Group A

Assignment No: 1

Title of the Assignment: Write a program non-recursive and recursive program to calculate Fibonacci numbers and analyze their time and space complexity.

Objective of the Assignment: Students should be able to perform non-recursive and recursive programs to calculate Fibonacci numbers and analyze their time and space complexity.

Prerequisite:

1. Basic of Python or Java Programming
2. Concept of Recursive and Non-recursive functions
3. Execution flow of calculate Fibonacci numbers
4. Basic of Time and Space complexity

Contents for Theory:

1. **Introduction to Fibonacci numbers**
2. **Time and Space complexity**

Introduction to Fibonacci numbers

- The Fibonacci series, named after Italian mathematician Leonardo Pisano Bogollo, laterknown as Fibonacci, is a series (sum) formed by Fibonacci numbers denoted as Fn. The numbers in Fibonacci sequence are given as: 0, 1, 1, 2, 3, 5, 8, 13, 21, 38, . . .
- In a Fibonacci series, every term is the sum of the preceding two terms, starting from 0 and 1 as first and second terms. In some old references, the term '0' might be omitted.

What is the Fibonacci Series?

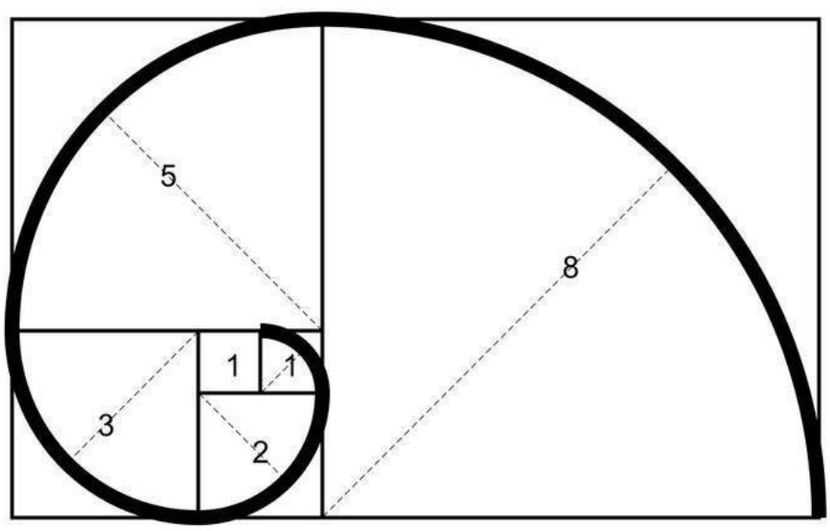
- The Fibonacci series is the sequence of numbers (also called Fibonacci numbers), where every number is the sum of the preceding two numbers, such that the first two terms are '0' and '1'.
- In some older versions of the series, the term '0' might be omitted. A Fibonacci series can thus be given as, 0, 1, 1, 2, 3, 5, 8, 13, 21, 34, . . . It can be thus be observed that every term can be calculated by adding the two terms before it.
- Given the first term, F0 and second term, F1 as '0' and '1', the third term here can be given as, F2 = 0 + 1 = 1

Similarly,

F3 = 1 + 1 = 2

F4 = 2 + 1 = 3

Given a number n, print n-th Fibonacci Number.



Fibonacci Sequence Formula

The Fibonacci sequence of numbers ‑Fn‖ is defined using the recursive relation with the seed values F0=0 and F1=1:

Fn = Fn-1+Fn-2

Here, the sequence is defined using two different parts, such as kick-off and recursive relation.

The kick-off part is F0=0 and F1=1.

The recursive relation part is Fn = Fn-1+Fn-2.

It is noted that the sequence starts with 0 rather than 1. So, F5 should be the 6th term of the sequence.

Examples:

Input : n = 2

Output : 1

Input : n = 9

Output : 34

The list of Fibonacci numbers are calculated as follows:

F_n	**Fibonacci Number**
0	0
1	1
2	1
3	2
4	3
5	5
6	8
7	13
8	21
9	34
… and so on.	… and so on.

Method 1 (Use Non-recursion)

A simple method that is a direct recursive implementation of mathematical recurrence relation is given above.

First, we'll store 0 and 1 in $F[0]$ and $F[1]$, respectively.
Next, we'll iterate through array positions 2 to $n-1$. At each position i, we store the sum of the two preceding array values in $F[i]$.

Finally, we return the value of $F[n-1]$, giving us the number at position n in the sequence.

Here's a visual representation of this process:

```
# Program to display the Fibonacci sequence up to n-th term

nterms = int(input("How many terms? "))

# first two terms

n1, n2 = 0, 1

count = 0

# check if the number of terms is valid

if nterms <= 0:

   print("Please enter a positive integer")

# if there is only one term, return n1

elif nterms == 1:

   print("Fibonacci sequence upto",nterms,":")

   print(n1)

# generate fibonacci sequence
else:

   print("Fibonacci sequence:")

   while count < nterms:

      print(n1)

      nth = n1 + n2

      # update values

      n1 = n2

      n2 = nth

      count += 1
```

Output

```
How many terms? 7

Fibonacci sequence:
0
1
1
2
3
5
8
```

Time and Space Complexity of Space Optimized Method

- The time complexity of the Fibonacci series is **T(N) i.e, linear**. We have to find the sum of two terms and it is repeated n times depending on the value of n.
- The space complexity of the Fibonacci series using dynamic programming is **O(1)**.

Time Complexity and Space Complexity of Dynamic Programming

- The time complexity of the above code is **T(N) i.e, linear**. We have to find the sum of two terms and it is repeated n times depending on the value of n.
- The space complexity of the above code is **O(N)**.

Method 2 (Use Recursion)

Let‘s start by defining F(n) as the function that returns the value of Fn.

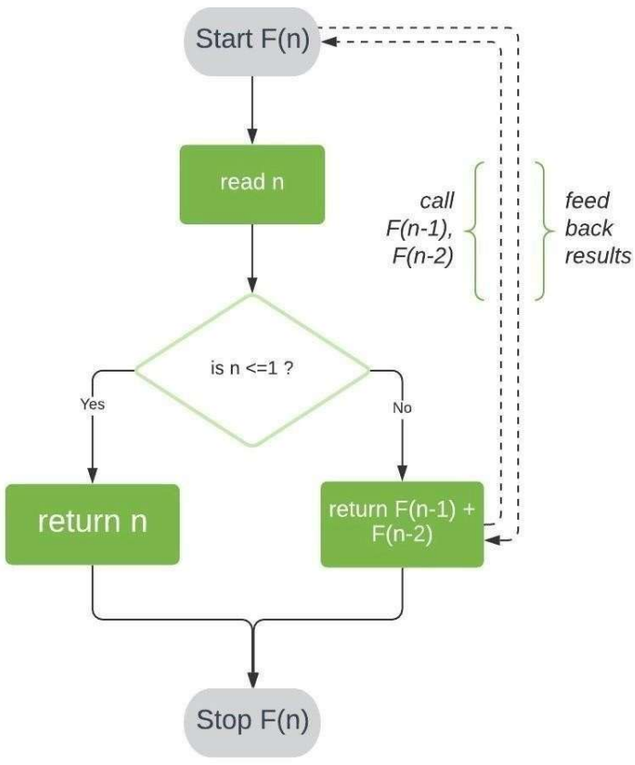
To evaluate *F*(*n*) for *n* > 1, we can reduce our problem into two smaller problems of the same kind: *F*(*n*-1) and *F*(*n*-2). We can further reduce *F*(*n*-1) and *F*(*n*-2) to *F*((*n*-1)-1) and *F*((*n*-1)-2); and *F*((*n*-2)-1) and *F*((*n*-2)-2), respectively.

If we repeat this reduction, we‘ll eventually reach our known base cases and, thereby, obtain a solution to *F*(*n*).

Employing this logic, our algorithm for *F*(*n*) will have two steps:

1. Check if $n \leq 1$. If so, return n.
2. Check if $n > 1$. If so, call our function F with inputs n-1 and n-2, and return the sum of the two results.

Here‘s a visual representation of this algorithm:



```
# Python program to display the Fibonacci sequence

def recur_fibo(n):

   if n <= 1:

      return n

   else:

      return(recur_fibo(n-1) + recur_fibo(n-2))

nterms = 7

# check if the number of terms is valid

if nterms <= 0:

   print("Plese enter a positive integer")

else:

   print("Fibonacci sequence:")

   for i in range(nterms):

      print(recur_fibo(i))
```

Output

```
Fibonacci sequence:

0

1

1

2

3

5

8
```

Time and Space Complexity

- The time complexity of the above code is **T(2^N) i.e, exponential**.

- The Space complexity of the above code is **O(N) for a recursive series.**

Method	Time complexity	Space complexity
Using recursion	**T(n) = T(n-1) + T(n-2)**	**O(n)**
Using DP	**O(n)**	**O(1)**
Space optimization of DP	**O(n)**	**O(1)**
Using the power of matrix method	**O(n)**	**O(1)**
Optimized matrix method	**O(log n)**	**O(log n)**
Recursive method in O(log n) time	**O(log n)**	**O(n)**
Using direct formula	**O(log n)**	**O(1)**
DP using memoization	**O(n)**	**O(1)**

Applications of Fibonacci Series

The Fibonacci series finds application in different fields in our day-to-day lives. The different patterns found in a varied number of fields from nature, to music, and to the human body follow the Fibonacci series. Some of the applications of the series are given as,

- It is used in the grouping of numbers and used to study different other special mathematical sequences.
- It finds application in Coding (computer algorithms, distributed systems, etc). For example, Fibonacci series are important in the computational run-time analysis of Euclid's algorithm, used for determining the GCF of two integers.
- It is applied in numerous fields of science like quantum mechanics, cryptography, etc.
- In finance market trading, Fibonacci retracement levels are widely used in technical analysis.

Conclusion- In this way we have explored Concept of Fibonacci series using recursive and non recursive method and also learn time and space complexity

Assignment Question

1. **What is the Fibonacci Sequence of numbers?**
2. **How do the Fibonacci work?**
3. **What is the Golden Ratio?**
4. **What is the Fibonacci Search technique?**
5. **What is the real application for Fibonacci series**

Reference link

- https://www.scaler.com/topics/fibonacci-series-in-c/
- https://www.baeldung.com/cs/fibonacci-computational-complexity

Group A

Assignment No: 2

Title of the Assignment: Write a program to implement Huffman Encoding using a greedy strategy.

Objective of the Assignment: Students should be able to understand and solve Huffman Encoding using greedy method

Prerequisite:

1. Basic of Python or Java Programming
2. Concept of Greedy method
3. Huffman Encoding concept

Contents for Theory:

1. **Greedy Method**
2. **Huffman Encoding**
3. **Example solved using huffman encoding**

What is a Greedy Method?

- A greedy algorithm is an approach for solving a problem by selecting the best option available at the moment. It doesn't worry whether the current best result will bring the overall optimal result.
- The algorithm never reverses the earlier decision even if the choice is wrong. It works in a top-down approach.
- This algorithm may not produce the best result for all the problems. It's because it always goes for the local best choice to produce the global best result.

Advantages of Greedy Approach

- The algorithm is **easier to describe**.
- This algorithm can **perform better** than other algorithms (but, not in all cases).

Drawback of Greedy Approach

- As mentioned earlier, the greedy algorithm doesn't always produce the optimal solution. This is the major disadvantage of the algorithm
- For example, suppose we want to find the longest path in the graph below from root to leaf.

Greedy Algorithm

1. To begin with, the solution set (containing answers) is empty.
2. At each step, an item is added to the solution set until a solution is reached.
3. If the solution set is feasible, the current item is kept.
4. Else, the item is rejected and never considered again.

Huffman Encoding

- Huffman Coding is a technique of compressing data to reduce its size without losing any of the details. It was first developed by David Huffman.
- Huffman Coding is generally useful to compress the data in which there are frequently occurring

characters.

- Huffman Coding is a famous Greedy Algorithm.
- It is used for the lossless compression of data.
- It uses variable length encoding.
- It assigns variable length code to all the characters.
- The code length of a character depends on how frequently it occurs in the given text.
- The character which occurs most frequently gets the smallest code.
- The character which occurs least frequently gets the largest code.
- It is also known as **Huffman Encoding**.

Prefix Rule-

- Huffman Coding implements a rule known as a prefix rule.
- This is to prevent the ambiguities while decoding.
- It ensures that the code assigned to any character is not a prefix of the code assigned to any other character

Major Steps in Huffman Coding-

There are two major steps in Huffman Coding-

1. Building a Huffman Tree from the input characters.
2. Assigning code to the characters by traversing the Huffman Tree.

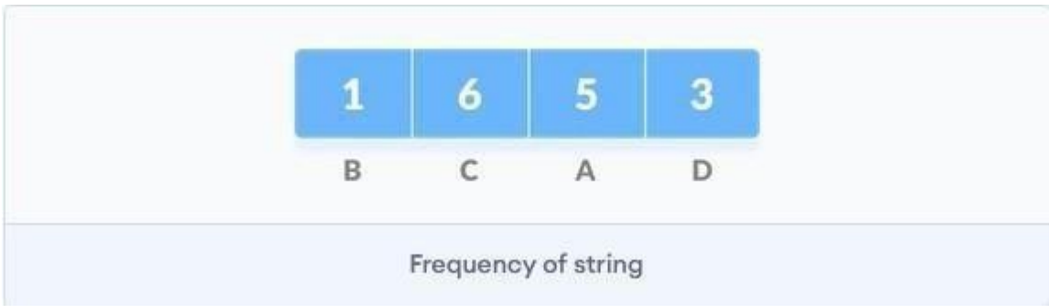
How does Huffman Coding work?

Suppose the string below is to be sent over a network.

- Each character occupies 8 bits. There are a total of 15 characters in the above string. Thus, a total of 8 * 15 = 120 bits are required to send this string.
- Using the Huffman Coding technique, we can compress the string to a smaller size.

- Huffman coding first creates a tree using the frequencies of the character and then generates code for each character.
- Once the data is encoded, it has to be decoded. Decoding is done using the same tree.
- Huffman Coding prevents any ambiguity in the decoding process using the concept of **prefix code** ie. a code associated with a character should not be present in the prefix of any other code. The tree created above helps in maintaining the property.
- Huffman coding is done with the help of the following steps.

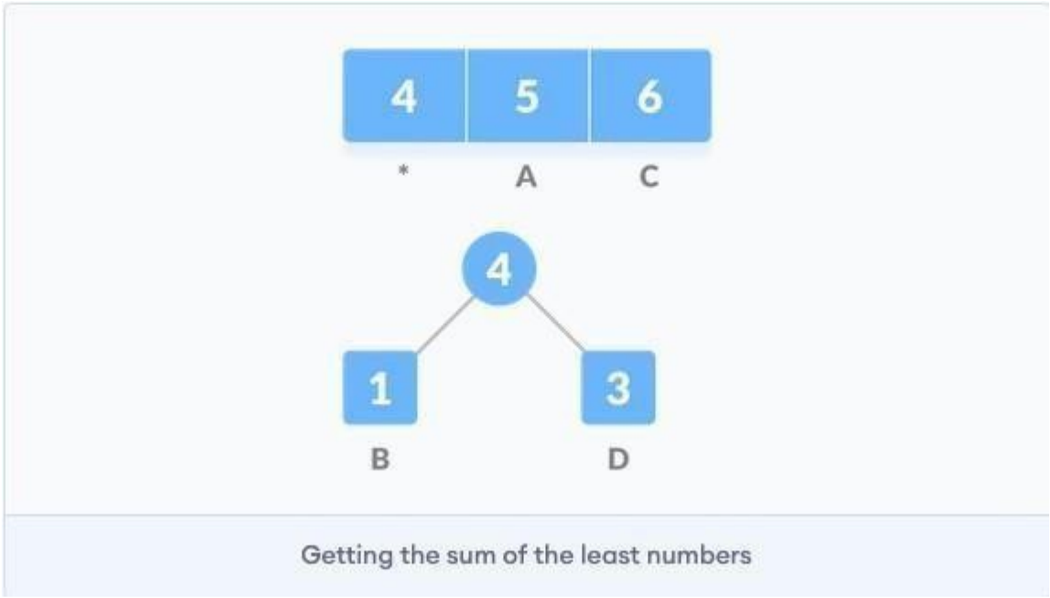
1. Calculate the frequency of each character in the string.



2. Sort the characters in increasing order of the frequency. These are stored in a priority queue Q.

3. Make each unique character as a leaf node.

4. Create an empty node z. Assign the minimum frequency to the left child of z and assign the second minimum frequency to the right child of z. Set the value of the z as the sum of the above two minimum frequencies.

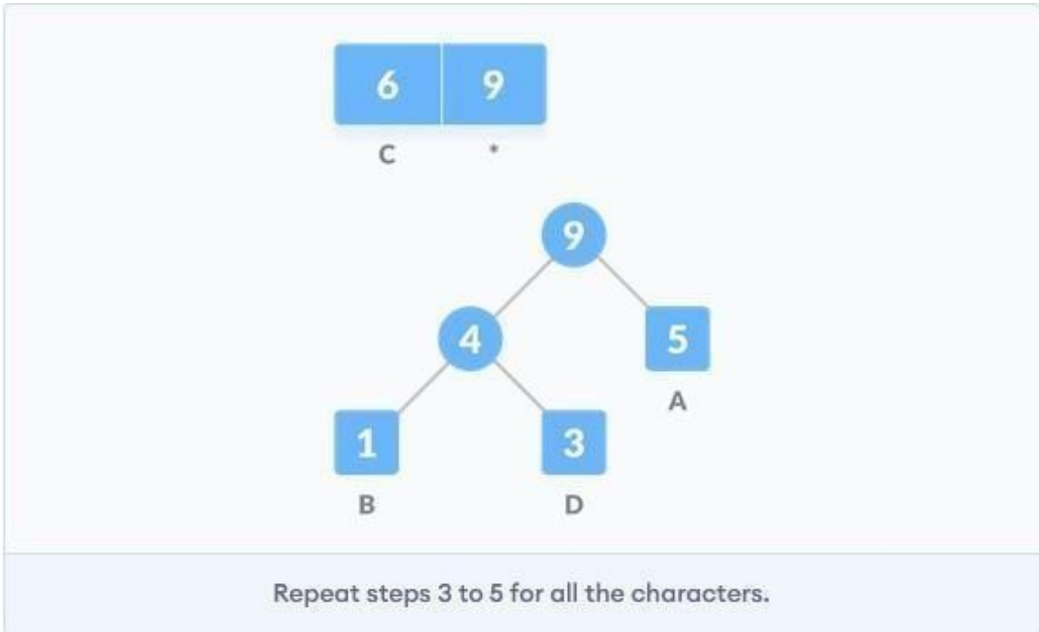


Getting the sum of the least numbers

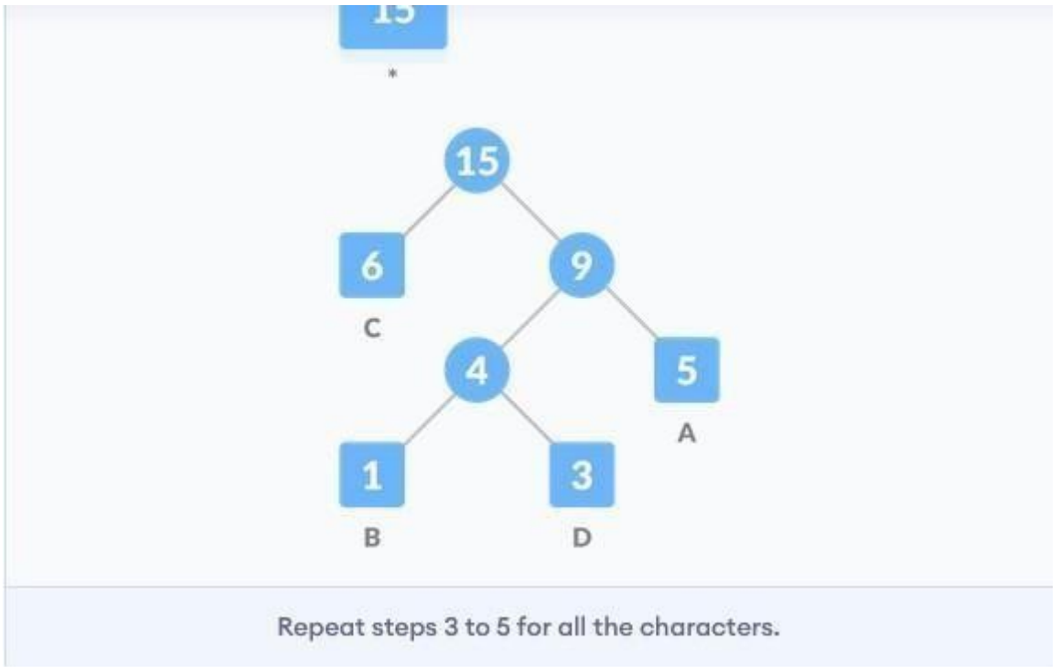
5. Remove these two minimum frequencies from Q and add the sum into the list of frequencies (* denote the internal nodes in the figure above).

6. Insert node z into the tree.

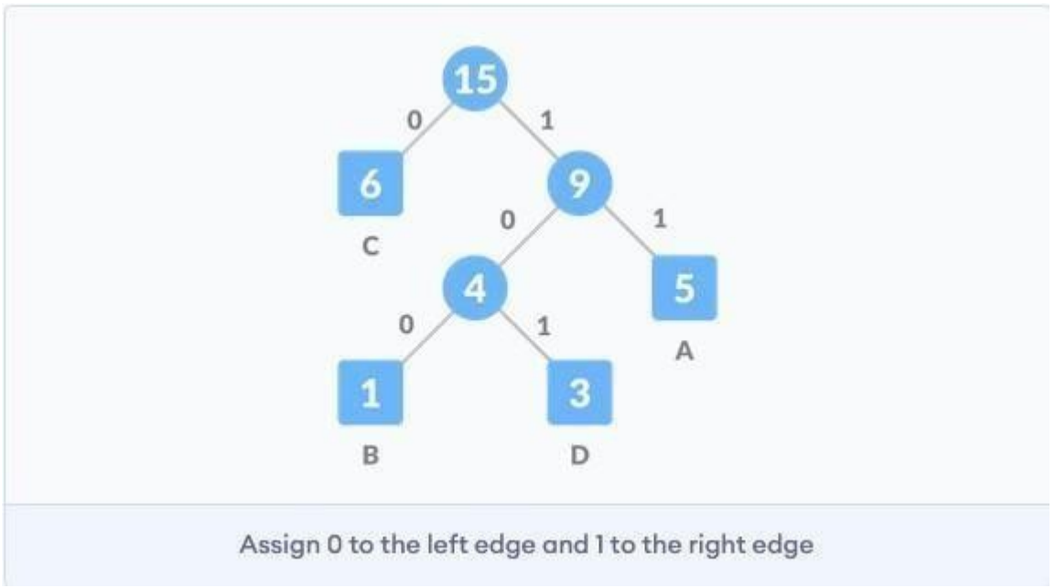
7. Repeat steps 3 to 5 for all the characters.



Repeat steps 3 to 5 for all the characters.



8. For each non-leaf node, assign 0 to the left edge and 1 to the right edge



For sending the above string over a network, we have to send the tree as well as the above compressed-code. The total size is given by the table below.

Character	Frequency	Code	Size
A	5	11	5*2 = 10
B	1	100	1*3 = 3
C	6	0	6*1 = 6
D	3	101	3*3 = 9
4 * 8 = 32 bits	15 bits		28 bits

Without encoding, the total size of the string was 120 bits. After encoding the size is reduced to 32 + 15 + 28 = 75.

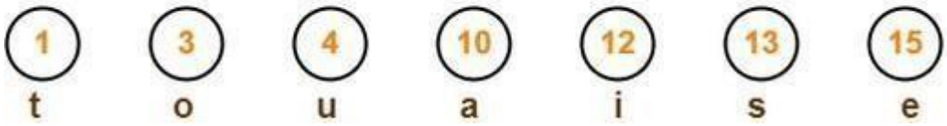
Example:

A file contains the following characters with the frequencies as shown. If Huffman Coding is used for data compression, determine-

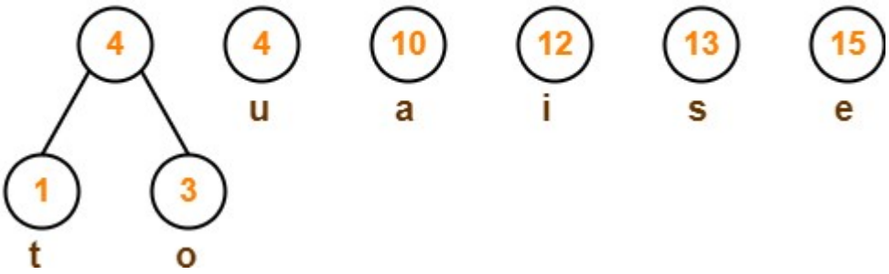
1. Huffman Code for each character
2. Average code length
3. Length of Huffman encoded message (in bits)

Characters	Frequencies
a	10
e	15
i	12
o	3
u	4
s	13
t	1

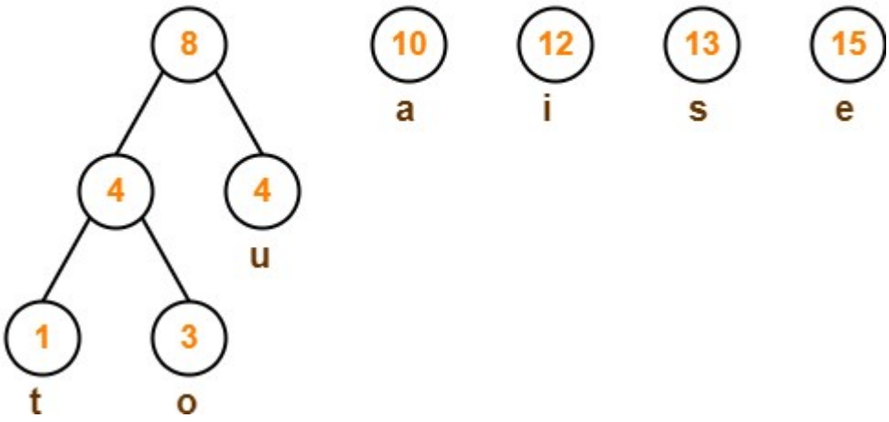
Step-01:



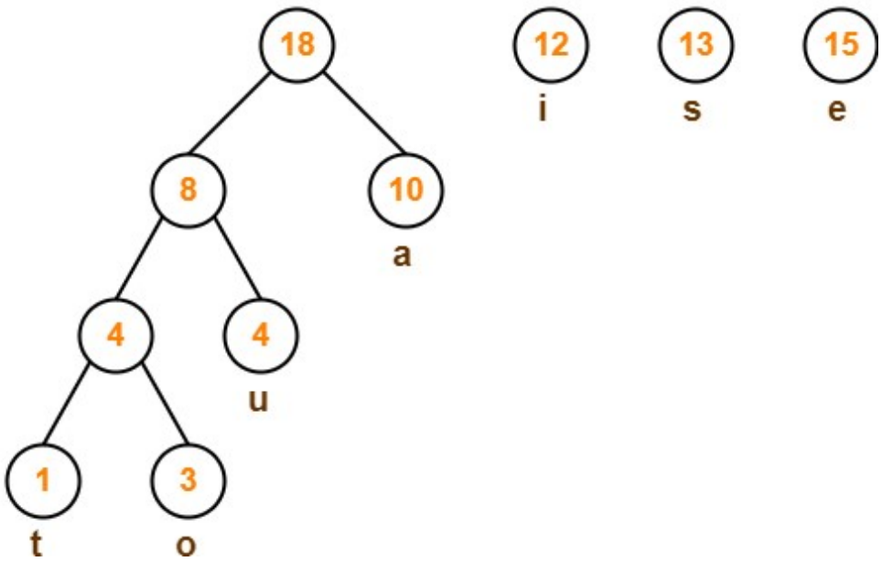
Step-02:



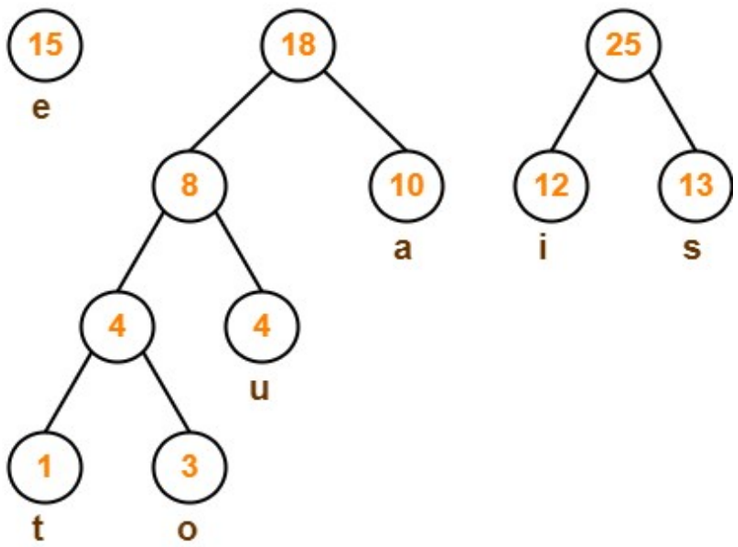
Step-03:



Step-04:



Step-06: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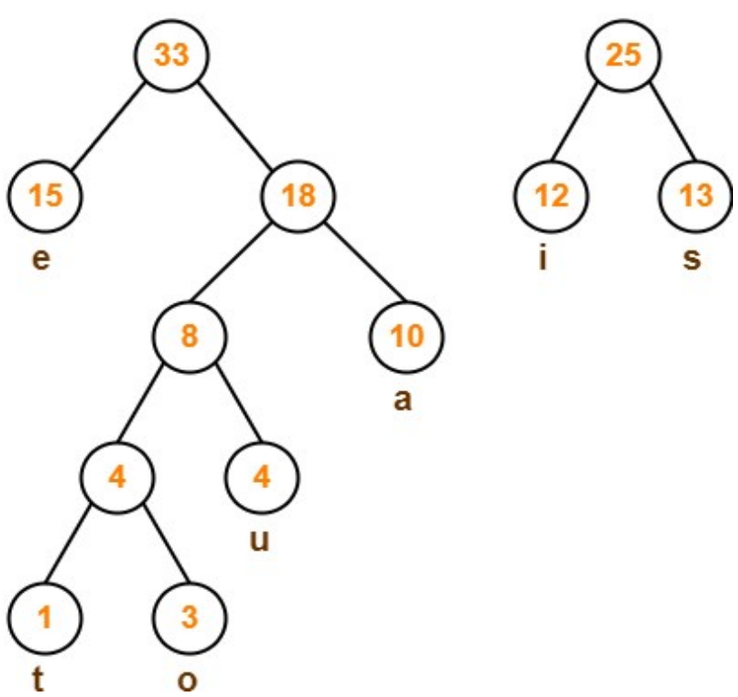
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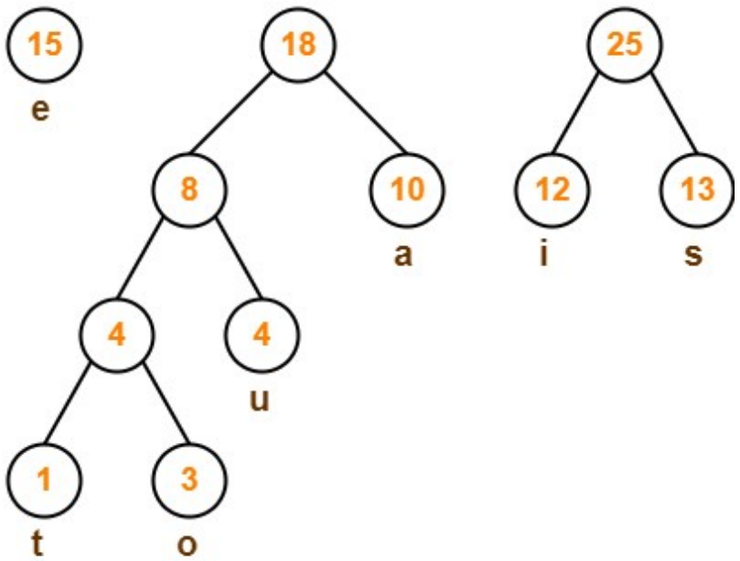
Step-06: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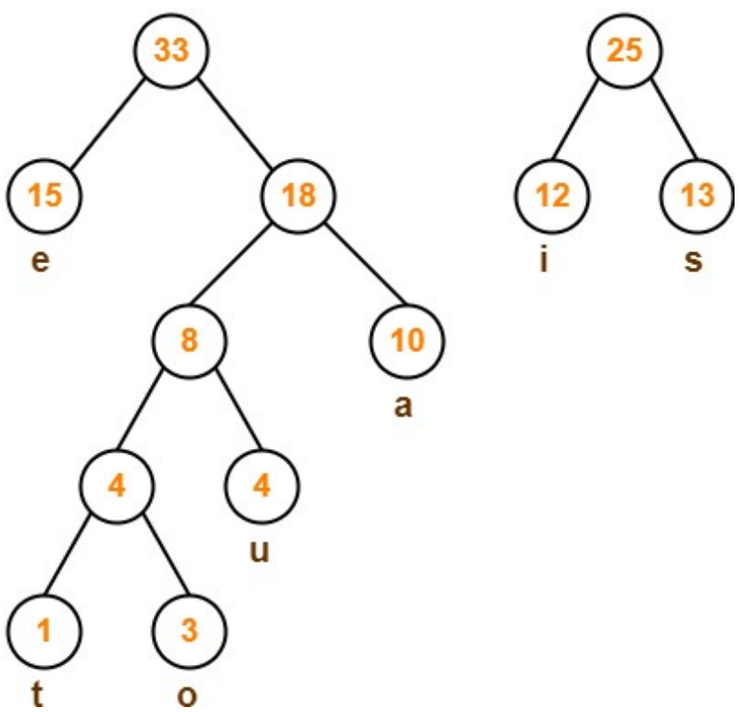
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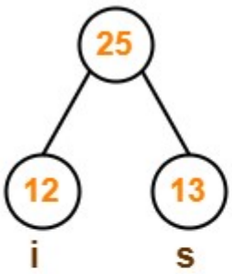
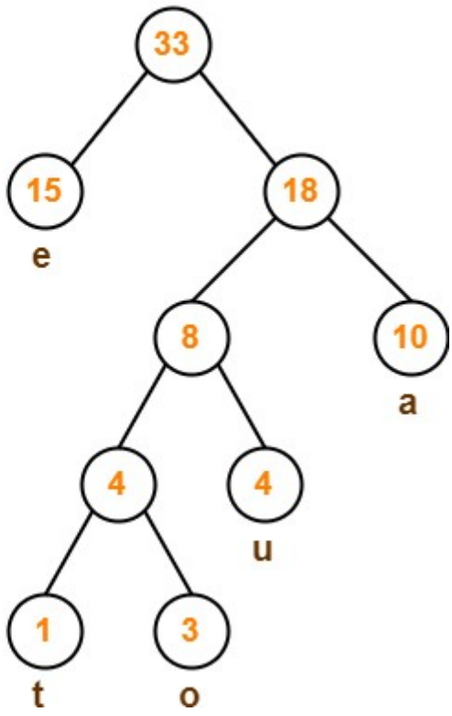
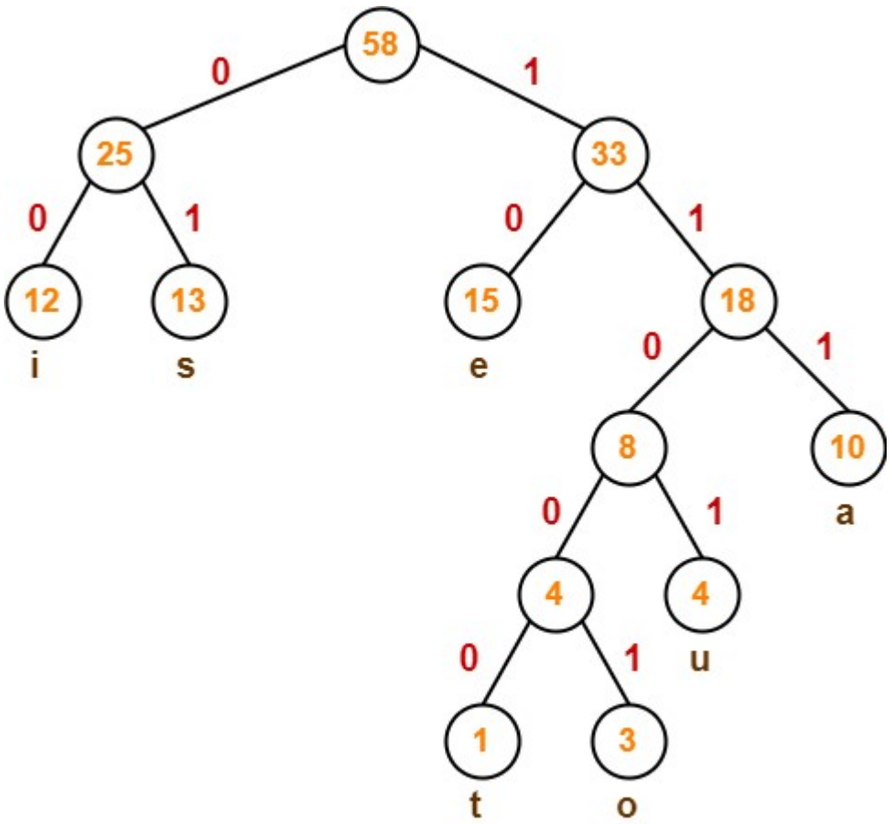
Step-07:







Huffman Tree

After assigning weight to all the edges, the modified Huffman Tree is shown above

To write Huffman Code for any character, traverse the Huffman Tree from root node to the leaf node of that character.

