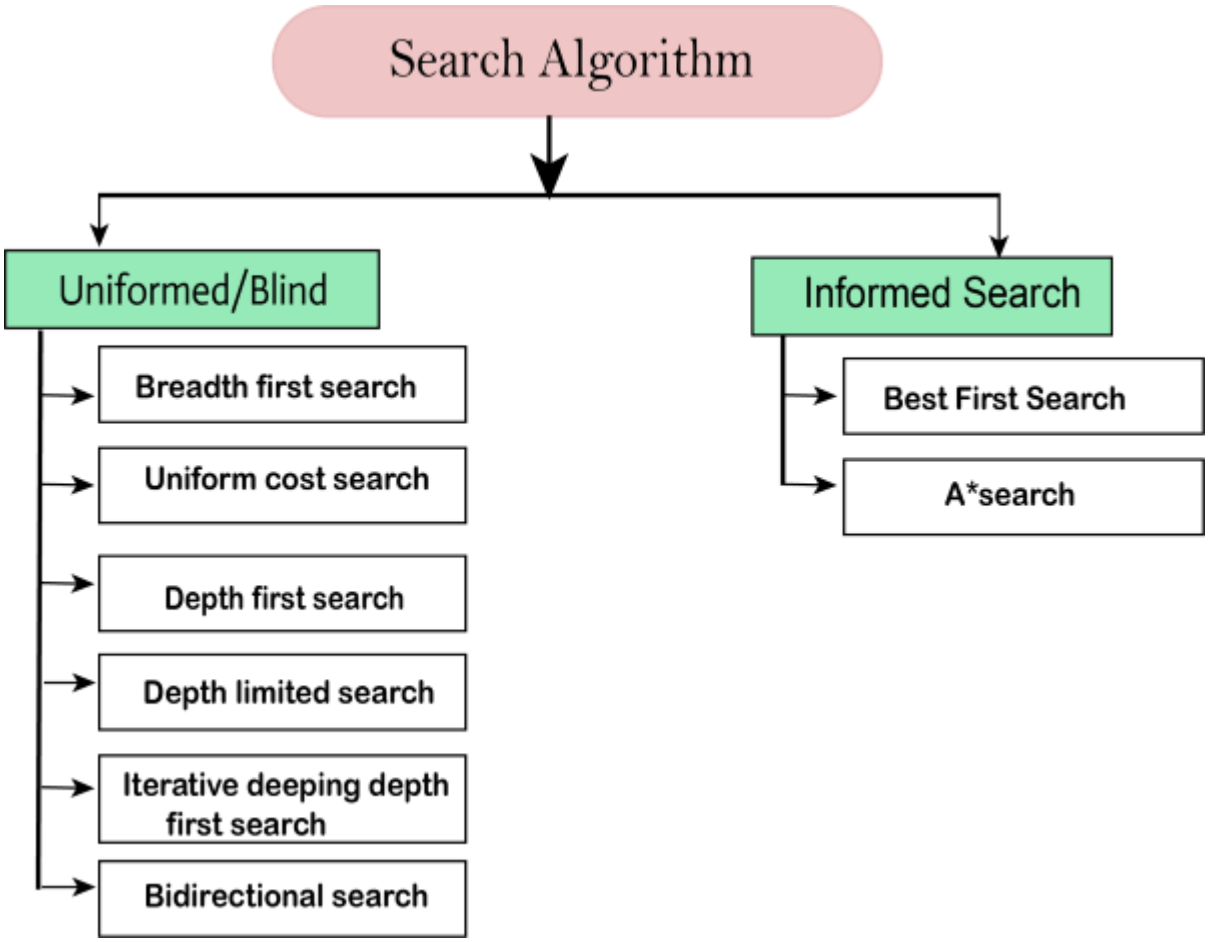
UNIT I PROBLEM SOLVING

Types of search algorithms

Based on the search problems we can classify the search algorithms into uninformed (Blind search) search and informed search (Heuristic search) algorithms.



Uninformed/Blind Search:

It can be divided into five main types:

- Breadth-first search
- Uniform cost search
- Depth-first search
- Iterative deepening depth-first search
- Bidirectional Search

Informed Search

An example of informed search algorithms is a traveling salesman problem.

1. Greedy Search
2. A* Search

Uninformed Search Algorithms

Uninformed search is a class of general-purpose search algorithms which operates in brute force-way. Uninformed search algorithms do not have additional information about state or search space other than how to traverse the tree, so it is also called blind search.

Following are the various types of uninformed search algorithms:

1. **Breadth-first Search**
2. **Depth-first Search**
3. **Depth-limited Search**
4. **Iterative deepening depth-first search**
5. **Uniform cost search**
6. **Bidirectional Search**

1. Breadth-first Search:

- Breadth-first search is the most common search strategy for traversing a tree or graph. This algorithm searches breadthwise in a tree or graph, so it is called breadth-first search.
- BFS algorithm starts searching from the root node of the tree and expands all successor node at the current level before moving to nodes of next level.
- The breadth-first search algorithm is an example of a general-graph search algorithm.
- Breadth-first search implemented using FIFO queue data structure.

Advantages:

- BFS will provide a solution if any solution exists.

- If there are more than one solutions for a given problem, then BFS will provide the minimal solution which requires the least number of steps.

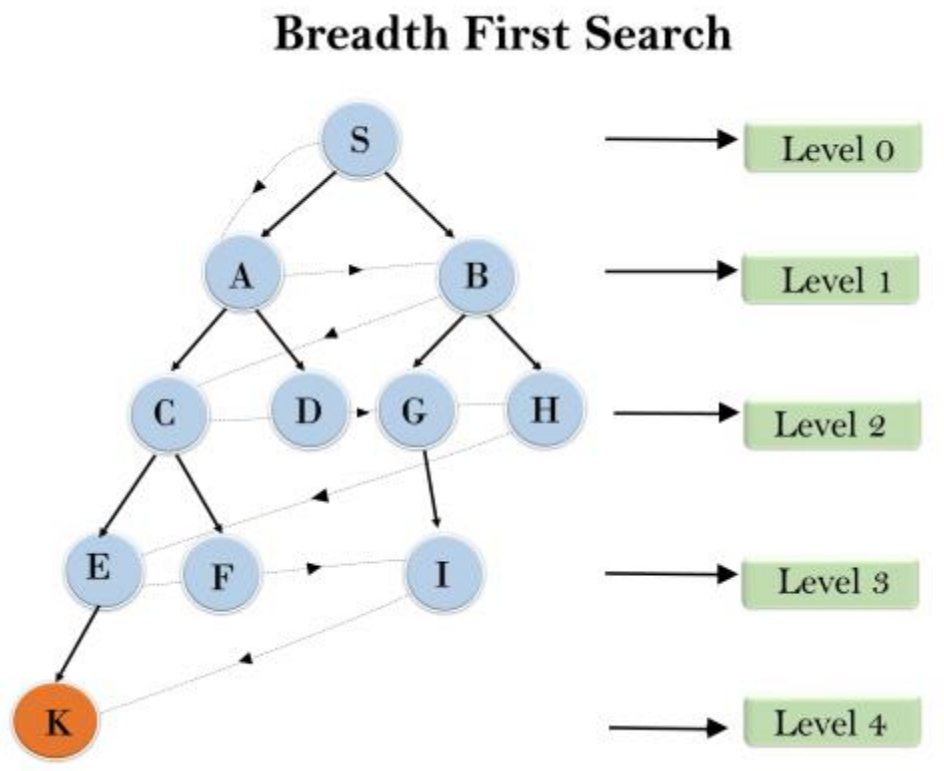
Disadvantages:

- It requires lots of memory since each level of the tree must be saved into memory to expand the next level.
- BFS needs lots of time if the solution is far away from the root node.

Example:

In the below tree structure, we have shown the traversing of the tree using BFS algorithm from the root node S to goal node K. BFS search algorithm traverse in layers, so it will follow the path which is shown by the dotted arrow, and the traversed path will be:

1. S---> A--->B---->C--->D---->G--->H--->E---->F---->I---->K



Time Complexity: Time Complexity of BFS algorithm can be obtained by the number of nodes traversed in BFS until the shallowest Node. Where the d= depth of shallowest solution and b is a node at every state.

$T(b) = 1+b^2+b^3+.....+ b^d = O(b^d)$

Space Complexity: Space complexity of BFS algorithm is given by the Memory size of frontier which is $O(b^d)$.

Completeness: BFS is complete, which means if the shallowest goal node is at some finite depth, then BFS will find a solution.

Optimality: BFS is optimal if path cost is a non-decreasing function of the depth of the node.

2. Depth-first Search

- Depth-first search isa recursive algorithm for traversing a tree or graph data structure.
- It is called the depth-first search because it starts from the root node and follows each path to its greatest depth node before moving to the next path.
- DFS uses a stack data structure for its implementation.
- The process of the DFS algorithm is similar to the BFS algorithm.

Advantage:

- DFS requires very less memory as it only needs to store a stack of the nodes on the path from root node to the current node.
- It takes less time to reach to the goal node than BFS algorithm (if it traverses in the right path).

Disadvantage:

- There is the possibility that many states keep re-occurring, and there is no guarantee of finding the solution.
- DFS algorithm goes for deep down searching and sometime it may go to the infinite loop.

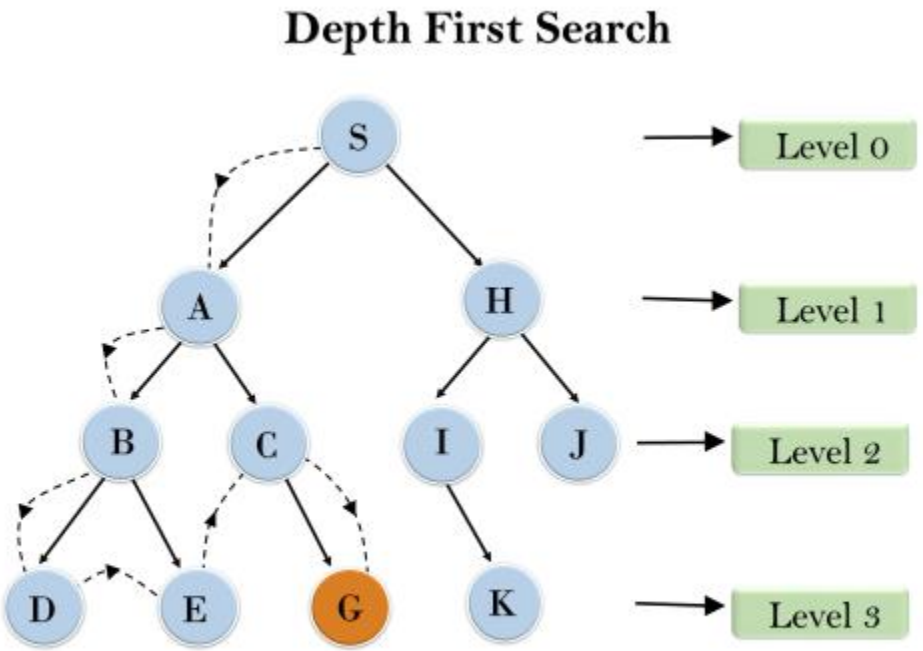
Example:

In the below search tree, we have shown the flow of depth-first search, and it will follow the order as:

Root node--->Left node ----> right node.

It will start searching from root node S, and traverse A, then B, then D and E, after traversing E, it will backtrack the tree as E has no other successor and still goal node is

not found. After backtracking it will traverse node C and then G, and here it will terminate as it found goal node.



Completeness: DFS search algorithm is complete within finite state space as it will expand every node within a limited search tree.

Time Complexity: Time complexity of DFS will be equivalent to the node traversed by the algorithm. It is given by:

$T(n)= 1+ n^2+ n^3 +.....+ n^m=O(n^m)$

Where, m= maximum depth of any node and this can be much larger than d (Shallowest solution depth)

Space Complexity: DFS algorithm needs to store only single path from the root node, hence space complexity of DFS is equivalent to the size of the fringe set, which is **O(bm)**.

Optimal: DFS search algorithm is non-optimal, as it may generate a large number of steps or high cost to reach to the goal node.

3. Depth-Limited Search Algorithm:

A depth-limited search algorithm is similar to depth-first search with a predetermined limit. Depth-limited search can solve the drawback of the infinite path in the Depth-first search. In this algorithm, the node at the depth limit will treat as it has no successor nodes further.

Depth-limited search can be terminated with two Conditions of failure:

- Standard failure value: It indicates that problem does not have any solution.
- Cutoff failure value: It defines no solution for the problem within a given depth limit.

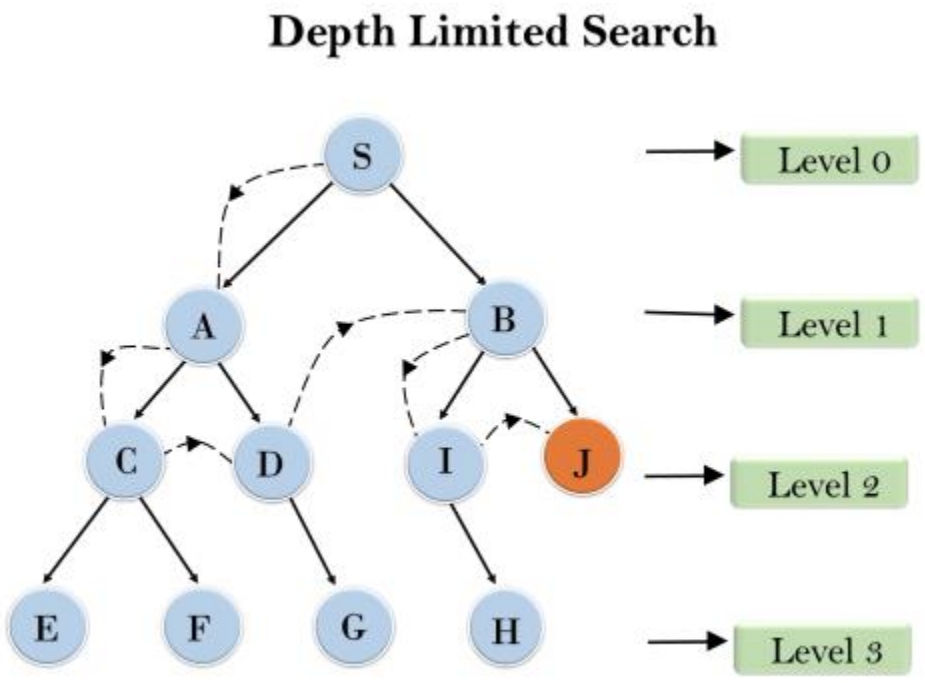
Advantages:

Depth-limited search is Memory efficient.

Disadvantages:

- Depth-limited search also has a disadvantage of incompleteness.
- It may not be optimal if the problem has more than one solution.

Example:



Completeness: DLS search algorithm is complete if the solution is above the depth-limit.

Time Complexity: Time complexity of DLS algorithm is **O(b^{ℓ})**.

Space Complexity: Space complexity of DLS algorithm is O**(b×ℓ)**.

Optimal: Depth-limited search can be viewed as a special case of DFS, and it is also not optimal even if ℓ>d.

4. Uniform-cost Search Algorithm:

Uniform-cost search is a searching algorithm used for traversing a weighted tree or graph. This algorithm comes into play when a different cost is available for each edge. The primary goal of the uniform-cost search is to find a path to the goal node which has the lowest cumulative cost. Uniform-cost search expands nodes according to their path costs form the root node. It can be used to solve any graph/tree where the optimal cost is in demand. A uniform-cost search algorithm is implemented by the priority queue. It gives maximum priority to the lowest cumulative cost. Uniform cost search is equivalent to BFS algorithm if the path cost of all edges is the same.

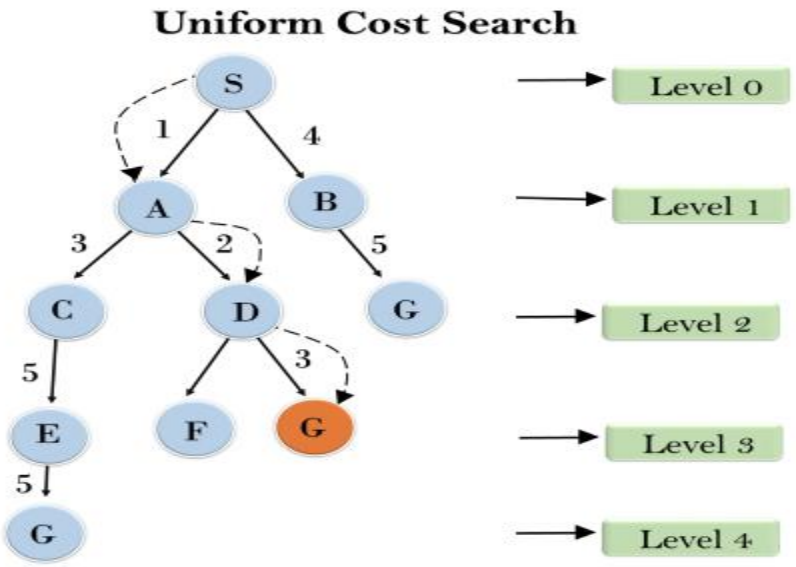
Advantages:

- Uniform cost search is optimal because at every state the path with the least cost is chosen.

Disadvantages:

- It does not care about the number of steps involve in searching and only concerned about path cost. Due to which this algorithm may be stuck in an infinite loop.

Example:



Completeness:

Uniform-cost search is complete, such as if there is a solution, UCS will find it.

Time Complexity:

Let C* **is Cost of the optimal solution**, and **ε** is each step to get closer to the goal node. Then the number of steps is = C*/ε+1. Here we have taken +1, as we start from state 0 and end to C*/ε.

Hence, the worst-case time complexity of Uniform-cost search is$\mathbf{O(b^{1 + [C^*/\varepsilon]})/}$.

Space Complexity:

The same logic is for space complexity so, the worst-case space complexity of Uniform-cost search is $\mathbf{O(b^{1 + [C^*/\varepsilon]})}$.

Optimal:

Uniform-cost search is always optimal as it only selects a path with the lowest path cost.

5. Iterative deepening depth-first Search:

The iterative deepening algorithm is a combination of DFS and BFS algorithms. This search algorithm finds out the best depth limit and does it by gradually increasing the limit until a goal is found.

This algorithm performs depth-first search up to a certain "depth limit", and it keeps increasing the depth limit after each iteration until the goal node is found.

This Search algorithm combines the benefits of Breadth-first search's fast search and depth-first search's memory efficiency.

The iterative search algorithm is useful uninformed search when search space is large, and depth of goal node is unknown.

Advantages:

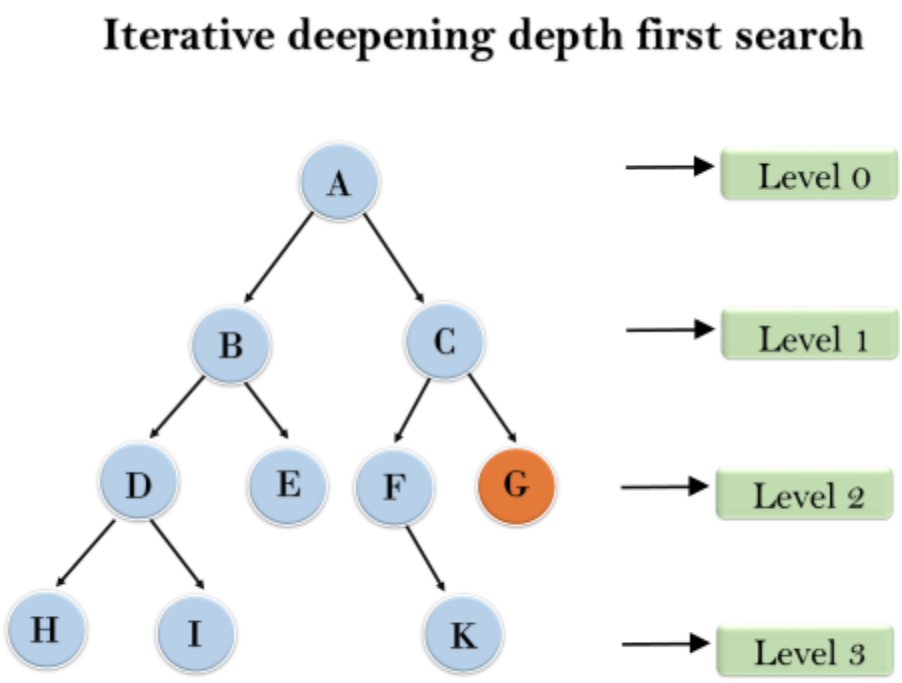
- Itcombines the benefits of BFS and DFS search algorithm in terms of fast search and memory efficiency.

Disadvantages:

- The main drawback of IDDFS is that it repeats all the work of the previous phase.

Example:

Following tree structure is showing the iterative deepening depth-first search. IDDFS algorithm performs various iterations until it does not find the goal node. The iteration performed by the algorithm is given as:



1'st Iteration-----> A
2'nd Iteration----> A, B, C
3'rd Iteration------>A, B, D, E, C, F, G
4'th Iteration------>A, B, D, H, I, E, C, F, K, G
In the fourth iteration, the algorithm will find the goal node.

Completeness:

This algorithm is complete is if the branching factor is finite.

Time Complexity:

Let's suppose b is the branching factor and depth is d then the worst-case time complexity is **$O(b^d)$**.

Space Complexity:

The space complexity of IDDFS will be **O(bd)**.

Optimal:

IDDFS algorithm is optimal if path cost is a non- decreasing function of the depth of the node.

6. Bidirectional Search Algorithm:

Bidirectional search algorithm runs two simultaneous searches, one form initial state called as forward-search and other from goal node called as backward-search, to find the goal node. Bidirectional search replaces one single search graph with two small subgraphs in which one starts the search from an initial vertex and other starts from goal vertex. The search stops when these two graphs intersect each other.

Bidirectional search can use search techniques such as BFS, DFS, DLS, etc.

Advantages:

- Bidirectional search is fast.
- Bidirectional search requires less memory

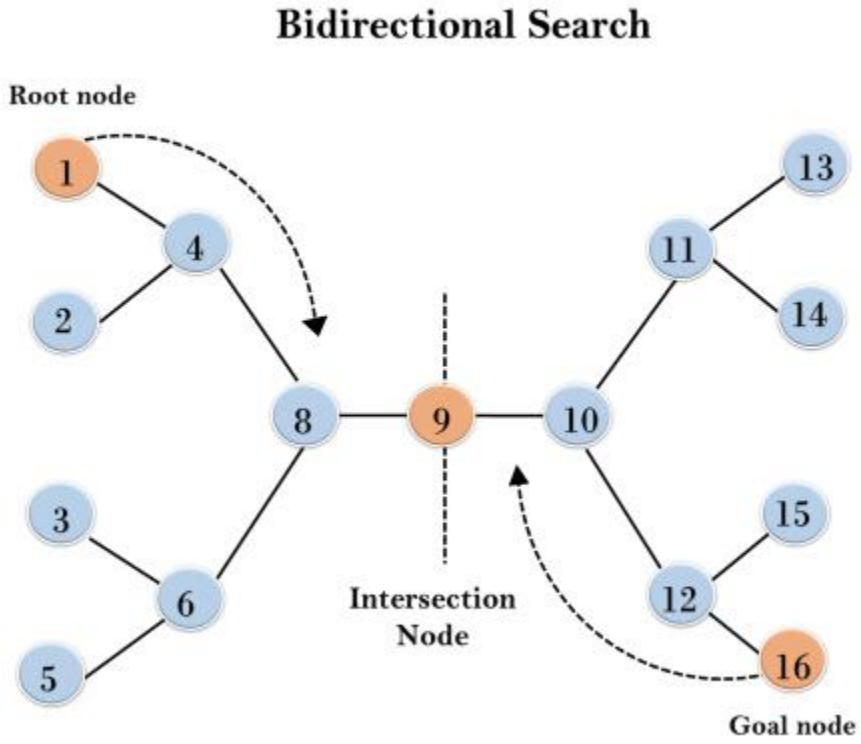
Disadvantages:

- Implementation of the bidirectional search tree is difficult.
- **In bidirectional search, one should know the goal state in advance.**

Example:

In the below search tree, bidirectional search algorithm is applied. This algorithm divides one graph/tree into two sub-graphs. It starts traversing from node 1 in the forward direction and starts from goal node 16 in the backward direction.

The algorithm terminates at node 9 where two searches meet.



Completeness: Bidirectional Search is complete if we use BFS in both searches.

Time Complexity: Time complexity of bidirectional search using BFS is **$O(b^d)$**.

Space Complexity: Space complexity of bidirectional search is **$O(b^d)$**.

Optimal: Bidirectional search is Optimal.

Informed Search Algorithms:

The informed search algorithm is more useful for large search space. Informed search algorithm uses the idea of heuristic, so it is also called Heuristic search.

Heuristics function: Heuristic is a function which is used in Informed Search, and it finds the most promising path. It takes the current state of the agent as its input and produces the estimation of how close agent is from the goal. The heuristic method, however, might not always give the best solution, but it guaranteed to find a good solution in reasonable time. Heuristic function estimates how close a state is to the goal. It is represented by h(n), and it calculates the cost of an optimal path between the pair of states. The value of the heuristic function is always positive.

Admissibility of the heuristic function is given as:

1. h(n) <= h*(n)

Here h(n) is heuristic cost, and h*(n) is the estimated cost. Hence heuristic cost should be less than or equal to the estimated cost.

In the informed search we will discuss two main algorithms which are given below:

- **Best First Search Algorithm(Greedy search)**
- **A* Search Algorithm**

1.) Best-first Search Algorithm (Greedy Search):

Greedy best-first search algorithm always selects the path which appears best at that moment. It is the combination of depth-first search and breadth-first search algorithms. It uses the heuristic function and search. Best-first search allows us to take the advantages of both algorithms. With the help of best-first search, at each step, we can choose the most promising node. In the best first search algorithm, we expand the node which is closest to the goal node and the closest cost is estimated by heuristic function, i.e.

1. f(n)= g(n).

Were, h(n)= estimated cost from node n to the goal.

The greedy best first algorithm is implemented by the priority queue.

Best first search algorithm:

- **Step 1:** Place the starting node into the OPEN list.
- **Step 2:** If the OPEN list is empty, Stop and return failure.
- **Step 3:** Remove the node n, from the OPEN list which has the lowest value of h(n), and places it in the CLOSED list.
- **Step 4:** Expand the node n, and generate the successors of node n.
- **Step 5:** Check each successor of node n, and find whether any node is a goal node or not. If any successor node is goal node, then return success and terminate the search, else proceed to Step 6.
- **Step 6:** For each successor node, algorithm checks for evaluation function f(n), and then check if the node has been in either OPEN or CLOSED list. If the node has not been in both list, then add it to the OPEN list.
- **Step 7:** Return to Step 2.

Advantages:

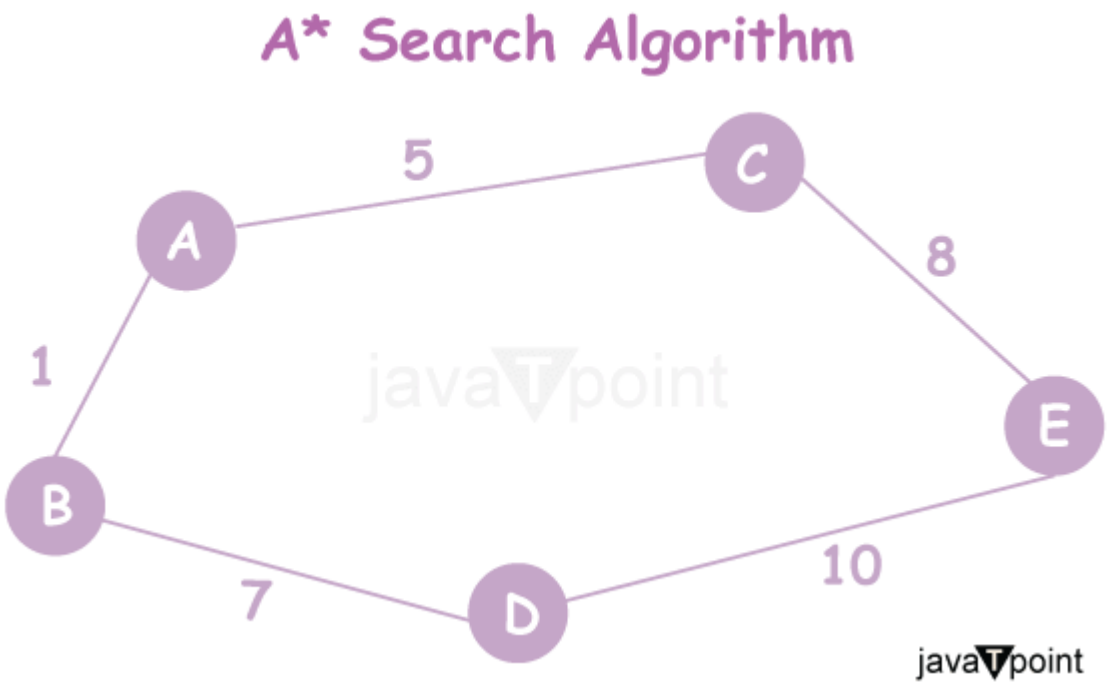
- Best first search can switch between BFS and DFS by gaining the advantages of both the algorithms.
- This algorithm is more efficient than BFS and DFS algorithms.

