A$, such that $\sum_{c \in A} \text{freq}(c) \cdot |\text{binarycode}(c)|$ is minimum, where $|\text{binarycode}(c)|$ represents the length of binary code of character c . That means the sum of the lengths of all character codes should be minimum [the sum of each character's frequency multiplied by the number of bits in the representation].

The basic idea behind the Huffman coding algorithm is to use fewer bits for more frequently occurring characters. The Huffman coding algorithm compresses the storage of data using variable length codes. We know that each character takes 8 bits for representation. But in general, we do not use all of them. Also, we use some characters more frequently than others. When reading a file, the system generally reads 8 bits at a time to read a single character. But this coding scheme is inefficient. The reason for this is that some characters are more frequently used than other characters. Let's say that the character 'e' is used 10 times more frequently than the character 'q'. It would then be advantageous for us to instead use a 7 bit code for e and a 9 bit code for q because that could reduce our overall message length.

On average, using Huffman coding on standard files can reduce them anywhere from 10% to 30% depending on the character frequencies. The idea behind the character coding is to give longer binary codes for less frequent characters and groups of characters. Also, the character coding is constructed in such a way that no two character codes are prefixes of each other.

An Example

Let's assume that after scanning a file we find the following character frequencies:

Character	Frequency
a	12
b	2
c	7
d	13
e	14
f	85

Given this, create a binary tree for each character that also stores the frequency with which it occurs (as shown below).

b-2

c-7

a-12

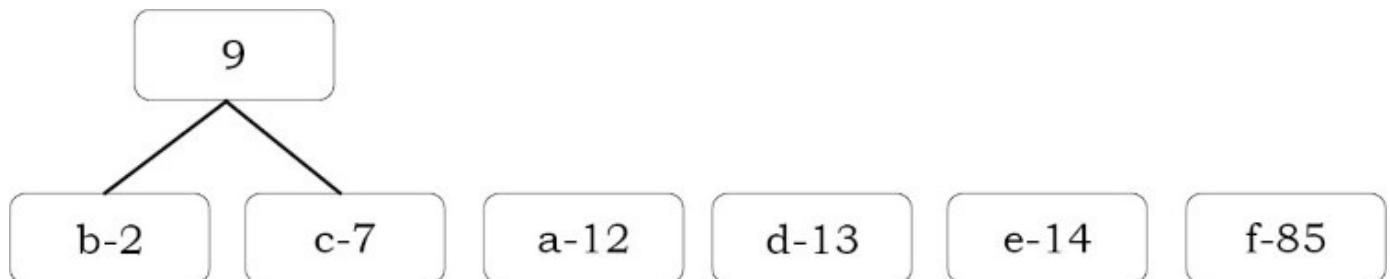
d-13

e-14

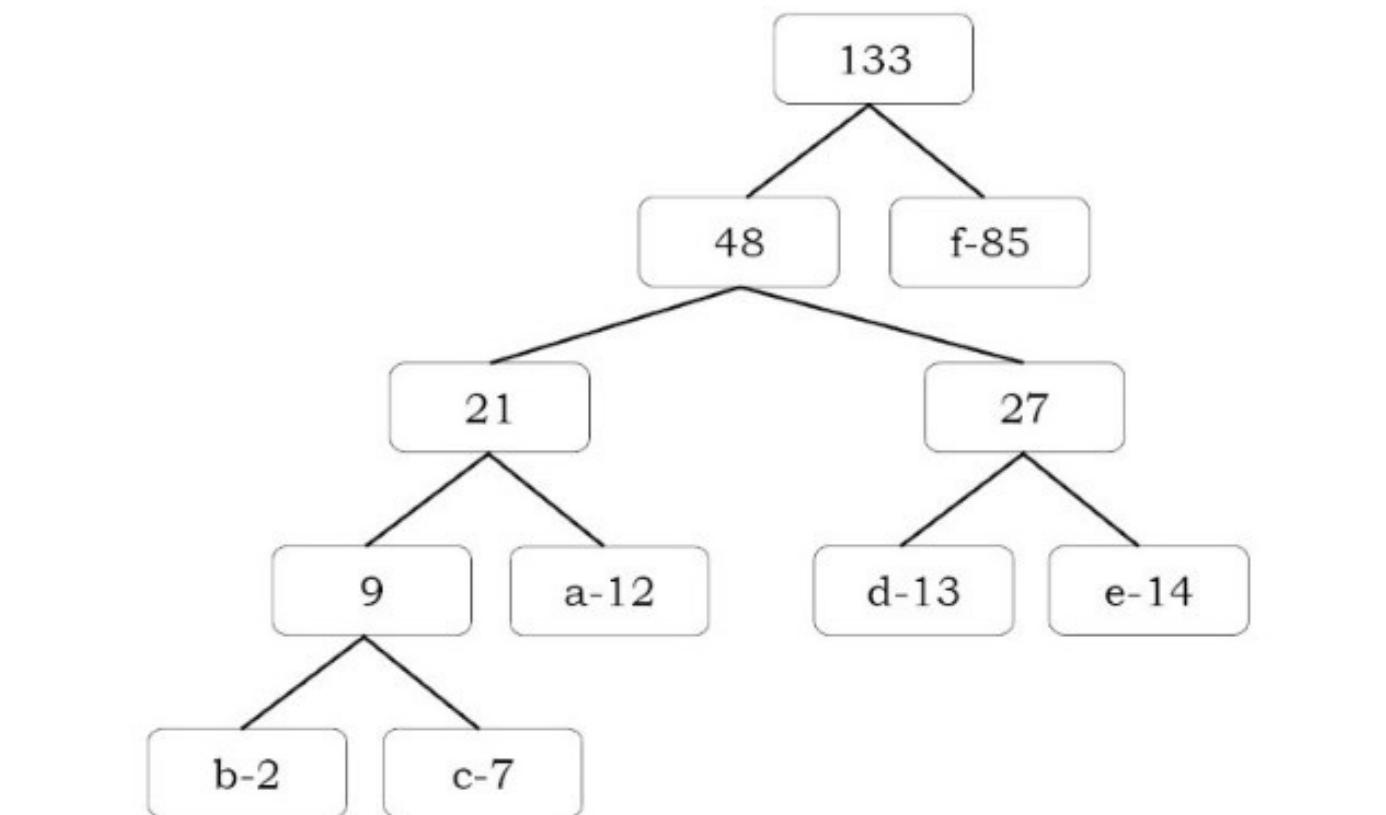
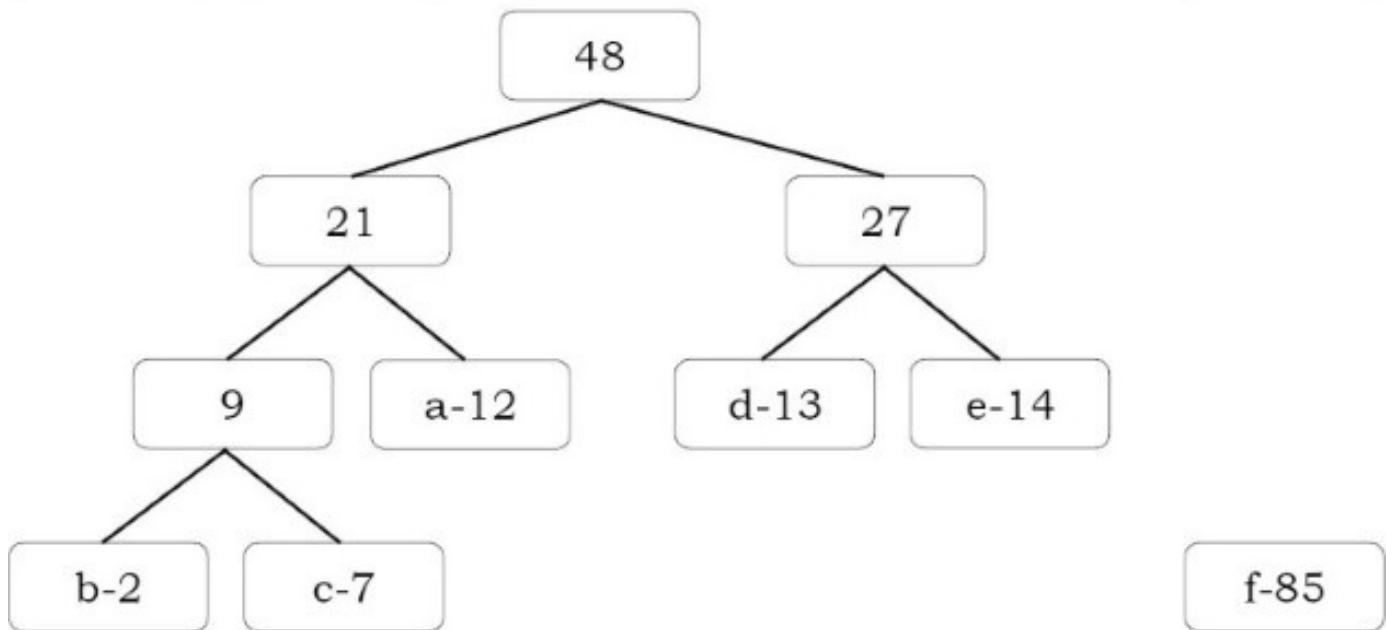
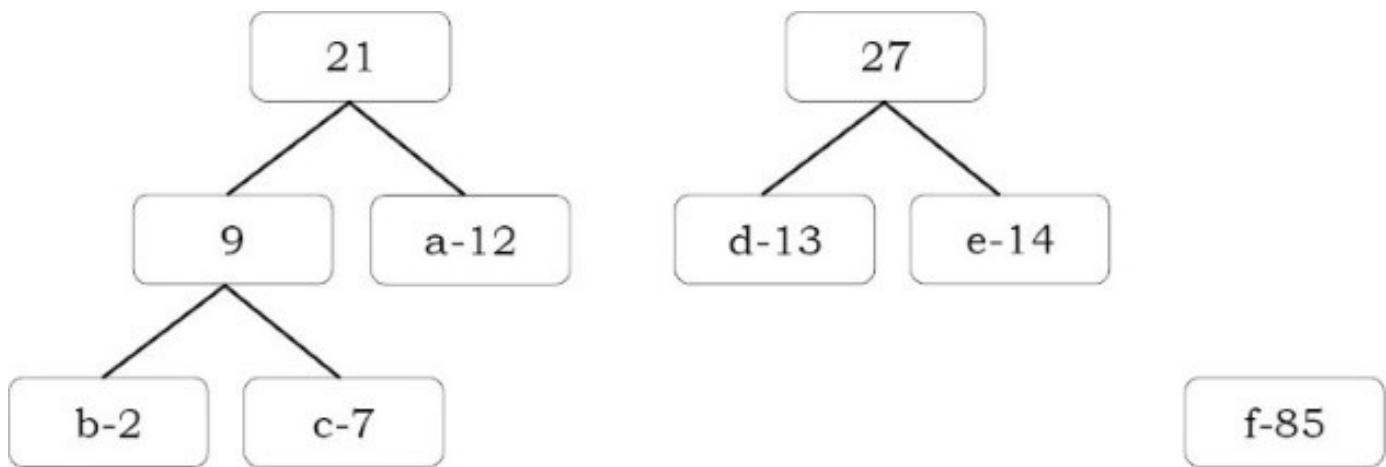
f-85

The algorithm works as follows: In the list, find the two binary trees that store minimum frequencies at their nodes.

Connect these two nodes at a newly created common node that will store no character but will store the sum of the frequencies of all the nodes connected below it. So our picture looks like this:



Repeat this process until only one tree is left:



Once the tree is built, each leaf node corresponds to a letter with a code. To determine the code for a particular node, traverse from the root to the leaf node. For each move to the left, append a 0 to the code, and for each move to the right, append a 1. As a result, for the above generated tree, we get the following codes:

Letter	Code
a	001
b	0000
c	0001
d	010
e	011
f	1

Calculating Bits Saved

Now, let us see how many bits that Huffman coding algorithm is saving. All we need to do for this calculation is see how many bits are originally used to store the data and subtract from that the number of bits that are used to store the data using the Huffman code. In the above example, since we have six characters, let's assume each character is stored with a three bit code. Since there are 133 such characters (multiply total frequencies by 3), the total number of bits used is $3 * 133 = 399$. Using the Huffman coding frequencies we can calculate the new total number of bits used:

Letter	Code	Frequency	Total Bits
a	001	12	36
b	0000	2	8
c	0001	7	28
d	010	13	39
e	011	14	42
f	1	85	85
Total			238

Thus, we saved $399 - 238 = 161$ bits, or nearly 40% of the storage space.

```

HuffmanCodingAlgorithm(int A[], int n) {
    Initialize a priority queue, PQ, to contain the n elements in A;
    struct BinaryTreeNode *temp;
    for (i = 1; i<n; i++) {
        temp = (struct *)malloc(sizeof(BinaryTreeNode));
        temp→left = Delete-Min(PQ);
        temp→right = Delete-Min(PQ);
        temp→data = temp→left→data + temp→right→data;
        Insert temp to PQ;
    }
    return PQ;
}

```

Time Complexity: $O(n \log n)$, since there will be *one* build_heap, $2n - 2$ delete_mins, and $n - 2$ inserts, on a priority queue that never has more than n elements. Refer to the [Priority Queues](#) chapter for details.

17.8 Greedy Algorithms: Problems & Solutions

Problem-1 Given an array F with size n . Assume the array content $F[i]$ indicates the length of the i^{th} file and we want to merge all these files into one single file. Check whether the following algorithm gives the best solution for this problem or not?

Algorithm: Merge the files contiguously. That means select the first two files and merge them. Then select the output of the previous merge and merge with the third file, and keep going...

Note: Given two files A and B with sizes m and n , the complexity of merging is $O(m + n)$.

Solution: This algorithm will not produce the optimal solution. For a counter example, let us consider the following file sizes array.

$$F = \{10, 5, 100, 50, 20, 15\}$$

As per the above algorithm, we need to merge the first two files (10 and 5 size files), and as a result we get the following list of files. In the list below, 15 indicates the cost of merging two files with sizes 10 and 5.

$$\{15, 100, 50, 20, 15\}$$

Similarly, merging 15 with the next file 100 produces: $\{115, 50, 20, 15\}$. For the subsequent steps

the list becomes

$$\{165,20,15\}, \{185,15\}$$

Finally,

$$\{200\}$$

The total cost of merging = Cost of all merging operations = $15 + 115 + 165 + 185 + 200 = 680$.

To see whether the above result is optimal or not, consider the order: $\{5,10,15,20,50,100\}$. For this example, following the same approach, the total cost of merging = $15 + 30 + 50 + 100 + 200 = 395$. So, the given algorithm is not giving the best (optimal) solution.

Problem-2 Similar to [Problem-1](#), does the following algorithm give the optimal solution?

Algorithm: Merge the files in pairs. That means after the first step, the algorithm produces the $n/2$ intermediate files. For the next step, we need to consider these intermediate files and merge them in pairs and keep going.

Note: Sometimes this algorithm is called 2-way merging. Instead of two files at a time, if we merge K files at a time then we call it K -way merging.

Solution: This algorithm will not produce the optimal solution and consider the previous example for a counter example. As per the above algorithm, we need to merge the first pair of files (10 and 5 size files), the second pair of files (100 and 50) and the third pair of files (20 and 15). As a result we get the following list of files.

$$\{15,150,35\}$$

Similarly, merge the output in pairs and this step produces [below, the third element does not have a pair element, so keep it the same]:

$$\{165,35\}$$

Finally,

$$\{185\}$$

The total cost of merging = Cost of all merging operations = $15 + 150 + 35 + 165 + 185 = 550$. This is much more than 395 (of the previous problem). So, the given algorithm is not giving the best (optimal) solution.

Problem-3 In [Problem-1](#), what is the best way to merge *all the files* into a single file?

Solution: Using the Greedy algorithm we can reduce the total time for merging the given files. Let us consider the following algorithm.

Algorithm:

1. Store file sizes in a priority queue. The key of elements are file lengths.
2. Repeat the following until there is only one file:
 - a. Extract two smallest elements X and Y .
 - b. Merge X and Y and insert this new file in the priority queue.

Variant of same algorithm:

1. Sort the file sizes in ascending order.
2. Repeat the following until there is only one file:
 - a. Take the first two elements (smallest) X and Y .
 - b. Merge X and Y and insert this new file in the sorted list.

To check the above algorithm, let us trace it with the previous example. The given array is:

$$F = \{10, 5, 100, 50, 20, 15\}$$

As per the above algorithm, after sorting the list it becomes: $\{5, 10, 15, 20, 50, 100\}$. We need to merge the two smallest files (5 and 10 size files) and as a result we get the following list of files. In the list below, 15 indicates the cost of merging two files with sizes 10 and 5.

$$\{15, 15, 20, 50, 100\}$$

Similarly, merging the two smallest elements (15 and 15) produces: $\{20, 30, 50, 100\}$. For the subsequent steps the list becomes

$$\begin{aligned} &\{50, 50, 100\} // \text{merging } 20 \text{ and } 30 \\ &\{100, 100\} // \text{merging } 20 \text{ and } 30 \end{aligned}$$

Finally,

$$\{200\}$$

The total cost of merging = Cost of all merging operations = $15 + 30 + 50 + 100 + 200 = 395$. So, this algorithm is producing the optimal solution for this merging problem.

Time Complexity: $O(n \log n)$ time using heaps to find best merging pattern plus the optimal cost of merging the files.

Problem-4 Interval Scheduling Algorithm: Given a set of n intervals $S = \{(start_i, end_i) | 1 \leq i \leq n\}$. Let us assume that we want to find a maximum subset S' of S such that no pair of intervals in S' overlaps. Check whether the following algorithm works or not.

Algorithm:

while (S is not empty) {

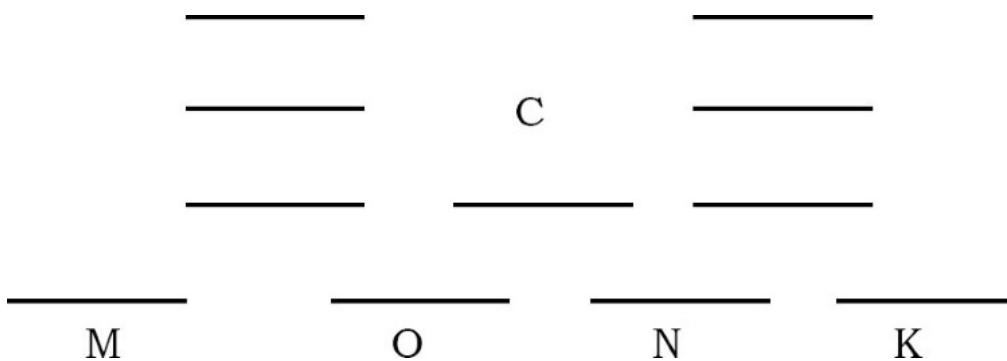
 Select the interval I that overlaps the least number of other intervals.

 Add I to final solution set S' .

 Remove all intervals from S that overlap with I .

}

Solution: This algorithm does not solve the problem of finding a maximum subset of non-overlapping intervals. Consider the following intervals. The optimal solution is $\{M,O,N,K\}$. However, the interval that overlaps with the fewest others is C , and the given algorithm will select C first.



Problem-5 In [Problem-4](#), if we select the interval that starts earliest (also not overlapping with already chosen intervals), does it give the optimal solution?

Solution: No. It will not give the optimal solution. Let us consider the example below. It can be seen that the optimal solution is 4 whereas the given algorithm gives 1.

Optimal Solution



Given Algorithm gives



Problem-6 In [Problem-4](#), if we select the shortest interval (but it is not overlapping the already chosen intervals), does it give the optimal solution?

Solution: This also will not give the optimal solution. Let us consider the example below. It can be seen that the optimal solution is 2 whereas the algorithm gives 1.

Optimal Solution



Current Algorithm gives

Problem-7 For [Problem-4](#), what is the optimal solution?

Solution: Now, let us concentrate on the optimal greedy solution.

Algorithm:

Sort intervals according to the right-most ends [end times];

for every consecutive interval {

- If the left-most end is after the right-most end of the last selected interval then we select this interval
- Otherwise we skip it and go to the next interval

}

Time complexity = Time for sorting + Time for scanning = $O(n \log n + n) = O(n \log n)$.

Problem-8 Consider the following problem.

Input: $S = \{(start_i, end_i) | 1 \leq i \leq n\}$ of intervals. The interval $(start_i, end_i)$ we can treat as a request for a room for a class with time start_i to time end_i.

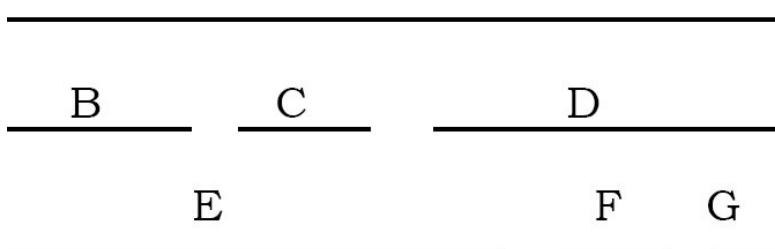
Output: Find an assignment of classes to rooms that uses the fewest number of rooms.

Consider the following iterative algorithm. Assign as many classes as possible to the first room, then assign as many classes as possible to the second room, then assign as many classes as possible to the third room, etc. Does this algorithm give the best solution?

Note: In fact, this problem is similar to the interval scheduling algorithm. The only difference is the application.

Solution: This algorithm does not solve the interval-coloring problem. Consider the following intervals:

A



Maximizing the number of classes in the first room results in having $\{B, C, F, G\}$ in one room, and classes A, D , and E each in their own rooms, for a total of 4. The optimal solution is to put A in one room, $\{B, C, D\}$ in another, and $\{E, F, G\}$ in another, for a total of 3 rooms.

Problem-9 For [Problem-8](#), consider the following algorithm. Process the classes in increasing order of start times. Assume that we are processing class C . If there is a room R such that R has been assigned to an earlier class, and C can be assigned to R without overlapping previously assigned classes, then assign C to R . Otherwise, put C in a new room. Does this algorithm solve the problem?

Solution: This algorithm solves the interval-coloring problem. Note that if the greedy algorithm creates a new room for the current class c_i , then because it examines classes in order of start times, c_i start point must intersect with the last class in all of the current rooms. Thus when greedy creates the last room, n , it is because the start time of the current class intersects with $n - 1$ other classes. But we know that for any single point in any class it can only intersect with at most s other class, so it must then be that $n \leq S$. As s is a lower bound on the total number needed, and greedy is feasible, it is thus also optimal.

Note: For optimal solution refer to [Problem-7](#) and for code refer to [Problem-10](#).

Problem-10 Suppose we are given two arrays $Start[1 .. n]$ and $Finish[1 .. n]$ listing the start and finish times of each class. Our task is to choose the largest possible subset $X \in \{1, 2, \dots, n\}$ so that for any pair $i, j \in X$, either $Start[i] > Finish[j]$ or $Start[j] > Finish[i]$

Solution: Our aim is to finish the first class as early as possible, because that leaves us with the most remaining classes. We scan through the classes in order of finish time, and whenever we encounter a class that doesn't conflict with the latest class so far, then we take that class.

```
int LargestTasks(int Start[], int n, int Finish[]) {
    sort Finish[];
    rearrange Start[] to match;
    count = 1;
    X[count] = 1;
    for (i = 2; i < n; i++) {
        if (Start[i] > Finish[X[count]]) {
            count = count + 1;
            X[count] = i;
        }
    }
    return X[1 .. count];
}
```

This algorithm clearly runs in $O(n \log n)$ time due to sorting.

Problem-11 Consider the making change problem in the country of India. The input to this problem is an integer M . The output should be the minimum number of coins to make M rupees of change. In India, assume the available coins are 1,5,10,20,25,50 rupees. Assume that we have an unlimited number of coins of each type.

For this problem, does the following algorithm produce the optimal solution or not?

Take as many coins as possible from the highest denominations. So for example, to make change for 234 rupees the greedy algorithm would take four 50 rupee coins, one 25 rupee coin, one 5 rupee coin, and four 1 rupee coins.

Solution: The greedy algorithm is not optimal for the problem of making change with the minimum number of coins when the denominations are 1,5,10,20,25, and 50. In order to make 40 rupees, the greedy algorithm would use three coins of 25,10, and 5 rupees. The optimal solution is to use two 20-shilling coins.

Note: For the optimal solution, refer to the [Dynamic Programming](#) chapter.

Problem-12 Let us assume that we are going for a long drive between cities A and B. In preparation for our trip, we have downloaded a map that contains the distances in miles between all the petrol stations on our route. Assume that our car's tanks can hold petrol for n miles. Assume that the value n is given. Suppose we stop at every point. Does it give the best solution?

Solution: Here the algorithm does not produce optimal solution. Obvious Reason: filling at each petrol station does not produce optimal solution.

Problem-13 For problem [Problem-12](#), stop if and only if you don't have enough petrol to make it to the next gas station, and if you stop, fill the tank up all the way. Prove or disprove that this algorithm correctly solves the problem.

Solution: The greedy approach works: We start our trip from A with a full tank. We check our map to determine the farthest petrol station on our route within n miles. We stop at that petrol station, fill up our tank and check our map again to determine the farthest petrol station on our route within n miles from this stop. Repeat the process until we get to B .

Note: For code, refer to [Dynamic Programming](#) chapter.

Problem-14 Fractional Knapsack problem: Given items t_1, t_2, \dots, t_n (items we might want to carry in our backpack) with associated weights s_1, s_2, \dots, s_n and benefit values v_1, v_2, \dots, v_n , how can we maximize the total benefit considering that we are subject to an absolute weight limit C ?

Solution:

Algorithm:

- 1) Compute value per size density for each item $d_i = \frac{v_i}{s_i}$.
- 2) Sort each item by its value density.
- 3) Take as much as possible of the density item not already in the bag

Time Complexity: $O(n \log n)$ for sorting and $O(n)$ for greedy selections.

Note: The items can be entered into a priority queue and retrieved one by one until either the bag is full or all items have been selected. This actually has a better runtime of $O(n + c \log n)$ where c is the number of items that actually get selected in the solution. There is a savings in runtime if $c = O(n)$, but otherwise there is no change in the complexity.

Problem-15 Number of railway-platforms: At a railway station, we have a time-table with the trains' arrivals and departures. We need to find the minimum number of platforms so that all the trains can be accommodated as per their schedule.

Example: The timetable is as given below, the answer is 3. Otherwise, the railway station will not be able to accommodate all the trains.

Rail	Arrival	Departure
Rail A	0900 hrs	0930 hrs
Rail B	0915 hrs	1300 hrs
Rail C	1030 hrs	1100 hrs
Rail D	1045 hrs	1145 hrs

Solution: Let's take the same example as described above. Calculating the number of platforms is done by determining the maximum number of trains at the railway station at any time.

First, sort all the arrival(A) and departure(D) times in an array. Then, save the corresponding arrivals and departures in the array also. After sorting, our array will look like this:

0900	0915	0930	1030	1045	1100	1145	1300
A	A	D	A	A	D	D	D

Now modify the array by placing 1 for A and -1 for D . The new array will look like this:

1	1	-1	1	1	-1	-1	-1
---	---	----	---	---	----	----	----

Finally make a cumulative array out of this:

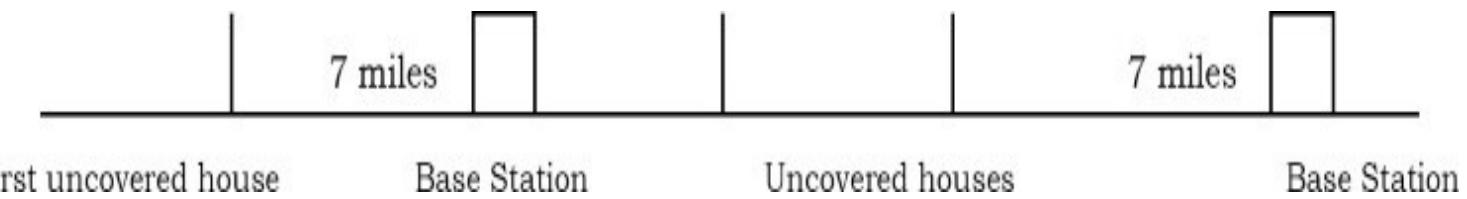
1	2	1	2	3	2	1	0
---	---	---	---	---	---	---	---

Our solution will be the maximum value in this array. Here it is 3.

Note: If we have a train arriving and another departing at the same time, then put the departure time first in the sorted array.

Problem-16 Consider a country with very long roads and houses along the road. Assume that the residents of all houses use cell phones. We want to place cell phone towers along the road, and each cell phone tower covers a range of 7 kilometers. Create an efficient algorithm that allow for the fewest cell phone towers.

Solution:



The algorithm to locate the least number of cell phone towers:

- 1) Start from the beginning of the road
- 2) Find the first uncovered house on the road
- 3) If there is no such house, terminate this algorithm. Otherwise, go to next step
- 4) Locate a cell phone tower 7 miles away after we find this house along the road
- 5) Go to step 2

Problem-17 Preparing Songs Cassette: Suppose we have a set of n songs and want to store these on a tape. In the future, users will want to read those songs from the tape. Reading a song from a tape is not like reading from a disk; first we have to fast-forward past all the other songs, and that takes a significant amount of time. Let $A[1 .. n]$ be an array listing the lengths of each song, specifically, song i has length $A[i]$. If the songs are stored in order from 1 to n , then the cost of accessing the k^{th} song is:

$$C(k) = \sum_{i=1}^k A[i]$$

The cost reflects the fact that before we read song k we must first scan past all the earlier songs on the tape. If we change the order of the songs on the tape, we change the cost of accessing the songs, with the result that some songs become more expensive to read, but others become cheaper. Different song orders are likely to result in different expected costs. If we assume that each song is equally likely to be accessed, which order should we use if we want the expected cost to be as small as possible?

Solution: The answer is simple. We should store the songs in the order from shortest to longest. Storing the short songs at the beginning reduces the forwarding times for the remaining jobs.

Problem-18 Let us consider a set of events at *HITEX (Hyderabad Convention Center)*. Assume that there are n events where each takes one unit of time. Event i will provide a profit of $P[i]$ rupees ($P[i] > 0$) if started at or before time $T[i]$, where $T[i]$ is an arbitrary number. If an event is not started by $T[i]$ then there is no benefit in scheduling it at all. All events can start as early as time 0. Give the efficient algorithm to find a schedule that maximizes the profit.

Solution:

Algorithm:

- Sort the jobs according to $\text{floor}(T[i])$ (sorted from largest to smallest).
- Let time t be the current time being considered (where initially $t = \text{floor}(T[i])$).
- All jobs i where $\text{floor}(T[i]) = t$ are inserted into a priority queue with the profit g_i used as the key.
- A *DeleteMax* is performed to select the job to run at time t .
- Then t is decremented and the process is continued.

Clearly the time complexity is $O(n \log n)$. The sort takes $O(n \log n)$ and there are at most n insert and *DeleteMax* operations performed on the priority queue, each of which takes $O(\log n)$ time.

Problem-19 Let us consider a customer-care server (say, mobile customer-care) with n customers to be served in the queue. For simplicity assume that the service time required by each customer is known in advance and it is w_t minutes for customer i . So if, for example, the customers are served in order of increasing i , then the i^{th} customer has to wait: $\sum_{j=1}^{n-1} w_j$ minutes. The total waiting time of all customers can be given as $= \sum_{i=1}^n \sum_{j=1}^{i-1} w_j$. What is the best way to serve the customers so that the total waiting time can be reduced?

Solution: This problem can be easily solved using greedy technique. Since our objective is to reduce the total waiting time, what we can do is, select the customer whose service time is less. That means, if we process the customers in the increasing order of service time then we can reduce the total waiting time.

Time Complexity: $O(n \log n)$.

CHAPTER

18



DIVIDE AND CONQUER ALGORITHMS

18.1 Introduction

In the *Greedy* chapter, we have seen that for many problems the Greedy strategy failed to provide optimal solutions. Among those problems, there are some that can be easily solved by using the *Divide and Conquer* (D & C) technique. Divide and Conquer is an important algorithm design technique based on recursion.

The D & C algorithm works by recursively breaking down a problem into two or more sub problems of the same type, until they become simple enough to be solved directly. The solutions to the sub problems are then combined to give a solution to the original problem.

18.2 What is Divide and Conquer Strategy?

The D & C strategy solves a problem by:

- 1) *Divide*: Breaking the problem into sub problems that are themselves smaller instances of the same type of problem.
- 2) *Recursion*: Recursively solving these sub problems.

- 3) *Conquer*: Appropriately combining their answers.

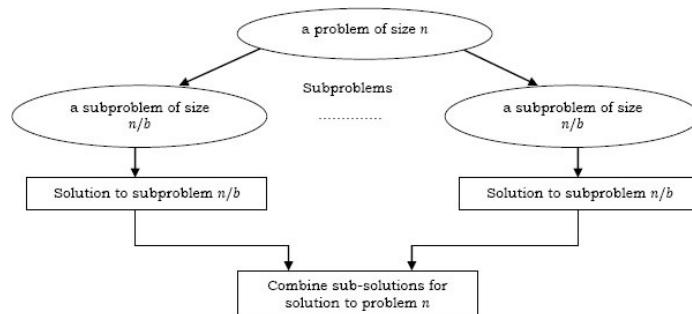
18.3 Does Divide and Conquer Always Work?

It's not possible to solve all the problems with the Divide & Conquer technique. As per the definition of D & C, the recursion solves the subproblems which are of the same type. For all problems it is not possible to find the subproblems which are the same size and D & C is not a choice for all problems.

18.4 Divide and Conquer Visualization

For better understanding, consider the following visualization. Assume that n is the size of the original problem. As described above, we can see that the problem is divided into sub problems with each of size n/b (for some constant b). We solve the sub problems recursively and combine their solutions to get the solution for the original problem.

```
DivideAndConquer ( P ) {
    if( small ( P ) )
        // P is very small so that a solution is obvious
        return solution ( n );
    divide the problem P into k sub problems P1, P2, ..., Pk;
    return (
        Combine (
            DivideAndConquer ( P1 ),
            DivideAndConquer ( P2 ),
            ...
            DivideAndConquer ( Pk )
        )
    );
}
```



18.5 Understanding Divide and Conquer

For a clear understanding of D & C, let us consider a story. There was an old man who was a rich farmer and had seven sons. He was afraid that when he died, his land and his possessions would be divided among his seven sons, and that they would quarrel with one another.

So he gathered them together and showed them seven sticks that he had tied together and told them that anyone who could break the bundle would inherit everything. They all tried, but no one could break the bundle. Then the old man untied the bundle and broke the sticks one by one. The brothers decided that they should stay together and work together and succeed together. The moral for problem solvers is different. If we can't solve the problem, divide it into parts, and solve one part at a time.

In earlier chapters we have already solved many problems based on D & C strategy: like Binary Search, Merge Sort, Quick Sort, etc.... Refer to those topics to get an idea of how D & C works. Below are a few other real-time problems which can easily be solved with D & C strategy. For all these problems we can find the subproblems which are similar to the original problem.

- Looking for a name in a phone book: We have a phone book with names in alphabetical order. Given a name, how do we find whether that name is there in the phone book or not?
- Breaking a stone into dust: We want to convert a stone into dust (very small stones).
- Finding the exit in a hotel: We are at the end of a very long hotel lobby with a long series of doors, with one door next to us. We are looking for the door that leads to the exit.
- Finding our car in a parking lot.