Following this rule, the Huffman Code for each character is-

a = 111

e = 10

i = 00

o = 11001

u = 1101

s = 01

t = 11000

Time Complexity-

The time complexity analysis of Huffman Coding is as follows-

- extractMin( ) is called 2 x (n-1) times if there are n nodes.
- As extractMin( ) calls minHeapify( ), it takes O(logn) time.

Thus, Overall time complexity of Huffman Coding becomes **O(nlogn)**.

Code :-

```
class Node:
    def __init__(self, prob, symbol, left=None, right=None):
        # probability of symbol
        self.prob = prob

        # symbol
        self.symbol = symbol

        # left node
        self.left = left

        # right node
        self.right = right

        # tree direction (0/1)
        self.code = ''
```

```
""" A helper function to calculate the probabilities of symbols in given data"""
def Calculate_Probability(data):
    symbols = dict()
    for element in data:
        if symbols.get(element) == None:
            symbols[element] = 1
        else:
            symbols[element] += 1
    return symbols
```

```
""" A helper function to obtain the encoded output"""
def Output_Encoded(data, coding):
    encoding_output = []
    for c in data:
        print(coding[c], end = '')
        encoding_output.append(coding[c])

    string = ''.join([str(item) for item in encoding_output])
    return string
```

```
""" A helper function to calculate the space difference between compressed and non co
def Total_Gain(data, coding):
    before_compression = len(data) * 8 # total bit space to stor the data before compr
    after_compression = 0
    symbols = coding.keys()
    for symbol in symbols:
        count = data.count(symbol)
        after_compression += count * len(coding[symbol]) #calculate how many bit is r
    print("Space usage before compression (in bits):", before_compression)
    print("Space usage after compression (in bits):",  after_compression)
```

```python
def Huffman_Encoding(data):
    symbol_with_probs = Calculate_Probability(data)
    symbols = symbol_with_probs.keys()
    probabilities = symbol_with_probs.values()
    print("symbols: ", symbols)
    print("probabilities: ", probabilities)

    nodes = []

    # converting symbols and probabilities into huffman tree nodes
    for symbol in symbols:
        nodes.append(Node(symbol_with_probs.get(symbol), symbol))

    while len(nodes) > 1:
        # sort all the nodes in ascending order based on their probability
        nodes = sorted(nodes, key=lambda x: x.prob)
        # for node in nodes:
        #       print(node.symbol, node.prob)

        # pick 2 smallest nodes
        right = nodes[0]
        left = nodes[1]

        left.code = 0
        right.code = 1

        # combine the 2 smallest nodes to create new node
        newNode = Node(left.prob+right.prob, left.symbol+right.symbol, left, right)

        nodes.remove(left)
        nodes.remove(right)
        nodes.append(newNode)

    huffman_encoding = Calculate_Codes(nodes[0])
    print(huffman_encoding)
    Total_Gain(data, huffman_encoding)
    encoded_output = Output_Encoded(data,huffman_encoding)
    print("Encoded output:", encoded_output)
    return encoded_output, nodes[0]
```

Output

```
AAAAAAABCCCCCCDDEEEEE
symbols:  dict_keys(['A', 'B', 'C', 'D', 'E'])
probabilities:  dict_values([7, 1, 6, 2, 5])
symbols with codes {'A': '00', 'C': '01', 'E': '10', 'D': '110', 'B': '111'}
Space usage before compression (in bits): 168
Space usage after compression (in bits): 45
Encoded output 00000000000000111010101010101110110101010101010
```

Conclusion- In this way we have explored Concept ofHuffman Encoding using greedy method

Assignment Question

1. What is Huffman Encoding?
2. How many bits may be required for encoding the message _mississippi‘?
3. Which tree is used in Huffman encoding?Give one Example
4. Why Huffman coding is lossless compression?

Reference link

- https://towardsdatascience.com/huffman-encoding-python-implementation-8448c3654328
- https://www.programiz.com/dsa/huffman-coding#cpp-code
- https://www.gatevidyalay.com/tag/huffman-coding-example-ppt/

Group A

Assignment No: 3

Title of the Assignment: Write a program to solve a fractional Knapsack problem using a greedy method.

Objective of the Assignment: Students should be able to understand and solve fractional Knapsack problems using a greedy method.

Prerequisite:

1. Basic of Python or Java Programming
2. Concept of Greedy method
3. fractional Knapsack problem

Contents for Theory:

1. **Greedy Method**
2. **Fractional Knapsack problem**
3. **Example solved using fractional Knapsack problem**

What is a Greedy Method?

- A greedy algorithm is an approach for solving a problem by selecting the best option available at the moment. It doesn't worry whether the current best result will bring the overall optimal result.
- The algorithm never reverses the earlier decision even if the choice is wrong. It works in a top-down approach.
- This algorithm may not produce the best result for all the problems. It's because it always goes for the local best choice to produce the global best result.

Advantages of Greedy Approach

- The algorithm is **easier to describe**.
- This algorithm can **perform better** than other algorithms (but, not in all cases).

Drawback of Greedy Approach

- As mentioned earlier, the greedy algorithm doesn't always produce the optimal solution. This is the major disadvantage of the algorithm
- For example, suppose we want to find the longest path in the graph below from root to leaf.

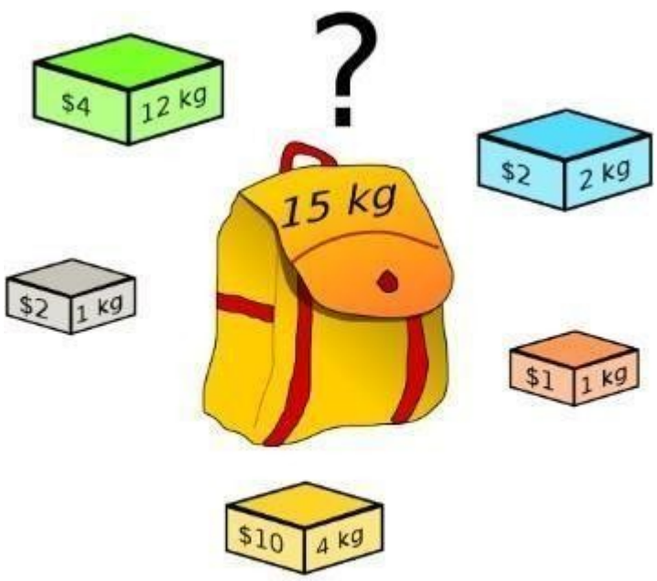
Greedy Algorithm

1. To begin with, the solution set (containing answers) is empty.
2. At each step, an item is added to the solution set until a solution is reached.
3. If the solution set is feasible, the current item is kept.
4. Else, the item is rejected and never considered again.

Knapsack Problem

You are given the following-

- A knapsack (kind of shoulder bag) with limited weight capacity.
- Few items each having some weight and value.



Knapsack Problem

The problem states-

Which items should be placed into the knapsack such that-

- The value or profit obtained by putting the items into the knapsack is maximum.
- And the weight limit of the knapsack does not exceed.

Knapsack Problem Variants

Knapsack problem has the following two variants-

1. Fractional Knapsack Problem
2. 0/1 Knapsack Problem

Fractional Knapsack Problem-

In Fractional Knapsack Problem,

- As the name suggests, items are divisible here.
- We can even put the fraction of any item into the knapsack if taking the complete item is not

possible.

- It is solved using the Greedy Method.

Fractional Knapsack Problem Using Greedy Method-

Fractional knapsack problem is solved using greedy method in the following steps-

Step-01:

For each item, compute its value / weight ratio.

Step-02:

Arrange all the items in decreasing order of their value / weight ratio.

Step-03:

Start putting the items into the knapsack beginning from the item with the highest ratio.

Put as many items as you can into the knapsack.

Problem-

For the given set of items and knapsack capacity = 60 kg, find the optimal solution for the fractional knapsack problem making use of greedy approach.

Item	Weight	Value
1	5	30
2	10	40
3	15	45
4	22	77
5	25	90

n = 5

w = 60 kg

(w1, w2, w3, w4, w5) = (5, 10, 15, 22, 25)

(b1, b2, b3, b4, b5) = (30, 40, 45, 77, 90)

Solution-

Step-01:

Compute the value / weight ratio for each item-

Items	Weight	Value	Ratio
1	5	30	6
2	10	40	4
3	15	45	3
4	22	77	3.5
5	25	90	3.6

Step-02:

Sort all the items in decreasing order of their value / weight ratio-

I1 I2 I5 I4 I3

(6) (4) (3.6) (3.5) (3)

Step-03:

Start filling the knapsack by putting the items into it one by one.

Knapsack Weight	Items in Knapsack	Cost
60	Ø	0
55	I1	30
45	I1, I2	70
20	I1, I2, I5	160

Now,

- Knapsack weight left to be filled is 20 kg but item-4 has a weight of 22 kg.
- Since in fractional knapsack problem, even the fraction of any item can be taken.
- So, knapsack will contain the following items-

< I1 , I2 , I5 , (20/22) I4 >

Total cost of the knapsack

= 160 + (20/22) x 77

= 160 + 70

= 230 units

Time Complexity-

- The main time taking step is the sorting of all items in decreasing order of their value / weight ratio.
- If the items are already arranged in the required order, then while loop takes O(n) time.
- The average time complexity of Quick Sort is O(nlogn).
- Therefore, total time taken including the sort is O(nlogn).

Code:-

```
class Item:
        def__init_(self, value, weight):
                self.value = value
                self.weight = weight

def fractionalKnapsack(W, arr):

        # Sorting Item on basis of ratio
        arr.sort(key=lambda x: (x.value/x.weight), reverse=True)

        # Result(value in Knapsack)
        finalvalue = 0.0

        # Looping through all Items
        for item in arr:

                # If adding Item won't overflow,
                # add it completely
                if item.weight <= W:
                        W -= item.weight
                        finalvalue += item.value

                # If we can't add current Item,
                # add fractional part of it
                else:
                        finalvalue += item.value * W / item.weight
                        break

        # Returning final value
        return finalvalue


# Driver Code
if__name__== "_main_":

        W = 50
        arr = [Item(60, 10), Item(100, 20), Item(120, 30)]

        # Function call
        max_val = fractionalKnapsack(W, arr)
        print(max_val)
```

Output

Maximum value we can obtain = 24

CONCLUSION: In this way we have explored Concept of Fractional Knapsack using greedy method

Assignment Question

1. **What is Greedy Approach?**
2. **Explain concept of fractional knapsack**
3. **Difference between Fractional and 0/1 Knapsack**
4. **Solve one example based on Fractional knapsack(Other than Manual)**

Reference link

- https://www.gatevidyalay.com/fractional-knapsack-problem-using-greedy-approach/

Group A

Assignment No: 4

Title of the Assignment: Write a program to solve a 0-1 Knapsack problem using dynamic programming or branch and bound strategy.

Objective of the Assignment: Students should be able to understand and solve 0-1 Knapsack problem using dynamic programming

Prerequisite:

1. Basic of Python or Java Programming
2. Concept of Dynamic Programming
3. 0/1 Knapsack problem

Contents for Theory:

1. **Greedy Method**
2. **0/1 Knapsack problem**
3. **Example solved using 0/1 Knapsack problem**

What is Dynamic Programming?

- Dynamic Programming is also used in optimization problems. Like divide-and-conquer method, Dynamic Programming solves problems by combining the solutions of subproblems.
- Dynamic Programming algorithm solves each sub-problem just once and then saves its answer in a table, thereby avoiding the work of re-computing the answer every time.
- Two main properties of a problem suggest that the given problem can be solved using Dynamic Programming. These properties are **overlapping sub-problems and optimal substructure**.
- Dynamic Programming also combines solutions to sub-problems. It is mainly used where thesolution of one sub-problem is needed repeatedly. The computed solutions are stored in a table, so that these don‘t have to be re-computed. Hence, this technique is needed where overlapping sub- problem exists.
- For example, Binary Search does not have overlapping sub-problem. Whereas recursive program of Fibonacci numbers have many overlapping sub-problems.

Steps of Dynamic Programming Approach

Dynamic Programming algorithm is designed using the following four steps −

- Characterize the structure of an optimal solution.
- Recursively define the value of an optimal solution.
- Compute the value of an optimal solution, typically in a bottom-up fashion.
- Construct an optimal solution from the computed information.

Applications of Dynamic Programming Approach

- Matrix Chain Multiplication
- Longest Common Subsequence
- Travelling Salesman Problem

Knapsack Problem

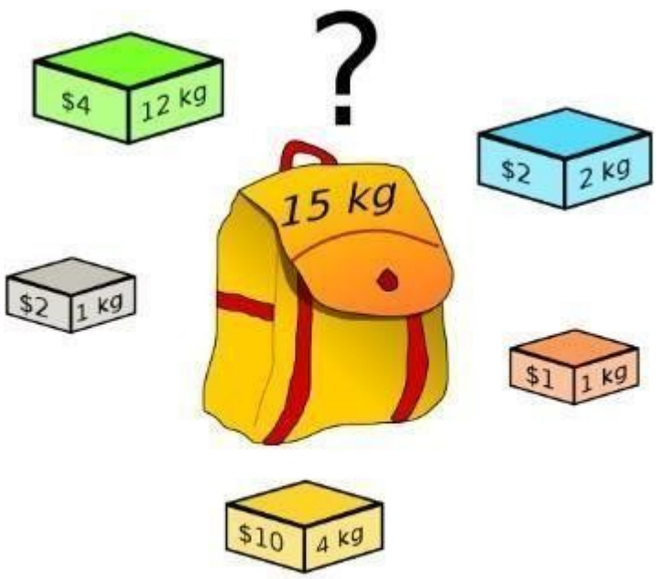
You are given the following-

- A knapsack (kind of shoulder bag) with limited weight capacity.
- Few items each having some weight and value.

The problem states-

Which items should be placed into the knapsack such that-

- The value or profit obtained by putting the items into the knapsack is maximum.
- And the weight limit of the knapsack does not exceed.



Knapsack Problem

Knapsack Problem Variants

Knapsack problem has the following two variants-

1. Fractional Knapsack Problem
2. 0/1 Knapsack Problem

0/1 Knapsack Problem-

In 0/1 Knapsack Problem,

- As the name suggests, items are indivisible here.
- We can not take a fraction of any item.
- We have to either take an item completely or leave it completely.
- It is solved using a dynamic programming approach.

0/1 Knapsack Problem Using Greedy Method-

Consider-

- Knapsack weight capacity = w
- Number of items each having some weight and value = n

0/1 knapsack problem is solved using dynamic programming in the following steps-

Step-01:

- Draw a table say _T' with (n+1) number of rows and (w+1) number of columns.
- Fill all the boxes of 0^{th} row and 0^{th} column with zeroes as shown-

	0	1	2	3	.....	W
0	0	0	0	0	.....	0
1	0					
2	0					
	.....					
n	0					

T-Table

Step-02:

Start filling the table row wise top to bottom from left to right.

Use the following formula-

$$T(i, j) = \max \{ T(i-1, j), value_i + T(i-1, j - weight_i) \}$$

Here, T(i , j) = maximum value of the selected items if we can take items 1 to i and have weight restrictions of j.

- This step leads to completely filling the table.
- Then, value of the last box represents the maximum possible value that can be put into the knapsack.

Step-03:

- To identify the items that must be put into the knapsack to obtain that maximum profit,
- Consider the last column of the table.
- Start scanning the entries from bottom to top.
- On encountering an entry whose value is not same as the value stored in the entry immediately above it, mark the row label of that entry.
- After all the entries are scanned, the marked labels represent the items that must be put into the knapsack

Problem-.

For the given set of items and knapsack capacity = 5 kg, find the optimal solution for the 0/1 knapsack problem making use of a dynamic programming approach.

Item	Weight	Value
1	2	3
2	3	4
3	4	5
4	5	6

n = 4

w = 5 kg

(w1, w2, w3, w4) = (2, 3, 4, 5)

(b1, b2, b3, b4) = (3, 4, 5, 6)

Solution-

Given

- Knapsack capacity (w) = 5 kg
- Number of items (n) = 4

Step-01:

- Draw a table say _T' with (n+1) = 4 + 1 = 5 number of rows and (w+1) = 5 + 1 = 6 number of columns.
- Fill all the boxes of 0^{th} row and 0^{th} column with 0.

	0	1	2	3	4	5
0	0	0	0	0	0	0
1	0					
2	0					
3	0					
4	0					

T-Table

Step-02:

Start filling the table row wise top to bottom from left to right using the formula-

$$T(i, j) = \max \{ T(i-1, j), value_i + T(i-1, j - weight_i) \}$$

Finding T(1,1)-

We have,

- i = 1
- j = 1
- $(value)_i = (value)_1 = 3$
- $(weight)_i = (weight)_1 = 2$

Substituting the values, we get-

$T(1,1) = \max \{ T(1-1, 1), 3 + T(1-1, 1-2) \}$

$T(1,1) = \max \{ T(0,1), 3 + T(0,-1) \}$

$T(1,1) = T(0,1)$ { Ignore T(0,-1) }

$T(1,1) = 0$

Finding T(1,2)-

We have,

- i = 1
- j = 2
- $(value)_i = (value)_1 = 3$
- $(weight)_i = (weight)_1 = 2$

Substituting the values, we get-

T(1,2) = max { T(1-1 , 2) , 3 + T(1-1 , 2-2) }

T(1,2) = max { T(0,2) , 3 + T(0,0) }

T(1,2) = max {0 , 3+0}

T(1,2) = 3

Finding T(1,3)-

We have,

- i = 1
- j = 3
- $(value)_i = (value)_1 = 3$
- $(weight)_i = (weight)_1 = 2$

Substituting the values, we get-

T(1,3) = max { T(1-1 , 3) , 3 + T(1-1 , 3-2) }

T(1,3) = max { T(0,3) , 3 + T(0,1) }

T(1,3) = max {0 , 3+0}

T(1,3) = 3

Finding T(1,4)-

We have,

- i = 1
- j = 4
- $(value)_i = (value)_1 = 3$
- $(weight)_i = (weight)_1 = 2$

Substituting the values, we get-

T(1,4) = max { T(1-1 , 4) , 3 + T(1-1 , 4-2) }

T(1,4) = max { T(0,4) , 3 + T(0,2) }

T(1,4) = max {0 , 3+0}

T(1,4) = 3

Finding T(1,5)-

We have,

- i = 1
- j = 5
- $(value)_i = (value)_1 = 3$
- $(weight)_i = (weight)_1 = 2$

Substituting the values, we get-

T(1,5) = max { T(1-1 , 5) , 3 + T(1-1 , 5-2) }

T(1,5) = max { T(0,5) , 3 + T(0,3) }

T(1,5) = max {0 , 3+0}

T(1,5) = 3

Finding T(2,1)-

We have,

- i = 2
- j = 1
- $(value)_i = (value)_2 = 4$
- (weight)i = (weight)2 = 3

Substituting the values, we get-

T(2,1) = max { T(2-1 , 1) , 4 + T(2-1 , 1-3) }

T(2,1) = max { T(1,1) , 4 + T(1,-2) }

T(2,1) = T(1,1) { Ignore T(1,-2) }

T(2,1) = 0

Finding T(2,2)-

We have,

- i = 2
- j = 2
- $(value)_i = (value)_2 = 4$
- $(weight)_i = (weight)_2 = 3$

Substituting the values, we get-

T(2,2) = max { T(2-1 , 2) , 4 + T(2-1 , 2-3) }

T(2,2) = max { T(1,2) , 4 + T(1,-1) }

T(2,2) = T(1,2) { Ignore T(1,-1) }

T(2,2) = 3

Finding T(2,3)-

We have,

- i = 2
- j = 3
- $(value)_i = (value)_2 = 4$
- $(weight)_i = (weight)_2 = 3$

Substituting the values, we get-

T(2,3) = max { T(2-1 , 3) , 4 + T(2-1 , 3-3) }

T(2,3) = max { T(1,3) , 4 + T(1,0) }

T(2,3) = max { 3 , 4+0 }

T(2,3) = 4

Similarly, compute all the entries.

After all the entries are computed and filled in the table, we get the following table-

	0	1	2	3	4	5
0	0	0	0	0	0	0
1	0	0	3	3	3	3
2	0	0	3	4	4	7
3	0	0	3	4	5	7
4	0	0	3	4	5	7

T-Table

- The last entry represents the maximum possible value that can be put into the knapsack.
- So, maximum possible value that can be put into the knapsack = 7.

Identifying Items To Be Put Into Knapsack

Following Step-04,

- We mark the rows labelled "1" and "2".
- Thus, items that must be put into the knapsack to obtain the maximum value 7 are-

Item-1 and Item-2

Time Complexity-

- Each entry of the table requires constant time $\theta(1)$ for its computation.
- It takes $\theta(nw)$ time to fill $(n+1)(w+1)$ table entries.
- It takes $\theta(n)$ time for tracing the solution since tracing process traces the n rows.
- Thus, overall $\theta(nw)$ time is taken to solve 0/1 knapsack problem using dynamic programming

Code :-

```
# code

# A Dynamic Programming based Python# Programfor 0-1 Knapsack problem # Returns the maximum value that can# be put in a knapsack of capacity W

defknapSack(W, wt, val, n):

dp =[0fori inrange(W+1)]  # Making the dp array
fori inrange(1, n+1):          # taking first i elements

forw inrange(W, 0, -1): # starting from back,so that we alsohave data of

# previous computation when taking i-1
items

ifwt[i-1] <=w:

# finding the maximum value

dp[w]  = max(dp[w],  dp[w-wt[i-1]]+val[i-1])


returndp[W]       # returning the maximum value of knapsack


# Driver code

val =[60, 100, 120]

wt =[10, 20, 30]

W =50

n  =len(val) print(knapSack(W, wt, val, n))
```

Output: 220

Conclusion-In this way we have explored Concept of 0/1 Knapsack using Dynamic approch

Assignment Question

1. **What is Dynamic Approach?**
2. **Explain concept of 0/1 knapsack**
3. **Difference between Dynamic and Branch and Bound Approach.Which is best?**
4. **Solve one example based on 0/1 knapsack(Other than Manual)**

Reference link

- https://www.gatevidyalay.com/0-1-knapsack-problem-using-dynamic-programming-appr oach/
- https://www.youtube.com/watch?v=mMhC9vuA-70
- https://www.tutorialspoint.com/design_and_analysis_of_algorithms/design_and_analysis_of_algorithms_fractional_knapsack.htm

Group A

Assignment No: 5

Title of the Assignment: Design n-Queens matrix having first Queen placed. Use backtracking to place remaining Queens to generate the final n-queen‘s matrix.

Objective of the Assignment: Students should be able to understand and solve n-Queen Problem,and understand basics of Backtracking

Prerequisite:

1. Basic of Python or Java Programming
2. Concept of backtracking method
3. N-Queen Problem

Contents for Theory:

1. **Introduction to Backtracking**
2. **N-Queen Problem**

Introduction to Backtracking

- Many problems are difficult to solve algorithmically. Backtracking makes it possible to solve at least some large instances of difficult combinatorial problems.

Suppose we have to make a series of decisions among various choices, where

- We don‘t have enough information to know what to choose
- Each decision leads to a new set of choices.
- Some sequence of choices (more than one choices) may be a solution to your problem.

What is backtracking?

Backtracking is finding the solution of a problem whereby the solution depends on the previous steps taken. For example, in a maze problem, the solution depends on all the steps you take one-by-one. If any of those steps is wrong, then it will not lead us to the solution. In a maze problem, we first choose a path and continue moving along it. But once we understand that the particular path is incorrect, then we just come back and change it. This is what backtracking basically is.

In backtracking, we first take a step and then we see if this step taken is correct or not i.e., whether it will give a correct answer or not. And if it doesn‘t, then we just come back and change our first step. In general, this is accomplished by recursion. Thus, in backtracking, we first start with a partial sub-solution of the problem (which may or may not lead us to the solution) and then check if we can proceed further with this sub-solution or not. If not, then we just come back and change it.

Thus, the general steps of backtracking are:

- start with a sub-solution
- check if this sub-solution will lead to the solution or not
- If not, then come back and change the sub-solution and continue again

Applications of Backtracking:

- N Queens Problem
- Sum of subsets problem
- Graph coloring
- Hamiltonian cycles.

N queens on NxN chessboard

One of the most common examples of the backtracking is to arrange N queens on an NxN chessboard such that no queen can strike down any other queen. A queen can attack horizontally, vertically, or diagonally. The solution to this problem is also attempted in a similar way. We first place the first queen anywhere arbitrarily and then place the next queen in any of the safe places. We continue this process until the number of unplaced queens becomes zero (a solution is found) or no safe place is left. If no safe place is left, then we change the position of the previously placed queen.

N-Queens Problem:

A classic combinational problem is to place n queens on a n*n chess board so that no two attack, i.,e no two queens are on the same row, column or diagonal.

What is the N Queen Problem?

N Queen problem is the classical Example of backtracking. N-Queen problem is defined as, –given N x N chess board, arrange N queens in such a way that no two queens attack each other by being in the same row, column or diagonal‖.

- For N = 1, this is a trivial case. For N = 2 and N = 3, a solution is not possible. So we start with N = 4 and we will generalize it for N queens

If we take n=4then the problem is called the 4 queens problem.

If we take n=8 then the problem is called the 8 queens problem.

Algorithm

1) Start in the leftmost column
2) If all queens are place return true
3) Try all rows in the current column.

Do following for every tried row.

a) If the queen can be placed safely in this row then mark this [row, column] as part of the solution and recursively check if placing queen here leads to a solution.

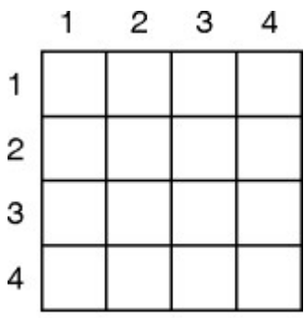
b) If placing the queen in [row, column] leads to a solution then return true.

c) If placing queen doesn't lead to a solution then unmark this [row, column] (Backtrack) and go to step (a) to try other rows.

4) If all rows have been tried and nothing worked,return false to trigger backtracking.

4- Queen Problem

Problem 1 : Given 4 x 4 chessboard, arrange four queens in a way, such that no two queens attack each other. That is, no two queens are placed in the same row, column, or diagonal.



4 x 4 Chessboard

- We have to arrange four queens, Q1, Q2, Q3 and Q4 in 4 x 4 chess board. We will put with queen in ith row. Let us start with position (1, 1). Q1 is the only queen, so there is no issue. partial solution is <1>
- We cannot place Q2 at positions (2, 1) or (2, 2). Position (2, 3) is acceptable. the partial solution is <1, 3>.
- Next, Q3 cannot be placed in position (3, 1) as Q1 attacks her. And it cannot be placed at (3, 2), (3, 3) or (3, 4) as Q2 attacks her. There is no way to put Q3 in the third row. Hence, the algorithm backtracks and goes back to the previous solution and readjusts the position of queen Q2. Q2 is moved from positions (2, 3) to
  (2, 4). Partial solution is <1, 4>

- Now, Q3 can be placed at position (3, 2). Partial solution is <1, 4, 3>.
- Queen Q4 cannot be placed anywhere in row four. So again, backtrack to the previous solution and readjust the position of Q3. Q3 cannot be placed on (3, 3) or(3, 4). So the algorithm backtracks even further.
- All possible choices for Q2 are already explored, hence the algorithm goes back to partial solution <1> and moves the queen Q1 from (1, 1) to (1, 2). And this process continues until a solution is found.

All possible solutions for 4-queen are shown in fig (a) & fig. (b)

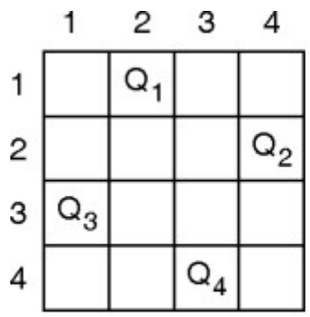


Fig. (a): Solution – 1

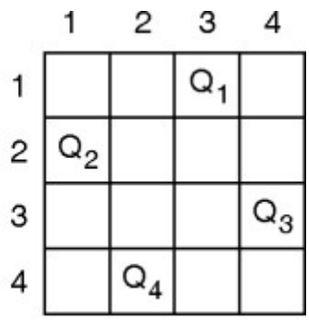
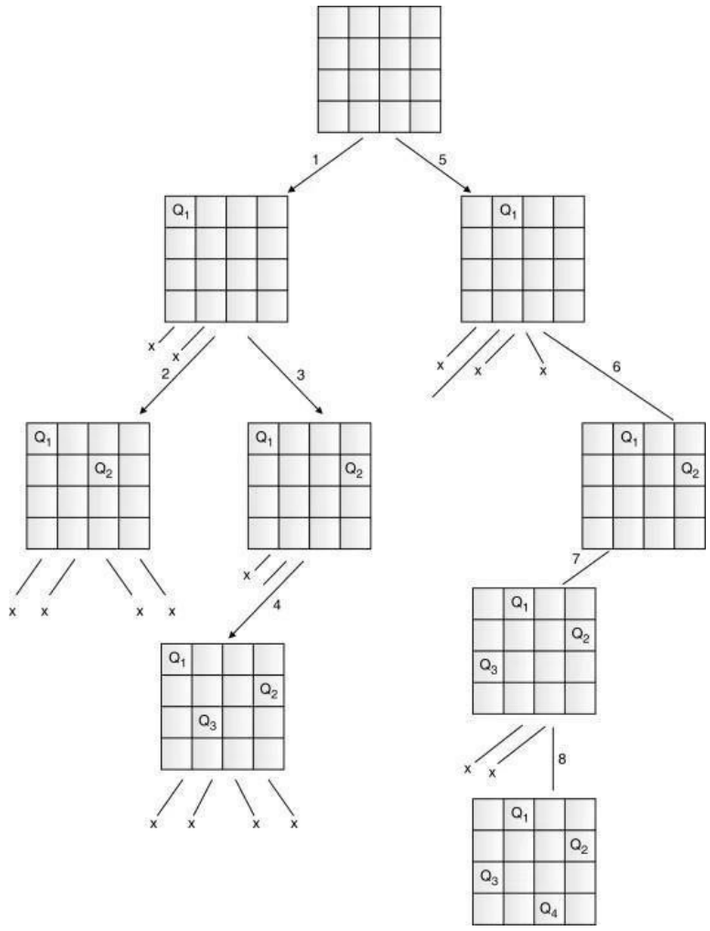


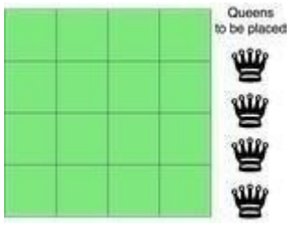
Fig. (b): Solution – 2

Fig. (d) describes the backtracking sequence for the 4-queen problem.

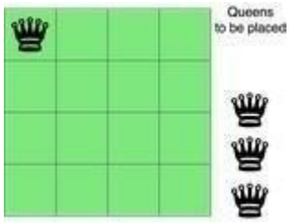


The solution of the 4-queen problem can be seen as four tuples (x_1, x_2, x_3, x_4), where x_i represents the column number of queen Q_i. Two possible solutions for the 4-queen problem are (2, 4, 1, 3) and (3, 1, 4, 2).

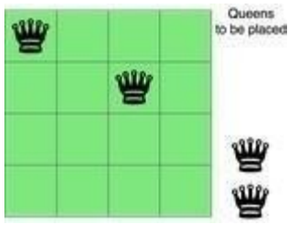
Explanation :

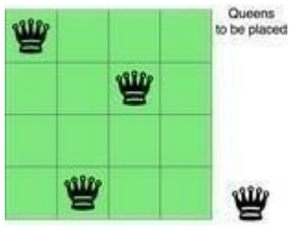


The above picture shows an NxN chessboard and we have to place N queens on it. So, we will start by placing the first queen.



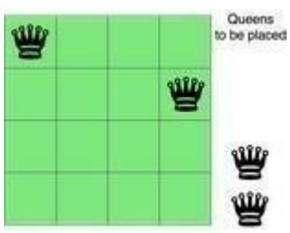
Now, the second step is to place the second queen in a safe position and then the third queen.



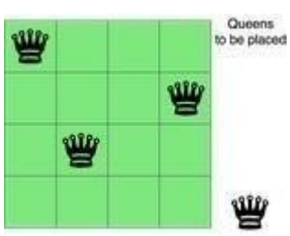


Now, you can see that there is no safe place where we can put the last queen. So, we will just change the position of the previous queen. And this is backtracking.