Disadvantages:

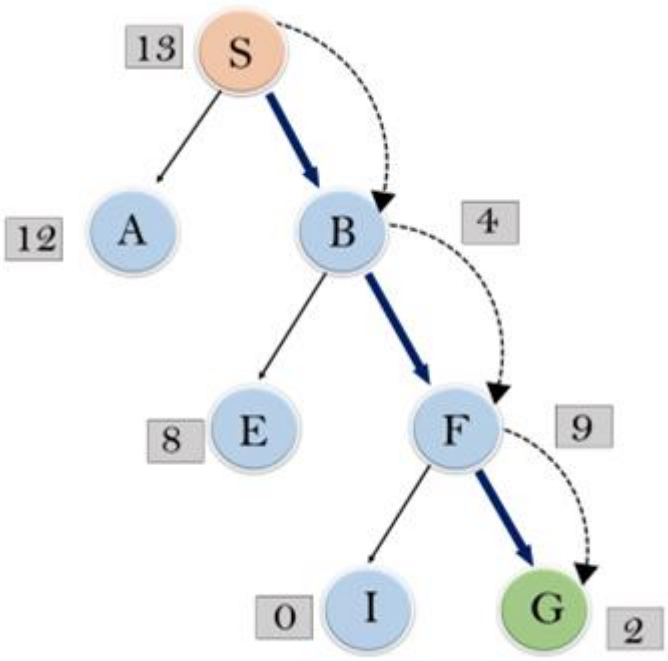
- It can behave as an unguided depth-first search in the worst case scenario.
- It can get stuck in a loop as DFS.
- This algorithm is not optimal.

Example:

Consider the below search problem, and we will traverse it using greedy best-first search. At each iteration, each node is expanded using evaluation function f(n)=h(n) , which is given in the below table.



In this search example, we are using two lists which are **OPEN** and **CLOSED** Lists. Following are the iteration for traversing the above example.



Expand the nodes of S and put in the CLOSED list

Initialization: Open [A, B], Closed [S]

Iteration1: Open [A], Closed [S,B]

Iteration2: Open[E,F,A],Closed[S,B]
: Open [E, A], Closed [S, B, F]

Iteration3: Open[I,G,E,A],Closed[S,B,F]
: Open [I, E, A], Closed [S,B,F,G]

Hence the final solution path will be: **S----> B----->F----> G**

Time Complexity: The worst case time complexity of Greedy best first search is $O(b^m)$.

Space Complexity: The worst case space complexity of Greedy best first search is $O(b^m)$. Where, m is the maximum depth of the search space.

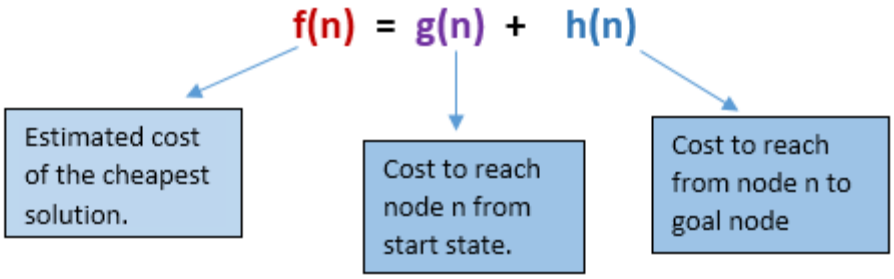
Complete: Greedy best-first search is also incomplete, even if the given state space is finite.

Optimal: Greedy best first search algorithm is not optimal.

2.) A* Search Algorithm:

A* search is the most commonly known form of best-first search. It uses heuristic function h(n), and cost to reach the node n from the start state g(n). It has combined features of UCS and greedy best-first search, by which it solve the problem efficiently. A* search algorithm finds the shortest path through the search space using the heuristic function. This search algorithm expands less search tree and provides optimal result faster. A* algorithm is similar to UCS except that it uses g(n)+h(n) instead of g(n).

In A* search algorithm, we use search heuristic as well as the cost to reach the node. Hence we can combine both costs as following, and this sum is called as a **fitness number**.



Algorithm of A* search:

Step1: Place the starting node in the OPEN list.

Step 2: Check if the OPEN list is empty or not, if the list is empty then return failure and stops.

Step 3: Select the node from the OPEN list which has the smallest value of evaluation function (g+h), if node n is goal node then return success and stop, otherwise

Step 4: Expand node n and generate all of its successors, and put n into the closed list. For each successor n', check whether n' is already in the OPEN or CLOSED list, if not then compute evaluation function for n' and place into Open list.

Step 5: Else if node n' is already in OPEN and CLOSED, then it should be attached to the back pointer which reflects the lowest g(n') value.

Step 6: Return to **Step 2**.

Advantages:

- A* search algorithm is the best algorithm than other search algorithms.
- A* search algorithm is optimal and complete.
- This algorithm can solve very complex problems.

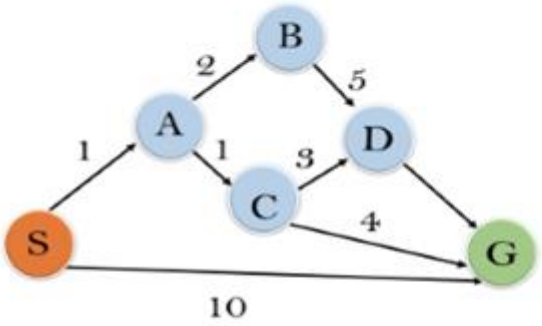
Disadvantages:

- It does not always produce the shortest path as it mostly based on heuristics and approximation.
- A* search algorithm has some complexity issues.

- The main drawback of A* is memory requirement as it keeps all generated nodes in the memory, so it is not practical for various large-scale problems.

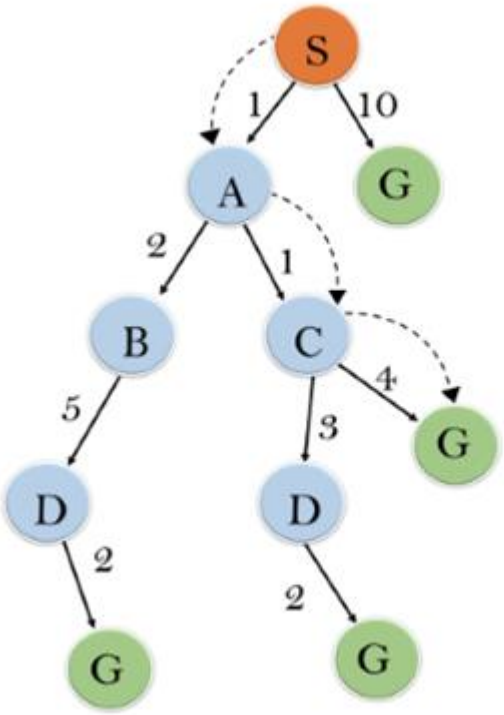
Example:

In this example, we will traverse the given graph using the A* algorithm. The heuristic value of all states is given in the below table so we will calculate the f(n) of each state using the formula f(n)= g(n) + h(n), where g(n) is the cost to reach any node from start state.
Here we will use OPEN and CLOSED list.



State	h(n)
S	5
A	3
B	4
C	2
D	6
G	0

Solution:



Initialization: {(S, 5)}

Iteration1: {(S--> A, 4), (S-->G, 10)}

Iteration2: {(S--> A-->C, 4), (S--> A-->B, 7), (S-->G, 10)}

Iteration3: {(S--> A-->C--->G, 6), (S--> A-->C--->D, 11), (S--> A-->B, 7), (S-->G, 10)}

Iteration 4 will give the final result, as **S--->A--->C--->G** it provides the optimal path with cost 6.

Points to remember:

- A* algorithm returns the path which occurred first, and it does not search for all remaining paths.
- The efficiency of A* algorithm depends on the quality of heuristic.
- A* algorithm expands all nodes which satisfy the condition f(n)<="" li="">

Complete: A* algorithm is complete as long as:

- Branching factor is finite.
- Cost at every action is fixed.

Optimal: A* search algorithm is optimal if it follows below two conditions:

- **Admissible:** the first condition requires for optimality is that h(n) should be an admissible heuristic for A* tree search. An admissible heuristic is optimistic in nature.
- **Consistency:** Second required condition is consistency for only A* graph-search.

If the heuristic function is admissible, then A* tree search will always find the least cost path.

Time Complexity: The time complexity of A* search algorithm depends on heuristic function, and the number of nodes expanded is exponential to the depth of solution d. So the time complexity is O(b^d), where b is the branching factor.

Space Complexity: The space complexity of A* search algorithm is **O(b^d).**

Hill Climbing Algorithm

- Hill climbing algorithm is a local search algorithm which continuously moves in the direction of increasing elevation/value to find the peak of the mountain or best solution to the problem. It terminates when it reaches a peak value where no neighbor has a higher value.
- Hill climbing algorithm is a technique which is used for optimizing the mathematical problems. One of the widely discussed examples of Hill climbing algorithm is Traveling-salesman Problem in which we need to minimize the distance traveled by the salesman.

- It is also called greedy local search as it only looks to its good immediate neighbor state and not beyond that.
- A node of hill climbing algorithm has two components which are state and value.
- Hill Climbing is mostly used when a good heuristic is available.
- In this algorithm, we don't need to maintain and handle the search tree or graph as it only keeps a single current state.

Features of Hill Climbing:

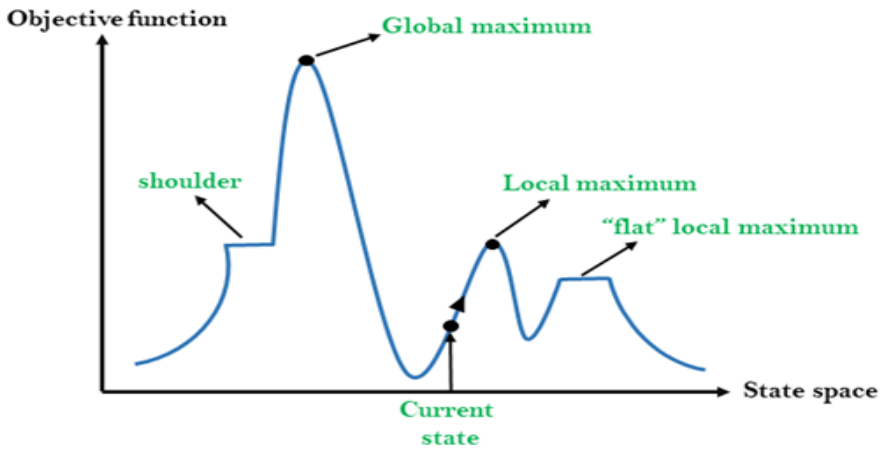
Following are some main features of Hill Climbing Algorithm:

- **Generate and Test variant:** Hill Climbing is the variant of Generate and Test method. The Generate and Test method produce feedback which helps to decide which direction to move in the search space.
- **Greedy approach:** Hill-climbing algorithm search moves in the direction which optimizes the cost.
- **No backtracking:** It does not backtrack the search space, as it does not remember the previous states.

State-space Diagram for Hill Climbing:

The state-space landscape is a graphical representation of the hill-climbing algorithm which is showing a graph between various states of algorithm and Objective function/Cost.

On Y-axis we have taken the function which can be an objective function or cost function, and state-space on the x-axis. If the function on Y-axis is cost then, the goal of search is to find the global minimum and local minimum. If the function of Y-axis is Objective function, then the goal of the search is to find the global maximum and local maximum.



Different regions in the state space landscape:

Local Maximum: Local maximum is a state which is better than its neighbour states, but there is also another state which is higher than it.

Global Maximum: Global maximum is the best possible state of state space landscape. It has the highest value of objective function.

Current state: It is a state in a landscape diagram where an agent is currently present.

Flat local maximum: It is a flat space in the landscape where all the neighbor states of current states have the same value.

Shoulder: It is a plateau region which has an uphill edge.

Types of Hill Climbing Algorithm:

- Simple hill Climbing:
- Steepest-Ascent hill-climbing:
- Stochastic hill Climbing:

1. Simple Hill Climbing:

Simple hill climbing is the simplest way to implement a hill climbing algorithm. **It only evaluates the neighbor node state at a time and selects the first one which optimizes current cost and set it as a current state**. It only checks it's one successor state, and if it finds better than the current state, then move else be in the same state. This algorithm has the following features:

- Less time consuming
- Less optimal solution and the solution is not guaranteed

Algorithm for Simple Hill Climbing:

- **Step 1:** Evaluate the initial state, if it is goal state then return success and Stop.
- **Step 2:** Loop Until a solution is found or there is no new operator left to apply.
- **Step 3:** Select and apply an operator to the current state.
- **Step 4:** Check new state:
    a. If it is goal state, then return success and quit.
    b. Else if it is better than the current state then assign new state as a current state.
    c. Else if not better than the current state, then return to step2.
- **Step 5:** Exit.

2. Steepest-Ascent hill climbing:

The steepest-Ascent algorithm is a variation of simple hill climbing algorithm. This algorithm examines all the neighbouring nodes of the current state and selects one neighbour node which is closest to the goal state. This algorithm consumes more time as it searches for multiple neighbours

Algorithm for Steepest-Ascent hill climbing:

- **Step 1:** Evaluate the initial state, if it is goal state then return success and stop, else make current state as initial state.
- **Step 2:** Loop until a solution is found or the current state does not change.
    a. Let SUCC be a state such that any successor of the current state will be better than it.
    b. For each operator that applies to the current state:
        a. Apply the new operator and generate a new state.
        b. Evaluate the new state.
        c. If it is goal state, then return it and quit, else compare it to the SUCC.
        d. If it is better than SUCC, then set new state as SUCC.
        e. If the SUCC is better than the current state, then set current state to SUCC.

- **Step 5:** Exit.

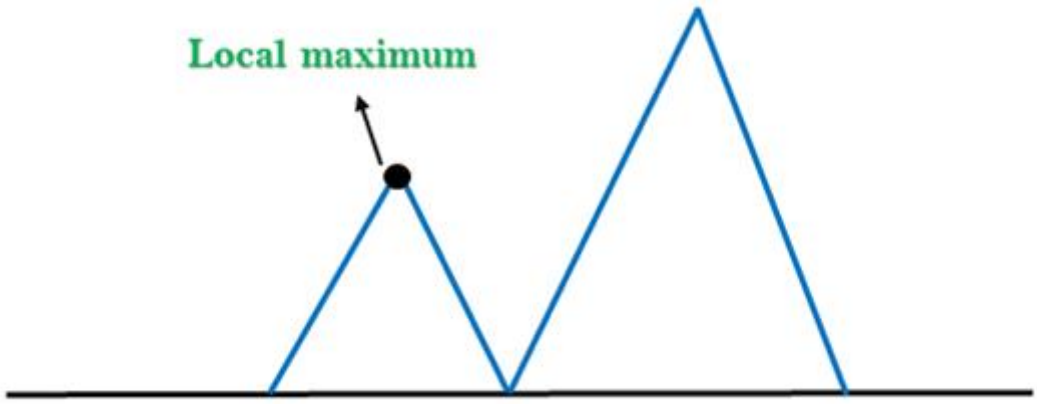
3. Stochastic hill climbing:

Stochastic hill climbing does not examine for all its neighbor before moving. Rather, this search algorithm selects one neighbor node at random and decides whether to choose it as a current state or examine another state.

Problems in Hill Climbing Algorithm:

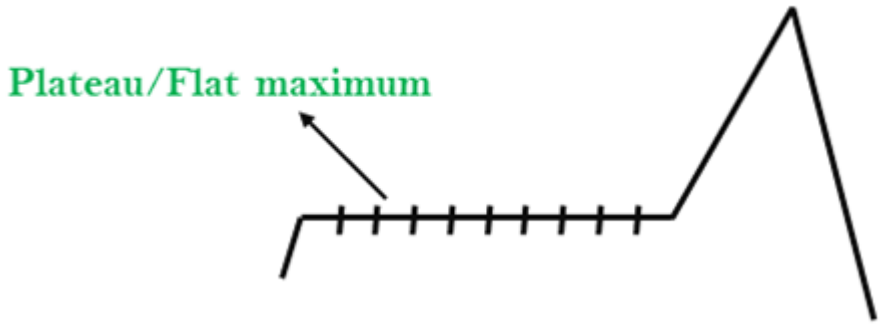
1. Local Maximum: A local maximum is a peak state in the landscape which is better than each of its neighboring states, but there is another state also present which is higher than the local maximum.

Solution: Backtracking technique can be a solution of the local maximum in state space landscape. Create a list of the promising path so that the algorithm can backtrack the search space and explore other paths as well.



2. Plateau: A plateau is the flat area of the search space in which all the neighbor states of the current state contains the same value, because of this algorithm does not find any best direction to move. A hill-climbing search might be lost in the plateau area.

Solution: The solution for the plateau is to take big steps or very little steps while searching, to solve the problem. Randomly select a state which is far away from the current state so it is possible that the algorithm could find non-plateau region.



3. Ridges: A ridge is a special form of the local maximum. It has an area which is higher than its surrounding areas, but itself has a slope, and cannot be reached in a single move.

Solution: With the use of bidirectional search, or by moving in different directions, we can improve this problem.

Simulated Annealing:

A hill-climbing algorithm which never makes a move towards a lower value guaranteed to be incomplete because it can get stuck on a local maximum. And if algorithm applies a random walk, by moving a successor, then it may complete but not efficient. **Simulated Annealing** is an algorithm which yields both efficiency and completeness.

In mechanical term **Annealing** is a process of hardening a metal or glass to a high temperature then cooling gradually, so this allows the metal to reach a low-energy crystalline state. The same process is used in simulated annealing in which the algorithm picks a random move, instead of picking the best move. If the random move improves the state, then it follows the same path. Otherwise, the algorithm follows the

path which has a probability of less than 1 or it moves downhill and chooses another path.

Mini-Max Algorithm

Mini-max algorithm is a recursive or backtracking algorithm which is used in decision-making and game theory. It provides an optimal move for the player assuming that opponent is also playing optimally.

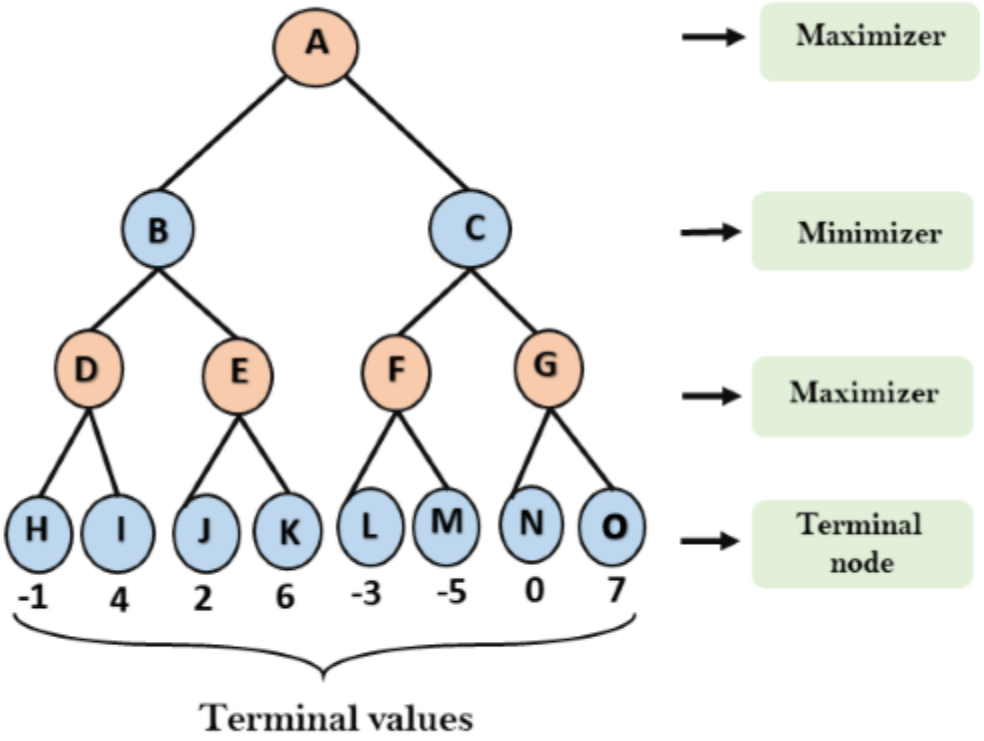
- Mini-Max algorithm uses recursion to search through the game-tree.
- Min-Max algorithm is mostly used for game playing in AI. Such as Chess, Checkers, tic-tac-toe, go, and various tow-players game. This Algorithm computes the minimax decision for the current state.
- In this algorithm two players play the game, one is called MAX and other is called MIN.
- Both the players fight it as the opponent player gets the minimum benefit while they get the maximum benefit.
- Both Players of the game are opponent of each other, where MAX will select the maximized value and MIN will select the minimized value.
- The minimax algorithm performs a depth-first search algorithm for the exploration of the complete game tree.
- The minimax algorithm proceeds all the way down to the terminal node of the tree, then backtrack the tree as the recursion.

Working of Min-Max Algorithm:

- The working of the minimax algorithm can be easily described using an example. Below we have taken an example of game-tree which is representing the two-player game.
- In this example, there are two players one is called Maximizer and other is called Minimizer.
- Maximizer will try to get the Maximum possible score, and Minimizer will try to get the minimum possible score.
- This algorithm applies DFS, so in this game-tree, we have to go all the way through the leaves to reach the terminal nodes.

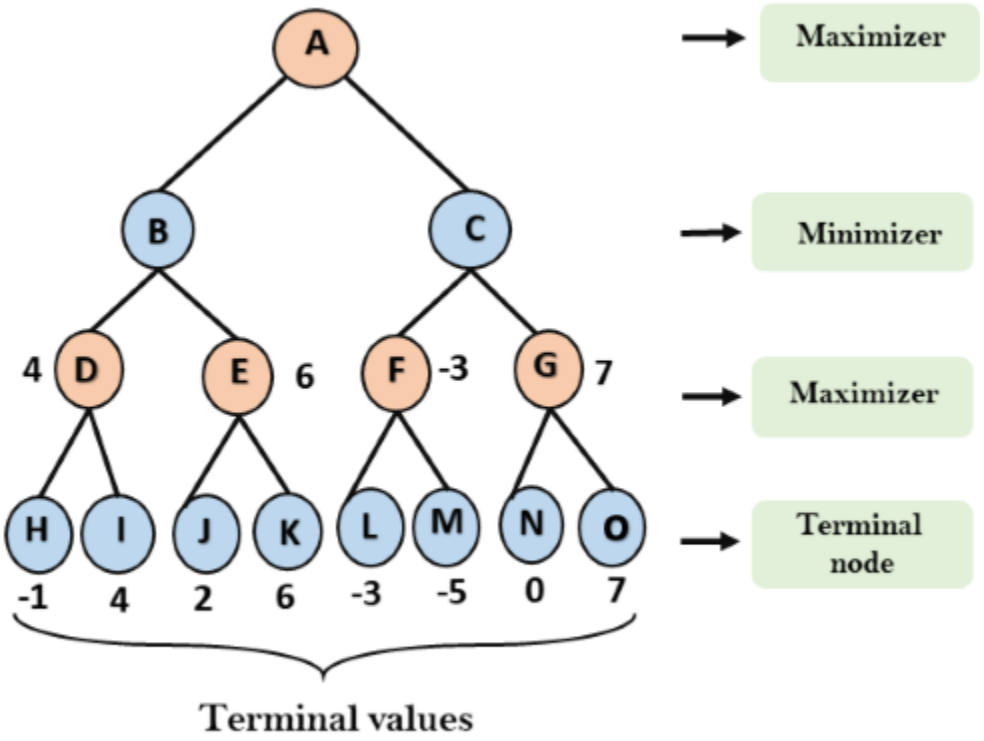
- At the terminal node, the terminal values are given so we will compare those value and backtrack the tree until the initial state occurs. Following are the main steps involved in solving the two-player game tree:

Step-1: In the first step, the algorithm generates the entire game-tree and apply the utility function to get the utility values for the terminal states. In the below tree diagram, let's take A is the initial state of the tree. Suppose maximizer takes first turn which has worst-case initial value =- infinity, and minimizer will take next turn which has worst-case initial value = +infinity.



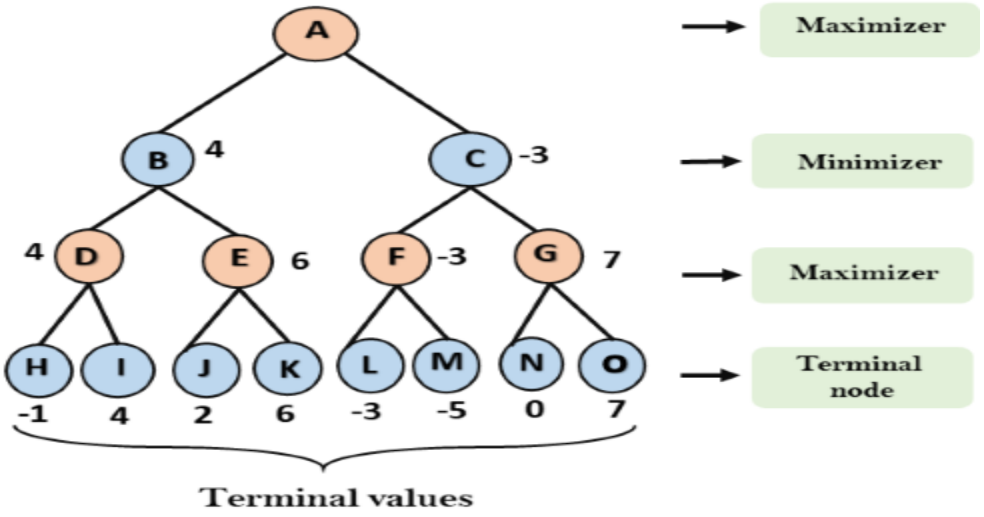
Step 2: Now, first we find the utilities value for the Maximizer, its initial value is -∞, so we will compare each value in terminal state with initial value of Maximizer and determines the higher nodes values. It will find the maximum among the all.