18.6 Advantages of Divide and Conquer

Solving difficult problems: D & C is a powerful method for solving difficult problems. As an example, consider the Tower of Hanoi problem. This requires breaking the problem into subproblems, solving the trivial cases and combining the subproblems to solve the original problem. Dividing the problem into subproblems so that subproblems can be combined again is a major difficulty in designing a new algorithm. For many such problems D & C provides a simple solution.

Parallelism: Since D & C allows us to solve the subproblems independently, this allows for execution in multiprocessor machines, especially shared-memory systems where the communication of data between processors does not need to be planned in advance, because different subproblems can be executed on different processors.

Memory access: D & C algorithms naturally tend to make efficient use of memory caches. This is because once a subproblem is small, all its subproblems can be solved within the cache, without

accessing the slower main memory.

18.7 Disadvantages of Divide and Conquer

One disadvantage of the *D & C* approach is that recursion is slow. This is because of the overhead of the repeated subproblem calls. Also, the *D & C* approach needs stack for storing the calls (the state at each point in the recursion). Actually this depends upon the implementation style. With large enough recursive base cases, the overhead of recursion can become negligible for many problems.

Another problem with *D & C* is that, for some problems, it may be more complicated than an iterative approach. For example, to add n numbers, a simple loop to add them up in sequence is much easier than a *D & C* approach that breaks the set of numbers into two halves, adds them recursively, and then adds the sums.

18.8 Master Theorem

As stated above, in the *D & C* method, we solve the sub problems recursively. All problems are generally defined in terms of recursive definitions. These recursive problems can easily be solved using Master theorem. For details on Master theorem, refer to the *Introduction to Analysis of Algorithms* chapter. Just for continuity, let us reconsider the Master theorem.

If the recurrence is of the form $T(n) = aT\left(\frac{n}{b}\right) + \Theta(n^k \log^p n)$, where $a \geq 1$, $b > 1$, $k \geq 0$ and p is a real number, then the complexity can be directly given as:

- 1) If $a > b^k$, then $T(n) = \Theta(n^{\log_b^a})$
- 2) If $a = b^k$
 - a. If $p > -1$, then $T(n) = \Theta(n^{\log_b^a} \log^{p+1} n)$
 - b. If $p = -1$, then $T(n) = \Theta(n^{\log_b^a} \log \log n)$
 - c. If $p < -1$, then $T(n) = \Theta(n^{\log_b^a})$
- 3) If $a < b^k$
 - a. If $p > 0$, then $T(n) = \Theta(n^k \log^p n)$
 - b. If $p < 0$, then $T(n) = O(n^k)$

18.9 Divide and Conquer Applications

- Binary Search
- Merge Sort and Quick Sort

- Median Finding
- Min and Max Finding
- Matrix Multiplication
- Closest Pair problem

18.10 Divide and Conquer: Problems & Solutions

Problem-1 Let us consider an algorithm A which solves problems by dividing them into five subproblems of half the size, recursively solving each subproblem, and then combining the solutions in linear time. What is the complexity of this algorithm?

Solution: Let us assume that the input size is n and $T(n)$ defines the solution to the given problem. As per the description, the algorithm divides the problem into 5 sub problems with each of size $\frac{n}{2}$. So we need to solve $5T\left(\frac{n}{2}\right)$ subproblems. After solving these sub problems, the given array (linear time) is scanned to combine these solutions. The total recurrence algorithm for this problem can be given as: $T(n) = 5T\left(\frac{n}{2}\right) + O(n)$. Using the Master theorem (of D & C), we get the complexity $O(n^{\log_2 5}) \approx O(n^{2+}) \approx O(n^3)$.

Problem-2 Similar to [Problem-1](#), an algorithm B solves problems of size n by recursively solving two subproblems of size $n - 1$ and then combining the solutions in constant time. What is the complexity of this algorithm?

Solution: Let us assume that the input size is n and $T(n)$ defines the solution to the given problem. As per the description of algorithm we divide the problem into 2 sub problems with each of size $n - 1$. So we have to solve $2T(n - 1)$ sub problems. After solving these sub problems, the algorithm takes only a constant time to combine these solutions. The total recurrence algorithm for this problem can be given as:

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

Using Master theorem (of *Subtract and Conquer*), we get the complexity as $O\left(n^0 2^{\frac{n}{1}}\right) = O(2^n)$. (Refer to [Introduction](#) chapter for more details).

Problem-3 Again similar to [Problem-1](#), another algorithm C solves problems of size n by dividing them into nine subproblems of size $\frac{n}{3}$, recursively solving each subproblem, and then combining the solutions in $O(n^2)$ time. What is the complexity of this algorithm?

Solution: Let us assume that input size is n and $T(n)$ defines the solution to the given problem. As per the description of algorithm we divide the problem into 9 sub problems with each of size $\frac{n}{3}$. So we need to solve $9T\left(\frac{n}{3}\right)$ sub problems. After solving the sub problems, the algorithm takes

quadratic time to combine these solutions. The total recurrence algorithm for this problem can be given as: $T(n) = 9T\left(\frac{n}{3}\right) + O(n^2)$. Using D & C Master theorem, we get the complexity as $O(n^2 \log n)$.

Problem-4 Write a recurrence and solve it.

```
void function(n) {
    if(n > 1) {
        printf("*");
        function( $\frac{n}{2}$ );
        function( $\frac{n}{2}$ );
    }
}
```

Solution: Let us assume that input size is n and $T(n)$ defines the solution to the given problem. As per the given code, after printing the character and dividing the problem into 2 subproblems with each of size $\frac{n}{2}$ and solving them. So we need to solve $2T\left(\frac{n}{2}\right)$ subproblems. After solving these subproblems, the algorithm is not doing anything for combining the solutions. The total recurrence algorithm for this problem can be given as:

$$T(n) = 2T\left(\frac{n}{2}\right) + O(1)$$

Using Master theorem (of D & C), we get the complexity as $O(n^{\log_2 2}) \approx O(n^1) = O(n)$.

Problem-5 Given an array, give an algorithm for finding the maximum and minimum.

Solution: Refer [Selection Algorithms](#) chapter.

Problem-6 Discuss Binary Search and its complexity.

Solution: Refer [Searching](#) chapter for discussion on Binary Search.

Analysis: Let us assume that input size is n and $T(n)$ defines the solution to the given problem. The elements are in sorted order. In binary search we take the middle element and check whether the element to be searched is equal to that element or not. If it is equal then we return that element.

If the element to be searched is greater than the middle element then we consider the right sub-array for finding the element and discard the left sub-array. Similarly, if the element to be searched is less than the middle element then we consider the left sub-array for finding the element and discard the right sub-array.

What this means is, in both the cases we are discarding half of the sub-array and considering the

remaining half only. Also, at every iteration we are dividing the elements into two equal halves.

As per the above discussion every time we divide the problem into 2 sub problems with each of size $\frac{n}{2}$ and solve one $T\left(\frac{n}{2}\right)$ sub problem. The total recurrence algorithm for this problem can be given as:

$$T(n) = 2T\left(\frac{n}{2}\right) + O(1)$$

Using Master theorem (of D & C), we get the complexity as $O(\log n)$.

Problem-7 Consider the modified version of binary search. Let us assume that the array is divided into 3 equal parts (ternary search) instead of 2 equal parts. Write the recurrence for this ternary search and find its complexity.

Solution: From the discussion on [Problem-5](#), binary search has the recurrence relation: $T(n) = T\left(\frac{n}{2}\right) + O(1)$. Similar to the [Problem-5](#) discussion, instead of 2 in the recurrence relation we use “3”. That indicates that we are dividing the array into 3 sub-arrays with equal size and considering only one of them. So, the recurrence for the ternary search can be given as:

$$T(n) = T\left(\frac{n}{3}\right) + O(1)$$

Using Master theorem (of D & C), we get the complexity as $O(\log_3^n) \approx O(\log n) \approx O(\log n)$ (we don't have to worry about the base of \log as they are constants).

Problem-8 In [Problem-5](#), what if we divide the array into two sets of sizes approximately one-third and two-thirds.

Solution: We now consider a slightly modified version of ternary search in which only one comparison is made, which creates two partitions, one of roughly $\frac{n}{3}$ elements and the other of $\frac{2n}{3}$. Here the worst case comes when the recursive call is on the larger $\frac{2n}{3}$ element part. So the recurrence corresponding to this worst case is:

$$T(n) = T\left(\frac{2n}{3}\right) + O(1)$$

Using Master theorem (of D & C), we get the complexity as $O(\log n)$. It is interesting to note that we will get the same results for general k -ary search (as long as k is a fixed constant which does not depend on n) as n approaches infinity.

Problem-9 Discuss Merge Sort and its complexity.

Solution: Refer to [Sorting](#) chapter for discussion on Merge Sort. In Merge Sort, if the number of elements are greater than 1, then divide them into two equal subsets, the algorithm is recursively

invoked on the subsets, and the returned sorted subsets are merged to provide a sorted list of the original set. The recurrence equation of the Merge Sort algorithm is:

$$T(n) = \begin{cases} 2T\left(\frac{n}{2}\right) + O(n), & \text{if } n > 1 \\ 0, & \text{if } n = 1 \end{cases}$$

If we solve this recurrence using D & C Master theorem it gives $O(n\log n)$ complexity.

Problem-10 Discuss Quick Sort and its complexity.

Solution: Refer to [Sorting](#) chapter for discussion on Quick Sort. For Quick Sort we have different complexities for best case and worst case.

Best Case: In *Quick Sort*, if the number of elements is greater than 1 then they are divided into two equal subsets, and the algorithm is recursively invoked on the subsets. After solving the sub problems we don't need to combine them. This is because in *Quick Sort* they are already in sorted order. But, we need to scan the complete elements to partition the elements. The recurrence equation of *Quick Sort* best case is

$$T(n) = \begin{cases} 2T\left(\frac{n}{2}\right) + O(n), & \text{if } n > 1 \\ 0, & \text{if } n = 1 \end{cases}$$

If we solve this recurrence using Master theorem of D & C gives $O(n\log n)$ complexity.

Worst Case: In the worst case, Quick Sort divides the input elements into two sets and one of them contains only one element. That means other set has $n - 1$ elements to be sorted. Let us assume that the input size is n and $T(n)$ defines the solution to the given problem. So we need to solve $T(n - 1)$, $T(1)$ subproblems. But to divide the input into two sets Quick Sort needs one scan of the input elements (this takes $O(n)$).

After solving these sub problems the algorithm takes only a constant time to combine these solutions. The total recurrence algorithm for this problem can be given as:

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

This is clearly a summation recurrence equation. So, $T(n) = \frac{n(n+1)}{2} = O(n^2)$.

Note: For the average case analysis, refer to [Sorting](#) chapter.

Problem-11 Given an infinite array in which the first n cells contain integers in sorted order and the rest of the cells are filled with some special symbol (say, \$). Assume we do not know the n value. Give an algorithm that takes an integer K as input and finds a position in the array containing K , if such a position exists, in $O(\log n)$ time.

Solution: Since we need an $O(\log n)$ algorithm, we should not search for all the elements of the given list (which gives $O(n)$ complexity). To get $O(\log n)$ complexity one possibility is to use binary search. But in the given scenario we cannot use binary search as we do not know the end of the list. Our first problem is to find the end of the list. To do that, we can start at the first element and keep searching with doubled index. That means we first search at index 1 then, 2,4,8 ...

```
int FindInInfiniteSeries(int A[]) {
    int mid, l = r = 1;
    while( A[r] != '$' ) {
        l = r;
        r = r * 2;
    }
    while( (r - l > 1) {
        mid = (r - l)/2 + l;
        if( A[mid] == '$' )
            r = mid;
        else
            l = mid;
    }
}
```

It is clear that, once we have identified a possible interval $A[i, \dots, 2i]$ in which K might be, its length is at most n (since we have only n numbers in the array A), so searching for K using binary search takes $O(\log n)$ time.

Problem-12 Given a sorted array of non-repeated integers $A[1.. n]$, check whether there is an index i for which $A[i] = i$. Give a divide-and-conquer algorithm that runs in time $O(\log n)$.

Solution: We can't use binary search on the array as it is. If we want to keep the $O(\log n)$ property of the solution we have to implement our own binary search. If we modify the array (in place or in a copy) and subtract i from $A[i]$, we can then use binary search. The complexity for doing so is $O(n)$.

Problem-13 We are given two sorted lists of size n . Give an algorithm for finding the median element in the union of the two lists.

Solution: We use the Merge Sort process. Use *merge* procedure of merge sort (refer to [Sorting](#) chapter). Keep track of the count while comparing elements of two arrays. If the count becomes n (since there are $2n$ elements), we have reached the median. Take the average of the elements at indexes $n - 1$ and n in the merged array.

Time Complexity: $O(n)$.

Problem-14 Can we give the algorithm if the size of the two lists are not the same?

Solution: The solution is similar to the previous problem. Let us assume that the lengths of two lists are m and n . In this case we need to stop when the counter reaches $(m + n)/2$.

Time Complexity: $O((m + n)/2)$.

Problem-15 Can we improve the time complexity of [Problem-13](#) to $O(\log n)$?

Solution: Yes, using the D & C approach. Let us assume that the given two lists are $L1$ and $L2$.

Algorithm:

1. Find the medians of the given sorted input arrays $L1[]$ and $L2[]$. Assume that those medians are $m1$ and $m2$.
2. If $m1$ and $m2$ are equal then return $m1$ (or $m2$).
3. If $m1$ is greater than $m2$, then the final median will be below two sub arrays.
4. From first element of $L1$ to $m1$.
5. From $m2$ to last element of $L2$.
6. If $m2$ is greater than $m1$, then median is present in one of the two sub arrays below.
7. From $m1$ to last element of $L1$.
8. From first element of $L2$ to $m2$.
9. Repeat the above process until the size of both the sub arrays becomes 2.
10. If size of the two arrays is 2, then use the formula below to get the median.
11. Median = $(\max(L1[0], L2[0]) + \min(L1[1], L2[1]))/2$

Time Complexity: $O(\log n)$ since we are considering only half of the input and throwing the remaining half.

Problem-16 Given an input array A . Let us assume that there can be duplicates in the list. Now search for an element in the list in such a way that we get the highest index if there are duplicates.

Solution: Refer to [Searching](#) chapter.

Problem-17 Discuss Strassen's Matrix Multiplication Algorithm using Divide and Conquer. That means, given two $n \times n$ matrices, A and B , compute the $n \times n$ matrix $C = A \times B$, where the elements of C are given by

$$C_{i,j} = \sum_{k=0}^{n-1} A_{i,k} B_{k,j}$$

Solution: Before Strassen's algorithm, first let us see the basic divide and conquer algorithm. The general approach we follow for solving this problem is given below. To determine, $C[i,j]$ we need to multiply the i^{th} row of A with j^{th} column of B .

```
// Initialize C.
for i = 1 to n
    for j = 1 to n
        for k = 1 to n
            C[i, j] += A[i, k] * B[k, j];
```

The matrix multiplication problem can be solved with the D & C technique. To implement a D & C algorithm we need to break the given problem into several subproblems that are similar to the original one. In this instance we view each of the $n \times n$ matrices as a 2×2 matrix, the elements of which are $\frac{n}{2} \times \frac{n}{2}$ submatrices. So, the original matrix multiplication, $C = A \times B$ can be written as:

$$\begin{bmatrix} C_{1,1} & C_{1,2} \\ C_{2,1} & C_{2,2} \end{bmatrix} = \begin{bmatrix} A_{1,1} & A_{1,2} \\ A_{2,1} & A_{2,2} \end{bmatrix} \times \begin{bmatrix} B_{1,1} & B_{1,2} \\ B_{2,1} & B_{2,2} \end{bmatrix}$$

where each $A_{i,j}$, $B_{i,j}$, and $C_{i,j}$ is a $\frac{n}{2} \times \frac{n}{2}$ matrix.

From the given definition of $C_{i,j}$, we get that the result sub matrices can be computed as follows:

$$\begin{aligned} C_{1,1} &= A_{1,1} \times B_{1,1} + A_{1,2} \times B_{2,1} \\ C_{1,2} &= A_{1,1} \times B_{1,2} + A_{1,2} \times B_{2,2} \\ C_{2,1} &= A_{2,1} \times B_{1,1} + A_{2,2} \times B_{2,1} \\ C_{2,2} &= A_{2,1} \times B_{1,2} + A_{2,2} \times B_{2,2} \end{aligned}$$

Here the symbols $+$ and \times are taken to mean addition and multiplication (respectively) of $\frac{n}{2} \times \frac{n}{2}$ matrices.

In order to compute the original $n \times n$ matrix multiplication we must compute eight $\frac{n}{2} \times \frac{n}{2}$ matrix products (*divide*) followed by four $\frac{n}{2} \times \frac{n}{2}$ matrix sums (*conquer*). Since matrix addition is an $O(n^2)$ operation, the total running time for the multiplication operation is given by the recurrence:

$$T(n) = \begin{cases} O(1) & , \text{for } n = 1 \\ 8T\left(\frac{n}{2}\right) + O(n^2) & , \text{for } n > 1 \end{cases}$$

Using master theorem, we get $T(n) = O(n^3)$.

Fortunately, it turns out that one of the eight matrix multiplications is redundant (found by Strassen). Consider the following series of seven $\frac{n}{2} \times \frac{n}{2}$ matrices:

$$\begin{aligned}
M_0 &= (A_{1,1} + A_{2,2}) \times (B_{1,1} + B_{2,2}) \\
M_1 &= (A_{1,2} - A_{2,2}) \times (B_{2,1} + B_{2,2}) \\
M_2 &= (A_{1,1} - A_{2,1}) \times (B_{1,1} + B_{1,2}) \\
M_3 &= (A_{1,1} + A_{1,2}) \times B_{2,2} \\
M_4 &= A_{1,1} \times (B_{1,2} - B_{2,2}) \\
M_5 &= A_{2,2} \times (B_{2,1} - B_{1,1}) \\
M_6 &= (A_{2,1} + A_{2,2}) \times B_{1,1}
\end{aligned}$$

Each equation above has only one multiplication. Ten additions and seven multiplications are required to compute M_0 through M_6 . Given M_0 through M_6 , we can compute the elements of the product matrix C as follows:

$$\begin{aligned}
C_{1,1} &= M_0 + M_1 - M_3 + M_5 \\
C_{1,2} &= M_3 + M_4 \\
C_{2,1} &= M_5 + M_6 \\
C_{2,2} &= M_0 - M_2 + M_4 - M_6
\end{aligned}$$

This approach requires seven $\frac{n}{2} \times \frac{n}{2}$ matrix multiplications and 18 $\frac{n}{2} \times \frac{n}{2}$ additions. Therefore, the worst-case running time is given by the following recurrence:

$$T(n) = \begin{cases} O(1) & , \text{for } n = 1 \\ 7T\left(\frac{n}{2}\right) + O(n^2) & , \text{for } n = 1 \end{cases}$$

Using master theorem, we get, $T(n) = O(n^{\log_2 7}) = O(n^{2.81})$.

Problem-18 Stock Pricing Problem: Consider the stock price of CareerMonk.com in n consecutive days. That means the input consists of an array with stock prices of the company. We know that the stock price will not be the same on all the days. In the input stock prices there may be dates where the stock is high when we can sell the current holdings, and there may be days when we can buy the stock. Now our problem is to find the day on which we can buy the stock and the day on which we can sell the stock so that we can make maximum profit.

Solution: As given in the problem, let us assume that the input is an array with stock prices [integers]. Let us say the given array is $A[1], \dots, A[n]$. From this array we have to find two days [one for buy and one for sell] in such a way that we can make maximum profit. Also, another point to make is that the buy date should be before sell date. One simple approach is to look at all possible buy and sell dates.

```

void StockStrategy(int A[], int n, int *buyDateIndex, int *sellDateIndex) {
    int j, profit=0;
    *buyDateIndex = 0; *sellDateIndex = 0;
    for (int i = 1; i < n; i++) //indicates buy date
        //indicates sell date
        for(j = i; j < n; j++)
            if(A[j] - A[i] > profit) {
                profit = A[j] - A[i];
                *buyDateIndex = i;
                *sellDateIndex = j;
            }
}

```

The two nested loops take $n(n + 1)/2$ computations, so this takes time $\Theta(n^2)$.

Problem-19 For [Problem-18](#), can we improve the time complexity?

Solution: Yes, by opting for the Divide-and-Conquer $\Theta(n \log n)$ solution. Divide the input list into two parts and recursively find the solution in both the parts. Here, we get three cases:

- *buyDateIndex* and *sellDateIndex* both are in the earlier time period.
- *buyDateIndex* and *sellDateIndex* both are in the later time period.
- *buyDateIndex* is in the earlier part and *sellDateIndex* is in the later part of the time period.

The first two cases can be solved with recursion. The third case needs care. This is because *buyDateIndex* is one side and *sellDateIndex* is on other side. In this case we need to find the minimum and maximum prices in the two sub-parts and this we can solve in linear-time.

```

void StockStrategy(int A[], int left, int right) {
    //Declare the necessary variables;
    if(left + 1 = right)
        return (0, left, left);
    mid = left + (right - left) / 2;

    (profitLeft, buyDateIndexLeft, sellDateIndexLeft) = StockStrategy(A, left, mid);
    (profitRight, buyDateIndexRight, sellDateIndexRight) = StockStrategy(A, mid, right);

    minLeft = Min(A, left, mid);
    maxRight = Max(A, mid, right);
    profit = A[maxRight] - A[minLeft];

    if(profitLeft > max(profitRight, profit))
        return (profitLeft, buyDateIndexLeft, sellDateIndexLeft);
    else if(profitRight > max(profitLeft, profit))
        return (profitRight, buyDateIndexRight, sellDateIndexRight);
    else return (profit, minLeft, maxRight);
}

```

Algorithm *StockStrategy* is used recursively on two problems of half the size of the input, and in addition $\Theta(n)$ time is spent searching for the maximum and minimum prices. So the time complexity is characterized by the recurrence $T(n) = 2T(n/2) + \Theta(n)$ and by the Master theorem we get $O(n\log n)$.

Problem-20 We are testing “unbreakable” laptops and our goal is to find out how unbreakable they really are. In particular, we work in an n -story building and want to find out the lowest floor from which we can drop the laptop without breaking it (call this “the ceiling”). Suppose we are given two laptops and want to find the highest ceiling possible. Give an algorithm that minimizes the number of tries we need to make $f(n)$ (hopefully, $f(n)$ is sub-linear, as a linear $f(n)$ yields a trivial solution).

Solution: For the given problem, we cannot use binary search as we cannot divide the problem and solve it recursively. Let us take an example for understanding the scenario. Let us say 14 is the answer. That means we need 14 drops to find the answer. First we drop from height 14, and if it breaks we try all floors from 1 to 13. If it doesn’t break then we are left 13 drops, so we will drop it from $14 + 13 + 1 = 28^{th}$ floor. The reason being if it breaks at the 28^{th} floor we can try all the floors from 15 to 27 in 12 drops (total of 14 drops). If it did not break, then we are left with 11 drops and we can try to figure out the floor in 14 drops.

From the above example, it can be seen that we first tried with a gap of 14 floors, and then followed by 13 floors, then 12 and so on. So if the answer is k then we are trying the intervals at $k, k - 1, k - 2 \dots 1$. Given that the number of floors is n , we have to relate these two. Since the maximum floor from which we can try is n , the total skips should be less than n . This gives:

$$\begin{aligned}
 k + (k - 1) + (k - 2) + \cdots + 1 &\leq n \\
 \frac{k(k + 1)}{2} &\leq n \\
 k &\leq \sqrt{n}
 \end{aligned}$$

Complexity of this process is $O(\sqrt{n})$.

Problem-21 Given n numbers, check if any two are equal.

Solution: Refer to [Searching](#) chapter.

Problem-22 Give an algorithm to find out if an integer is a square? E.g. 16 is, 15 isn't.

Solution: Initially let us say $i = 2$. Compute the value $i \times i$ and see if it is equal to the given number. If it is equal then we are done; otherwise increment the i value. Continue this process until we reach $i \times i$ greater than or equal to the given number.

Time Complexity: $O(\sqrt{n})$. Space Complexity: $O(1)$.

Problem-23 Given an array of $2n$ integers in the following format $a_1\ a_2\ a_3\ \dots\ a_n\ b_1\ b_2\ b_3\ \dots\ b_n$. Shuffle the array to $a_1\ b_1\ a_2\ b_2\ a_3\ b_3\ \dots\ a_n\ b_n$ without any extra memory [MA].

Solution: Let us take an example (for brute force solution refer to [Searching](#) chapter)

1. Start with the array: $a_1\ a_2\ a_3\ a_4\ b_1\ b_2\ b_3\ b_4$
2. Split the array into two halves: $a_1\ a_2\ a_3\ a_4 : b_1\ b_2\ b_3\ b_4$
3. Exchange elements around the center: exchange $a_3\ a_4$ with $b_1\ b_2$ you get: $a_1\ a_2\ b_1\ b_2\ a_3\ a_4\ b_3\ b_4$
4. Split $a_1\ a_2\ b_1\ b_2$ into $a_1\ a_2 : b_1\ b_2$ then split $a_3\ a_4\ b_3\ b_4$ into $a_3\ a_4 : b_3\ b_4$
5. Exchange elements around the center for each subarray you get: $a_1\ b_1\ a_2\ b_2$ and $a_3\ b_3\ a_4\ b_4$

Please note that this solution only handles the case when $n = 2^i$ where $i = 0, 1, 2, 3$, etc. In our example $n = 2^2 = 4$ which makes it easy to recursively split the array into two halves. The basic idea behind swapping elements around the center before calling the recursive function is to produce smaller size problems. A solution with linear time complexity may be achieved if the elements are of a specific nature. For example you can calculate the new position of the element using the value of the element itself. This is a hashing technique.

```

void ShuffleArray(int A[], int l, int r) {
    //Array center
    int c = l + (r-l)/2, q = l + l + (c-l)/2;
    if(l == r) //Base case when the array has only one element
        return;
    for (int k = 1, i = q; i <= c; i++, k++) {
        //Swap elements around the center
        int tmp = A[i]; A[i] = A[c + k]; A[c + k] = tmp;
    }
    ShuffleArray(A, l, c);           //Recursively call the function on the left and right
    ShuffleArray(A, c + 1, r); );   //Recursively call the function on the right
}

```

Time Complexity: $O(n \log n)$.

Problem-24 Nuts and Bolts Problem: Given a set of n nuts of different sizes and n bolts such that there is a one-to-one correspondence between the nuts and the bolts, find for each nut its corresponding bolt. Assume that we can only compare nuts to bolts (cannot compare nuts to nuts and bolts to bolts).

Solution: Refer to [Sorting](#) chapter.

Problem-25 Maximum Value Contiguous Subsequence: Given a sequence of n numbers $A(1) \dots A(n)$, give an algorithm for finding a contiguous subsequence $A(i) \dots A(j)$ for which the sum of elements in the subsequence is maximum. **Example :** $\{-2, 11, -4, 13, -5, 2\} \rightarrow 20$ and $\{1, -3, 4, -2, -1, 6\} \rightarrow 7$.

Solution: Divide this input into two halves. The maximum contiguous subsequence sum can occur in one of 3 ways:

- Case 1: It can be completely in the first half
- Case 2: It can be completely in the second half
- Case 3: It begins in the first half and ends in the second half

We begin by looking at case 3. To avoid the nested loop that results from considering all $n/2$ starting points and $n/2$ ending points independently, replace two nested loops with two consecutive loops. The consecutive loops, each of size $n/2$, combine to require only linear work. Any contiguous subsequence that begins in the first half and ends in the second half must include both the last element of the first half and the first element of the second half. What we can do in cases 1 and 2 is apply the same strategy of dividing into more halves. In summary, we do the following:

1. Recursively compute the maximum contiguous subsequence that resides entirely in the first half.
2. Recursively compute the maximum contiguous subsequence that resides entirely in the

second half.

3. Compute, via two consecutive loops, the maximum contiguous subsequence sum that begins in the first half but ends in the second half.
4. Choose the largest of the three sums.

```
int MaxSumRec(int A[], int left, int right) {  
    int MaxLeftBorderSum = 0, MaxRightBorderSum = 0, LeftBorderSum = 0, RightBorderSum = 0;  
    int mid = left + (right - left) / 2;  
    if(left == right) // Base Case  
        return A[left] > 0 ? A[left] : 0;  
    int MaxLeftSum = MaxSumRec(A, left, mid);  
    int MaxRightSum = MaxSumRec(A, mid + 1, right);  
    for (int i = mid; i >= left; i--) {  
        LeftBorderSum += A[i];  
        if(LeftBorderSum > MaxLeftBorderSum)  
            MaxLeftBorderSum = LeftBorderSum;  
    }  
    for (int j = mid + 1; j <= right; j++) {  
        RightBorderSum += A[j];  
        if(RightBorderSum > MaxRightBorderSum)  
            MaxRightBorderSum = RightBorderSum;  
    }  
    return Max(MaxLeftSum, MaxRightSum, MaxLeftBorderSum + MaxRightBorderSum);  
}  
int MaxSubsequenceSum(int A, int n) {  
    return n > 0 ? MaxSumRec(A, 0, n - 1) : 0;  
}
```

The base case cost is 1. The program performs two recursive calls plus the linear work involved in computing the maximum sum for case 3. The recurrence relation is:

$$\begin{aligned} T(1) &= 1 \\ T(n) &= 2T(n/2) + n \end{aligned}$$

Using D & C Master theorem, we get the time complexity as $T(n) = O(n \log n)$.

Note: For an efficient solution refer to the [Dynamic Programming](#) chapter.

Problem-26 Closest-Pair of Points: Given a set of n points, $S = \{p_1, p_2, p_3, \dots, p_n\}$, where $p_i = (x_i, y_i)$. Find the pair of points having the smallest distance among all pairs (assume that all points are in one dimension).

Solution: Let us assume that we have sorted the points. Since the points are in one dimension, all the points are in a line after we sort them (either on X-axis or Y-axis). The complexity of sorting is $O(n\log n)$. After sorting we can go through them to find the consecutive points with the least difference. So the problem in one dimension is solved in $O(n\log n)$ time which is mainly dominated by sorting time.

Time Complexity: $O(n\log n)$.

Problem-27 For [Problem-26](#), how do we solve it if the points are in two-dimensional space?

Solution: Before going to the algorithm, let us consider the following mathematical equation:

$$\text{distance}(p_1, p_2) = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2}$$

The above equation calculates the distance between two points $p_1 = (x_1, y_1)$ and $p_2 = (x_2, y_2)$.

Brute Force Solution:

- Calculate the distances between all the pairs of points. From n points there are n_{C_2} ways of selecting 2 points. ($n_{C_2} = O(n^2)$).
- After finding distances for all n^2 possibilities, we select the one which is giving the minimum distance and this takes $O(n^2)$.

The overall time complexity is $O(n^2)$.

Problem-28 Give $O(n\log n)$ solution for *closest pair* problem (Problem-27)?

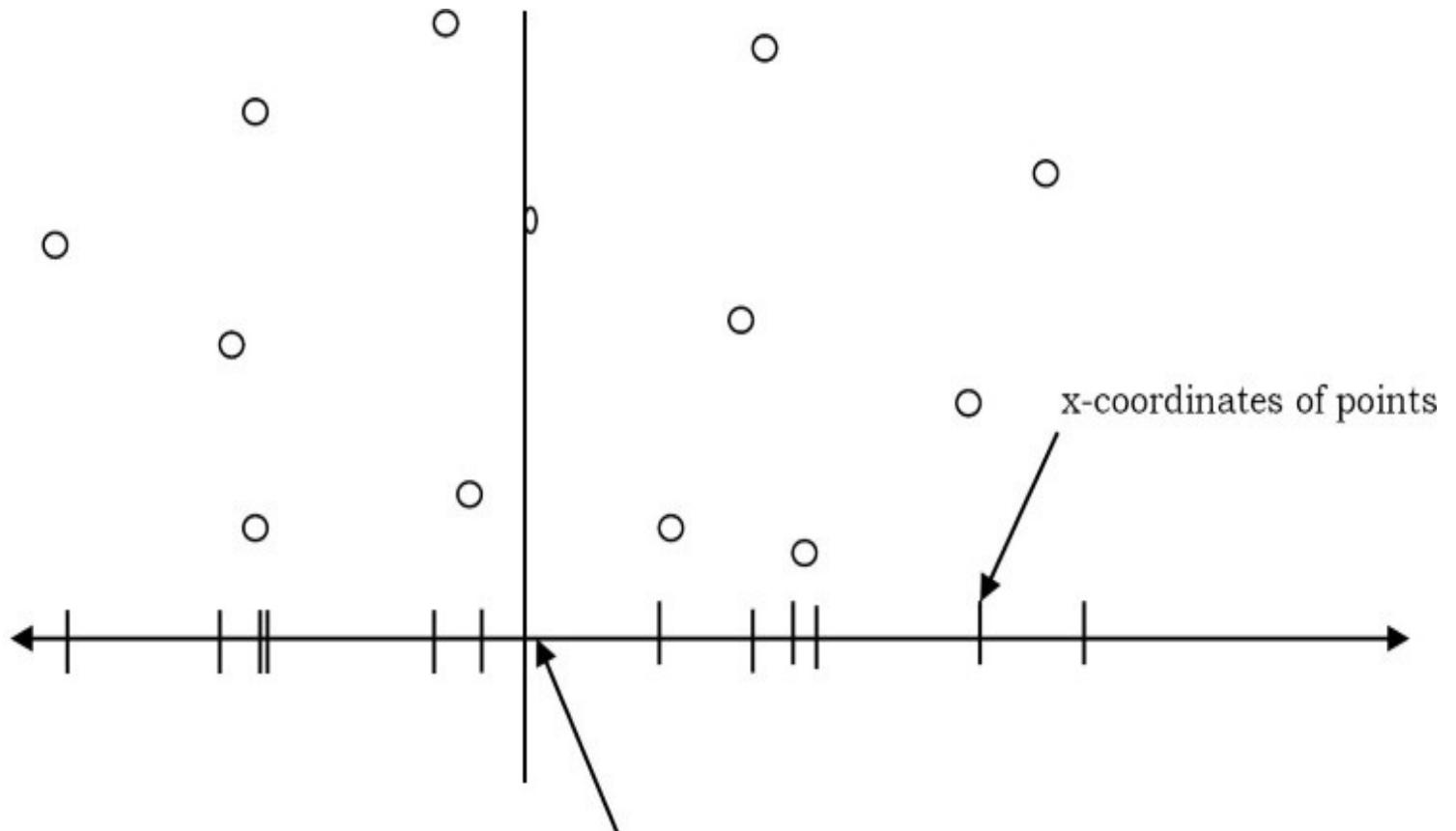
Solution: To find $O(n\log n)$ solution, we can use the D & C technique. Before starting the divide-and-conquer process let us assume that the points are sorted by increasing x -coordinate. Divide the points into two equal halves based on median of x -coordinates. That means the problem is divided into that of finding the closest pair in each of the two halves. For simplicity let us consider the following algorithm to understand the process.