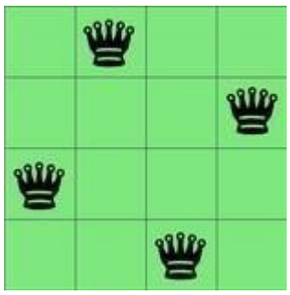
Also, there is no other position where we can place the third queen so we will go back one more step and change the position of the second queen.



And now we will place the third queen again in a safe position until we find a solution.

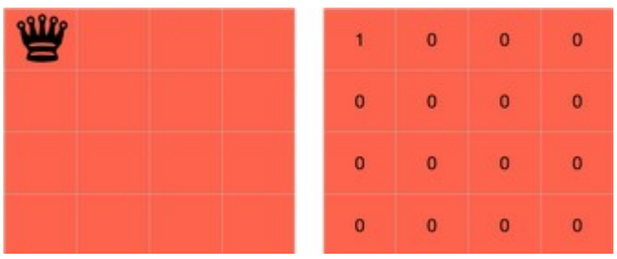


We will continue this process and finally, we will get the solution as shown below.

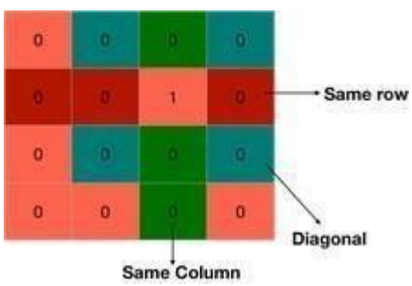


We need to check if a cell (i, j) is under attack or not. For that, we will pass these two in our function along with the chessboard and its size - IS-ATTACK(i, j, board, N).

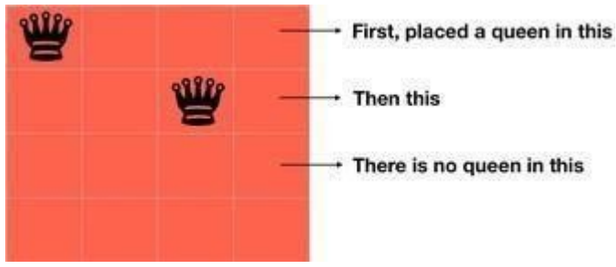
If there is a queen in a cell of the chessboard, then its value will be 1, otherwise, 0.



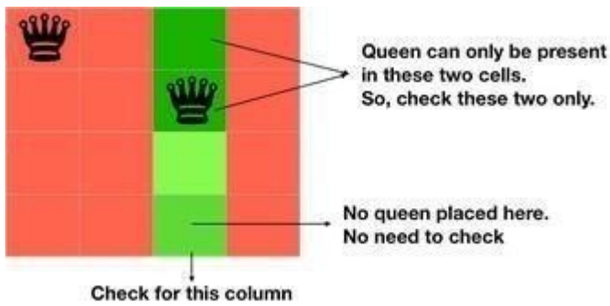
The cell (i,j) will be under attack in three condition - if there is any other queen in row i, if there is any other queen in the column j or if there is any queen in the diagonals.



We are already proceeding row-wise, so we know that all the rows above the current row(i) are filled but not the current row and thus, there is no need to check for row i.



We can check for the column j by changing k from 1 to i-1 in board[k][j] because only the rows from 1 to i-1 are filled.



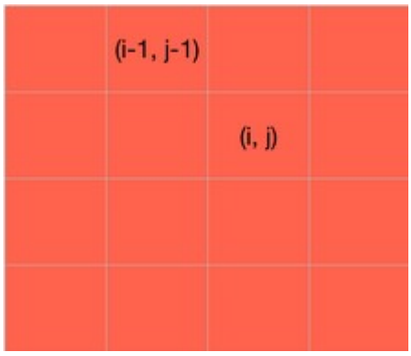

```
for k in 1 to i-1
  if board[k][j]==1

    return TRUE
```

Now, we need to check for the diagonal. We know that all the rows below the row i are empty, so we need to check only for the diagonal elements which above the row i.

If we are on the cell (i, j), then decreasing the value of i and increasing the value of j will make us traverse over the diagonal on the right side, above the row i.

```
k = i-1

l = j+1

while k>=1 and l<=N

  if board[k][l] == 1

  return TRUE

  k=k-1

  l=l+1
```

Also if we reduce both the values of i and j of cell (i, j) by 1, we will traverse over the left diagonal, above the row i.




```
k = i-1

l = j-1

while k>=1 and l>=1

  if board[k][l] == 1

  return TRUE

  k=k-1

  l=l-1
```

At last, we will return false as it will be return true is not returned by the above statements and the cell (i,j) is safe.

We can write the entire code as:

```
IS-ATTACK(i, j, board, N)
 // checking in the column j
 for k in 1 to i-1
  if board[k][j]==1
        return TRUE
 // checking upper right diagonal
 k = i-1
 l = j+1
 while k>=1 and l<=N
  if board[k][l] == 1
        return TRUE
  k=k+1
  l=l+1
 // checking upper left diagonal
 k = i-1
 l = j-1
   while k>=1 and l>=1\
    if board[k][l] == 1
     return TRUE
    k=k-1
    l=l-1
   return FALSE
```

Now, let's write the real code involving backtracking to solve the N Queen problem.
Our function will take the row, number of queens, size of the board and the board itself - N-QUEEN(row, n, N,board).

If the number of queens is 0, then we have already placed all the queens.

```
if n==0
  return TRUE
```

Otherwise, we will iterate over each cell of the board in the row passed to the function and for each cell, we will check if we can place the queen in that cell or not. We can't place the queen in a cell if it is under attack.

```
for j in 1 to N
  if !IS-ATTACK(row, j, board, N)
        board[row][j] = 1
```

After placing the queen in the cell, we will check if we are able to place the next queen with this arrangement or not. If not, then we will choose a different position for the current queen.

```
  for j in 1 to N

        if N-QUEEN(row+1, n-1, N, board)
              return TRUE
        board[row][j] = 0
```

if N-QUEEN(row+1, n-1, N, board) - We are placing the rest of the queens with the current arrangement. Also, sinceall the rows up to 'row' are occupied, so we will start from 'row+1'. If this returns true, then we are successfulin placing all the queen, if not, then we have to change the position of our current queen. So, we are leaving the currentcell board[row][j] = 0 and then iteration will find another place for the queen and this is backtracking.

Take a note that we have already covered the base case - if n==0 → return TRUE. It means when all queens willbe placed correctly, then N-QUEEN(row, 0, N, board) will be called and this will return true.

At last, if true is not returned, then we didn't find any way, so we will return false.N-QUEEN(row, n, N, board)

```
...
return FALSE
```

```
N-QUEEN(row, n, N, board)
 if n==0
  return TRUE
 for j in 1 to N
  if !IS-ATTACK(row, j, board, N)
        board[row][j] = 1
```

```
    if N-QUEEN(row+1, n-1, N, board)
      return TRUE
    board[row][j] = 0 //backtracking, changing current decision
  return FALSE
```

Code :-

```
# Python3 program to solve N Queen
# Problem using backtracking
global N
N = 4

def printSolution(board):
        for i in range(N):
                for j in range(N):
                        print(board[i][j], end = " ")
                print()

# A utility function to check if a queen can
# be placed on board[row][col]. Note that this
# function is called when "col" queens are
# already placed in columns from 0 to col -1.
# So we need to check only left side for
# attacking queens
def isSafe(board, row, col):
        # Check this row on left side
        for i in range(col):
                if board[row][i] == 1:
                        return False
        # Check upper diagonal on left side
        for i, j in zip(range(row, -1, -1),
                                        range(col, -1, -1)):
                if board[i][j] == 1:
                        return False
        # Check lower diagonal on left side
        for i, j in zip(range(row, N, 1),
                                        range(col, -1, -1)):
                if board[i][j] == 1:
                        return False
        return True
def solveNQUtil(board, col):
        # base case: If all queens are placed
        # then return true
        if col >= N:
                return True
        # Consider this column and try placing
        # this queen in all rows one by one
        for i in range(N):
                if isSafe(board, i, col):
                        # Place this queen in board[i][col]
                        Board[i][col]=1
                        # recur to place rest of the queens
                        if solveNQUtil(board, col + 1) == True:
                                return True

                        # If placing queen in board[i][col
                        # doesn't lead to a solution, then
                        # queen from board[i][col]
                        board[i][col] = 0
```

```
        # if the queen can not be placed in any row in
        # this column col then return false
        return False

# This function solves the N Queen problem using
# Backtracking. It mainly uses solveNQUtil() to
# solve the problem. It returns false if queens
# cannot be placed, otherwise return true and
# placement of queens in the form of 1s.
# note that there may be more than one
# solutions, this function prints one of the
# feasible solutions.
def solveNQ():
        board = [ [0, 0, 0, 0],
                        [0, 0, 0, 0],
                        [0, 0, 0, 0],
                        [0, 0, 0, 0] ]

        if solveNQUtil(board, 0) == False:
                print ("Solution does not exist")
                return False

        printSolution(board)
        return True

# Driver Code
solveNQ()
```

Output:-

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

Conclusion- In this way we have explored Concept of Backtracking method and solve n-Queen problem using backtracking method

Assignment Question

1. **What is backtracking? Give the general Procedure.**
2. **Give the problem statement of the n-queens problem. Explain the solution**
3. **Write an algorithm for N-queens problem using backtracking?**
4. **Why it is applicable to N=4 and N=8 only?**

Reference link

- https://www.codesdope.com/blog/article/backtracking-explanation-and-n-queens-problem/

MINI PROJECT 1

Title: Write a program to implement matrix multiplication. Also implement multithreaded matrix multiplication with either one thread per row or one thread per cell. Analyze and compare their performance.

Objective of the Assignment: Students will be able to implement and analyze matrix multiplication and multithreaded matrix multiplication with either one thread per row or one thread per cell.
Prerequisite:

1. Basic Knowledge of python or Java
2. Concept of Matrix Multiplication

Theory

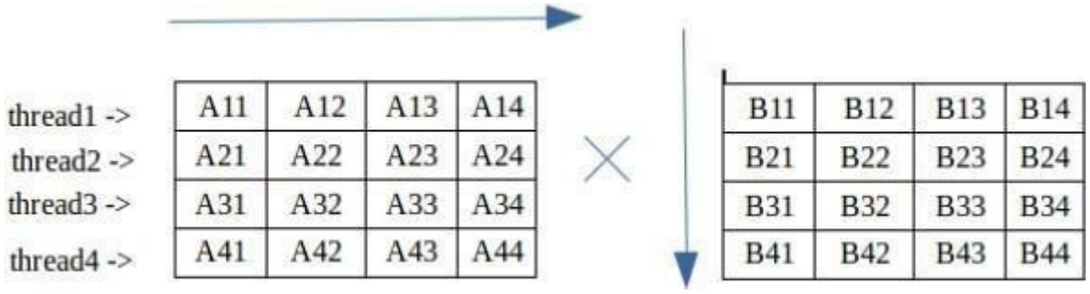
Multiplication of matrix does take time surely. Time complexity of matrix multiplication is O(n^3) using normal matrix multiplication. And Strassen algorithm improves it and its time complexity is O(n^(2.8074)).

But, Is there any way to improve the performance of matrix multiplication using the normalmethod.

Multi-threading can be done to improve it. In multi-threading, instead of utilizing a single core of your processor, we utilizes all or more core to solve the problem.
We create different threads, each thread evaluating some part of matrix multiplication.

Depending upon the number of cores your processor has, you can create the number of threads required. Although you can create as many threads as you need, a better way is to create each thread for one core.

In second approach,we create a separate thread for each element in resultant matrix. Using pthread_exit() we return computed value from each thread which is collected by pthread_join().This approach does not make use of any global variables.



To compare the performance of matrix multiplication with one thread per row and one thread per cell, we'll analyze the execution times and consider factors like matrix size and the number of CPU threads available. In general, the choice of which method is more efficient will depend on the specific use case and hardware configuration. Let's analyze the performance:

1. **Matrix Size (m, n, p)**: In this example, we used matrices of size 1000x1000 for A and B. Smaller matrices may not demonstrate significant performance differences, while larger matrices may show more noticeable speedups from parallelization.

2. **Multithreading Overhead**: The use of multiple threads introduces overhead in terms of thread creation, synchronization, and context switching. For smaller matrices, this overhead can dominate, and one thread per cell may perform better. For larger matrices, the actual matrix multiplication work may dominate, and one thread per row may perform better.

3. **Number of CPU Threads**: The number of available CPU threads can affect the performance. If there are fewer threads than rows/columns, it might not make sense to use one thread per row or cell. On a multi-core CPU, if you have many threads available, parallelization can be more beneficial.

4. **Cache and Memory**: The efficiency of cache usage can play a role in performance. One thread per row may perform better when it utilizes the cache more effectively.
5. **Optimized Libraries**: Specialized libraries like NumPy have highly optimized matrix multiplication routines that can outperform custom multithreaded implementations.
6. **Hardware**: The performance can vary based on the specific hardware and CPU architecture.
7. **Implementation Overheads**: The specific implementation of the matrix multiplication algorithm and the way it's parallelized can also impact performance. In this example, we used a basic approach.
8. **Load Balancing**: Load balancing is important when using one thread per row. Uneven workloads can lead to inefficient use of CPU resources.
9. **Scaling**: The performance may not scale linearly with the number of threads. Beyond a certain point, adding more threads may not lead to significant improvements due to the limitations of the hardware

Code :-

```
// CPP Program to multiply two matrix using pthreads
#include <bits/stdc++.h>
using namespace std;

// maximum size of
matrix#define MAX 4

// maximum number of threads
#define MAX_THREAD 4

int
matA[MAX][MAX];
int
matB[MAX][MAX];
int
matC[MAX][MAX];
int step_i = 0;

void* multi(void* arg)
{
    int i = step_i++; //i denotes row number of resultant matC

    for (int j = 0; j < MAX;
    j++) for (int k = 0; k <
    MAX; k++)
            matC[i][j] += matA[i][k] * matB[k][j];
}

// Driver
Codeint
main()
{
    // Generating random values in matA and matB
    for (int i = 0; i < MAX; i++) {
            for (int j = 0; j < MAX; j++) {
                    matA[i][j] = rand() %
                    10;
                    matB[i][j] = rand() % 10;
            }
```

```
    }

    // Displaying
    matAcout << endl
            << "Matrix A" <<
    endl;for (int i = 0; i < MAX;
    i++) {
            for (int j = 0; j < MAX; j++)
                    cout << matA[i][j] << "
            ";cout << endl;
    }

    // Displaying
    matBcout << endl
            << "Matrix B" <<
    endl;for (int i = 0; i < MAX;
    i++) {
            for (int j = 0; j < MAX; j++)
                    cout << matB[i][j] << "
            ";cout << endl;
    }

    // declaring four threads
    pthread_t threads[MAX_THREAD];

    // Creating four threads, each evaluating its own partfor
    (int i = 0; i < MAX_THREAD; i++) {
            int* p;
            pthread_create(&threads[i], NULL, multi, (void*)(p));
    }

    // joining and waiting for all threads to complete
    for (int i = 0; i < MAX_THREAD; i++)
            pthread_join(threads[i], NULL);

    // Displaying the result
    matrixcout << endl
            << "Multiplication of A and B" <<
    endl;for (int i = 0; i < MAX; i++) {
            for (int j = 0; j < MAX; j++)
                    cout << matC[i][j] << "
            ";cout << endl;
    }
    return 0;
}
```

Conclusion

Hence we have successfully completed the implementation of this Mini Project.

Group B
Assignment No : 1

Title of the Assignment: Predict the price of the Uber ride from a given pickup point to the agreed drop-off location. Perform following tasks:

1. Pre-process the dataset.
2. Identify outliers.
3. Check the correlation.
4. Implement linear regression and random forest regression models.
5. Evaluate the models and compare their respective scores like R2, RMSE, etc.

Dataset Description: The project is about on world's largest taxi company Uber inc. In this project, we're looking to predict the fare for their future transactional cases. Uber delivers service to lakhs of customers daily. Now it becomes really important to manage their data properly to come up with new business ideas to get best results. Eventually, it becomes really important to estimate the fare prices accurately.

Link for Dataset:https://www.kaggle.com/datasets/yasserh/uber-fares-dataset **Objective of**

the Assignment:
Students should be able to preprocess dataset and identify outliers, to check correlation and implement linear regression and random forest regression models. Evaluate them with respective scores like R2, RMSE etc.

Prerequisite:

1. Basic knowledge of Python
2. Concept of preprocessing data
3. Basic knowledge of Data Science and Big Data Analytics.

Contents of the Theory:

1. Data Preprocessing
2. Linear regression
3. Random forest regression models
4. Box Plot
5. Outliers
6. Haversine
7. Mathplotlib
8. Mean Squared Error

Data Preprocessing:

Data preprocessing is a process of preparing the raw data and making it suitable for amachine learning model. It is the first and crucial step while creating a machine learning model.

When creating a machine learning project, it is not always a case that we come across the clean and formatted data. And while doing any operation with data, it is mandatory to clean itand put in a formatted way. So for this, we use data preprocessing task.

Why do we need Data Preprocessing?

A real-world data generally contains noises, missing values, and maybe in an unusable format which cannot be directly used for machine learning models. Data preprocessing is required tasks for cleaning thedata and making it suitable for a machine learning model which also increases the accuracy and efficiency of a machine learning model.

It involves below steps:

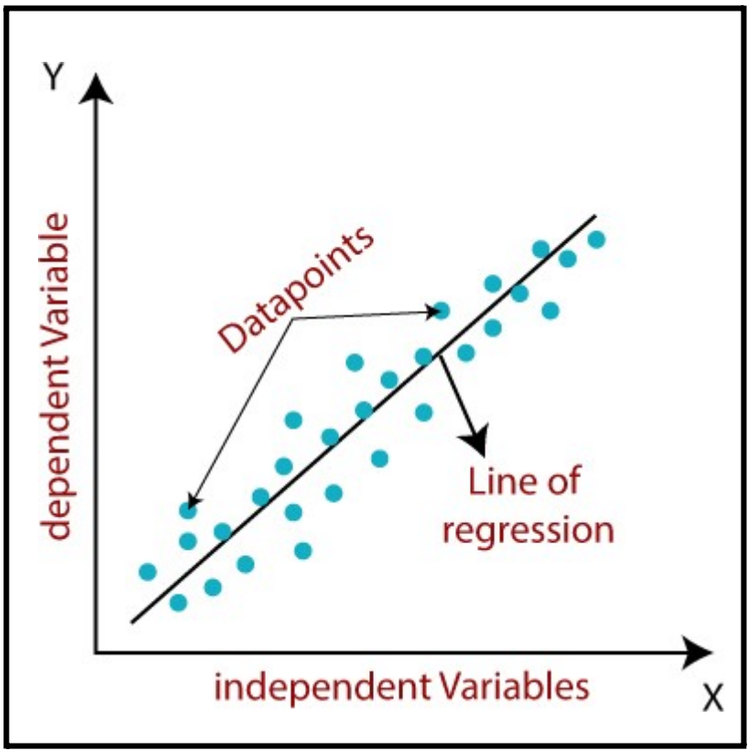
- Getting the dataset
- Importing libraries
- Importing datasets
- Finding Missing Data
- Encoding Categorical Data
- Splitting dataset into training and test set
- Feature scaling

Linear Regression:

Linear regression is one of the easiest and most popular Machine Learning algorithms. It is a statistical method that is used for predictive analysis. Linear regression makes predictions for continuous/real or numeric variables such as**sales, salary, age, product price,**etc.

Linear regression algorithm shows a linear relationship between a dependent (y) and one or more independent (y) variables, hence called as linear regression. Since linear regression shows the linear relationship, which means it nds how the value of the dependent variable is changing according to the value of the independent variable.

The linear regression model provides a sloped straight line representing the relationship between the variables. Consider the below image:



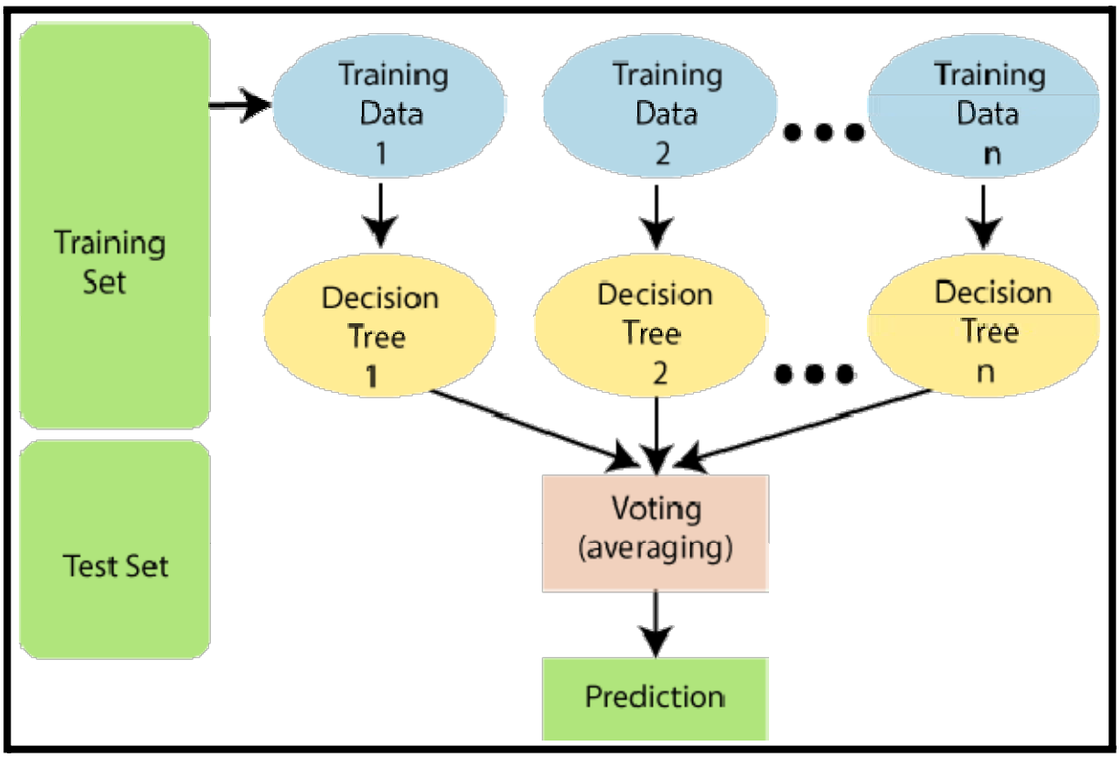
Random Forest Regression Models:

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

As the name suggests,***"Random Forest is a classi er 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
nal output.

The greater number of trees in the forest leads to higher accuracy and prevents theproblem of over tting.



Boxplot:

Boxplots are a measure of how well data is distributed across a data set. This divides thedata set into three quartiles. This graph represents the minimum, maximum, average, rst quartile, and the third quartile in the data set. Boxplot is also useful in comparing thedistribution of data in a data set by drawing a boxplot for each of them.

R provides a boxplot() function to create a boxplot. There is the following syntax of boxplot()function:

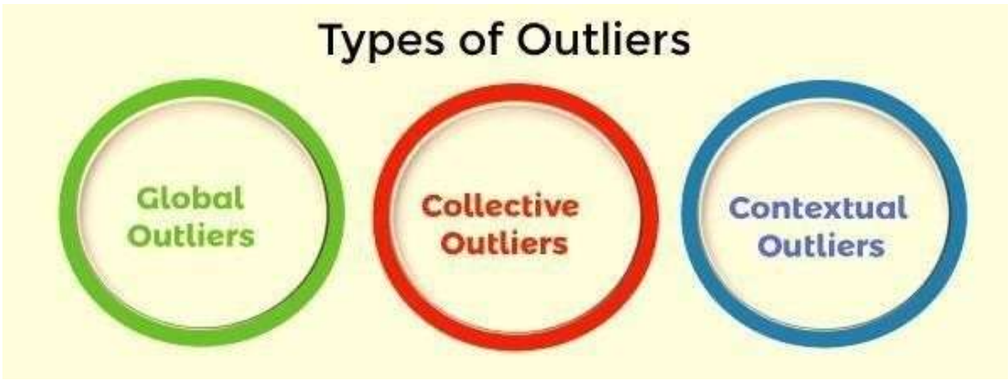
boxplot(x, data, notch, varwidth, names, main)

Here,

S.No	Parameter	Description
1.	x	It is a vector or a formula.
2.	data	It is the data frame.
3.	notch	It is a logical value set as true to draw a notch.
4.	varwidth	It is also a logical value set as true to draw the width of the boxsameas the sample size.
5.	names	It is the group of labels that will be printed under each boxplot.
6.	main	It is used to give a title to the graph.

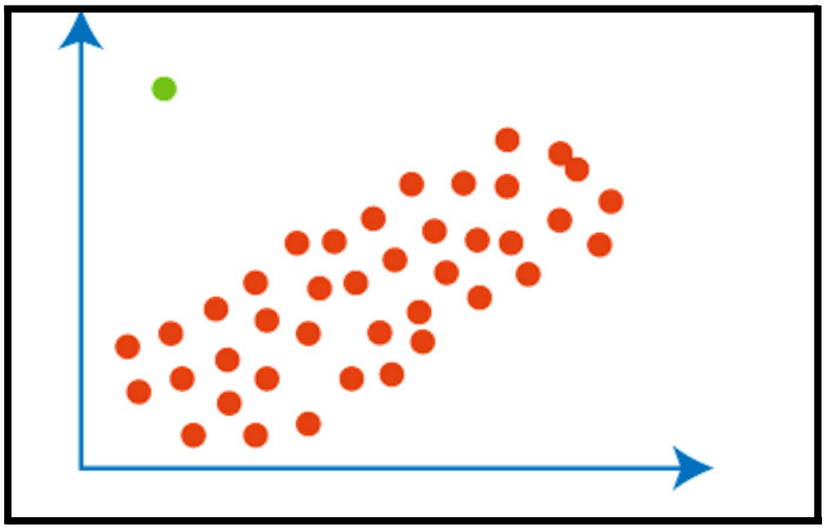
Outliers:

As the name suggests, "outliers" refer to the data points that exist outside of what is to beexpected. The major thing about the outliers is what you do with them. If you are going toanalyze any task to analyze data sets, you will always have some assumptions based onhow this data is generated. If you nd some data points that are likely to contain some form of error, then these are de nitely outliers, and depending on the context, you want toovercome those errors. The data mining process involves the analysis and prediction of datathat the data holds. In 1969, Grubbs introduced the rst de nition of outliers.



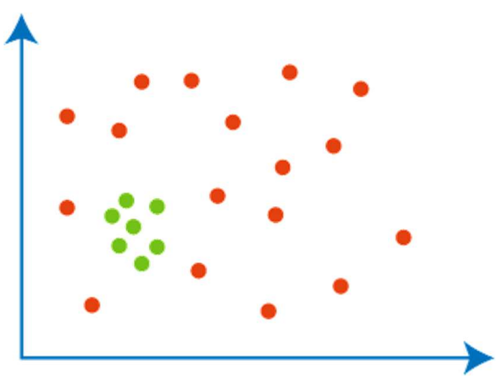
Global Outliers

Global outliers are also called point outliers. Global outliers are taken as the simplest form of outliers. When data points deviate from all the rest of the data points in a given data set, it is known as the global outlier. In most cases, all the outlier detection procedures are targeted to determine the global outliers. The green data point is the global outlier.



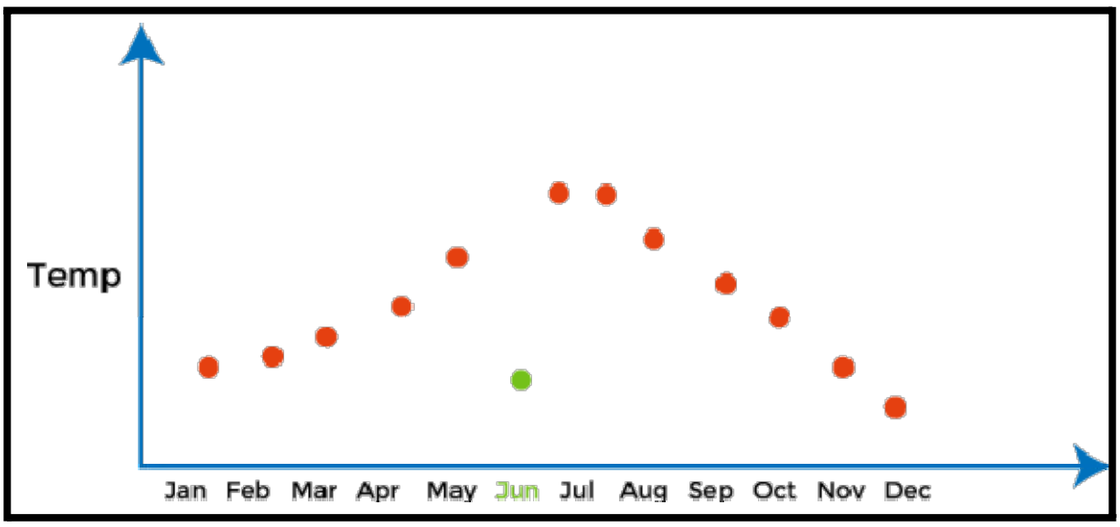
Collective Outliers

In a given set of data, when a group of data points deviates from the rest of the data set is called collective outliers. Here, the particular set of data objects may not be outliers, but when you consider the data objects as a whole, they may behave as outliers. To identify thetypes of different outliers, you need to go through background information about the relationship between the behavior of outliers shown by different data objects. For example, in an Intrusion Detection System, the DOS package from one system to another is taken as normal behavior. Therefore, if this happens with the various computer simultaneously, it is considered abnormal behavior, and as a whole, they are called collective outliers.The greendata points as a whole represent the collective outlier.



Contextual Outliers

As the name suggests, "Contextual" means this outlier introduced within a context. For example, in the speech recognition technique, the single background noise. Contextual outliers are also known as Conditional outliers. These types of outliers happen if a data object deviates from the other data points because of any speci c condition in a given data set. As we know, there are two types of attributes of objects of data: contextual attributes and behavioral attributes. Contextual outlier analysis enables the users to examine outliers in different contexts and conditions, which can be useful in various applications. For example, A temperature reading of 45 degrees Celsius may behave as an outlier in a rainy season. Still, it will behave like a normal data point in the context of a summer season. In thegiven diagram, a green dot representing the low-temperature value in June is a contextual outlier since the same value in December is not an outlier.



Haversine:

The Haversine formula calculates the shortest distance between two points on a sphere using their latitudes and longitudes measured along the surface. It is important for use in navigation.

Matplotlib:

Matplotlib is an amazing visualization library in Python for 2D plots of arrays. Matplotlib is a multi-platform data visualization library built on NumPy arrays and designed to work with the broader SciPy stack. It was introduced by John Hunter in the year 2002.

One of the greatest benefits of visualization is that it allows us visual access to huge amounts of data in easily digestible visuals. Matplotlib consists of several plots like line, bar, scatter, histogram etc.

Mean Squared Error;

The**Mean Squared Error (MSE)**or**Mean Squared Deviation (MSD)**of an estimator measures the average of error squares i.e. the average squared difference between theestimated values and true value. It is a risk function, corresponding to the expected value ofthe squared error loss. It is always non – negative and values close to zero are better. TheMSE is the second moment of the error (about the origin) and thus incorporates both thevariance of the estimator and its bias.

Code :- https://www.kaggle.com/code/proxzima/uber-fare-price-prediction

Conclusion:

In this way we have explored Concept correlation and implement linear regression andrandom forest regression models.

Assignment Questions:

1. What is data preprocessing?
2. De ne Outliers?
3. What is Linear Regression?
4. What is Random Forest Algorithm?
5. Explain: pandas, numpy?

Group B

Assignment No : 2

Title of the Assignment: Classify the email using the binary classification method. Email Spam detection has two states:
a) Normal State – Not Spam,
b) Abnormal State – Spam.
Use K-Nearest Neighbors and Support Vector Machine for classification. Analyze theirperformance.

Dataset Description: The csv file contains 5172 rows, each row for each email. There are 3002 columns. The first column indicates Email name. The name has been set with numbers and not recipients' name to protect privacy. The last column has the labels for prediction : 1for spam, 0 for not spam. The remaining 3000 columns are the 3000 most common words inall the emails, after excluding the non-alphabetical characters/words. For each row, thecount of each word(column) in that email(row) is stored in the respective cells. Thus,information regarding all 5172 emails are stored in a compact dataframe rather than asseparate text files.

Link:https://www.kaggle.com/datasets/balaka18/email-spam-classification-dataset-csv **Objective of the**

Assignment:

Students should be able to classify email using the binary Classification and implement email spam detection technique by using K-Nearest Neighbors and Support Vector Machine algorithm.

Prerequisite:

1. Basic knowledge of Python
2. Concept of K-Nearest Neighbors and Support Vector Machine for classification.

Contents of the Theory:

1. Data Preprocessing
2. Binary Classification
3. K-Nearest Neighbours
4. Support Vector Machine
5. Train, Test and Split Procedure

Data Preprocessing:
Data preprocessing is a process of preparing the raw data and making it suitable for amachine learning model. It is the first and crucial step while creating a machine learning model.
When creating a machine learning project, it is not always a case that we come across the clean and formatted data. And while doing any operation with data, it is mandatory to clean itand put in a formatted way. So for this, we use data preprocessing task.

Why do we need Data Preprocessing?

A real-world data generally contains noises, missing values, and maybe in an unusable format which cannot be directly used for machine learning models. Data preprocessing is required tasks for cleaning thedata and making it suitable for a machine learning model which also increases the accuracy and efficiency of a machine learning model.
It involves below steps:

- Getting the dataset
- Importing libraries
- Importing datasets
- Finding Missing Data
- Encoding Categorical Data
- Splitting dataset into training and test set
- Feature scaling

Code :- https://www.kaggle.com/code/mfaisalqureshi/email-spam-detection-98-accuracy/notebook

Binary classification

Binary classification is a supervised machine learning task where the goal is to assign each data point to one of two classes or categories. Classification into one of two classes is a common machine learning problem. You might want to predict whether or not a customer is likely to make a purchase, whether or not a credit card transaction was fraudulent, whether deep space signals show evidence of a new planet, or a medical test evidence of a disease. These are all binary classification problems.

Two common algorithms used for binary classification are K-Nearest Neighbors (K-NN) and Support Vector Machine (SVM). Here's an overview of these algorithms and the train-test split procedure:

1. **K-Nearest Neighbors (K-NN):**

    - K-NN is a simple classification algorithm that makes predictions based on the majority class of the k-nearest data points to a given test point.To use K-NN for binary classification, you need labeled data with two classes (e.g., positive and negative).
    - K-NN is a lazy learner because it doesn't build a specific model during the training phase; it memorizes the training data.
    - The choice of 'k' is a hyperparameter that can significantly affect the model's performance. A small 'k' may make the model sensitive to noise, while a large 'k' might lead to oversmoothing. K-NN can be computationally expensive for large datasets, as it requires calculating distances to all data points.
    - Feature scaling is essential because K-NN relies on distance calculations. Features with different scales can bias the results. K-NN works well for simple and small to medium-sized datasets but may not be suitable for high-dimensional data or datasets with imbalanced class distributions.
    - It's important to choose an appropriate distance metric based on the nature of your data and the problem you're trying to solve. K-NN is a versatile algorithm, and while it has its limitations, it can be a useful tool for various classification tasks, especially when the dataset is well-preprocessed, and the choice of 'k' is well-tuned
    - The steps for using K-NN for binary classification are as follows:
    - a. Collect and preprocess your data.
    - b. Split the data into a training set and a test set.
    - c. Choose a value for 'k' (the number of nearest neighbors to consider).
    - d. Train the K-NN model on the training data.