- For node D max(-1,- -∞) => max(-1,4)= 4
- For Node E max(2, -∞) => max(2, 6)= 6
- For Node F max(-3, -∞) => max(-3,-5) = -3
- For node G max(0, -∞) = max(0, 7) = 7



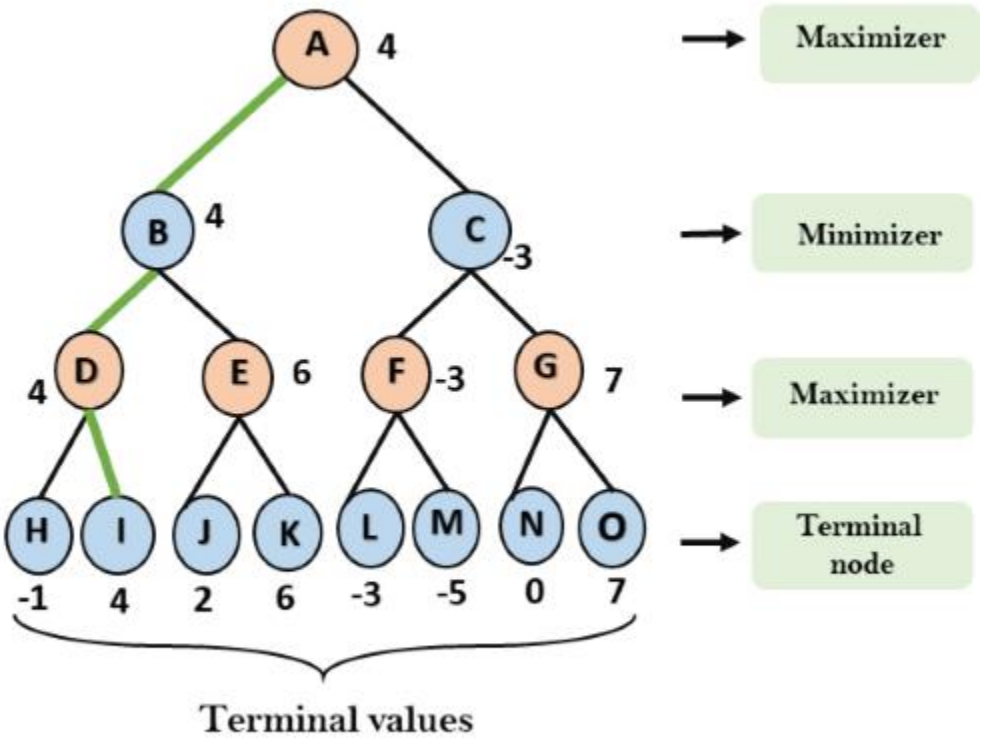
Step 3: In the next step, it's a turn for minimizer, so it will compare all nodes value with +∞, and will find the 3rd layer node values.

- For node B= min(4,6) = 4
- For node C= min (-3, 7) = -3



Step 4: Now it's a turn for Maximizer, and it will again choose the maximum of all nodes value and find the maximum value for the root node. In this game tree, there are only 4 layers, hence we reach immediately to the root node, but in real games, there will be more than 4 layers.

- For node A max(4, -3)= 4



That was the complete workflow of the minimax two player game.

Properties of Mini-Max algorithm:

- **Complete-** Min-Max algorithm is Complete. It will definitely find a solution (if exist), in the finite search tree.
- **Optimal-** Min-Max algorithm is optimal if both opponents are playing optimally.
- **Time complexity-** As it performs DFS for the game-tree, so the time complexity of Min-Max algorithm is **$O(b^m)$**, where b is branching factor of the game-tree, and m is the maximum depth of the tree.

- **Space Complexity-** Space complexity of Mini-max algorithm is also similar to DFS which is **O(bm)**.

Limitation of the minimax Algorithm:

The main drawback of the minimax algorithm is that it gets really slow for complex games such as Chess, go, etc. This type of games has a huge branching factor, and the player has lots of choices to decide. This limitation of the minimax algorithm can be improved from **alpha-beta pruning** which we have discussed in the next topic.

Alpha-Beta Pruning

- Alpha-beta pruning is a modified version of the minimax algorithm. It is an optimization technique for the minimax algorithm.
- As we have seen in the minimax search algorithm that the number of game states it has to examine are exponential in depth of the tree. Since we cannot eliminate the exponent, but we can cut it to half. Hence there is a technique by which without checking each node of the game tree we can compute the correct minimax decision, and this technique is called **pruning**. This involves two threshold parameter Alpha and beta for future expansion, so it is called **alpha-beta pruning**. It is also called as **Alpha-Beta Algorithm**.
- Alpha-beta pruning can be applied at any depth of a tree, and sometimes it not only prune the tree leaves but also entire sub-tree.
- The two-parameter can be defined as:
    a. **Alpha:** The best (highest-value) choice we have found so far at any point along the path of Maximizer. The initial value of alpha is **-∞**.
    b. **Beta:** The best (lowest-value) choice we have found so far at any point along the path of Minimizer. The initial value of beta is **+∞**.
- The Alpha-beta pruning to a standard minimax algorithm returns the same move as the standard algorithm does, but it removes all the nodes which are not really affecting the final decision but making algorithm slow. Hence by pruning these nodes, it makes the algorithm fast.

Condition for Alpha-beta pruning:

The main condition which required for alpha-beta pruning is:

1. α>=β

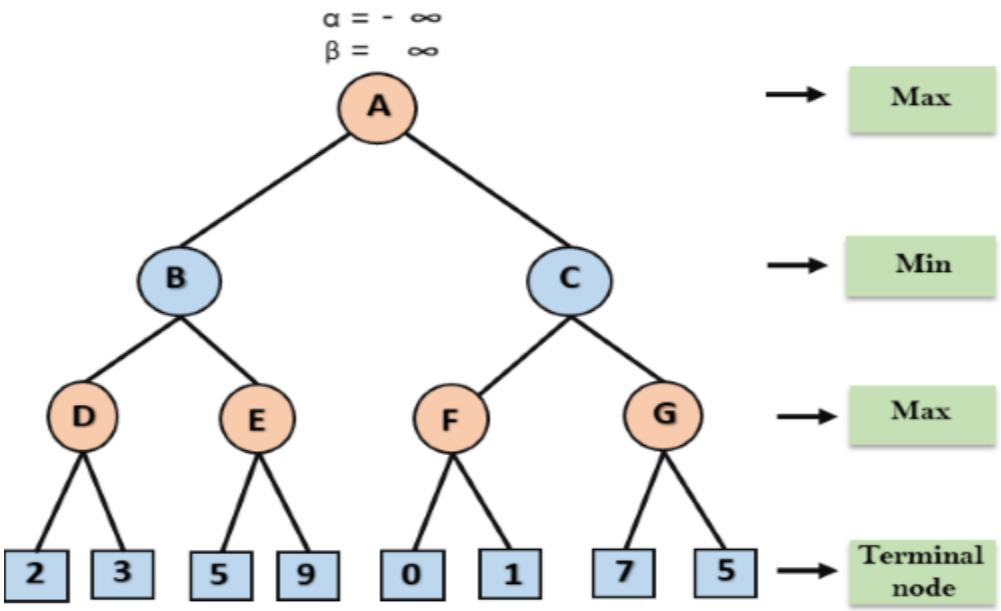
Key points about alpha-beta pruning:

- The Max player will only update the value of alpha.
- The Min player will only update the value of beta.
- While backtracking the tree, the node values will be passed to upper nodes instead of values of alpha and beta.
- We will only pass the alpha, beta values to the child nodes.

Working of Alpha-Beta Pruning:

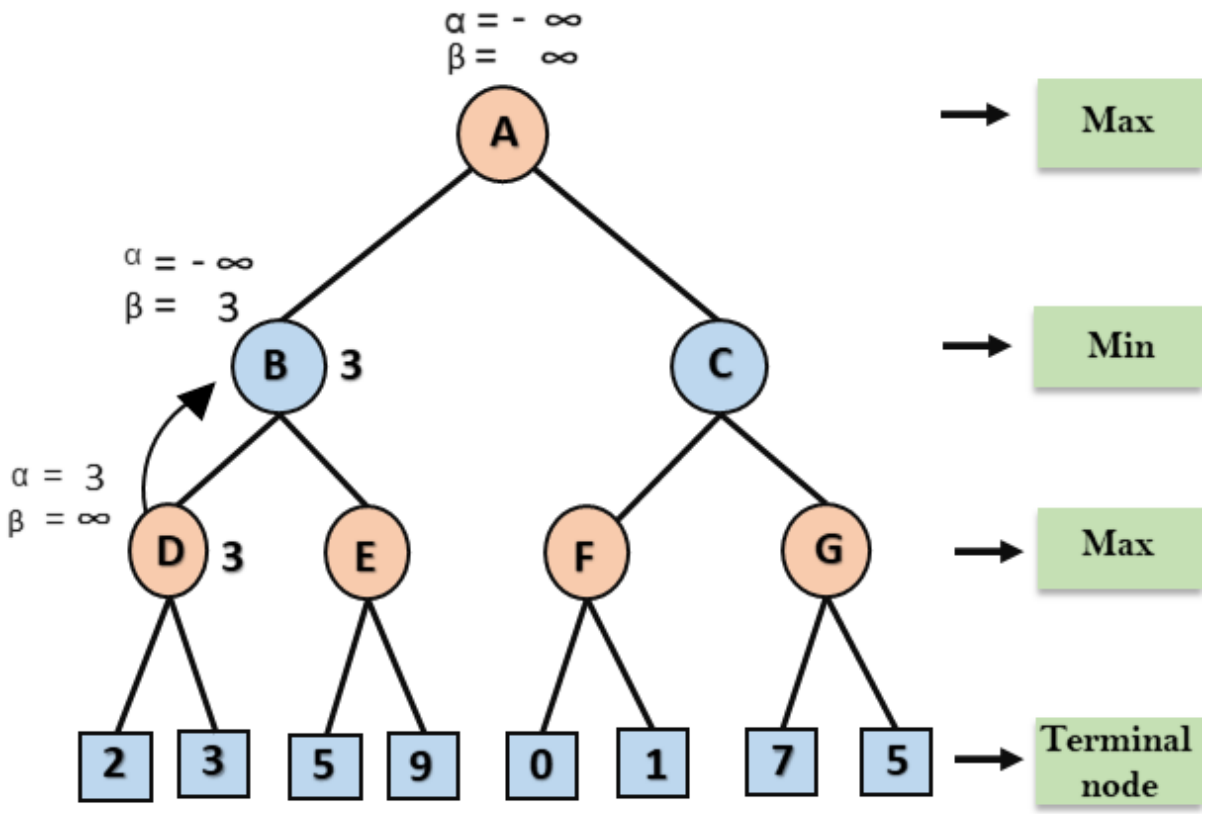
Let's take an example of two-player search tree to understand the working of Alpha-beta pruning

Step 1: At the first step the, Max player will start first move from node A where α= -∞ and β= +∞, these value of alpha and beta passed down to node B where again α= -∞ and β= +∞, and Node B passes the same value to its child D.



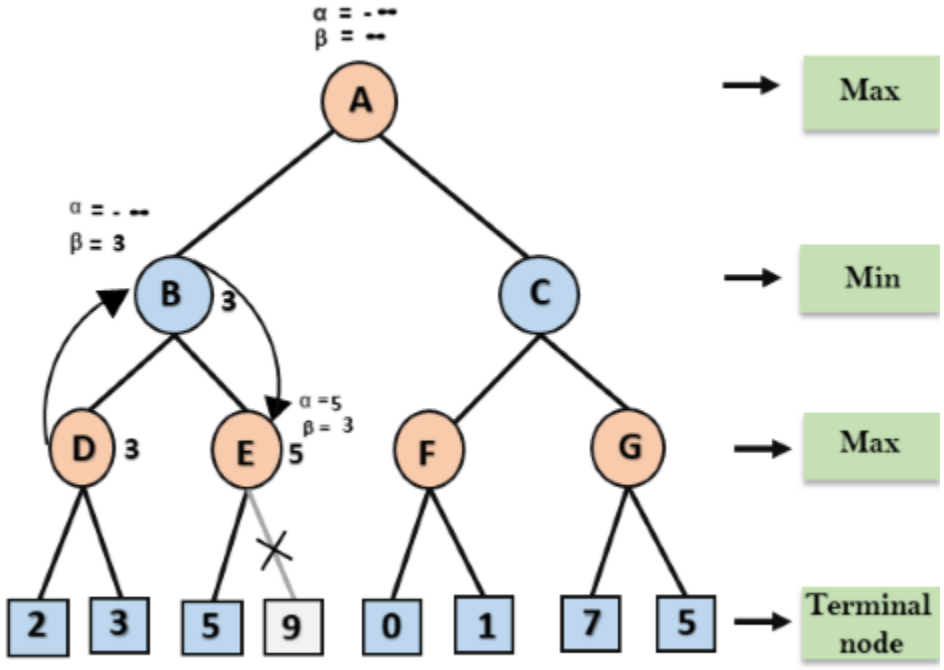
Step 2: At Node D, the value of α will be calculated as its turn for Max. The value of α is compared with firstly 2 and then 3, and the max (2, 3) = 3 will be the value of α at node D and node value will also 3.

Step 3: Now algorithm backtrack to node B, where the value of β will change as this is a turn of Min, Now β= +∞, will compare with the available subsequent nodes value, i.e. min (∞, 3) = 3, hence at node B now α= -∞, and β= 3.



In the next step, algorithm traverse the next successor of Node B which is node E, and the values of α= -∞, and β= 3 will also be passed.

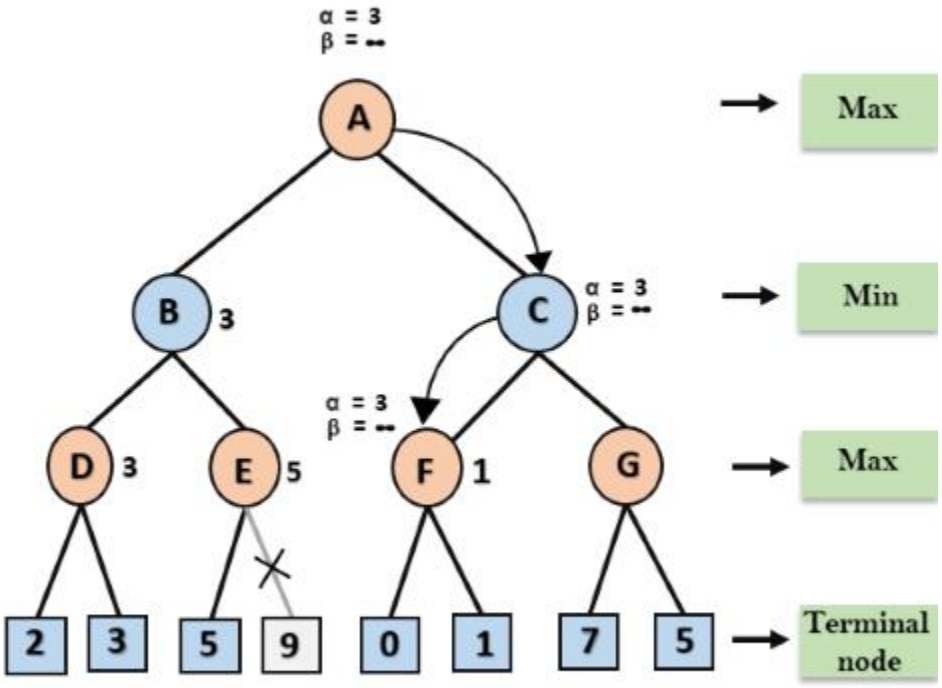
Step 4: At node E, Max will take its turn, and the value of alpha will change. The current value of alpha will be compared with 5, so max (-∞, 5) = 5, hence at node E α= 5 and β= 3, where α>=β, so the right successor of E will be pruned, and algorithm will not traverse it, and the value at node E will be 5.



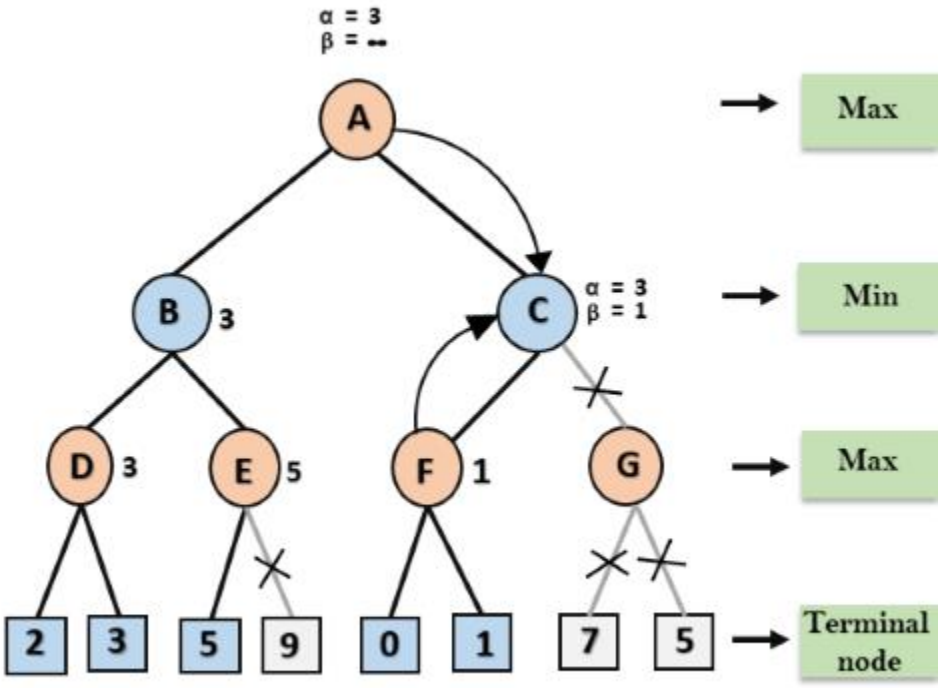
Step 5: At next step, algorithm again backtrack the tree, from node B to node A. At node A, the value of alpha will be changed the maximum available value is 3 as max (-∞, 3)= 3, and β= +∞, these two values now passes to right successor of A which is Node C.

At node C, α=3 and β= +∞, and the same values will be passed on to node F.

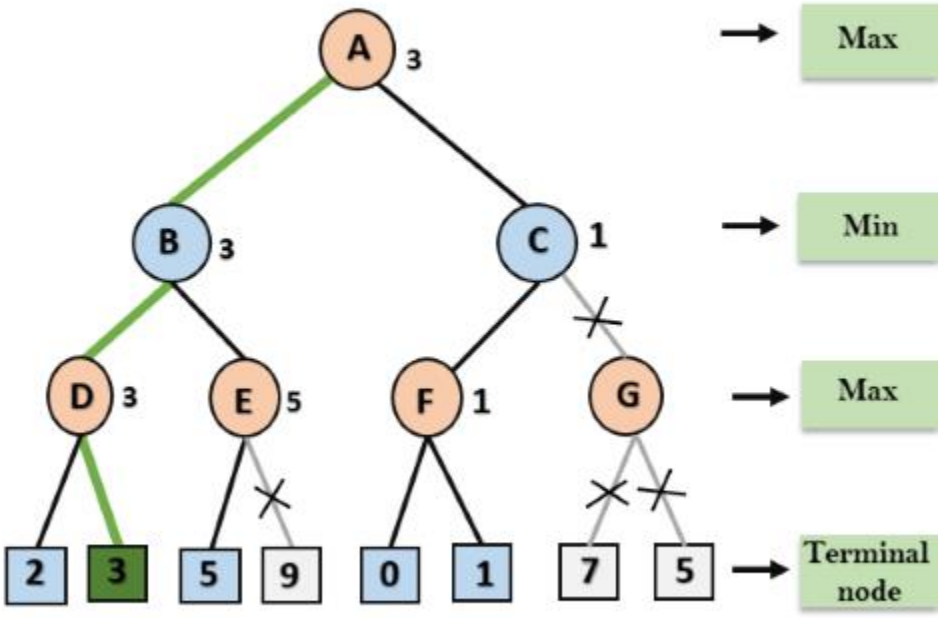
Step 6: At node F, again the value of α will be compared with left child which is 0, and max(3,0)= 3, and then compared with right child which is 1, and max(3,1)= 3 still α remains 3, but the node value of F will become 1.



Step 7: Node F returns the node value 1 to node C, at C α= 3 and β= +∞, here the value of beta will be changed, it will compare with 1 so min (∞, 1) = 1. Now at C, α=3 and β= 1, and again it satisfies the condition α>=β, so the next child of C which is G will be pruned, and the algorithm will not compute the entire sub-tree G.



Step 8: C now returns the value of 1 to A here the best value for A is max (3, 1) = 3. Following is the final game tree which is the showing the nodes which are computed and nodes which has never computed. Hence the optimal value for the maximizer is 3 for this example.



Move Ordering in Alpha-Beta pruning:

The effectiveness of alpha-beta pruning is highly dependent on the order in which each node is examined. Move order is an important aspect of alpha-beta pruning.

It can be of two types:

- **Worst ordering:** In some cases, alpha-beta pruning algorithm does not prune any of the leaves of the tree, and works exactly as minimax algorithm. In this case, it also consumes more time because of alpha-beta factors, such a move of pruning is called worst ordering. In this case, the best move occurs on the right side of the tree. The time complexity for such an order is $O(b^m)$.
- **Ideal ordering:** The ideal ordering for alpha-beta pruning occurs when lots of pruning happens in the tree, and best moves occur at the left side of the tree. We apply DFS hence it first search left of the tree and go deep twice as minimax algorithm in the same amount of time. Complexity in ideal ordering is $O(b^{m/2})$.

Rules to find good ordering:

Following are some rules to find good ordering in alpha-beta pruning:

- Occur the best move from the shallowest node.
- Order the nodes in the tree such that the best nodes are checked first.
- Use domain knowledge while finding the best move. Ex: for Chess, try order: captures first, then threats, then forward moves, backward moves.
- We can bookkeep the states, as there is a possibility that states may repeat.

UNIT II PROBABILISTIC REASONING

Probabilistic reasoning in Artificial intelligence

Uncertainty:

Till now, we have learned knowledge representation using first-order logic and propositional logic with certainty, which means we were sure about the predicates. With this knowledge representation, we might write A→B, which means if A is true then B is true, but consider a situation where we are not sure about whether A is true or not then we cannot express this statement, this situation is called uncertainty.

So to represent uncertain knowledge, where we are not sure about the predicates, we need uncertain reasoning or probabilistic reasoning.

Causes of uncertainty:

Following are some leading causes of uncertainty to occur in the real world.

1. Information occurred from unreliable sources.
2. Experimental Errors
3. Equipment fault
4. Temperature variation
5. Climate change.

Probabilistic reasoning:

Probabilistic reasoning is a way of knowledge representation where we apply the concept of probability to indicate the uncertainty in knowledge. In probabilistic reasoning, we combine probability theory with logic to handle the uncertainty.

We use probability in probabilistic reasoning because it provides a way to handle the uncertainty that is the result of someone's laziness and ignorance.

In the real world, there are lots of scenarios, where the certainty of something is not confirmed, such as "It will rain today," "behavior of someone for some situations," "A match between two teams or two players." These are probable sentences for which we can assume that it will happen but not sure about it, so here we use probabilistic reasoning.

Need of probabilistic reasoning in AI:

- When there are unpredictable outcomes.
- When specifications or possibilities of predicates becomes too large to handle.
- When an unknown error occurs during an experiment.

In probabilistic reasoning, there are two ways to solve problems with uncertain knowledge:

- **Bayes' rule**
- **Bayesian Statistics**

As probabilistic reasoning uses probability and related terms, so before understanding probabilistic reasoning, let's understand some common terms:

Probability: Probability can be defined as a chance that an uncertain event will occur. It is the numerical measure of the likelihood that an event will occur. The value of probability always remains between 0 and 1 that represent ideal uncertainties.

1. $0 \leq P(A) \leq 1$, where P(A) is the probability of an event A.
1. $P(A) = 0$, indicates total uncertainty in an event A.
1. $P(A) = 1$, indicates total certainty in an event A.

We can find the probability of an uncertain event by using the below formula.

$$\textbf{Probability of occurrence} = \frac{\text{Number of desired outcomes}}{\text{Total number of outcomes}}$$

- P(¬A) = probability of a not happening event.
- P(¬A) + P(A) = 1.

Event: Each possible outcome of a variable is called an event.

Sample space: The collection of all possible events is called sample space.

Random variables: Random variables are used to represent the events and objects in the real world.

Prior probability: The prior probability of an event is probability computed before observing new information.

Posterior Probability: The probability that is calculated after all evidence or information has taken into account. It is a combination of prior probability and new information.

Conditional probability:

Conditional probability is a probability of occurring an event when another event has already happened.

Let's suppose, we want to calculate the event A when event B has already occurred, "the probability of A under the conditions of B", it can be written as:

$$P(A|B) = \frac{P(A \wedge B)}{P(B)}$$

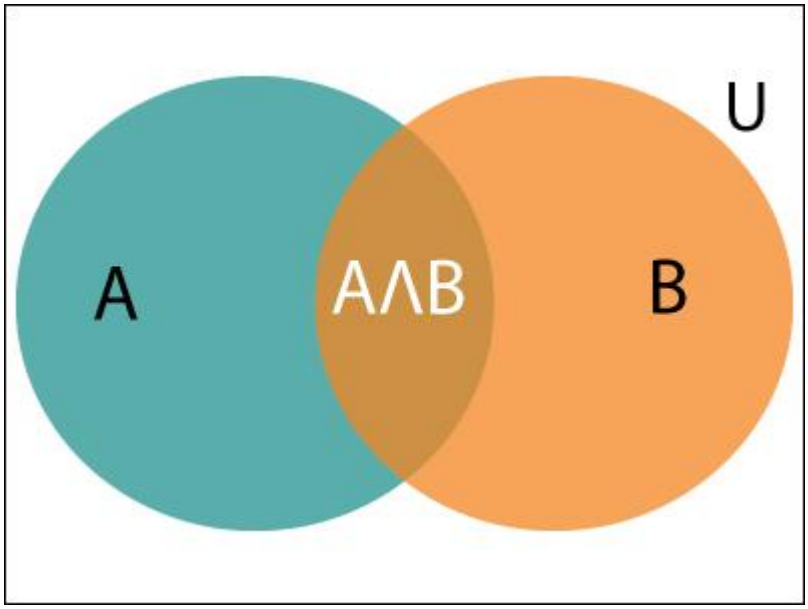
Where $P(A \wedge B)$= Joint probability of a and B

P(B)= Marginal probability of B.

If the probability of A is given and we need to find the probability of B, then it will be given as:

$$P(B|A) = \frac{P(A \wedge B)}{P(A)}$$

It can be explained by using the below Venn diagram, where B is occurred event, so sample space will be reduced to set B, and now we can only calculate event A when event B is already occurred by dividing the probability of **$P(A \wedge B)$ by P(B)**.



Example:

In a class, there are 70% of the students who like English and 40% of the students who likes English and mathematics, and then what is the percent of students those who like English also like mathematics?

Solution:

Let, A is an event that a student likes Mathematics

B is an event that a student likes English.

$$P(A|B) = \frac{P(A \wedge B)}{P(B)} = \frac{0.4}{0.7} = 57\%$$

Hence, 57% are the students who like English also like Mathematics.

Bayes' theorem in Artificial intelligence

Bayes' theorem:

Bayes' theorem is also known as **Bayes' rule, Bayes' law**, or **Bayesian reasoning**, which determines the probability of an event with uncertain knowledge.

In probability theory, it relates the conditional probability and marginal probabilities of two random events.

Bayes' theorem was named after the British mathematician **Thomas Bayes**. The **Bayesian inference** is an application of Bayes' theorem, which is fundamental to Bayesian statistics.

It is a way to calculate the value of P(B|A) with the knowledge of P(A|B).

Bayes' theorem allows updating the probability prediction of an event by observing new information of the real world.

Example: If cancer corresponds to one's age then by using Bayes' theorem, we can determine the probability of cancer more accurately with the help of age.

Bayes' theorem can be derived using product rule and conditional probability of event A with known event B:

As from product rule we can write:

1. P(A ∧ B)= P(A|B) P(B) or

Similarly, the probability of event B with known event A:

1. P(A ∧ B)= P(B|A) P(A)

Equating right hand side of both the equations, we will get:

$$P(A|B) = \frac{P(B|A)\,P(A)}{P(B)} \quad \text{....(a)}$$

The above equation (a) is called as **Bayes' rule** or **Bayes' theorem**. This equation is basic of most modern AI systems for **probabilistic inference**.

It shows the simple relationship between joint and conditional probabilities. Here,

P(A|B) is known as **posterior**, which we need to calculate, and it will be read as Probability of hypothesis A when we have occurred an evidence B.

P(B|A) is called the likelihood, in which we consider that hypothesis is true, then we calculate the probability of evidence.

P(A) is called the **prior probability**, probability of hypothesis before considering the evidence

P(B) is called **marginal probability**, pure probability of an evidence.

In the equation (a), in general, we can write P (B) = P(A)*P(B|Ai), hence the Bayes' rule can be written as:

$$P(A_i|B) = \frac{P(A_i)*P(B|A_i)}{\sum_{i=1}^{k} P(A_i)*P(B|A_i)}$$

Where A_1, A_2, A_3,....., A_n is a set of mutually exclusive and exhaustive events.