Algorithm:

- 1) Sort the given points in S (given set of points) based on their x –coordinates. Partition S into two subsets, S_1 and S_2 , about the line l through median of S . This step is the *Divide* part of the *D & C* technique.
- 2) Find the closest-pairs in S_1 and S_2 and call them L and R recursively.
- 3) Now, steps 4 to 8 form the Combining component of the *D & C* technique.
- 4) Let us assume that $\delta = \min(L, R)$.
- 5) Eliminate points that are farther than δ apart from l .
- 6) Consider the remaining points and sort based on their y -coordinates.
- 7) Scan the remaining points in the y order and compute the distances of each point to all its neighbors that are distanced no more than $2 \times \delta$ (that's the reason for sorting

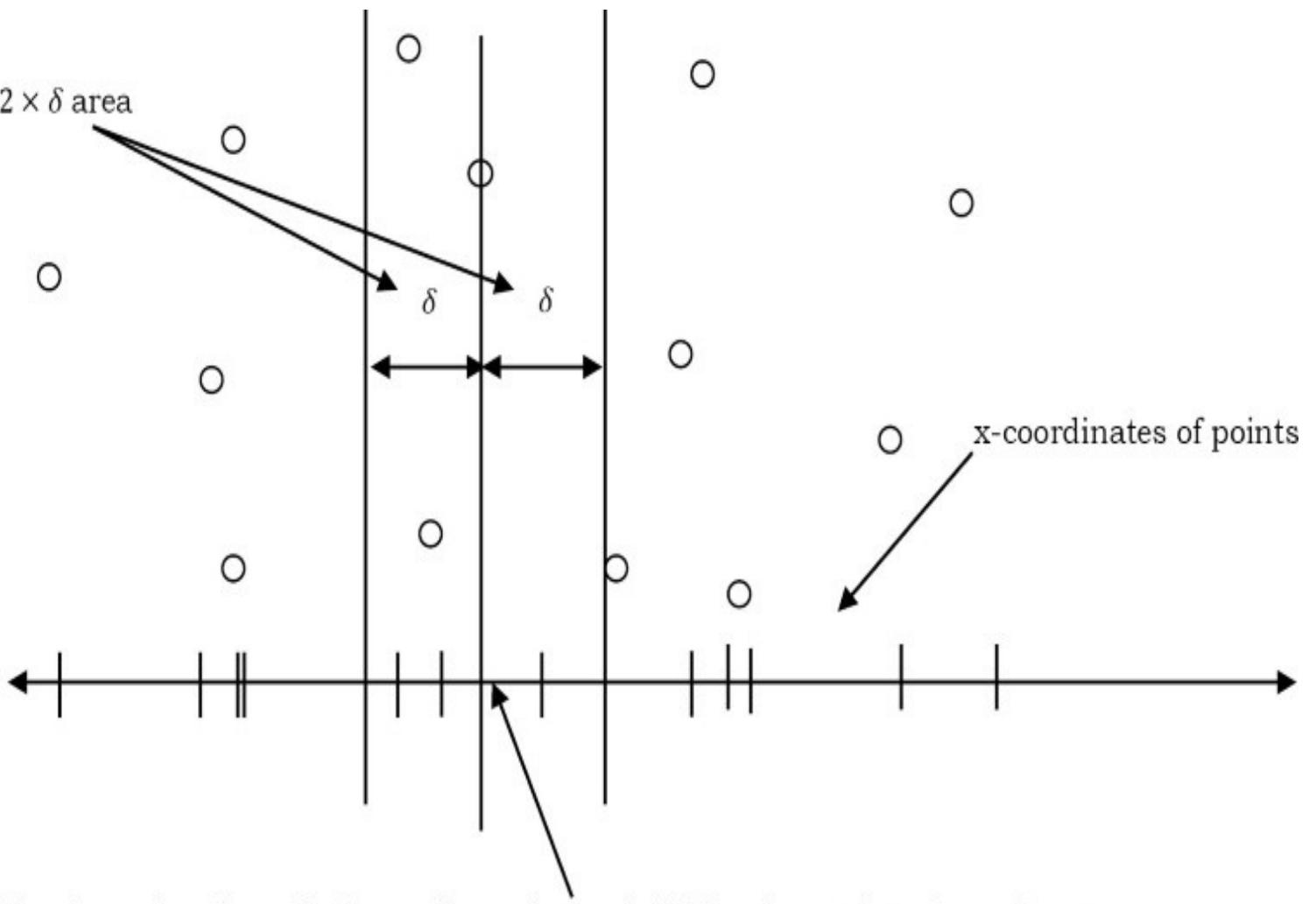
according to y).

- 8) If any of these distances is less than δ then update δ .



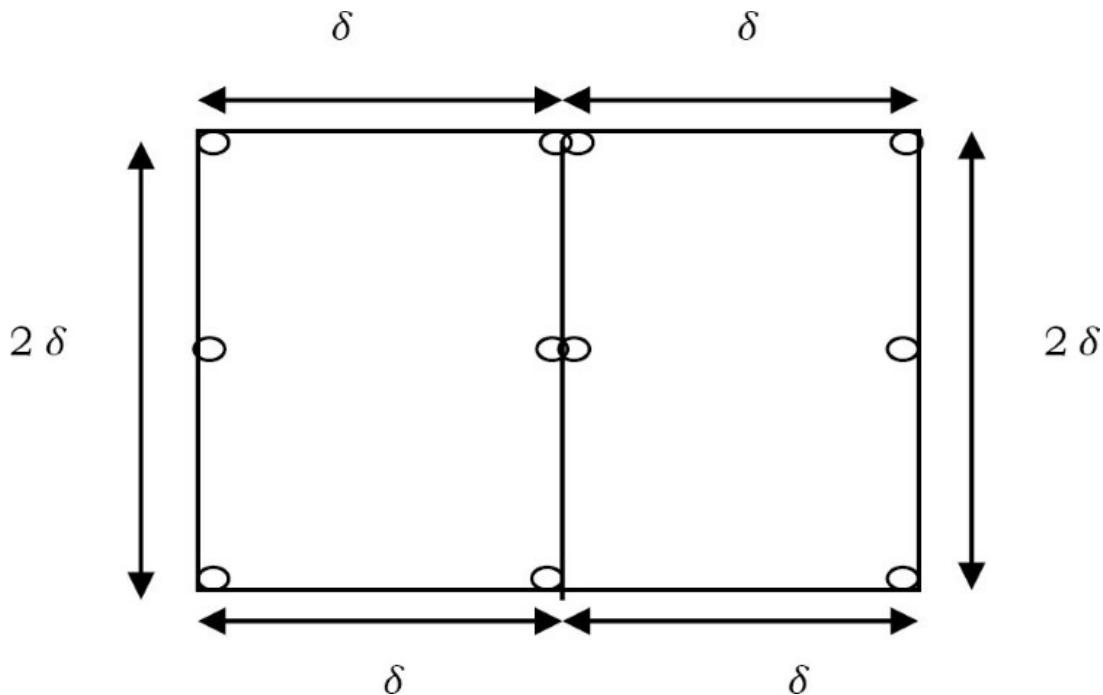
Line l passing through the median point and divides the set into 2 equal parts

Combining the results in linear time



Line l passing through the median point and divides the set into 2 equal parts

Let $\delta = \min(L, R)$, where L is the solution to first sub problem and R is the solution to second sub problem. The possible candidates for closest-pair, which are across the dividing line, are those which are less than δ distance from the line. So we need only the points which are inside the $2 \times \delta$ area across the dividing line as shown in the figure. Now, to check all points within distance δ from the line, consider the following figure.



From the above diagram we can see that a maximum of 12 points can be placed inside the square with a distance not less than δ . That means, we need to check only the distances which are within 11 positions in the sorted list. This is similar to the one above, but with the difference that in the above combining of subproblems, there are no vertical bounds. So we can apply the 12-point box tactic over all the possible boxes in the $2 \times \delta$ area with the dividing line as the middle line. As there can be a maximum of n such boxes in the area, the total time for finding the closest pair in the corridor is $O(n)$.

Analysis:

- 1) Step-1 and Step-2 take $O(n \log n)$ for sorting and recursively finding the minimum.
- 2) Step-4 takes $O(1)$.
- 3) Step-5 takes $O(n)$ for scanning and eliminating.
- 4) Step-6 takes $O(n \log n)$ for sorting.
- 5) Step-7 takes $O(n)$ for scanning.

The total complexity: $T(n) = O(n \log n) + O(1) + O(n) + O(n) + O(n) \approx O(n \log n)$.

Problem-29 To calculate k^n , give algorithm and discuss its complexity.

Solution: The naive algorithm to compute k^n is: start with 1 and multiply by k until reaching k^n . For this approach; there are $n - 1$ multiplications and each takes constant time giving a $\Theta(n)$ algorithm.

But there is a faster way to compute k^n . For example,

$$9^{24} = (9^{12})^2 = ((9^6)^2)^2 = (((9^3)^2)^2)^2 = (((9^2 \cdot 9)^2)^2)^2$$

Note that taking the square of a number needs only one multiplication; this way, to compute 9^{24} we need only 5 multiplications instead of 23.

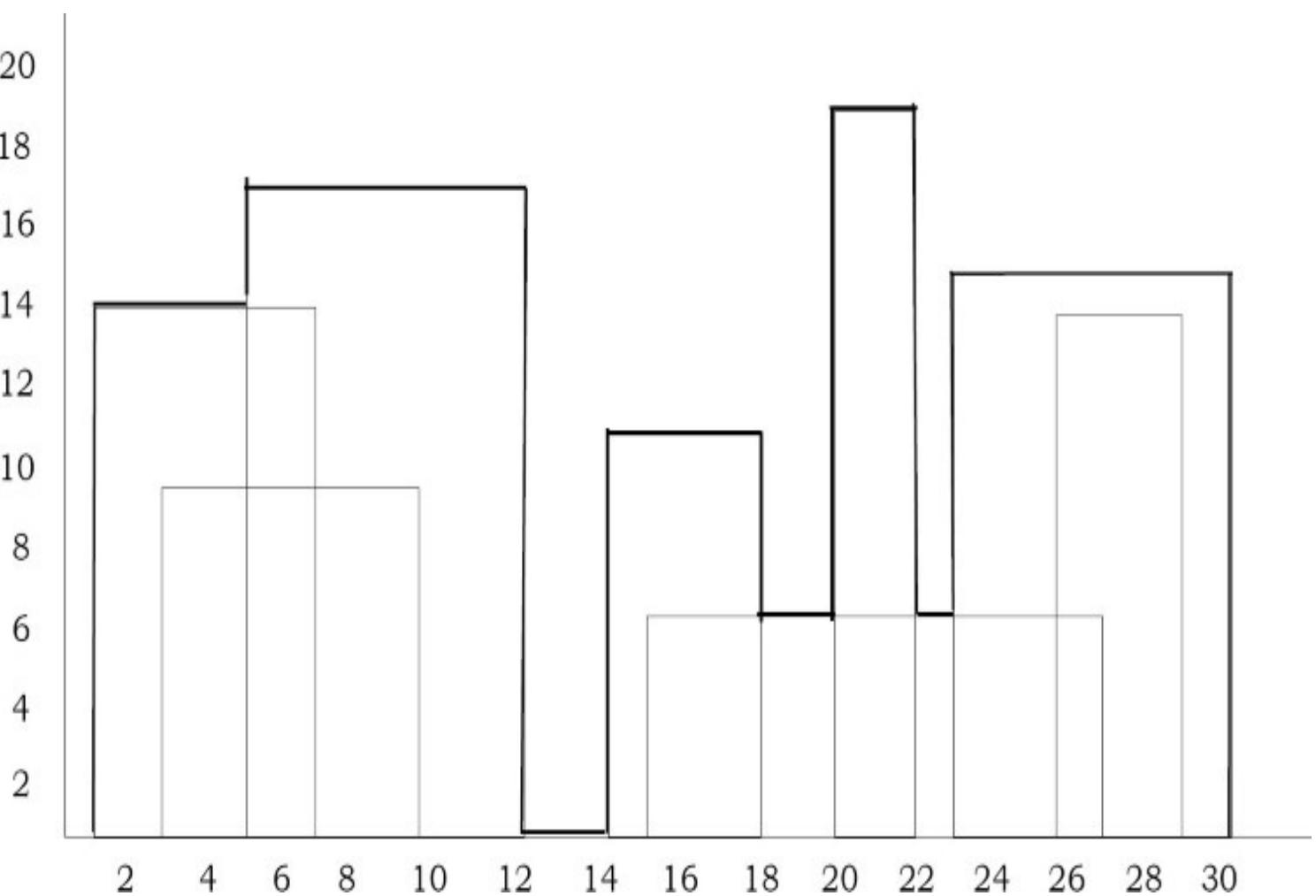
```
int Exponential(int k, int n) {
    if (k == 0)
        return 1;
    else{
        if (n%2 == 1){
            a = Exponential(k, n-1);
            return a*k;
        }
        else{
            a= Exponential(k, n/2);
            return a*a;
        }
    }
}
```

Let $T(n)$ be the number of multiplications required to compute k^n . For simplicity, assume $k = 2^i$ for some $i \geq 1$.

$$T(n) = T\left(\frac{n}{2}\right) + 1$$

Using master theorem we get $T(n) = O(\log n)$.

Problem-30 The Skyline Problem: Given the exact locations and shapes of n rectangular buildings in a 2-dimensional city. There is no particular order for these rectangular buildings. Assume that the bottom of all buildings lie on a fixed horizontal line (bottom edges are collinear). The input is a list of triples; one per building. A building B_i is represented by the triple (l_i, h_i, r_i) where l_i denote the x -position of the left edge and r_i denote the x -position of the right edge, and h_i denotes the building's height. Give an algorithm that computes the skyline (in 2 dimensions) of these buildings, eliminating hidden lines. In the diagram below there are 8 buildings, represented from left to right by the triplets $(1, 14, 7), (3, 9, 10), (5, 17, 12), (14, 11, 18), (15, 6, 27), (20, 19, 22), (23, 15, 30)$ and $(26, 14, 29)$.



The output is a collection of points which describe the path of the skyline. In some versions of the problem this collection of points is represented by a sequence of numbers p_1, p_2, \dots, p_n , such that the point p_i represents a horizontal line drawn at height p_i if i is even, and it represents a vertical line drawn at position p_i if i is odd. In our case the collection of points will be a sequence of p_1, p_2, \dots, p_n pairs of (x_i, h_i) where $p_i(x_i, h_i)$ represents the h_i height of the skyline at position x_i . In the diagram above the skyline is drawn with a thick line around the buildings and it is represented by the sequence of position-height pairs $(1, 14), (5, 17), (12, 0), (14, 11), (18, 6), (20, 19), (22, 6), (23, 15)$ and $(30, 0)$. Also, assume that R_i of the right most building can be maximum of 1000. That means, the L_i co-ordinate of left building can be minimum of 1 and R_i of the right most building can be maximum of 1000.

Solution: The most important piece of information is that we know that the left and right coordinates of each and every building are non-negative integers less than 1000. Now why is this important? Because we can assign a height-value to every distinct x_i coordinate where i is between 0 and 9,999.

Algorithm:

- Allocate an array for 1000 elements and initialize all of the elements to 0. Let's call this array *auxHeights*.

- Iterate over all of the buildings and for every B_i building iterate on the range of $[l_i..r_i]$ where l_i is the left, r_i is the right coordinate of the building B_i .
- For every x_j element of this range check if $h_i > auxHeights[x_j]$, that is if building B_i is taller than the current height-value at position x_j . If so, replace $auxHeights[x_j]$ with h_i .

Once we checked all the buildings, the $auxHeights$ array stores the heights of the tallest buildings at every position. There is one more thing to do: convert the $auxHeights$ array to the expected output format, that is to a sequence of position-height pairs. It's also easy: just map each and every i index to an $(i, auxHeights[i])$ pair.

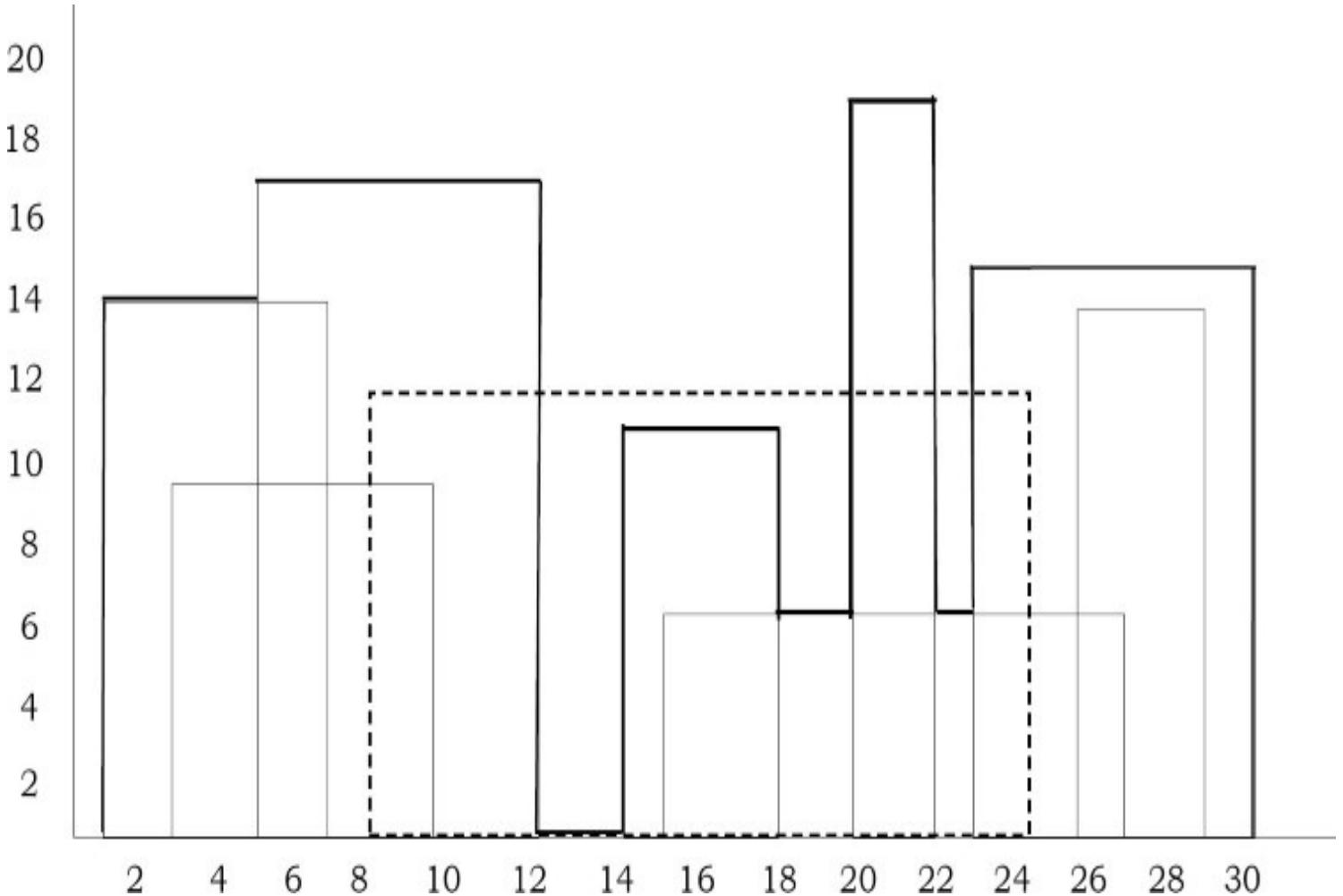
```
#include<stdio.h>
#define MaxRightMostBuildingRi 1000
int auxHeights[MaxRightMostBuildingRi];
int SkyLineBruteForce(){
    int left,h,right,i,prev;
    int rightMostBuildingRi=0;
    while(scanf("%d %d %d", &left, &h, &right)==3){
        for(i=left;i<right;i++){
            if(auxHeights[i]<h)
                auxHeights[i]=h;
            if(rightMostBuildingRi<right)
                rightMostBuildingRi=right;
        }
        prev = 0;
        for(i=1;i<rightMostBuildingRi;i++){
            if(prev!=auxHeights[i]){
                printf("%d %d ", i, auxHeights[i]);
                prev=auxHeights[i];
            }
        }
        printf("%d %d\n", rightMostBuildingRi, auxHeights[rightMostBuildingRi]);
        return 0;
    }
}
```

Let's have a look at the time complexity of this algorithm. Assume that, n indicates the number of buildings in the input sequence and m indicates the maximum coordinate (right most building r_i). From the above code, it is clear that for every new input building, we are traversing from $left$ (l_i) to $right$ (r_i) to update the heights. In the worst case, with n equal-size buildings, each having $l = 0$ left and $r = m - 1$ right coordinates, that is every building spans over the whole $[0..m)$ interval.

Thus the running time of setting the height of every position is $O(n \times m)$. The overall time-complexity is $O(n \times m)$, which is a lot larger than $O(n^2)$ if $m > n$.

Problem-31 Can we improve the solution of the [Problem-30](#)?

Solution: It would be a huge speed-up if somehow we could determine the skyline by calculating the height for those coordinates only where it matters, wouldn't it? Intuition tells us that if we can insert a building into an *existing skyline* then instead of all the coordinates the building spans over we only need to check the height at the left and right coordinates of the building plus those coordinates of the skyline the building overlaps with and may modify.



Is merging two skylines substantially different from merging a building with a skyline? The answer is, of course, No. This suggests that we use divide-and-conquer. Divide the input of n buildings into two equal sets. Compute (recursively) the skyline for each set then merge the two skylines. Inserting the buildings one after the other is not the fastest way to solve this problem as we've seen it above. If, however, we first merge pairs of buildings into skylines, then we merge pairs of these skylines into bigger skylines (and not two sets of buildings), and then merge pairs of these bigger skylines into even bigger ones, then - since the problem size is halved in every step -after $\log n$ steps we can compute the final skyline.

```
class SkyLineDivideandConquer {
public:
    vector<pair<int, int>> getSkyline(int start, int end, vector<vector<int>>& buildings) {
        if (start == end) {
            vector<pair<int, int>> result;
            result.push_back(pair<int, int>(buildings[start][0], buildings[start][1]));
            result.push_back(pair<int, int>(buildings[start][2], 0));
            return result;
        }
        int mid = (end + start) / 2;
        vector<pair<int, int>> leftSkyline = getSkyline(start, mid, buildings);

```

```

vector<pair<int, int>> rightSkyline = getSkyline(mid + 1, end, buildings);
vector<pair<int, int>> result = mergeSkylines(leftSkyline, rightSkyline);
return result;
}

vector<pair<int, int>> mergeSkylines(vector<pair<int, int>>& leftSkyline, vector<pair<int, int>>& rightSkyline) {
    vector<pair<int, int>> result;
    int i = 0, j = 0, currentHeight1 = 0, currentHeight2 = 0;
    int maxH = max(currentHeight1, currentHeight2);
    while (i != leftSkyline.size() && j != rightSkyline.size()) {
        if (leftSkyline[i].first < rightSkyline[j].first) {
            currentHeight1 = leftSkyline[i].second;
            if (maxH != max(currentHeight1, currentHeight2))
                result.push_back(pair<int, int>(leftSkyline[i].first, max(currentHeight1, currentHeight2)));
            maxH = max(currentHeight1, currentHeight2);
            i++;
        }
        else if (leftSkyline[i].first > rightSkyline[j].first) {
            currentHeight2 = rightSkyline[j].second;
            if (maxH != max(currentHeight1, currentHeight2))
                result.push_back(pair<int, int>(rightSkyline[j].first, max(currentHeight1, currentHeight2)));
            maxH = max(currentHeight1, currentHeight2);
            j++;
        }
        else {
            if(leftSkyline[i].second >= rightSkyline[j].second) {
                currentHeight1 = leftSkyline[i].second;
                currentHeight2 = rightSkyline[j].second;
                if(maxH != max(currentHeight1, currentHeight2))
                    result.push_back(pair<int, int>(leftSkyline[i].first, leftSkyline[i].second));
                maxH = max(currentHeight1, currentHeight2);
                i++;
                j++;
            }
            else {
                currentHeight1 = leftSkyline[i].second;
                currentHeight2 = rightSkyline[j].second;
                if(maxH != max(currentHeight1, currentHeight2))
                    result.push_back(pair<int, int>(rightSkyline[j].first, rightSkyline[j].second));
                maxH = max(currentHeight1, currentHeight2);
                i++;
                j++;
            }
        }
    }
    while (j < rightSkyline.size()) {
        result.push_back(rightSkyline[j]);
        j++;
    }
    while (i != leftSkyline.size()) {
        result.push_back(leftSkyline[i]);
        i++;
    }
    return result;
}
};

```

For example, given two skylines A=($a_1, ha_1, a_2, ha_2, \dots, a_n, 0$) and B=($b_1, hb_1, b_2, hb_2, \dots, b_m, 0$), we merge these lists as the new list: ($c_1, hc_1, c_2, hc_2, \dots, c_{n+m}, 0$). Clearly, we merge the list of a 's and b 's just like in the standard Merge algorithm. But, in addition to that, we have to decide on the correct height in between these boundary values. We use two variables $currentHeight1$ and $currentHeight2$ (note that these are the heights prior to encountering the heads of the lists) to store the current height of the first and the second skyline, respectively. When comparing the head entries ($currentHeight1, currentHeight2$) of the two skylines, we introduce a new strip (and append to the output skyline) whose x-coordinate is the minimum of the entries' x-coordinates and whose height is the maximum of $currentHeight1$ and $currentHeight2$. This algorithm has a structure similar to Mergesort. So the overall running time of the divide and conquer approach will be $O(n \log n)$.

DYNAMIC PROGRAMMING

CHAPTER 19



19.1 Introduction

In this chapter we will try to solve the problems for which we failed to get the optimal solutions using other techniques (say, *Divide & Conquer* and *Greedy* methods). Dynamic Programming (DP) is a simple technique but it can be difficult to master. One easy way to identify and solve DP problems is by solving as many problems as possible. The term *Programming* is not related to coding but it is from literature, and means filling tables (similar to *Linear Programming*).

19.2 What is Dynamic Programming Strategy?

Dynamic programming and memoization work together. The main difference between dynamic programming and divide and conquer is that in the case of the latter, sub problems are independent, whereas in DP there can be an overlap of sub problems. By using memoization [maintaining a table of sub problems already solved], dynamic programming reduces the exponential complexity to polynomial complexity ($O(n^2)$, $O(n^3)$, etc.) for many problems. The major components of DP are:

- Recursion: Solves sub problems recursively.

- Memoization: Stores already computed values in table (*Memoization* means caching).

$$\text{Dynamic Programming} = \text{Recursion} + \text{Memoization}$$

19.3 Properties of Dynamic Programming Strategy

The two dynamic programming properties which can tell whether it can solve the given problem or not are:

- *Optimal substructure*: an optimal solution to a problem contains optimal solutions to sub problems.
- *Overlapping sub problems*: a recursive solution contains a small number of distinct sub problems repeated many times.

19.4 Can Dynamic Programming Solve All Problems?

Like Greedy and Divide and Conquer techniques, DP cannot solve every problem. There are problems which cannot be solved by any algorithmic technique [Greedy, Divide and Conquer and Dynamic Programming].

The difference between Dynamic Programming and straightforward recursion is in memoization of recursive calls. If the sub problems are independent and there is no repetition then memoization does not help, so dynamic programming is not a solution for all problems.

19.5 Dynamic Programming Approaches

Basically there are two approaches for solving DP problems:

- Bottom-up dynamic programming
- Top-down dynamic programming

Bottom-up Dynamic Programming

In this method, we evaluate the function starting with the smallest possible input argument value and then we step through possible values, slowly increasing the input argument value. While computing the values we store all computed values in a table (memory). As larger arguments are evaluated, pre-computed values for smaller arguments can be used.

Top-down Dynamic Programming

In this method, the problem is broken into sub problems; each of these sub problems is solved; and the solutions remembered, in case they need to be solved. Also, we save each computed value as the final action of the recursive function, and as the first action we check if pre-computed value exists.

Bottom-up versus Top-down Programming

In bottom-up programming, the programmer has to select values to calculate and decide the order of calculation. In this case, all sub problems that might be needed are solved in advance and then used to build up solutions to larger problems. In top-down programming, the recursive structure of the original code is preserved, but unnecessary recalculation is avoided. The problem is broken into sub problems, these sub problems are solved and the solutions remembered, in case they need to be solved again.

Note: Some problems can be solved with both the techniques and we will see examples in the next section.

19.6 Examples of Dynamic Programming Algorithms

- Many string algorithms including longest common subsequence, longest increasing subsequence, longest common substring, edit distance.
- Algorithms on graphs can be solved efficiently: Bellman-Ford algorithm for finding the shortest distance in a graph, Floyd's All-Pairs shortest path algorithm, etc.
- Chain matrix multiplication
- Subset Sum
- 0/1 Knapsack
- Travelling salesman problem, and many more

19.7 Understanding Dynamic Programming

Before going to problems, let us understand how DP works through examples.

Fibonacci Series

In Fibonacci series, the current number is the sum of previous two numbers. The Fibonacci series is defined as follows:

$$\begin{aligned} Fib(n) &= 0, && \text{for } n = 0 \\ &= 1, && \text{for } n = 1 \\ &= Fib(n-1) + Fib(n-2), && \text{for } n > 1 \end{aligned}$$

The recursive implementation can be given as:

```
int RecursiveFibonacci(int n) {  
    if(n == 0) return 0;  
    if(n == 1) return 1;  
    return RecursiveFibonacci(n -1) + RecursiveFibonacci(n -2);  
}
```

Solving the above recurrence gives:

$$T(n) = T(n - 1) + T(n - 2) + 1 \approx \left(\frac{1+\sqrt{5}}{2}\right)^n \approx 2^n = O(2^n)$$

Note: For proof, refer to [Introduction](#) chapter.

How does Memoization help?

Calling $fib(5)$ produces a call tree that calls the function on the same value many times:

```
fib(5)  
fib(4) + fib(3)  
(fib(3) + fib(2)) + (fib(2) + fib(1))  
((fib(2) + fib(1)) + (fib(1) + fib(0))) + ((fib(1) + fib(0)) + fib(1))  
(((fib(1) + fib(0)) + fib(1)) + (fib(1) + fib(0))) + ((fib(1) + fib(0)) + fib(1))
```

In the above example, $fib(2)$ was calculated three times (overlapping of subproblems). If n is big, then many more values of fib (sub problems) are recalculated, which leads to an exponential time algorithm. Instead of solving the same sub problems again and again we can store the previous calculated values and reduce the complexity.

Memoization works like this: Start with a recursive function and add a table that maps the function's parameter values to the results computed by the function. Then if this function is called twice with the same parameters, we simply look up the answer in the table.

Improving: Now, we see how DP reduces this problem complexity from exponential to polynomial. As discussed earlier, there are two ways of doing this. One approach is bottom-up: these methods start with lower values of input and keep building the solutions for higher values.

```

int fib[n];
int fib(int n) {
    // Check for base cases
    if(n == 0 || n == 1) return 1;
    fib[0] = 1;
    fib[1] = 1;
    for (int i = 2; i < n; i++)
        fib[i] = fib[i - 1] + fib[i - 2];
    return fib[n - 1];
}

```

The other approach is top-down. In this method, we preserve the recursive calls and use the values if they are already computed. The implementation for this is given as:

```

int fib[n];
int fibonacci( int n ) {
    if(n == 1)
        return 1;
    if(n == 2)
        return 1;
    if( fib[n] != 0) return fib[n] ;
    return fib[n] = fibonacci(n-1) + fibonacci(n -2) ;
}

```

Note: For all problems, it may not be possible to find both top-down and bottom-up programming solutions.

Both versions of the Fibonacci series implementations clearly reduce the problem complexity to $O(n)$. This is because if a value is already computed then we are not calling the subproblems again. Instead, we are directly taking its value from the table.

Time Complexity: $O(n)$. Space Complexity: $O(n)$, for table.

Further Improving: One more observation from the Fibonacci series is: The current value is the sum of the previous two calculations only. This indicates that we don't have to store all the previous values. Instead, if we store just the last two values, we can calculate the current value. The implementation for this is given below:

```

int fibonacci(int n) {
    int a = 0, b = 1, sum, i;
    for (i=0;i < n;i++) {
        sum = a + b;
        a = b;
        b = sum;
    }
    return sum;
}

```

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

Note: This method may not be applicable (available) for all problems.

Observations

While solving the problems using DP, try to figure out the following:

- See how the problems are defined in terms of subproblems recursively.
- See if we can use some table [memoization] to avoid the repeated calculations.

Factorial of a Number

As another example, consider the factorial problem: $n!$ is the product of all integers between n and 1. The definition of recursive factorial can be given as:

$$n! = n * (n - 1)!$$

$$1! = 1$$

$$0! = 1$$

This definition can easily be converted to implementation. Here the problem is finding the value of $n!$, and the sub-problem is finding the value of $(n - 1)!$. In the recursive case, when n is greater than 1, the function calls itself to find the value of $(n - 1)!$ and multiplies that with n . In the base case, when n is 0 or 1, the function simply returns 1.

```

int fact(int n) {
    if(n == 1) return 1;
    else if(n == 0) return 1;
    else // recursive case: multiply n by (n - 1) factorial
        return n *fact(n -1);
}

```

The recurrence for the above implementation can be given as: $T(n) = n \times T(n - 1) \approx O(n)$
Time Complexity: $O(n)$. Space Complexity: $O(n)$, recursive calls need a stack of size n .

In the above recurrence relation and implementation, for any n value, there are no repetitive calculations (no overlapping of sub problems) and the factorial function is not getting any benefits with dynamic programming. Now, let us say we want to compute a series of $m!$ for some arbitrary value m . Using the above algorithm, for each such call we can compute it in $O(m)$. For example, to find both $n!$ and $m!$ we can use the above approach, wherein the total complexity for finding $n!$ and $m!$ is $O(m + n)$.

Time Complexity: $O(n + m)$.

Space Complexity: $O(\max(m,n))$, recursive calls need a stack of size equal to the maximum of m and n .

Improving: Now let us see how DP reduces the complexity. From the above recursive definition it can be seen that $\text{fact}(n)$ is calculated from $\text{fact}(n - 1)$ and n and nothing else. Instead of calling $\text{fact}(n)$ every time, we can store the previous calculated values in a table and use these values to calculate a new value. This implementation can be given as:

```
int facto[n];
int fact(int n) {
    if(n == 1) return 1;
    else if(n == 0)
        return 1;
    //Already calculated case
    else if(facto[n]!=0)
        return facto[n];
    else // recursive case: multiply n by (n - 1) factorial
        return facto[n]= n *fact(n -1);
}
```

For simplicity, let us assume that we have already calculated $n!$ and want to find $m!$. For finding $m!$, we just need to see the table and use the existing entries if they are already computed. If $m < n$ then we do not have to recalculate $m!$. If $m > n$ then we can use $n!$ and call the factorial on the remaining numbers only.

The above implementation clearly reduces the complexity to $O(\max(m,n))$. This is because if the $\text{fact}(n)$ is already there, then we are not recalculating the value again. If we fill these newly computed values, then the subsequent calls further reduce the complexity.

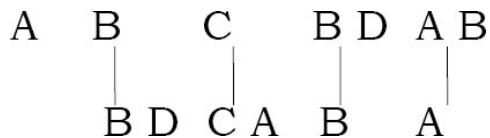
Time Complexity: $O(\max(m,n))$. Space Complexity: $O(\max(m,n))$ for table.

19.8 Longest Common Subsequence

Given two strings: string X of length m [$X(1..m)$], and string Y of length n [$Y(1..n)$], find the longest common subsequence: the longest sequence of characters that appear left-to-right (but not necessarily in a contiguous block) in both strings. For example, if $X = \text{"ABCBDAB"}$ and $Y = \text{"BDCABA"}$, the $LCS(X, Y) = \{\text{"BCBA"}, \text{"BDAB"}, \text{"BCAB"}\}$. We can see there are several optimal solutions.

Brute Force Approach: One simple idea is to check every subsequence of $X[1..m]$ (m is the length of sequence X) to see if it is also a subsequence of $Y[1..n]$ (n is the length of sequence Y). Checking takes $O(n)$ time, and there are 2^m subsequences of X . The running time thus is exponential $O(n \cdot 2^m)$ and is not good for large sequences.