- e. Use the trained model to make predictions on the test data.
- f. Evaluate the model's performance using metrics like accuracy, precision, recall, and F1-score.

2. Support Vector Machine (SVM):

- SVM is a powerful classification algorithm that finds a hyperplane that best separates the two classes in a way that maximizes the margin between them.
- SVM is effective in cases where the data is not linearly separable by transforming it into a higher-dimensional space. The choice of kernel and its hyperparameters can have a significant impact on the SVM's performance. SVM is capable of finding a decision boundary that maximizes the margin, making it robust against overfitting.
- SVM can handle both balanced and imbalanced datasets. SVM can be computationally intensive, especially for large datasets. Techniques like stochastic gradient descent and linear SVMs may be used for efficiency. Support vectors are essential for defining the decision boundary, so they play a crucial role in the SVM's performance. Support Vector Machines are a versatile algorithm that works well in a wide range of applications, including image classification, text classification, and anomaly detection, among others.
- Steps for using SVM for binary classification:
- a. Collect and preprocess your data.
- b. Split the data into a training set and a test set.
- c. Choose a suitable kernel (e.g., linear, polynomial, or radial basis function) and kernel parameters.
- d. Train the SVM model on the training data.
- e. Use the trained model to make predictions on the test data.
- f. Evaluate the model's performance, typically using metrics like accuracy, precision, recall, and F1-score.

3. Train-Test Split Procedure:

- The train-test split is a critical step in machine learning to assess the model's performance. It involves dividing the dataset into two parts: a training set and a test set.
- The training set is used to train the machine learning model, while the test set is used to evaluate the model's performance and generalization.
- The steps for the train-test split procedure are as follows:

- a. Randomly shuffle the dataset to ensure that the data is evenly distributed between the training and test sets.
- b. Split the dataset into two parts, typically with a ratio like 70-30 or 80-20,where the training set gets the larger portion.
- c. Ensure that the two sets are mutually exclusive, meaning that no data point appears in both sets.
- d. Use the training set to train the machine learning model.
- e. Use the test set to evaluate the model's performance by making predictionsand comparing them to the actual labels.
- f. Calculate various evaluation metrics to assess the model's accuracy and generalization, such as accuracy, precision, recall, and F1-score.

The train-test split procedure helps you estimate how well your model is likely to perform onnew, unseen data and avoid overfitting, where the model performs well on the training data but poorly on new data.

Conclusion

Hence in this way we have studied the Concept of K-Nearest Neighbors and Support Vector

Group B
Assignment No : 3

Title of the Assignment: Given a bank customer, build a neural network-based classifier that can determine whether they will leave or not in the next 6 months

Dataset Description: The case study is from an open-source dataset from Kaggle. The dataset contains 10,000 sample points with 14 distinct features such as CustomerId, CreditScore, Geography, Gender, Age, Tenure, Balance, etc.

Link for Dataset:https://www.kaggle.com/barelydedicated/bank-customer-churn-modeling **Perform**

the following steps:

1. Read the dataset.
2. Distinguish the feature and target set and divide the data set into training and test sets.
3. Normalize the train and test data.
4. Initialize and build the model. Identify the points of improvement and implement the same.
5. Print the accuracy score and confusion matrix (5 points).

Objective of the Assignment:

Students should be able to distinguish the feature and target set and divide the data set into training and test sets and normalize them and students should build the model on the basis of that.

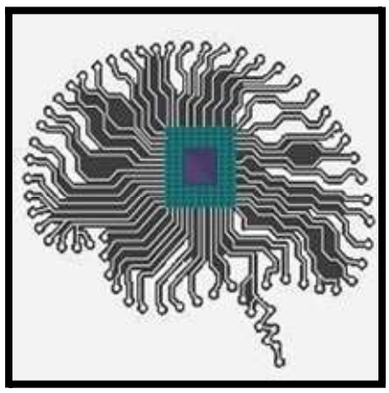
Prerequisite:

1. Basic knowledge of Python
2. Concept of Confusion Matrix

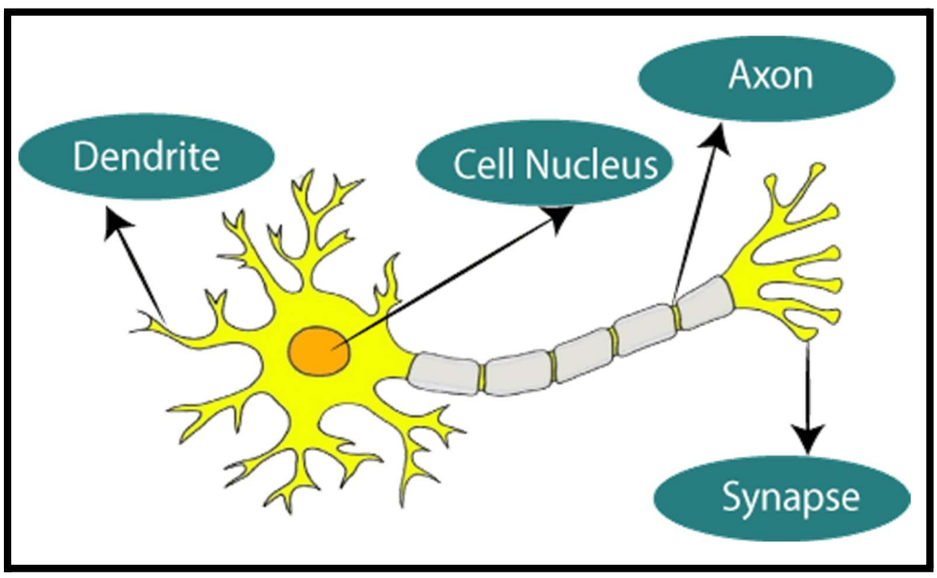
Contents of the Theory:

1. Artificial Neural Network
2. Keras
3. tensorflow
4. Normalization
5. Confusion Matrix

Artificial Neural Network:

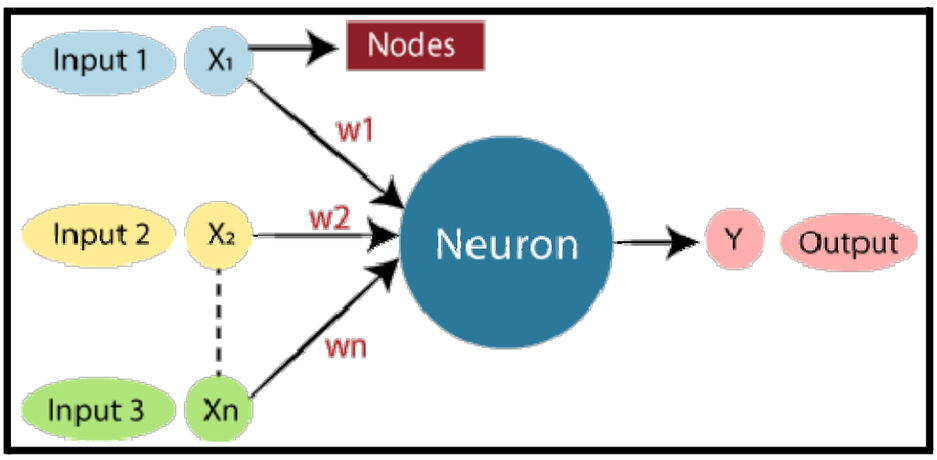


The term "Arti cial Neural Network" is derived from Biological neural networks that develop the structure of a human brain. Similar to the human brain that has neurons interconnected to one another, arti cial neural networks also have neurons that are interconnected to one another in various layers of the networks. These neurons are known as nodes.



The given gure illustrates the typical diagram of Biological Neural Network.

The typical Arti cial Neural Network looks something like the given gure.



Dendrites from Biological Neural Network represent inputs in Arti cial Neural Networks, cellnucleus represents Nodes, synapse represents Weights, and Axon represents Output.

Relationship between Biological neural network and arti cial neural network:

Biological Neural Network	**Artificial Neural Network**
Dendrites	Inputs
Cell nucleus	Nodes
Synapse	Weights
Axon	Output

An**Arti cial Neural Network**in the eld of**Arti cial intelligence**where it attempts to mimic the network of neurons makes up a human brain so that computers will have an option tounderstand things and make decisions in a human-like manner. The arti cial neural networkis designed by programming computers to behave simply like interconnected brain cells.

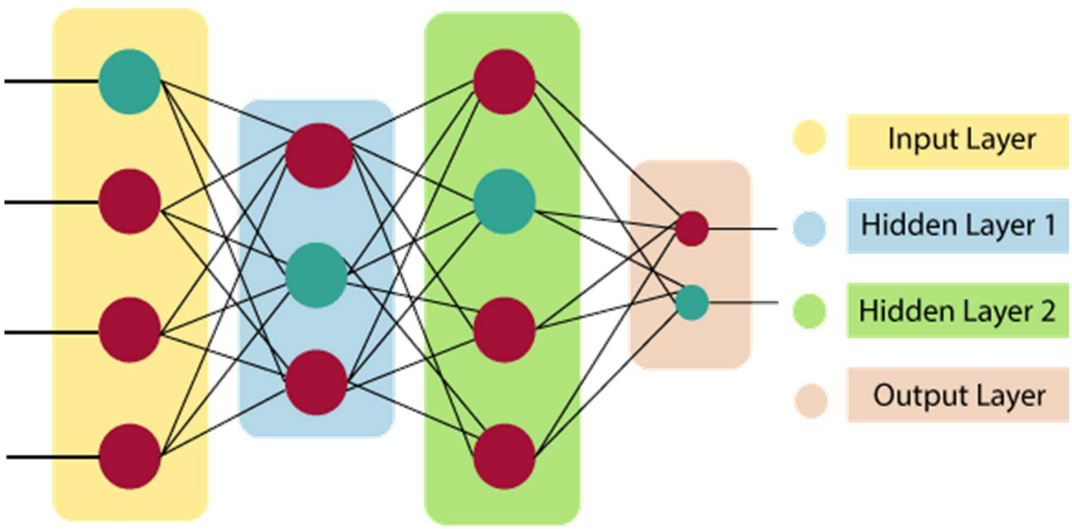
There are around 1000 billion neurons in the human brain. Each neuron has an association point somewhere in the range of 1,000 and 100,000. In the human brain, data is stored in such a manner as to be distributed, and we can extract more than one piece of this data when necessary from our memory parallelly. We can say that the human brain is made up ofincredibly amazing parallel processors.

We can understand the artificial neural network with an example, consider an example of adigital logic gate that takes an input and gives an output. "OR" gate, which takes two inputs. If one or both the inputs are "On," then we get "On" in output. If both the inputs are "Off," thenwe get "Off" in output. Here the output depends upon input. Our brain does not perform the same task. The outputs to inputs relationship keep changing because of the neurons in our brain, which are "learning."

The architecture of an artificial neural network:

To understand the concept of the architecture of an artificial neural network, we have to understand what a neural network consists of. In order to define a neural network that consists of a large number of artificial neurons, which are termed units arranged in a sequence of layers. Lets us look at various types of layers available in an artificial neural network.

Artificial Neural Network primarily consists of three layers:



Input Layer:

As the name suggests, it accepts inputs in several different formats provided by the programmer.

Hidden Layer:

The hidden layer presents in-between input and output layers. It performs all the calculationsto find hidden features and patterns.

Output Layer:

The input goes through a series of transformations using the hidden layer, which finally results in output that is conveyed using this layer.

The artificial neural network takes input and computes the weighted sum of the inputs andincludes a bias. This computation is represented in the form of a transfer function.

$$\sum_{i=1}^{n} Wi * Xi + b$$

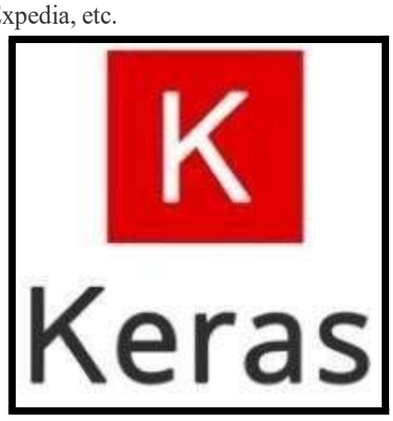
It determines weighted total is passed as an input to an activation function to produce the output. Activation functions choose whether a node should fire or not. Only those who are fired make it to the output layer. There are distinctive activation functions available that canbe applied upon the sort of task we are performing.

Keras:

Keras is an open-source high-level Neural Network library, which is written in Python is capable enough to run on Theano, TensorFlow, or CNTK. It was developed by one of the Google engineers, Francois Chollet. It is made user-friendly, extensible, and modular for facilitating faster experimentation with deep neural networks. It not only supports Convolutional Networks and Recurrent Networks individually but also their combination.

It cannot handle low-level computations, so it makes use of the**Backend**library to resolve it.The backend library act as a high-level API wrapper for the low-level API, which lets it run onTensorFlow, CNTK, or Theano.

Initially, it had over 4800 contributors during its launch, which now has gone up to 250,000 developers. It has a 2X growth ever since every year it has grown. Big companies like Microsoft, Google, NVIDIA, and Amazon have actively contributed to the development of Keras. It has an amazing industry interaction, and it is used in the development of popular
[rms likes Net[ix, Uber, Google, Expedia, etc.



Tensor□ow:

TensorFlow is a Google product, which is one of the most famous deep learning tools widelyused in the research area of machine learning and deep neural network. It came into the market on 9th November 2015 under the Apache License 2.0. It is built in such a way that it can easily run on multiple CPUs and GPUs as well as on mobile operating systems. It consists of various wrappers in distinct languages such asJava, C++, or Python.

Normalization:

Normalization is a scaling technique in Machine Learning applied during data preparation tochange the values of numeric columns in the dataset to use a common scale. It is not necessary for all datasets in a model. It is required only when features of machine learning models have different ranges.

Mathematically, we can calculate normalization with the below formula:Xn = (X -

Xminimum) / (Xmaximum - Xminimum)

Where,

- Xn = Value of Normalization
- Xmaximum = Maximum value of a feature
- Xminimum = Minimum value of a feature

Example: Let's assume we have a model dataset having maximum and minimum values of feature as mentioned above. To normalize the machine learning model, values are shiftedand rescaled so their range can vary between 0 and 1. This technique is also known asMin-Max scaling. In this scaling technique, we will change the feature values as follows:

Case1-If the value of X is minimum, the value of Numerator will be 0; hence Normalizationwill also be 0.

Xn = (X - Xminimum) / (Xmaximum - Xminimum) ----------formula

Put X =Xminimum in above formula, we get;

Xn = Xminimum- Xminimum/ (Xmaximum - Xminimum)Xn = 0

Case2-If the value of X is maximum, then the value of the numerator is equal to the denominator; hence Normalization will be 1.

Xn = (X - Xminimum) / (Xmaximum - Xminimum)Put X

=Xmaximum in above formula, we get;

Xn = Xmaximum - Xminimum/ (Xmaximum - Xminimum)Xn = 1

Case3-On the other hand, if the value of X is neither maximum nor minimum, then values of normalization will also be between 0 and 1.

Hence, Normalization can be de ned as a scaling method where values are shifted and rescaled to maintain their ranges between 0 and 1, or in other words; it can be referred to as Min-Max scaling technique.

Normalization techniques in Machine Learning

Although there are so many feature normalization techniques in Machine Learning, few of them are most frequently used. These are as follows:

- **Min-Max Scaling:**This technique is also referred to as scaling. As we have already discussed above, the Min-Max scaling method helps the dataset to shift and rescalethe values of their attributes, so they end up ranging between 0 and 1.
- **Standardization scaling:**

Standardization scaling is also known as**Z-score**normalization, in which values are centered around the mean with a unit standard deviation, which means the attributebecomes zero and the resultant distribution has a unit standard deviation. Mathematically,we can calculate the standardization by subtracting the feature value from the mean anddividing it by standard deviation.

Hence, standardization can be expressed as follows:

$$X' = \frac{X - \mu}{\sigma}$$

Here,**μ**represents the mean of feature value, and**σ**represents the standard deviation offeature values.

However, unlike Min-Max scaling technique, feature values are not restricted to a speci crange in the standardization technique.

This technique is helpful for various machine learning algorithms that use distance measures suchas**KNN, K-means clustering, and Principal component analysis**, etc. Further,it is also important that themodel is built on assumptions and data is normally distributed.

When to use Normalization or Standardization?

Which is suitable for our machine learning model, Normalization or Standardization? This is probably a big confusion among all data scientists as well as machine learning engineers. Although both terms have the almost same meaning choice of using normalization or standardization will depend on your problem and the algorithm you are using in models.

1. Normalization is a transformation technique that helps to improve the performance as well as the accuracy of your model better. Normalization of a machine learning model is useful when you don't know feature distribution exactly. In other words, the feature distribution of data does not follow a**Gaussian**(bell curve) distribution. Normalization must

have an abounding range, so if you have outliers in data, they will be affected by Normalization.

Further, it is also useful for data having variable scaling techniques such as**KNN, artificial neural network**s. Hence, you can't use assumptions for the distribution of data.

2. Standardization in the machine learning model is useful when you are exactly aware of the feature distribution of data or, in other words, your data follows a Gaussian distribution. However, this does not have to be necessarily true. Unlike Normalization, Standardization does not necessarily have a bounding range, so if you have outliers in your data, they will notbe affected by Standardization.

Further, it is also useful when data has variable dimensions and techniques such as**linear regression, logistic regression, and linear discriminant analysis**.

Example: Let's understand an experiment where we have a dataset having two attributes, i.e., age and salary. Where the age ranges from 0 to 80 years old, and the income varies from 0 to 75,000 dollars or more. Income is assumed to be 1,000 times that of age. As a result, the ranges of these two attributes are much different from one another.

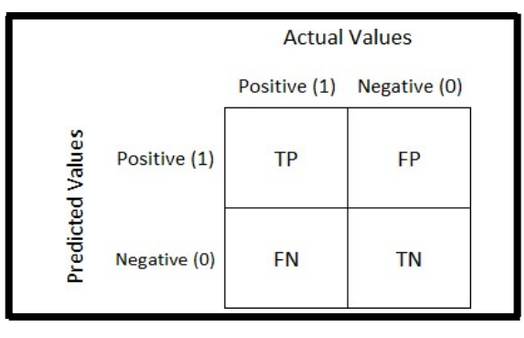
Because of its bigger value, the attributed income will organically in uence the conclusion more when we undertake further analysis, such as multivariate linear regression. However, this does not necessarily imply that it is a better predictor. As a result, we normalize the dataso that all of the variables are in the same range.

Further, it is also helpful for the prediction of credit risk scores where normalization isapplied to all numeric data except the class column. It uses the**tanh transformation** technique, which converts all numeric features into values of range between 0 to 1.

Confusion Matrix:

The confusion matrix is a matrix used to determine the performance of the classi cation models for a given set of test data. It can only be determined if the true values for test data are known. The matrix itselfcan be easily understood, but the related terminologies may beconfusing. Since it shows the errors in the model performance in the form of a matrix, hence also known as an**error matrix**. Some features of Confusion matrix are given below:

- For the 2 prediction classes of classi ers, the matrix is of 2*2 table, for 3 classes, it is3*3 table, and so on.
- The matrix is divided into two dimensions, that are**predicted values**and**actual values**along with the total number of predictions.
- Predicted values are those values, which are predicted by the model, and actualvalues are the true values for the given observations.
- It looks like the below table:



The above table has the following cases:

- **True Negative:**Model has given prediction No, and the real or actual value was alsoNo.
- **True Positive:**The model has predicted yes, and the actual value was also true.
- **False Negative:**The model has predicted no, but the actual value was Yes, it is alsocalled as**Type-II error**.
- **False Positive:**The model has predicted Yes, but the actual value was No. It is alsocalled a**Type-I error.**

Need for Confusion Matrix in Machine learning

- It evaluates the performance of the classi cation models, when they makepredictions on test data, and tells how good our classi cation model is.
- It not only tells the error made by the classi ers but also the type of errors such as itis either type-I or type-II error.
- With the help of the confusion matrix, we can calculate the different parameters forthe model, such as accuracy, precision, etc.

Example: We can understand the confusion matrix using an example.

Suppose we are trying to create a model that can predict the result for the disease that iseither a person has that disease or not. So, the confusion matrix for this is given as:

n = 100	Actual: No	Actual: Yes	
Predicted: No	TN: 65	FP: 3	68
Predicted: Yes	FN: 8	TP: 24	32
	73	27	

From the above example, we can conclude that:

- The table is given for the two-class classifier, which has two predictions "Yes" and "NO." Here, Yes defines that patient has the disease, and No defines that patient doesnot has that disease.
- The classifier has made a total of **100 predictions**. Out of 100 predictions, **89 are true predictions**, and **11 are incorrect predictions**.
- The model has given prediction "yes" for 32 times, and "No" for 68 times. Whereas theactual "Yes" was 27, and actual "No" was 73 times.

Calculations using Confusion Matrix:

We can perform various calculations for the model, such as the model's accuracy, using thismatrix. These calculations are given below:

- **Classification Accuracy:** It is one of the important parameters to determine the accuracy of the classification problems. It defines how often the model predicts thecorrect output. It can be calculated as the ratio of the number of correct predictionsmade by the classifier to all number of predictions made by the classifiers. The formula is given below:

$$\text{Accuracy} = \frac{TP+TN}{TP+FP+FN+TN}$$

- **Misclassification rate:** It is also termed as Error rate, and it defines how often the model gives the wrong predictions. The value of error rate can be calculated as thenumber of incorrect predictions to all number of the predictions made by the classifier. The formula is given below:

$$\text{Error rate} = \frac{FP+FN}{TP+FP+FN+TN}$$

- **Precision:** It can be defined as the number of correct outputs provided by the model or out of all positive classes that have predicted correctly by the model, how many ofthem were actually true. It can be calculated using the below formula:

$$\text{Precision} = \frac{TP}{TP+FP}$$

- **Recall:** It is defined as the out of total positive classes, how our model predicted correctly. The recall must be as high as possible.

$$\text{Recall} = \frac{TP}{TP+FN}$$

- **F-measure:** If two models have low precision and high recall or vice versa, it is difficult to compare these models. So, for this purpose, we can use F-score. This score helps us to evaluate the recall and precision at the same time. The F-score is maximum if the recall is equal to the precision. It can be calculated using the below formula:

$$\text{F-measure} = \frac{2*Recall*Precision}{Recall+Precision}$$

Other important terms used in Confusion Matrix:

- **Null Error rate:** It defines how often our model would be incorrect if it always predicted the majority class. As per the accuracy paradox, it is said that "*the best classifier has a higher error rate than the null error rate.*"

- **ROC Curve:** The ROC is a graph displaying a classifier's performance for all possible thresholds. The graph is plotted between the true positive rate (on the Y-axis) and the false Positive rate (on the x-axis).

Code :- https://www.kaggle.com/code/jaysadguru00/starter-bank-customer-churn-modeling-6dbfe05e-a

Conclusion:

In this way we build a a neural network-based classifier that can determine whether they will leave or not in the next 6 months

Group B

Assignment No : 4

Title of the Assignment: Implement K-Nearest Neighbors algorithm on diabetes.csv dataset.Compute confusion matrix, accuracy, error rate, precision and recall on the given dataset.

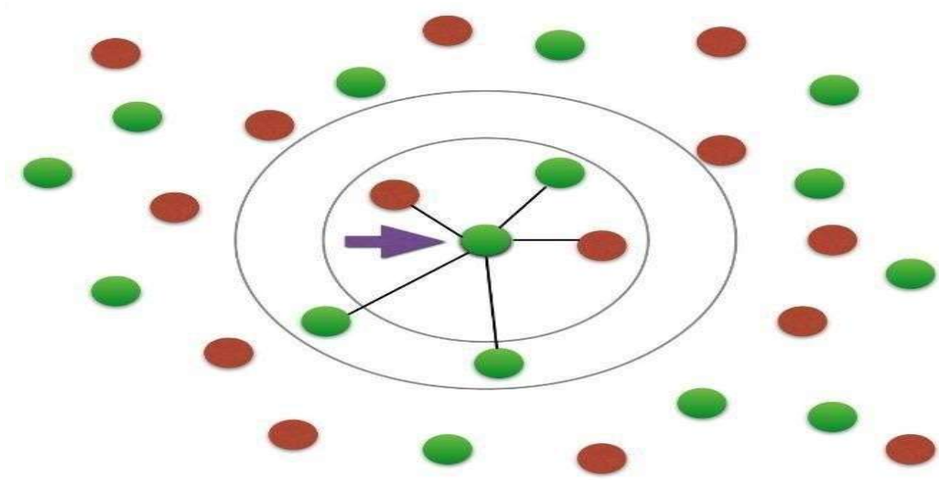
Dataset Description: We will try to build a machine learning model to accurately predict whether or not the patients in the dataset have diabetes or not?
The datasets consists of several medical predictor variables and one target variable, Outcome. Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and so on.

Link for Dataset: Diabetes predication system with KNN algorithm | Kaggle

Objective of the Assignment:
Students should be able to preprocess dataset and identify outliers, to check correlation and implement KNN algorithm and random forest classification models. Evaluate them with respective scores like confusion_matrix, accuracy_score, mean_squared_error, r2_score, roc_auc_score, roc_curve etc.

Prerequisite:

1. Basic knowledge of Python
2. Concept of Confusion Matrix
3. Concept of roc_auc curve.
4. Concept of Random Forest and KNN algorithms



k-Nearest-Neighbors (k-NN) is a supervised machine learning model. Supervised learning is when a model learns from data that is already labeled. A supervised learning model takes in a set of input objects and output values. The model then trains on that data to learn how to map the inputs to the desired output so it can learn to make predictions on unseen data.
k-NN models work by taking a data point and looking at the _k' closest labeled data points. The data point is then assigned the label of the majority of the _k' closest points.
For example, if k = 5, and 3 of points are _green' and 2 are _red', then the data point in question would be labeled _green', since _green' is the majority (as shown in the above graph).
Scikit-learn is a machine learning library for Python. In this tutorial, we will build a k-NN model using Scikit-learn to predict whether or not a patient has diabetes.
Reading in the training data

For our k-NN model, the first step is to read in the data we will use as input. For this example, we are using the diabetes dataset. To start, we will use Pandas to read in the data. I will not go into detail on Pandas, but it is a library you should become familiar with if you're looking to dive further into data science and machine learning.

```
import pandas as pd#read in the data using pandas
df = pd.read_csv(_data/diabetes_data.csv')#check data has been read in properly
df.head()
```

	pregnancies	glucose	diastolic	triceps	insulin	bmi	dpf	age	diabetes
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

Next, let's see how much data we have. We will call the _shape' function on our dataframe to see how many rows and columns there are in our data. The rows indicate the number of patients and the columns indicate the number of features (age, weight, etc.) in the dataset for each patient.


```
#check number of rows and columns in dataset
df.shape

Op → (768,9)
```

We can see that we have 768 rows of data (potential diabetes patients) and 9 columns (8 input features and 1 target output).

Split up the dataset into inputs and targets

Now let‘s split up our dataset into inputs (X) and our target (y). Our input will be every column except ‗diabetes‘ because ‗diabetes‘ is what we will be attempting to predict. Therefore, ‗diabetes‘ will be our target.

We will use pandas ‗drop‘ function to drop the column ‗diabetes‘ from our dataframe and store it in the variable ‗X‘. This will be our input.

```
#create a dataframe with all training data except the target column
X = df.drop(columns=['diabetes'])#check that the target variable has been removed
X.head()
```

	pregnancies	glucose	diastolic	triceps	insulin	bmi	dpf	age
0	6	148	72	35	0	33.6	0.627	50
1	1	85	66	29	0	26.6	0.351	31
2	8	183	64	0	0	23.3	0.672	32
3	1	89	66	23	94	28.1	0.167	21
4	0	137	40	35	168	43.1	2.288	33

We will insert the ‗diabetes‘ column of our dataset into our target variable (y).

```
#separate target values
y = df['diabetes'].values#view target values
y[0:5]
```

```
array([1, 0, 1, 0, 1])
```

Split the dataset into train and test data

Now we will split the dataset into into training data and testing data. The training data is the data thatthe model will learn from. The testing data is the data we will use to see how well the model performs on unseen data.

Scikit-learn has a function we can use called ‚train_test_split‘ that makes it easy for us to split our dataset into training and testing data.

```
from sklearn.model_selection import train_test_split#split dataset into train and test data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=1, stratify=y)
```

‚train_test_split‘ takes in 5 parameters. The first two parameters are the input and target data we split up earlier. Next, we will set ‚test_size‘ to 0.2. This means that 20% of all the data will be used for testing, which leaves 80% of the data as training data for the model to learn from. Setting ‚random_state‘ to 1 ensures that we get the same split each time so we can reproduce our results.

Setting ‚stratify‘ to y makes our training split represent the proportion of each value in the y variable. For example, in our dataset, if 25% of patients have diabetes and 75% don‘t have diabetes, setting ‚stratify‘ to y will ensure that the random split has 25% of patients with diabetes and 75% of patients without diabetes.

Building and training the model

Next, we have to build the model. Here is the code:

```
from sklearn.neighbors import KNeighborsClassifier# Create KNN classifier
knn = KNeighborsClassifier(n_neighbors = 3)# Fit the classifier to the data
knn.fit(X_train,y_train)
```

First, we will create a new k-NN classifier and set ‚n_neighbors‘ to 3. To recap, this means that if at least 2 out of the 3 nearest points to an new data point are patients without diabetes, then the new data point will be labeled as ‚no diabetes‘, and vice versa. In other words, a new data point is labeled with by majority from the 3 nearest points.

We have set ‚n_neighbors‘ to 3 as a starting point. We will go into more detail below on how to better select a value for ‚n_neighbors‘ so that the model can improve its performance.

Next, we need to train the model. In order to train our new model, we will use the ‗fit' function and pass in our training data as parameters to fit our model to the training data.

Testing the model

Once the model is trained, we can use the ‗predict' function on our model to make predictions on our test data. As seen when inspecting ‗y' earlier, 0 indicates that the patient does not have diabetes and 1 indicates that the patient does have diabetes. To save space, we will only show print the first 5 predictions of our test set.

```
#show first 5 model predictions on the test data
knn
```

```
array([0, 0, 0, 0, 1])
```

We can see that the model predicted ‗no diabetes' for the first 4 patients in the test set and ‗has diabetes' for the 5th patient.

Now let's see how our accurate our model is on the full test set. To do this, we will use the ‗score' function and pass in our test input and target data to see how well our model predictions match up to the actual results.

```
#check accuracy of our model on the test data
knn.score(X_test, y_test)
```

```
0.6688311688311688
```

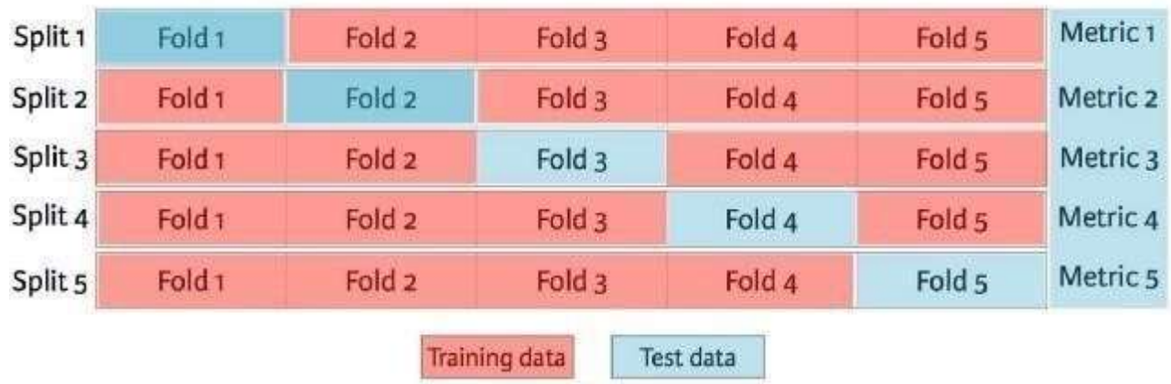
Our model has an accuracy of approximately 66.88%. It's a good start, but we will see how we can increase model performance below.

Congrats! You have now built an amazing k-NN model!

k-Fold Cross-Validation

Cross-validation is when the dataset is randomly split up into ‗k' groups. One of the groups is used as the test set and the rest are used as the training set. The model is trained on the training set and scored on the test set. Then the process is repeated until each unique group as been used as the test set.

For example, for 5-fold cross validation, the dataset would be split into 5 groups, and the model would be trained and tested 5 separate times so each group would get a chance to be the test set. This can be seen in the graph below.



5- fold cross validation (image credit)

The train-test-split method we used in earlier is called ‗holdout'. Cross-validation is better than using the holdout method because the holdout method score is dependent on how the data is split into trainand test sets. Cross-validation gives the model an opportunity to test on multiple splits so we can get a better idea on how the model will perform on unseen data.

In order to train and test our model using cross-validation, we will use the ‗cross_val_score' function with a cross-validation value of 5. ‗cross_val_score' takes in our k-NN model and our data as parameters. Then it splits our data into 5 groups and fits and scores our data 5 seperate times, recording the accuracy score in an array each time. We will save the accuracy scores in the
‗cv_scores' variable.

To find the average of the 5 scores, we will use numpy's mean function, passing in ‗cv_score'. Numpy is a useful math library in Python.

```
from sklearn.model_selection import cross_val_score
import numpy as np#create a new KNN model
knn_cv = KNeighborsClassifier(n_neighbors=3)#train model with cv of 5
cv_scores = cross_val_score(knn_cv, X, y, cv=5)#print each cv score (accuracy) and average them
print(cv_scores)
print( cv_scores mean:{}'.format(np.mean(cv_scores)))
```

```
[ 0.68181818  0.69480519  0.75324675  0.75163399  0.68627451]
cv_scores mean:0.7135557253204311
```


Using cross-validation, our mean score is about 71.36%. This is a more accurate representation of how our model will perform on unseen data than our earlier testing using the holdout method.

Hypertuning model parameters using GridSearchCV

When built our initial k-NN model, we set the parameter ‗n_neighbors' to 3 as a starting point with no real logic behind that choice.

Hypertuning parameters is when you go through a process to find the optimal parameters for yourmodel to improve accuracy. In our case, we will use GridSearchCV to find the optimal value for ‗n_neighbors'.

GridSearchCV works by training our model multiple times on a range of parameters that we specify. That way, we can test our model with each parameter and figure out the optimal values to get the best accuracy results.

For our model, we will specify a range of values for ‗n_neighbors' in order to see which value works best for our model. To do this, we will create a dictionary, setting ‗n_neighbors' as the key and using numpy to create an array of values from 1 to 24.