Applying Bayes' rule:

Bayes' rule allows us to compute the single term P(B|A) in terms of P(A|B), P(*B*), and P(A). This is very useful in cases where we have a good probability of these three terms and want to determine the fourth one. Suppose we want to perceive the effect of some unknown cause, and want to compute that cause, then the Bayes' rule becomes:

$$\mathbf{P(cause|effect)} = \frac{P(effect|cause)\,P(cause)}{P(effect)}$$

Example-1:

Question: what is the probability that a patient has diseases meningitis with a stiff neck?

Given Data:

A doctor is aware that disease meningitis causes a patient to have a stiff neck, and it occurs 80% of the time. He is also aware of some more facts, which are given as follows:

- The Known probability that a patient has meningitis disease is 1/30,000.
- The Known probability that a patient has a stiff neck is 2%.

Let a be the proposition that patient has stiff neck and b be the proposition that patient has meningitis. , so we can calculate the following as:

P(a|b) = 0.8

P(b) = 1/30000

P(a)= .02

$$P(b|a) = \frac{P(a|b)P(b)}{P(a)} = \frac{0.8*(\frac{1}{30000})}{0.02} = 0.001333333.$$

Hence, we can assume that 1 patient out of 750 patients has meningitis disease with a stiff neck.

Example-2:

Question: From a standard deck of playing cards, a single card is drawn. The probability that the card is king is 4/52, then calculate posterior probability P(King|Face), which means the drawn face card is a king card.

Solution:

$$P(king|face) = \frac{P(Face|king)*P(King)}{P(Face)} \quad .....(i)$$

P(king): probability that the card is King= 4/52= 1/13

P(face): probability that a card is a face card= 3/13

P(Face|King): probability of face card when we assume it is a king = 1

Putting all values in equation (i) we will get:

$$P(king|face) = \frac{1*(\frac{1}{13})}{(\frac{3}{13})} = 1/3,$$ **it is a probability that a face card is a king card.**

Application of Bayes' theorem in Artificial intelligence:

Following are some applications of Bayes' theorem:

- It is used to calculate the next step of the robot when the already executed step is given.
- Bayes' theorem is helpful in weather forecasting.
- It can solve the Monty Hall problem.

Bayesian Belief Network in artificial intelligence

Bayesian belief network is key computer technology for dealing with probabilistic events and to solve a problem which has uncertainty. We can define a Bayesian network as:

"A Bayesian network is a probabilistic graphical model which represents a set of variables and their conditional dependencies using a directed acyclic graph."

It is also called a **Bayes network, belief network, decision network**, or **Bayesian model**.

Bayesian networks are probabilistic, because these networks are built from a **probability distribution**, and also use probability theory for prediction and anomaly detection.

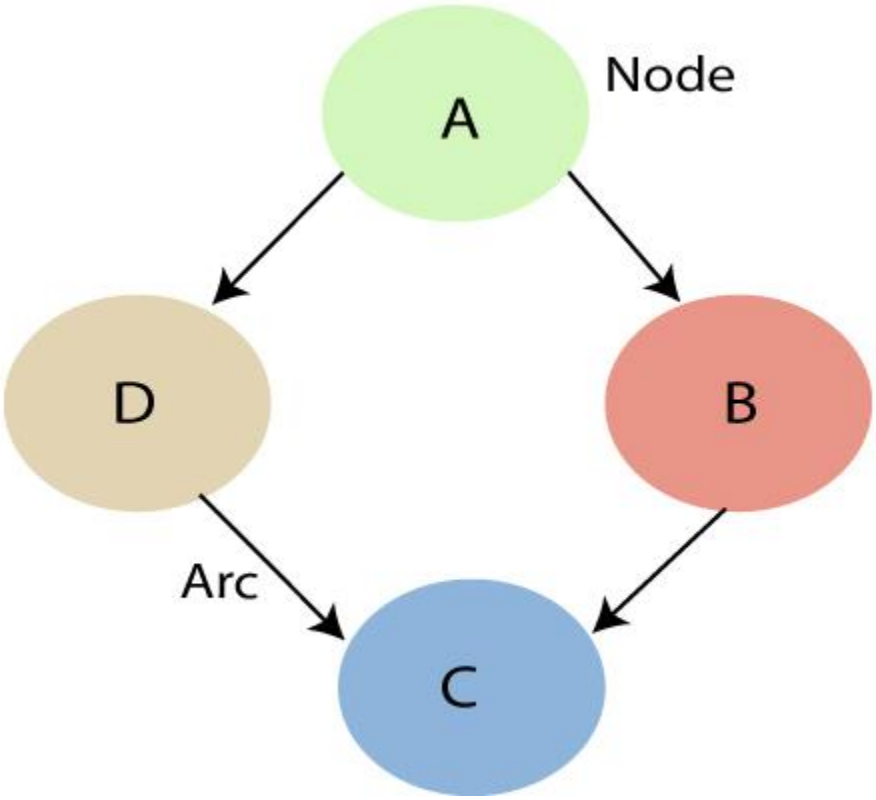
Real world applications are probabilistic in nature, and to represent the relationship between multiple events, we need a Bayesian network. It can also be used in various tasks including **prediction, anomaly detection, diagnostics, automated insight, reasoning, time series prediction**, and **decision making under uncertainty**.

Bayesian Network can be used for building models from data and experts opinions, and it consists of two parts:

- **Directed Acyclic Graph**
- **Table of conditional probabilities.**

The generalized form of Bayesian network that represents and solve decision problems under uncertain knowledge is known as an **Influence diagram**.

A Bayesian network graph is made up of nodes and Arcs (directed links), where:



- Each **node** corresponds to the random variables, and a variable can be **continuous** or **discrete**.
- **Arc or directed arrows** represent the causal relationship or conditional probabilities between random variables. These directed links or arrows connect the pair of nodes in the graph.
  These links represent that one node directly influence the other node, and if there is no directed link that means that nodes are independent with each other
  - **In the above diagram, A, B, C, and D are random variables represented by the nodes of the network graph.**
  - **If we are considering node B, which is connected with node A by a directed arrow, then node A is called the parent of Node B.**
  - **Node C is independent of node A.**

The Bayesian network has mainly two components:

- **Causal Component**
- **Actual numbers**

Each node in the Bayesian network has condition probability distribution **$P(X_i \mid Parent(X_i))$**, which determines the effect of the parent on that node.

Bayesian network is based on Joint probability distribution and conditional probability. So let's first understand the joint probability distribution:

Joint probability distribution:

If we have variables x1, x2, x3,....., xn, then the probabilities of a different combination of x1, x2, x3.. xn, are known as Joint probability distribution.

$P[x_1, x_2, x_3,...., x_n]$, it can be written as the following way in terms of the joint probability distribution.

$= P[x_1| x_2, x_3,...., x_n]P[x_2, x_3,...., x_n]$

$= P[x_1| x_2, x_3,...., x_n]P[x_2|x_3,...., x_n]....P[x_{n-1}|x_n]P[x_n].$

In general for each variable Xi, we can write the equation as:

$$P(X_i|X_{i-1},.....,X_1) = P(X_i|Parents(X_i))$$

Explanation of Bayesian network:

Let's understand the Bayesian network through an example by creating a directed acyclic graph:

Example: Harry installed a new burglar alarm at his home to detect burglary. The alarm reliably responds at detecting a burglary but also responds for minor earthquakes. Harry has two neighbors David and Sophia, who have taken a responsibility to inform Harry at work when they hear the alarm. David always calls Harry when he hears the alarm, but sometimes he got confused with the phone ringing and calls at that time too. On the other hand, Sophia likes to listen to high music, so sometimes she misses to hear the alarm. Here we would like to compute the probability of Burglary Alarm.

Problem:

Calculate the probability that alarm has sounded, but there is neither a burglary, nor an earthquake occurred, and David and Sophia both called the Harry.

Solution:

- The Bayesian network for the above problem is given below. The network structure is showing that burglary and earthquake is the parent node of the alarm and directly affecting the probability of alarm's going off, but David and Sophia's calls depend on alarm probability.

- The network is representing that our assumptions do not directly perceive the burglary and also do not notice the minor earthquake, and they also not confer before calling.
- The conditional distributions for each node are given as conditional probabilities table or CPT.
- Each row in the CPT must be sum to 1 because all the entries in the table represent an exhaustive set of cases for the variable.
- In CPT, a boolean variable with k boolean parents contains 2^K probabilities. Hence, if there are two parents, then CPT will contain 4 probability values

List of all events occurring in this network:

- **Burglary (B)**
- **Earthquake(E)**
- **Alarm(A)**
- **David Calls(D)**
- **Sophia calls(S)**

We can write the events of problem statement in the form of probability: **P[D, S, A, B, E]**, can rewrite the above probability statement using joint probability distribution:

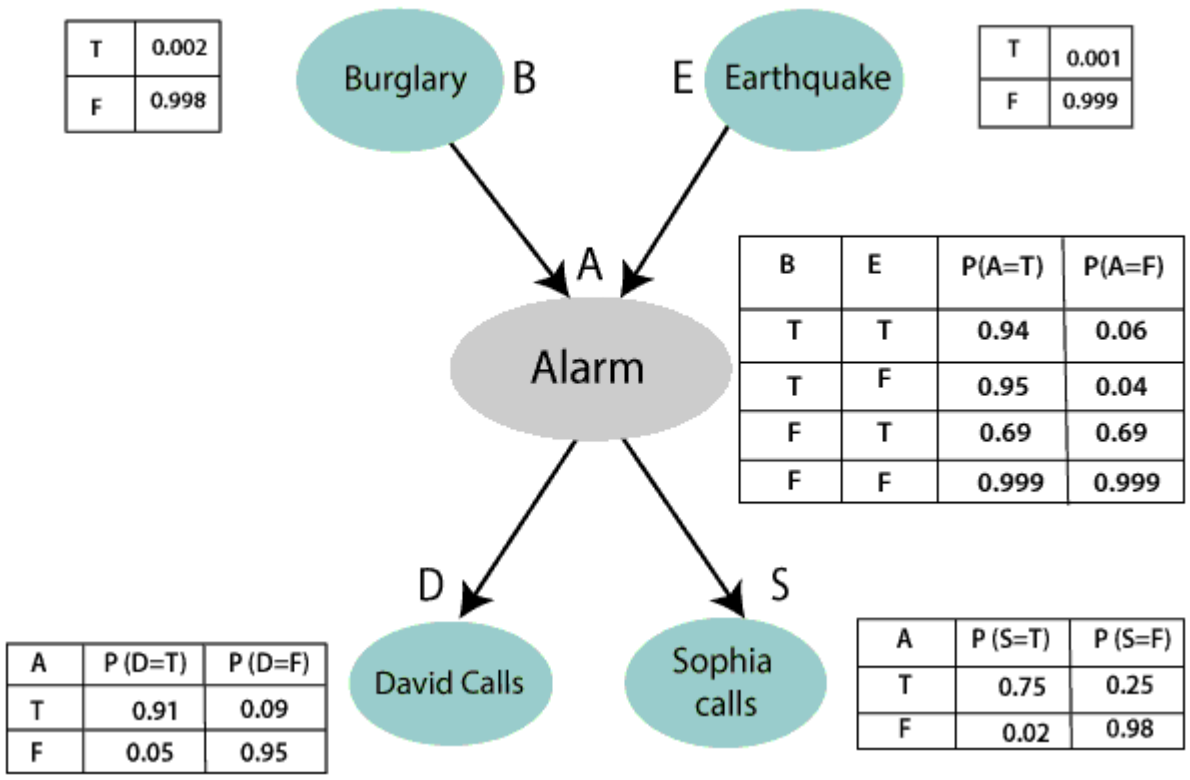
P[D, S, A, B, E]= P[D | S, A, B, E]. P[S, A, B, E]

=P[D | S, A, B, E]. P[S | A, B, E]. P[A, B, E]

= P [D| A]. P [S| A, B, E]. P[A, B, E]

= P[D | A]. P[S | A]. P[A| B, E]. P[B, E]

= P[D | A]. P[S | A]. P[A| B, E]. P[B |E]. P[E]



Let's take the observed probability for the Burglary and earthquake component:

P(B= True) = 0.002, which is the probability of burglary.

P(B= False)= 0.998, which is the probability of no burglary.

P(E= True)= 0.001, which is the probability of a minor earthquake

P(E= False)= 0.999, Which is the probability that an earthquake not occurred.

We can provide the conditional probabilities as per the below tables:

Conditional probability table for Alarm A:

The Conditional probability of Alarm A depends on Burglar and earthquake:

B	E	P(A= True)	P(A= False)
True	True	0.94	0.06
True	False	0.95	0.04
False	True	0.31	0.69

False	False	0.001	0.999

Conditional probability table for David Calls:

The Conditional probability of David that he will call depends on the probability of Alarm.

A	P(D= True)	P(D= False)
True	0.91	0.09
False	0.05	0.95

Conditional probability table for Sophia Calls:

The Conditional probability of Sophia that she calls is depending on its Parent Node "Alarm."

A	P(S= True)	P(S= False)
True	0.75	0.25
False	0.02	0.98

From the formula of joint distribution, we can write the problem statement in the form of probability distribution:

P(S, D, A, ¬B, ¬E) = P (S|A) *P (D|A)*P (A|¬B ^ ¬E) *P (¬B) *P (¬E).

= 0.75* 0.91* 0.001* 0.998*0.999

= 0.00068045.

Hence, a Bayesian network can answer any query about the domain by using Joint distribution.

The semantics of Bayesian Network:

There are two ways to understand the semantics of the Bayesian network, which is given below:

1. To understand the network as the representation of the Joint probability distribution.

It is helpful to understand how to construct the network.

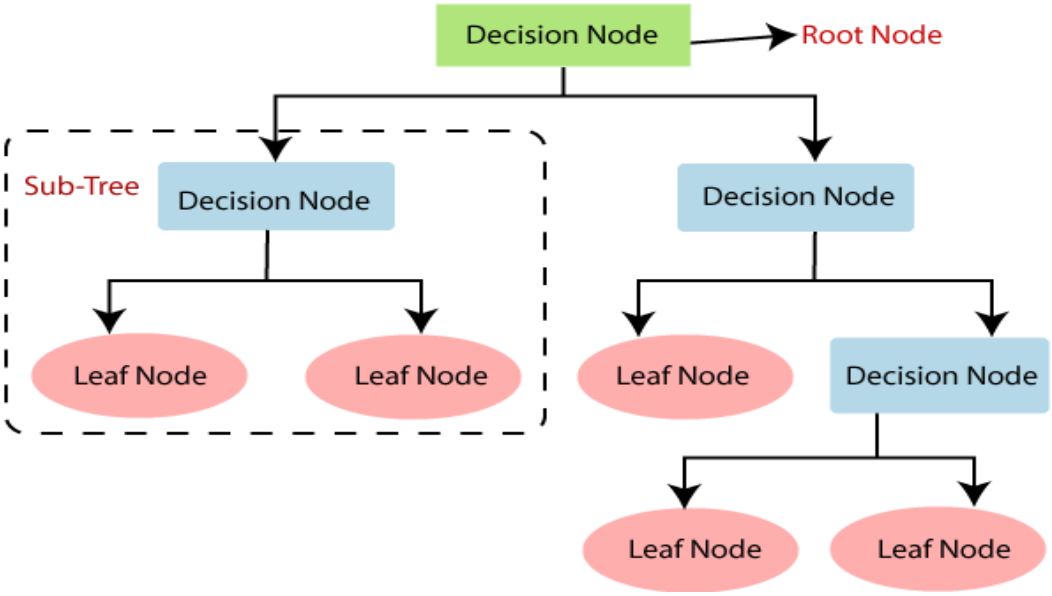
2. To understand the network as an encoding of a collection of conditional independence statements.

It is helpful in designing inference procedure.

UNIT III SUPERVISED LEARNING

Decision Tree Algorithm

- Decision Tree is a **Supervised learning technique** that can be used for both classification and Regression problems, but mostly it is preferred for solving Classification problems. It is a tree-structured classifier, where **internal nodes represent the features of a dataset, branches represent the decision rules** and **each leaf node represents the outcome.**
- In a Decision tree, there are two nodes, which are the **Decision Node** and **Leaf Node.** Decision nodes are used to make any decision and have multiple branches, whereas Leaf nodes are the output of those decisions and do not contain any further branches.
- The decisions or the test are performed on the basis of features of the given dataset.
- ***It is a graphical representation for getting all the possible solutions to a problem/decision based on given conditions.***
- It is called a decision tree because, similar to a tree, it starts with the root node, which expands on further branches and constructs a tree-like structure.
- In order to build a tree, we use the **CART algorithm,** which stands for **Classification and Regression Tree algorithm.**
- A decision tree simply asks a question, and based on the answer (Yes/No), it further split the tree into subtrees.
- Below diagram explains the general structure of a decision tree:



Why use Decision Trees?

There are various algorithms in Machine learning, so choosing the best algorithm for the given dataset and problem is the main point to remember while creating a machine learning model. Below are the two reasons for using the Decision tree:

- Decision Trees usually mimic human thinking ability while making a decision, so it is easy to understand.
- The logic behind the decision tree can be easily understood because it shows a tree-like structure.

Decision Tree Terminologies

- **Root Node:** Root node is from where the decision tree starts. It represents the entire dataset, which further gets divided into two or more homogeneous sets.
- **Leaf Node:** Leaf nodes are the final output node, and the tree cannot be segregated further after getting a leaf node.
- **Splitting:** Splitting is the process of dividing the decision node/root node into sub-nodes according to the given conditions.
- **Branch/Sub Tree:** A tree formed by splitting the tree.
- **Pruning:** Pruning is the process of removing the unwanted branches from the tree.
- **Parent/Child node:** The root node of the tree is called the parent node, and other nodes are called the child nodes.

How does the Decision Tree algorithm Work?

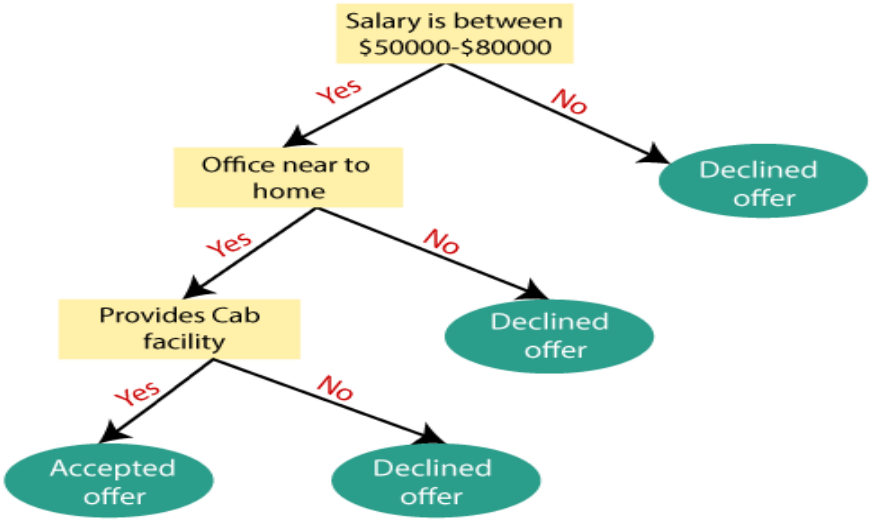
In a decision tree, for predicting the class of the given dataset, the algorithm starts from the root node of the tree. This algorithm compares the values of root attribute

with the record (real dataset) attribute and, based on the comparison, follows the branch and jumps to the next node.

For the next node, the algorithm again compares the attribute value with the other sub-nodes and move further. It continues the process until it reaches the leaf node of the tree. The complete process can be better understood using the below algorithm:

- **Step-1:** Begin the tree with the root node, says S, which contains the complete dataset.
- **Step-2:** Find the best attribute in the dataset using **Attribute Selection Measure (ASM).**
- **Step-3:** Divide the S into subsets that contains possible values for the best attributes.
- **Step-4:** Generate the decision tree node, which contains the best attribute.
- **Step-5:** Recursively make new decision trees using the subsets of the dataset created in step -3. Continue this process until a stage is reached where you cannot further classify the nodes and called the final node as a leaf node.

Example: Suppose there is a candidate who has a job offer and wants to decide whether he should accept the offer or Not. So, to solve this problem, the decision tree starts with the root node (Salary attribute by ASM). The root node splits further into the next decision node (distance from the office) and one leaf node based on the corresponding labels. The next decision node further gets split into one decision node (Cab facility) and one leaf node. Finally, the decision node splits into two leaf nodes (Accepted offers and Declined offer). Consider the below diagram:



Attribute Selection Measures

While implementing a Decision tree, the main issue arises that how to select the best attribute for the root node and for sub-nodes. So, to solve such problems there is a technique which is called as **Attribute selection measure or ASM.** By this measurement, we can easily select the best attribute for the nodes of the tree. There are two popular techniques for ASM, which are:

- **Information Gain**
- **Gini Index**

1. Information Gain:

- Information gain is the measurement of changes in entropy after the segmentation of a dataset based on an attribute.
- It calculates how much information a feature provides us about a class.
- According to the value of information gain, we split the node and build the decision tree.
- A decision tree algorithm always tries to maximize the value of information gain, and a node/attribute having the highest information gain is split first. It can be calculated using the below formula:

1. Information Gain= Entropy(S)- [(Weighted Avg) *Entropy(each feature)

Entropy: Entropy is a metric to measure the impurity in a given attribute. It specifies randomness in data. Entropy can be calculated as:

```
Entropy(s)= -P(yes)log2 P(yes)- P(no) log2 P(no)
```

Where,

- **S= Total number of samples**
- **P(yes)= probability of yes**
- **P(no)= probability of no**

2. Gini Index:

- Gini index is a measure of impurity or purity used while creating a decision tree in the CART(Classification and Regression Tree) algorithm.
- An attribute with the low Gini index should be preferred as compared to the high Gini index.

- It only creates binary splits, and the CART algorithm uses the Gini index to create binary splits.
- Gini index can be calculated using the below formula:

$$\text{Gini Index} = 1 - \sum_j P_j^2$$

Pruning: Getting an Optimal Decision tree

Pruning is a process of deleting the unnecessary nodes from a tree in order to get the optimal decision tree.

A too-large tree increases the risk of overfitting, and a small tree may not capture all the important features of the dataset. Therefore, a technique that decreases the size of the learning tree without reducing accuracy is known as Pruning. There are mainly two types of tree **pruning** technology used:

- **Cost Complexity Pruning**
- **Reduced Error Pruning.**

Advantages of the Decision Tree

- It is simple to understand as it follows the same process which a human follow while making any decision in real-life.
- It can be very useful for solving decision-related problems.
- It helps to think about all the possible outcomes for a problem.
- There is less requirement of data cleaning compared to other algorithms.

Disadvantages of the Decision Tree

- The decision tree contains lots of layers, which makes it complex.
- It may have an overfitting issue, which can be resolved using the **Random Forest algorithm.**
- For more class labels, the computational complexity of the decision tree may increase.

Python Implementation of Decision Tree

- **Data Pre-processing step**
- **Fitting a Decision-Tree algorithm to the Training set**

- **Predicting the test result**
- **Test accuracy of the result(Creation of Confusion matrix)**
- **Visualizing the test set result.**

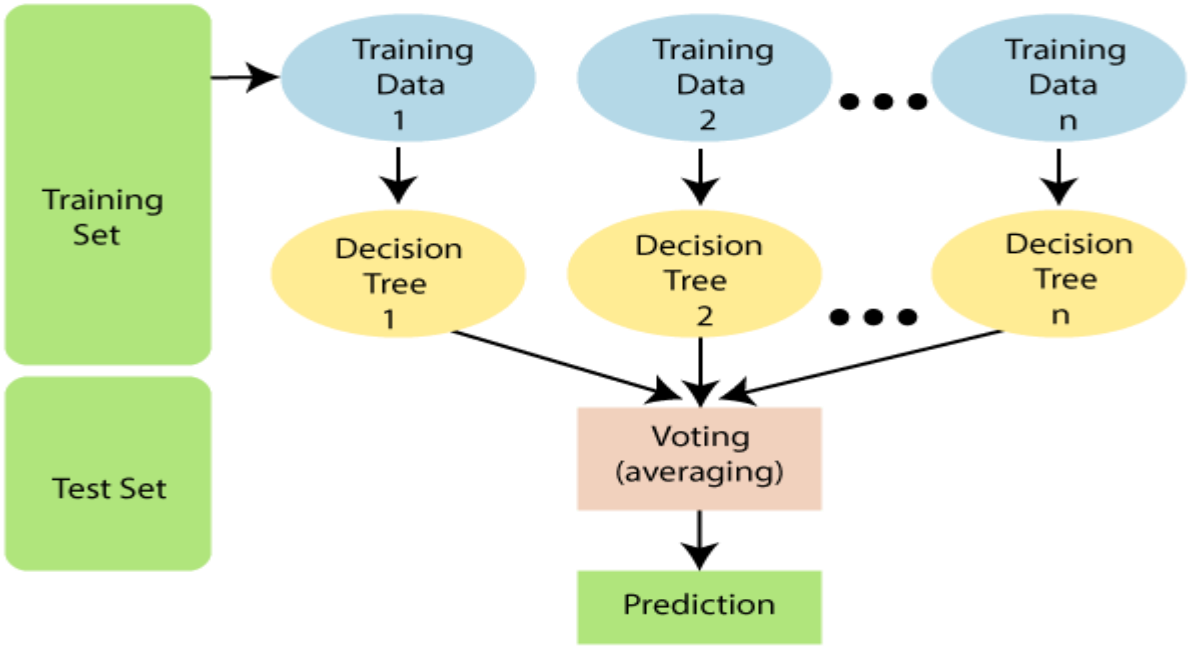
Random Forest Algorithm

Random Forest is a popular machine learning algorithm that belongs to the supervised learning technique. It can be used for both Classification and Regression problems in ML. It is based on the concept of **ensemble learning,** which is a process of *combining multiple classifiers to solve a complex problem and to improve the performance of the model.*

As the name suggests, **"*Random Forest is a classifier that contains a number of decision trees on various subsets of the given dataset and takes the average to improve the predictive accuracy of that dataset.*"** Instead of relying on one decision tree, the random forest takes the prediction from each tree and based on the majority votes of predictions, and it predicts the final output.

The greater number of trees in the forest leads to higher accuracy and prevents the problem of overfitting.

The below diagram explains the working of the Random Forest algorithm:



Assumptions for Random Forest

Since the random forest combines multiple trees to predict the class of the dataset, it is possible that some decision trees may predict the correct output, while others may not. But together, all the trees predict the correct output. Therefore, below are two assumptions for a better Random forest classifier:

- There should be some actual values in the feature variable of the dataset so that the classifier can predict accurate results rather than a guessed result.
- The predictions from each tree must have very low correlations.

Why use Random Forest?

Below are some points that explain why we should use the Random Forest algorithm:

<=”” |i=””>

- It takes less training time as compared to other algorithms.
- It predicts output with high accuracy, even for the large dataset it runs efficiently.
- It can also maintain accuracy when a large proportion of data is missing.

How does Random Forest algorithm work?

Random Forest works in two-phase first is to create the random forest by combining N decision tree, and second is to make predictions for each tree created in the first phase.

The Working process can be explained in the below steps and diagram:

Step-1: Select random K data points from the training set.

Step-2: Build the decision trees associated with the selected data points (Subsets).