Recursive Solution: Before going to DP solution, let us form the recursive solution for this and later we can add memoization to reduce the complexity. Let's start with some simple observations about the LCS problem. If we have two strings, say “ABCBDAB” and “BDCABA”, and if we draw lines from the letters in the first string to the corresponding letters in the second, no two lines cross:



From the above observation, we can see that the current characters of X and Y may or may not match. That means, suppose that the two first characters differ. Then it is not possible for both of them to be part of a common subsequence - one or the other (or maybe both) will have to be removed. Finally, observe that once we have decided what to do with the first characters of the strings, the remaining sub problem is again a *LCS* problem, on two shorter strings. Therefore we can solve it recursively.

The solution to *LCS* should find two sequences in X and Y and let us say the starting index of sequence in X is i and the starting index of sequence in Y is j . Also, assume that $X[i \dots m]$ is a substring of X starting at character i and going until the end of X , and that $Y[j \dots n]$ is a substring of Y starting at character j and going until the end of Y .

Based on the above discussion, here we get the possibilities as described below:

- 1) If $X[i] == Y[j]$: $1 + LCS(i + 1, j + 1)$
- 2) If $X[i] \neq Y[j]$: $LCS(i, j + 1)$ // skipping j^{th} character of Y
- 3) If $X[i] \neq Y[j]$: $LCS(i + 1, j)$ // skipping i^{th} character of X

In the first case, if $X[i]$ is equal to $Y[j]$, we get a matching pair and can count it towards the total length of the *LCS*. Otherwise, we need to skip either i^{th} character of X or j^{th} character of Y and find the longest common subsequence. Now, $LCS(i, j)$ can be defined as:

$$LCS(i, j) = \begin{cases} 0, & \text{if } i = m \text{ or } j = n \\ \max\{LCS(i, j+1), LCS(i+1, j)\}, & \text{if } X[i] \neq Y[j] \\ 1 + LCS[i+1, j+1], & \text{if } X[i] == Y[j] \end{cases}$$

LCS has many applications. In web searching, if we find the smallest number of changes that are needed to change one word into another. A *change* here is an insertion, deletion or replacement of a single character.

```
//Initial Call: LCSLength(X, 0, m-1, Y, 0, n-1);
int LCSLength( int X[], int i, int m, int Y[], int j, int n) {
    if (i == m || j == n)
        return 0;
    else if (X[i] == Y[j]) return 1 + LCSLength(X, i+1, m, Y, j+1, n);
    else return max( LCSLength(X, i+1, m, Y, j, n), LCSLength(X, i, m, Y, j+1, n));
}
```

This is a correct solution but it is very time consuming. For example, if the two strings have no matching characters, the last line always gets executed which gives (if $m == n$) close to $O(2^n)$.

DP Solution: Adding Memoization: The problem with the recursive solution is that the same subproblems get called many different times. A subproblem consists of a call to `LCS_length`, with the arguments being two suffixes of X and Y , so there are exactly $(i + 1)(j + 1)$ possible subproblems (a relatively small number). If there are nearly 2^n recursive calls, some of these subproblems must be being solved over and over.

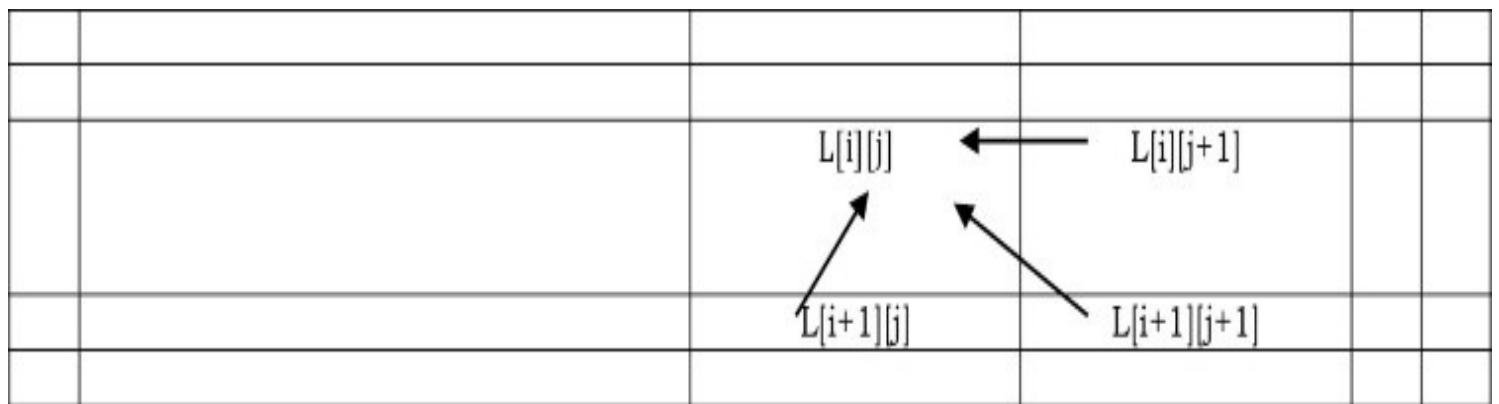
The DP solution is to check, whenever we want to solve a sub problem, whether we've already done it before. So we look up the solution instead of solving it again. Implemented in the most direct way, we just add some code to our recursive solution. To do this, look up the code. This can be given as:

```

int LCS[1024][1024];
int LCSLength( int X[], int m, int Y[], int n) {
    for( int i = 0; i <= m; i++ )
        LCS[i][n] = 0;
    for( int j = 0; j <= n; j++ )
        LCS[m][j] = 0;
    for( int i = m - 1; i >= 0; i--) {
        for( int j = n - 1; j >= 0; j--) {
            LCS[i][j] = LCS[i + 1][j + 1]; // matching X[i] to Y[j]
            if( X[i] == Y[j] )
                LCS[i][j]++;
            // the other two cases - inserting a gap
            if(LCS[i][j + 1] > LCS[i][j] )
                LCS[i][j] = LCS[i][j + 1];
            if(LCS[i + 1][j] > LCS[i][j] )
                LCS[i][j] = LCS[i + 1][j];
        }
    }
    return LCS[0][0];
}

```

First, take care of the base cases. We have created an *LCS* table with one row and one column larger than the lengths of the two strings. Then run the iterative DP loops to fill each cell in the table. This is like doing recursion backwards, or bottom up.



The value of $LCS[i][j]$ depends on 3 other values ($LCS[i + 1][j + 1]$, $LCS[i][j + 1]$ and $LCS[i + 1][j]$), all of which have larger values of i or j . They go through the table in the order of decreasing i and j values. This will guarantee that when we need to fill in the value of $LCS[i][j]$, we already know the values of all the cells on which it depends.

Time Complexity: $O(mn)$, since i takes values from 1 to m and j takes values from 1 to n .

Space Complexity: $O(mn)$.

Note: In the above discussion, we have assumed $LCS(i,j)$ is the length of the LCS with $X[i \dots m]$ and $Y[j \dots n]$. We can solve the problem by changing the definition as $LCS(i,j)$ is the length of the LCS with $X[1 \dots i]$ and $Y[1 \dots j]$.

Printing the subsequence: The above algorithm can find the length of the longest common subsequence but cannot give the actual longest subsequence. To get the sequence, we trace it through the table. Start at cell $(0,0)$. We know that the value of $LC5[0][0]$ was the maximum of 3 values of the neighboring cells. So we simply recompute $LC5[0][0]$ and note which cell gave the maximum value. Then we move to that cell (it will be one of $(1,1)$, $(0,1)$ or $(1,0)$) and repeat this until we hit the boundary of the table. Every time we pass through a cell (i,j') where $X[i] == Y[j]$, we have a matching pair and print $X[i]$. At the end, we will have printed the longest common subsequence in $O(mn)$ time.

An alternative way of getting path is to keep a separate table for each cell. This will tell us which direction we came from when computing the value of that cell. At the end, we again start at cell $(0,0)$ and follow these directions until the opposite corner of the table.

From the above examples, I hope you understood the idea behind DP. Now let us see more problems which can be easily solved using the DP technique.

Note: As we have seen above, in DP the main component is recursion. If we know the recurrence then converting that to code is a minimal task. For the problems below, we concentrate on getting the recurrence.

19.9 Dynamic Programming: Problems & Solutions

Problem-1 Convert the following recurrence to code.

$$T(0) = T(1) = 2$$
$$T(n) = \sum_{i=1}^{n-1} 2 \times T(i) \times T(i - 1), \text{ for } n > 1$$

Solution: The code for the given recursive formula can be given as:

```

int f(int n) {
    int sum = 0;
    if(n==0 || n==1) //Base Case
        return 2;
    //recursive case
    for(int i=1; i < n;i++)
        sum += 2 * f(i) * f(i-1);
    return sum;
}

```

Problem-2 Can we improve the solution to [Problem-1](#) using memoization of DP?

Solution: Yes. Before finding a solution, let us see how the values are calculated.

$$\begin{aligned}
 T(0) &= T(1) = 2 \\
 T(2) &= 2 * T(1) * T(0) \\
 T(3) &= 2 * T(1) * T(0) + 2 * T(2) * T(1) \\
 T(4) &= 2 * T(1) * T(0) + 2 * T(2) * T(1) + 2 * T(3) * T(2)
 \end{aligned}$$

From the above calculations it is clear that there are lots of repeated calculations with the same input values. Let us use a table for avoiding these repeated calculations, and the implementation can be given as:

```

int f(int n) {
    T[0] = T[1] = 2;
    for(int i=2; i <= n; i++) {
        T[i] = 0;
        for (int j=1; j < i; j++)
            T[i] += 2 * T[j] * T[j-1];
    }
    return T[n];
}

```

Time Complexity: $O(n^2)$, two *for* loops. Space Complexity: $O(n)$, for table.

Problem-3 Can we further improve the complexity of [Problem-2](#)?

Solution: Yes, since all sub problem calculations are dependent only on previous calculations, code can be modified as:

```

int f(int n) {
    T[0] = T[1] = 2;
    T[2] = 2 * T[0] * T[1];
    for(int i=3; i <= n; i++)
        T[i]=T[i-1] + 2 * T[i-1] * T[i-2];
    return T[n];
}

```

Time Complexity: $O(n)$, since only one *for* loop. Space Complexity: $O(n)$.

Problem-4 Maximum Value Contiguous Subsequence: Given an array of n numbers, give an algorithm for finding a contiguous subsequence $A(i) \dots A(j)$ for which the sum of elements is maximum. **Example:** $\{-2, 11, -4, 13, -5, 2\} \rightarrow 20$ and $\{1, -3, 4, -2, -1, 6\} \rightarrow 7$

Solution:

Input: Array. $A(1) \dots A(n)$ of n numbers.

Goal: If there are no negative numbers, then the solution is just the sum of all elements in the given array. If negative numbers are there, then our aim is to maximize the sum [there can be a negative number in the contiguous sum].

One simple and brute force approach is to see all possible sums and select the one which has maximum value.

```

int MaxContiguousSum(int A[], int n) {
    int maxSum = 0;
    for(int i = 0; i < n; i++) // for each possible start point
        for(int j = i; j < n; j++) { // for each possible end point
            int currentSum = 0;
            for(int k = i; k <= j; k++)
                currentSum += A[k];
            if(currentSum > maxSum)
                maxSum = currentSum;
        }
    return maxSum;
}

```

Time Complexity: $O(n^3)$. Space Complexity: $O(1)$.

Problem-5 Can we improve the complexity of [Problem-4](#)?

Solution: Yes. One important observation is that, if we have already calculated the sum for the subsequence $i, \dots, j - 1$, then we need only one more addition to get the sum for the subsequence i, \dots, j . But, the [Problem-4](#) algorithm ignores this information. If we use this fact, we can get an improved algorithm with the running time $O(n^2)$.

```
int MaxContiguousSum(int A[], int n) {
    int maxSum = 0;
    for( int i = 0; i < n; i++ ) {
        int currentSum = 0;
        for( int j = i; j < n; j++ ) {
            currentSum += a[j];
            if(currentSum > maxSum)
                maxSum = currentSum;
        }
    }
    return maxSum;
}
```

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-6 Can we solve [Problem-4](#) using Dynamic Programming?

Solution: Yes. For simplicity, let us say, $M(i)$ indicates maximum sum over all windows ending at i .

Given Array, A : recursive formula considers the case of selecting i^{th} element

	?	
--	-------	---	--

$A[i]$

To find maximum sum we have to do one of the following and select maximum among them.

- Either extend the old sum by adding $A[i]$
- or start new window starting with one element $A[i]$

$$M(i) = \text{Max} \begin{cases} M(i-1) + A[i] \\ 0 \end{cases}$$

Where, $M(i-1) + A[i]$ indicates the case of extending the previous sum by adding $A[i]$ and 0 indicates the new window starting at $A[i]$.

```

int MaxContiguousSum(int A[], int n) {
    int M[n] = 0, maxSum = 0;
    if(A[0] > 0)
        M[0] = A[0];
    else M[0] = 0;
    for( int i = 1; i < n; i++) {
        if( M[i-1] + A[i] > 0)
            M[i] = M[i-1] + A[i];
        else      M[i] = 0;
    }
    for( int i = 0; i < n; i++)
        if(M[i] > maxSum)
            maxSum = M[i];
    return maxSum;
}

```

Time Complexity: $O(n)$. Space Complexity: $O(n)$, for table.

Problem-7 Is there any other way of solving [Problem-4](#)?

Solution: Yes. We can solve this problem without DP too (without memory). The algorithm is a little tricky. One simple way is to look for all positive contiguous segments of the array (*sumEndingHere*) and keep track of the maximum sum contiguous segment among all positive segments (*sumSoFar*). Each time we get a positive sum compare it (*sumEndingHere*) with *sumSoFar* and update *sumSoFar* if it is greater than *sumSoFar*. Let us consider the following code for the above observation.

```

int MaxContiguousSum(int A[], int n) {
    int sumSoFar = 0, sumEndingHere = 0;
    for(int i = 0; i < n; i++)  {
        sumEndingHere = sumEndingHere + A[i];
        if(sumEndingHere < 0) {
            sumEndingHere = 0;
            continue;
        }
        if(sumSoFar < sumEndingHere)
            sumSoFar = sumEndingHere;
    }
    return sumSoFar;
}

```

Note: The algorithm doesn't work if the input contains all negative numbers. It returns 0 if all numbers are negative. To overcome this, we can add an extra check before the actual implementation. The phase will look if all numbers are negative, and if they are it will return maximum of them (or smallest in terms of absolute value).

Time Complexity: $O(n)$, because we are doing only one scan. Space Complexity: $O(1)$, for table.

Problem-8 In [Problem-7](#) solution, we have assumed that $M(i)$ indicates maximum sum over all windows ending at i . Can we assume $M(i)$ indicates maximum sum over all windows starting at i and ending at n ?

Solution: Yes. For simplicity, let us say, $M(i)$ indicates maximum sum over all windows starting at i .

Given Array, A: recursive formula considers the case of selecting i^{th} element

	?
--	-------	---	-------

$A[i]$

To find maximum window we have to do one of the following and select maximum among them.

- Either extend the old sum by adding $A[i]$
- Or start new window starting with one element $A[i]$

$$M(i) = \begin{cases} M(i + 1) + A[i], & \text{if } M(i + 1) + A[i] > 0 \\ 0, & \text{if } M(i + 1) + A[i] \leq 0 \end{cases}$$

Where, $M(i + 1) + A[t]$ indicates the case of extending the previous sum by adding $A[i]$, and 0 indicates the new window starting at $A[i]$.

Time Complexity: $O(n)$. Space Complexity: $O(n)$, for table.

Note: For $O(n\log n)$ solution, refer to the [Divide and Conquer](#) chapter.

Problem-9 Given a sequence of n numbers $A(1) \dots A(n)$, give an algorithm for finding a contiguous subsequence $A(i) \dots A(j)$ for which the sum of elements in the subsequence is maximum. Here the condition is we should not select two contiguous numbers.

Solution: Let us see how DP solves this problem. Assume that $M(i)$ represents the maximum sum from 1 to i numbers without selecting two contiguous numbers. While computing $M(i)$, the decision we have to make is, whether to select the i^{th} element or not. This gives us two possibilities and based on this we can write the recursive formula as:

$$M(i) = \begin{cases} \max\{A[i] + M(i-2), M(i-1)\}, & \text{if } i > 2 \\ A[1], & \text{if } i = 1 \\ \max\{A[1], A[2]\}, & \text{if } i = 2 \end{cases}$$

- The first case indicates whether we are selecting the i^{th} element or not. If we don't select the i^{th} element then we have to maximize the sum using the elements 1 to $i - 1$. If i^{th} element is selected then we should not select $i - 1^{th}$ element and need to maximize the sum using 1 to $i - 2$ elements.
- In the above representation, the last two cases indicate the base cases.

Given Array, A: recursive formula considers the case of selecting i^{th} element

	?	
--	-------	-------	---	--

A[i-2] A[i-1] A[i]

```
int maxSumWithNoTwoContinuousNumbers(int A[], int n) {
    int M[n+1];
    M[0]=A[0];
    M[1]=(A[0]>A[1]?A[0]:A[1]);
    for(i=2, i<n; i++)
        M[i]= (M[i-1]>M[i-2]+A[i]? M[i-1]: M[i-2]+A[i]);
    return M[n-1];
}
```

Time Complexity: O(n). Space Complexity: O(n).

Problem-10 In [Problem-9](#), we assumed that $M(i)$ represents the maximum sum from 1 to i numbers without selecting two contiguous numbers. Can we solve the same problem by changing the definition as: $M(i)$ represents the maximum sum from i to n numbers without selecting two contiguous numbers?

Solution: Yes. Let us assume that $M(i)$ represents the maximum sum from i to n numbers without selecting two contiguous numbers:

Given Array, A: recursive formula considers the case of selecting i^{th} element

	?	
--	---	-------	-------	--

A[i] A[i+1] A[i+2]

As similar to [Problem-9](#) solution, we can write the recursive formula as:

$$M(i) = \begin{cases} \max\{A[i] + M(i+2), M(i+1)\}, & \text{if } i > 2 \\ A[1], & \text{if } i = 1 \\ \max\{A[1], A[2]\}, & \text{if } i = 2 \end{cases}$$

- The first case indicates whether we are selecting the i^{th} element or not. If we don't select the i^{th} element then we have to maximize the sum using the elements $i + 1$ to n . If i^{th} element is selected then we should not select $i + 1^{th}$ element need to maximize the sum using $i + 2$ to n elements.
- In the above representation, the last two cases indicate the base cases.

Time Complexity: $O(n)$. Space Complexity: $O(n)$.

Problem-11 Given a sequence of n numbers $A(1) \dots A(n)$, give an algorithm for finding a contiguous subsequence $A(i) \dots A(j)$ for which the sum of elements in the subsequence is maximum. Here the condition is we should not select *three* continuous numbers.

Solution: Input: Array $A(1) \dots A(n)$ of n numbers.

Given Array, A: recursive formula considers the case of selecting i^{th} element

	?	
--	-------	-------	-------	---	--

$A[i-3] \quad A[i-2] \quad A[i-1] \quad A[i]$

Assume that $M(i)$ represents the maximum sum from 1 to i numbers without selecting three contiguous numbers. While computing $M(i)$, the decision we have to make is, whether to select i^{th} element or not. This gives us the following possibilities:

$$M(i) = \max \begin{cases} A[i] + A[i-1] + M(i-3) \\ A[i] + M(i-2) \\ M(i-1) \end{cases}$$

- In the given problem the restriction is not to select three continuous numbers, but we can select two elements continuously and skip the third one. That is what the first case says in the above recursive formula. That means we are skipping $A[i-2]$.
- The other possibility is, selecting i^{th} element and skipping second $i - 1^{th}$ element. This is the second case (skipping $A[i-1]$).
- The third term defines the case of not selecting i^{th} element and as a result we should solve the problem with $i - 1$ elements.

Time Complexity: O(n). Space Complexity: O(n).

Problem-12 In [Problem-11](#), we assumed that $M(i)$ represents the maximum sum from 1 to i numbers without selecting three contiguous numbers. Can we solve the same problem by changing the definition as: $M(i)$ represents the maximum sum from i to n numbers without selecting three contiguous numbers?

Solution: Yes. The reasoning is very much similar. Let us see how DP solves this problem. Assume that $M(i)$ represents the maximum sum from i to n numbers without selecting three contiguous numbers.

Given Array, A: recursive formula considers the case of selecting i^{th} element

	?	
	A[i]	A[i+1]	A[i+2]	A[i+3]	

While computing $M(i)$, the decision we have to make is, whether to select i^{th} element or not. This gives us the following possibilities:

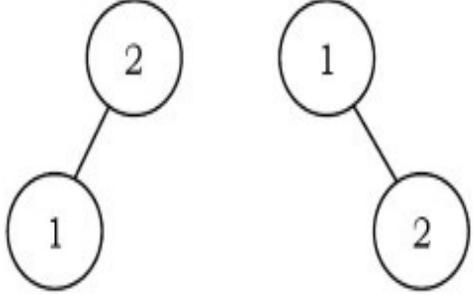
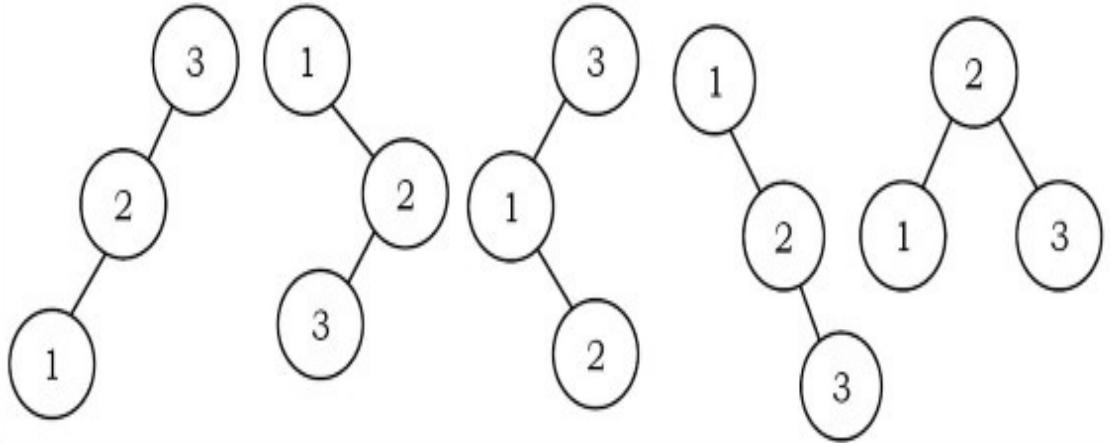
$$M(i) = \text{Max} \begin{cases} A[i] + A[i + 1] + M(i + 3) \\ A[i] + M(i + 2) \\ M(i + 1) \end{cases}$$

- In the given problem the restriction is to not select three continuous numbers, but we can select two elements continuously and skip the third one. That is what the first case says in the above recursive formula. That means we are skipping $A[i + 2]$.
- The other possibility is, selecting i^{th} element and skipping second $i - 1^{th}$ element. This is the second case (skipping $A[i + 1]$).
- And the third case is not selecting i^{th} element and as a result we should solve the problem with $i + 1$ elements.

Time Complexity: O(n). Space Complexity: O(n).

Problem-13 Catalan Numbers: How many binary search trees are there with n vertices?

Solution: Binary Search Tree (BST) is a tree where the left subtree elements are less than the root element, and the right subtree elements are greater than the root element. This property should be satisfied at every node in the tree. The number of BSTs with n nodes is called *Catalan Number* and is denoted by C_n . For example, there are 2 BSTs with 2 nodes (2 choices for the root) and 5 BSTs with 3 nodes.

Number of nodes, n	Number of Trees
1	
2	
3	

Let us assume that the nodes of the tree are numbered from 1 to n . Among the nodes, we have to select some node as root, and then divide the nodes which are less than root node into left sub tree, and elements greater than root node into right sub tree. Since we have already numbered the vertices, let us assume that the root element we selected is i^{th} element.

If we select i^{th} element as root then we get $i - 1$ elements on left sub-tree and $n - i$ elements on right sub tree. Since C_n is the Catalan number for n elements, C_{i-1} represents the Catalan number for left sub tree elements ($i - 1$ elements) and C_{n-i} represents the Catalan number for right sub tree elements. The two sub trees are independent of each other, so we simply multiply the two numbers. That means, the Catalan number for a fixed i value is $C_{i-1} \times C_{n-i}$.

Since there are n nodes, for i we will get n choices. The total Catalan number with n nodes can be given as:

$$C_n = \sum_{i=1}^n C_{i-1} \times C_{n-i}$$

```

int CatalanNumber( int n ) {
    if( n == 0 )
        return 1;
    int count = 0;
    for( int i = 1; i <= n; i++ )
        count += CatalanNumber( i - 1 ) * CatalanNumber( n - i );
    return count;
}

```

Time Complexity: $O(4^n)$. For proof, refer [Introduction](#) chapter.

Problem-14 Can we improve the time complexity of [Problem-13](#) using DP?

Solution: The recursive call C_n depends only on the numbers C_0 to C_{n-1} and for any value of i , there are a lot of recalculations. We will keep a table of previously computed values of C_i . If the function *CatalanNumber()* is called with parameter **i**, and if it has already been computed before, then we can simply avoid recalculating the same subproblem.

```

int Table[1024];
int CatalanNumber( int n ) {
    if( Table[n] != 1 )
        return Table[n];
    Table[n] = 0;
    for( int i = 1; i <= n; i++ )
        Table[n] += CatalanNumber( i - 1 ) * CatalanNumber( n - i );
    return Table[n];
}

```

The time complexity of this implementation $O(n^2)$, because to compute $CatalanNumber(n)$, we need to compute all of the $CatalanNumber(i)$ values between 0 and $n - 1$, and each one will be computed exactly once, in linear time.

In mathematics, Catalan Number can be represented by direct equation as: $\frac{(2n)!}{n!(n+1)!}$

Problem-15 Matrix Product Parenthesizations: Given a series of matrices: $A_1 \times A_2 \times A_3 \times \dots \times A_n$ with their dimensions, what is the best way to parenthesize them so that it produces the minimum number of total multiplications. Assume that we are using standard matrix and not Strassen's matrix multiplication algorithm.

Solution: Input: Sequence of matrices $A_1 \times A_2 \times A_3 \times \dots \times A_n$, where A_i is a $P_{i-1} \times P_i$. The dimensions are given in an array P.

Goal: Parenthesize the given matrices in such a way that it produces the optimal number of multiplications needed to compute $A_1 \times A_2 \times A_3 \times \dots \times A_n$.

For the matrix multiplication problem, there are many possibilities. This is because matrix multiplication is associative. It does not matter how we parenthesize the product, the result will be the same. As an example, for four matrices A, B, C, and D, the possibilities could be:

$$(ABC)D = (AB)(CD) = A(BCD) = A(BC)D = ..$$

Multiplying $(p \times q)$ matrix with $(q \times r)$ matrix requires pqr multiplications. Each of the above possibilities produces a different number of products during multiplication. To select the best one, we can go through each possible parenthesization (brute force), but this requires $O(2^n)$ time and is very slow. Now let us use DP to improve this time complexity. Assume that, $M[i,j]$ represents the least number of multiplications needed to multiply $A_i \dots A_j$.

$$M[i, j] = \begin{cases} 0 & , if i = j \\ \min\{M[i, k] + M[k + 1, j] + P_{i-1}P_kP_j\}, & if i < j \end{cases}$$

The above recursive formula says that we have to find point k such that it produces the minimum number of multiplications. After computing all possible values for k , we have to select the k value which gives minimum value. We can use one more table (say, $S[i,j]$) to reconstruct the optimal parenthesizations. Compute the $M[i,j]$ and $S[i,j]$ in a bottom-up fashion.

```

/* P is the sizes of the matrices, Matrix i has the dimension P[i-1] x P[i].
M[i,j] is the best cost of multiplying matrices i through j
S[i,j] saves the multiplication point and we use this for back tracing */
void MatrixChainOrder(int P[], int length) {
    int n = length - 1, M[n][n], S[n][n];
    for (int i = 1; i <= n; i++)
        M[i][i] = 0;
    // Fills in matrix by diagonals
    for (int l=2; l<= n; l++) {           // l is chain length
        for (int i=1; i<= n-l+1; i++) {
            int j = i+l-1;
            M[i][j] = MAX_VALUE;
            // Try all possible division points i..k and k..j
            for (int k=i; k<=j-1; k++) {
                int thisCost = M[i][k] + M[k+1][j] + P[i-1]*P[k]*P[j];
                if(thisCost < M[i][j]) {
                    M[i][j] = thisCost;
                    S[i][j] = k;
                }
            }
        }
    }
}

```

How many sub problems are there? In the above formula, i can range from 1 to n and j can range from 1 to n . So there are a total of n^2 subproblems, and also we are doing $n - 1$ such operations [since the total number of operations we need for $A_1 \times A_2 \times A_3 \times \dots \times A_n$ is $n - 1$]. So the time complexity is $O(n^3)$.

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

Problem-16 For the [Problem-15](#), can we use greedy method?

Solution: *Greedy* method is not an optimal way of solving this problem. Let us go through some counter example for this. As we have seen already, *greedy* method makes the decision that is good locally and it does not consider the future optimal solutions. In this case, if we use *Greedy*, then we always do the cheapest multiplication first. Sometimes it returns a parenthesization that is not optimal.

Example: Consider $A_1 \times A_2 \times A_3$ with dimensions 3×100 , 100×2 and 2×2 . Based on *greedy* we parenthesize them as: $A_1 \times (A_2 \times A_3)$ with $100 \cdot 2 \cdot 2 + 3 \cdot 100 \cdot 2 = 1000$ multiplications. But the optimal solution to this problem is: $(A_1 \times A_2) \times A_3$ with $3 \cdot 100 \cdot 2 + 3 \cdot 2 \cdot 2 = 612$

multiplications. \therefore we cannot use *greedy* for solving this problem.

Problem-17 Integer Knapsack Problem [Duplicate Items Permitted]: Given n types of items, where the i^{th} item type has an integer size s_i and a value v_i . We need to fill a knapsack of total capacity C with items of maximum value. We can add multiple items of the same type to the knapsack.

Note: For Fractional Knapsack problem refer to [Greedy Algorithms](#) chapter.

Solution: Input: n types of items where i^{th} type item has the size s_i and value v_i . Also, assume infinite number of items for each item type.

Goal: Fill the knapsack with capacity C by using n types of items and with maximum value.

One important note is that it's not compulsory to fill the knapsack completely. That means, filling the knapsack completely [of size C] if we get a value V and without filling the knapsack completely [let us say $C - 1$] with value U and if $V < U$ then we consider the second one. In this case, we are basically filling the knapsack of size $C - 1$. If we get the same situation for $C - 1$ also, then we try to fill the knapsack with $C - 2$ size and get the maximum value.

Let us say $M(j)$ denotes the maximum value we can pack into a j size knapsack. We can express $M(j)$ recursively in terms of solutions to sub problems as follows:

$$M(j) = \begin{cases} \max\{M(j - 1), \max_{i=1 \text{ to } n}(M(j - s_i)) + v_i\}, & \text{if } j \geq 1 \\ 0, & \text{if } j \leq 0 \end{cases}$$

For this problem the decision depends on whether we select a particular i^{th} item or not for a knapsack of size j .

- If we select i^{th} item, then we add its value v_i to the optimal solution and decrease the size of the knapsack to be solved to $j - s_i$.
- If we do not select the item then check whether we can get a better solution for the knapsack of size $j - 1$.

The value of $M(C)$ will contain the value of the optimal solution. We can find the list of items in the optimal solution by maintaining and following “back pointers”.

Time Complexity: Finding each $M(j)$ value will require $\Theta(n)$ time, and we need to sequentially compute C such values. Therefore, total running time is $\Theta(nC)$.

Space Complexity: $\Theta(C)$.

Problem-18 0-1 Knapsack Problem: For [Problem-17](#), how do we solve it if the items are not duplicated (not having an infinite number of items for each type, and each item is allowed to be used for 0 or 1 time)?

Real-time example: Suppose we are going by flight, and we know that there is a limitation on the luggage weight. Also, the items which we are carrying can be of different types (like laptops, etc.). In this case, our objective is to select the items with maximum value. That means, we need to tell the customs officer to select the items which have more weight and less value (profit).

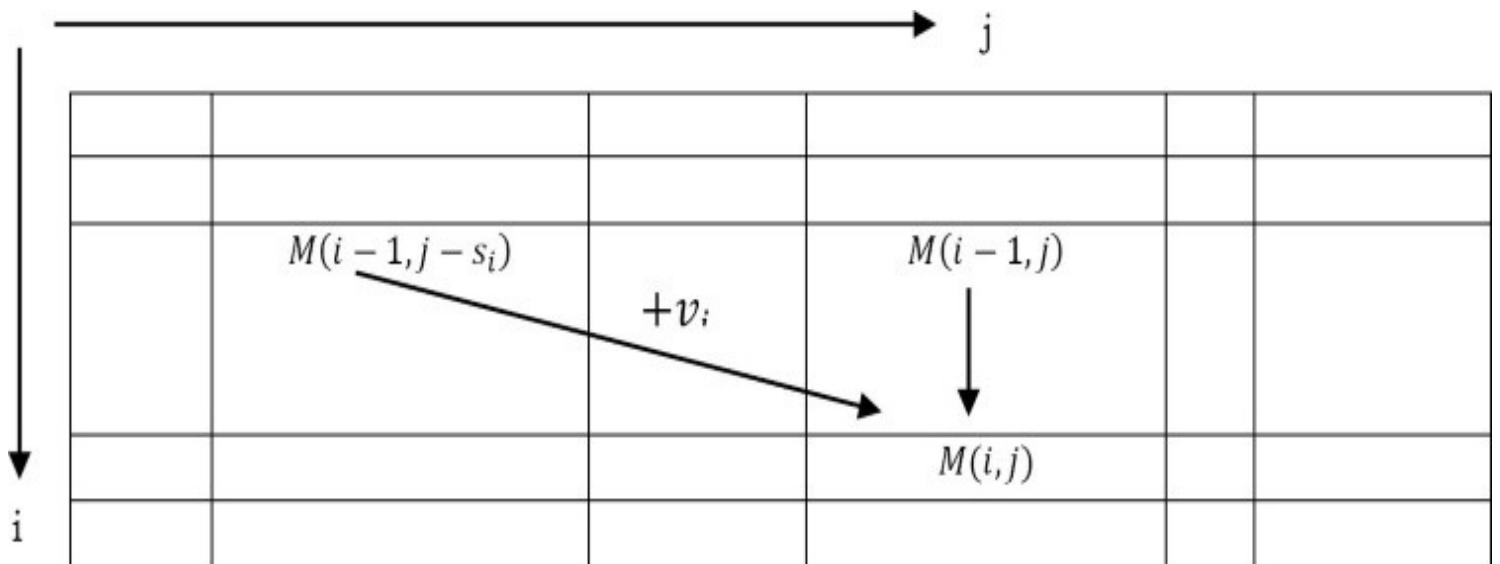
Solution: Input is a set of n items with sizes s_i and values v_i and a Knapsack of size C which we need to fill with a subset of items from the given set. Let us try to find the recursive formula for this problem using DP. Let $M(i,j)$ represent the optimal value we can get for filling up a knapsack of size j with items $1 \dots i$. The recursive formula can be given as:

$$M(i,j) = \text{Max}\{M(i-1,j), M(i-1,j-s_i) + v_i\}$$

\uparrow \uparrow
ith item is not used *ith item is used*

Time Complexity: $O(nC)$, since there are nC subproblems to be solved and each of them takes $O(1)$ to compute. Space Complexity: $O(nC)$, whereas Integer Knapsack takes only $O(C)$.