Our new model using grid search will take in a new k-NN classifier, our param_grid and a cross-validation value of 5 in order to find the optimal value for ‗n_neighbors'.

```
from sklearn.model_selection import GridSearchCV#create new a knn model
knn2 = KNeighborsClassifier()#create a dictionary of all values we want to test for n_neighbors
param_grid = {‗n_neighbors': np.arange(1, 25)}#use gridsearch to test all values for n_neighbors
knn_gscv = GridSearchCV(knn2, param_grid, cv=5)#fit model to data
knn_gscv.fit(X, y)
```

After training, we can check which of our values for ‗n_neighbors' that we tested performed the best. To do this, we will call ‗best_params_' on our model.

```
#check top performing n_neighbors value
knn_gscv.best_params_
```

```
{'n_neighbors': 14}
```

We can see that 14 is the optimal value for ‗n_neighbors'. We can use the ‗best_score_' function to check the accuracy of our model when ‗n_neighbors' is 14. ‗best_score_' outputs the mean accuracy of the scores obtained through cross-validation.

```
#check mean score for the top performing value of n_neighbors
knn_gscv.best_score_
```

```
0.7578125
```

By using grid search to find the optimal parameter for our model, we have improved our model accuracy by over 4%!

Code :- https://www.kaggle.com/code/shrutimechlearn/step-by-step-diabetes-classification-knn-detailed

Conclusion:

In this way we build a a neural network-based classifier that can determine whether they willleave or not in the next 6 months

Group B

Assignment No : 5

Title of the Assignment: Implement K-Means clustering/ hierarchical clustering on sales_data_sample.csv dataset. Determine the number of clusters using the elbow method.

Dataset Description: The data includes the following features:

1. Customer ID
2. Customer Gender
3. Customer Age
4. Annual Income of the customer (in Thousand Dollars)
5. Spending score of the customer (based on customer behavior and spending nature)

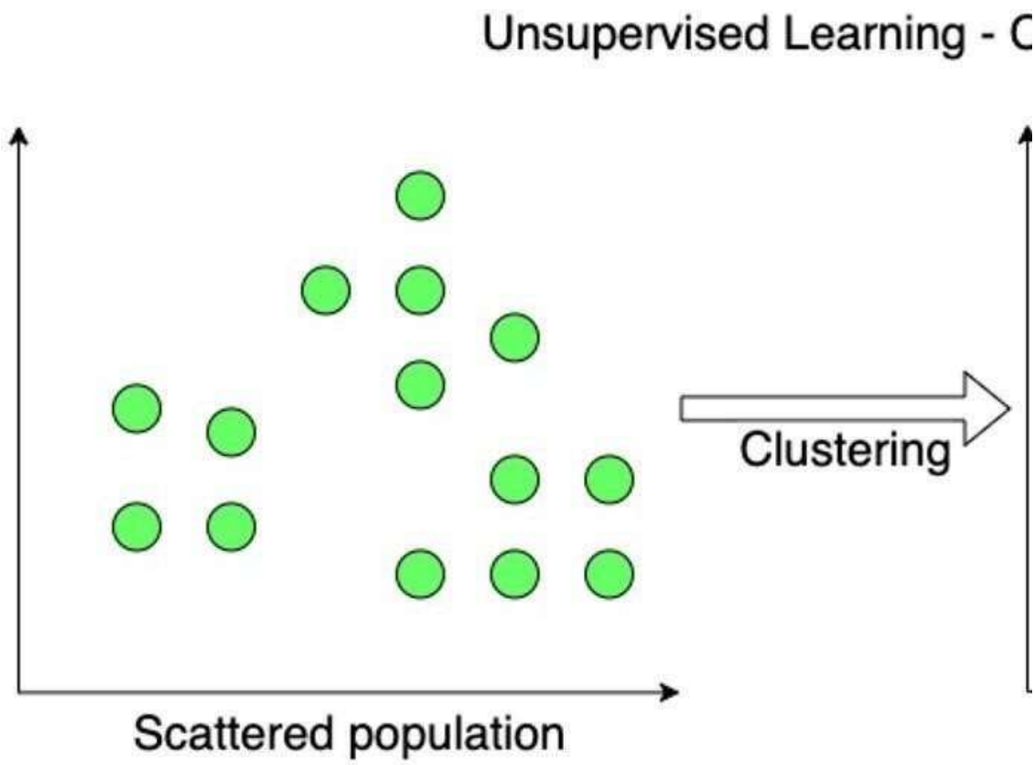
Objective of the Assignment:

Students should able to understand how to use unsupervised learning to segment different-different clusters or groups and used to them to train your model to predict future things.

Prerequisite:

1. Knowledge of Python
2. Unsupervised learning
3. Clustering
4. Elbow method

Clustering algorithms try to find natural clusters in data, the various aspects of how the algorithms to cluster data can be tuned and modified. Clustering is based on the principle that items within the same cluster must be similar to each other. The data is grouped in such a way that related elements are close to each other.



Diverse and different types of data are subdivided into smaller groups.

Uses of Clustering

Marketing:

In the field of marketing, clustering can be used to identify various customer groups with existing customer data. Based on that, customers can be provided with discounts, offers, promo codes etc.

Real Estate:

Clustering can be used to understand and divide various property locations based on value and importance. Clustering algorithms can process through the data and identify various groups of property on the basis of probable price.

BookStore and Library management:

Libraries and Bookstores can use Clustering to better manage the book database. With proper book ordering, better operations can be implemented.

Document Analysis:

Often, we need to group together various research texts and documents according to similarity. And in such cases, we don‘t have any labels. Manually labelling large amounts of data is also not possible. Using clustering, the algorithm can process the text and group it into different themes.

These are some of the interesting use cases of clustering.

K-Means Clustering

K-Means clustering is an unsupervised machine learning algorithm that divides the given data into the given number of clusters. Here, the –K‖ is the given number of predefined clusters, that need to be created.

It is a centroid based algorithm in which each cluster is associated with a centroid. The main idea is to reduce the distance between the data points and their respective cluster centroid.

The algorithm takes raw unlabelled data as an input and divides the dataset into clusters and the process is repeated until the best clusters are found.

K-Means is very easy and simple to implement. It is highly scalable, can be applied to both small and large datasets. There is, however, a problem with choosing the number of clusters or K. Also, with the increase in dimensions, stability decreases. But, overall K Means is a simple and robust algorithm that makes clustering very easy.

```
#Importing the necessary librariesimport
numpy as np
import pandas as pd
import matplotlib.pyplot as pltimport
seaborn as sns
from mpl_toolkits.mplot3d import Axes3D
%matplotlib inline
```

The necessary libraries are imported.

```
#Reading the excel file data=pd.read_excel("Mall_Customers.xlsx")
```

The data is read. I will share a link to the entire code and excel data at the end of the article.

The data has 200 entries, that is data from 200 customers.

```
data.head()
```

So let us have a look at the data.

	CustomerID	Gender	Age	Annual Income (k$)	Spending Score (1-100)
0	1	Male	19	15	39
1	2	Male	21	15	81
2	3	Female	20	16	6
3	4	Female	23	16	77
4	5	Female	31	17	40

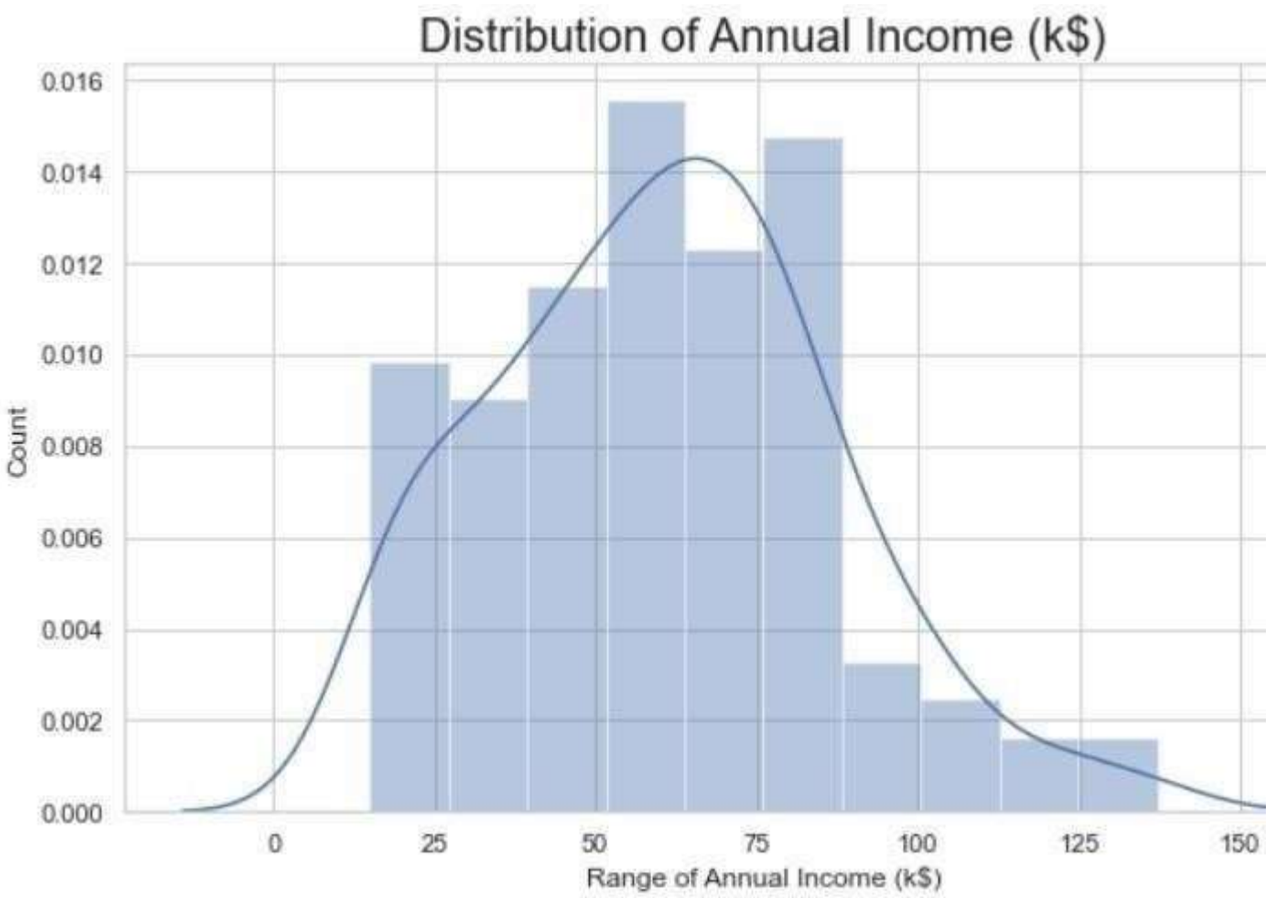
data.corr()

	CustomerID	Age	Annual Income (k$)	Spending Score (
CustomerID	1.000000	-0.026763	0.977548	0.013835
Age	-0.026763	1.000000	-0.012398	-0.327227
Annual Income (k$)	0.977548	-0.012398	1.000000	0.009903
Spending Score (1-100)	0.013835	-0.327227	0.009903	1.000000

The data seems to be interesting. Let us look at the data distribution.

Annual Income Distribution:

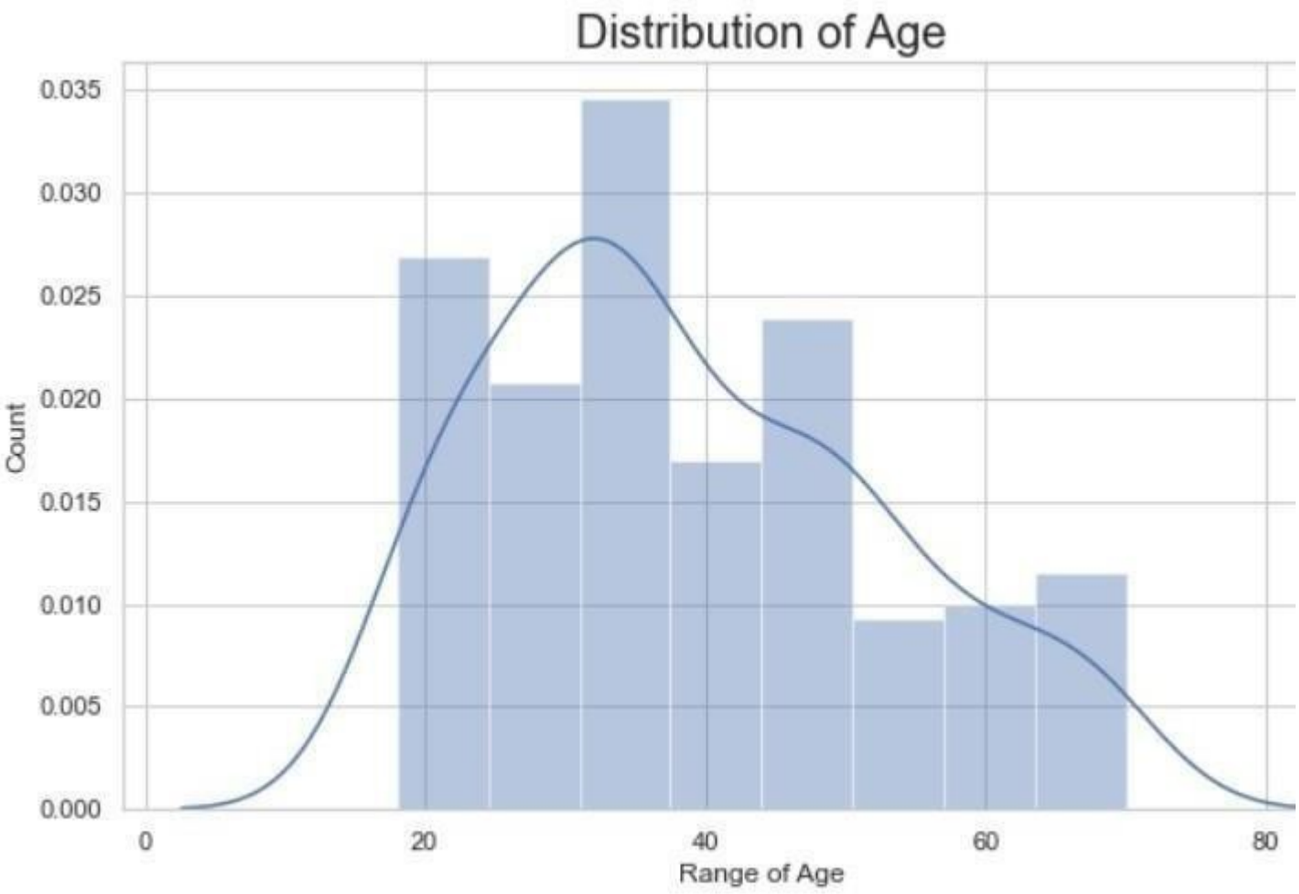
```
#Distribution of Annnual Income
plt.figure(figsize=(10, 6)) sns.set(style = 'whitegrid')
sns.distplot(data['Annual Income (k$)'])
plt.title('Distribution of Annual Income (k$)', fontsize = 20)plt.xlabel('Range of
Annual Income (k$)')
plt.ylabel('Count')
```



Most of the annual income falls between 50K to 85K.

Age Distribution:

```
#Distribution of age
plt.figure(figsize=(10, 6)) sns.set(style
= 'whitegrid')sns.distplot(data['Age'])
plt.title('Distribution of Age', fontsize = 20)plt.xlabel('Range of
Age')
plt.ylabel('Count')
```



There are customers of a wide variety of ages.

Spending Score Distribution:

#Distribution of spending score

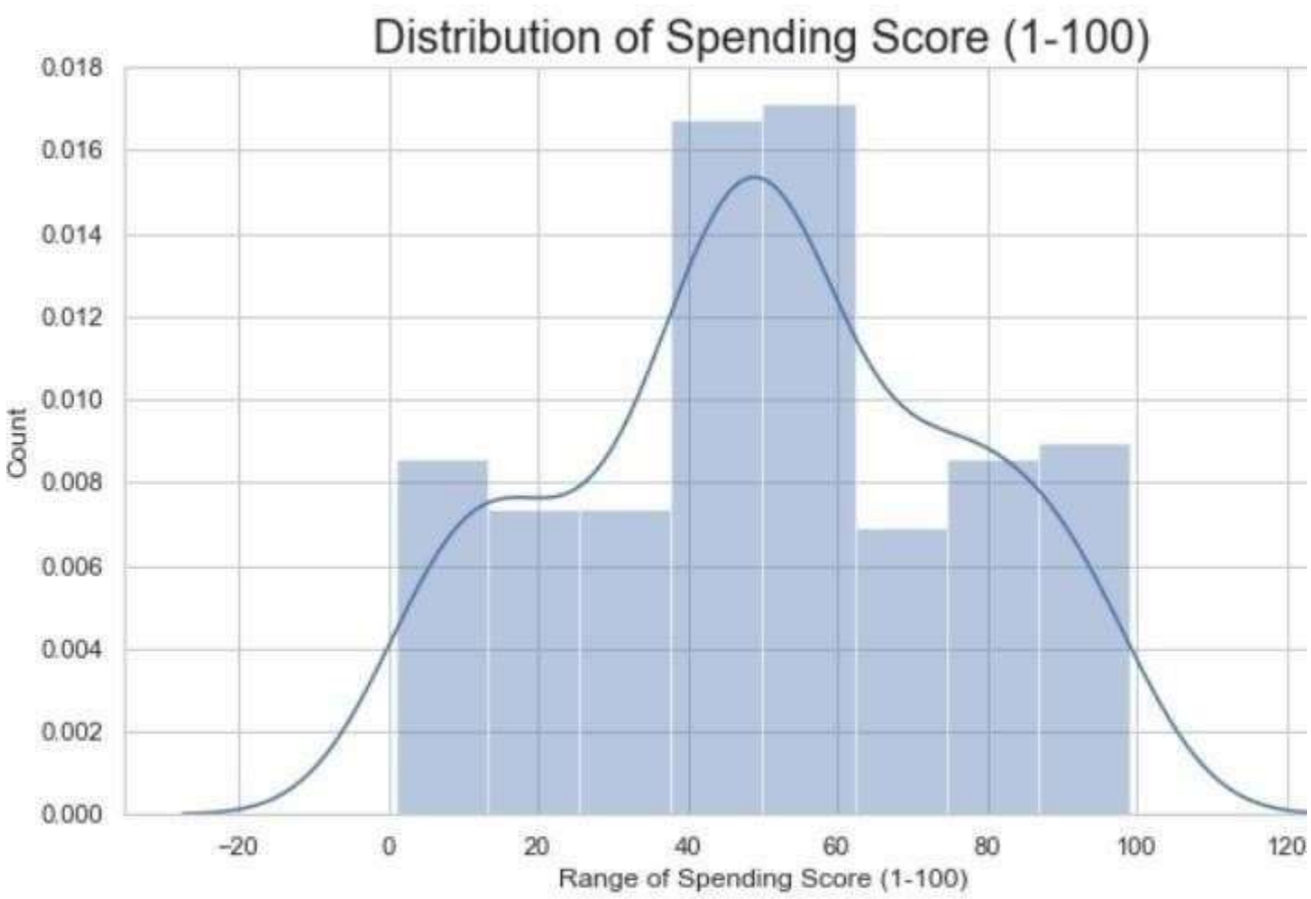
plt.figure(figsize=(10, 6)) sns.set(style =

'whitegrid')

sns.distplot(data['Spending Score (1-100)']) plt.title('Distribution of Spending Score (1-

100)', fontsize = 20)plt.xlabel('Range of Spending Score (1-100)')

plt.ylabel('Count')



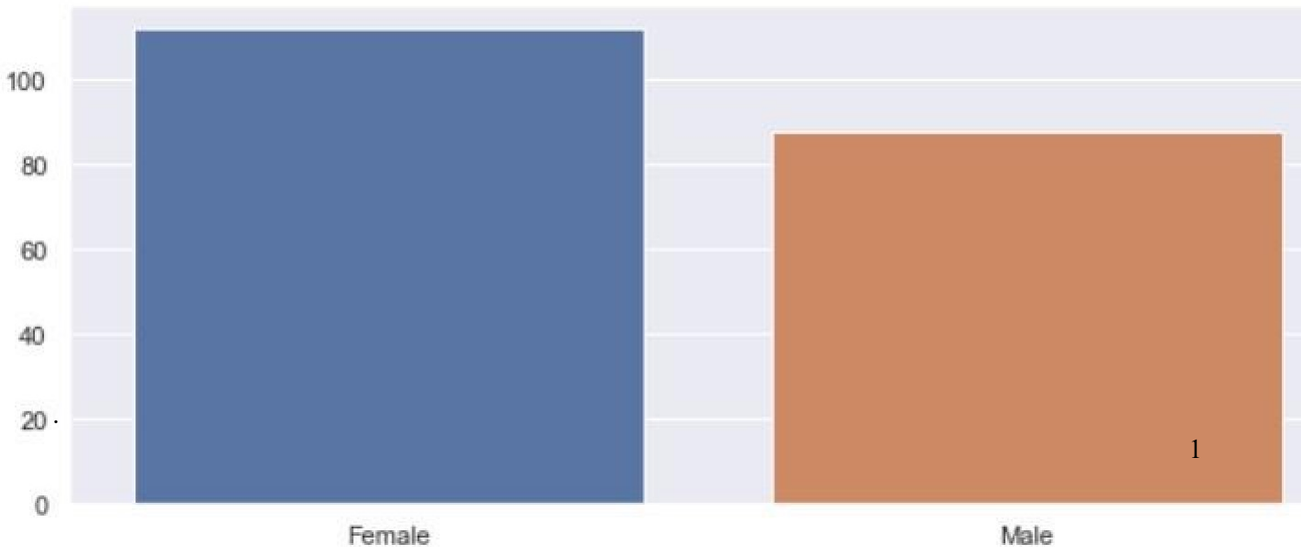
The maximum spending score is in the range of 40 to 60.

Gender Analysis:

genders = data.Gender.value_counts() sns.set_style("darkgrid")

plt.figure(figsize=(10,4)) sns.barplot(x=genders.index,

y=genders.values)plt.show()



More female customers than male.

I have made more visualizations. Do have a look at the GitHub link at the end to understand the data analysis and overall data exploration.

Clustering based on 2 features

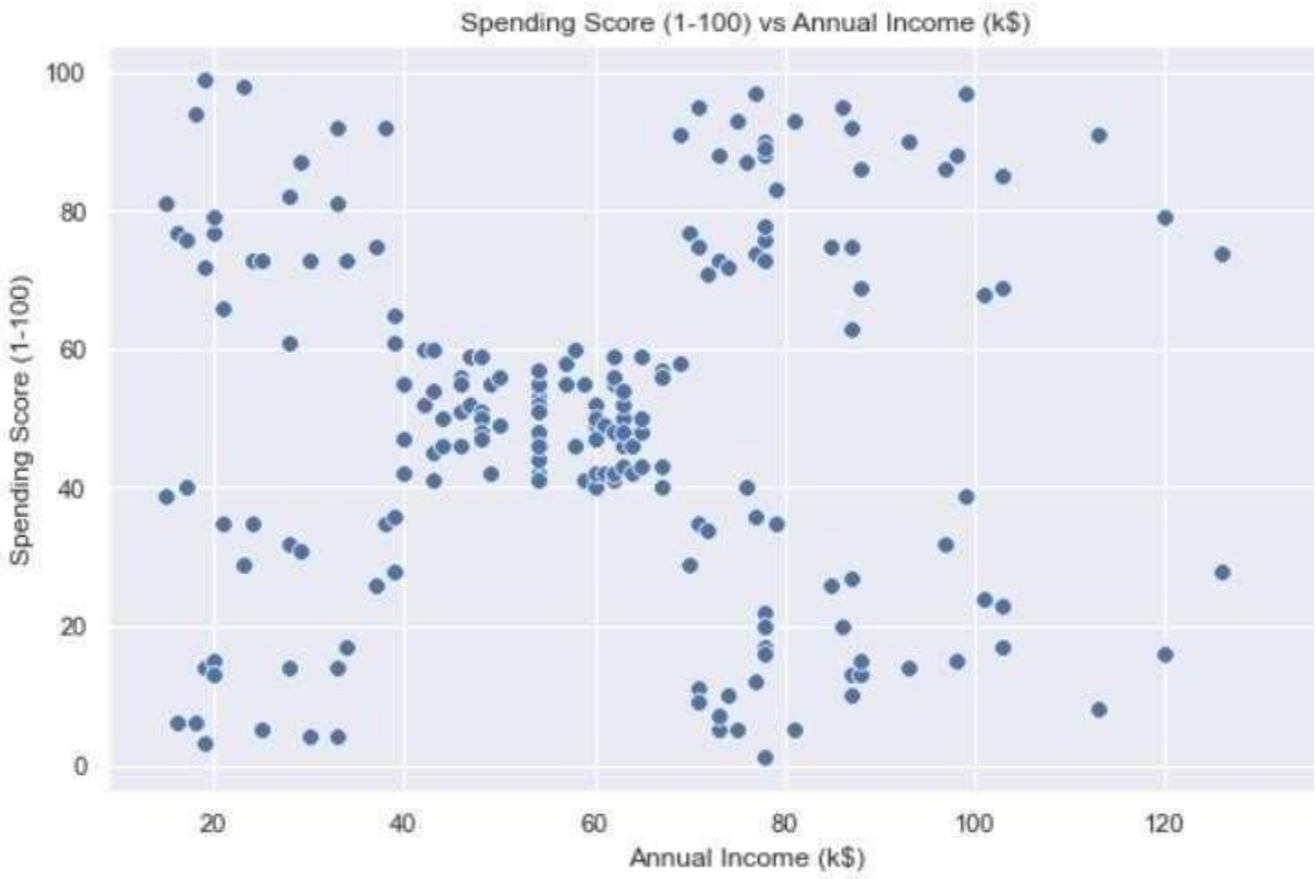
First, we work with two features only, annual income and spending score.

```
#We take just the Annual Income and Spending score df1=data[["CustomerID","Gender","Age","Annual Income
(k$)","Spending Score (1-100)"]]X=df1[["Annual Income (k$)","Spending Score (1-100)"]]
#The input data
X.head()
```

	Annual Income (k$)	Spending Score (1-100)
0	15	39
1	15	81
2	16	6
3	16	77
4	17	40

```
#Scatterplot of the input data
plt.figure(figsize=(10,6))
sns.scatterplot(x = 'Annual Income (k$)',y = 'Spending Score (1-100)',  data = X   ,s = 60
)
plt.xlabel('Annual Income (k$)') plt.ylabel('Spending
Score (1-100)')
plt.title('Spending Score (1-100) vs Annual Income (k$)')plt.show()
```

The data does seem to hold some patterns.

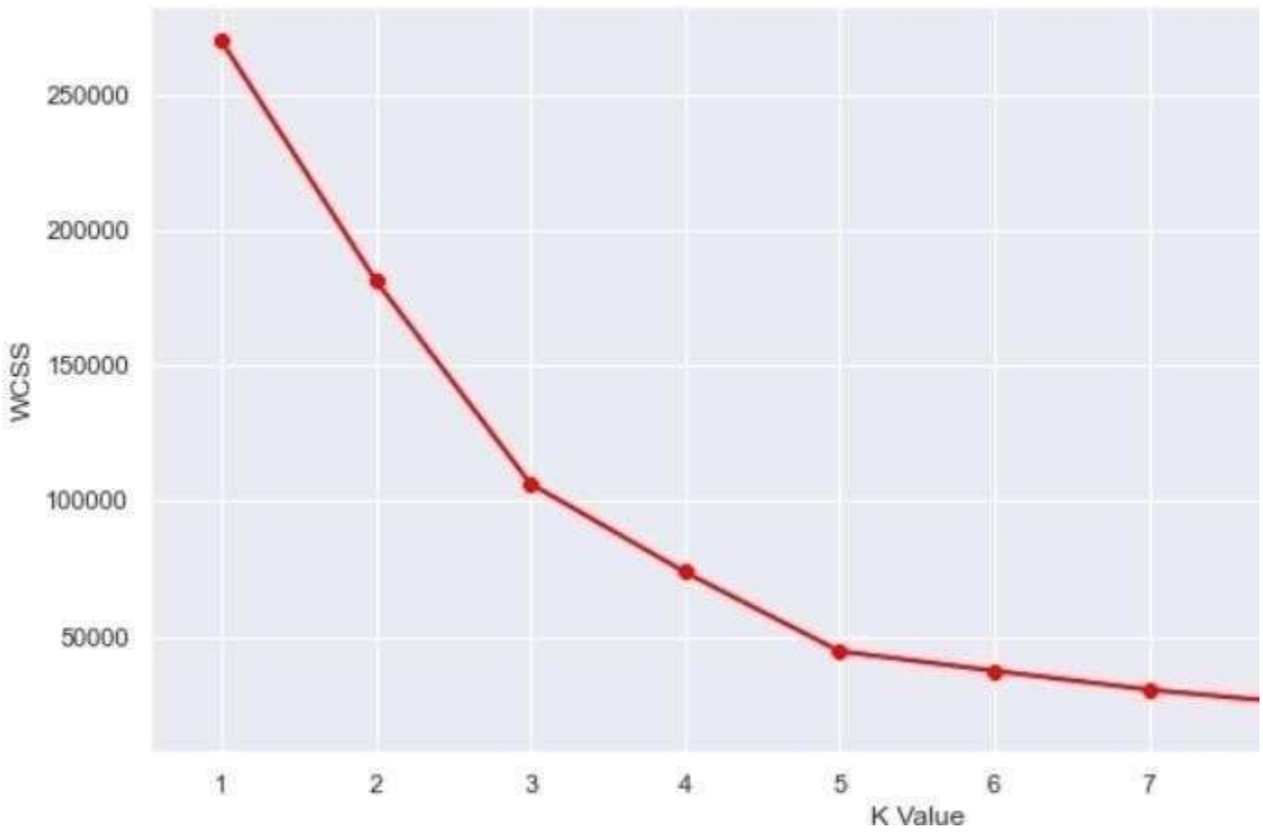



```
#Importing KMeans from sklearn from
sklearn.cluster import KMeans
```

Now we calculate the Within Cluster Sum of Squared Errors (WSS) for different values of k. Next, we choose the k for which WSS first starts to diminish. This value of K gives us the best number of clusters to make from the raw data.

```
wcss=[]
for i in range(1,11):
    km=KMeans(n_clusters=i)km.fit(X)
    wcss.append(km.inertia_)
#The elbow curve plt.figure(figsize=(12,6))
plt.plot(range(1,11),wcss)
plt.plot(range(1,11),wcss, linewidth=2, color="red", marker ="8")plt.xlabel("K Value")
plt.xticks(np.arange(1,11,1))
plt.ylabel("WCSS") plt.show()
```

The plot:



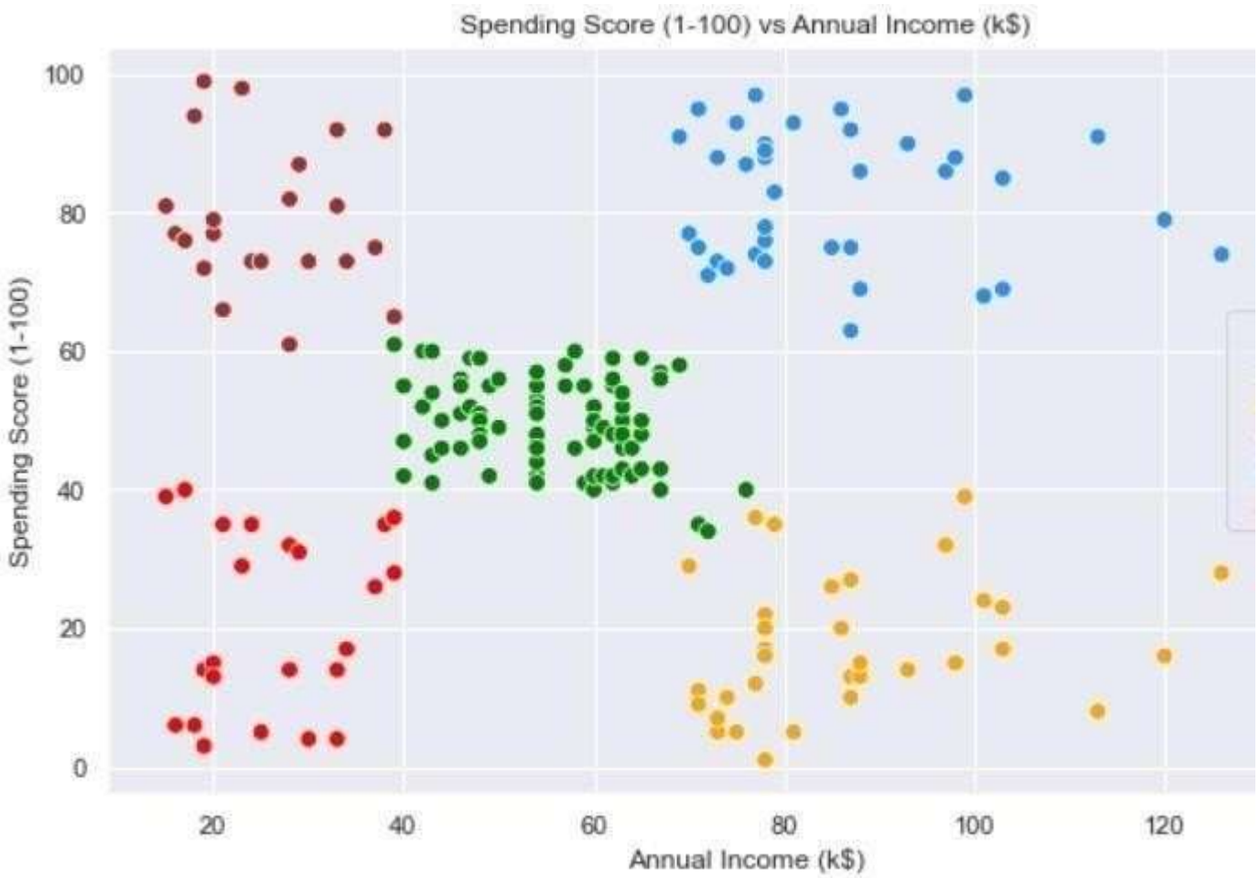
This is known as the elbow graph, the x-axis being the number of clusters, the number of clusters is taken at the elbow joint point. This point is the point where making clusters is most relevant as here the value of WCSS suddenly stops decreasing. Here in the graph, after 5 the drop is minimal, so we take 5 to be the number of clusters.

```
#Taking 5 clusters
km1=KMeans(n_clusters=5)#Fitting the
input data km1.fit(X)
#predicting the labels of the input data
y=km1.predict(X)
#adding the labels to a column named labeldf1["label"] =
y
#The new dataframe with the clustering donedf1.head()
```

The labels added to the data.

	CustomerID	Gender	Age	Annual Income (k$)	Spending Score (1-100)	label
0	1	Male	19	15	39	4
1	2	Male	21	15	81	2
2	3	Female	20	16	6	4
3	4	Female	23	16	77	2
4	5	Female	31	17	40	4

```
#Scatterplot of the clusters
plt.figure(figsize=(10,6))
sns.scatterplot(x = 'Annual Income (k$)',y = 'Spending Score (1-100)',hue="label",
                palette=['green','orange','brown','dodgerblue','red'],legend='full',data = df1  ,s = 60 )
plt.xlabel('Annual Income (k$)') plt.ylabel('Spending
Score (1-100)')
plt.title('Spending Score (1-100) vs Annual Income (k$)')plt.show()
```



We can clearly see that 5 different clusters have been formed from the data. The red cluster is the customers with the least income and least spending score, similarly, the blue cluster is the customers with the most income and most spending score.