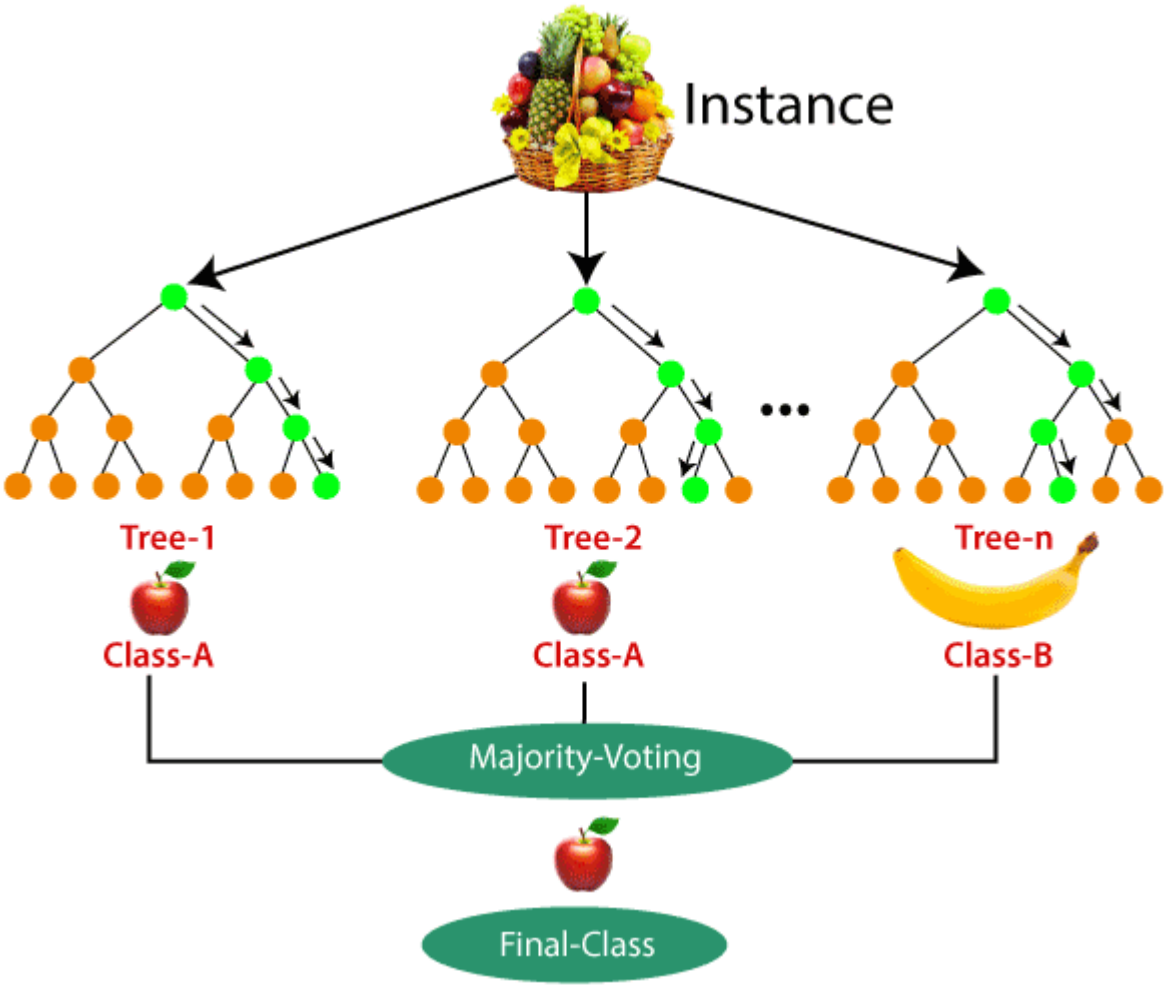
Step-3: Choose the number N for decision trees that you want to build.

Step-4: Repeat Step 1 & 2.

Step-5: For new data points, find the predictions of each decision tree, and assign the new data points to the category that wins the majority votes.

The working of the algorithm can be better understood by the below example:

Example: Suppose there is a dataset that contains multiple fruit images. So, this dataset is given to the Random forest classifier. The dataset is divided into subsets and given to each decision tree. During the training phase, each decision tree produces a prediction result, and when a new data point occurs, then based on the majority of results, the Random Forest classifier predicts the final decision. Consider the below image:



Applications of Random Forest

There are mainly four sectors where Random forest mostly used:

1. **Banking:** Banking sector mostly uses this algorithm for the identification of loan risk.
2. **Medicine:** With the help of this algorithm, disease trends and risks of the disease can be identified.
3. **Land Use:** We can identify the areas of similar land use by this algorithm.
4. **Marketing:** Marketing trends can be identified using this algorithm.

Advantages of Random Forest

- Random Forest is capable of performing both Classification and Regression tasks.
- It is capable of handling large datasets with high dimensionality.
- It enhances the accuracy of the model and prevents the overfitting issue.

Disadvantages of Random Forest

- Although random forest can be used for both classification and regression tasks, it is not more suitable for Regression tasks.

Python Implementation of Random Forest Algorithm

Implementation Steps are given below:

- Data Pre-processing step
- Fitting the Random forest algorithm to the Training set
- Predicting the test result
- Test accuracy of the result (Creation of Confusion matrix)
- Visualizing the test set result.

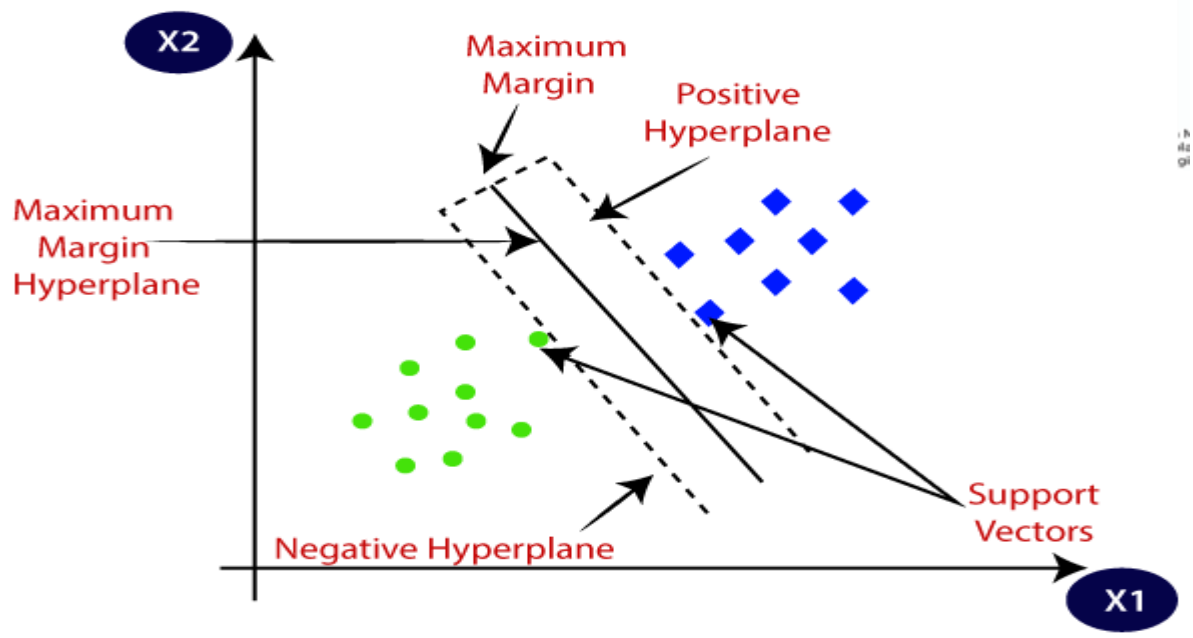
Support Vector Machine Algorithm

Support Vector Machine or SVM is one of the most popular Supervised Learning algorithms, which is used for Classification as well as Regression problems. However, primarily, it is used for Classification problems in Machine Learning.

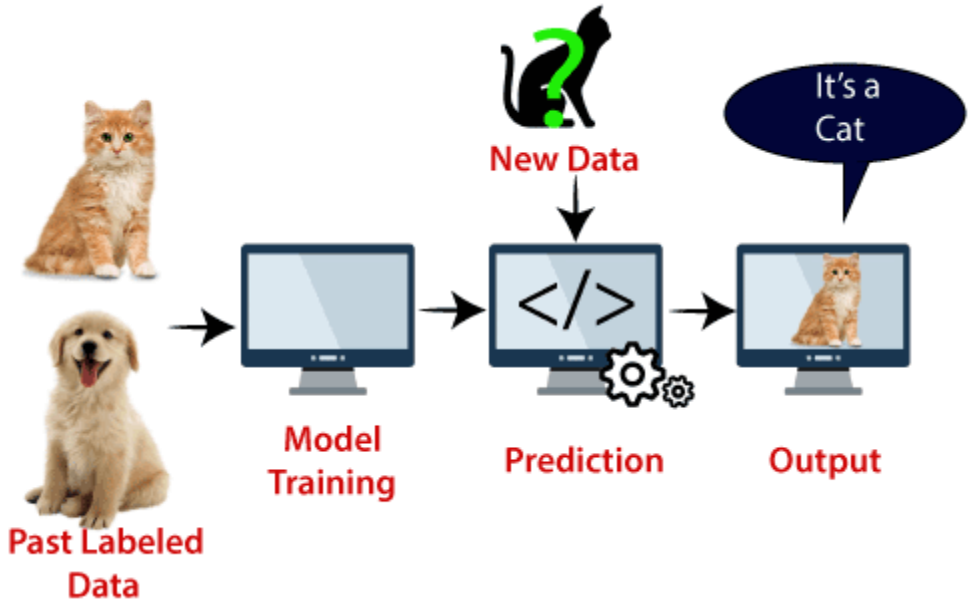
The goal of the SVM algorithm is to create the best line or decision boundary that can segregate n-dimensional space into classes so that we can easily put the new data point in the correct category in the future. This best decision boundary is called a hyperplane.

SVM chooses the extreme points/vectors that help in creating the hyperplane. These extreme cases are called as support vectors, and hence algorithm is termed as Support

Vector Machine. Consider the below diagram in which there are two different categories that are classified using a decision boundary or hyperplane:



Example: SVM can be understood with the example that we have used in the KNN classifier. Suppose we see a strange cat that also has some features of dogs, so if we want a model that can accurately identify whether it is a cat or dog, so such a model can be created by using the SVM algorithm. We will first train our model with lots of images of cats and dogs so that it can learn about different features of cats and dogs, and then we test it with this strange creature. So as support vector creates a decision boundary between these two data (cat and dog) and choose extreme cases (support vectors), it will see the extreme case of cat and dog. On the basis of the support vectors, it will classify it as a cat. Consider the below diagram:



SVM algorithm can be used for **Face detection, image classification, text categorization,** etc.

Types of SVM

SVM can be of two types:

- **Linear SVM:** Linear SVM is used for linearly separable data, which means if a dataset can be classified into two classes by using a single straight line, then such data is termed as linearly separable data, and classifier is used called as Linear SVM classifier.
- **Non-linear SVM:** Non-Linear SVM is used for non-linearly separated data, which means if a dataset cannot be classified by using a straight line, then such data is termed as non-linear data and classifier used is called as Non-linear SVM classifier.

Hyperplane and Support Vectors in the SVM algorithm:

Hyperplane: There can be multiple lines/decision boundaries to segregate the classes in n-dimensional space, but we need to find out the best decision boundary that helps to classify the data points. This best boundary is known as the hyperplane of SVM.

The dimensions of the hyperplane depend on the features present in the dataset, which means if there are 2 features (as shown in image), then hyperplane will be a straight line. And if there are 3 features, then hyperplane will be a 2-dimension plane.

We always create a hyperplane that has a maximum margin, which means the maximum distance between the data points.

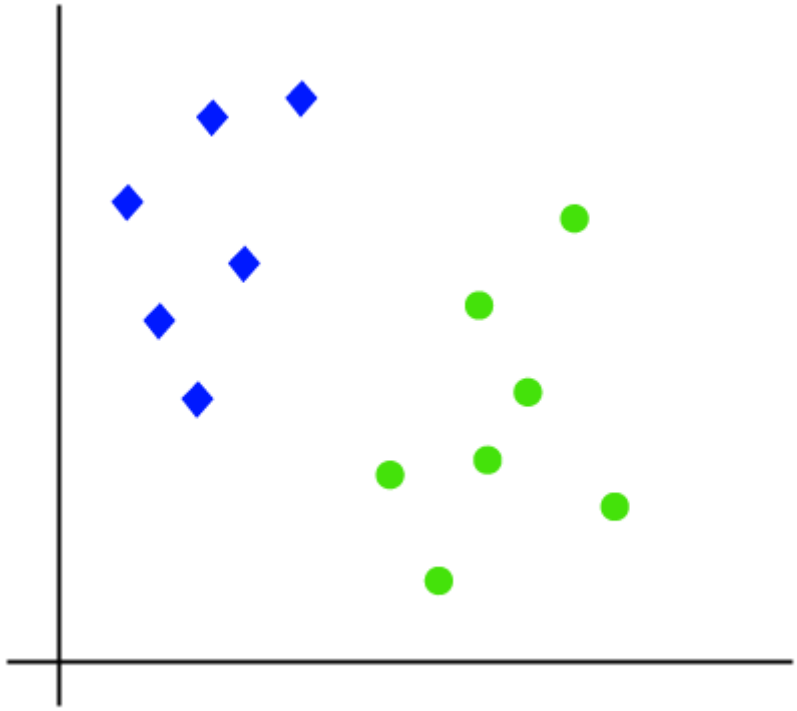
Support Vectors:

The data points or vectors that are the closest to the hyperplane and which affect the position of the hyperplane are termed as Support Vector. Since these vectors support the hyperplane, hence called a Support vector.

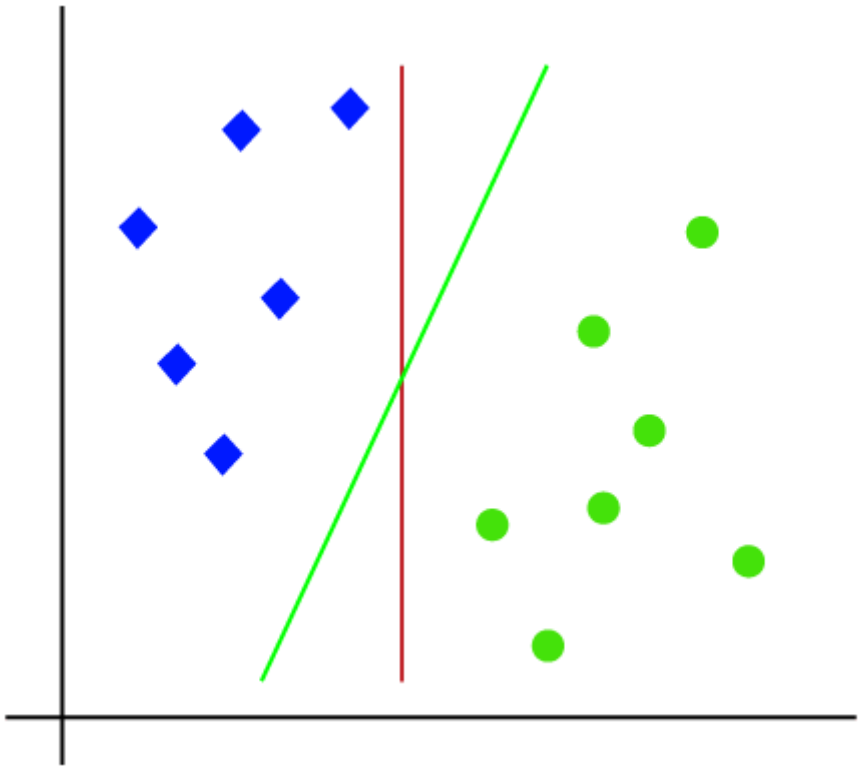
How does SVM works?

Linear SVM:

The working of the SVM algorithm can be understood by using an example. Suppose we have a dataset that has two tags (green and blue), and the dataset has two features x1 and x2. We want a classifier that can classify the pair(x1, x2) of coordinates in either green or blue. Consider the below image:

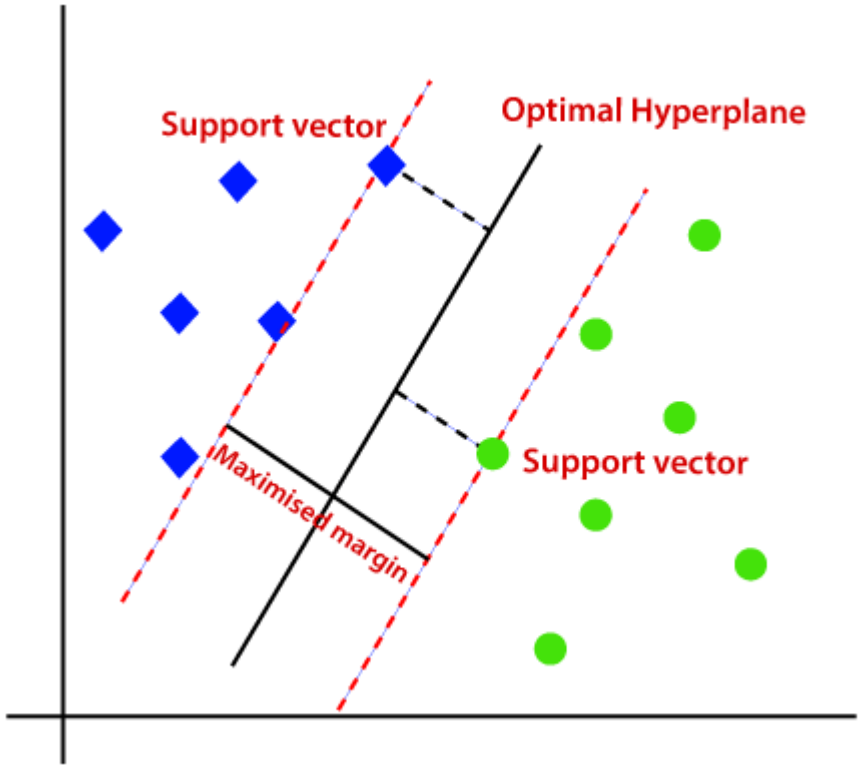


So as it is 2-d space so by just using a straight line, we can easily separate these two classes. But there can be multiple lines that can separate these classes. Consider the below image:



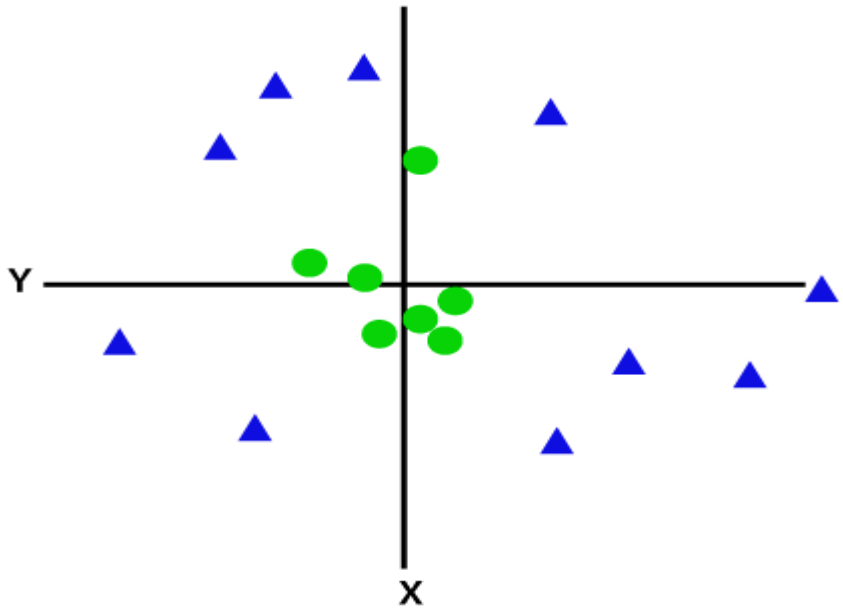
Hence, the SVM algorithm helps to find the best line or decision boundary; this best boundary or region is called as a **hyperplane**. SVM algorithm finds the closest point

of the lines from both the classes. These points are called support vectors. The distance between the vectors and the hyperplane is called as **margin**. And the goal of SVM is to maximize this margin. The **hyperplane** with maximum margin is called the **optimal hyperplane**.



Non-Linear SVM:

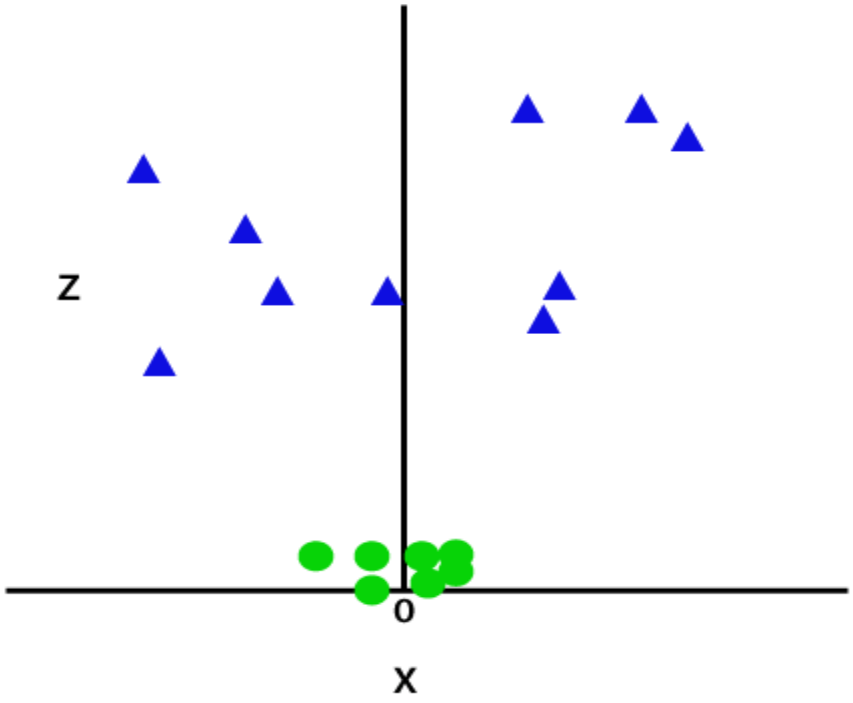
If data is linearly arranged, then we can separate it by using a straight line, but for non-linear data, we cannot draw a single straight line. Consider the below image:



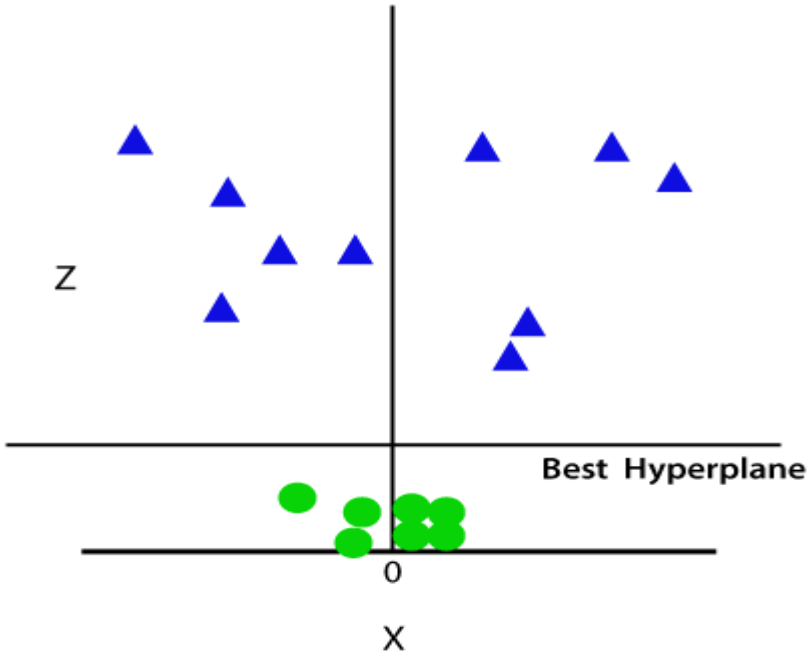
So to separate these data points, we need to add one more dimension. For linear data, we have used two dimensions x and y, so for non-linear data, we will add a third dimension z. It can be calculated as:

$$z=x^2 +y^2$$

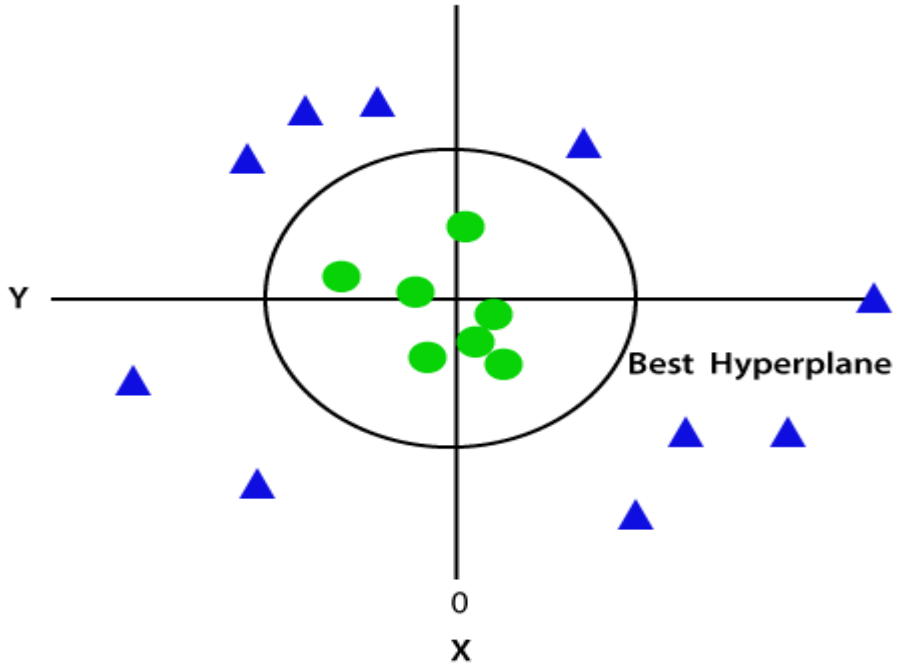
By adding the third dimension, the sample space will become as below image:



So now, SVM will divide the datasets into classes in the following way. Consider the below image:



Since we are in 3-d Space, hence it is looking like a plane parallel to the x-axis. If we convert it in 2d space with z=1, then it will become as:



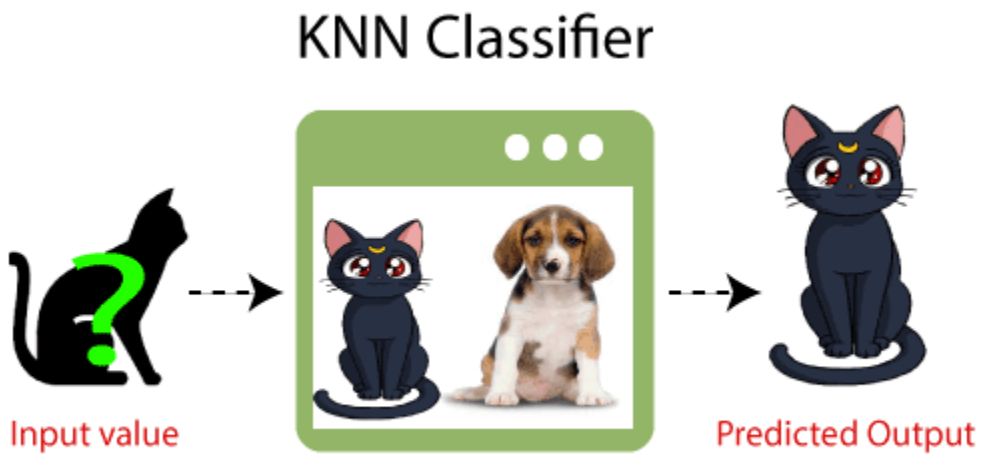
Hence we get a circumference of radius 1 in case of non-linear data.