Now let us consider the following diagram which helps us in reconstructing the optimal solution and also gives further understanding. Size of below matrix is M .



Since i takes values from $1 \dots n$ and j takes values from $1 \dots C$, there are a total of nC subproblems. Now let us see what the above formula says:

- $M(i-1, j)$: Indicates the case of not selecting the i^{th} item. In this case, since we are not adding any size to the knapsack we have to use the same knapsack size for subproblems but excluding the i^{th} item. The remaining items are $i-1$.
- $M(i-1, j-s_i) + v_i$ indicates the case where we have selected the i^{th} item. If we add

the i^{th} item then we have to reduce the subproblem knapsack size to $j - s_i$ and at the same time we need to add the value v_i to the optimal solution. The remaining items are $i - 1$.

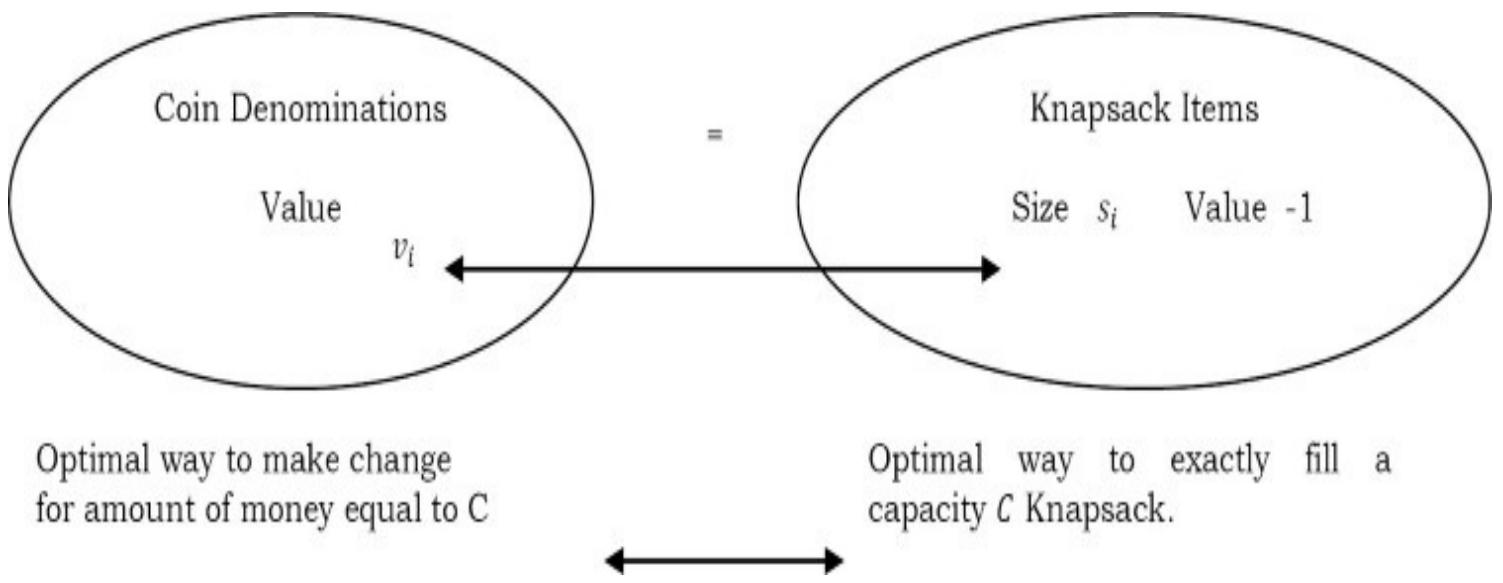
Now, after finding all $M(i,j)$ values, the optimal objective value can be obtained as:
 $\text{Max}_j\{M(n,j)\}$

This is because we do not know what amount of capacity gives the best solution.

In order to compute some value $M(i,j)$, we take the maximum of $M(i - 1,j)$ and $M(i - 1,j - s_i) + v_i$. These two values ($M(i,j)$ and $M(i - 1,j - s_i)$) appear in the previous row and also in some previous columns. So, $M(i,j)$ can be computed just by looking at two values in the previous row in the table.

Problem-19 Making Change: Given n types of coin denominations of values $v_1 < v_2 < \dots < v_n$ (integers). Assume $v_1 = 1$, so that we can always make change for any amount of money C . Give an algorithm which makes change for an amount of money C with as few coins as possible.

Solution:



This problem is identical to the Integer Knapsack problem. In our problem, we have coin denominations, each of value v_i . We can construct an instance of a Knapsack problem for each item that has a size s_i , which is equal to the value of v_i coin denomination. In the Knapsack we can give the value of every item as -1 .

Now it is easy to understand an optimal way to make money C with the fewest coins is completely equivalent to the optimal way to fill the Knapsack of size C . This is because since every value has a value of -1 , and the Knapsack algorithm uses as few items as possible which correspond to as few coins as possible.

Let us try formulating the recurrence. Let $M(j)$ indicate the minimum number of coins required to make change for the amount of money equal to j .

$$M(j) = \text{Min}_i\{M(j - v_i)\} + 1$$

What this says is, if coin denomination i was the last denomination coin added to the solution, then the optimal way to finish the solution with that one is to optimally make change for the amount of money $j - v_i$ and then add one extra coin of value v_i .

```
int Table[128] ; //Initialization
int MakingChange(int n) {
    if(n < 0) return -1;
    if(n == 0)
        return 0;
    if(Table[n] != -1)
        return Table[n];
    int ans = -1;
    for ( int i = 0 ; i < num_denomination ; ++i )
        ans = Min( ans , MakingChange(n - denominations [ i ]) );
    return Table[ n ] = ans + 1 ;
}
```

Time Complexity: $O(nC)$. Since we are solving C sub-problems and each of them requires minimization of n terms. Space Complexity: $O(nC)$.

Problem-20 Longest Increasing Subsequence: Given a sequence of n numbers $A_1 \dots A_n$, determine a subsequence (not necessarily contiguous) of maximum length in which the values in the subsequence form a strictly increasing sequence.

Solution:

Input: Sequence of n numbers $A_1 \dots A_n$.

Goal: To find a subsequence that is just a subset of elements and does not happen to be contiguous. But the elements in the subsequence should form a strictly increasing sequence and at the same time the subsequence should contain as many elements as possible.

For example, if the sequence is (5,6,2,3,4,1,9,9,8,9,5), then (5,6), (3,5), (1,8,9) are all increasing sub-sequences. The longest one of them is (2,3,4,8,9), and we want an algorithm for finding it.

First, let us concentrate on the algorithm for finding the longest subsequence. Later, we can try printing the sequence itself by tracing the table. Our first step is finding the recursive formula.

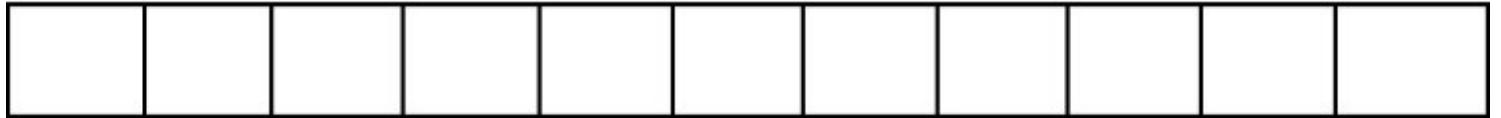
First, let us create the base conditions. If there is only one element in the input sequence then we don't have to solve the problem and we just need to return that element. For any sequence we can start with the first element ($A[1]$). Since we know the first number in the LIS, let's find the second number ($A[2]$). If $A[2]$ is larger than $A[1]$ then include $A[2]$ also. Otherwise, we are done - the LIS is the one element sequence($A[1]$).

Now, let us generalize the discussion and decide about i^{th} element. Let $L(i)$ represent the optimal subsequence which is starting at position $A[1]$ and ending at $A[i]$. The optimal way to obtain a strictly increasing subsequence ending at position i is to extend some subsequence starting at some earlier position j . For this the recursive formula can be written as:

$$L(i) = \text{Max}_{j < i \text{ and } A[j] < A[i]} \{L(j)\} + 1$$

The above recurrence says that we have to select some earlier position j which gives the maximum sequence. The 1 in the recursive formula indicates the addition of i^{th} element.

1 j i



Now after finding the maximum sequence for all positions we have to select the one among all positions which gives the maximum sequence and it is defined as:

$$\text{Max}_i \{L(i)\}$$

```

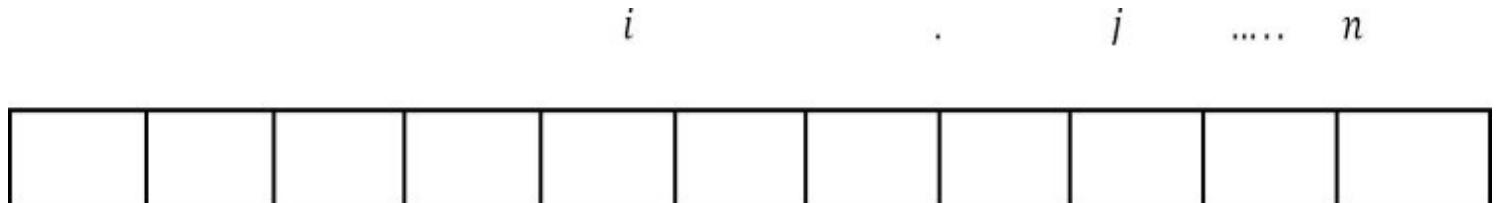
int LISTable [1024];
int LongestIncreasingSequence( int A[], int n ) {
    int i, j, max = 0;
    for ( i = 0; i < n; i++ )
        LISTable[i] = 1;
    for ( i = 0; i < n; i++ ) {
        for ( j = 0; j < i; j++ ) {
            if( A[i] > A[j] && LISTable[i] < LISTable[j] + 1 )
                LISTable[i] = LISTable[j] + 1;
        }
    }
    for ( i = 0; i < n; i++ ) {
        if( max < LISTable[i] )
            max = LISTable[i];
    }
    return max;
}

```

Time Complexity: $O(n^2)$, since two *for* loops. Space Complexity: $O(n)$, for table.

Problem-21 Longest Increasing Subsequence: In [Problem-20](#), we assumed that $L(i)$ represents the optimal subsequence which is starting at position $A[1]$ and ending at $A[i]$. Now, let us change the definition of $L(i)$ as: $L(i)$ represents the optimal subsequence which is starting at position $A[i]$ and ending at $A[n]$. With this approach can we solve the problem?

Solution: Yes.



Let $L(i)$ represent the optimal subsequence which is starting at position $A[i]$ and ending at $A[n]$. The optimal way to obtain a strictly increasing subsequence starting at position i is going to be to extend some subsequence starting at some later position j . For this the recursive formula can be written as:

$$L(i) = \max_{j < i \text{ and } A[j] < A[i]} \{L(j)\} + 1$$

We have to select some later position j which gives the maximum sequence. The 1 in the recursive formula is the addition of i^{th} element. After finding the maximum sequence for all positions select

the one among all positions which gives the maximum sequence and it is defined as:

$$\text{Max}_i\{L(i)\}$$

```
int LISTable [1024];
int LongestIncreasingSequence( int A[], int n ) {
    int i, j, max = 0;
    for ( i = 0; i < n; i++ )
        LISTable[i] = 1;
    for ( i = n - 1; i >= 0; i++ ) {
        // try picking a larger second element
        for ( j = i + 1; j < n; j++ ) {
            if( A[i] < A[j] && LISTable [i] < LISTable [j] + 1)
                LISTable[i] = LISTable[j] + 1;
        }
    }
    for ( i = 0; i < n; i++ ) {
        if( max < LISTable[i] )
            max = LISTable[i];
    }
    return max;
}
```

Time Complexity: $O(n^2)$ since two nested *for* loops. Space Complexity: $O(n)$, for table.

Problem-22 Is there an alternative way of solving *Problem-21*?

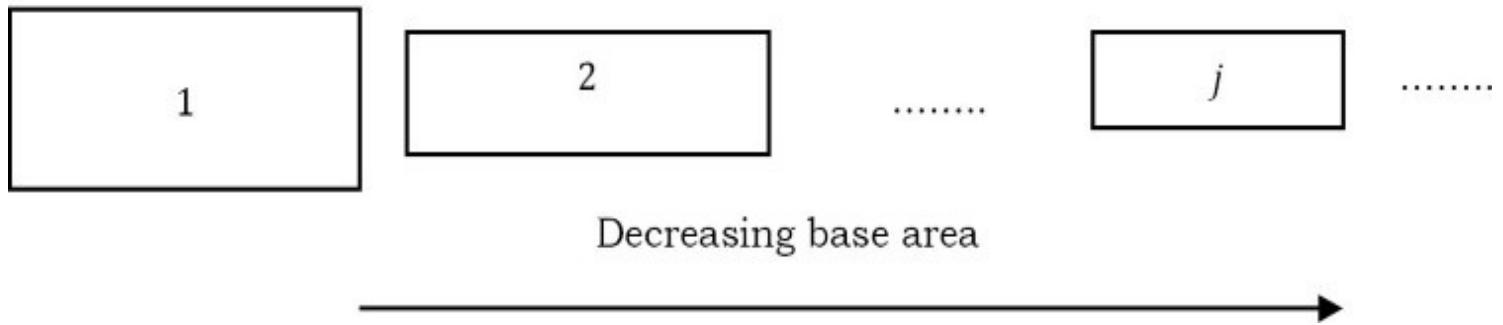
Solution: Yes. The other method is to sort the given sequence and save it into another array and then take out the “Longest Common Subsequence” (LCS) of the two arrays. This method has a complexity of $O(n^2)$. For LCS problem refer *theory section* of this chapter.

Problem-23 Box Stacking: Assume that we are given a set of n rectangular 3 – D boxes. The dimensions of i^{th} box are height h_i , width w_i and depth d_i . Now we want to create a stack of boxes which is as tall as possible, but we can only stack a box on top of another box if the dimensions of the 2 – D base of the lower box are each strictly larger than those of the 2 – D base of the higher box. We can rotate a box so that any side functions as its base. It is possible to use multiple instances of the same type of box.

Solution: Box stacking problem can be reduced to LIS [*Problem-21*].

Input: n boxes where i^{th} with height h_i , width w_i and depth d_i . For all n boxes we have to consider all the orientations with respect to rotation. That is, if we have, in the original set, a box with dimensions $1 \times 2 \times 3$, then we consider 3 boxes,

$$1 \times 2 \times 3 \Rightarrow \begin{cases} 1 \times (2 \times 3), \text{with height 1, base 2 and width 3} \\ 2 \times (1 \times 3), \text{with height 2, base 1 and width 3} \\ 3 \times (1 \times 2), \text{with height 3, base 1 and width 2} \end{cases}$$



This simplification allows us to forget about the rotations of the boxes and we just focus on the stacking of n boxes with each height as h_i and a base area of $(w_i \times d_i)$. Also assume that $w_i \leq d_i$. Now what we do is, make a stack of boxes that is as tall as possible and has maximum height. We allow a box i on top of box j only if box i is smaller than box j in both the dimensions. That means, if $w_i < w_j \text{ and } d_i < d_j$. Now let us solve this using DP. First select the boxes in the order of decreasing base area.

Now, let us say $H(j)$ represents the tallest stack of boxes with box j on top. This is very similar to the LIS problem because the stack of n boxes with ending box j is equal to finding a subsequence with the first j boxes due to the sorting by decreasing base area. The order of the boxes on the stack is going to be equal to the order of the sequence.

Now we can write $H(j)$ recursively. In order to form a stack which ends on box j , we need to extend a previous stack ending at i . That means, we need to put j box at the top of the stack [i box is the current top of the stack]. To put j box at the top of the stack we should satisfy the condition $w_i > w_j \text{ and } d_i > d_j$ [this ensures that the low level box has more base than the boxes above it]. Based on this logic, we can write the recursive formula as:

$$H(j) = \max_{i < j \text{ and } w_i > w_j \text{ and } d_i > d_j} \{H(i)\} + h_i$$

Similar to the LIS problem, at the end we have to select the best j over all potential values. This is because we are not sure which box might end up on top.

$$\max_j \{H(j)\}$$

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

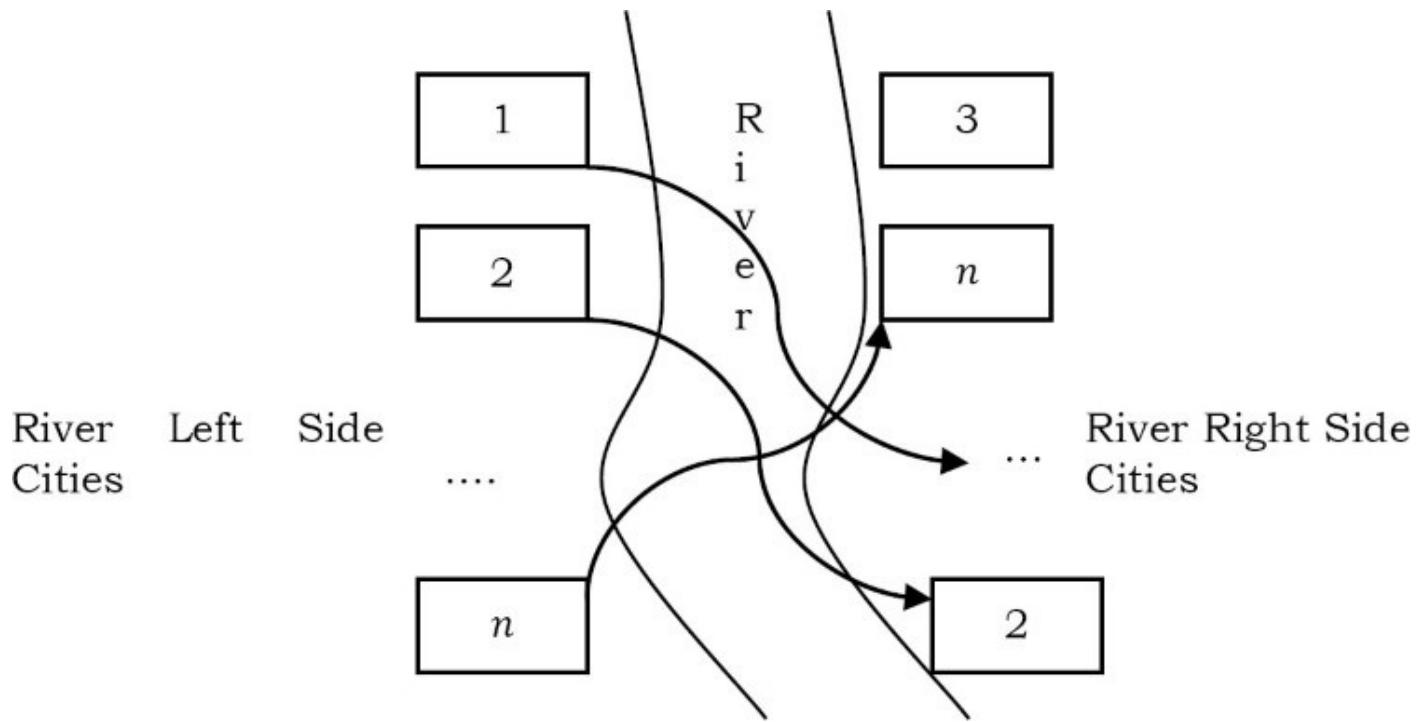
Problem-24 Building Bridges in India: Consider a very long, straight river which moves from north to south. Assume there are n cities on both sides of the river: n cities on the left of the river and n cities on the right side of the river. Also, assume that these cities are numbered from 1 to n but the order is not known. Now we want to connect as many left-

right pairs of cities as possible with bridges such that no two bridges cross. When connecting cities, we can only connect city i on the left side to city i on the right side.

Solution:

Input: Two pairs of sets with each numbered from 1 to n .

Goal: Construct as many bridges as possible without any crosses between left side cities to right side cities of the river.



To understand better let us consider the diagram below. In the diagram it can be seen that there are n cities on the left side of river and n cities on the right side of river. Also, note that we are connecting the cities which have the same number [a requirement in the problem]. Our goal is to connect the maximum cities on the left side of river to cities on the right side of the river, without any cross edges. Just to make it simple, let us sort the cities on one side of the river.

If we observe carefully, since the cities on the left side are already sorted, the problem can be simplified to finding the maximum increasing sequence. That means we have to use the LIS solution for finding the maximum increasing sequence on the right side cities of the river.

Time Complexity: $O(n^2)$, (same as LIS).

Problem-25 Subset Sum: Given a sequence of n positive numbers $A_1 \dots A_n$, give an algorithm which checks whether there exists a subset of A whose sum of all numbers is T ?

Solution: This is a variation of the Knapsack problem. As an example, consider the following array:

$$A = [3, 2, 4, 19, 3, 7, 13, 10, 6, 11]$$

Suppose we want to check whether there is any subset whose sum is 17. The answer is yes, because the sum of $4 + 13 = 17$ and therefore $\{4, 13\}$ is such a subset.

Let us try solving this problem using DP. We will define $n \times T$ matrix, where n is the number of elements in our input array and T is the sum we want to check.

Let, $M[i, j] = 1$ if it is possible to find a subset of the numbers 1 through i that produce sum/ and $M[i, j] = 0$ otherwise.

$$M[i, j] = \text{Max}(M[i - 1, j], M[i - 1, j - A_i])$$

According to the above recursive formula similar to the Knapsack problem, we check if we can get the sum j by not including the element i in our subset, and we check if we can get the sum j by including i and checking if the sum $j - A_i$ exists without the i^{th} element. This is identical to Knapsack, except that we are storing 0/1's instead of values. In the below implementation we can use binary OR operation to get the maximum among $M[i - 1, j]$ and $M[i - 1, j - A_i]$.

```
int SubsetSum( int A[], int n, int T ) {
    int i, j, M[n+1][T+1];
    M[0][0]=0;
    for (i=1; i<= T; i++)
        M[0][i]= 0;
    for (i=1; i<=n; i++) {
        for (j = 0; j<= T; j++) {
            M[i][j] = M[i-1][j] || M[i-1][j - A[i]];
        }
    }
    return M[n][T];
}
```

How many subproblems are there? In the above formula, i can range from 1 to n and j can range from 1 to T . There are a total of nT subproblems and each one takes $O(1)$. So the time complexity is $O(nT)$ and this is not polynomial as the running time depends on two variables [n and T], and we can see that they are an exponential function of the other.

Space Complexity: $O(nT)$.

Problem-26 Given a set of n integers and the sum of all numbers is at most n . Find the subset of these n elements whose sum is exactly half of the total sum of n numbers.

Solution: Assume that the numbers are $A_1 \dots A_n$. Let us use DP to solve this problem. We will

create a boolean array T with size equal to $K + 1$. Assume that $T[x]$ is 1 if there exists a subset of given n elements whose sum is x . That means, after the algorithm finishes, $T[K]$ will be 1, if and only if there is a subset of the numbers that has sum K . Once we have that value then we just need to return $T[K/2]$. If it is 1, then there is a subset that adds up to half the total sum.

Initially we set all values of T to 0. Then we set $T[0]$ to 1. This is because we can always build 0 by taking an empty set. If we have no numbers in A , then we are done! Otherwise, we pick the first number, $A[0]$. We can either throw it away or take it into our subset. This means that the new $T[]$ should have $T[0]$ and $T[A[0]]$ set to 1. This creates the base case. We continue by taking the next element of A .

Suppose that we have already taken care of the first $i - 1$ elements of A . Now we take $A[i]$ and look at our table $T[]$. After processing $i - 1$ elements, the array T has a 1 in every location that corresponds to a sum that we can make from the numbers we have already processed. Now we add the new number, $A[i]$. What should the table look like? First of all, we can simply ignore $A[i]$. That means, no one should disappear from $T[]$ - we can still make all those sums. Now consider some location of $T[j]$ that has a 1 in it. It corresponds to some subset of the previous numbers that add up to j . If we add $A[i]$ to that subset, we will get a new subset with total sum $j + A[i]$. So we should set $T[j + A[i]]$ to 1 as well. That's all. Based on the above discussion, we can write the algorithm as:

```

bool T[10240];
bool SubsetHalfSum( int A[], int n ) {
    int K = 0;
    for( int i = 0; i < n; i++ )
        K += A[i];
    T[0] = 1;          // initialize the table
    for( int i = 1; i <= K; i++ )
        T[i] = 0;
    // process the numbers one by one
    for( int i = 0; i < n; i++ ) {
        for( int j = K - A[i]; j >= 0; j-- ) {
            if( T[j] )
                T[j + A[i]] = 1;
        }
    }
    return T[K / 2];
}

```

In the above code, j loop moves from right to left. This reduces the double counting problem. That means, if we move from left to right, then we may do the repeated calculations.

Time Complexity: $O(nK)$, for the two *for* loops. Space Complexity: $O(K)$, for the boolean table T .

Problem-27 Can we improve the performance of [Problem-26](#)?

Solution: Yes. In the above code what we are doing is, the inner j loop is starting from K and moving left. That means, it is unnecessarily scanning the whole table every time.

What we actually want is to find all the 1 entries. At the beginning, only the 0th entry is 1. If we keep the location of the rightmost 1 entry in a variable, we can always start at that spot and go left instead of starting at the right end of the table.

To take full advantage of this, we can sort $A[]$ first. That way, the rightmost 1 entry will move to the right as slowly as possible. Finally, we don't really care about what happens in the right half of the table (after $T[K/2]$) because if $T[x]$ is 1, then $T[Kx]$ must also be 1 eventually – it corresponds to the complement of the subset that gave us x . The code based on above discussion is given below.

```
int T[10240];
int SubsetHalfSumEfficient( int A[], int n ) {
    int K = 0;
    for( int i = 0; i < n; i++ )
        K += A[i];
    Sort(A,n));
    T[0] = 1;           // initialize the table
    for( int i = 1; i <= sum; i++ )
        T[i] = 0;
    int R = 0; // rightmost 1 entry
    for( int i = 0; i < n; i++ ) {           // process the numbers one by one
        for( int j = R; j >= 0; j-- ) {
            if( T[j] )
                T[j + A[i]] = 1;
            R = min(K / 2, R + C[i]);
        }
    }
    return T[K / 2];
}
```

After the improvements, the time complexity is still $O(nK)$, but we have removed some useless steps.

Problem-28 Partition partition problem is to determine whether a given set can be partitioned into two subsets such that the sum of elements in both subsets is the same [the same as the previous problem but a different way of asking]. For example, if $A[] = \{1, 5,$

$\{11, 5\}$, the array can be partitioned as $\{1, 5, 5\}$ and $\{11\}$. Similarly, if $A[] = \{1, 5, 3\}$, the array cannot be partitioned into equal sum sets.

Solution: Let us try solving this problem another way. Following are the two main steps to solve this problem:

1. Calculate the sum of the array. If the sum is odd, there cannot be two subsets with an equal sum, so return false.
2. If the sum of the array elements is even, calculate $sum/2$ and find a subset of the array with a sum equal to $sum/2$.

The first step is simple. The second step is crucial, and it can be solved either using recursion or Dynamic Programming.

Recursive Solution: Following is the recursive property of the second step mentioned above. Let $subsetSum(A, n, sum/2)$ be the function that returns true if there is a subset of $A[0..n-1]$ with sum equal to $sum/2$. The $isSubsetSum$ problem can be divided into two sub problems:

- a) $isSubsetSum()$ without considering last element (reducing n to $n - 1$)
- b) $isSubsetSum$ considering the last element (reducing $sum/2$ by $A[n-1]$ and n to $n - 1$)

If any of the above sub problems return true, then return true.

$$subsetSum (A,n,sum/2) = isSubsetSum (A,n - 1,sum/2) \text{ || } subsetSum (A,n - 1,sum/2 - A[n - 1])$$

```

// A utility function that returns true if there is a subset of A[] with sum equal to given sum
bool subsetSum (int A[], int n, int sum){
    if (sum == 0)
        return true;
    if (n == 0 && sum != 0)
        return false;
    // If last element is greater than sum, then ignore it
    if (A[n-1] > sum)
        return subsetSum (A, n-1, sum);
    return subsetSum (A, n-1, sum) || subsetSum (A, n-1, sum-A[n-1]);
}

```

```

// Returns true if A[] can be partitioned in two subsets of equal sum, otherwise false
bool findPartition (int A[], int n){
    // calculate sum of all elements
    int sum = 0;
    for (int i = 0; i < n; i++)
        sum += A[i];
    // If sum is odd, there cannot be two subsets with equal sum
    if (sum%2 != 0)
        return false;
    // Find if there is subset with sum equal to half of total sum
    return subsetSum (A, n, sum/2);
}

```

Time Complexity: $O(2^n)$ In worst case, this solution tries two possibilities (whether to include or exclude) for every element.

Dynamic Programming Solution: The problem can be solved using dynamic programming when the sum of the elements is not too big. We can create a 2D array $\text{part}[][]$ of size $(\text{sum}/2)*(n + 1)$. And we can construct the solution in a bottom-up manner such that every filled entry has a following property

$\text{part}[i][j] = \text{true if a subset of } \{A[0], A[1], \dots, A[j-1]\} \text{ has sum equal to } \text{sum}/2, \text{ otherwise false}$

```

// Returns true if A[] can be partitioned in two subsets of equal sum, otherwise false
bool findPartition (int A[], int n){
    int sum = 0;
    int i, j;
    // calculate sum of all elements
    for (i = 0; i < n; i++)
        sum += A[i];
    if (sum%2 != 0)
        return false;
    bool part[sum/2+1][n+1];
    // initialize top row as true
    for (i = 0; i <= n; i++)
        part[0][i] = true;
    // initialize leftmost column, except part[0][0], as 0
    for (i = 1; i <= sum/2; i++)
        part[i][0] = false;
    // Fill the partition table in bottom up manner
    for (i = 1; i <= sum/2; i++) {
        for (j = 1; j <= n; j++) {
            part[i][j] = part[i][j-1];
            if (i >= A[j-1])
                part[i][j] = part[i][j] || part[i - A[j-1]][j-1];
        }
    }
    return part[sum/2][n];
}

```

Time Complexity: $O(sum \times n)$. Space Complexity: $O(sum \times n)$. Please note that this solution will not be feasible for arrays with a big sum.

Problem-29 Counting Boolean Parenthesizations: Let us assume that we are given a boolean expression consisting of symbols ‘true’, ‘false’, ‘and’, ‘or’, and ‘xor’. Find the number of ways to parenthesize the expression such that it will evaluate to *true*. For example, there is only 1 way to parenthesize ‘*true and false xor true*’ such that it evaluates to *true*.

Solution: Let the number of symbols be n and between symbols there are boolean operators like and, or, xor, etc. For example, if $n = 4$, $T \text{ or } F \text{ and } T \text{ xor } F$. Our goal is to count the numbers of ways to parenthesize the expression with boolean operators so that it evaluates to *true*. In the above case, if we use $T \text{ or } ((F \text{ and } T) \text{ xor } F)$ then it evaluates to *true*.

$$T \text{ or} \{ (F \text{ and } T) \text{ xor } F \} = \text{True}$$

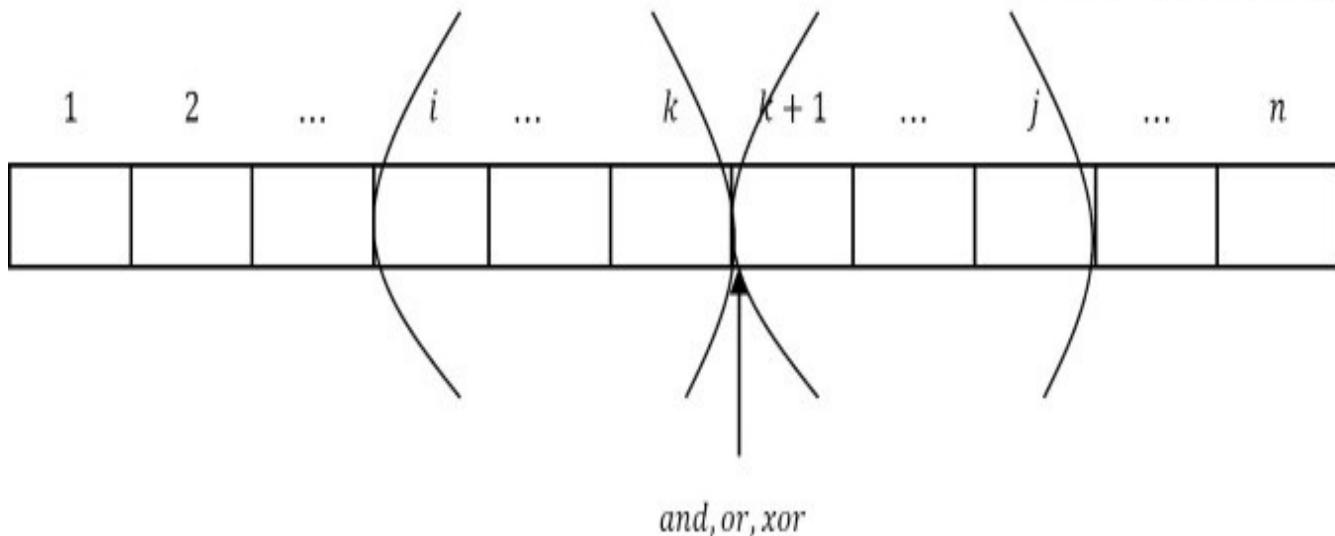
Now let us see how DP solves this problem. Let $T(i,j)$ represent the number of ways to parenthesize the sub expression with symbols $i \dots j$ [symbols means only T and F and not the operators] with boolean operators so that it evaluates to *true*. Also, i and j take the values from 1 to n . For example, in the above case, $T(2,4) = 0$ because there is no way to parenthesize the expression F and T xor F to make it *true*.

Just for simplicity and similarity, let $F(i,j)$ represent the number of ways to parenthesize the sub expression with symbols $i \dots j$ with boolean operators so that it evaluates to *false*. The base cases are $T(i,i)$ and $F(i,i)$.

Now we are going to compute $T(i, i + 1)$ and $F(i, i + 1)$ for all values of i . Similarly, $T(i, i + 2)$ and $F(i, i + 2)$ for all values of i and so on. Now let's generalize the solution.

$$T(i,j) = \sum_{k=i}^{j-1} \begin{cases} T(i,k)T(k+1,j), & \text{for "and"} \\ \text{Total}(i,k)\text{Total}(k+1,j) - F(i,k)F(k+1,j), & \text{for "or"} \\ T(i,k)F(k+1,j) + F(i,k)T(k+1,j), & \text{for "xor"} \end{cases}$$

Where, $\text{Total}(i,k) = T(i,k) + F(i,k)$.



What this above recursive formula says is, $T(i,j)$ indicates the number of ways to parenthesize the expression. Let us assume that we have some sub problems which are ending at k . Then the total number of ways to parenthesize from i to j is the sum of counts of parenthesizing from i to k and from $k + 1$ to j . To parenthesize between k and $k + 1$ there are three ways: “*and*”, “*or*” and “*xor*”.

- If we use “*and*” between k and $k + 1$, then the final expression becomes *true* only when both are *true*. If both are *true* then we can include them to get the final count.
- If we use “*or*”, then if at least one of them is *true*, the result becomes *true*. Instead of including all three possibilities for “*or*”, we are giving one alternative where we are subtracting the “*false*” cases from total possibilities.