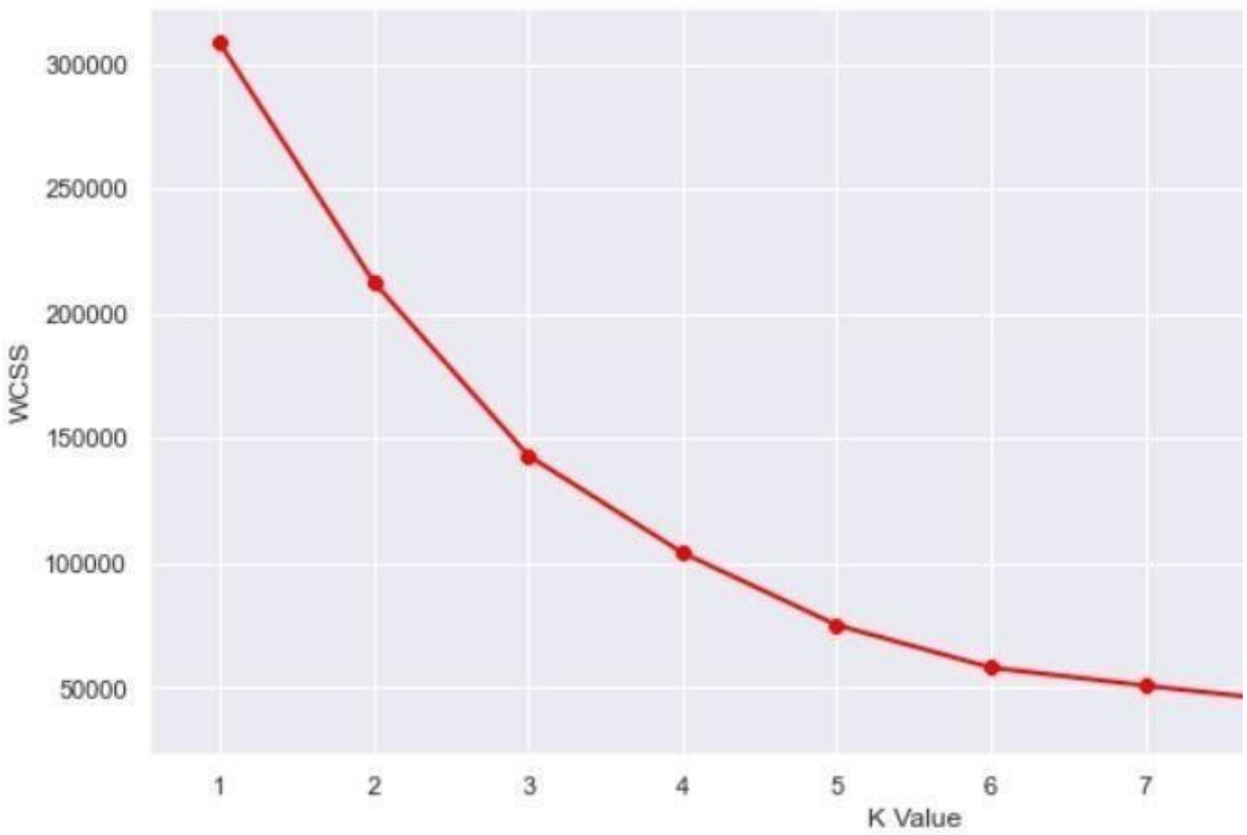
k-Means Clustering on the basis of 3D data

Now, we shall be working on 3 types of data. Apart from the spending score and

annual income of customers, we shall also take in the age of the customers.

```
#Taking the features
X2=df2[["Age","Annual Income (k$)","Spending Score (1-100)"]]
#Now we calculate the Within Cluster Sum of Squared Errors (WSS) for different values ofk.
wcss = []
for k in range(1,11):
    kmeans = KMeans(n_clusters=k, init="k-means++")kmeans.fit(X2)
    wcss.append(kmeans.inertia_)
plt.figure(figsize=(12,6))
plt.plot(range(1,11),wcss, linewidth=2, color="red", marker ="8")plt.xlabel("K Value")
plt.xticks(np.arange(1,11,1))
plt.ylabel("WCSS") plt.show()
```

The WCSS curve.



Here can assume that K=5 will be a good value.

```
#We choose the k for which WSS starts to diminishkm2 =
KMeans(n_clusters=5)
y2 = km.fit_predict(X2)
df2["label"] = y2
#The data with labels
df2.head()
```

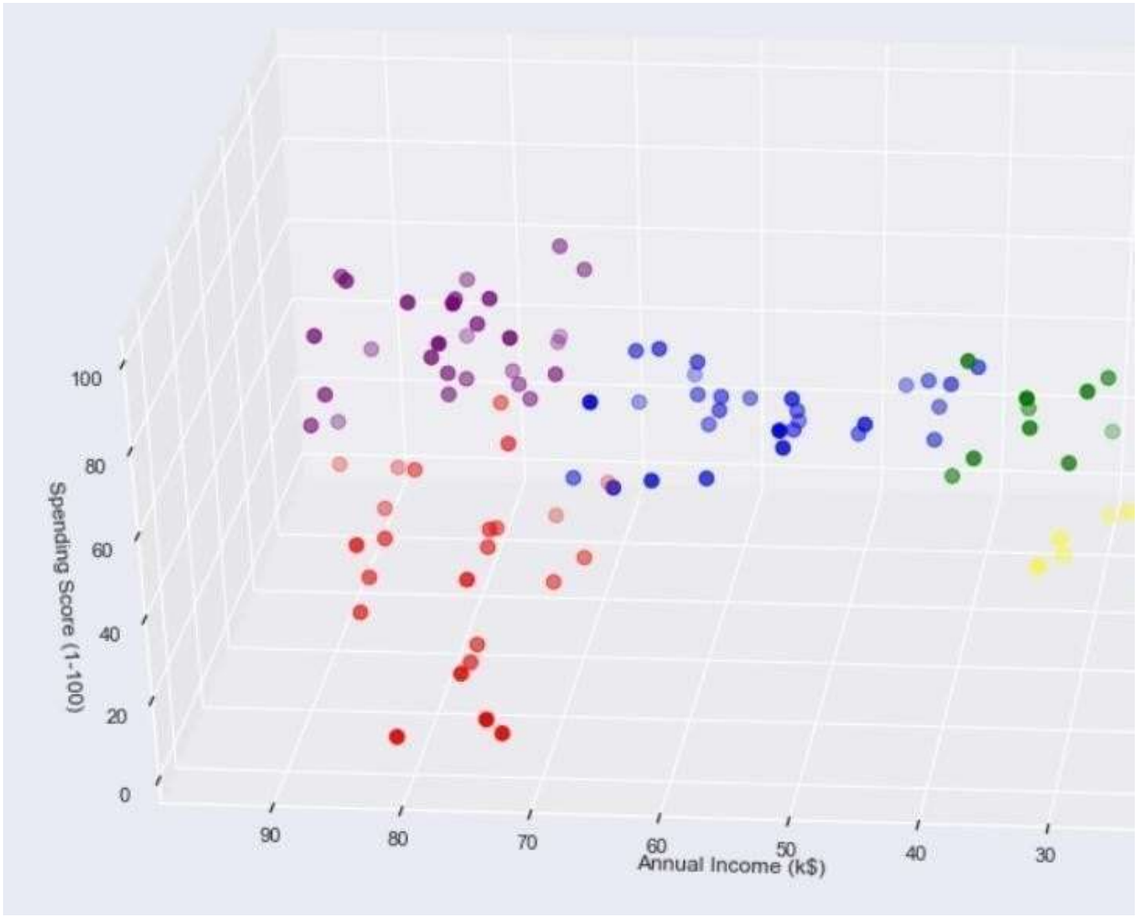
The data:

	CustomerID	Gender	Age	Annual Income (k$)	Spending Score (1-100)	label
0	1	Male	19	15	39	5
1	2	Male	21	15	81	3
2	3	Female	20	16	6	4
3	4	Female	23	16	77	3
4	5	Female	31	17	40	5

Now we plot it.

```
#3D Plot as we did the clustering on the basis of 3 input featuresfig =

plt.figure(figsize=(20,10))

ax = fig.add_subplot(111, projection='3d')

ax.scatter(df2.Age[df2.label == 0], df2["Annual Income (k$)"][df2.label == 0],df2["Spending Score (1-
100)"][df2.label == 0], c='purple', s=60)

ax.scatter(df2.Age[df2.label == 1], df2["Annual Income (k$)"][df2.label == 1],df2["Spending Score (1-
100)"][df2.label == 1], c='red', s=60)

ax.scatter(df2.Age[df2.label == 2], df2["Annual Income (k$)"][df2.label == 2],df2["Spending Score (1-
100)"][df2.label == 2], c='blue', s=60)

ax.scatter(df2.Age[df2.label == 3], df2["Annual Income (k$)"][df2.label == 3],df2["Spending Score (1-
100)"][df2.label == 3], c='green', s=60)

ax.scatter(df2.Age[df2.label == 4], df2["Annual Income (k$)"][df2.label == 4],df2["Spending Score (1-
100)"][df2.label == 4], c='yellow', s=60)

ax.view_init(35, 185) plt.xlabel("Age")

plt.ylabel("Annual Income (k$)")

ax.set_zlabel('Spending Score (1-100)')plt.show()
```

The output:



What we get is a 3D plot. Now, if we want to know the customer IDs, we can do that too.

```
cust1=df2[df2["label"]==1]
print('Number of customer in 1st group=', len(cust1))print('They are -',
cust1["CustomerID"].values) print("                                                ")
cust2=df2[df2["label"]==2]
print('Number of customer in 2nd group=', len(cust2))print('They are -',
cust2["CustomerID"].values) print("                                                ")
cust3=df2[df2["label"]==0]
print('Number of customer in 3rd group=', len(cust3))print('They are -',
cust3["CustomerID"].values) print("                                                ")
cust4=df2[df2["label"]==3]
print('Number of customer in 4th group=', len(cust4))
print('They are -', cust4["CustomerID"].values) print("----------------------")
cust5=df2[df2["label"]==4]
print('Number of customer in 5th group=', len(cust5))print('They are -',
cust5["CustomerID"].values)
```

```
print("  ....................................................................................")
```

The output we get:

```
Number of customer in 1st group= 24
They are - [129 131 135 137 139 141 145 147 149 151 153 155 157 159 161  163  165  167
169 171 173 175 177 179]

---------------------------------------------------------------------------

Number of the customer in 2nd group= 29
They are - [ 47 51 55 56 57 60 67 72 77 78 80 82 84 86 90 93 94 97
99 102 105 108 113 118 119 120 122 123 127]

---------------------------------------------------------------------------

Number of the customer in 3rd group= 28

They are - [124 126 128 130 132 134 136 138 140 142 144 146 148 150 152  154  156  158

160 162 164 166 168 170 172 174 176 178]

---------------------------------------------------------------------------

Number of the customer in 4th group= 22
They are - [ 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42  46]
--------------------------------------------------------------------------------
Number of customer in 5th group= 12
They are - [ 3 7 9 11 13 15 23 25 31 33 35 37]

---------------------------------------------------------------------------
```

So, we used K-Means clustering to understand customer data. K-Means is a good clustering algorithm. Almost all the clusters have similar density. It is also fast and efficient in terms of computational cost.

MINI PROJECT 2

Problem Statement: - Build a machine learning model that predicts the type of people who survived the Titanic shipwreck using passenger data (i.e. name, age, gender, socio-economic class,etc.).

Objective: Students should learn to build a machine learning model.

Theory:

Here's a step-by-step guide on how to approach this problem using Python and some popular libraries:

1. **Data Collection and Understanding**:
    - Start by obtaining the Titanic dataset, which contains passenger information and survival labels. You can find datasets on websites like Kaggle.
2. **Data Pre-processing**:
    - Clean the data by handling missing values, outliers, and redundant features.
    - Perform feature engineering to create relevant features or transform existing ones.
    - Encode categorical variables into numerical format using techniques like one-hot encoding.
3. **Data Splitting**:
    - Split your dataset into a training set and a test set. This allows you to evaluate your model's performance on unseen data.
4. **Select a Machine Learning Algorithm**:
    - Choose a classification algorithm suitable for this problem. Common choices include Decision Trees, Random Forests, Logistic Regression, Support Vector Machines, or Gradient Boosting.
5. **Model Training**:
    - Fit your chosen algorithm to the training data. The model learns patterns from the data.
6. **Model Evaluation**:
    - Evaluate your model's performance using metrics like accuracy, precision, recall, F1-score, and the ROC-AUC score. Cross-validation can help in assessing how well the model generalizes to new data.
7. **Hyperparameter Tuning**:
    - Experiment with different hyperparameters to optimize your model's performance. Techniques like grid search or random search can be helpful.
8. **Model Interpretation**:
    - Understand the feature importance or coefficients of your model to interpret how different features affect survival.
9. **Prediction**:
    - Use your trained model to make predictions on new, unseen data or the test set.
10. **Post-processing**:

- You may need to further process the model's output, such as setting a threshold for classification.

Importing the Libraries

```
# linear algebra
import numpy as np

# data processing
import pandas as pd

# data visualization
import seaborn as sns
%matplotlib inline
from matplotlib import pyplot as plt
from matplotlib import style

# Algorithms
from sklearn import linear_model
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import Perceptron
from sklearn.linear_model import SGDClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC, LinearSVC
from sklearn.naive_bayes import GaussianNB
```

Getting the Data

```
test_df = pd.read_csv("test.csv")
train_df = pd.read_csv("train.csv")
```

Data Exploration/Analysis

```
train_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 891 entries, 0 to 890
Data columns (total 12 columns):
PassengerId     891 non-null int64
Survived        891 non-null int64
Pclass          891 non-null int64
Name            891 non-null object
Sex             891 non-null object
Age             714 non-null float64
SibSp           891 non-null int64
Parch           891 non-null int64
Ticket          891 non-null object
Fare            891 non-null float64
Cabin           204 non-null object
Embarked        889 non-null object
dtypes: float64(2), int64(5), object(5)
memory usage: 83.6+ KB
```

The training-set has 891 examples and 11 features + the target variable (survived). 2 of the features are floats, 5 are integers and 5 areobjects. Below I have listed the features with a short description:

survival: Survival

```
PassengerId: Unique Id of a passenger.
pclass:    Ticket class
sex:    Sex
Age:    Age in years
sibsp:  # of siblings / spouses aboard the Titanic
parch:  # of parents / children aboard the Titanic
ticket:  Ticket number
fare:   Passenger  fare
cabin:    Cabin number
embarked:    Port of Embarkationtrain_df.describe()
```

	PassengerId	Survived	Pclass	Age	SibSp	Parch	Fare
count	891.000000	891.000000	891.000000	714.000000	891.000000	891.000000	891.000000
mean	446.000000	0.383838	2.308642	29.699118	0.523008	0.381594	32.204208
std	257.353842	0.486592	0.836071	14.526497	1.102743	0.806057	49.693429
min	1.000000	0.000000	1.000000	0.420000	0.000000	0.000000	0.000000
25%	223.500000	0.000000	2.000000	20.125000	0.000000	0.000000	7.910400
50%	446.000000	0.000000	3.000000	28.000000	0.000000	0.000000	14.454200
75%	668.500000	1.000000	3.000000	38.000000	1.000000	0.000000	31.000000
max	891.000000	1.000000	3.000000	80.000000	8.000000	6.000000	512.329200

Above we can see that **38% out of the training-set survived the Titanic**. We can also see that the passenger ages range from 0.4 to 80. Ontop of that we can already detect some features, that contain missing values, like the „Age" feature.

```
train_df.head(8)
```

	PassengerId	Survived	Pclass	Name	Sex	Age	SibSp	Parch	Ticket	Fare	Cabin	Embarked
				Harris								
1	2	1	1	Cumings, Mrs. John Bradley (Florence Briggs Th...	female	38.0	1	0	PC 17599	71.2833	C85	C
2	3	1	3	Heikkinen, Miss. Laina	female	26.0	0	0	STON/O2. 3101282	7.9250	NaN	S
3	4	1	1	Futrelle, Mrs. Jacques Heath (Lily May Peel)	female	35.0	1	0	113803	53.1000	C123	S
4	5	0	3	Allen, Mr. William Henry	male	35.0	0	0	373450	8.0500	NaN	S
5	6	0	3	Moran, Mr. James	male	NaN	0	0	330877	8.4583	NaN	Q
6	7	0	1	McCarthy, Mr. Timothy J	male	54.0	0	0	17463	51.8625	E46	S
7	8	0	3	Palsson, Master. Gosta Leonard	male	2.0	3	1	349909	21.0750	NaN	S
8	9	1	3	Johnson, Mrs. Oscar W (Elisabeth Vilhelmina Berg)	female	27.0	0	2	347742	11.1333	NaN	S

From the table above, we can note a few things. First of all, that we **need to convert a lot of features into numeric** ones later on, so that the machine learning algorithms can process them. Furthermore, we can see that the **features have widely different ranges**, that we will need to convert into roughly the same scale. We can also spot some more features,that contain missing values (NaN = not a number), that wee need to deal with.

Let's take a more detailed look at what data is actually missing:

```
total = train_df.isnull().sum().sort_values(ascending=False)
percent_1 = train_df.isnull().sum()/train_df.isnull().count()*100
percent_2 = (round(percent_1, 1)).sort_values(ascending=False)
missing_data = pd.concat([total, percent_2], axis=1, keys=['Total',
'%'])
missing data.head(5)
```

	Total	%
Cabin	687	77.1
Age	177	19.9
Embarked	2	0.2
Fare	0	0.0
Ticket	0	0.0

The Embarked feature has only 2 missing values, which can easily be filled. It will be much more tricky, to deal with the „Age" feature, which has177 missing values. The „Cabin" feature needs further investigation, but it looks like that we might want to drop it from the dataset, since 77 % of it are missing.

```
train_df.columns.values
```

```
array(['PassengerId', 'Survived', 'Pclass', 'Name', 'Sex', 'Age', 'SibSp',
       'Parch', 'Ticket', 'Fare', 'Cabin', 'Embarked'], dtype=object)
```

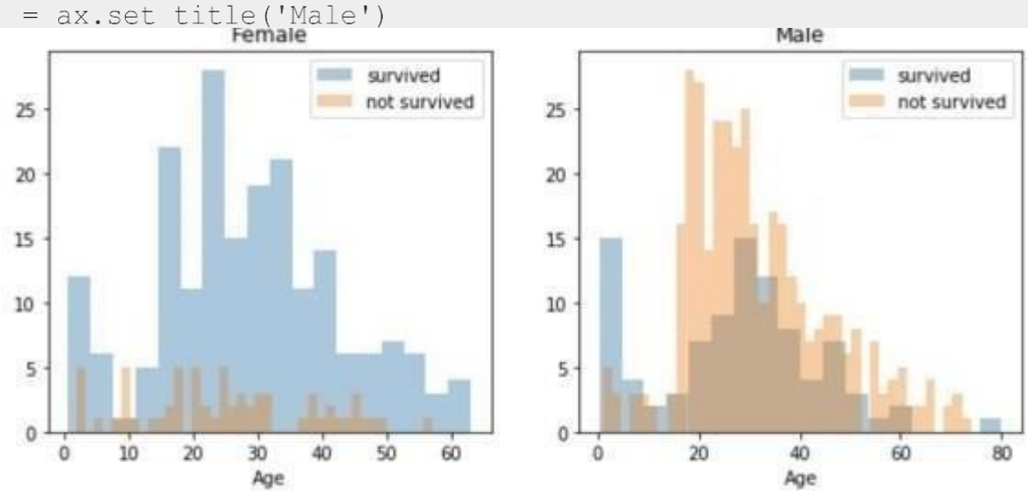
Above you can see the 11 features + the target variable (survived). **Whatfeatures could contribute to a high survival rate ?**

To me it would make sense if everything except „PassengerId", „Ticket" and„Name" would be correlated with a high survival rate.

1. Age and Sex:

```
survived = 'survived'
not_survived = 'not survived'
fig, axes = plt.subplots(nrows=1, ncols=2,figsize=(10, 4))
women = train_df[train_df['Sex']=='female']
men = train_df[train_df['Sex']=='male']
ax = sns.distplot(women[women['Survived']==1].Age.dropna(), bins=18,
label = survived, ax = axes[0], kde =False)
ax = sns.distplot(women[women['Survived']==0].Age.dropna(), bins=40,
label = not_survived, ax = axes[0], kde =False)
ax.legend()
ax.set_title('Female')
ax = sns.distplot(men[men['Survived']==1].Age.dropna(), bins=18, label
= survived, ax = axes[1], kde = False)
```

```
ax = sns.distplot(men[men['Survived']==0].Age.dropna(), bins=40, label
= not_survived, ax = axes[1], kde = False)
ax.legend()
  = ax.set_title('Male')
```



You can see that men have a high probability of survival when they are between 18 and 30 years old, which is also a little bit true for women butnot fully. For women the survival chances are higher between 14 and 40.

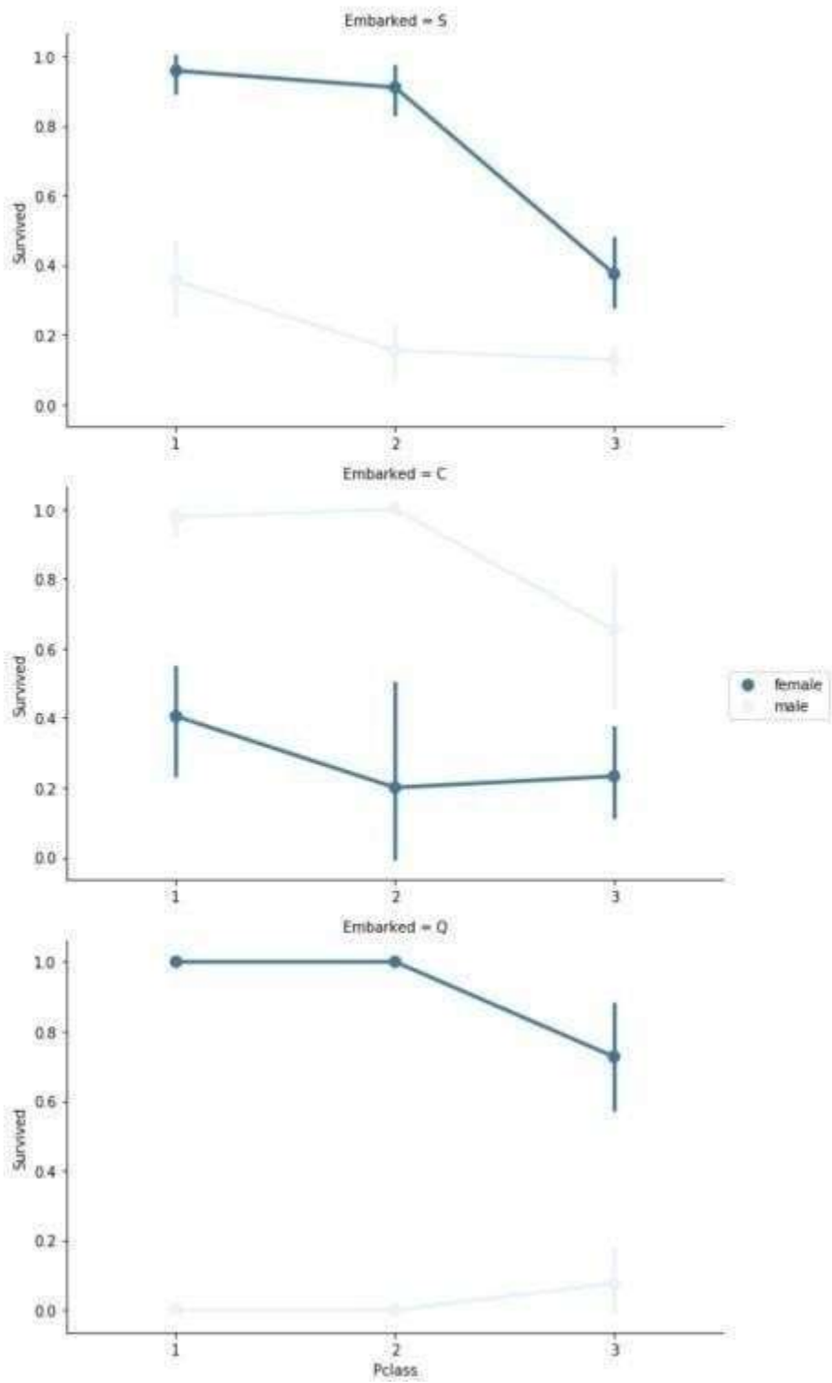
For men the probability of survival is very low between the age of 5 and 18,but that isn‟t true for women. Another thing to note is that infants also have a little bit higher probability of survival.

Since there seem to be **certain ages, which have increased odds ofsurvival** and because I want every feature to be roughly on the same scale, I will create age groups later on.

3. Embarked, Pclass and Sex:

```
FacetGrid = sns.FacetGrid(train_df, row='Embarked', size=4.5,
aspect=1.6)
FacetGrid.map(sns.pointplot, 'Pclass', 'Survived', 'Sex',
palette=None, order=None, hue_order=None )
FacetGrid.add_legend()
```

```
<seaborn.axisgrid.FacetGrid at 0x10ba485c0>
```



Embarked seems to be correlated with survival, depending on the gender.

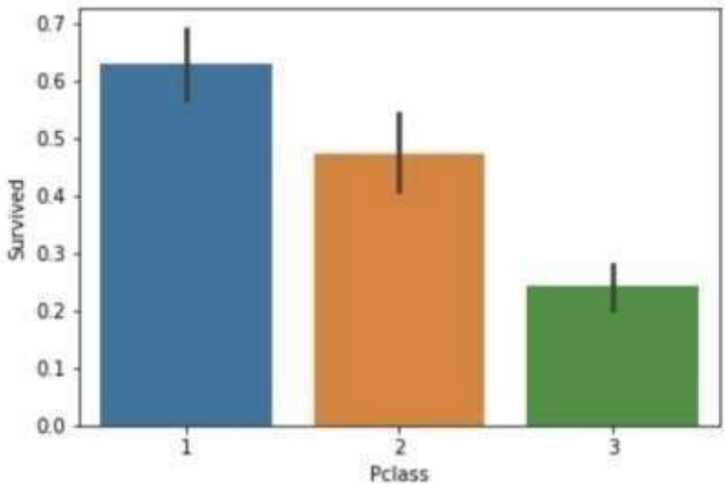
Women on port Q and on port S have a higher chance of survival. The inverse is true, if they are at port C. Men have a high survival probability ifthey are on port C, but a low probability if they are on port Q or S.

Pclass also seems to be correlated with survival. We will generate anotherplot of it below.

4. Pclass:

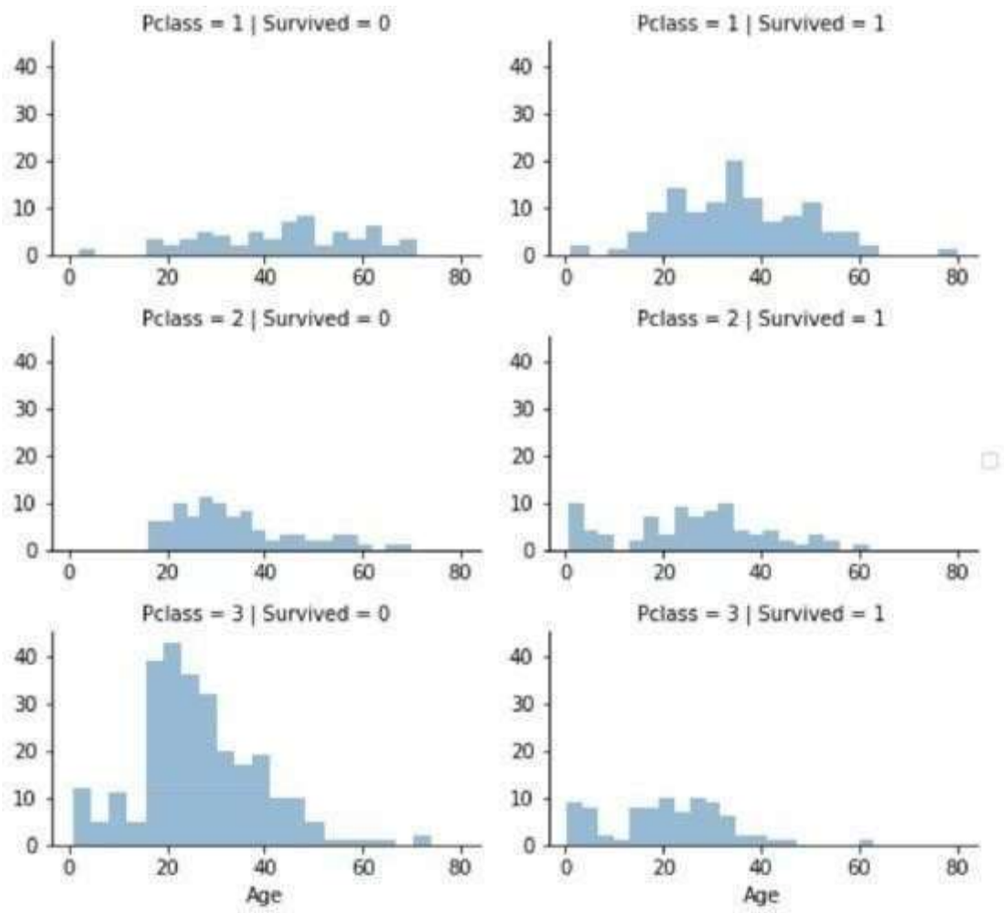
```
sns.barplot(x='Pclass',y='Survived',data=train_df)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x10d1dc7b8>
```



Here we see clearly, that Pclass is contributing to a persons chance of survival, especially if this person is in class 1. We will create another pclassplot below.

```
grid = sns.FacetGrid(train_df, col='Survived', row='Pclass', size=2.2,
aspect=1.6)
grid.map(plt.hist, 'Age', alpha=.5, bins=20)
grid.add_legend();
```



The plot above confirms our assumption about pclass 1, but we can alsospot a high probability that aperson in pclass 3 will not survive.

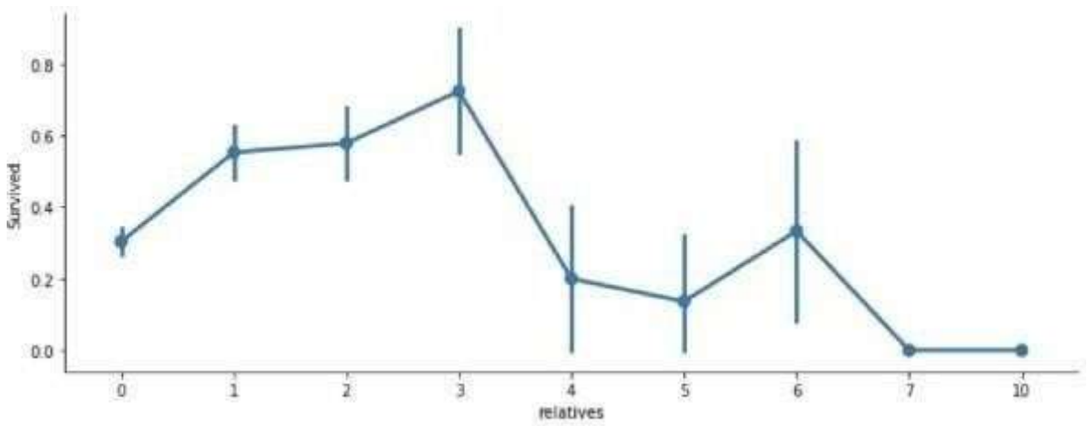
5. SibSp and Parch:

SibSp and Parch would make more sense as a combined feature, thatshows the total number of relatives, a person has on the Titanic. I willcreate it below and also a feature that sows if someone is not alone.

```
data = [train_df, test_df]
for dataset in data:
    dataset['relatives'] = dataset['SibSp'] + dataset['Parch']
    dataset.loc[dataset['relatives'] > 0, 'not_alone'] = 0
    dataset.loc[dataset['relatives'] == 0, 'not_alone'] = 1
    dataset['not_alone'] =
dataset['not alone'].astype(int)train df['not alone'].value counts()
```

```
1    537
0    354
Name: not_alone, dtype: int64
```

```
axes = sns.factorplot('relatives','Survived',
                      data=train df, aspect = 2.5, )
```



Here we can see that you had a high probabilty of survival with 1 to 3 realitves, but a lower one if you had less than 1 or more than 3 (except forsome cases with 6 relatives).

Data Preprocessing

First, I will drop „PassengerId" from the train set, because it does not contribute to a persons survival probability. I will not drop it from the testset, since it is required there for the submission.

```
train df = train df.drop(['PassengerId'], axis=1)
```

Missing Data:

Cabin:

As a reminder, we have to deal with Cabin (687), Embarked (2) and Age(177). First I thought, we have to delete the „Cabin" variable but then I

found something interesting. A cabin number looks like „C123“ and
the **letter refers to the deck**. Therefore we“re going to extract these andcreate a new feature, that contains a persons deck. Afterwords we will convert the feature into a numeric variable. The missing values will be converted to zero. In the picture below you can see the actual decks of thetitanic, ranging from A to G.

```
import re
deck = {"A": 1, "B": 2, "C": 3, "D": 4, "E": 5, "F": 6, "G": 7, "U":
8}
data = [train_df, test_df]

for dataset in data:
    dataset['Cabin'] = dataset['Cabin'].fillna("U0")
    dataset['Deck'] = dataset['Cabin'].map(lambda x: re.compile("([a-
zA-Z]+)").search(x).group())
    dataset['Deck'] = dataset['Deck'].map(deck)
    dataset['Deck'] = dataset['Deck'].fillna(0)
    dataset['Deck'] = dataset['Deck'].astype(int)# we can now drop the
cabin feature
train_df = train_df.drop(['Cabin'], axis=1)
test_df = test_df.drop(['Cabin'], axis=1)
```

Age:

Now we can tackle the issue with the age features missing values. I will create an array that contains random numbers, which are computed basedon the mean age value in regards to the standard deviation and is_null.

```
data = [train_df, test_df]

for dataset in data:
    mean = train_df["Age"].mean()
    std = test_df["Age"].std()
    is_null = dataset["Age"].isnull().sum()
    # compute random numbers between the mean, std and is_null
    rand_age = np.random.randint(mean - std, mean + std, size =
is_null)
    # fill NaN values in Age column with random values generated
    age_slice = dataset["Age"].copy()
    age_slice[np.isnan(age_slice)] = rand_age
    dataset["Age"] = age_slice
    dataset["Age"] =
train df["Age"].astype(int)train df["Age"].isnull().sum()
```

```
0
```


Embarked:

Since the Embarked feature has only 2 missing values, we will just fillthese with the most common one.

```
train_df['Embarked'].describe()
```

```
count     889
unique      3
top         S
freq      644
Name: Embarked, dtype: object
```

```
common_value = 'S'
data = [train_df, test_df]

for dataset in data:
    dataset['Embarked'] = dataset['Embarked'].fillna(common value)
```

Converting Features:

train_df.info()

```
RangeIndex: 891 entries, 0 to 890
Data columns (total 13 columns):
Survived     891 non-null int64
Pclass       891 non-null int64
Name         891 non-null object
Sex          891 non-null object
Age          891 non-null int64
SibSp        891 non-null int64
Parch        891 non-null int64
Ticket       891 non-null object
Fare         891 non-null float64
Embarked     891 non-null object
relatives    891 non-null int64
not_alone    891 non-null int64
Deck         891 non-null int64
dtypes: float64(1), int64(8), object(4)
memory usage: 90.6+ KB
```

Above you can see that „Fare" is a float and we have to deal with 4 categorical features: Name, Sex, Ticket and Embarked. Lets investigateand transfrom one after another.