UNIT IV ENSEMBLE TECHNIQUES AND UNSUPERVISED LEARNING

K-Nearest Neighbour(KNN) Algorithm

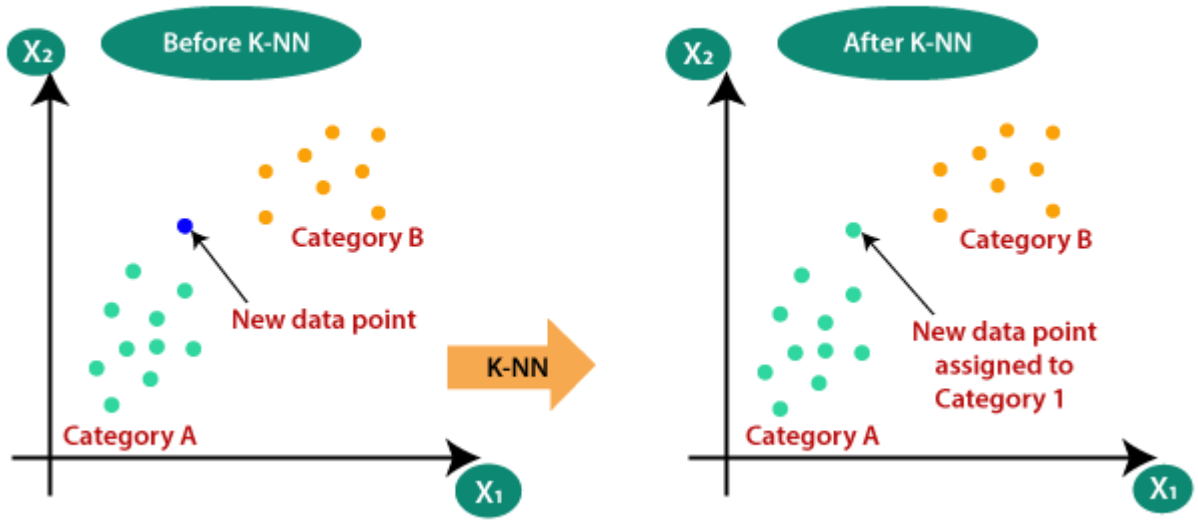
- K-Nearest Neighbour is one of the simplest Machine Learning algorithms based on Supervised Learning technique.
- K-NN algorithm assumes the similarity between the new case/data and available cases and put the new case into the category that is most similar to the available categories.
- K-NN algorithm stores all the available data and classifies a new data point based on the similarity. This means when new data appears then it can be easily classified into a well suite category by using K- NN algorithm.
- K-NN algorithm can be used for Regression as well as for Classification but mostly it is used for the Classification problems.

- K-NN is a **non-parametric algorithm**, which means it does not make any assumption on underlying data.
- It is also called a **lazy learner algorithm** because it does not learn from the training set immediately instead it stores the dataset and at the time of classification, it performs an action on the dataset.
- KNN algorithm at the training phase just stores the dataset and when it gets new data, then it classifies that data into a category that is much similar to the new data.
- **Example:** Suppose, we have an image of a creature that looks similar to cat and dog, but we want to know either it is a cat or dog. So for this identification, we can use the KNN algorithm, as it works on a similarity measure. Our KNN model will find the similar features of the new data set to the cats and dogs images and based on the most similar features it will put it in either cat or dog category.



Why do we need a K-NN Algorithm?

Suppose there are two categories, i.e., Category A and Category B, and we have a new data point x1, so this data point will lie in which of these categories. To solve this type of problem, we need a K-NN algorithm. With the help of K-NN, we can easily identify the category or class of a particular dataset. Consider the below diagram:

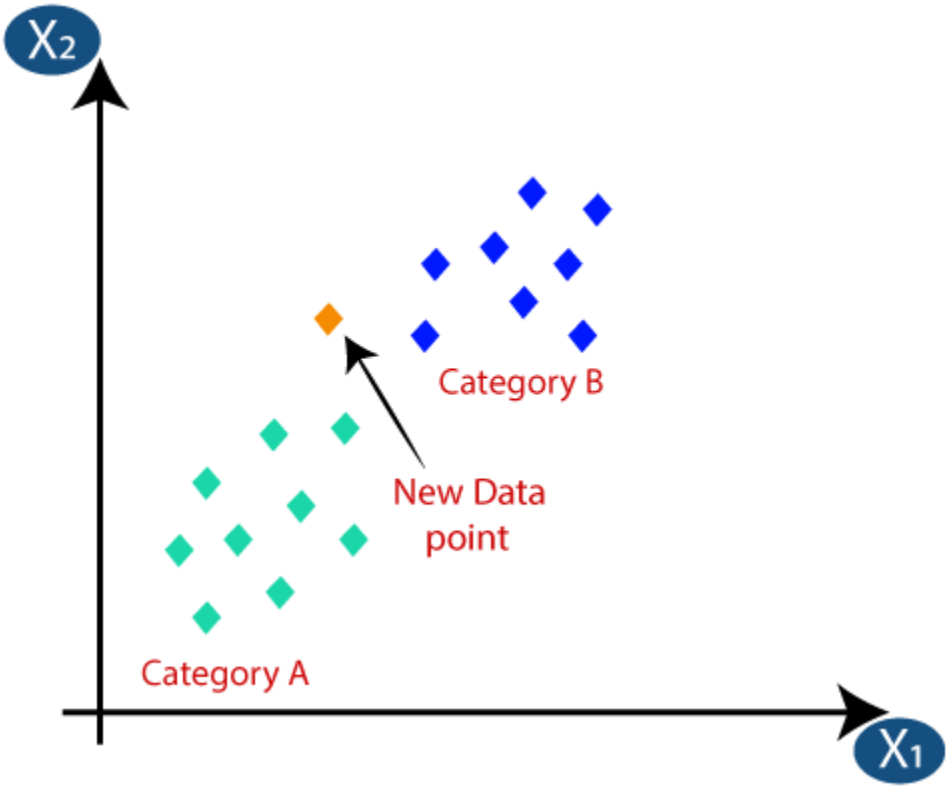


How does K-NN work?

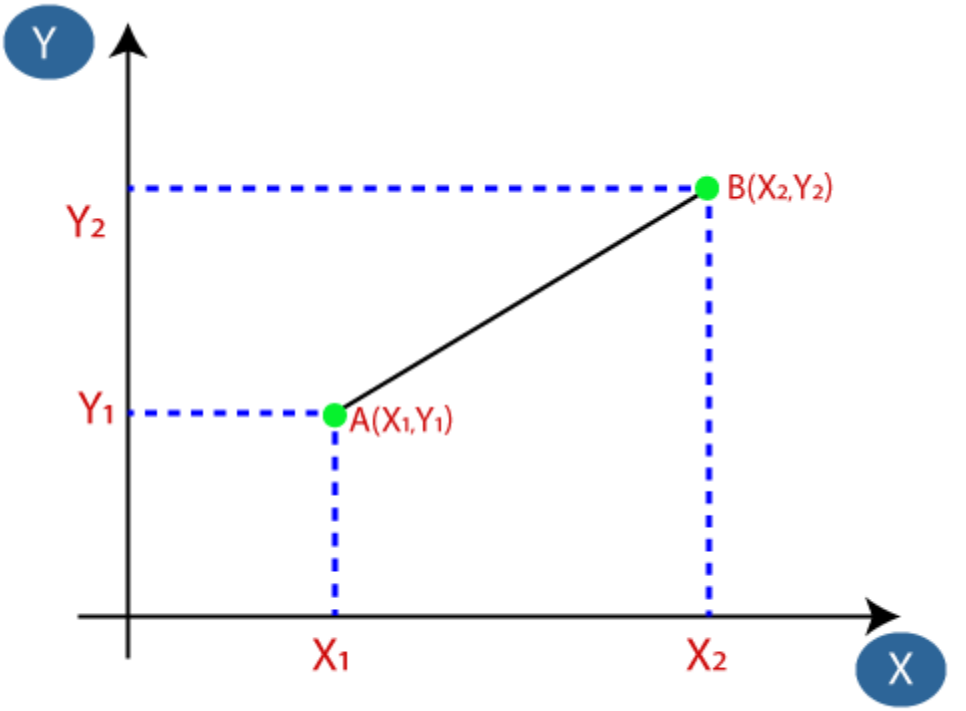
The K-NN working can be explained on the basis of the below algorithm:

- **Step-1:** Select the number K of the neighbors
- **Step-2:** Calculate the Euclidean distance of **K number of neighbors**
- **Step-3:** Take the K nearest neighbors as per the calculated Euclidean distance.
- **Step-4:** Among these k neighbors, count the number of the data points in each category.
- **Step-5:** Assign the new data points to that category for which the number of the neighbor is maximum.
- **Step-6:** Our model is ready.

Suppose we have a new data point and we need to put it in the required category. Consider the below image:

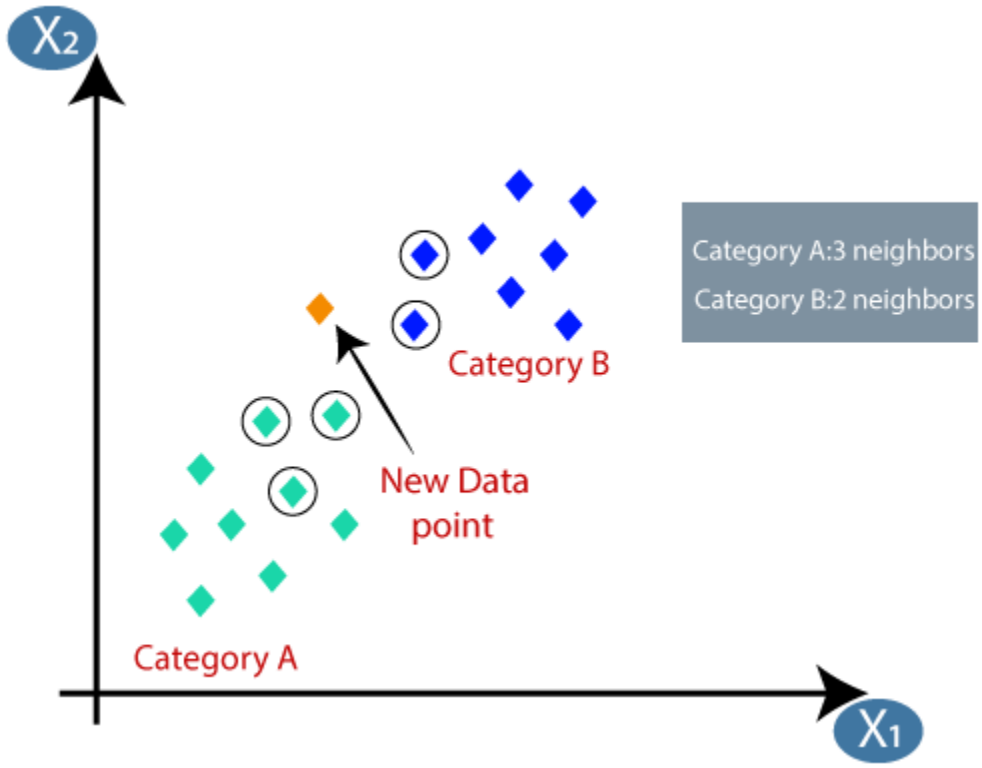


- Firstly, we will choose the number of neighbors, so we will choose the k=5.
- Next, we will calculate the **Euclidean distance** between the data points. The Euclidean distance is the distance between two points, which we have already studied in geometry. It can be calculated as:



Euclidean Distance between A_1 and B_2 = $\sqrt{(X_2-X_1)^2+(Y_2-Y_1)^2}$

- By calculating the Euclidean distance we got the nearest neighbors, as three nearest neighbors in category A and two nearest neighbors in category B. Consider the below image:



- As we can see the 3 nearest neighbors are from category A, hence this new data point must belong to category A.

How to select the value of K in the K-NN Algorithm?

Below are some points to remember while selecting the value of K in the K-NN algorithm:

- There is no particular way to determine the best value for "K", so we need to try some values to find the best out of them. The most preferred value for K is 5.
- A very low value for K such as K=1 or K=2, can be noisy and lead to the effects of outliers in the model.
- Large values for K are good, but it may find some difficulties.

Advantages of KNN Algorithm:

- It is simple to implement.
- It is robust to the noisy training data

- It can be more effective if the training data is large.

Disadvantages of KNN Algorithm:

- Always needs to determine the value of K which may be complex some time.
- The computation cost is high because of calculating the distance between the data points for all the training samples.

Python implementation of the KNN algorithm

Steps to implement the K-NN algorithm:

- Data Pre-processing step
- Fitting the K-NN algorithm to the Training set
- Predicting the test result
- Test accuracy of the result(Creation of Confusion matrix)
- Visualizing the test set result.

K-Means Clustering Algorithm

K-Means Clustering is an unsupervised learning algorithm that is used to solve the clustering problems in machine learning or data science. In this topic, we will learn what is K-means clustering algorithm, how the algorithm works, along with the Python implementation of k-means clustering.

What is K-Means Algorithm?

K-Means Clustering is an Unsupervised Learning algorithm, which groups the unlabeled dataset into different clusters. Here K defines the number of pre-defined clusters that need to be created in the process, as if K=2, there will be two clusters, and for K=3, there will be three clusters, and so on.

It is an iterative algorithm that divides the unlabeled dataset into k different clusters in such a way that each dataset belongs only one group that has similar properties.

It allows us to cluster the data into different groups and a convenient way to discover the categories of groups in the unlabeled dataset on its own without the need for any training.

It is a centroid-based algorithm, where each cluster is associated with a centroid. The main aim of this algorithm is to minimize the sum of distances between the data point and their corresponding clusters.

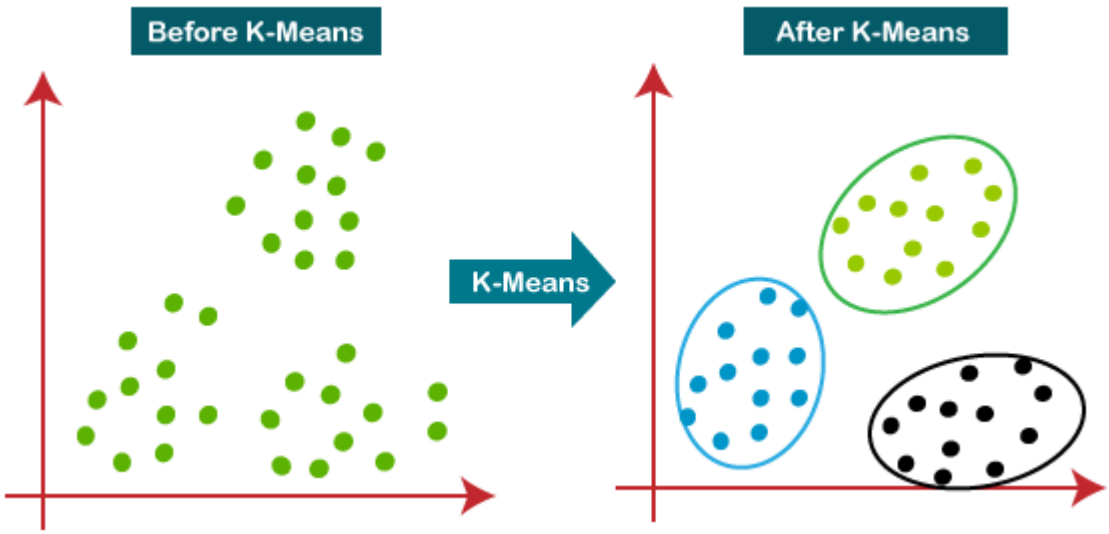
The algorithm takes the unlabeled dataset as input, divides the dataset into k-number of clusters, and repeats the process until it does not find the best clusters. The value of k should be predetermined in this algorithm.

The k-means clustering algorithm mainly performs two tasks:

- Determines the best value for K center points or centroids by an iterative process.
- Assigns each data point to its closest k-center. Those data points which are near to the particular k-center, create a cluster.

Hence each cluster has datapoints with some commonalities, and it is away from other clusters.

The below diagram explains the working of the K-means Clustering Algorithm:



How does the K-Means Algorithm Work?

The working of the K-Means algorithm is explained in the below steps:

Step-1: Select the number K to decide the number of clusters.

Step-2: Select random K points or centroids. (It can be other from the input dataset).

Step-3: Assign each data point to their closest centroid, which will form the predefined K clusters.

Step-4: Calculate the variance and place a new centroid of each cluster.

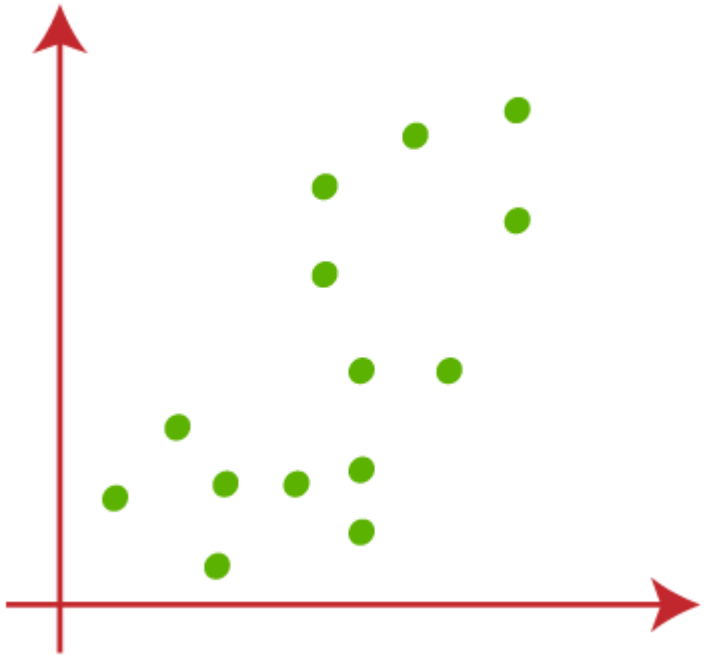
Step-5: Repeat the third steps, which means reassign each datapoint to the new closest centroid of each cluster.

Step-6: If any reassignment occurs, then go to step-4 else go to FINISH.

Step-7: The model is ready.

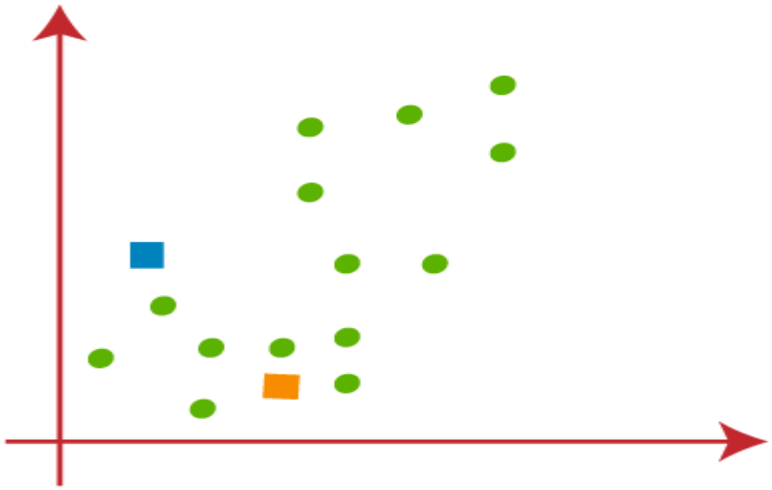
Let's understand the above steps by considering the visual plots:

Suppose we have two variables M1 and M2. The x-y axis scatter plot of these two variables is given below:

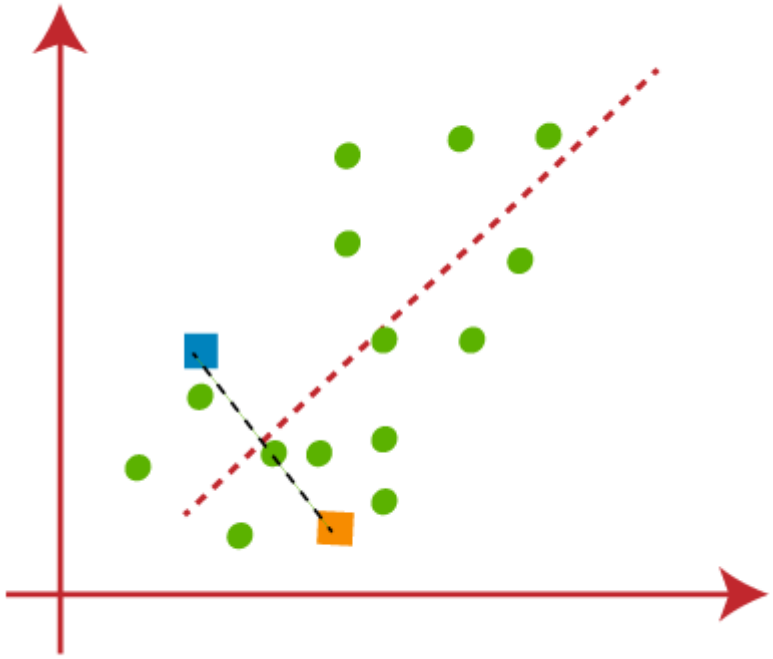


- Let's take number k of clusters, i.e., K=2, to identify the dataset and to put them into different clusters. It means here we will try to group these datasets into two different clusters.
- We need to choose some random k points or centroid to form the cluster. These points can be either the points from the dataset or any other point. So, here we are selecting the below two points as k points, which are not the part of our

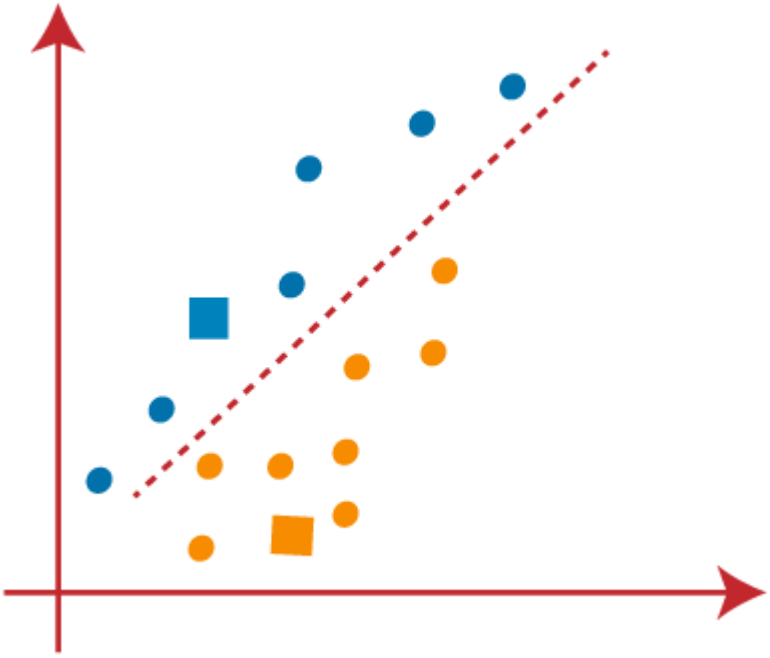
dataset. Consider the below image:



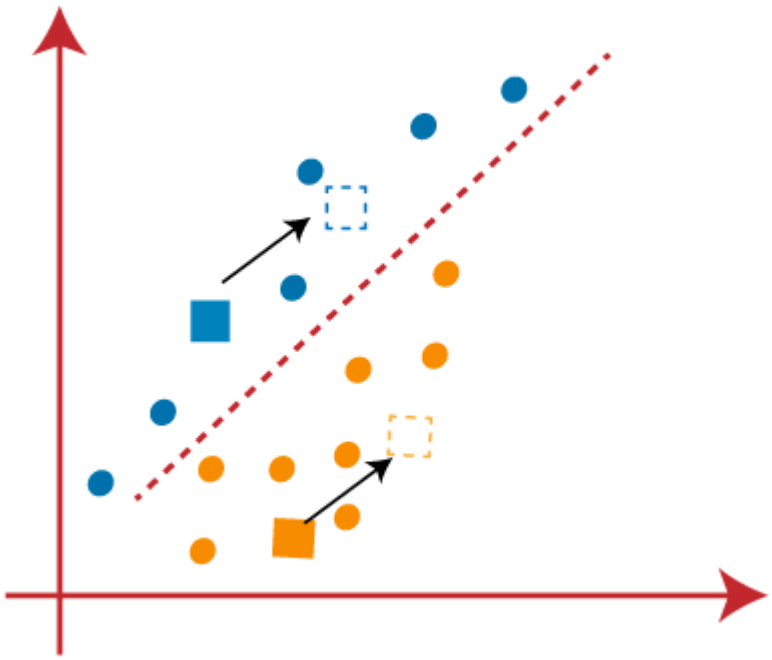
- Now we will assign each data point of the scatter plot to its closest K-point or centroid. We will compute it by applying some mathematics that we have studied to calculate the distance between two points. So, we will draw a median between both the centroids. Consider the below image:



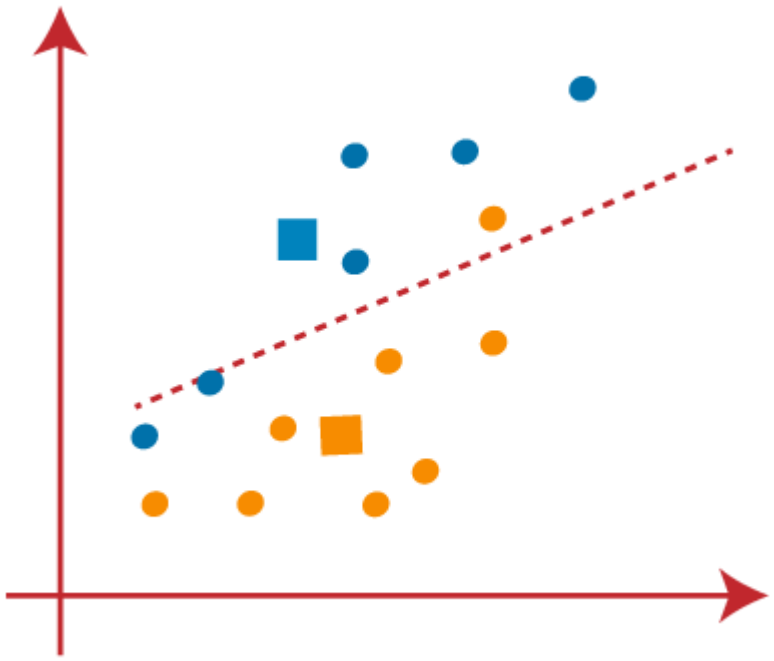
From the above image, it is clear that points left side of the line is near to the K1 or blue centroid, and points to the right of the line are close to the yellow centroid. Let's color them as blue and yellow for clear visualization.



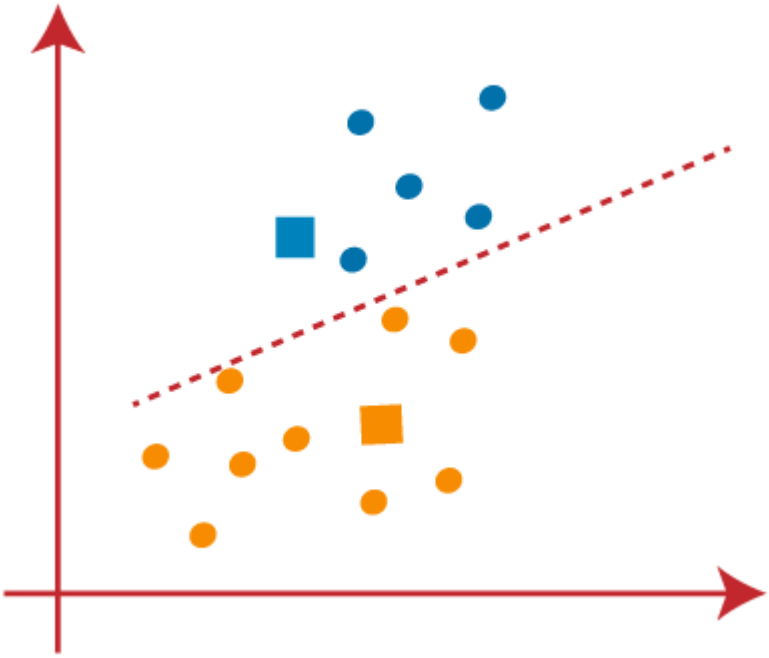
- As we need to find the closest cluster, so we will repeat the process by choosing **a new centroid**. To choose the new centroids, we will compute the center of gravity of these centroids, and will find new centroids as below:



- Next, we will reassign each datapoint to the new centroid. For this, we will repeat the same process of finding a median line. The median will be like below image:



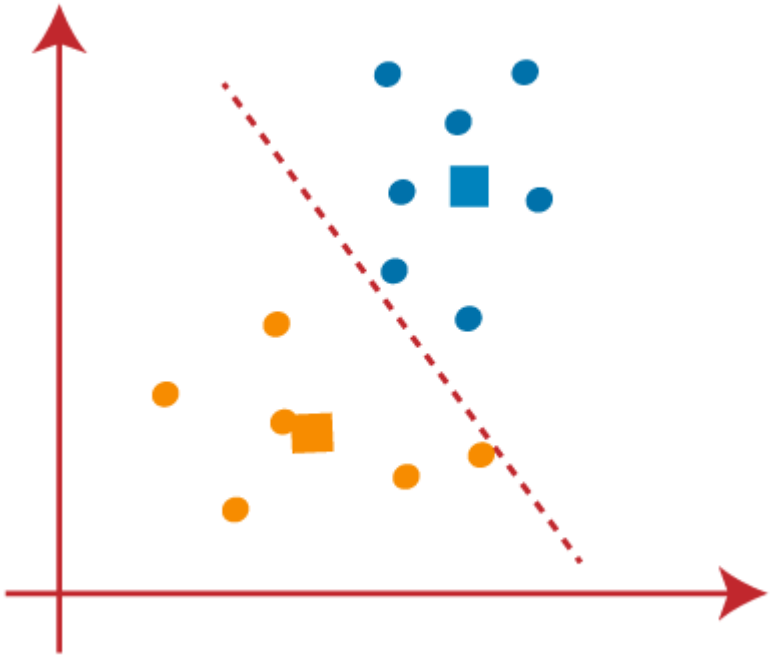
From the above image, we can see, one yellow point is on the left side of the line, and two blue points are right to the line. So, these three points will be assigned to new centroids.