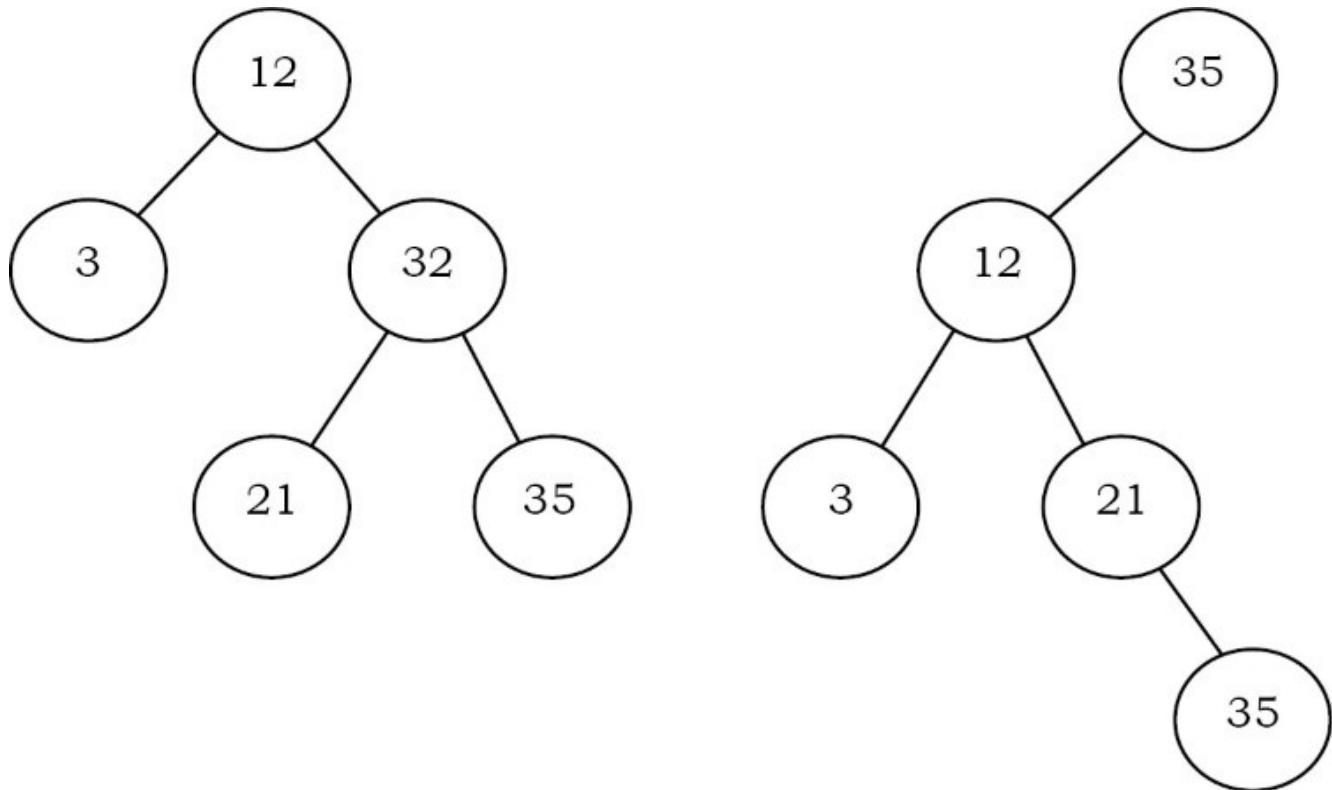
- The same is the case with “*xor*”. The conversation is as in the above two cases.

After finding all the values we have to select the value of k , which produces the maximum count, and for k there are i to $j - 1$ possibilities.

How many subproblems are there? In the above formula, i can range from 1 to n , and j can range from 1 to n . So there are a total of n^2 subproblems, and also we are doing summation for all such values. So the time complexity is $O(n^3)$.

Problem-30 Optimal Binary Search Trees: Given a set of n (sorted) keys $A[1..n]$, build the best binary search tree for the elements of A . Also assume that each element is associated with *frequency* which indicates the number of times that a particular item is searched in the binary search trees. That means we need to construct a binary search tree so that the total search time will be reduced.

Solution: Before solving the problem let us understand the problem with an example. Let us assume that the given array is $A = [3, 12, 21, 32, 35]$. There are many ways to represent these elements, two of which are listed below.



Of the two, which representation is better? The search time for an element depends on the depth of the node. The average number of comparisons for the first tree is: $\frac{1+2+2+3+3}{5} = \frac{11}{5}$ and for the second tree, the average number of comparisons is: $\frac{1+2+3+3+4}{5} = \frac{13}{5}$. Of the two, the first tree gives better results.

If frequencies are not given and if we want to search all elements, then the above simple

calculation is enough for deciding the best tree. If the frequencies are given, then the selection depends on the frequencies of the elements and also the depth of the elements. For simplicity let us assume that the given array is A and the corresponding frequencies are in array F . $F[i]$ indicates the frequency of i^{th} element $A[i]$. With this, the total search time $S(\text{root})$ of the tree with root can be defined as:

$$S(\text{root}) = \sum_{i=1}^n (\text{depth}(\text{root}, i) + 1) \times F[i]$$

In the above expression, $\text{depth}(\text{root}, i) + 1$ indicates the number of comparisons for searching the i^{th} element. Since we are trying to create a binary search tree, the left subtree elements are less than root element and the right subtree elements are greater than root element. If we separate the left subtree time and right subtree time, then the above expression can be written as:

$$S(\text{root}) = \sum_{i=1}^{r-1} (\text{depth}(\text{root}, i) + 1) \times F[i] + \sum_{i=1}^r F[i] + \sum_{i=r+1}^n (\text{depth}(\text{root}, i) + 1) \times F[i]$$

Where r indicates the position of the root element in the array.

If we replace the left subtree and right subtree times with their corresponding recursive calls, then the expression becomes:

$$S(\text{root}) = S(\text{root} \rightarrow \text{left}) + S(\text{root} \rightarrow \text{right}) + + \sum_{i=1}^n F[i]$$

Binary Search Tree node declaration

Refer to [Trees](#) chapter.

Implementation:

```

struct BinarySearchTreeNode *OptimalBST(int A[], int F[], int low, int high) {
    int r, minTime = 0;
    struct BinarySearchTreeNode *newNode=(struct BinarySearchTreeNode *)
        malloc(sizeof(struct BinarySearchTreeNode));
    if(!newNode) {
        printf("Memory Error");
        return;
    }
    for (r = 0, r <= n-1; r++) {
        root->left = OptimalBST(A, F, low, r-1);
        root->right = OptimalBST(A, F, r+1, high);
        root->data = A[r];
        if(minTime > S(root)) minTime = S(root);
    }
    return minTime;
}

```

Problem-31 Edit Distance: Given two strings A of length m and B of length n , transform A into B with a minimum number of operations of the following types: delete a character from A , insert a character into A , or change some character in A into a new character. The minimal number of such operations required to transform A into B is called the *edit distance* between A and B .

Solution:

Input: Two text strings A of length m and B of length n .

Goal: Convert string A into B with minimal conversions.

Before going to a solution, let us consider the possible operations for converting string A into B .

- If $m > n$, we need to remove some characters of A
- If $m == n$, we may need to convert some characters of A
- If $m < n$, we need to remove some characters from A

So the operations we need are the insertion of a character, the replacement of a character and the deletion of a character, and their corresponding cost codes are defined below.

Costs of operations:

Insertion of a character	c_i
Replacement of a character	c_r

Now let us concentrate on the recursive formulation of the problem. Let, $T(i,j)$ represents the minimum cost required to transform first i characters of A to first j characters of B . That means, $A[1\dots i]$ to $B[1\dots j]$.

$$T(i,j) = \min \begin{cases} c_d + T(i-1, j) \\ T(i, j-1) + c_i \\ \begin{cases} T(i-1, j-1), & \text{if } A[i] == B[j] \\ T(i-1, j-1) + c_r & \text{if } A[i] \neq B[j] \end{cases} \end{cases}$$

Based on the above discussion we have the following cases.

- If we delete i^{th} character from A , then we have to convert remaining $i - 1$ characters of A to j characters of B
- If we insert i^{th} character in A , then convert these i characters of A to $j - 1$ characters of B
- If $A[i] == B[j]$, then we have to convert the remaining $i - 1$ characters of A to $j - 1$ characters of B
- If $A[i] \neq B[j]$, then we have to replace i^{th} character of A to j^{th} character of B and convert remaining $i - 1$ characters of A to $j - 1$ characters of B

After calculating all the possibilities we have to select the one which gives the lowest cost.

How many subproblems are there? In the above formula, i can range from 1 to m and j can range from 1 to n . This gives mn subproblems and each one takes $O(1)$ and the time complexity is $O(mn)$. Space Complexity: $O(mn)$ where m is number of rows and n is number of columns in the given matrix.

Problem-32 All Pairs Shortest Path Problem: Floyd's Algorithm: Given a weighted directed graph $G = (V,E)$, where $V = \{1,2,\dots,n\}$. Find the shortest path between any pair of nodes in the graph. Assume the weights are represented in the matrix $C[V][V]$, where $C[i][j]$ indicates the weight (or cost) between the nodes i and j . Also, $C[i][j] = \infty$ or -1 if there is no path from node i to node j .

Solution: Let us try to find the DP solution (Floyd's algorithm) for this problem. The Floyd's algorithm for all pairs shortest path problem uses matrix $A[1..n][1..n]$ to compute the lengths of the shortest paths. Initially,

$$\begin{aligned} A[i,j] &= C[i,j] \quad \text{if } i \neq j \\ &= 0 \quad \text{if } i = j \end{aligned}$$

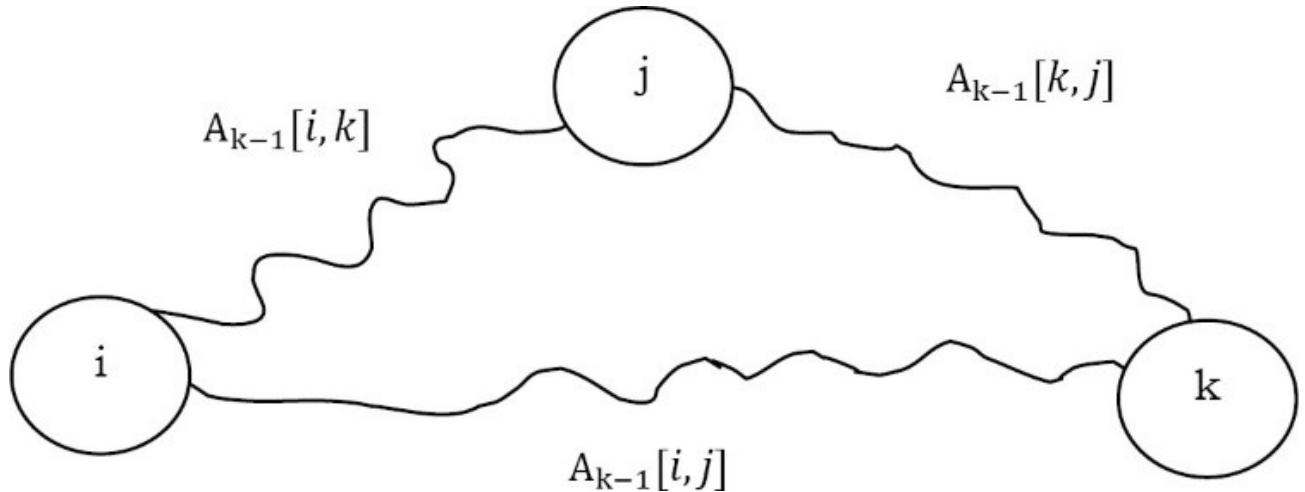
From the definition, $C[i,j] = \infty$ if there is no path from i to j . The algorithm makes n passes over A . Let A_0, A_1, \dots, A_n be the values of A on the n passes, with A_0 being the initial value.

Just after the $k - 1^{\text{th}}$ iteration, $A_{k-1}[i,j] = \text{smallest length of any path from vertex } i \text{ to vertex } j \text{ that does not pass through the vertices } \{k+1, k+2, \dots, n\}$. That means, it passes through the vertices possibly through $\{1, 2, 3, \dots, k-1\}$.

In each iteration, the value $A[i][j]$ is updated with minimum of $A_{k-1}[i,j]$ and $A_{k-1}[i,k] + A_{k-1}[k,j]$.

$$A[i,j] = \min \begin{cases} A_{k-1}[i,j] \\ A_{k-1}[i,k] + A_{k-1}[k,j] \end{cases}$$

The k^{th} pass explores whether the vertex k lies on an optimal path from i to j , for all i, j . The same is shown in the diagram below.



```
void Floyd(int C[][], int A[][], int n) {
    int i, j, k;
    for(i = 0; i <= n - 1; i++)
        for(j = 0; j <= n - 1; j++)
            A[i][j] = C[i][j];
    for(i = 0; i <= n - 1; i++)
        A[i][i] = 0;
    for(k = 0; k <= n - 1; k++) {
        for(i = 0; i <= n - 1; i++) {
            for(j = 0; j <= n - 1; j++) {
                if(A[i][k] + A[k][j] < A[i][j])
                    A[i][j] = A[i][k] + A[k][j];
            }
        }
    }
}
```

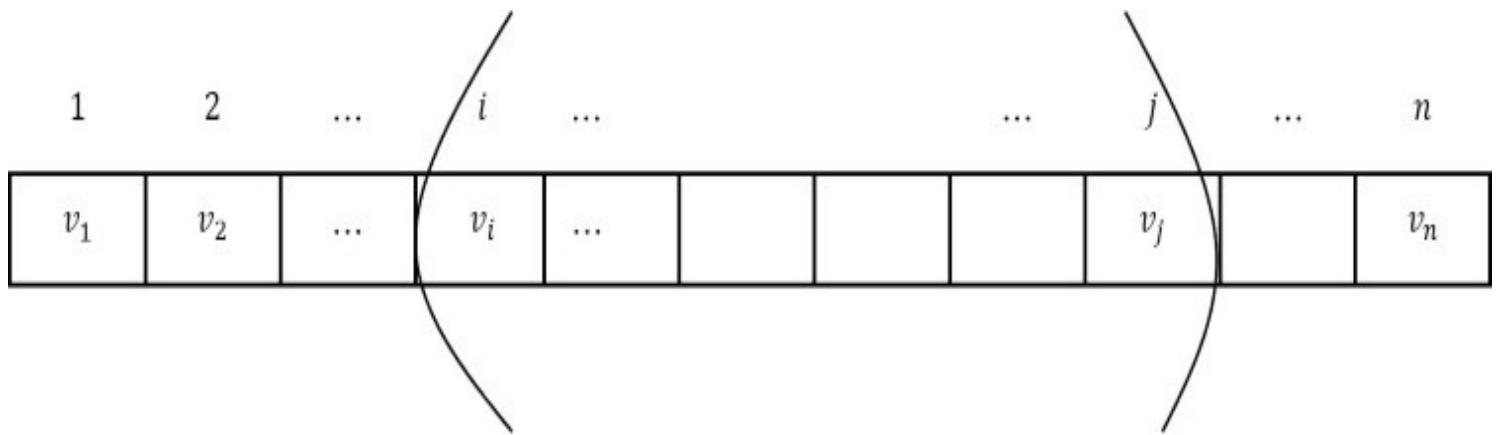
Time Complexity: $O(n^3)$.

Problem-33 Optimal Strategy for a Game: Consider a row of n coins of values $v_1 \dots v_n$, where n is even [since it's a two player game]. We play this game with the opponent. In each turn, a player selects either the first or last coin from the row, removes it from the row permanently, and receives the value of the coin. Determine the maximum possible amount of money we can definitely win if we move first.

Alternative way of framing the question: Given n pots, each with some number of gold coins, are arranged in a line. You are playing a game against another player. You take turns picking a pot of gold. You may pick a pot from either end of the line, remove the pot, and keep the gold pieces. The player with the most gold at the end wins. Develop a strategy for playing this game.

Solution: Let us solve the problem using our DP technique. For each turn either we or our opponent selects the coin only from the ends of the row. Let us define the subproblems as:

$V(i,j)$: denotes the maximum possible value we can definitely win if it is our turn and the only coins remaining are $v_i \dots v_j$.



Base Cases: $V(i,i), V(i, i + 1)$ for all values of i .

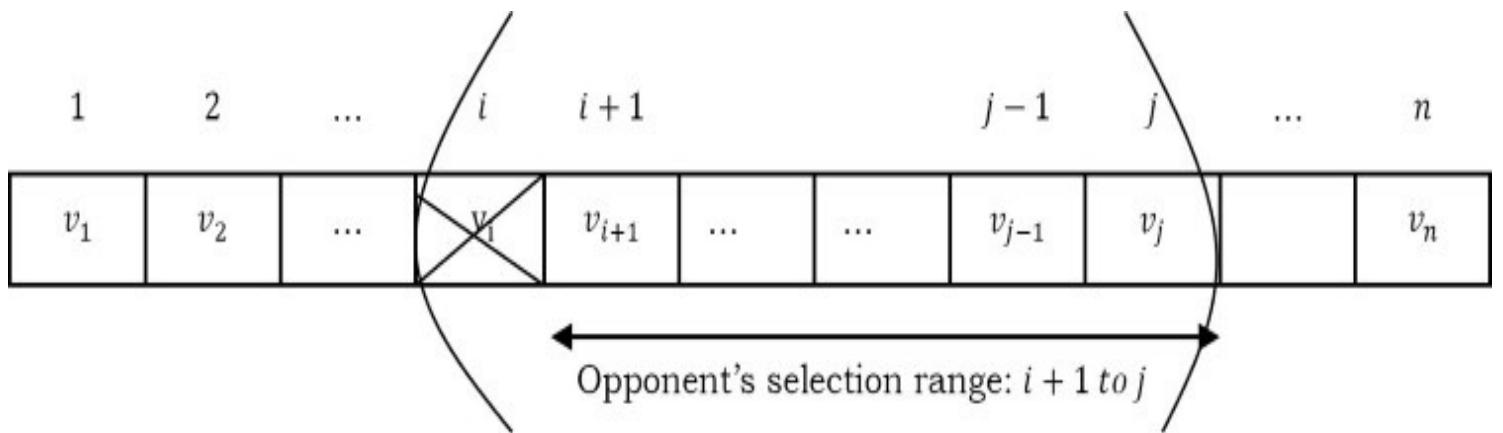
From these values, we can compute $V(i, i + 2), V(i, i + 3)$ and so on. Now let us define $V(i,j)$ for each sub problem as:

$$V(i,j) = \text{Max} \left\{ \text{Min} \left\{ \frac{V(i+1, j-1)}{V(i+2, j)} \right\} + v_i, \text{Min} \left\{ \frac{V(i, j-2)}{V(i+1, j-1)} \right\} + v_j \right\}$$

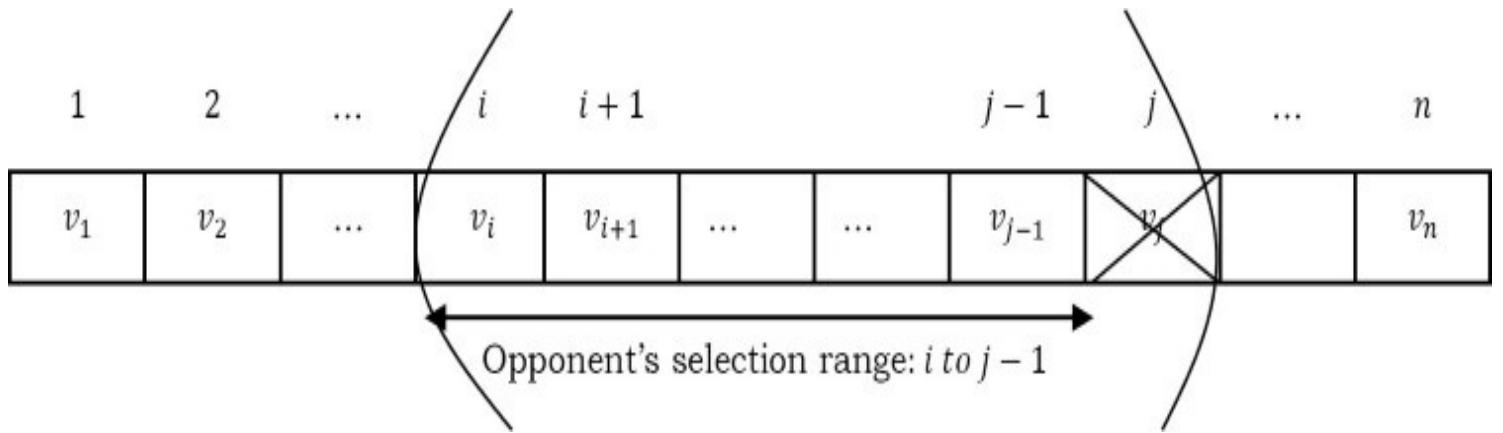
In the recursive call we have to focus on i^{th} coin to j^{th} coin ($v_i \dots v_j$). Since it is our turn to pick the coin, we have two possibilities: either we can pick v_i or v_j . The first term indicates the case if we select i^{th} coin (v_i) and the second term indicates the case if we select j^{th} coin (v_j). The outer *Max* indicates that we have to select the coin which gives maximum value. Now let us focus on the terms:

- Selecting i^{th} coin: If we select the i^{th} coin then the remaining range is from $i + 1$ to j . Since we selected the i^{th} coin we get the value v_i for that. From the remaining range

$i + 1$ to j , the opponents can select either $i + 1^{th}$ coin or j^{th} coin. But the oponents selection should be minimized as much as possible [the *Min* term]. The same is described in the below figure.



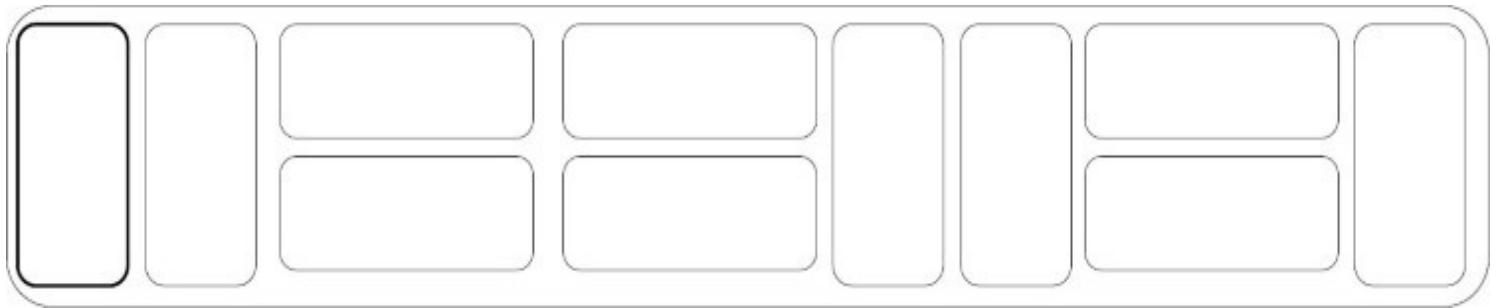
- Selecting the j^{th} coin: Here also the argument is the same as above. If we select the j^{th} coin, then the remaining range is from i to $j - 1$. Since we selected the j^{th} coin we get the value v_j for that. From the remaining range i to $j - 1$, the opponent can select either the i^{th} coin or the $j - 1^{th}$ coin. But the opponent's selection should be minimized as much as possible [the *Min* term].



How many subproblems are there? In the above formula, i can range from 1 to n and j can range from 1 to n . There are a total of n^2 subproblems and each takes $O(1)$ and the total time complexity is $O(n^2)$.

Problem-34 Tiling: Assume that we use dominoes measuring 2×1 to tile an infinite strip of height 2. How many ways can one tile a $2 \times n$ strip of square cells with 1×2 dominoes?

Solution: Notice that we can place tiles either vertically or horizontally. For placing vertical tiles, we need a gap of at least 2×2 . For placing horizontal tiles, we need a gap of 2×1 . In this manner, the problem is reduced to finding the number of ways to partition n using the numbers 1 and 2 with order considered relevant [1]. For example: $11 = 1 + 2 + 2 + 1 + 2 + 2 + 1$.



If we have to find such arrangements for 12, we can either place a 1 at the end or we can add 2 in the arrangements possible with 10. Similarly, let us say we have F_n possible arrangements for n . Then for $(n + 1)$, we can either place just 1 at the end or we can find possible arrangements for $(n - 1)$ and put a 2 at the end. Going by the above theory:

$$F_{n+1} = F_n + F_{n-1}$$

Let's verify the above theory for our original problem:

- In how many ways can we fill a 2×1 strip: 1 → Only one vertical tile.
- In how many ways can we fill a 2×2 strip: 2 → Either 2 horizontal or 2 vertical tiles.
- In how many ways can we fill a 2×3 strip: 3 → Either put a vertical tile in the 2 solutions possible for a 2×2 strip, or put 2 horizontal tiles in the only solution possible for a 2×1 strip. ($2 + 1 = 3$).
- Similarly, in how many ways can we fill a $2 \times n$ strip: Either put a vertical tile in the solutions possible for $2 \times (n - 1)$ strip or put 2 horizontal tiles in the solution possible for a $2 \times (n - 2)$ strip. ($F_{n-1} + F_{n-2}$).
- That's how we verified that our final solution is: $F_n = F_{n-1} + F_{n-2}$ with $F_1 = 1$ and $F_2 = 2$.

Problem-35 Longest Palindrome Subsequence: A sequence is a palindrome if it reads the same whether we read it left to right or right to left. For example A, C, G, G, G, G, C, A . Given a sequence of length n , devise an algorithm to output the length of the longest palindrome subsequence. For example, the string $A, G, C, T, C, B, M, A, A, C, T, G, G, A, M$ has many palindromes as subsequences, for instance: $A, G, T, C, M, C, T, G, A$ has length 9.

Solution: Let us use DP to solve this problem. If we look at the sub-string $A[i, \dots, j]$ of the string A , then we can find a palindrome sequence of length at least 2 if $A[i] == A[j]$. If they are not the same, then we have to find the maximum length palindrome in subsequences $A[i + 1, \dots, j]$ and $A[i, \dots, j - 1]$.

Also, every character $A[i]$ is a palindrome of length 1. Therefore the base cases are given by $A[i, i] = 1$. Let us define the maximum length palindrome for the substring $A[i, \dots, j]$ as $L(i, j)$.

$$L(i, j) = \begin{cases} L(i + 1, j - 1) + 2, & \text{if } A[i] == A[j] \\ \max\{L(i + 1, j), L(i, j - 1)\}, & \text{otherwise} \end{cases}$$

$$L(i, i) = 1 \text{ for all } i = 1 \text{ to } n$$

```

int LongestPalindromeSubsequence(int A[], int n) {
    int max = 1;
    int i, k, L[n][n];
    for (i = 1; i <= n - 1; i++) {
        L[i][i] = 1;
        if(A[i]==A[i+1]) {
            L[i][i + 1] = 1;
            max = 2;
        }
        else
            L[i][i + 1] = 0;
    }
    for (k=3;k<= n;k++) {
        for (i = 1; i <= n-k + 1; i++) {
            j = i + k - 1;
            if(A[i] == A[j])
                {
                    L[i, j] = 2 + L[i + 1][j - 1];
                    max = k;
                }
            else
                L[i, j] = max(L[i + 1][j - 1], L[i][j - 1]);
        }
    }
    return max;
}

```

Time Complexity: First ‘for’ loop takes $O(n)$ time while the second ‘for’ loop takes $O(n - k)$ which is also $O(n)$. Therefore, the total running time of the algorithm is given by $O(n^2)$.

Problem-36 Longest Palindrome Substring: Given a string A , we need to find the longest sub-string of A such that the reverse of it is exactly the same.

Solution: The basic difference between the longest palindrome substring and the longest palindrome subsequence is that, in the case of the longest palindrome substring, the output string should be the contiguous characters, which gives the maximum palindrome; and in the case of the longest palindrome subsequence, the output is the sequence of characters where the characters might not be contiguous but they should be in an increasing sequence with respect to their positions in the given string.

Brute-force solution exhaustively checks all $n(n + 1)/2$ possible substrings of the given n-length string, tests each one if it's a palindrome, and keeps track of the longest one seen so far. This has worst-case complexity $O(n^3)$, but we can easily do better by realizing that a palindrome is centered on either a letter (for odd-length palindromes) or a space between letters (for even-length palindromes). Therefore we can examine all $n + 1$ possible centers and find the longest palindrome for that center, keeping track of the overall longest palindrome. This has worst-case complexity $O(n^2)$.

Let us use DP to solve this problem. It is worth noting that there are no more than $O(n^2)$ substrings in a string of length n (while there are exactly 2^n subsequences). Therefore, we could scan each substring, check for a palindrome, and update the length of the longest palindrome substring discovered so far. Since the palindrome test takes time linear in the length of the substring, this idea takes $O(n^3)$ algorithm. We can use DP to improve this. For $1 \leq i \leq j \leq n$, define

$$L(i, j) = \begin{cases} 1, & \text{if } A[i] \dots A[j] \text{ is a palindrome substring,} \\ 0, & \text{otherwise} \end{cases}$$

$$L[i, i] = 1,$$

$$L[i, j] = L[i, i + 1], \text{ if } A[i] == A[i + 1], \text{ for } 1 \leq i \leq j \leq n - 1.$$

Also, for string of length at least 3,

$$L[i, j] = (L[i + 1, j - 1] \text{ and } A[i] = A[j]).$$

Note that in order to obtain a well-defined recurrence, we need to explicitly initialize two distinct diagonals of the boolean array $L[i, j]$, since the recurrence for entry $[i, j]$ uses the value $[i - 1, j - 1]$, which is two diagonals away from $[i, j]$ (that means, for a substring of length k , we need to know the status of a substring of length $k - 2$).

```

int LongestPalindromeSubstring(int A[], int n) {
    int max = 1;
    int i,k, L[n][n];
    for (i = 1; i<=n-1; i++) {
        L[i][i] = 1;
        if(A[i]==A[i+1]) {
            L[i][i + 1] = 1;
            max = 2;
        }
        else
            L[i][i + 1] = 0;
    }
    for (k=3;k<=n;k++) {
        for (i = 1;i <= n-k+1; i++) {
            j = i + k - 1;
            if(A[i] == A[j] && L[i + 1][j - 1]) {
                L[i][j] = 1;
                max = k;
            }
            else
                L[i][j] = 0;
        }
    }
    return max;
}

```

Time Complexity: First for loop takes $O(n)$ time while the second for loop takes $O(n - k)$ which is also $O(n)$. Therefore the total running time of the algorithm is given by $O(n^2)$.

Problem-37 Given two strings S and T , give an algorithm to find the number of times S appears in T . It's not compulsory that all characters of S should appear contiguous to T . For example, if $S = ab$ and $T = abadcb$ then the solution is 4, because ab is appearing 4 times in $abadcb$.

Solution:

Input: Given two strings $S[1.. m]$ and $T[1 ...m]$.

Goal: Count the number of times that S appears in T .

Assume $L(i,j)$ represents the count of how many times i characters of S are appearing in j characters of T .

$$L(i, j) = \text{Max} \begin{cases} 0, & \text{if } j = 0 \\ 1, & \text{if } i = 0 \\ L(i - 1, j - 1) + L(i, j - 1), & \text{if } S[i] == T[j] \\ L(i - 1, j), & \text{if } S[i] \neq T[j] \end{cases}$$

If we concentrate on the components of the above recursive formula,

- If $j = 0$, then since T is empty the count becomes 0.
- If $i = 0$, then we can treat empty string S also appearing in T and we can give the count as 1.
- If $S[i] == T[i]$, it means i^{th} character of S and j^{th} character of T are the same. In this case we have to check the subproblems with $i - 1$ characters of S and $j - 1$ characters of T and also we have to count the result of i characters of S with $j - 1$ characters of T . This is because even all i characters of S might be appearing in $j - 1$ characters of T .
- If $S[i] \neq T[i]$, then we have to get the result of subproblem with $i - 1$ characters of S and j characters of T .

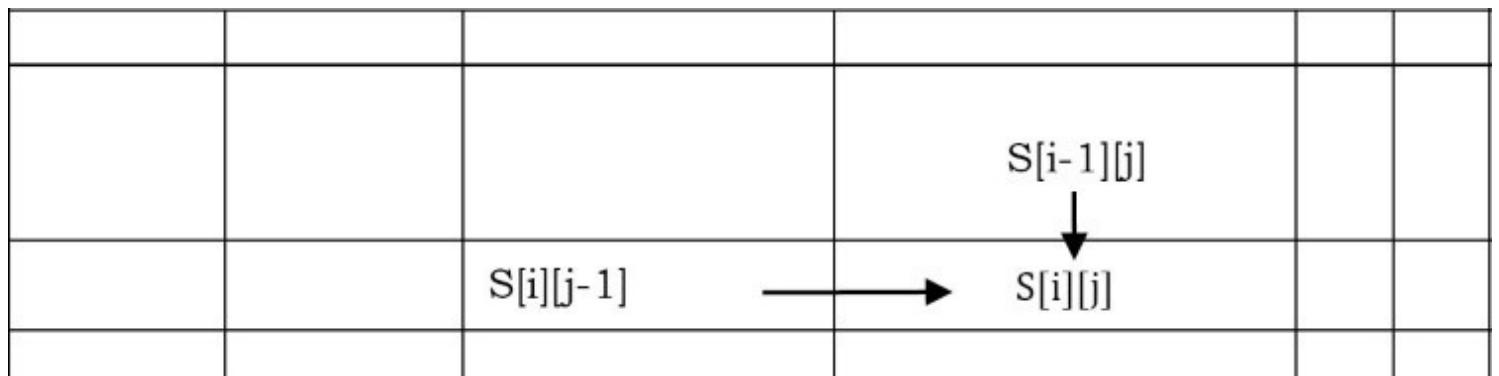
After computing all the values, we have to select the one which gives the maximum count.

How many subproblems are there? In the above formula, i can range from 1 to m and j can range from 1 to n . There are a total of mn subproblems and each one takes $O(1)$. Time Complexity is $O(mn)$.

Space Complexity: $O(mn)$ where m is number of rows and n is number of columns in the given matrix.

Problem-38 Given a matrix with n rows and m columns ($n \times m$). In each cell there are a number of apples. We start from the upper-left corner of the matrix. We can go down or right one cell. Finally, we need to arrive at the bottom-right corner. Find the maximum number of apples that we can collect. When we pass through a cell, we collect all the apples left there.

Solution: Let us assume that the given matrix is $A[n][m]$. The first thing that must be observed is that there are at most 2 ways we can come to a cell - from the left (if it's not situated on the first column) and from the top (if it's not situated on the most upper row).