Fare:

Converting ‑Fare‖ from float to int64, using the ‑astype()‖ function pandasprovides:

```
data = [train_df, test_df]

for dataset in data:
    dataset['Fare'] = dataset['Fare'].fillna(0)
    dataset['Fare'] = dataset['Fare'].astype(int)
```

Name:

We will use the Name feature to extract the Titles from the Name, so thatwe can build a new feature out of that.

```
data = [train_df, test_df]
titles = {"Mr": 1, "Miss": 2, "Mrs": 3, "Master": 4, "Rare": 5}

for dataset in data:
    # extract titles
```

```
    dataset['Title'] = dataset.Name.str.extract(' ([A-Za-z]+)\.',
expand=False)
    # replace titles with a more common title or as Rare
    dataset['Title'] = dataset['Title'].replace(['Lady',
'Countess','Capt', 'Col','Don', 'Dr',\
                                            'Major', 'Rev', 'Sir',
'Jonkheer', 'Dona'], 'Rare')
    dataset['Title'] = dataset['Title'].replace('Mlle', 'Miss')
    dataset['Title'] = dataset['Title'].replace('Ms', 'Miss')
    dataset['Title'] = dataset['Title'].replace('Mme', 'Mrs')
    # convert titles into numbers
    dataset['Title'] = dataset['Title'].map(titles)
    # filling NaN with 0, to get safe
    dataset['Title'] = dataset['Title'].fillna(0)train_df =
train_df.drop(['Name'], axis=1)
test df = test df.drop(['Name'], axis=1)
```

Sex:

Convert „Sex" feature into numeric.

```
genders = {"male": 0, "female": 1}
data = [train_df, test_df]

for dataset in data:
    dataset['Sex'] = dataset['Sex'].map(genders)
```

Ticket:

```
train df['Ticket'].describe()
```

```
count      891
unique     681
top       1601
freq         7
Name: Ticket, dtype: object
```

Since the Ticket attribute has 681 unique tickets, it will be a bit tricky toconvert them into useful categories. So we will drop it from the dataset.

```
train_df = train_df.drop(['Ticket'], axis=1)
test_df = test_df.drop(['Ticket'], axis=1)
```

Embarked:

Convert „Embarked" feature into numeric.

```
ports = {"S": 0, "C": 1, "Q": 2}
data = [train_df, test_df]

for dataset in data:
    dataset['Embarked'] = dataset['Embarked'].map(ports)
```

Creating Categories:

We will now create categories within the following features:

Age:

Now we need to convert the „age‟ feature. First we will convert it from floatinto integer. Then we will create the new „AgeGroup‖ variable, by categorizing every age into a group. Note that it is important to place attention on how you form these groups, since you don‟t want for examplethat 80% of your data falls into group 1.

```
data = [train_df, test_df]
for dataset in data:
    dataset['Age'] = dataset['Age'].astype(int)
    dataset.loc[ dataset['Age'] <= 11, 'Age'] = 0
    dataset.loc[(dataset['Age'] > 11) & (dataset['Age'] <= 18), 'Age']
= 1
    dataset.loc[(dataset['Age'] > 18) & (dataset['Age'] <= 22), 'Age']
= 2
    dataset.loc[(dataset['Age'] > 22) & (dataset['Age'] <= 27), 'Age']
= 3
    dataset.loc[(dataset['Age'] > 27) & (dataset['Age'] <= 33), 'Age']
= 4
    dataset.loc[(dataset['Age'] > 33) & (dataset['Age'] <= 40), 'Age']
= 5
    dataset.loc[(dataset['Age'] > 40) & (dataset['Age'] <= 66), 'Age']
= 6
    dataset.loc[ dataset['Age'] > 66, 'Age'] = 6

# let's see how it's distributed train df['Age'].value counts()
```

```
4    165
6    158
5    147
3    129
2    124
1    100
0     68
Name: Age, dtype: int64
```

Fare:

For the „Fare‟ feature, we need to do the same as with the „Age‟ feature. Butit isn‟t that easy, because if we cut the range of the fare values into a few equally big categories, 80% of the values would fall into the first category. Fortunately, we can use sklearn -qcut()‖ function, that we can use to see,

how we can form the categories.

```
train_df.head(10)
```

	Survived	Pclass	Sex	Age	SibSp	Parch	Fare	Embarked	relatives	not_alone	Deck	Title
0	0	3	0	2	1	0	7	0	1	0	8	1
1	1	1	1	5	1	0	71	1	1	0	3	3
2	1	3	1	3	0	0	7	0	0	1	8	2
3	1	1	1	5	1	0	53	0	1	0	3	3
4	0	3	0	5	0	0	8	0	0	1	8	1
5	0	3	0	4	0	0	8	2	0	1	8	1
6	0	1	0	6	0	0	51	0	0	1	5	1
7	0	3	0	0	3	1	21	0	4	0	8	4
8	1	3	1	3	0	2	11	0	2	0	8	3
9	1	2	1	1	1	0	30	1	1	0	8	3

```
data = [train_df, test_df]

for dataset in data:
    dataset.loc[ dataset['Fare'] <= 7.91, 'Fare'] = 0
    dataset.loc[(dataset['Fare'] > 7.91) & (dataset['Fare'] <=
14.454), 'Fare'] = 1
    dataset.loc[(dataset['Fare'] > 14.454) & (dataset['Fare'] <= 31),
'Fare']   = 2
    dataset.loc[(dataset['Fare'] > 31) & (dataset['Fare'] <= 99),
'Fare']   = 3
    dataset.loc[(dataset['Fare'] > 99) & (dataset['Fare'] <= 250),
'Fare']   = 4
    dataset.loc[ dataset['Fare'] > 250, 'Fare'] = 5
    dataset['Fare'] = dataset['Fare'].astype(int)
```

Creating new Features

I will add two new features to the dataset, that I compute out of otherfeatures.

1. Age times Class

```
data = [train_df, test_df]
for dataset in data:
    dataset['Age Class']= dataset['Age']* dataset['Pclass']
```

2. Fare per Person

```
for dataset in data:
    dataset['Fare_Per_Person'] =
dataset['Fare']/(dataset['relatives']+1)
    dataset['Fare_Per_Person'] =
dataset['Fare_Per_Person'].astype(int)# Let's take a last look at the
training set, before we start training the models.
train df.head(10)
```

	Survived	Pclass	Sex	Age	SibSp	Parch	Fare	Embarked	relatives	not_alone	Deck	Title	Age_Class	Fare_Per_Pers
0	0	3	0	2	1	0	0	0	1	0	8	1	6	0
1	1	1	1	5	1	0	3	1	1	0	3	3	5	1
2	1	3	1	3	0	0	0	0	0	1	8	2	9	0
3	1	1	1	5	1	0	3	0	1	0	3	3	5	1
4	0	3	0	5	0	0	1	0	0	1	8	1	15	1
5	0	3	0	4	0	0	1	2	0	1	8	1	12	1
6	0	1	0	6	0	0	3	0	0	1	5	1	6	3
7	0	3	0	0	3	1	2	0	4	0	8	4	0	0
8	1	3	1	3	0	2	1	0	2	0	8	3	9	0
9	1	2	1	1	1	0	2	1	1	0	8	3	2	1
10	1	3	1	0	1	1	2	0	2	0	7	2	0	0

Building Machine Learning Models

Now we will train several Machine Learning models and compare their results. Note that because the dataset does not provide labels for their testing-set, we need to use the predictions on the training set to comparethe algorithms with each other. Later on, we will use cross validation.

```
X_train = train_df.drop("Survived", axis=1)
Y_train = train_df["Survived"]
X test  = test df.drop("PassengerId", axis=1).copy()
```

Stochastic Gradient Descent (SGD):

```
sgd = linear_model.SGDClassifier(max_iter=5, tol=None)
sgd.fit(X_train, Y_train)
Y_pred = sgd.predict(X_test)

sgd.score(X_train, Y_train)

acc sgd = round(sgd.score(X train, Y train) * 100, 2)
```

Random Forest:

```
random_forest = RandomForestClassifier(n_estimators=100)
random_forest.fit(X_train, Y_train)

Y_prediction = random_forest.predict(X_test)

random_forest.score(X_train, Y_train)
acc_random_forest = round(random_forest.score(X_train, Y_train) * 100,
2)
```

Logistic Regression:

```
logreg = LogisticRegression()
logreg.fit(X_train, Y_train)

Y_pred = logreg.predict(X_test)

acc log = round(logreg.score(X train, Y train) * 100, 2)
```

K Nearest Neighbor:

```
# KNN knn = KNeighborsClassifier(n_neighbors = 3) knn.fit(X_train,
Y_train) Y_pred = knn.predict(X_test) acc_knn =
round(knn.score(X_train, Y_train) * 100, 2)
```

Gaussian Naive Bayes:

```
gaussian = GaussianNB() gaussian.fit(X_train, Y_train) Y_pred =
gaussian.predict(X_test)  acc_gaussian = round(gaussian.score(X_train,
Y_train) * 100, 2)
```

Perceptron:

```
perceptron = Perceptron(max_iter=5)
perceptron.fit(X_train, Y_train)

Y_pred = perceptron.predict(X_test)

acc perceptron = round(perceptron.score(X train, Y train) * 100, 2)
```

Linear Support Vector Machine:

```
linear_svc = LinearSVC()
linear_svc.fit(X_train, Y_train)

Y_pred = linear_svc.predict(X_test)

acc linear svc = round(linear svc.score(X train, Y train) * 100, 2)
```

Decision Tree

```
decision_tree = DecisionTreeClassifier() decision_tree.fit(X_train,
Y_train) Y_pred = decision_tree.predict(X_test) acc_decision_tree =
round(decision_tree.score(X_train, Y_train) * 100, 2)
```

Which is the best Model ?

```
results = pd.DataFrame({
    'Model': ['Support Vector Machines', 'KNN', 'Logistic Regression',
              'Random Forest', 'Naive Bayes', 'Perceptron',
              'Stochastic Gradient Decent',
              'Decision Tree'],
    'Score': [acc_linear_svc, acc_knn, acc_log,
              acc_random_forest, acc_gaussian, acc_perceptron,
              acc_sgd, acc_decision_tree]})
result_df = results.sort_values(by='Score', ascending=False)
result_df = result_df.set_index('Score')
result_df.head(9)
```

Score	Model
92.82	Random Forest
92.82	Decision Tree
87.32	KNN
81.14	Logistic Regression
80.81	Support Vector Machines
80.70	Perceptron
77.10	Naive Bayes
76.99	Stochastic Gradient Decent

As we can see, the Random Forest classifier goes on the first place. Butfirst, let us check, how random-forest performs, when we use cross validation.

K-Fold Cross Validation:

K-Fold Cross Validation randomly splits the training data into **K subsetscalled folds**. Let‟s image we would split our data into 4 folds (K = 4). Ourrandom forest model would be trained and evaluated 4 times, using a different fold for evaluation everytime, while it would be trained on the remaining 3 folds.

The image below shows the process, using 4 folds (K = 4). Every row represents one training + evaluation process. In the first row, the model get‟s trained on the first, second and third subset and evaluated on the fourth. In the second row, the model get‟s trained on the second, third andfourth subset and evaluated on the first. K-Fold Cross Validation repeats this process till every fold acted once as an evaluation fold.

Training	Training	Training	Evaluation
1	2	3	**4**
2	3	4	**1**
3	4	1	**2**
4	1	2	**3**

The result of our K-Fold Cross Validation example would be an array thatcontains 4 different scores. We then need to compute the mean and the standard deviation for these scores.

The code below perform K-Fold Cross Validation on our random forestmodel, using 10 folds (K = 10). Therefore it outputs an array with 10 different scores.

```
from sklearn.model_selection import cross_val_score
rf = RandomForestClassifier(n_estimators=100)
scores = cross_val_score(rf, X_train, Y_train, cv=10, scoring =
"accuracy")print("Scores:", scores)
print("Mean:", scores.mean())
print("Standard Deviation:", scores.std())
```

```
Scores: [ 0.76666667  0.82222222  0.7752809   0.82022472  0.85393258  0.86516854
  0.83146067  0.76404494  0.85393258  0.852272731
Mean: 0.820520655998
Standard Deviation: 0.0367328665466
```

This looks much more realistic than before. Our model has a average accuracy of 82% with a standard deviation of 4 %. The standard deviationshows us, how precise the estimates are .

This means in our case that the accuracy of our model can differ + — 4%.

I think the accuracy is still really good and since random forest is an easyto use model, we will try to increase it‟s performance even further in the following section.

Random Forest

What is Random Forest ?

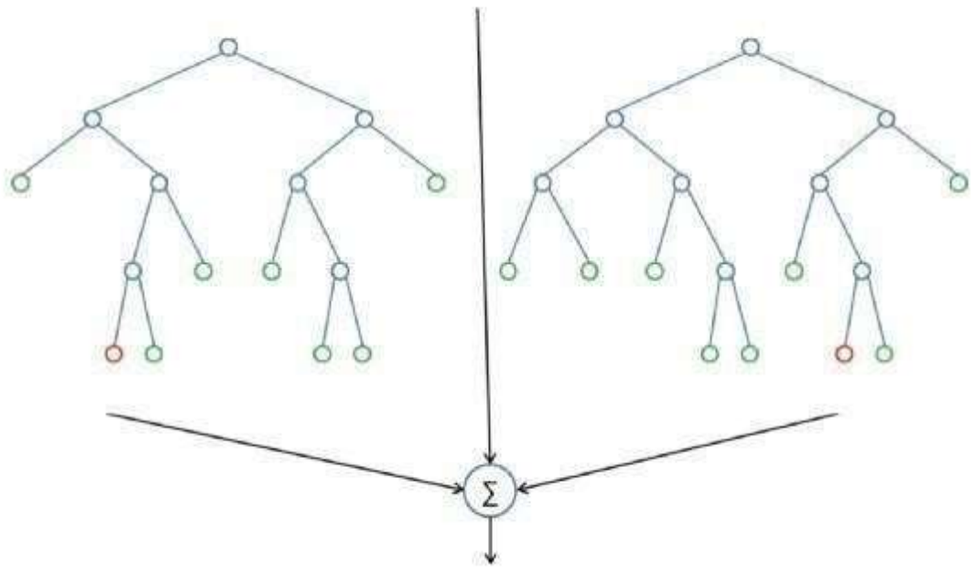
Random Forest is a supervised learning algorithm. Like you can already see from it‟s name, it creates a forest and makes it somehow random. The
„forest– it builds, is an ensemble of Decision Trees, most of the time trained with the ‑bagging‖ method. The general idea of the bagging method is that a combination of learning models increases the overallresult.

To say it in simple words: Random forest builds multiple decision treesand merges them together to get a more accurate and stable prediction.

One big advantage of random forest is, that it can be used for both classification and regression problems, which form the majority of currentmachine learning systems. With a few exceptions a random-forest classifier has all the hyperparameters of a decision-tree classifier and alsoall the hyperparameters of a bagging classifier, to control the ensemble itself.

The random-forest algorithm brings extra randomness into the model, when it is growing the trees. Instead of searching for the best feature whilesplitting a node, it searches for the best feature among a random subset offeatures. This process creates a wide diversity, which generally results in abetter model. Therefore when you are growing a tree in random forest, only a random subset of the features is considered for splitting a node. Youcan even make trees more random, by using random thresholds on top of it, for each feature rather than searching for the best possible thresholds (like a normal decision tree does).

Below you can see how a random forest would look like with two trees:



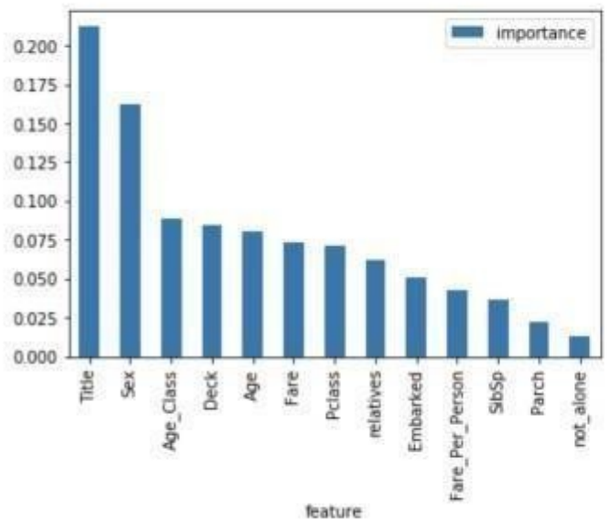
nodes, that use that

feature, reduce impurity on average (across all trees in the forest). It computes this score automaticall for each feature after training and scalesthe results so that the sum of all importances is equal to 1. We will acces this below:

```
importances =
pd.DataFrame({'feature':X_train.columns,'importance':np.round(random_f
orest.feature_importances_,3)})
importances =
importances.sort_values('importance',ascending=False).set_index('featu
re')importances.head(15)
```

	importance
feature	
Title	0.212
Sex	0.162
Age_Class	0.089
Deck	0.084
Age	0.080
Fare	0.073
Pclass	0.071
relatives	0.062
Embarked	0.051
Fare_Per_Person	0.043
SibSp	0.036
Parch	0.022
not_alone	0.013

```
<matplotlib.axes._subplots.AxesSubplot at 0x1a157c1e10>
```



Conclusion:

not_alone and Parch doesn‟t play a significant role in our random forestclassifiers prediction process.Because of that I will drop them from thedataset and train the classifier again. We could also remove more or less features, but this would need a more detailed investigation of the featureseffect on our model. But Ithink it‟s just fine to remove only Alone and Parch.

```
train_df  = train_df.drop("not_alone", axis=1)
test_df  = test_df.drop("not_alone", axis=1)

train_df  = train_df.drop("Parch", axis=1)
test_df  = test_df.drop("Parch", axis=1)
```

Training random forest again:

```
# Random Forest

random_forest = RandomForestClassifier(n_estimators=100, oob_score =
True)
random_forest.fit(X_train, Y_train)
Y_prediction = random_forest.predict(X_test)

random_forest.score(X_train, Y_train)

acc_random_forest = round(random_forest.score(X_train, Y_train) * 100,
2)
print(round(acc random forest,2,), "%")
```

92.82%

Our random forest model predicts as good as it did before. A general ruleis that, **the more features you have, the more likely your model will suffer from overfitting** and vice versa. But I think our data looksfine for now and hasn't too much features.

There is also another way to evaluate a random-forest classifier, which is probably much more accurate than the score we used before. What I am talking about is the **out-of-bag samples** to estimate the generalization accuracy. I will not go into details here about how it works. Just note that out-of-bag estimate is as accurate as using a test set of the same size as thetraining set. Therefore, using the out-of-bag error estimate removes the need for a set aside test set.

oob score: 81.82 %

```
print("oob score:", round(random_forest.oob_score_, 4)*100, "%")
```

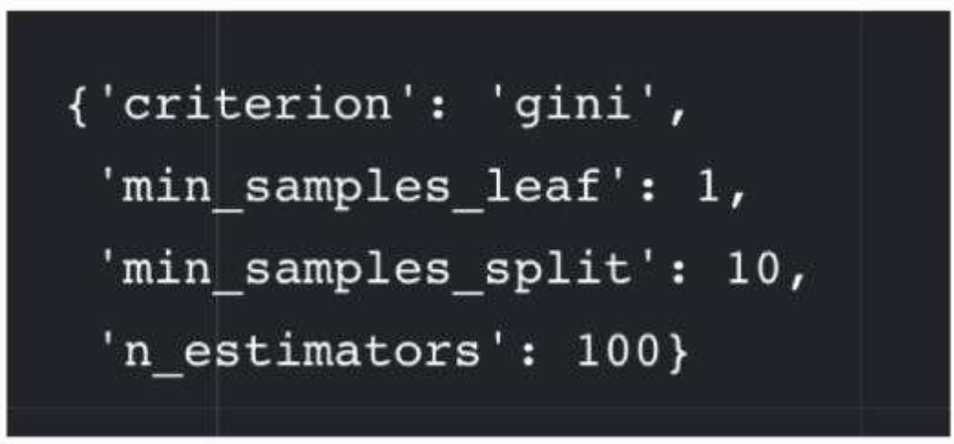

Now we can start tuning the hyperameters of random forest.

Hyperparameter Tuning

Below you can see the code of the hyperparamter tuning for the parameters criterion, min_samples_leaf, min_samples_split andn_estimators.

I put this code into a markdown cell and not into a code cell, because it takes a long time to run it. Directly underneeth it, I put a screenshot of thegridsearch's output.

```
param_grid = { "criterion" : ["gini", "entropy"], "min_samples_leaf" :
[1, 5, 10, 25, 50, 70], "min_samples_split" : [2, 4, 10, 12, 16, 18,
25, 35], "n_estimators": [100, 400, 700, 1000, 1500]}from
sklearn.model_selection import GridSearchCV, cross_val_scorerf =
RandomForestClassifier(n_estimators=100, max_features='auto',
oob_score=True, random_state=1, n_jobs=-1)clf =
GridSearchCV(estimator=rf, param_grid=param_grid, n_jobs=-
1)clf.fit(X_train, Y_train)clf.best_params
```



Test new Parameters:

```
# Random Forest
random_forest = RandomForestClassifier(criterion = "gini",
                                       min_samples_leaf = 1,
                                       min_samples_split = 10,
                                       n_estimators=100,
                                       max_features='auto',
                                       oob_score=True,
                                       random_state=1,
                                       n_jobs=-1)

random_forest.fit(X_train, Y_train)
Y_prediction = random_forest.predict(X_test)

random_forest.score(X_train, Y_train)

print("oob score:", round(random_forest.oob_score_, 4)*100, "%")
```

oob score: 83.05 %

Now that we have a proper model, we can start evaluating it‟s performace in a more accurate way. Previously we only used accuracy and the oob score, which is just another form of accuracy. The problem is just, that it‟smore complicated to evaluate a classification model than a regression model. We will talk about this in the following section.

Further Evaluation

Confusion Matrix:

```
from sklearn.model_selection import cross_val_predict
from sklearn.metrics import confusion_matrix
predictions = cross_val_predict(random_forest, X_train, Y_train, cv=3)
confusion_matrix(Y_train, predictions)
```

```
array([[488,  61],
       [ 95, 247]])
```

The first row is about the not-survived-predictions: **493 passengers were correctly classified as not survived** (called true negatives) and **56 where wrongly classified as not survived** (false positives).

The second row is about the survived-predictions: **93 passengers wherewrongly classified as survived** (false negatives) and **249 where correctly classified as survived** (true positives).

A confusion matrix gives you a lot of information about how well yourmodel does, but theres a way to get even more, like computing the classifiers precision.

Precision and Recall:

```
from sklearn.metrics import precision_score, recall_score

print("Precision:", precision_score(Y_train, predictions))
print("Recall:",recall_score(Y_train, predictions))
```

Precision: 0.801948051948

Recall: 0.722222222222

Our model predicts 81% of the time, a passengers survival correctly (precision). The recall tells us that it predicted the survival of 73 % of thepeople who actually survived.

F-Score

You can combine precision and recall into one score, which is called the F-score. The F-score is computed with the harmonic mean of precision and recall. Note that it assigns much more weight to low values. As a result of that, the classifier will only get a high F-score, if both recall and precision are high.

```
from sklearn.metrics import f1_score
f1_score(Y_train, predictions)
```

0.7599999999999

There we have it, a 77 % F-score. The score is not that high, because we have a recall of 73%. But unfortunately the F-score is not perfect, because it favors classifiers that have a similar precision and recall. This is a problem, because you sometimes want a high precision and sometimes a high recall. The thing is that an increasing precision, sometimes results inan decreasing recall and vice versa (depending on the threshold). This is called the precision/recall tradeoff. We will discuss this in the following section.

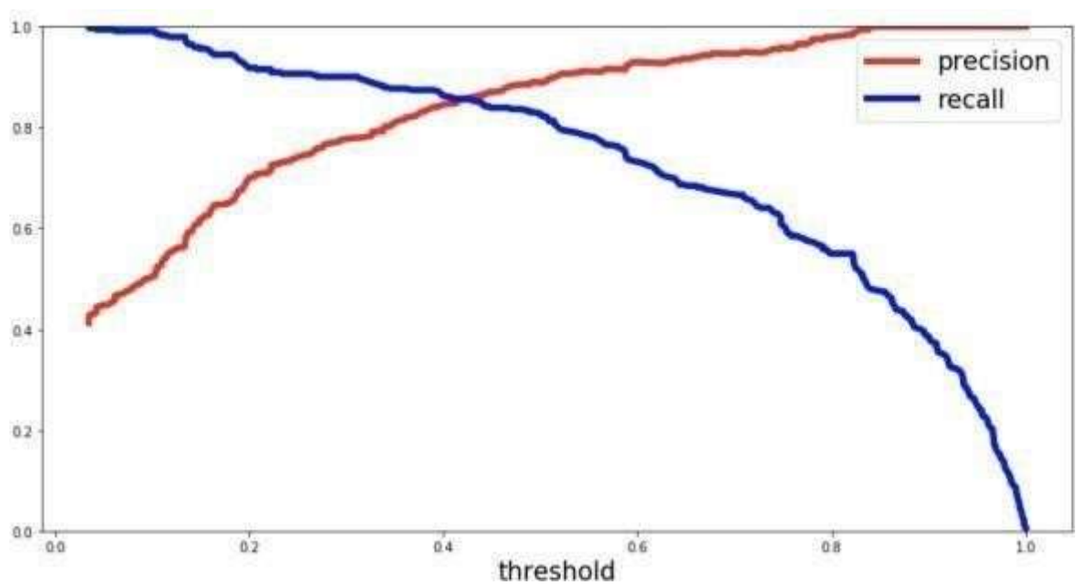
Precision Recall Curve

For each person the Random Forest algorithm has to classify, it computesa probability based on a function and it classifies the person as survived (when the score is bigger the than threshold) or as not survived (when thescore is smaller than the threshold). That‟s why the threshold plays an important part.

We will plot the precision and recall with the threshold using matplotlib:

```
from sklearn.metrics import precision_recall_curve

# getting the probabilities of our predictions
y_scores = random_forest.predict_proba(X_train)
y_scores = y_scores[:,1]

precision, recall, threshold = precision recall curve(Y train,
```

```
y_scores)def plot_precision_and_recall(precision, recall, threshold):
    plt.plot(threshold, precision[:-1], "r-", label="precision",
linewidth=5)
    plt.plot(threshold, recall[:-1], "b", label="recall", linewidth=5)
    plt.xlabel("threshold", fontsize=19)
    plt.legend(loc="upper right", fontsize=19)
    plt.ylim([0, 1])

plt.figure(figsize=(14, 7))
plot_precision_and_recall(precision, recall, threshold)
plt.show()
```

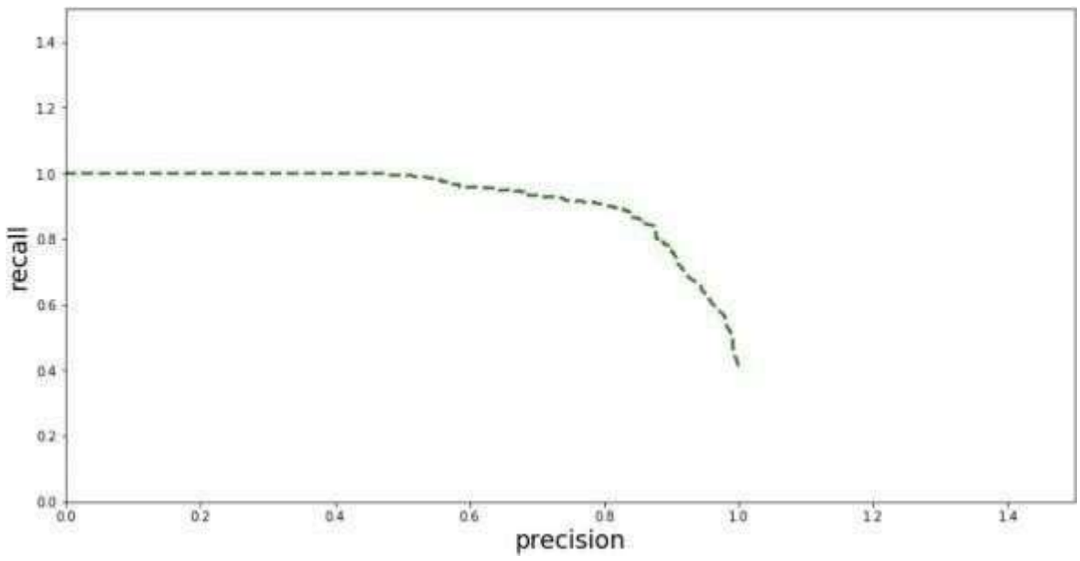


Above you can clearly see that the recall is falling of rapidly at a precision of around 85%. Because of that you may want to select the precision/recalltradeoff before that — maybe at around 75 %.

You are now able to choose a threshold, that gives you the best precision/recall tradeoff for your current machine learning problem. If youwant for example a precision of 80%, you can easily look at the plots and see that you would need a threshold of around 0.4. Then you could train a model with exactly that threshold and would get the desired accuracy.

Another way is to plot the precision and recall against each other:

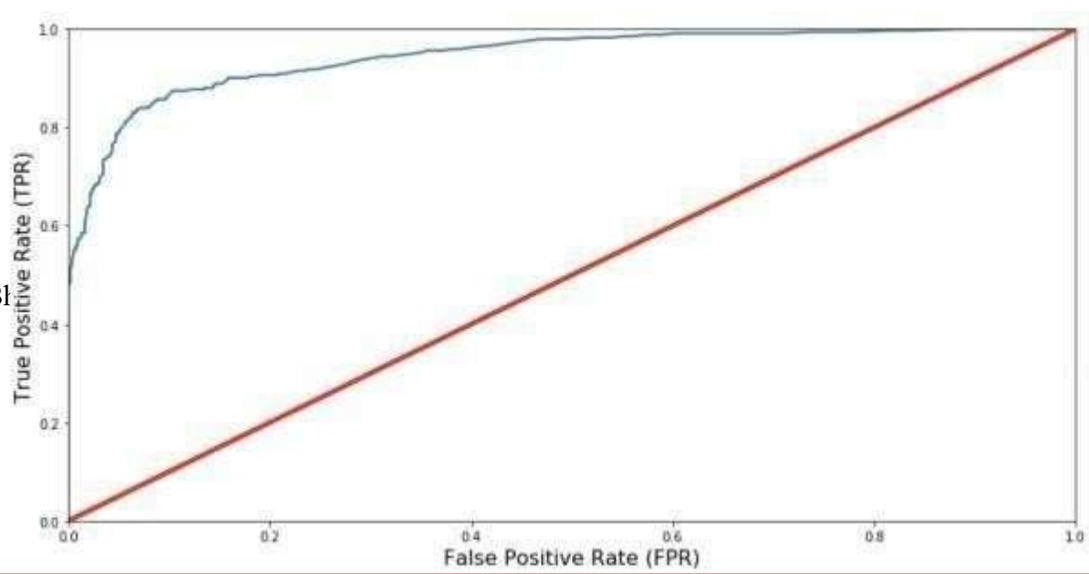
```
def plot_precision_vs_recall(precision, recall):
    plt.plot(recall, precision, "g--", linewidth=2.5)
    plt.ylabel("recall", fontsize=19)
    plt.xlabel("precision", fontsize=19)
    plt.axis([0, 1.5, 0, 1.5])

plt.figure(figsize=(14, 7))
plot_precision_vs_recall(precision, recall)
plt.show()
```



ROC AUC Curve

Another way to evaluate and compare your binary classifier is provided bythe ROC AUC Curve. This curve plots the true positive rate (also called recall) against the false positive rate (ratio of incorrectly classified negativeinstances), instead of plotting the precision versus the recall.

```
from sklearn.metrics import roc_curve
# compute true positive rate and false positive rate
false_positive_rate, true_positive_rate, thresholds =
roc_curve(Y_train, y_scores)# plotting them against each other
def plot_roc_curve(false_positive_rate, true_positive_rate,
label=None):
    plt.plot(false_positive_rate, true_positive_rate, linewidth=2,
label=label)
    plt.plot([0, 1], [0, 1], 'r', linewidth=4)
    plt.axis([0, 1, 0, 1])
    plt.xlabel('False Positive Rate (FPR)', fontsize=16)
    plt.ylabel('True Positive Rate (TPR)', fontsize=16)

plt.figure(figsize=(14, 7))
plot_roc_curve(false_positive_rate, true_positive_rate)
plt.show()
```



Bl

The red line in the middel represents a purely random classifier (e.g a coin flip) and therefore your classifier should be as far away from it as possible.Our Random Forest model seems to do a good job.

Of course we also have a tradeoff here, because the classifier producesmore false positives, the higher the true positive rate is.

ROC AUC Score

The ROC AUC Score is the corresponding score to the ROC AUC Curve. Itis simply computed by measuring the area under the curve, which is calledAUC.

A classifiers that is 100% correct, would have a ROC AUC Score of 1 and a completely random classiffier would have a score of 0.5.

```
from sklearn.metrics import roc_auc_score
r_a_score = roc_auc_score(Y_train, y_scores)
print("ROC-AUC-Score:", r_a_score)
```

Group C
Assignment No : 1

Title of the Assignment: Installation of MetaMask and study spending Ether per transaction

Objective of the Assignment: Students should be able to learn new technology such as metamask.Its application and implementations

Prerequisite:

1. Basic knowledge of cryptocurrency
2. Basic knowledge of distributed computing concept
3. Working of blockchain

Contents for Theory:

1. **Introduction Blockchain**
2. **Cryptocurrency**
3. **Transaction Wallets**
4. **Ether transaction**
5. **Installation Process of Metamask**

Introduction to Blockchain

- Blockchain can be described as a data structure that holds transactional records and while ensuring security, transparency, and decentralization. You can also think of it as a chain or records stored in the forms of blocks which are controlled by no single authority.
- A blockchain is a distributed ledger that is completely open to any and everyone on the network. Once an information is stored on a blockchain, it is extremely difficult to change or alter it.
- Each transaction on a blockchain is secured with a digital signature that proves its authenticity. Due to the use of encryption and digital signatures, the data stored on the blockchain is tamper-proof and cannot be changed.
- Blockchain technology allows all the network participants to reach an agreement, commonly known as consensus. All the data stored on a blockchain is recordeddigitally and has a common history which is available for all the network participants. This way, the chances of any fraudulent activity or duplication of transactions is eliminated without the need of a third-party.