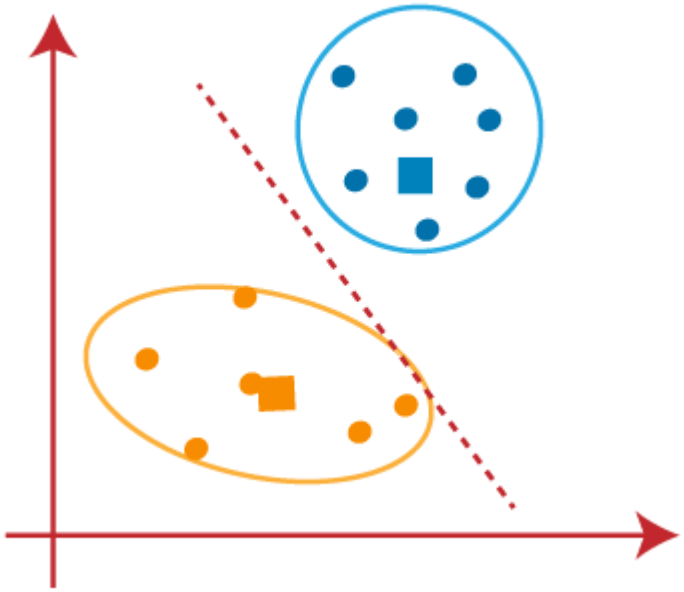
As reassignment has taken place, so we will again go to the step-4, which is finding new centroids or K-points.

- We will repeat the process by finding the center of gravity of centroids, so the new centroids will be as shown in the below image:

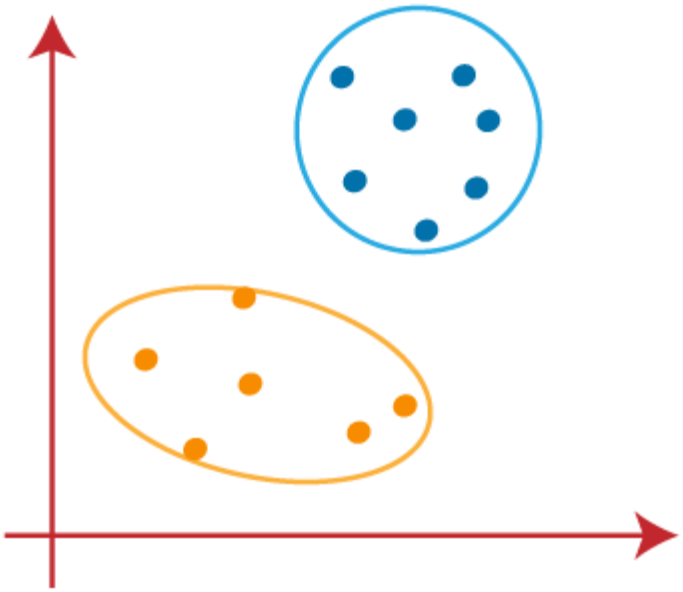
- As we got the new centroids so again will draw the median line and reassign the data points. So, the image will be:



- We can see in the above image; there are no dissimilar data points on either side of the line, which means our model is formed. Consider the below image:



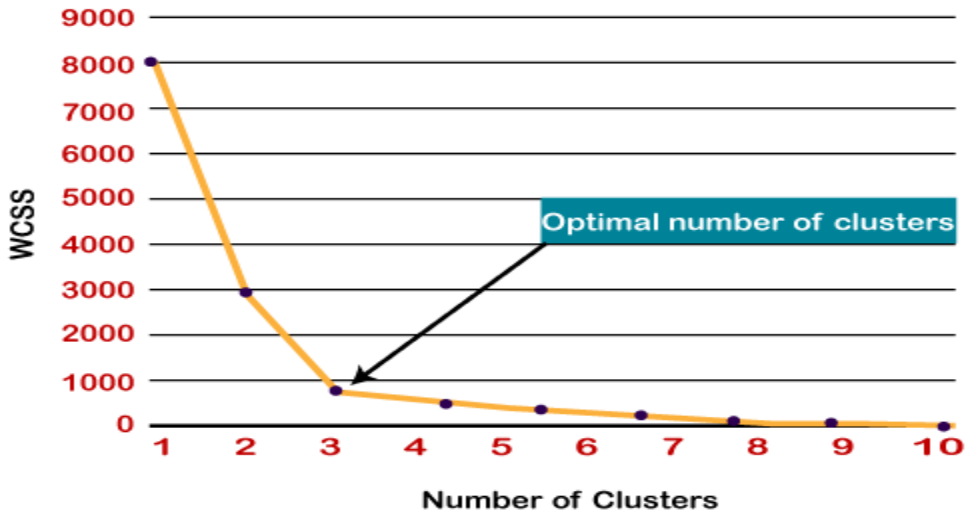
As our model is ready, so we can now remove the assumed centroids, and the two final clusters will be as shown in the below image:



To find the optimal value of clusters, the elbow method follows the below steps:

- It executes the K-means clustering on a given dataset for different K values (ranges from 1-10).
- For each value of K, calculates the WCSS value.
- Plots a curve between calculated WCSS values and the number of clusters K.
- The sharp point of bend or a point of the plot looks like an arm, then that point is considered as the best value of K.

Since the graph shows the sharp bend, which looks like an elbow, hence it is known as the elbow method. The graph for the elbow method looks like the below image:



Python Implementation of K-means Clustering Algorithm

The steps to be followed for the implementation are given below:

- **Data Pre-processing**
- **Finding the optimal number of clusters using the elbow method**
- **Training the K-means algorithm on the training dataset**
- **Visualizing the clusters**

Ensemble Learning

• The idea of ensemble learning is to employ multiple learners and combine their predictions. If we have a committee of M models with uncorrelated errors, simply by averaging them the average error of a model can be reduced by a factor of M.
• Unformtunately, the key assumption that the errors due to the individual models are uncorrelated is unrealistic; in practice, the errors are typically highly correlated, so the reduction in overall error is generally small.
• Ensemble modeling is the process of running two or more related but different analytical models and then synthesizing the results into a single score or spread in order to improve the accuracy of predictive analytics and data mining applications.
• Ensembles of classifiers is a set of classifiers whose individual decisions combined in some way to classify new examples.
• Ensemble methods combine several decision trees classifiers to produce better predictive performance than a single decision tree classifier. The main principle behind the ensemble model is that a group of weak learners come together to form a strong learner, thus increasing the accuracy of the model.
• Why do ensemble methods work?
• Based on one of two basic observations :
1. Variance reduction: If the training sets are completely independent, it will always helps to average an ensemble because this will reduce variance without affecting bias (e.g., bagging) and reduce sensitivity to individual data points.

2. Bias reduction: For simple models, average of models has much greater capacity than single model Averaging models can reduce bias substantially by increasing capacity and control variance by Citting one component at a time.

Bagging

• Bagging is also called Bootstrap aggregating. Bagging and boosting are meta - algorithms that pool decisions from multiple classifiers. It creates ensembles feed by repeatedly randomly resampling the training data.

• Bagging was the first effective method of ensemble learning and is one of the simplest methods of arching. The meta- algorithm, which is a special case of the model averaging, was originally designed for classification and is usually applied to decision tree models, but it can be used with any type of model for classification or regression.

• Ensemble classifiers such as bagging, boosting and model averaging are known to have improved accuracy and robustness over a single model. Although unsupervised models, such as clustering, do not directly generate label prediction for each individual, they provide useful constraints for the joint prediction of a set of related objects.

• For given a training set of size n, create m samples of size n by drawing n examples from the original data, with replacement. Each bootstrap sample will on average contain 63.2 % of the unique training examples, the rest are replicates. It combines the m resulting models using simple majority vote.

• In particular, on each round, the base learner is trained on what is often called a "bootstrap replicate" of the original training set. Suppose the training set consists motor of n examples. Then a bootstrap replicate is a new training set that also consists of n examples, and which is formed by repeatedly selecting uniformly at random and with replacement n examples from the original training set. This means that the same example may appear multiple times in the bootstrap replicate, or it may appear not at all.

• It also decreases error by decreasing the variance in the results due to unstable learners, algorithms (like decision trees) whose output can change dramatically when the training data is slightly changed.

Pseudocode:

1. Given training data $(x_1, y_1), ..., (x_m, Y_m)$

2. For t = 1,..., T:

a. Form bootstrap replicate dataset S_t by selecting m random examples from the training set with replacement.

b. Let h_t be the result of training base learning algorithm on S_t.

3. Output combined classifier:

$H(x) = \text{majority } (h_1(x), ..., h_T(x))$.

Bagging Steps:

1. Suppose there are N observations and M features in training data set. A sample aside from training data set is taken randomly with replacement.

2. A subset of M features is selected randomly and whichever feature gives the best split is used to split the node iteratively.

3. The tree is grown to the largest.

4. Above steps are repeated n times and prediction is given based on the aggregation of predictions from n number of trees.

Advantages of Bagging:

1. Reduces over -fitting of the model.

2. Handles higher dimensionality data very well.

3. Maintains accuracy for missing data.

Disadvantages of Bagging:

1. Since final prediction is based on the mean predictions from subset trees, it won't give precise values for the classification and regression model.

Boosting

• Boosting is a very different method to generate multiple predictions (function mob estimates) and combine them linearly. Boosting refers to a general and provably effective method of producing a very accurate classifier by combining rough and moderately inaccurate rules of thumb.

• Originally developed by computational learning theorists to guarantee performance improvements on fitting training data for a weak learner that only needs to generate a hypothesis with a training accuracy greater than 0.5. Final result is the weighted sum of the results of weak classifiers.

• A learner is weak if it produces a classifier that is only slightly better than random guessing, while a learner is said to be strong if it produces a classifier that achieves a low error with high confidence for a given concept.

• Revised to be a practical algorithm, AdaBoost, for building ensembles that empirically improves generalization performance. Examples are given weights. At each iteration, a new hypothesis is learned and the examples are reweighted to focus the system on examples that the most recently learned classifier got wrong.

• Boosting is a bias reduction technique. It typically improves the performance of a single tree model. A reason for this is that we often cannot construct trees which are sufficiently large due to thinning out of observations in the terminal nodes.
• Boosting is then a device to come up with a more complex solution by taking linear combination of trees. In presence of high-dimensional predictors, boosting is also very useful as a regularization technique for additive or interaction modeling.
• To begin, we define an algorithm for finding the rules of thumb, which we call a weak learner. The boosting algorithm repeatedly calls this weak learner, each time feeding it a different distribution over the training data. Each call generates a weak classifier and we must combine all of these into a single classifier that, hopefully, is much more accurate than any one of the rules.
• Train a set of weak hypotheses: h_1,..., h_T. The combined hypothesis H is a weighted majority vote of the T weak hypotheses. During the training, focus on the examples that are misclassified.

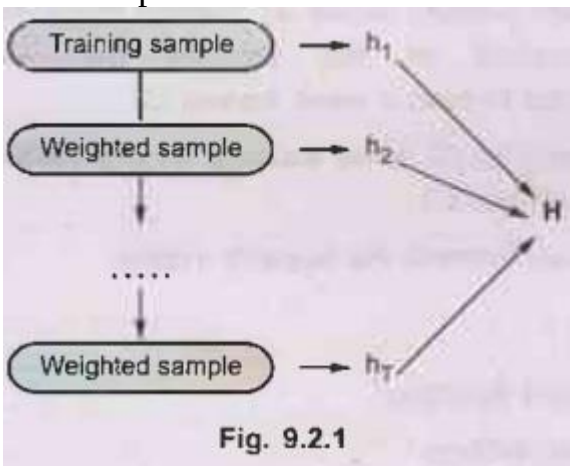


Fig. 9.2.1

AdaBoost:

• AdaBoost, short for "Adaptive Boosting", is a machine learning meta - algorithm formulated by Yoav Freund and Robert Schapire who won the prestigious "Gödel Prize" in 2003 for their work. It can be used in conjunction with many other types of learning algorithms to improve their performance.
• It can be used to learn weak classifiers and final classification based on weighted vote of weak classifiers.
• It is linear classifier with all its desirable properties. It has good generalization properties.
• To use the weak learner to form a highly accurate prediction rule by calling the weak learner repeatedly on different distributions over the training examples.

• Initially, all weights are set equally, but each round the weights of incorrectly classified examples are increased so that those observations that the previously classifier poorly predicts receive greater weight on the next iteration.

• **Advantages of AdaBoost:**

1. Very simple to implement
2. Fairly good generalization
3. The prior error need not be known ahead of time.

• **Disadvantages of AdaBoost:**

1. Sub optimal solution
2. Can over fit in presence of noise.

Boosting Steps:

1. Draw a random subset of training samples d1 without replacement from the training set D to train a weak learner C1
2. Draw second random training subset d2 without replacement from the training set and add 50 percent of the samples that were previously falsely classified/misclassified to train a weak learner C2
3. Find the training samples d3 in the training set D on which C1 and C2 disagree to train a third weak learner C3
4. Combine all the weak learners via majority voting.

Advantages of Boosting:

1. Supports different loss function.
2. Works well with interactions.

Disadvantages of Boosting:

1. Prone to over-fitting.
2. Requires careful tuning of different hyper - parameters.

Stacking

• Stacking, sometimes called stacked generalization, is an ensemble machine learning method that combines multiple heterogeneous base or component models via a meta-model.

• The base model is trained on the complete training data, and then the meta-model is trained on the predictions of the base models. The advantage of stacking is the ability to explore the solution space with different models in the same problem.

• The stacking based model can be visualized in levels and has at least two levels of the models. The first level typically trains the two or more base learners(can be heterogeneous) and the second level might be a single meta learner that utilizes the base models predictions as input and gives the final result as output. A stacked model can have more than two such levels but increasing the levels doesn't always guarantee better performance.

• In the classification tasks, often logistic regression is used as a meta learner, while linear regression is more suitable as a meta learner for regression-based tasks.

• Stacking is concerned with combining multiple classifiers generated by different learning algorithms $L_1,..., L_N$ on a single dataset S, which is composed by a feature vector $S_1 = (x_i, t_i)$.

• The stacking process can be broken into two phases:

1. Generate a set of base - level classifiers $C_1,..., C_N$ where $C_i = L_i$ (S)

2. Train a meta - level classifier to combine the outputs of the base – level classifiers.

• Fig. 9.2.2 shows stacking frame.

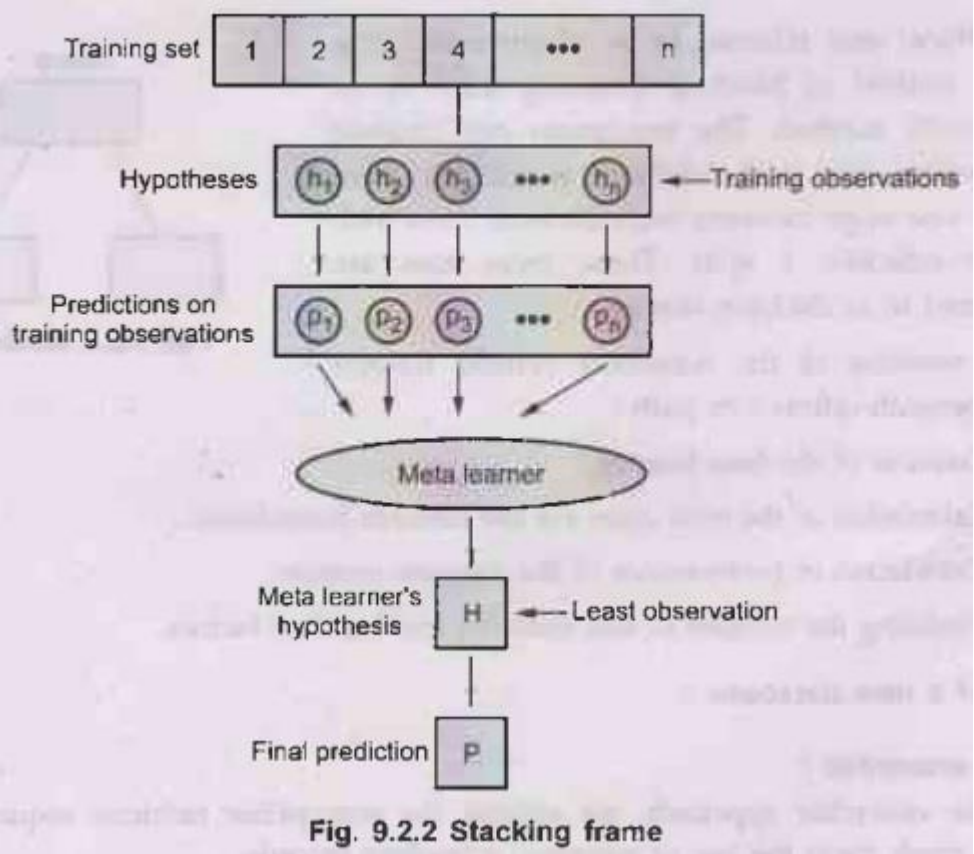


Fig. 9.2.2 Stacking frame

• The training set for the meta- level classifier is generated through a leave - one - out cross validation process.

$\nabla_i = 1, ..., n$ and $\nabla_k = 1,..., N$: C^j_k

$= L_k (S-s_i)$

• The learned classifiers are then used to generate predictions for s_i : $\hat{y}^k_i = C^i_k (x_i)$

• The meta- level dataset consists of examples of the form $((\hat{y},...,\hat{y}^n_i), y_i)$, where the features are the predictions of the base - level classifiers and the class is the correct class of the example in hand.

• Why do ensemble methods work?

• Based on one of two basic observations:

1. Variance reduction: If the training sets are completely independent, it will always helps to average an ensemble because this will reduce variance without affecting bias (e.g. - bagging) and reduce sensitivity to individual data points.

2. Bias reduction: For simple models, average of models has much greater capacity than single model Averaging models can reduce bias substantially by increasing capacity and control variance by Citting one component at a time.

Adaboost

• AdaBoost also referred to as adaptive boosting Stumpis a method in Machine Learning used as an ensemble method. The maximum not unusual algorithm used with AdaBoost is selection trees with one stage meaning with decision trees with most effective 1 split. These trees also are referred to as decision stumps.

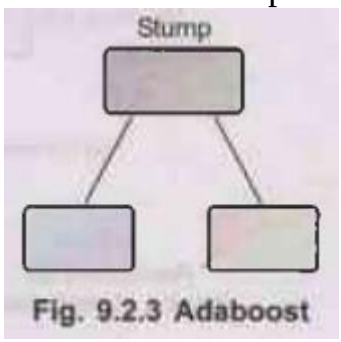


Fig. 9.2.3 Adaboost

• The working of the AdaBoost version follows the beneath-referred to path:

• Creation of the base learner.

• Calculation of the total error via the beneath formulation.

• Calculation of performance of the decision stumps.

• Updating the weights in line with the misclassified factors.

Creation of a new database:

AdaBoost ensemble:

• In the ensemble approach, we upload the susceptible fashions sequentially and then teach them the use of weighted schooling records.
• We hold to iterate the process till we gain the advent of a pre-set range of vulnerable learners or we can not look at further improvement at the dataset. At the end of the algorithm, we are left with some vulnerable learners with a stage fee.

Difference between Bagging and Boosting

Sr. No.	Bagging	Boosting
1.	Bagging is a technique that builds multiple homogeneous models from different subsamples of the same training dataset to obtain more accurate predictions than its individual models	Boosting refers to a group of algorithms that utilize weighted averages to make weak learning algorithms stronger learning algorithms.
2.	Learns them independently from each other in parallel	Learns them sequentially in a very adaptative way
3.	It helps in reducing variance.	It helps in reducing bias and variance.
4.	Every model receives an equal weight.	Models are weighted by their performance.

UNIT V NEURAL NETWORKS

Gradient Descent in Machine Learning

Gradient Descent is known as one of the most commonly used optimization algorithms to train machine learning models by means of minimizing errors between actual and expected results. Further, gradient descent is also used to train Neural Networks.

In mathematical terminology, Optimization algorithm refers to the task of minimizing/maximizing an objective function f(x) parameterized by x. Similarly, in machine learning, optimization is the task of minimizing the cost function parameterized by the model's parameters. The main objective of gradient descent is to minimize the convex function using iteration of parameter updates. Once these machine learning models are optimized, these models can be used as powerful tools for Artificial Intelligence and various computer science applications.

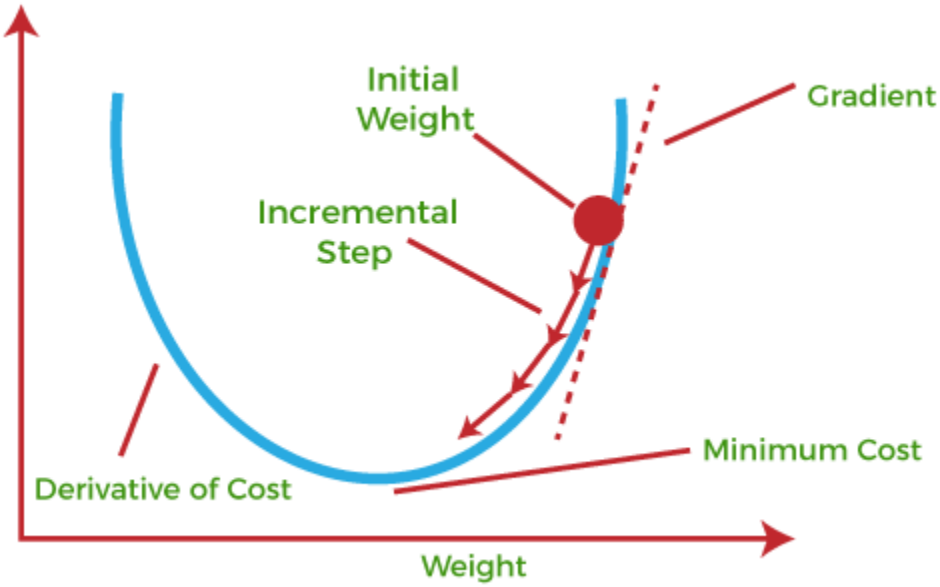
In this tutorial on Gradient Descent in Machine Learning, we will learn in detail about gradient descent, the role of cost functions specifically as a barometer within Machine Learning, types of gradient descents, learning rates, etc.

What is Gradient Descent or Steepest Descent?

Gradient descent was initially discovered by **"Augustin-Louis Cauchy"** in mid of 18th century. ***Gradient Descent is defined as one of the most commonly used iterative optimization algorithms of machine learning to train the machine learning and deep learning models. It helps in finding the local minimum of a function.***

The best way to define the local minimum or local maximum of a function using gradient descent is as follows:

- If we move towards a negative gradient or away from the gradient of the function at the current point, it will give the **local minimum** of that function.
- Whenever we move towards a positive gradient or towards the gradient of the function at the current point, we will get the **local maximum** of that function.



This entire procedure is known as Gradient Ascent, which is also known as steepest descent. ***The main objective of using a gradient descent algorithm is to minimize the cost function using iteration.*** To achieve this goal, it performs two steps iteratively:

- Calculates the first-order derivative of the function to compute the gradient or slope of that function.

- Move away from the direction of the gradient, which means slope increased from the current point by alpha times, where Alpha is defined as Learning Rate. It is a tuning parameter in the optimization process which helps to decide the length of the steps.

What is Cost-function?

The cost function is defined as the measurement of difference or error between actual values and expected values at the current position and present in the form of a single real number. It helps to increase and improve machine learning efficiency by providing feedback to this model so that it can minimize error and find the local or global minimum. Further, it continuously iterates along the direction of the negative gradient until the cost function approaches zero. At this steepest descent point, the model will stop learning further. Although cost function and loss function are considered synonymous, also there is a minor difference between them. The slight difference between the loss function and the cost function is about the error within the training of machine learning models, as loss function refers to the error of one training example, while a cost function calculates the average error across an entire training set.

The cost function is calculated after making a hypothesis with initial parameters and modifying these parameters using gradient descent algorithms over known data to reduce the cost function.

Hypothesis:

Parameters:

Cost function:

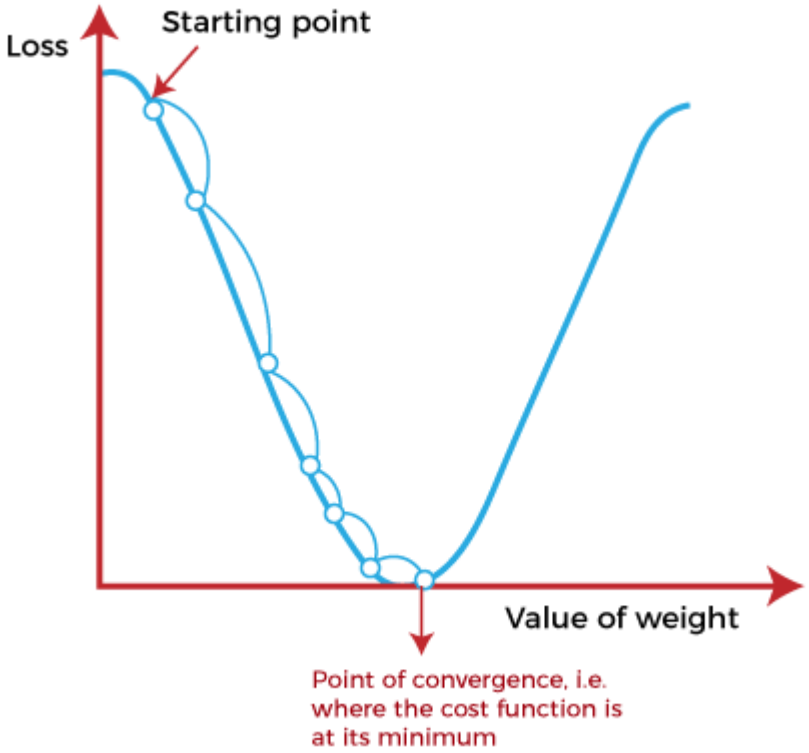
Goal:

How does Gradient Descent work?

Before starting the working principle of gradient descent, we should know some basic concepts to find out the slope of a line from linear regression. The equation for simple linear regression is given as:

1. $Y=mX+c$

Where 'm' represents the slope of the line, and 'c' represents the intercepts on the y-axis.



The starting point(shown in above fig.) is used to evaluate the performance as it is considered just as an arbitrary point. At this starting point, we will derive the first derivative or slope and then use a tangent line to calculate the steepness of this slope. Further, this slope will inform the updates to the parameters (weights and bias).