To find the best solution for that cell, we have to have already found the best solutions for all of the cells from which we can arrive to the current cell. From above, a recurrent relation can be easily obtained as:

$$S(i,j) = \begin{cases} A[i][j] + \text{Max} \left\{ \begin{array}{ll} S(i,j-1), & \text{if } j > 0 \\ S(i-1,j), & \text{if } i > 0 \end{array} \right\} \end{cases}$$

$S(i,j)$ must be calculated by going first from left to right in each row and process the rows from top to bottom, or by going first from top to bottom in each column and process the columns from left to right.

```
int FindApplesCount(int A[][], int n, int m) {
    int S[n][m];
    for( int i = 1;i<=n;i++ ) {
        for(int j = 1;j<=m;j++) {
            S[i][j] = A[i][j];
            if(j>0 && S[i][j] < S[i][j] + S[i][j-1])
                S[i][j] += S[i][j-1];
            if(i>0 && S[i][j] < S[i][j] + S[i-1][j])
                S[i][j] += S[i-1][j];
        }
    }
    return S[n][m];
}
```

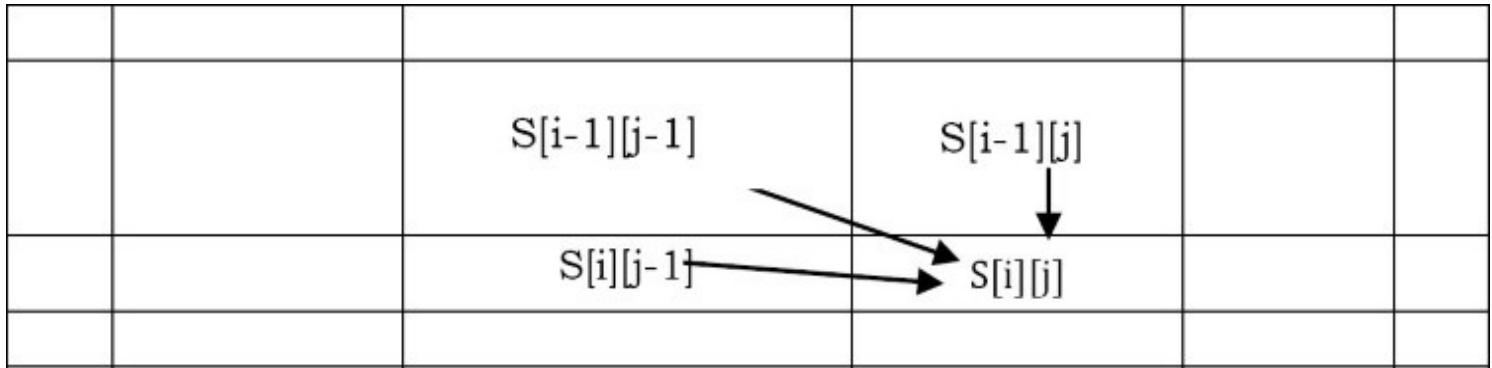
How many such subproblems are there? In the above formula, i can range from 1 to n and j can range from 1 to m . There are a total of nm subproblems and each one takes $O(1)$. Time Complexity is $O(nm)$. Space Complexity: $O(nm)$, where m is number of rows and n is number of columns in the given matrix.

Problem-39 Similar to [Problem-38](#), assume that we can go down, right one cell, or even in a diagonal direction. We need to arrive at the bottom-right corner. Give DP solution to find the maximum number of apples we can collect.

Solution: Yes. The discussion is very similar to [Problem-38](#). Let us assume that the given matrix is $A[n][m]$. The first thing that must be observed is that there are at most 3 ways we can come to a cell - from the left, from the top (if it's not situated on the uppermost row) or from the top diagonal. To find the best solution for that cell, we have to have already found the best solutions for all of the cells from which we can arrive to the current cell. From above, a recurrent relation can be easily obtained:

$$S(i,j) = \begin{cases} S(i,j-1), & \text{if } j > 0 \\ A[i][j] + \text{Max} \left\{ \begin{array}{l} S(i-1,j), \\ S(i-1,j-1), \text{ if } i > 0 \text{ and } j > 0 \end{array} \right\}, & \text{if } i > 0 \end{cases}$$

$S(i,j)$ must be calculated by going first from left to right in each row and process the rows from top to bottom, or by going first from top to bottom in each column and process the columns from left to right.



How many such subproblems are there? In the above formula, i can range from 1 to n and j can range from 1 to m . There are a total of mn subproblems and each one takes $O(1)$. Time Complexity is $O(nm)$.

Space Complexity: $O(nm)$ where m is number of rows and n is number of columns in the given matrix.

Problem-40 Maximum size square sub-matrix with all 1's: Given a matrix with 0's and 1's, give an algorithm for finding the maximum size square sub-matrix with all 1's. For example, consider the binary matrix below.

0	1	1	0	1
1	1	0	1	0
0	1	1	1	0
1	1	1	1	0
1	1	1	1	1
0	0	0	0	0

The maximum square sub-matrix with all set bits is

1	1	1
1	1	1
1	1	1

Solution: Let us try solving this problem using DP. Let the given binary matrix be $B[m][m]$. The idea of the algorithm is to construct a temporary matrix $L[][]$ in which each entry $L[i][j]$ represents size of the square sub-matrix with all 1's including $B[i][j]$ and $B[i][j]$ is the rightmost

and bottom-most entry in the sub-matrix.

Algorithm:

- 1) Construct a sum matrix $L[m][n]$ for the given matrix $B[m][n]$.
 - a. Copy first row and first columns as is from $B[][]$ to $L[][]$.
 - b. For other entries, use the following expressions to construct $L[][]$

```
if( $B[i][j]$  )  
     $L[i][j] = \min(L[i][j - 1], L[i - 1][j], L[i - 1][j - 1]) + 1;$   
else  $L[i][j] = 0;$ 
```

- 2) Find the maximum entry in $L[m][n]$.
- 3) Using the value and coordinates of maximum entry in $L[i]$, print sub-matrix of $B[][]$.

```

void MatrixSubSquareWithAllOnes(int B[][], int m, int n) {
    int i, j, L[m][n], max_of_s, max_i, max_j;
    // Setting first column of L[][]
    for(i = 0; i < m; i++)
        L[i][0] = B[i][0];
    // Setting first row of L[][]
    for(j = 0; j < n; j++)
        L[0][j] = B[0][j];
    // Construct other entries of L[][]
    for(i = 1; i < m; i++) {
        for(j = 1; j < n; j++) {
            if(B[i][j] == 1)
                L[i][j] = min(L[i][j-1], L[i-1][j], L[i-1][j-1]) + 1;
            else
                L[i][j] = 0;
        }
    }
    max_of_s = L[0][0]; max_i = 0; max_j = 0;
    for(i = 0; i < m; i++) {
        for(j = 0; j < n; j++) {
            if(L[i][j] > max_of_s){
                max_of_s = L[i][j];
                max_i = i;
                max_j = j;
            }
        }
    }
    printf("Maximum sub-matrix");
    for(i = max_i; i > max_i - max_of_s; i--) {
        for(j = max_j; j > max_j - max_of_s; j--)
            printf("%d", B[i][j]);
    }
}

```

How many subproblems are there? In the above formula, i can range from 1 to n and j can range from 1 to m . There are a total of nm subproblems and each one takes $O(1)$. Time Complexity is $O(nm)$. Space Complexity is $O(nm)$, where n is number of rows and m is number of columns in the given matrix.

Problem-41 Maximum size sub-matrix with all 1's: Given a matrix with 0's and 1's, give an algorithm for finding the maximum size sub-matrix with all Is. For example, consider

the binary matrix below.

1	1	0	0	1	0
0	1	1	1	1	1
1	1	1	1	1	0
0	0	1	1	0	0

The maximum sub-matrix with all set bits is

1	1	1	1
1	1	1	1

Solution: If we draw a histogram of all 1's cells in the above rows for a particular row, then maximum all 1's sub-matrix ending in that row will be equal to maximum area rectangle in that histogram. Below is an example for 3rdrow in the above discussed matrix [1]:

1	1	0	0	1	0
0	1	1	1	1	1
1	1	1	1	1	0
0	0	1	1	0	0

If we calculate this area for all the rows, maximum area will be our answer. We can extend our solution very easily to find start and end co-ordinates. For this, we need to generate an auxiliary matrix $S[][]$ where each element represents the number of Is above and including it, up until the first 0. $S[][]$ for the above matrix will be as shown below:

1	1	0	0	1	0
0	2	1	1	2	1
1	3	2	2	3	0
0	0	3	3	0	0

Now we can simply call our maximum rectangle in histogram on every row in $S[][]$ and update the maximum area every time. Also we don't need any extra space for saving S . We can update original matrix (A) to S and after calculation, we can convert S back to A .

```

#define ROW 10
#define COL 10
int find_max_matrix(int A[ROW][COL]) {
    int max, cur_max = 0;
    //Calculate Auxiliary matrix
    for (int i=1; i<ROW; i++) {
        for(int j=0; j<COL; j++) {
            if(A[i][j] == 1)
                A[i][j] = A[i-1][j] + 1;
        }
    }
    //Calculate maximum area in S for each row
    for (int i=0; i<ROW; i++) {
        max = MaxRectangleArea(A[i], COL);           //Refer Stacks Chapter
        if(max > cur_max)
            cur_max = max;
    }
    //Regenerate Original matrix
    for (int i=ROW-1; i>0; i--)
        for(int j=0; j<COL; j++) {
            if(A[i][j])
                A[i][j] = A[i][j] - A[i-1][j];
        }
    return cur_max;
}

```

Problem-42 Maximum sum sub-matrix: Given an $n \times n$ matrix M of positive and negative integers, give an algorithm to find the sub-matrix with the largest possible sum.

Solution: Let $Aux[r, c]$ represent the sum of rectangular subarray of M with one corner at entry $[1,1]$ and the other at $[r,c]$. Since there are n^2 such possibilities, we can compute them in $O(n^2)$ time. After computing all possible sums, the sum of any rectangular subarray of M can be computed in constant time. This gives an $O(n^4)$ algorithm: we simply guess the lower-left and the upper-right corner of the rectangular subarray and use the Aux table to compute its sum.

Problem-43 Can we improve the complexity of [Problem-42](#)?

Solution: We can use the [Problem-4](#) solution with little variation, as we have seen that the maximum sum array of a 1 – D array algorithm scans the array one entry at a time and keeps a running total of the entries. At any point, if this total becomes negative, then set it to 0. This algorithm is called *Kadane's* algorithm. We use this as an auxiliary function to solve a two-dimensional problem in the following way.

```

public void FindMaximumSubMatrix(int[][] A, int n){
    //computing the vertical prefix sum for columns
    int[][] M = new int[n][n];
    for (int i = 0; i < n; i++) {
        for (int j = 0; j < n; j++) {
            if (j == 0)
                M[j][i] = A[j][i];
            else
                M[j][i] = A[j][i] + M[j - 1][i];
        }
    }
    int maxSoFar = 0, min, subMatrix;
    //iterate over the possible combinations applying Kadane's Alg.
    for (int i = 0; i < n; i++) {
        for (int j = i; j < n; j++) {
            min = 0;
            subMatrix = 0;
            for (int k = 0; k < n; k++) {
                if (i == 0)
                    subMatrix += M[j][k];
                else
                    subMatrix += M[j][k] - M[i - 1][k];
                if (subMatrix < min)
                    min = subMatrix;
                if ((subMatrix - min) > maxSoFar)
                    maxSoFar = subMatrix - min;
            }
        }
    }
}

```

Time Complexity: $O(n^3)$.

Problem-44 Given a number n , find the minimum number of squares required to sum a given number n .

Examples: $\min[1] = 1 = 1^2$, $\min[2] = 2 = 1^2 + 1^2$, $\min[4] = 1 = 2^2$, $\min[13] = 2 = 3^2 + 2^2$.

Solution: This problem can be reduced to a coin change problem. The denominations are 1 to \sqrt{n} . Now, we just need to make change for n with a minimum number of denominations.

Problem-45 Finding Optimal Number of Jumps To Reach Last Element: Given an array, start from the first element and reach the last by jumping. The jump length can be at most the value at the current position in the array. The optimum result is when you reach the goal

in the minimum number of jumps. **Example:** Given array A = {2,3,1,1,4}. Possible ways to reach the end (index list) are:

- 0,2,3,4 (jump 2 to index 2, and then jump 1 to index 3, and then jump 1 to index 4)
- 0,1,4 (jump 1 to index 1, and then jump 3 to index 4)

Since second solution has only 2 jumps it is the optimum result.

Solution: This problem is a classic example of Dynamic Programming. Though we can solve this by brute-force, it would be complex. We can use the LIS problem approach for solving this. As soon as we traverse the array, we should find the minimum number of jumps for reaching that position (index) and update our result array. Once we reach the end, we have the optimum solution at last index in result array.

How can we find the optimum number of jumps for every position (index)? For first index, the optimum number of jumps will be zero. Please note that if value at first index is zero, we can't jump to any element and return infinite. For $n + 1^{th}$ element, initialize $\text{result}[n + 1]$ as infinite. Then we should go through a loop from 0 ... n , and at every index i , we should see if we are able to jump to $n + 1$ from i or not. If possible, then see if total number of jumps ($\text{result}[i] + 1$) is less than $\text{result}[n + 1]$, then update $\text{result}[n + 1]$, else just continue to next index.

```

//Define MAX 1 less so that adding 1 doesn't make it 0
#define MAX 0xFFFFFFFF;
unsigned int jump(int *array, int n) {
    unsigned answer, int *result = new unsigned int[n];
    int i, j;
    //Boundary conditions
    if(n==0 || array[0] == 0)
        return MAX;
    result[0] = 0; //no need to jump at first element
    for (i = 1; i < n; i++) {
        result[i] = MAX; //Initialization of result[i]
        for (j = 0; j < i; j++) {
            //check if jump is possible from j to i
            if(array[j] >= (i-j)) {
                //check if better solution available
                if(result[j] + 1) < result[i])
                    result[i] = result[j] + 1; //updating result[i]
            }
        }
    }
    answer = result[n-1]; //return result[n-1]
    delete[] result;
    return answer;
}

```

The above code will return optimum number of jumps. To find the jump indexes as well, we can very easily modify the code as per requirement.

Time Complexity: Since we are running 2 loops here and iterating from 0 to i in every loop then total time takes will be $1 + 2 + 3 + 4 + \dots + n - 1$. So time efficiency $O(n) = O(n * (n - 1)/2) = O(n^2)$.

Space Complexity: $O(n)$ space for result array.

Problem-46 Explain what would happen if a dynamic programming algorithm is designed to solve a problem that does not have overlapping sub-problems.

Solution: It will be just a waste of memory, because the answers of sub-problems will never be used again. And the running time will be the same as using the Divide & Conquer algorithm.

Problem-47 Christmas is approaching. You're helping Santa Claus to distribute gifts to children. For ease of delivery, you are asked to divide n gifts into two groups such that the weight difference of these two groups is minimized. The weight of each gift is a positive integer. Please design an algorithm to find an optimal division minimizing the value

difference. The algorithm should find the minimal weight difference as well as the groupings in $O(nS)$ time, where S is the total weight of these n gifts. Briefly justify the correctness of your algorithm.

Solution: This problem can be converted into making one set as close to $\frac{S}{2}$ as possible. We consider an equivalent problem of making one set as close to $W = \left\lfloor \frac{S}{2} \right\rfloor$ as possible. Define $FD(i, w)$ to be the minimal gap between the weight of the bag and W when using the first i gifts only. WLOG, we can assume the weight of the bag is always less than or equal to W . Then fill the DP table for $0 \leq i \leq n$ and $0 \leq w \leq W$ in which $F(0, w) = W$ for all w , and

$$FD(i, w) = \min\{FD(i - 1, w - w_i) + w_i, FD(i - 1, w)\} \text{ if } \{FD(i - 1, w - w_i) \geq w_i\} \\ = FD(i - 1, w) \text{ otherwise}$$

This takes $O(nS)$ time. $FD(n, W)$ is the minimum gap. Finally, to reconstruct the answer, we backtrack from (n, W) . During backtracking, if $FD(i, j) = FD(i - 1, j)$ then i is not selected in the bag and we move to $F(i - 1, j)$. Otherwise, i is selected and we move to $F(i - 1, j - w_i)$.

Problem-48 A circus is designing a tower routine consisting of people standing atop one another's shoulders. For practical and aesthetic reasons, each person must be both shorter and lighter than the person below him or her. Given the heights and weights of each person in the circus, write a method to compute the largest possible number of people in such a tower.

Solution: It is same as Box stacking and Longest increasing subsequence (LIS) problem.

COMPLEXITY CLASSES

CHAPTER 20



20.1 Introduction

In the previous chapters we have solved problems of different complexities. Some algorithms have lower rates of growth while others have higher rates of growth. The problems with lower rates of growth are called *easy* problems (or *easy solved problems*) and the problems with higher rates of growth are called *hard* problems (or *hard solved problems*). This classification is done based on the running time (or memory) that an algorithm takes for solving the problem.

Time Complexity	Name	Example	Problems
$O(1)$	Constant	Adding an element to the front of a linked list	Easy solved problems
$O(\log n)$	Logarithmic	Finding an element in a binary search tree	
$O(n)$	Linear	Finding an element in an unsorted array	
$O(n \log n)$	Linear Logarithmic	Merge sort	
$O(n^2)$	Quadratic	Shortest path between two nodes in a graph	
$O(n^3)$	Cubic	Matrix Multiplication	
$O(2^n)$	Exponential	The Towers of Hanoi problem	
$O(n!)$	Factorial	Permutations of a string	Hard solved problems

There are lots of problems for which we do not know the solutions. All the problems we have seen so far are the ones which can be solved by computer in deterministic time. Before starting our discussion let us look at the basic terminology we use in this chapter.

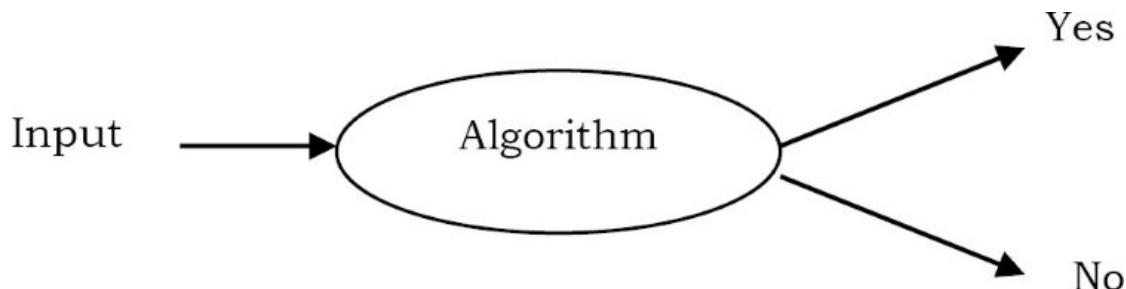
20.2 Polynomial/Exponential Time

Exponential time means, in essence, trying every possibility (for example, backtracking algorithms) and they are very slow in nature. Polynomial time means having some clever algorithm to solve a problem, and we don't try every possibility. Mathematically, we can represent these as:

- Polynomial time is $O(n^k)$, for some k .
- Exponential time is $O(k^n)$, for some k .

20.3 What is a Decision Problem?

A decision problem is a question with a *yes/no* answer and the answer depends on the values of input. For example, the problem “Given an array of n numbers, check whether there are any duplicates or not?” is a decision problem. The answer for this problem can be either *yes* or *no* depending on the values of the input array.



20.4 Decision Procedure

For a given decision problem let us assume we have given some algorithm for solving it. The process of solving a given decision problem in the form of an algorithm is called a *decision procedure* for that problem.

20.5 What is a Complexity Class?

In computer science, in order to understand the problems for which solutions are not there, the problems are divided into classes and we call them as complexity classes. In complexity theory, a *complexity class* is a set of problems with related complexity. It is the branch of theory of computation that studies the resources required during computation to solve a given problem.

The most common resources are time (how much time the algorithm takes to solve a problem) and space (how much memory it takes).

20.6 Types of Complexity Classes

P Class

The complexity class *P* is the set of decision problems that can be solved by a deterministic machine in polynomial time (*P* stands for polynomial time). *P* problems are a set of problems whose solutions are easy to find.

NP Class

The complexity class *NP* (*NP* stands for non-deterministic polynomial time) is the set of decision problems that can be solved by a non-deterministic machine in polynomial time. *NP* class problems refer to a set of problems whose solutions are hard to find, but easy to verify.

For better understanding let us consider a college which has 500 students on its roll. Also, assume that there are 100 rooms available for students. A selection of 100 students must be paired together in rooms, but the dean of students has a list of pairings of certain students who cannot room together for some reason.

The total possible number of pairings is too large. But the solutions (the list of pairings) provided to the dean, are easy to check for errors. If one of the prohibited pairs is on the list, that's an error. In this problem, we can see that checking every possibility is very difficult, but the result is easy to validate.

That means, if someone gives us a solution to the problem, we can tell them whether it is right or not in polynomial time. Based on the above discussion, for NP class problems if the answer is *yes*, then there is a proof of this fact, which can be verified in polynomial time.

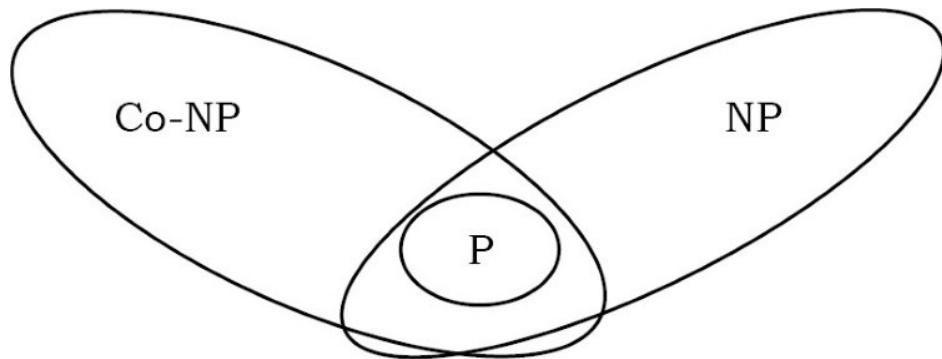
Co-NP Class

$Co - NP$ is the opposite of NP (complement of NP). If the answer to a problem in $Co - NP$ is *no*, then there is a proof of this fact that can be checked in polynomial time.

P	Solvable in polynomial time
NP	<i>Yes</i> answers can be checked in polynomial time
$Co-NP$	<i>No</i> answers can be checked in polynomial time

Relationship between P, NP and Co-NP

Every decision problem in P is also in NP . If a problem is in P , we can verify YES answers in polynomial time. Similarly, any problem in P is also in $Co - NP$.



One of the important open questions in theoretical computer science is whether or not $P = NP$. Nobody knows. Intuitively, it should be obvious that $P \neq NP$, but nobody knows how to prove it.

Another open question is whether NP and $Co - NP$ are different. Even if we can verify every YES answer quickly, there's no reason to think that we can also verify NO answers quickly.

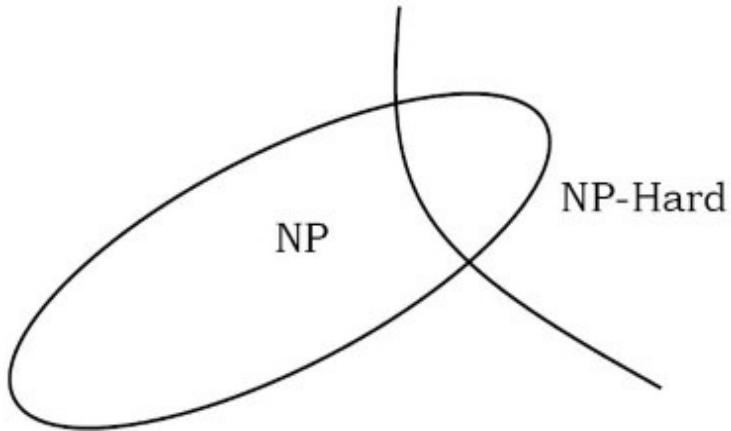
It is generally believed that $NP \neq Co - NP$, but again nobody knows how to prove it.

NP-hard Class

It is a class of problems such that every problem in NP reduces to it. All NP -hard problems are not in NP , so it takes a long time to even check them. That means, if someone gives us a solution for NP -hard problem, it takes a long time for us to check whether it is right or not.

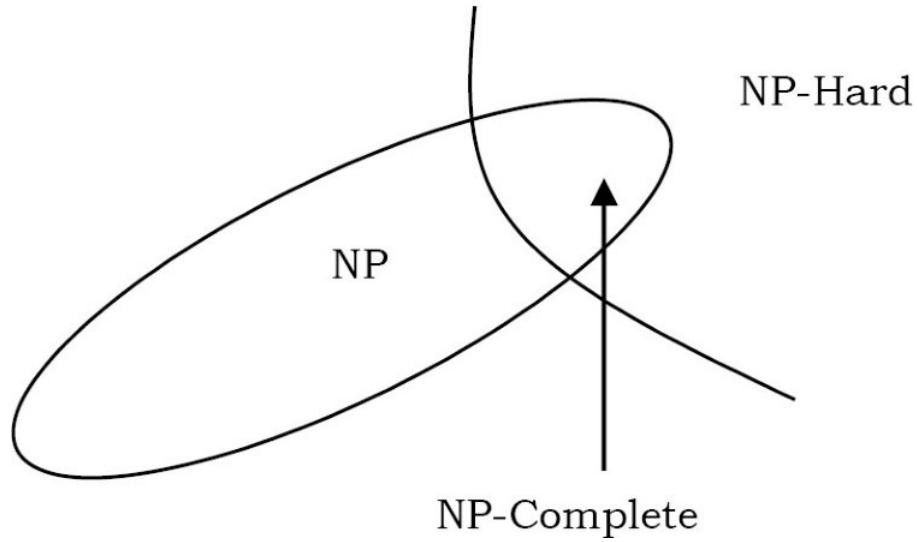
A problem K is NP -hard indicates that if a polynomial-time algorithm (solution) exists for K then a polynomial-time algorithm for every problem is NP . Thus:

K is NP -hard implies that if K can be solved in polynomial time, then $P = NP$



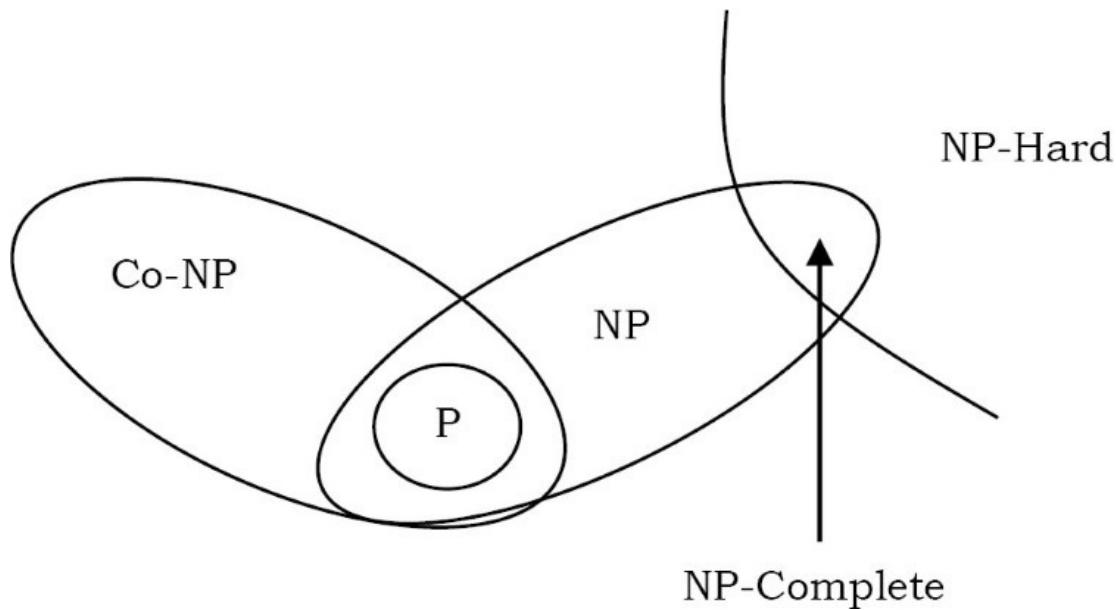
NP-complete Class

Finally, a problem is NP -complete if it is part of both NP -hard and NP . NP -complete problems are the hardest problems in NP . If anyone finds a polynomial-time algorithm for one NP -complete problem, then we can find polynomial-time algorithm for every NP -complete problem. This means that we can check an answer fast and every problem in NP reduces to it.



Relationship between P, NP Co-NP, NP-Hard and NP-Complete

From the above discussion, we can write the relationships between different components as shown below (remember, this is just an assumption).



The set of problems that are *NP-hard* is a strict superset of the problems that are *NP-complete*. Some problems (like the halting problem) are *NP-hard*, but not in *NP*. *NP-hard* problems might be impossible to solve in general. We can tell the difference in difficulty between *NP-hard* and *NP-complete* problems because the class *NP* includes everything easier than its “toughest” problems - if a problem is not in *NP*, it is harder than all the problems in *NP*.

Does $P=NP$?

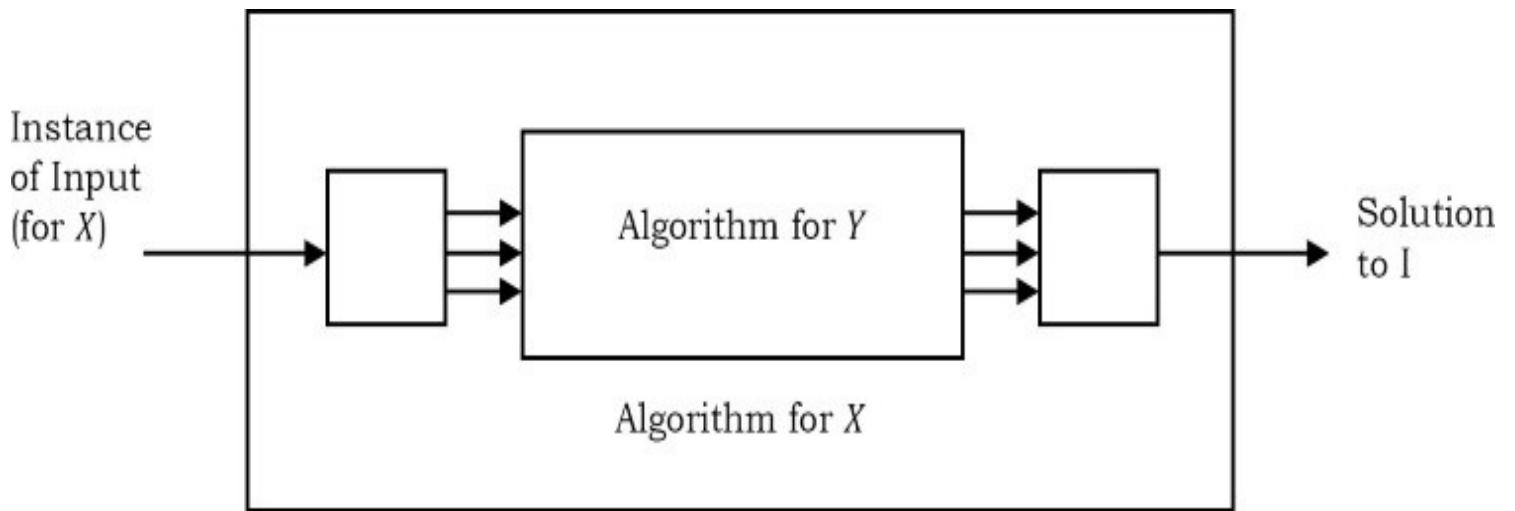
If $P = NP$, it means that every problem that can be checked quickly can be solved quickly (remember the difference between checking if an answer is right and actually solving a problem).

This is a big question (and nobody knows the answer), because right now there are lots of *NP-complete* problems that can't be solved quickly. If $P = NP$, that means there is a way to solve them fast. Remember that “quickly” means not trial-and-error. It could take a billion years, but as long as we didn't use trial and error, it was quick. In future, a computer will be able to change that billion years into a few minutes.

20.7 Reductions

Before discussing reductions, let us consider the following scenario. Assume that we want to solve problem X but feel it's very complicated. In this case what do we do?

The first thing that comes to mind is, if we have a similar problem to that of X (let us say Y), then we try to map X to Y and use Y 's solution to solve X also. This process is called reduction.



In order to map problem X to problem Y , we need some algorithm and that may take linear time or more. Based on this discussion the cost of solving problem X can be given as:

$$\text{Cost of solving } X = \text{Cost of solving } Y + \text{Reduction time}$$

Now, let us consider the other scenario. For solving problem X , sometimes we may need to use Y 's algorithm (solution) multiple times. In that case,

$$\text{Cost of solving } X = \text{Number of Times} * \text{Cost of solving } X + \text{Reduction time}$$

The main thing in *NP*-Complete is reducibility. That means, we reduce (or transform) given *NP*-Complete problems to other known *NP*-Complete problem. Since the *NP*-Complete problems are hard to solve and in order to prove that given *NP*-Complete problem is hard, we take one existing hard problem (which we can prove is hard) and try to map given problem to that and finally we prove that the given problem is hard.

Note: It's not compulsory to reduce the given problem to known hard problem to prove its hardness. Sometimes, we reduce the known hard problem to given problem.

Important NP-Complete Problems (Reductions)

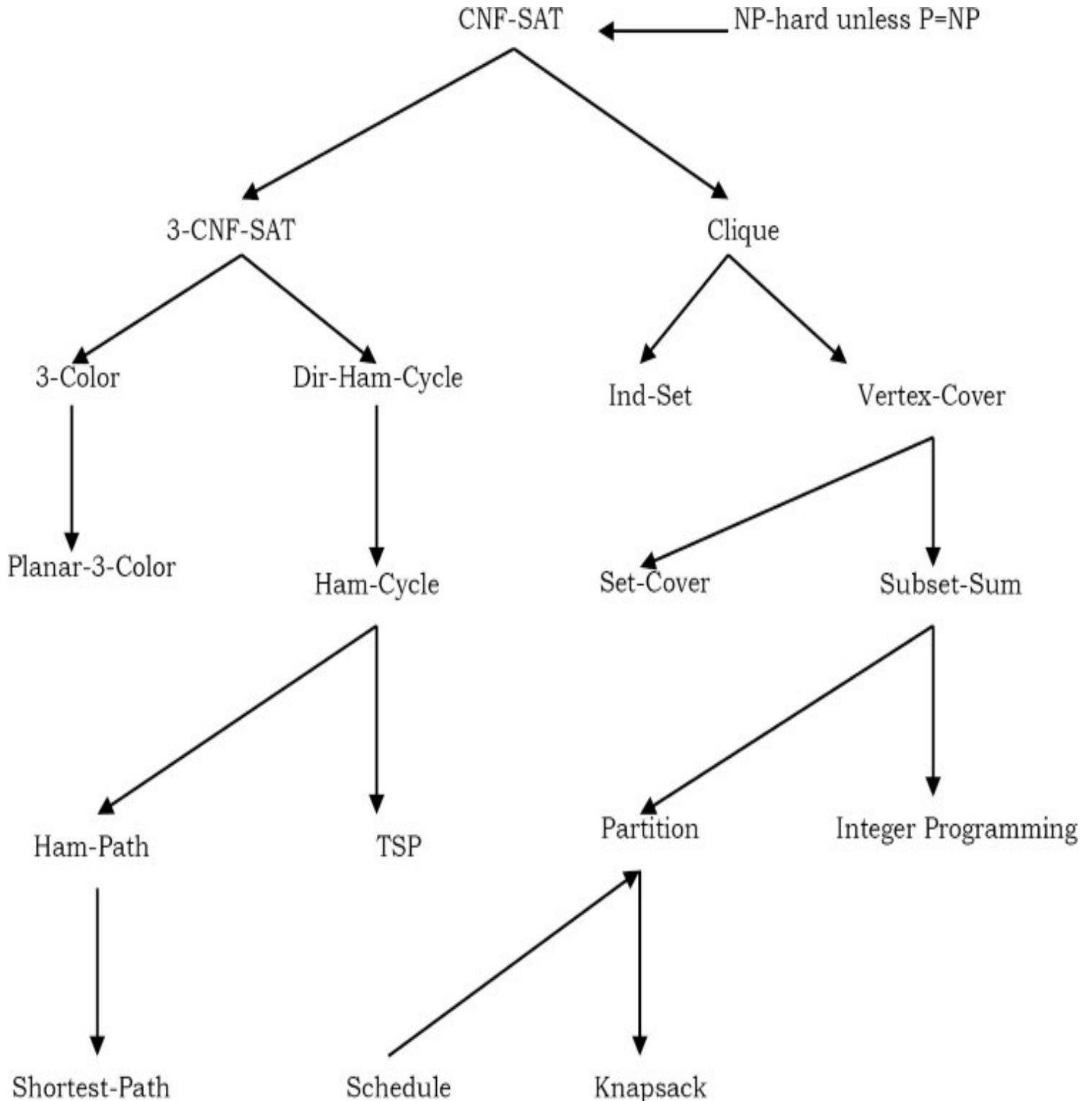
Satisfiability Problem: A boolean formula is in *conjunctive normal form* (CNF) if it is a conjunction (AND) of several clauses, each of which is the disjunction (OR) of several literals, each of which is either a variable or its negation. For example: $(a \vee b \vee c \vee d \vee e) \wedge (b \vee \neg c \vee \neg d) \wedge (\neg a \vee c \vee d) \vee (a \vee \neg b)$

A 3-CNF formula is a CNF formula with exactly three literals per clause. The previous example is not a 3-CNF formula, since its first clause has five literals and its last clause has only two.

2-SAT Problem: 3-SAT is just SAT restricted to 3-CNF formulas: Given a 3-CNF formula, is there an assignment to the variables so that the formula evaluates to TRUE?

2-SAT Problem: 2-SAT is just SAT restricted to 2-CNF formulas: Given a 2-CNF formula, is there an assignment to the variables so that the formula evaluates to TRUE?

Circuit-Satisfiability Problem: Given a boolean combinational circuit composed of AND, OR and NOT gates, is it satisfiable?. That means, given a boolean circuit consisting of AND, OR and NOT gates properly connected by wires, the Circuit-SAT problem is to decide whether there exists an input assignment for which the output is TRUE.



Hamiltonian Path Problem (Ham-Path): Given an undirected graph, is there a path that visits

every vertex exactly once?

Hamiltonian Cycle Problem (Ham-Cycle): Given an undirected graph, is there a cycle (where start and end vertices are same) that visits every vertex exactly once?

Directed Hamiltonian Cycle Problem (Dir-Ham-Cycle): Given a directed graph, is there a cycle (where start and end vertices are same) that visits every vertex exactly once?

Travelling Salesman Problem (TSP): Given a list of cities and their pair-wise distances, the problem is to find the shortest possible tour that visits each city exactly once.

Shortest Path Problem (Shortest-Path): Given a directed graph and two vertices s and t , check whether there is a shortest simple path from s to t .

Graph Coloring: A k -coloring of a graph is to map one of k ‘colors’ to each vertex, so that every edge has two different colors at its endpoints. The graph coloring problem is to find the smallest possible number of colors in a legal coloring.

3-Color problem: Given a graph, is it possible to color the graph with 3 colors in such a way that every edge has two different colors?

Clique (also called complete graph): Given a graph, the *CLIQUE* problem is to compute the number of nodes in its largest complete subgraph. That means, we need to find the maximum subgraph which is also a complete graph.

Independent Set Problem (Ind_Set): Let G be an arbitrary graph. An independent set in G is a subset of the vertices of G with no edges between them. The maximum independent set problem is the size of the largest independent set in a given graph.

Vertex Cover Problem (Vertex-Cover): A vertex cover of a graph is a set of vertices that touches every edge in the graph. The vertex cover problem is to find the smallest vertex cover in a given graph.

Subset Sum Problem (Subset-Sum): Given a set S of integers and an integer T , determine whether S has a subset whose elements sum to T .

Integer Programming: Given integers b_i , a_{ij} find 0/1 variables x_i that satisfy a linear system of equations.

$$\sum_{j=1}^N a_{ij}x_j = b_i \quad 1 \leq i \leq M$$
$$x_j \in \{0,1\} \quad 1 \leq j \leq N$$

In the figure, arrows indicate the reductions. For example, Ham-Cycle (Hamiltonian Cycle Problem) can be reduced to CNF-SAT. Same is the case with any pair of problems. For our discussion, we can ignore the reduction process for each of the problems. There is a theorem called *Cook's Theorem* which proves that Circuit satisfiability problem is NP-hard. That means, Circuit satisfiability is a known NP-hard problem.

Note: Since the problems below are NP-Complete, they are NP and NP-hard too. For simplicity we can ignore the proofs for these reductions.

20.8 Complexity Classes: Problems & Solutions

Problem-1 What is a quick algorithm?

Solution: A quick algorithm (solution) means not trial-and-error solution. It could take a billion years, but as long as we do not use trial and error, it is efficient. Future computers will change those billion years to a few minutes.

Problem-2 What is an efficient algorithm?

Solution: An algorithm is said to be efficient if it satisfies the following properties:

- Scale with input size.
- Don't care about constants.
- Asymptotic running time: polynomial time.

Problem-3 Can we solve all problems in polynomial time?

Solution: No. The answer is trivial because we have seen lots of problems which take more than polynomial time.

Problem-4 Are there any problems which are NP-hard?

Solution: By definition, NP-hard implies that it is very hard. That means it is very hard to prove and to verify that it is hard. Cook's Theorem proves that Circuit satisfiability problem is NP-hard.

Problem-5 For 2-SAT problem, which of the following are applicable?

- (a) P
- (b) NP
- (c) $CoNP$
- (d) $NP\text{-Hard}$
- (e) $CoNP\text{-Hard}$
- (f) $NP\text{-Complete}$
- (g) $CoNP\text{-Complete}$

Solution: 2-SAT is solvable in poly-time. So it is P , NP , and $CoNP$.

Problem-6 For 3-SAT problem, which of the following are applicable?

- (a) P
- (b) NP
- (c) $CoNP$
- (d) $NP\text{-Hard}$
- (e) $CoNP\text{-Hard}$
- (f) $NP\text{-Complete}$
- (g) $CoNP\text{-Complete}$

Solution: 3-SAT is NP-complete. So it is NP, NP-Hard, and NP-complete.

Problem-7 For 2-Clique problem, which of the following are applicable?

- (a) P
- (b) NP
- (c) $CoNP$
- (d) $NP\text{-Hard}$
- (e) $CoNP\text{-Hard}$
- (f) $NP\text{-Complete}$
- (g) $CoNP\text{-Complete}$

Solution: 2-Clique is solvable in poly-time (check for an edge between all vertex-pairs in $O(n^2)$ time). So it is P , NP , and $CoNP$.

Problem-8 For 3-Clique problem, which of the following are applicable?

- (a) P
- (b) NP
- (c) $CoNP$
- (d) $NP\text{-Hard}$
- (e) $CoNP\text{-Hard}$
- (f) $NP\text{-Complete}$
- (g) $CoNP\text{-Complete}$

Solution: 3-Clique is solvable in poly-time (check for a triangle between all vertex-triplets in $O(n^3)$ time). So it is P , NP , and $CoNP$.

Problem-9 Consider the problem of determining. For a given boolean formula, check whether every assignment to the variables satisfies it. Which of the following is applicable?

- (a) P
- (b) NP
- (c) $CoNP$
- (d) $NP\text{-Hard}$
- (e) $CoNP\text{-Hard}$
- (f) $NP\text{-Complete}$
- (g) $CoNP\text{-Complete}$

Solution: Tautology is the complimentary problem to Satisfiability, which is NP-complete, so Tautology is $CoNP$ -complete. So it is $CoNP$, $CoNP$ -hard, and $CoNP$ -complete.

Problem-10 Let S be an NP -complete problem and Q and R be two other problems not known to be in NP . Q is polynomial time reducible to S and S is polynomial-time reducible to R . Which one of the following statements is true?

- (a) R is NP -complete
- (b) R is NP -hard
- (c) Q is NP -complete
- (d) Q is NP -hard.

Solution: R is NP -hard (b).

Problem-11 Let A be the problem of finding a Hamiltonian cycle in a graph $G = (V, E)$, with $|V|$ divisible by 3 and B the problem of determining if Hamiltonian cycle exists in such graphs. Which one of the following is true?

- (a) Both A and B are NP -hard
- (b) A is NP -hard, but B is not
- (c) A is NP -hard, but B is not
- (d) Neither A nor B is NP -hard

Solution: Both A and B are NP -hard (a).

Problem-12 Let A be a problem that belongs to the class NP . State which of the following is true?

- (a) There is no polynomial time algorithm for A .
- (b) If A can be solved deterministically in polynomial time, then $P = NP$.
- (c) If A is NP -hard, then it is NP -complete.
- (d) A may be undecidable.

Solution: If A is NP -hard, then it is NP -complete (c).

Problem-13 Suppose we assume *Vertex – Cover* is known to be NP -complete. Based on our reduction, can we say *Independent – Set* is NP -complete?

Solution: Yes. This follows from the two conditions necessary to be NP -complete:

- *Independent Set* is in NP , as stated in the problem.
- A reduction from a known NP -complete problem.

Problem-14 Suppose *Independent Set* is known to be NP -complete. Based on our reduction, is *Vertex Cover* NP -complete?

Solution: No. By reduction from *Vertex-Cover* to *Independent-Set*, we do not know the difficulty of solving *Independent-Set*. This is because *Independent-Set* could still be a much harder problem than *Vertex-Cover*. We have not proved that.

Problem-15 The class of NP is the class of languages that cannot be accepted in polynomial time. Is it true? Explain.

Solution:

- The class of NP is the class of languages that can be *verified* in *polynomial time*.
- The class of P is the class of languages that can be *decided* in *polynomial time*.
- The class of P is the class of languages that can be *accepted* in *polynomial time*.

$P \subseteq NP$ and “languages in P can be accepted in polynomial time”, the description “languages in NP cannot be accepted in polynomial time” is wrong.

The term NP comes from nondeterministic polynomial time and is derived from an alternative characterization by using nondeterministic polynomial time Turing machines. It has nothing to do with “cannot be accepted in polynomial time”.

Problem-16 Different encodings would cause different time complexity for the same algorithm. Is it true?

Solution: True. The time complexity of the same algorithm is different between unary encoding and binary encoding. But if the two encodings are polynomially related (e.g. base 2 & base 3 encodings), then changing between them will not cause the time complexity to change.

Problem-17 If $P = NP$, then NPC (NP Complete) $\subseteq P$. Is it true?

Solution: True. If $P = NP$, then for any language $L \in NP$ C (1) $L \in NPC$ (2) L is NP-hard. By the first condition, $L \in NPC \subseteq NP = P \Rightarrow NPC \subseteq P$.

Problem-18 If $NPC \subseteq P$, then $P = NP$. Is it true?

Solution: True. All the NP problem can be reduced to arbitrary NPC problem in polynomial time, and NPC problems can be solved in polynomial time because $NPC \subseteq P \Rightarrow$ NP problem solvable in polynomial time $\Rightarrow NP \subseteq P$ and trivially $P \subseteq NP$ implies $NP = P$.

MISCELLANEOUS CONCEPTS

CHAPTER 21



21.1 Introduction

In this chapter we will cover the topics which are useful for interviews and exams.

21.2 Hacks on Bitwise Programming

In *C* and *C++* we can work with bits effectively. First let us see the definitions of each bit operation and then move onto different techniques for solving the problems. Basically, there are six operators that *C* and *C++* support for bit manipulation:

Symbol	Operation
&	Bitwise AND
	Bitwise OR
^	Bitwise Exclusive-OR
<<	Bitwise left shift

<code>>></code>	Bitwise right shift
<code>~</code>	Bitwise complement

21.2.1 Bitwise AND

The bitwise AND tests two binary numbers and returns bit values of 1 for positions where both numbers had a one, and bit values of 0 where both numbers did not have one:

$$\begin{array}{r}
 01001011 \\
 \& 00010101 \\
 \hline
 00000001
 \end{array}$$

21.2.2 Bitwise OR

The bitwise OR tests two binary numbers and returns bit values of 1 for positions where either bit or both bits are one, the result of 0 only happens when both bits are 0:

$$\begin{array}{r}
 01001011 \\
 | 00010101 \\
 \hline
 01011111
 \end{array}$$

21.2.3 Bitwise Exclusive-OR

The bitwise Exclusive-OR tests two binary numbers and returns bit values of 1 for positions where both bits are different; if they are the same then the result is 0:

$$\begin{array}{r}
 01001011 \\
 ^ 00010101 \\
 \hline
 01011110
 \end{array}$$

21.2.4 Bitwise Left Shift

The bitwise left shift moves all bits in the number to the left and fills vacated bit positions with 0.

01001011	
<< 2	

	00101100

21.2.5 Bitwise Right Shift

The bitwise right shift moves all bits in the number to the right.

01001011	
>> 2	

	??010010

Note the use of ? for the fill bits. Where the left shift filled the vacated positions with 0, a right shift will do the same only when the value is unsigned. If the value is signed then a right shift will fill the vacated bit positions with the sign bit or 0, whichever one is implementation-defined. So the best option is to never right shift signed values.

21.2.6 Bitwise Complement

The bitwise complement inverts the bits in a single binary number.

01001011	
~	

	10110100

21.2.7 Checking Whether K-th Bit is Set or Not

Let us assume that the given number is n . Then for checking the K^{th} bit we can use the expression: $n \& (1 \ll K - 1)$. If the expression is true then we can say the K^{th} bit is set (that means, set to 1).

Example:

$$\begin{array}{l}
 n = 01001011 \text{ and } K = 4 \\
 1 \ll K - 1 \quad 00001000 \\
 n \& (1 \ll K - 1) \quad 00001000
 \end{array}$$

21.2.8 Setting K-th Bit

For a given number n , to set the K^{th} bit we can use the expression: $n \mid 1 \ll (K - 1)$

Example:

$$\begin{array}{l} n = 01001011 \text{ and } K = 3 \\ 1 \ll K - 1 \quad 00000100 \\ n \mid (1 \ll K - 1) \quad 01001111 \end{array}$$

21.2.9 Clearing K-th Bit

To clear K^{th} bit of a given number n , we can use the expression: $n \& \sim(1 \ll K - 1)$

Example:

$$\begin{array}{l} n = 01001011 \text{ and } K = 4 \\ 1 \ll K - 1 \quad 00001000 \\ \sim(1 \ll K - 1) \quad 11110111 \\ n \& \sim(1 \ll K - 1) \quad 01000011 \end{array}$$

21.2.10 Toggling K-th Bit

For a given number n , for toggling the K^{th} bit we can use the expression: $n \wedge (1 \ll K - 1)$

Example:

$$\begin{array}{l} n = 01001011 \text{ and } K = 3 \\ 1 \ll K - 1 \quad 00000100 \\ n \wedge (1 \ll K - 1) \quad 01001111 \end{array}$$

21.2.11 Toggling Rightmost One Bit

For a given number n , for toggling rightmost one bit we can use the expression: $n \& n - 1$

Example:

$$\begin{array}{l} n = 01001011 \\ n - 1 \quad 01001010 \\ n \& n - 1 \quad 01001010 \end{array}$$

21.2.12 Isolating Rightmost One Bit

For a given number n , for isolating rightmost one bit we can use the expression: $n \& -n$

Example:

$$\begin{array}{rcl} n & = & 01001011 \\ -n & & 10110101 \\ n \& -n & 00000001 \end{array}$$

Note: For computing $-n$, use two's complement representation. That means, toggle all bits and add 1.

21.2.13 Isolating Rightmost Zero Bit

For a given number n , for isolating rightmost zero bit we can use the expression: $\sim n \& n + 1$

Example:

$$\begin{array}{rcl} n & = & 01001011 \\ \sim n & & 10110100 \\ n + 1 & & 01001100 \\ \sim n \& n + 1 & 00000100 \end{array}$$

21.2.14 Checking Whether Number is Power of 2 or Not

Given number n , to check whether the number is in 2^n form for not, we can use the expression:
 $if(n \& n - 1 == 0)$

Example:

$$\begin{array}{rcl} n & = & 01001011 \\ n - 1 & & 01001010 \\ n \& n - 1 & 01001010 \\ if(n \& n - 1 == 0) & & 0 \end{array}$$

21.2.15 Multiplying Number by Power of 2

For a given number n , to multiply the number with 2^K we can use the expression: $n \ll K$

Example:

$$\begin{array}{l} n = 00001011 \text{ and } K = 2 \\ n \ll K \quad 00101100 \end{array}$$

21.2.16 Dividing Number by Power of 2

For a given number n , to divide the number with 2^K we can use the expression: $n \gg K$

Example:

$$\begin{array}{l} n = 00001011 \text{ and } K = 2 \\ n \gg K \quad 00010010 \end{array}$$

21.2.17 Finding Modulo of a Given Number

For a given number n , to find the $\%8$ we can use the expression: $n \& 0x7$. Similarly, to find $\%32$, use the expression: $n \& 0x1F$

Note: Similarly, we can find modulo value of any number.

21.2.18 Reversing the Binary Number

For a given number n , to reverse the bits (reverse (mirror) of binary number) we can use the following code snippet:

```
unsigned int n, nReverse = n;
int s = sizeof(n);
for (; n; n >>= 1) {
    nReverse <<= 1;
    nReverse |= n & 1;
    s--;
}
nReverse <<= s;
```

Time Complexity: This requires one iteration per bit and the number of iterations depends on the size of the number.

21.2.19 Counting Number of One's in Number

For a given number n , to count the number of 1's in its binary representation we can use any of the following methods.

Method 1: Process bit by bit with bitwise and operator

```
unsigned int n;
unsigned int count=0;
while(n) {
    count += n & 1;
    n >>= 1;
}
```

Time Complexity: This approach requires one iteration per bit and the number of iterations depends on system.

Method 2: Using modulo approach

```
unsigned int n;
unsigned int count=0;
while(n) {
    if(n%2 ==1)
        count++;
    n = n/2;
}
```

Time Complexity: This requires one iteration per bit and the number of iterations depends on system.

Method 3: Using toggling approach: $n \& n - 1$

```
unsigned int n;
unsigned int count=0;
while(n) {
    count++;
    n &= n - 1;
}
```

Time Complexity: The number of iterations depends on the number of 1 bits in the number.

Method 4: Using preprocessing idea. In this method, we process the bits in groups. For example if we process them in groups of 4 bits at a time, we create a table which indicates the number of one's for each of those possibilities (as shown below).

0000→0	0100→1	1000→1	1100→2
0001→1	0101→2	1001→2	1101→3
0010→1	0110→2	1010→2	1110→3
0011→2	0111→3	1011→3	1111→4

The following code to count the number of Is in the number with this approach:

```
int Table = {0,1,1,2,1,2,2,3,1,2,2,3,2,3,3,4};
int count = 0;
for(; n; n >>= 4)
    count = count + Table[n & 0xF];
return count;
```

Time Complexity: This approach requires one iteration per 4 bits and the number of iterations depends on system.

21.2.20 Creating Mask for Trailing Zero's

For a given number n , to create a mask for trailing zeros, we can use the expression: $(n \& -n) - 1$

Example:

$$\begin{array}{ll}
 n & 01001011 \\
 -n & 10110101 \\
 n \& -n & 00000001 \\
 (n \& -n) - 1 & 00000000
 \end{array}$$

Note: In the above case we are getting the mask as all zeros because there are no trailing zeros.

27.2.21 Swap all odd and even bits

Example:

$$\begin{array}{ll}
 n = & 01001011 \\
 \text{Find even bits of given number (evenN)} = & n \& 0xAA \quad 00001010 \\
 \text{Find odd bits of given number (oddN)} = & n \& 0x55 \quad 01000001 \\
 & \text{evenN} >>= 1 \quad 00000101 \\
 & \text{oddN} <<= 1 \quad 10000010 \\
 \text{Final Expression: evenN | oddN} & \quad 10000111
 \end{array}$$

21.2.22 Performing Average without Division

Is there a bit-twiddling algorithm to replace $mid = (low + high) / 2$ (used in Binary Search and Merge Sort) with something much faster?

We can use $mid = (low + high) \gg 1$. Note that using $(low + high) / 2$ for midpoint calculations won't work correctly when integer overflow becomes an issue. We can use bit shifting and also overcome a possible overflow issue: $low + ((high - low) / 2)$ and the bit shifting operation for this is $low + ((high - low) \gg 1)$.

21.3 Other Programming Questions with Solutions

Problem-1 Give an algorithm for printing the matrix elements in spiral order.

Solution: Non-recursive solution involves directions right, left, up, down, and dealing their corresponding indices. Once the first row is printed, direction changes (from right) to down, the row is discarded by incrementing the upper limit. Once the last column is printed, direction changes to left, the column is discarded by decrementing the right hand limit.

```
void Spiral(int **A, int n) {
    int rowStart=0, columnStart=0;
    int rowEnd=n-1, columnEnd=n-1;
    while(rowStart<=rowEnd && columnStart<=columnEnd) {
        int i=rowStart, j=columnStart;
        for(j=columnStart; j<=columnEnd; j++)
            printf("%d ",A[i][j]);
        for(i=rowStart+1, j--; i<=rowEnd; i++)
            printf("%d ",A[i][j]);
        for(j=columnEnd-1, i--; j>=columnStart; j--)
            printf("%d ",A[i][j]);
        for(i=rowEnd-1, j++; i>=rowStart+1; i--)
            printf("%d ",A[i][j]);
        rowStart++; columnStart++; rowEnd--; columnEnd--;
    }
}
```

Time Complexity: $O(n^2)$. Space Complexity: $O(1)$.

Problem-2 Give an algorithm for shuffling the desk of cards.

Solution: Assume that we want to shuffle an array of 52 cards, from 0 to 51 with no repeats, such as we might want for a deck of cards. First fill the array with the values in order, then go through

the array and exchange each element with a randomly chosen element in the range from itself to the end. It's possible that an element will swap with itself, but there is no problem with that.

```
void Shuffle(int cards[], int n){  
    srand(time(0)); // initialize seed randomly  
    for (int i=0; i<n; i++)  
        cards[i] = i; // filling the array with card number  
    for (int i=0; i<n; i++) {  
        int r = i + (rand() % (52-i)); // Random remaining position.  
        int temp = cards[i];  
        cards[i] = cards[r];  
        cards[r] = temp;  
    }  
    printf("Shuffled Cards: ");  
    for (int i=0; i<n; i++)  
        printf("%d ", cards[i]);  
}
```

Time Complexity: O(n). Space Complexity: O(1).

Problem-3 Reversal algorithm for array rotation: Write a function rotate(A[], d, n) that rotates A[] of size n by d elements. For example, the array 1,2,3,4,5,6,7 becomes 3,4,5,6,7,1,2 after 2 rotations.

Solution: Consider the following algorithm.

Algorithm:

```
rotate(Array[], d, n)  
reverse(Array[], 1, d) ; reverse(Array[], d + 1, n);  
reverse(Array[], 1, n);
```

Let AB be the two parts of the input Arrays where A = Array[0..d-1] and B = Array[d..n-1]. The idea of the algorithm is:

Reverse A to get ArB. /* Ar is reverse of A */

Reverse B to get ArBr. /* Br is reverse of B */

Reverse all to get (ArBr) r = BA.

For example, if Array[] = [1, 2, 3, 4, 5, 6, 7], d = 2 and n = 7 then, A = [1, 2] and B = [3, 4, 5, 6, 7]

Reverse A, we get ArB = [2, 1, 3, 4, 5, 6, 7], Reverse B, we get ArBr = [2, 1, 7, 6, 5, 4, 3]

Reverse all, we get (ArBr)r = [3, 4, 5, 6, 7, 1, 2]

Implementation :

```

//Function to left rotate Array[] of size n by d
void leftRotate(int Array[], int d, int n) {
    rvereseArrayay(Array, 0, d-1);
    rvereseArrayay(Array, d, n-1);
    rvereseArrayay(Array, 0, n-1);
}
//UTILITY FUNCTIONS: function to print an Arrays
void printArrayay(int Array[], int size){
    for(int i = 0; i < size; i++)
        printf("%d ", Array[i]);
    printf("%\n ");
}
//Function to reverse Array[] from index start to end
void rvereseArrayay(int Array[], int start, int end) {
    int i;
    int temp;
    while(start < end){
        temp = Array[start];
        Array[start] = Array[end];
        Array[end] = temp;
        start++;
        end--;
    }
}

```

Problem-4 Suppose you are given an array $s[1...n]$ and a procedure $\text{reverse}(s, i, j)$ which reverses the order of elements in between positions i and j (both inclusive). What does the following sequence

do, where $1 < k \leq n$:

reverse (s , 1 , k);
 reverse (s , $k + 1$, n);
 reverse (s , 1 , n);

- a) Rotates s left by k positions
- b) Leaves s unchanged
- c) Reverses all elements of s
- d) None of the above

Solution: (b). Effect of the above 3 reversals for any k is equivalent to left rotation of the array of size n by k [refer [Problem-3](#)].

Problem-5 Finding Anagrams in Dictionary: you are given these 2 files: dictionary.txt and jumbles.txt

The jumbles.txt file contains a bunch of scrambled words. Your job is to print out those jumbled words, 1 word to a line. After each jumbled word, print a list of real dictionary words that could be formed by unscrambling the jumbled word. The dictionary words that you have to choose from are in the dictionary.txt file. Sample content of jumbles.txt:

nwae: wean anew wane
eslyep: sleepy
rpeoims: semipro imposer promise
ettniner: renitent
ahicryrhe: hierarchy
dica: acid cadi caid
dobol: blood
.....
%

Solution: Step-By-Step

Step 1: Initialization

- Open the dictionary.txt file and read the words into an array (before going further verify by echoing out the words back from the array out to the screen).
- Declare a hash table variable.

Step 2: Process the Dictionary for each dictionary word in the array. Do the following:

We now have a hash table where each key is the sorted form of a dictionary word and the value associated to it is a string or array of dictionary words that sort to that same key.

- Remove the newline off the end of each word via chomp(\$word);
- Make a sorted copy of the word - i.e. rearrange the individual chars in the string to be sorted alphabetically
- Think of the sorted word as the key value and think of the set of all dictionary words that sort to the exact same key word as being the value of the key
- Query the hashtable to see if the sortedWord is already one of the keys
- If it is not already present then insert the sorted word as key and the unsorted original of the word as the value
- Else concat the unsorted word onto the value string already out there (put a space in between)

Step 3: Process the jumbled word file

- Read through the jumbled word file one word at a time. As you read each jumbled word chomp it and make a sorted copy (the sorted copy is your key)
- Print the unsorted jumble word
- Query the hashtable for the sorted copy. If found, print the associated value on same line as key and then a new line.

Step 4: Celebrate, we are all done

Sample code in Perl:

```

#step 1
open("MYFILE",<dictionary.txt>);
while(<MYFILE>){
    $row = $_;
    chomp($row);
    push(@words,$row);
}
my %hashdic = ();
#step 2
foreach $words(@words){
    @not_sorted=split (' ', $words);

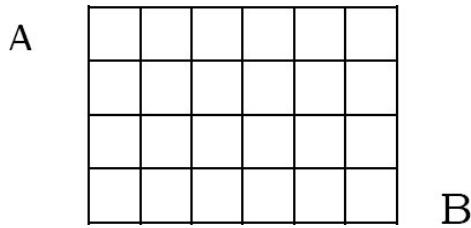
    @sorted = sort (@not_sorted);

    $name=join("",@sorted);
    if (exists $hashdic{$name}) {
        $hashdic{$name}." $words";
    }
    else {
        $hashdic{$name}=$words;
    }
}
$size=keys %hashdic;
#step 3
open("jumbled",<jumbles.txt>);
while(<jumbled>){
    $jum = $_;
    chomp($jum);
    @not_sorted1=split (' ', $jum);
    @sorted1 = sort(@not_sorted1);
    $name1=join("",@sorted1);
    if(length($hashdic{$name1})<1) {
        print "\n$jum : NO MATCHES";
    }
    else {
        @value=split(/ /,$hashdic{$name1});
        print "\n$jum : @values";
    }
}

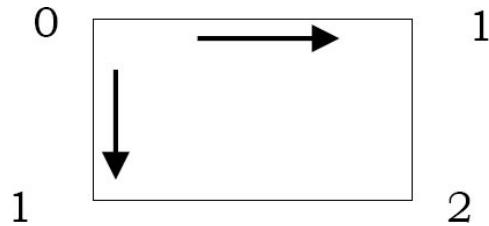
```

Problem-6 Pathways: Given a matrix as shown below, calculate the number of ways for

reaching destination *B* from *A*.



Solution: Before finding the solution, we try to understand the problem with a simpler version. The smallest problem that we can consider is the number of possible routes in a 1×1 grid.



From the above figure, it can be seen that:

- From both the bottom-left and the top-right corners there's only one possible route to the destination.
- From the top-left corner there are trivially two possible routes.

Similarly, for 2×2 and 3×3 grids, we can fill the matrix as:

0	1
1	2

0	1	1
1	2	3
1	3	6

From the above discussion, it is clear that to reach the bottom right corner from left top corner, the paths are overlapping. As unique paths could overlap at certain points (grid cells), we could try to alter the previous algorithm, as a way to avoid following the same path again. If we start filling 4×4 and 5×5 , we can easily figure out the solution based on our childhood mathematics concepts.

0	1	1	1
1	2	3	4
1	3	6	10
1	4	10	20

0	1	1	1	1
1	2	3	4	5
1	3	6	10	15
1	4	10	20	35
1	5	15	35	70

Are you able to figure out the pattern? It is the same as *Pascals* triangle. So, to find the number of ways, we can simply scan through the table and keep counting them while we move from left to right and top to bottom (starting with left-top). We can even solve this problem with mathematical equation of *Pascals* triangle.

Problem-7 Given a string that has a set of words and spaces, write a program to move the spaces to *front* of string. You need to traverse the array only once and you need to adjust the string in place.

Input = “move these spaces to beginning” *Output* =“ movethesepaces to beginning”

Solution: Maintain two indices i and j ; traverse from end to beginning. If the current index contains char, swap chars in index i with index j . This will move all the spaces to beginning of the array.

```
void mySwap(char A[],int i,int j){  
    char temp=A[i];  
    A[i]=A[j];  
    A[j]=temp;  
}  
void moveSpacesToBegin(char A[]){  
    int i=strlen(A)-1;  
    int j=i;  
    for(; j>=0; j--){  
        if(!isspace(A[j]))  
            mySwap(A,i--,j);  
    }  
}
```

```
void testCode(int argc, char * argv[]){  
    char sparr[]="move these spaces to beginning";  
    printf("Value of A is: %s\n", sparr);  
    moveSpacesToBegin(sparr);  
    printf("Value of A is: %s", sparr);  
}
```

Time Complexity: $O(n)$ where n is the number of characters in the input array. Space Complexity: $O(1)$.

Problem-8 For the [Problem-7](#), can we improve the complexity?

Solution: We can avoid a swap operation with a simple counter. But, it does not reduce the overall complexity.

```
void moveSpacesToBegin(char A[]){  
    int n=strlen(A)-1,count=n;  
    int i=n;  
    for(;i>=0;i--){  
        if(A[i]!=' ')  
            A[count--]=A[i];  
    }  
    while(count>=0)  
        A[count--]=' ';  
}
```

```
int testCode(){  
    char sparr[]="move these spaces to beginning";  
    printf("Value of A is: %s\n", sparr);  
    moveSpacesToBegin(sparr);  
    printf("Value of A is: %s", sparr);  
}
```

Time Complexity: $O(n)$ where n is the number of characters in input array. Space Complexity: $O(1)$.

Problem-9 Given a string that has a set of words and spaces, write a program to move the spaces to *end* of string. You need to traverse the array only once and you need to adjust the string in place.

Input = “move these spaces to end” *Output* = “movethesepacestoend”

Solution: Traverse the array from left to right. While traversing, maintain a counter for non-space elements in array. For every non-space character $A[i]$, put the element at $A[\text{count}]$ and increment count . After complete traversal, all non-space elements have already been shifted to front end and count is set as index of first 0. Now, all we need to do is run a loop which fills all elements with spaces from count till end of the array.

```
void moveSpacesToEnd(char A[]){
    // Count of non-space elements
    int count = 0;
    int n = strlen(A)-1;
    int i = 0;
    for (; i <= n; i++)
        if (!isspace(A[i]))
            A[count++] = A[i];
    while (count <= n)
        A[++count] = ' ';
}
```

```
void testCode(int argc, char * argv[]){
    char sparr[]="move these spaces to end";
    printf("Value of A is: %s\n", sparr);
    moveSpacesToEnd(sparr);
    printf("Value of A is: %s", sparr);
}
```

Time Complexity: $O(n)$ where n is number of characters in input array. Space Complexity: $O(1)$.

Problem-10 Moving Zeros to end: Given an array of n integers, move all the zeros of a given array to the end of the array. For example, if the given array is $\{1, 9, 8, 4, 0, 0, 2, 7, 0, 6, 0\}$, it should be changed to $\{1, 9, 8, 4, 2, 7, 6, 0, 0, 0, 0\}$. The order of all other elements should be same.

Solution: Maintain two variables i and j ; and initialize with 0. For each of the array element $A[i]$, if $A[i]$ non-zero element, then replace the element $A[j]$ with element $A[i]$. Variable i will always be incremented till $n - 1$ but we will increment j only when the element pointed by i is non-zero.

```

void moveZerosToEnd(int A[], int size){
    int i=0,j=0;
    while (i <= size - 1){
        if (A[i] != 0){
            A[j++] = A[i];
        }
        i++;
    }
    while (j <= size - 1)
        A[j++] = 0;
}

```

```

int testCode(){
    int A[ ] = {1,9,8,4,0,0,2,7,0,6,0};
    int i;
    int size = sizeof(A) / sizeof(A[0]);
    moveZerosToEnd(A, size);
    for (i = 0; i <= size - 1; i++)
        printf("%d ", A[i]);
    return 0;
}

```

Time Complexity: O(n). Space Complexity: O(1).

Problem-11 For [Problem-10](#), can we improve the complexity?

Solution: Using simple swap technique we can avoid the unnecessary second *while* loop from the above code.

```

void mySwap(int A[],int i,int j){
    int temp=A[i]; A[i]=A[j]; A[j]=temp;
}
void moveZerosToEnd(int A[], int len){
    int i, j;
    for(i=0,j=0; i<len; i++) {
        if (A[i] !=0)
            mySwap(A,j++,i);
    }
}

```

Time Complexity: O(n). Space Complexity: O(1).

Problem-12 Variant of [Problem-10](#) and [Problem-11](#): Given an array containing negative and positive numbers; give an algorithm for separating positive and negative numbers in it. Also, maintain the relative order of positive and negative numbers. Input: -5, 3, 2, -1, 4, -8
Output: -5-1 -8342

Solution: In the *moveZerosToEnd* function, just replace the condition $A[i] \neq 0$ with $A[i] < 0$.

Problem-13 Given a number, swap odd and even bits.

Solution:

```

int swap(int num){
    int mask1 = 0xAAAAAAAA;
    int mask2 = 0x55555555;
    return (num << 1 & mask1) | (num >> 1 & mask2);
}

```

Problem-14 Count the number of set bits in all numbers from 1 to n

Solution: We can use the technique of [section 21.2.19](#) and iterate through all the numbers from 1 to n.

```

int countingNumberofOnesIn1toN(unsigned int n){
    int count = 0, i = 0, j;
    for (i = 1; i <= n; i++){
        j = i;
        while(j){
            j = j & (j-1);
            count++;
        }
    }
    return count;
}

```

Problem-15 Count the number of set bits in all numbers from 1 to n

Solution: We can use the technique of [section 21.2.19](#) and iterate through all the numbers from 1 to n.

```

int countingNumberofOnesIn1toN(unsigned int n){
    int count = 0, i = 0, j;
    for (i = 1; i <= n; i++){
        j = i;
        while(j){
            j = j & (j-1);
            count++;
        }
    }
    return count;
}

```

Time complexity: O(number of set bits in all numbers from 1 to n).

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