The slope becomes steeper at the starting point or arbitrary point, but whenever new parameters are generated, then steepness gradually reduces, and at the lowest point, it approaches the lowest point, which is called **a point of convergence.**

The main objective of gradient descent is to minimize the cost function or the error between expected and actual. To minimize the cost function, two data points are required:

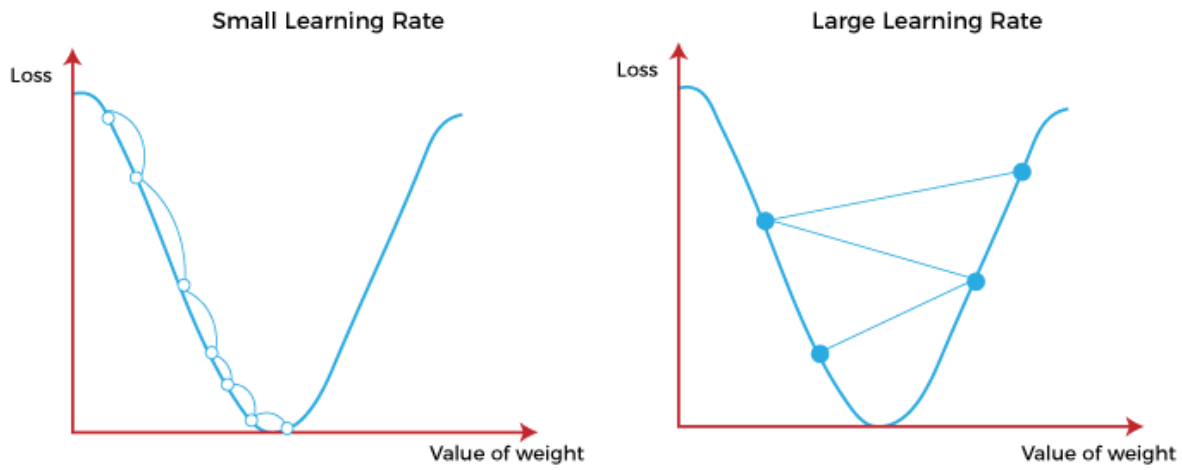
Direction & Learning Rate

These two factors are used to determine the partial derivative calculation of future iteration and allow it to the point of convergence or local minimum or global minimum. Let's discuss learning rate factors in brief;

Learning Rate:

It is defined as the step size taken to reach the minimum or lowest point. This is typically a small value that is evaluated and updated based on the behavior of the cost function. If the learning rate is high, it results in larger steps but also leads to risks of

overshooting the minimum. At the same time, a low learning rate shows the small step sizes, which compromises overall efficiency but gives the advantage of more precision.



Types of Gradient Descent

Based on the error in various training models, the Gradient Descent learning algorithm can be divided into **Batch gradient descent, stochastic gradient descent, and mini-batch gradient descent.** Let's understand these different types of gradient descent:

1. Batch Gradient Descent:

Batch gradient descent (BGD) is used to find the error for each point in the training set and update the model after evaluating all training examples. This procedure is known as the training epoch. In simple words, it is a greedy approach where we have to sum over all examples for each update.

Advantages of Batch gradient descent:

- It produces less noise in comparison to other gradient descent.
- It produces stable gradient descent convergence.
- It is Computationally efficient as all resources are used for all training samples.

2. Stochastic gradient descent

Stochastic gradient descent (SGD) is a type of gradient descent that runs one training example per iteration. Or in other words, it processes a training epoch for each

example within a dataset and updates each training example's parameters one at a time. As it requires only one training example at a time, hence it is easier to store in allocated memory. However, it shows some computational efficiency losses in comparison to batch gradient systems as it shows frequent updates that require more detail and speed. Further, due to frequent updates, it is also treated as a noisy gradient. However, sometimes it can be helpful in finding the global minimum and also escaping the local minimum.

Advantages of Stochastic gradient descent:

In Stochastic gradient descent (SGD), learning happens on every example, and it consists of a few advantages over other gradient descent.

- It is easier to allocate in desired memory.
- It is relatively fast to compute than batch gradient descent.
- It is more efficient for large datasets.

3. MiniBatch Gradient Descent:

Mini Batch gradient descent is the combination of both batch gradient descent and stochastic gradient descent. It divides the training datasets into small batch sizes then performs the updates on those batches separately. Splitting training datasets into smaller batches make a balance to maintain the computational efficiency of batch gradient descent and speed of stochastic gradient descent. Hence, we can achieve a special type of gradient descent with higher computational efficiency and less noisy gradient descent.

Advantages of Mini Batch gradient descent:

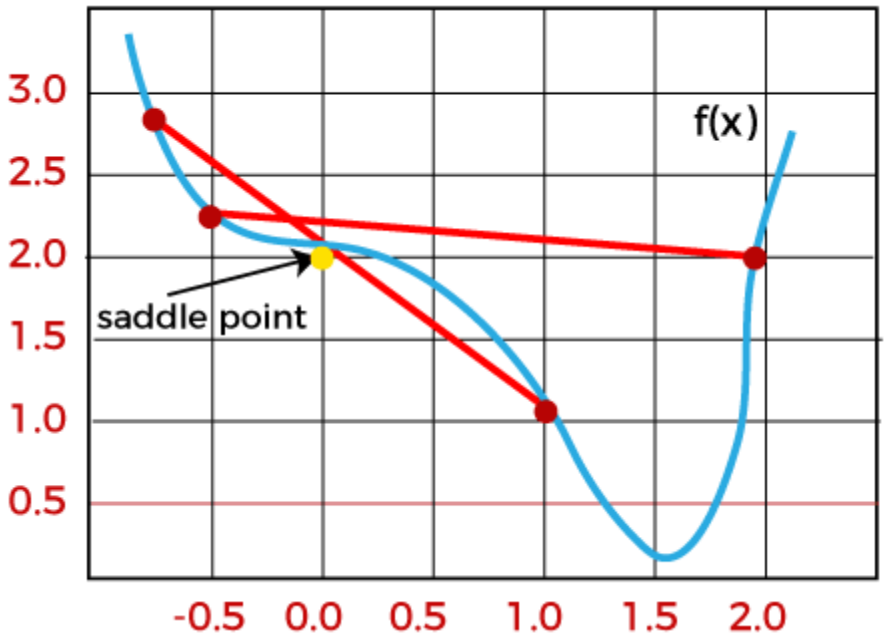
- It is easier to fit in allocated memory.
- It is computationally efficient.
- It produces stable gradient descent convergence.

Challenges with the Gradient Descent

Although we know Gradient Descent is one of the most popular methods for optimization problems, it still also has some challenges. There are a few challenges as follows:

1. Local Minima and Saddle Point:

For convex problems, gradient descent can find the global minimum easily, while for non-convex problems, it is sometimes difficult to find the global minimum, where the machine learning models achieve the best results.



Whenever the slope of the cost function is at zero or just close to zero, this model stops learning further. Apart from the global minimum, there occur some scenarios that can show this slop, which is saddle point and local minimum. Local minima generate the shape similar to the global minimum, where the slope of the cost function increases on both sides of the current points.

In contrast, with saddle points, the negative gradient only occurs on one side of the point, which reaches a local maximum on one side and a local minimum on the other side. The name of a saddle point is taken by that of a horse's saddle.

The name of local minima is because the value of the loss function is minimum at that point in a local region. In contrast, the name of the global minima is given so because the value of the loss function is minimum there, globally across the entire domain the loss function.

2. Vanishing and Exploding Gradient

In a deep neural network, if the model is trained with gradient descent and backpropagation, there can occur two more issues other than local minima and saddle point.

Vanishing Gradients:

Vanishing Gradient occurs when the gradient is smaller than expected. During backpropagation, this gradient becomes smaller that causing the decrease in the learning rate of earlier layers than the later layer of the network. Once this happens, the weight parameters update until they become insignificant.

Exploding Gradient:

Exploding gradient is just opposite to the vanishing gradient as it occurs when the Gradient is too large and creates a stable model. Further, in this scenario, model weight increases, and they will be represented as NaN. This problem can be solved using the dimensionality reduction technique, which helps to minimize complexity within the model.

Perceptron in Machine Learning

In Machine Learning and Artificial Intelligence, Perceptron is the most commonly used term for all folks. It is the primary step to learn Machine Learning and Deep Learning technologies, which consists of a set of weights, input values or scores, and a threshold. ***Perceptron is a building block of an Artificial Neural Network***. Initially, in the mid of 19th century, **Mr. Frank Rosenblatt** invented the Perceptron for performing certain calculations to detect input data capabilities or business intelligence. Perceptron is a linear Machine Learning algorithm used for supervised learning for various binary classifiers. This algorithm enables neurons to learn elements and processes them one by one during preparation. In this tutorial, "Perceptron in Machine Learning," we will discuss in-depth knowledge of Perceptron and its basic functions in brief. Let's start with the basic introduction of Perceptron.

What is the Perceptron model in Machine Learning?

Perceptron is Machine Learning algorithm for supervised learning of various binary classification tasks. Further, ***Perceptron is also understood as an Artificial Neuron or neural network unit that helps to detect certain input data computations in business intelligence***.

Perceptron model is also treated as one of the best and simplest types of Artificial Neural networks. However, it is a supervised learning algorithm of binary classifiers. Hence, we can consider it as a single-layer neural network with four main parameters, i.e., **input values, weights and Bias, net sum, and an activation function.**

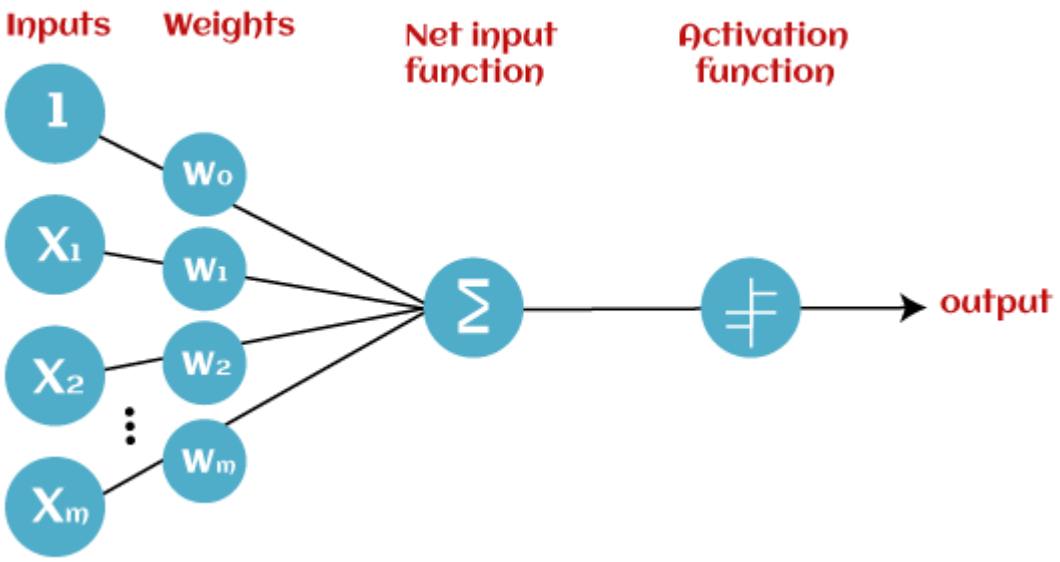
What is Binary classifier in Machine Learning?

In Machine Learning, binary classifiers are defined as the function that helps in deciding whether input data can be represented as vectors of numbers and belongs to some specific class.

Binary classifiers can be considered as linear classifiers. In simple words, we can understand it as a ***classification algorithm that can predict linear predictor function in terms of weight and feature vectors.***

Basic Components of Perceptron

Mr. Frank Rosenblatt invented the perceptron model as a binary classifier which contains three main components. These are as follows:



- **Input Nodes or Input Layer:**

This is the primary component of Perceptron which accepts the initial data into the system for further processing. Each input node contains a real numerical value.

- **Wight and Bias:**

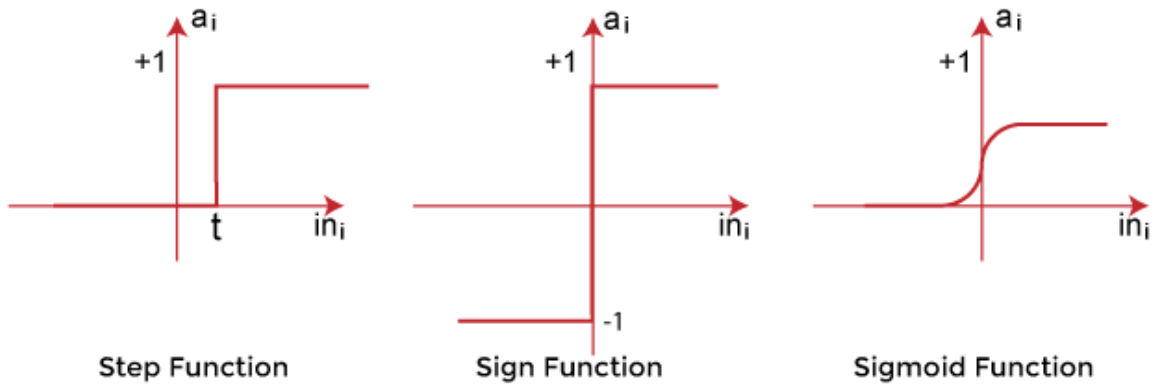
Weight parameter represents the strength of the connection between units. This is another most important parameter of Perceptron components. Weight is directly proportional to the strength of the associated input neuron in deciding the output. Further, Bias can be considered as the line of intercept in a linear equation.

- **Activation Function:**

These are the final and important components that help to determine whether the neuron will fire or not. Activation Function can be considered primarily as a step function.

Types of Activation functions:

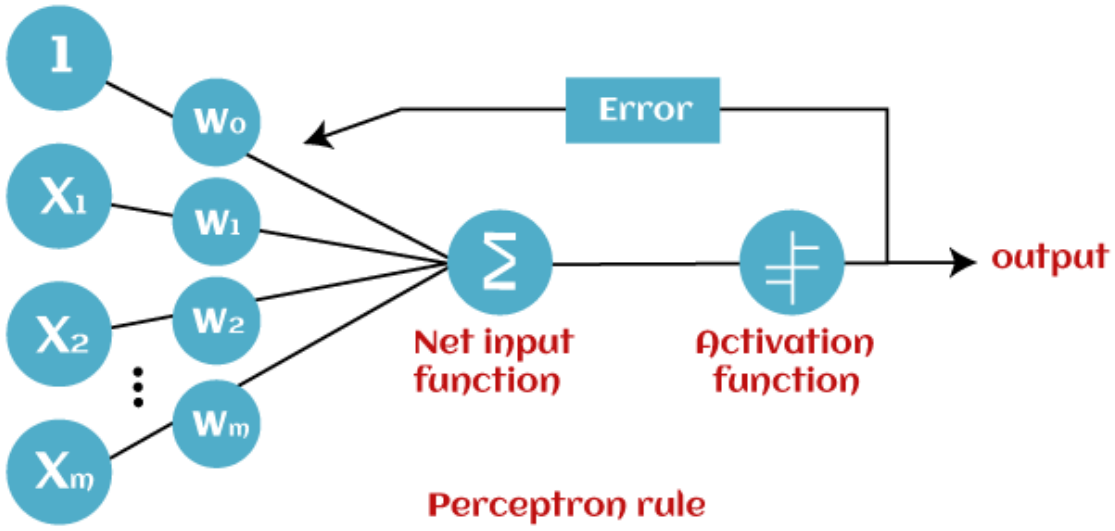
- Sign function
- Step function, and
- Sigmoid function



The data scientist uses the activation function to take a subjective decision based on various problem statements and forms the desired outputs. Activation function may differ (e.g., Sign, Step, and Sigmoid) in perceptron models by checking whether the learning process is slow or has vanishing or exploding gradients.

How does Perceptron work?

In Machine Learning, Perceptron is considered as a single-layer neural network that consists of four main parameters named input values (Input nodes), weights and Bias, net sum, and an activation function. The perceptron model begins with the multiplication of all input values and their weights, then adds these values together to create the weighted sum. Then this weighted sum is applied to the activation function 'f' to obtain the desired output. This activation function is also known as the **step function** and is represented by **'f'**.



This step function or Activation function plays a vital role in ensuring that output is mapped between required values (0,1) or (-1,1). It is important to note that the weight of input is indicative of the strength of a node. Similarly, an input's bias value gives the ability to shift the activation function curve up or down.

Perceptron model works in two important steps as follows:

Step-1

In the first step first, multiply all input values with corresponding weight values and then add them to determine the weighted sum. Mathematically, we can calculate the weighted sum as follows:

∑wi*xi = x1*w1 + x2*w2 +...wn*xn

Add a special term called **bias 'b'** to this weighted sum to improve the model's performance.

∑wi*xi + b

Step-2

In the second step, an activation function is applied with the above-mentioned weighted sum, which gives us output either in binary form or a continuous value as follows:

Y = f(∑wi*xi + b)

Types of Perceptron Models

Based on the layers, Perceptron models are divided into two types. These are as follows:

1. Single-layer Perceptron Model
2. Multi-layer Perceptron model

Single Layer Perceptron Model:

This is one of the easiest Artificial neural networks (ANN) types. A single-layered perceptron model consists feed-forward network and also includes a threshold transfer function inside the model. The main objective of the single-layer perceptron model is to analyze the linearly separable objects with binary outcomes.

In a single layer perceptron model, its algorithms do not contain recorded data, so it begins with inconstantly allocated input for weight parameters. Further, it sums up all inputs (weight). After adding all inputs, if the total sum of all inputs is more than a pre-determined value, the model gets activated and shows the output value as +1.

If the outcome is same as pre-determined or threshold value, then the performance of this model is stated as satisfied, and weight demand does not change. However, this model consists of a few discrepancies triggered when multiple weight inputs values are fed into the model. Hence, to find desired output and minimize errors, some changes should be necessary for the weights input.

"*Single-layer perceptron can learn only linearly separable patterns.*"

Multi-Layered Perceptron Model:

Like a single-layer perceptron model, a multi-layer perceptron model also has the same model structure but has a greater number of hidden layers.

The multi-layer perceptron model is also known as the Backpropagation algorithm, which executes in two stages as follows:

- **Forward Stage:** Activation functions start from the input layer in the forward stage and terminate on the output layer.
- **Backward Stage:** In the backward stage, weight and bias values are modified as per the model's requirement. In this stage, the error between actual output

and demanded originated backward on the output layer and ended on the input layer.

Hence, a multi-layered perceptron model has considered as multiple artificial neural networks having various layers in which activation function does not remain linear, similar to a single layer perceptron model. Instead of linear, activation function can be executed as sigmoid, TanH, ReLU, etc., for deployment.

A multi-layer perceptron model has greater processing power and can process linear and non-linear patterns. Further, it can also implement logic gates such as AND, OR, XOR, NAND, NOT, XNOR, NOR.

Advantages of Multi-Layer Perceptron:

- A multi-layered perceptron model can be used to solve complex non-linear problems.
- It works well with both small and large input data.
- It helps us to obtain quick predictions after the training.
- It helps to obtain the same accuracy ratio with large as well as small data.

Disadvantages of Multi-Layer Perceptron:

- In Multi-layer perceptron, computations are difficult and time-consuming.
- In multi-layer Perceptron, it is difficult to predict how much the dependent variable affects each independent variable.
- The model functioning depends on the quality of the training.

Perceptron Function

Perceptron function ''f(x)'' can be achieved as output by multiplying the input 'x' with the learned weight coefficient 'w'.

Mathematically, we can express it as follows:

f(x)=1; if w.x+b>0

otherwise, f(x)=0

- 'w' represents real-valued weights vector
- 'b' represents the bias
- 'x' represents a vector of input x values.

Characteristics of Perceptron

The perceptron model has the following characteristics.

1. Perceptron is a machine learning algorithm for supervised learning of binary classifiers.
2. In Perceptron, the weight coefficient is automatically learned.
3. Initially, weights are multiplied with input features, and the decision is made whether the neuron is fired or not.
4. The activation function applies a step rule to check whether the weight function is greater than zero.
5. The linear decision boundary is drawn, enabling the distinction between the two linearly separable classes +1 and -1.
6. If the added sum of all input values is more than the threshold value, it must have an output signal; otherwise, no output will be shown.

Limitations of Perceptron Model

A perceptron model has limitations as follows:

- The output of a perceptron can only be a binary number (0 or 1) due to the hard limit transfer function.
- Perceptron can only be used to classify the linearly separable sets of input vectors. If input vectors are non-linear, it is not easy to classify them properly.

Activation Functions in Neural Networks

A paradigm for information processing that draws inspiration from the brain is called an artificial neural network (ANN). ANNs learn via imitation just like people do. Through a learning process, an ANN is tailored for a particular purpose, including such pattern classification or data classification. The synapses interconnections that exist between both the neurons change because of learning.

What input layer to employ with in hidden layer and at the input level of the network is one of the decisions you get to make while creating a neural network. This article discusses a few of the alternatives.

Neural Network Components

Layers are the vertically stacked parts that make up a neural network. The image's dotted lines each signify a layer. A NN has three different types of layers.

Input Layer

The input layer is first. The data will be accepted by this layer and forwarded to the remainder of the network. This layer allows feature input. It feeds the network with data from the outside world; no calculation is done here; instead, nodes simply transmit the information (features) to the hidden units.

Hidden Layer

Since they are a component of the abstraction that any neural network provides, the nodes in this layer are not visible to the outside world. Any features entered through to the input layer are processed by the hidden layer in any way, with the results being sent to the output layer. The concealed layer is the name given to the second kind of layer. For a neural network, either there are one or many hidden layers. The number inside the example above is 1. In reality, hidden layers are what give neural networks their exceptional performance and intricacy.

Output Layer

This layer raises the knowledge that the network has acquired to the outside world. The output layer is the final kind of layer The output layer contains the answer to the issue. We receive output from the output layer after passing raw photos to the input layer.

Activation Function

Definition

In artificial neural networks, an activation function is one that outputs a smaller value for tiny inputs and a higher value if its inputs are greater than a threshold. An activation function "fires" if the inputs are big enough; otherwise, nothing happens. An activation function, then, is a gate that verifies how an incoming value is higher than a threshold value.

Need of Non-linear Activation Functions

An interconnected regression model without an activation function is all that a neural network is. Input is transformed nonlinearly by the activation function, allowing the system to learn and perform more challenging tasks.

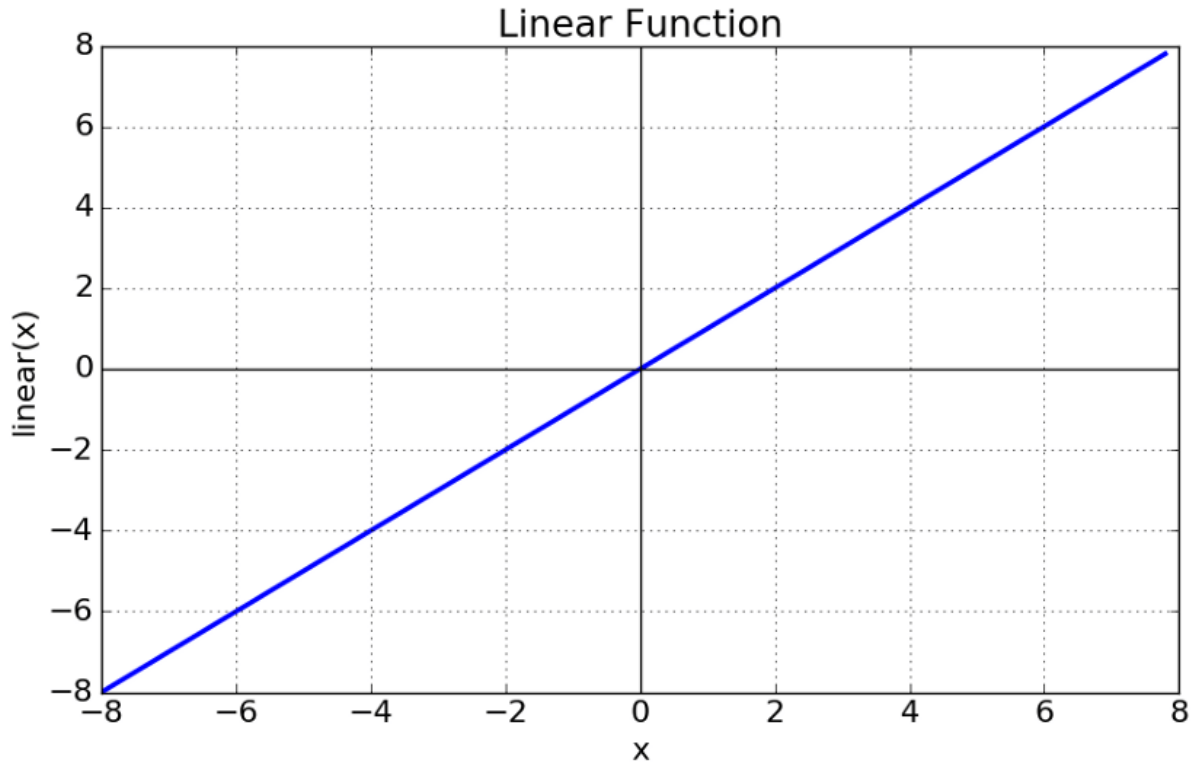
It is merely a thing procedure that is used to obtain a node's output. It also goes by the name Transfer Function.

The two main categories of activation functions are:

- Linear Activation Function
- Non-linear Activation Functions

Linear Activation Function

As can be observed, the functional is linear or linear. Therefore, no region will be employed to restrict the functions' output.



The normal data input to neural networks is unaffected by the complexity or other factors.

Non-linear Activation Function

The normal data input to neural networks is unaffected by the complexity or other factors.

Activation Function

- **Linear Function**

Equation: A linear function's equation, which is y = x, is similar to the eqn of a single direction.

The ultimate activation function of the last layer is nothing more than a linear function of input from the first layer, regardless of how many levels we have if they are all linear in nature. -inf to +inf is the range.

Uses: The output layer is the only location where the activation function's function is applied.

If we separate a linear function to add non-linearity, the outcome will no longer depend on the input "x," the function will become fixed, and our algorithm won't exhibit any novel behaviour.

A good example of a regression problem is determining the cost of a house. We can use linear activation at the output layer since the price of a house may have any huge or little value. The neural network's hidden layers must perform some sort of non-linear function even in this circumstance.

- **Sigmoid Function**

It is a functional that is graphed in a "S" shape.

A is equal to 1/(1 + e-x).

Non-linear in nature. Observe that while Y values are fairly steep, X values range from -2 to 2. To put it another way, small changes in x also would cause significant shifts in the value of Y. spans from 0 to 1.

Uses: Sigmoid function is typically employed in the output nodes of a classi?cation, where the result may only be either 0 or 1. Since the value for the sigmoid function only ranges from 0 to 1, the result can be easily anticipated to be 1 if the value is more than 0.5 and 0 if it is not.

- **Tanh Function**

The activation that consistently outperforms sigmoid function is known as tangent hyperbolic function. It's actually a sigmoid function that has been mathematically adjusted. Both are comparable to and derivable from one another.

```
f(x) = tanh(x) = 2/(1 + e^-2x) - 1
OR
tanh(x) = 2 * sigmoid(2x) - 1
```

Range of values: -1 to +1. non-linear nature

Uses: - Since its values typically range from -1 to 1, the mean again for hidden layer of a neural network will be 0 or very near to it. This helps to centre the data by getting the mean close to 0. This greatly facilitates learning for the following layer.

Equation:

max A(x) (0, x). If x is positive, it outputs x; if not, it outputs 0.

Value Interval: [0, inf]

Nature: non-linear, which allows us to simply backpropagate the mistakes and have the ReLU function activate many layers of neurons.

Uses: Because ReLu includes simpler mathematical processes than tanh and sigmoid, it requires less computer time to run. The system is sparse and efficient for computation since only a limited number of neurons are activated at any given time.

Simply said, RELU picks up information considerably more quickly than sigmoid and Tanh functions.

- **ReLU (Rectified Linear Unit) Activation Function**

Currently, the ReLU is the activation function that is employed the most globally. Since practically all convolutional neural networks and deep learning systems employ it.

The derivative and the function are both monotonic.

However, the problem is that all negative values instantly become zero, which reduces the model's capacity to effectively fit or learn from the data. This means that any negative input to a ReLU activation function immediately becomes zero in the graph, which has an impact on the final graph by improperly mapping the negative values.

- **Softmax Function**

Although it is a subclass of the sigmoid function, the softmax function comes in handy when dealing with multiclass classification issues.

Used frequently when managing several classes. In the output nodes of image classification issues, the softmax was typically present. The softmax function would split by the sum of the outputs and squeeze all outputs for each category between 0 and 1.

The output unit of the classifier, where we are actually attempting to obtain the probabilities to determine the class of each input, is where the softmax function is best applied.

The usual rule of thumb is to utilise RELU, which is a usual perceptron in hidden layers and is employed in the majority of cases these days, if we really are unsure of what encoder to apply.

A very logical choice for the output layer is the sigmoid function if your input is for binary classification. If our output involves multiple classes, Softmax can be quite helpful in predicting the odds for each class.