Blockchain Features

The following features make the revolutionary technology of blockchain stand out:

- **Decentralized**

  Blockchains are decentralized in nature meaning that no single person or group holds the authority of the overall network. While everybody in the network has the copy of the distributed ledger with them, no one can modify it on his or her own. This unique feature of blockchain allows transparency and security while giving power to the users.

- **Peer-to-Peer Network**

  With the use of Blockchain, the interaction between two parties through a peer-to-peer model is easily accomplished without the requirement of any third party. Blockchain uses P2P protocol which allows all the network participants to hold an identical copy of transactions, enabling approval through a machine consensus. For example, if you wish to make any transaction from one part of the world to another, you can do that with blockchain all by yourself within a few seconds. Moreover, any interruptions or extra charges will not be deducted in the transfer.

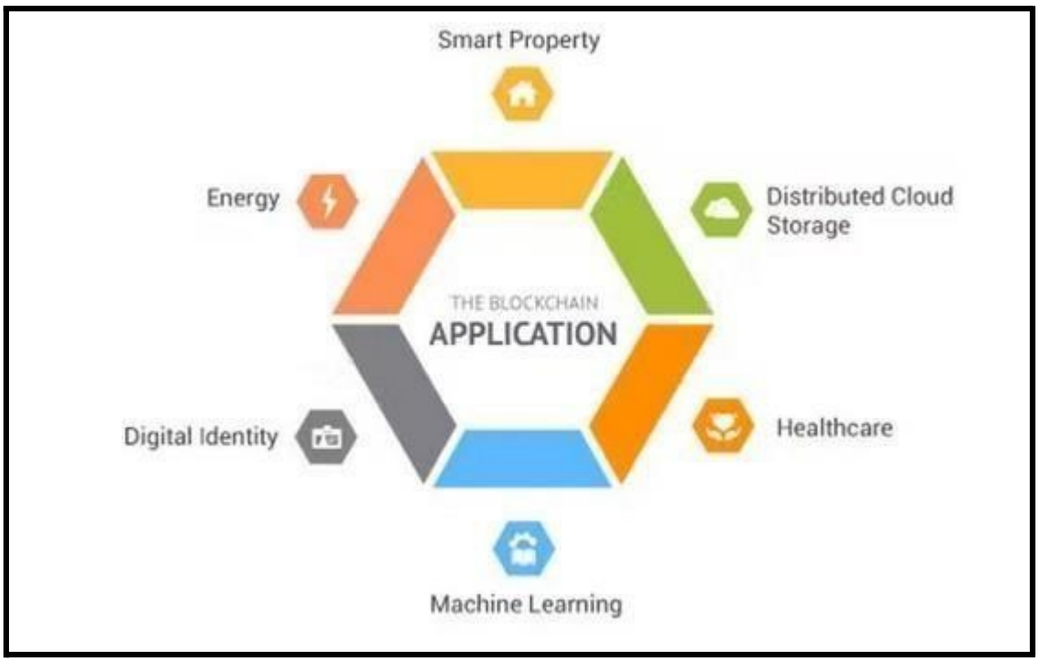
- **Immutable**

  The immutability property of a blockchain refers to the fact that any data once written on the blockchain cannot be changed. To understand immutability, consider sending email as an example. Once you send an email to a bunch of people, you cannot take it back. In order to find a way around, you'll have to ask all the recipients to delete your email which is pretty tedious. This is how immutability works.

- **Tamper-Proof**

  With the property of immutability embedded in blockchains, it becomes easier to detect tampering of any data. Blockchains are considered tamper-proof as any change in even one single block can be detected and addressed smoothly. There are two key ways of detecting tampering namely, hashes and blocks.

Popular Applications of Blockchain Technology



Benefits of Blockchain Technology:

- **Time-saving:** No central Authority verification needed for settlements making the process faster and cheaper.
- **Cost-saving:** A Blockchain network reduces expenses in several ways. No need for third-party verification. Participants can share assets directly. Intermediaries are reduced. Transaction efforts are minimized as every participant has a copy of shared ledger.
- **Tighter security:** No one can temper with Blockchain Data as it is shared among

millions of participants. The system is safe against cybercrimes and Fraud.

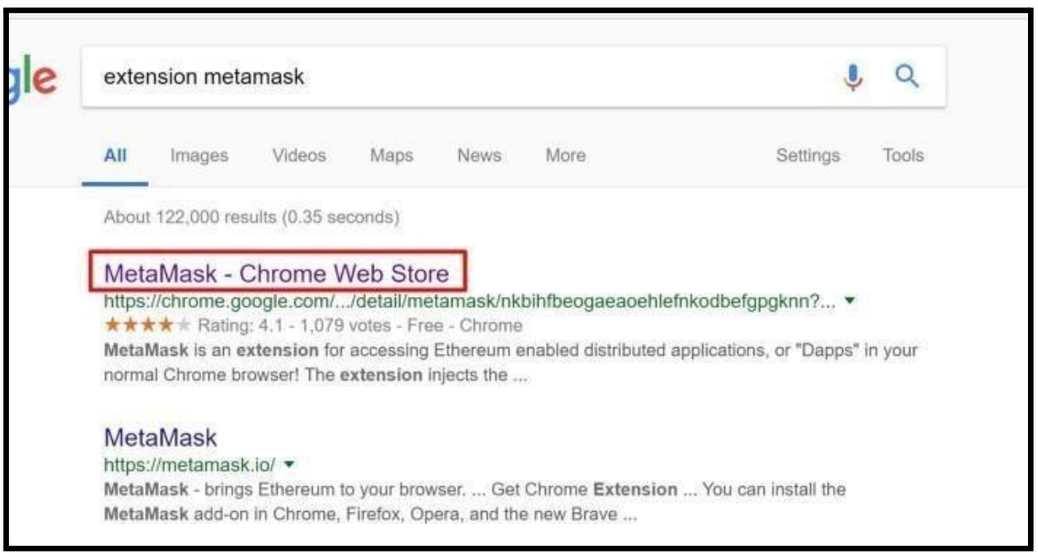
- In finance market trading, Fibonacci retracement levels are widely used in technical analysis.

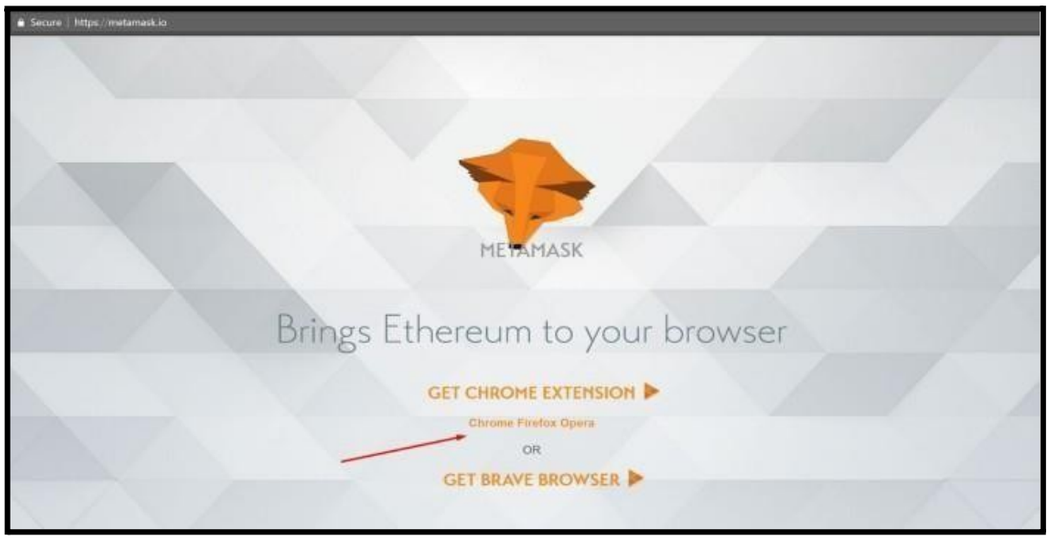
How to use MetaMask: A step by step guide

MetaMask is one of the most popular browser extensions that serves as a way of storing your Ethereum and other ERC-20 Tokens. The extension is free and secure, allowing web applications to read and interact with Ethereum‘s blockchain.

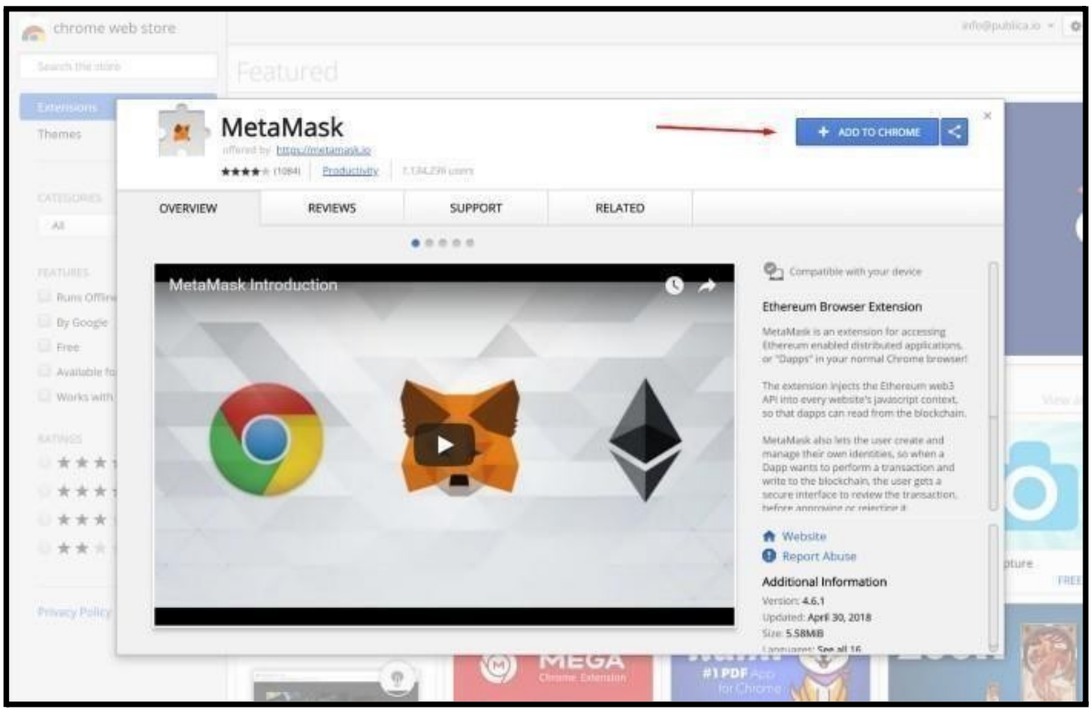
Step 1. Install MetaMask on your browser.

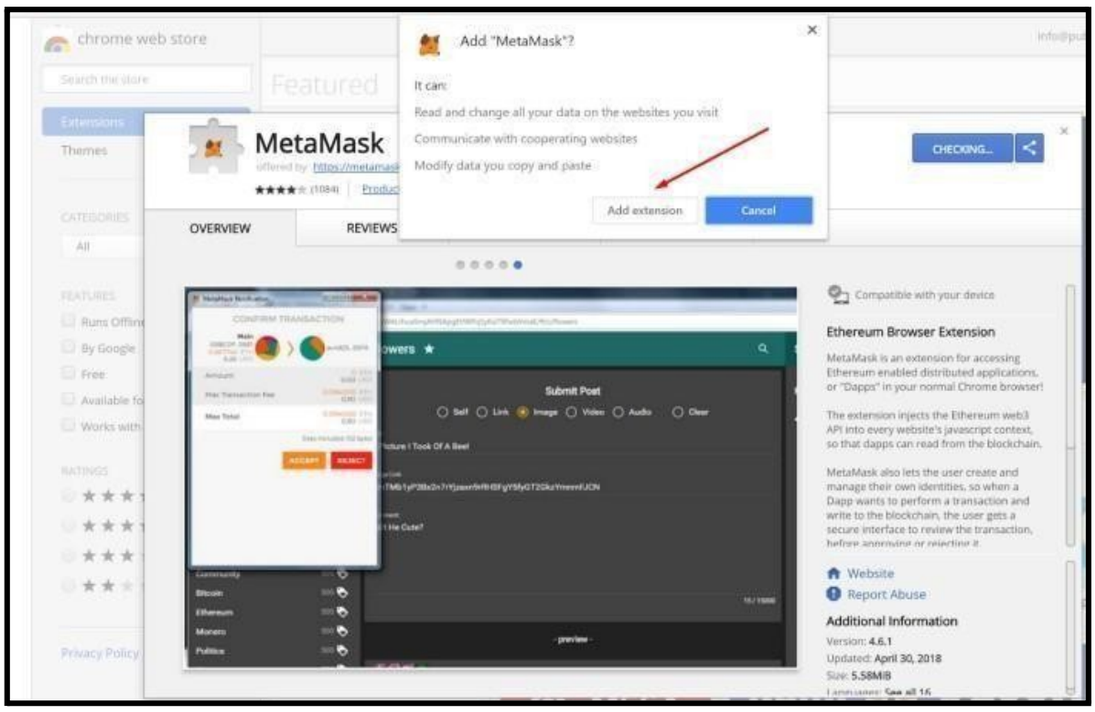
To create a new wallet, you have to install the extension first. Depending on your browser, there are different marketplaces to find it. Most browsers have MetaMask on their stores, so it‘s not that hard to see it, but either way, here they are Chrome, Firefox, and Opera.





- Click on **Install MetaMask** as a Google Chrome extension.
- Click **Add to Chrome**.
- Click **Add Extension**.

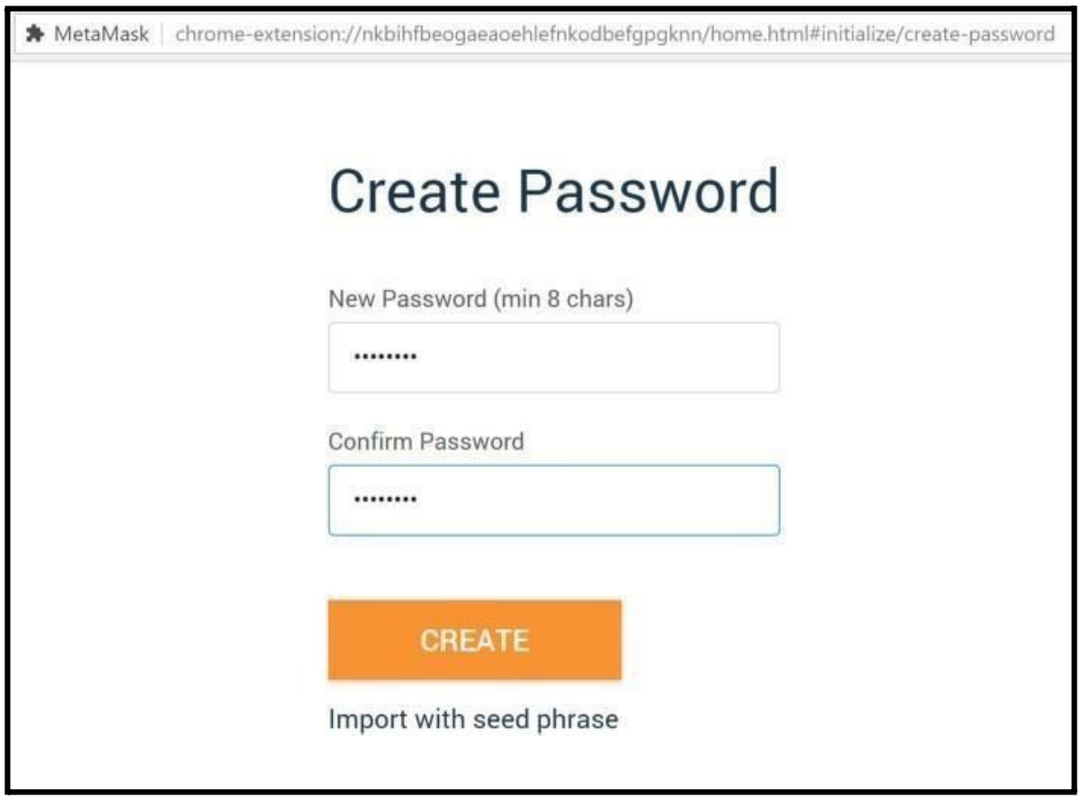




and it‘s as easy as that to install the extension on your browser, continue reading the next stepto figure out how to create an account.

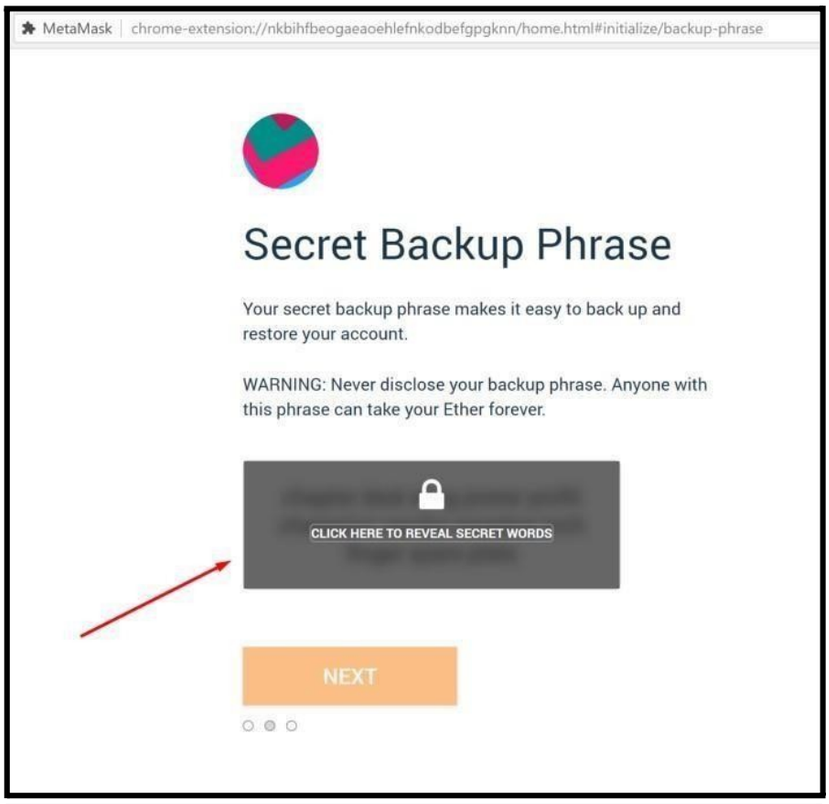
Step 2. Create an account.

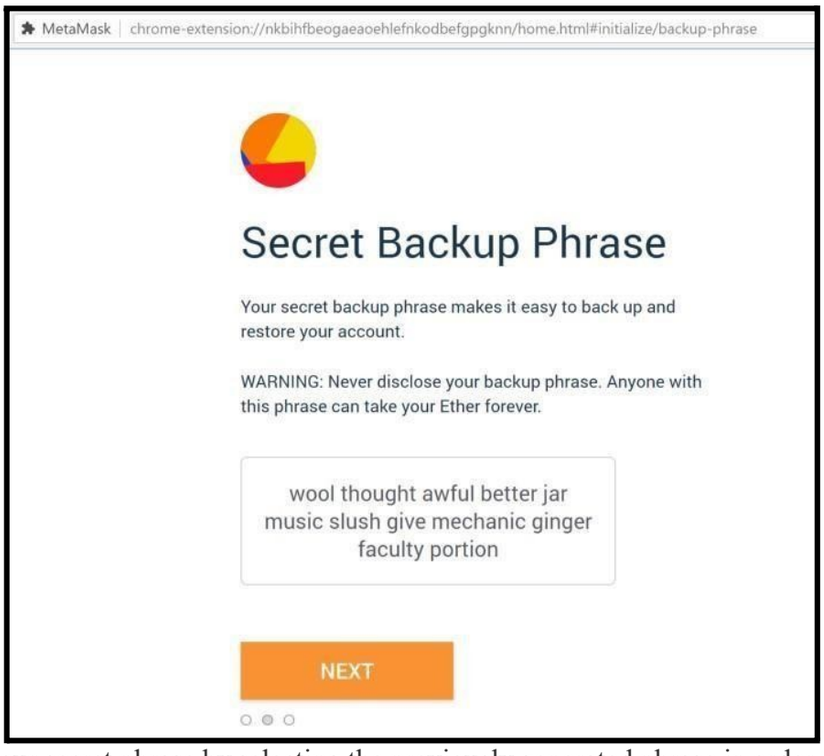
- Click on the extension icon in the upper right corner to open MetaMask.
- To install the latest version and be up to date, **click Try it now**.
- **Click Continue**.
- You will be prompted to create a new password. **Click Create**.



- Proceed by **clicking Next** and accept the Terms of Use.

Click Reveal Secret Words. There you will see a 12 words seed phrase. This is really important and usually not a good idea to store digitally, so take your time and write it down





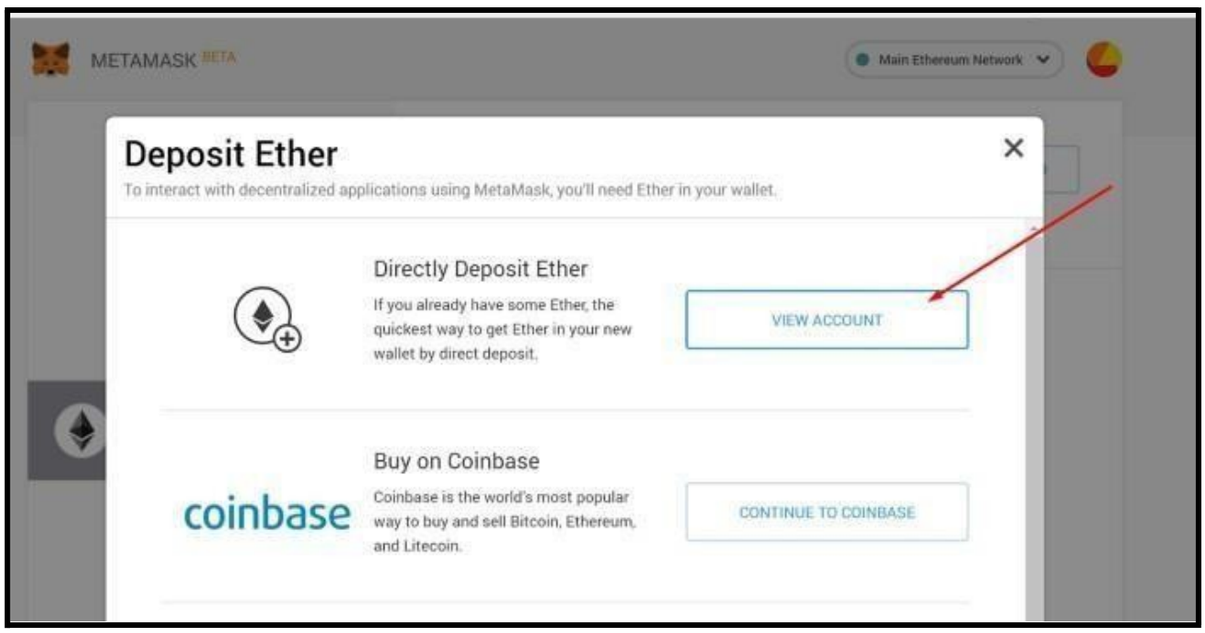
- Verify your secret phrase by selecting the previously generated phrase in order. **Click Confirm**.

And that‘s it; now you have created your MetaMask account successfully. A new Ethereum wallet

address has just been created for you. It‘s waiting for you to deposit funds, and if you want to learn how to do that, look at the next step below.

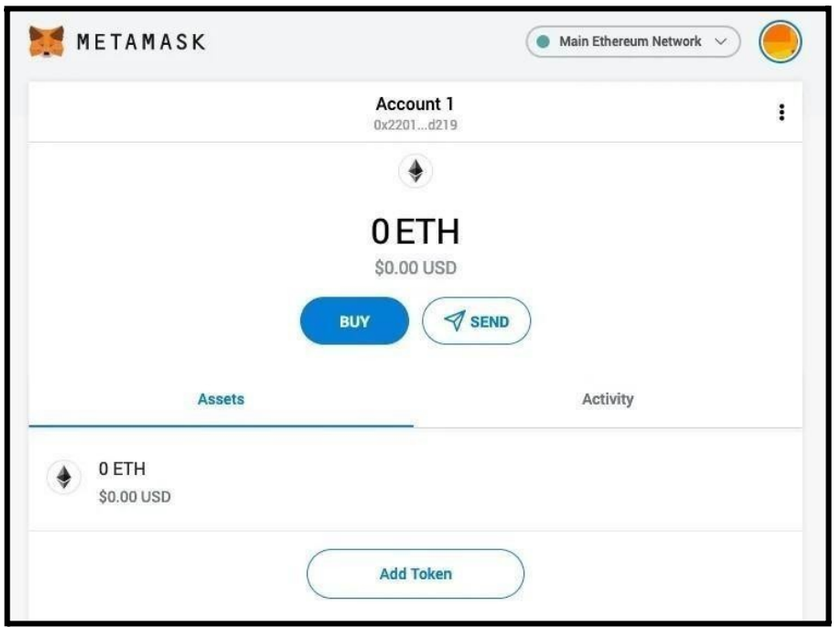
Step 3. Depositing funds.

- Click on **View Account**.



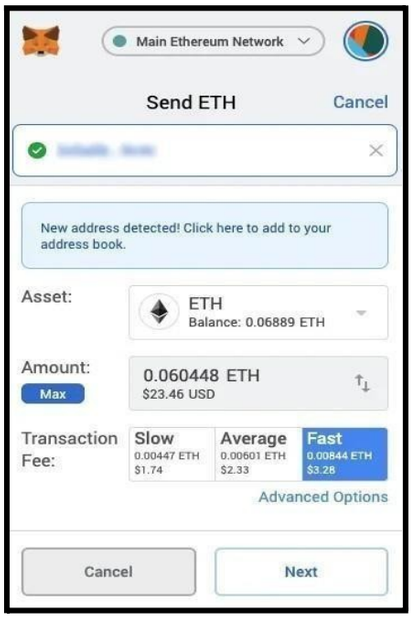
You can now see your public address and share it with other people. There are some methods to buy coins offered by MetaMask, but you can do it differently as well; you just need your address.

If you ever get logged out, you‘ll be able to log back in again by clicking the MetaMask icon, which will have been added to your web browser (usually found next to the URL bar).



You can now access your list of assets in the _Assets‘ tab and view your transaction history in the _Activity‘ tab.

- Sending crypto is as simple as clicking the _Send‘ button, entering the recipient address and amount to send, and selecting a transaction fee. You can also manually adjust the transaction fee using the _Advanced Options‘ button, using information from ETH Gas Station or similar platforms to choose a more acceptable gas price.
- After clicking _Next‘, you will then be able to either confirm or reject the transaction on the subsequent page.



- To use MetaMask to interact with a dapp or smart contract, you'll usually need to find a _Connect to Wallet' button or similar element on the platform you are trying to use. After clicking this, you should then see a prompt asking whether you want to let the dapp connect to your wallet.

What advantages does MetaMask have?

- **Popular** - It is commonly used, so users only need one plugin to access a wide range of dapps.
- **Simple** - Instead of managing private keys, users just need to remember a list of words, and transactions are signed on their behalf.
- **Saves space** - Users don't have to download the Ethereum blockchain, as MetaMask sends requests to nodes outside of the user's computer.
- **Integrated** - Dapps are designed to work with MetaMask, so it becomes much easier to send Ether in and out.

Conclusion- In this way we have explored Concept Blockchain and metamat wallet for transaction of digital currency

Assignment Question

1. **What Are the Different Types of Blockchain Technology?**
2. **What Are the Key Features/Properties of Blockchain?**
3. **What Type of Records You Can Keep in A Blockchain?**
4. **What is the difference between Ethereum and Bitcoin?**
5. **What are Merkle Trees? Explain their concept.**
6. **What is Double Spending in transaction operation**
7. **Give real-life use cases of blockchain.**

Reference link

- https://hackernoon.com/blockchain-technology-explained-introduction-meaning-and-applications-edbd6759a2b2
- https://levelup.gitconnected.com/how-to-use-metamask-a-step-by-step-guide-f380a3943fb1
- https://decrypt.co/resources/metamask

Group C
Assignment No:2

Title: Create your own wallet using MetaMask for crypto transactions.

Objective: Understand and explore the working of Blockchain technology and its applications.

Course Outcome:

CO6:Interpret the basic concepts in Blockchain technology and its application.

Description:

MetaMask is a cryptocurrency wallet used to interact with the Ethereum Blockchain. It can be accessed through an app or through a browser extension.MetaMask is a popular cryptocurrency wallet known for its ease of use, availability on both desktops and mobile devices, the ability to buy, send, and receive cryptocurrency from within the wallet, and collect non-fungible tokens (NFTs) across two block chains. While experienced crypto users will appreciate the simplicity and fast transactions, those new in the space are at a higher risk of losing their tokens from lost secret phrases, malicious websites, and other cryptocurrency scams

Similarly, you‟ll need a crypto wallet to transact with a Blockchain.

A wallet is your personal key to interact with the cryptographic world. It powers you to buy, sell or transfer assets on the Blockchain.

And MetaMask is a wallet for the most diverse Blockchain in existence–Ethereum. It‟s your gateway to its DeFi ecosystem, non-fungible tokens (NFTs), ERC-20 tokens, and practically–everything Ethereum.

It‟s available as an app for iOS and Android. In addition, you can use this as an extension with a few web browsers: Chrome, Firefox, Brave, and Edge.

Let‟s take a look at some of the prominent features of this wallet:

Ease of use

Starting with MetaMask is easy, quick, and anonymous. You don‟t even need an email address. Just set up a password and remember (and store) the secret recovery phrase, and you‟re done.

Security

Your information is encrypted in your browser that nobody has access to. In the event ofa lost password, you have the 12-word secret recovery phase (also called a seed phrase) for recovery. Notably, it‟s essential to keep the seed phrase safe, as even MetaMask has noinformation about it. Once lost, it can‟t be retrieved.

Built-In Crypto Store

If you‟re wondering, no, you can‟t buy Bitcoin with MetaMask. It only supports Ether and other Ether-related tokens, including the famous ERC-20 tokens. Cryptocurrencies (excluding Ether) on Ethereum are built as ERC-20 tokens.

Backup and Restore

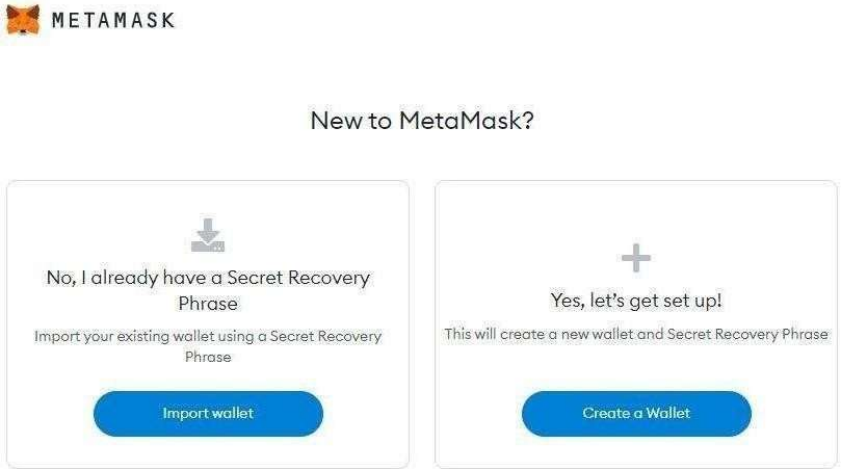
MetaMask stores your information locally. So, in case you switch browsers or machines, you can restore your MetaMask wallet with your secret recovery phrase.

Community Support

As of August 2021, MetaMask was home to 10 million monthly active users around the world. It‟s simple and intuitive user interface keeps pushing these numbers with a recorded 1800% increase from July 2020.

Conclusively, try MetaMask if hot wallets are your pick. Let‟s begin with the installation before moving to its use cases. Further sections entail the illustration for Chrome web browser and Android mobile platform.

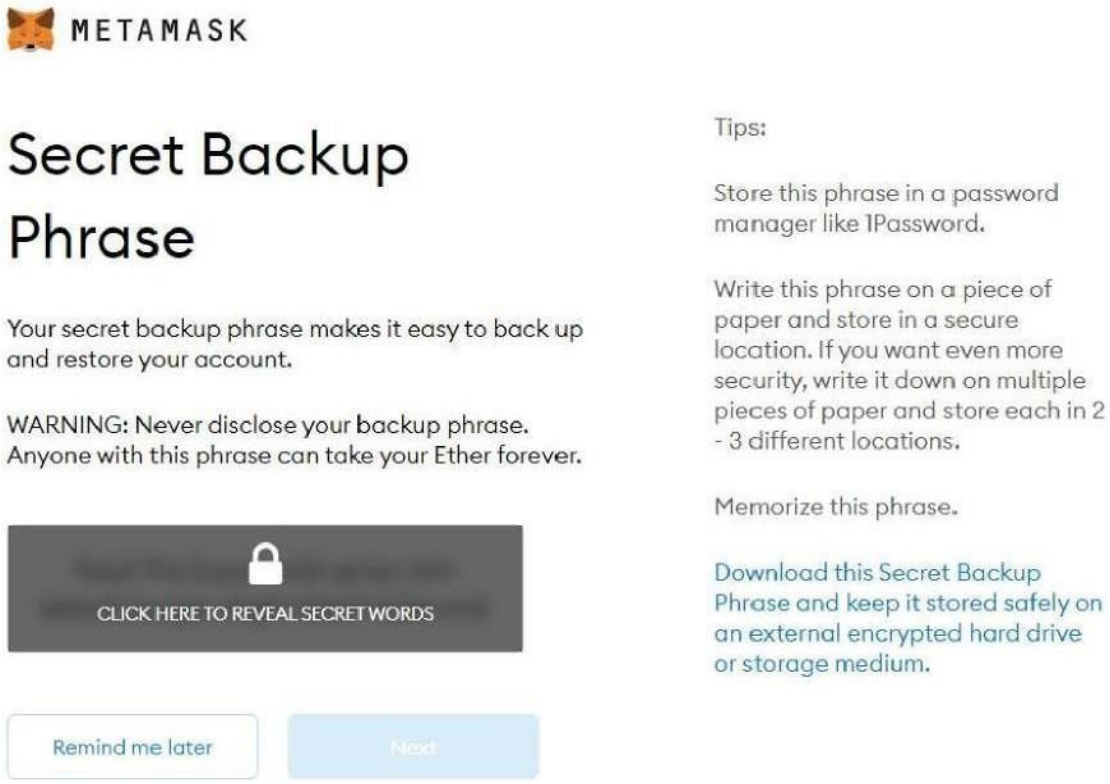
Step 1: Click on the ―Create a wallet‖.



Step 2: Create a password for your wallet. This password is to be entered every time the browser is launched and wants to use MetaMask. A new password needs to be created if chrome is uninstalled or if there is a switching of browsers. In that case, go through the Import Wallet button. This is because MetaMask stores the keys in the browser. Agree to Terms of Use.

Step 3:Click on the dark area which says *Click here to reveal secret words* to get your secret phrase.

Step 4: This is the most important step. Back up your secret phrase properly. Do not store your secret phrase on your computer. Please read everything on this screen until you understand it completely before proceeding. The secret phrase is the only way to access your wallet if you forget your password. Once done click the Next button.

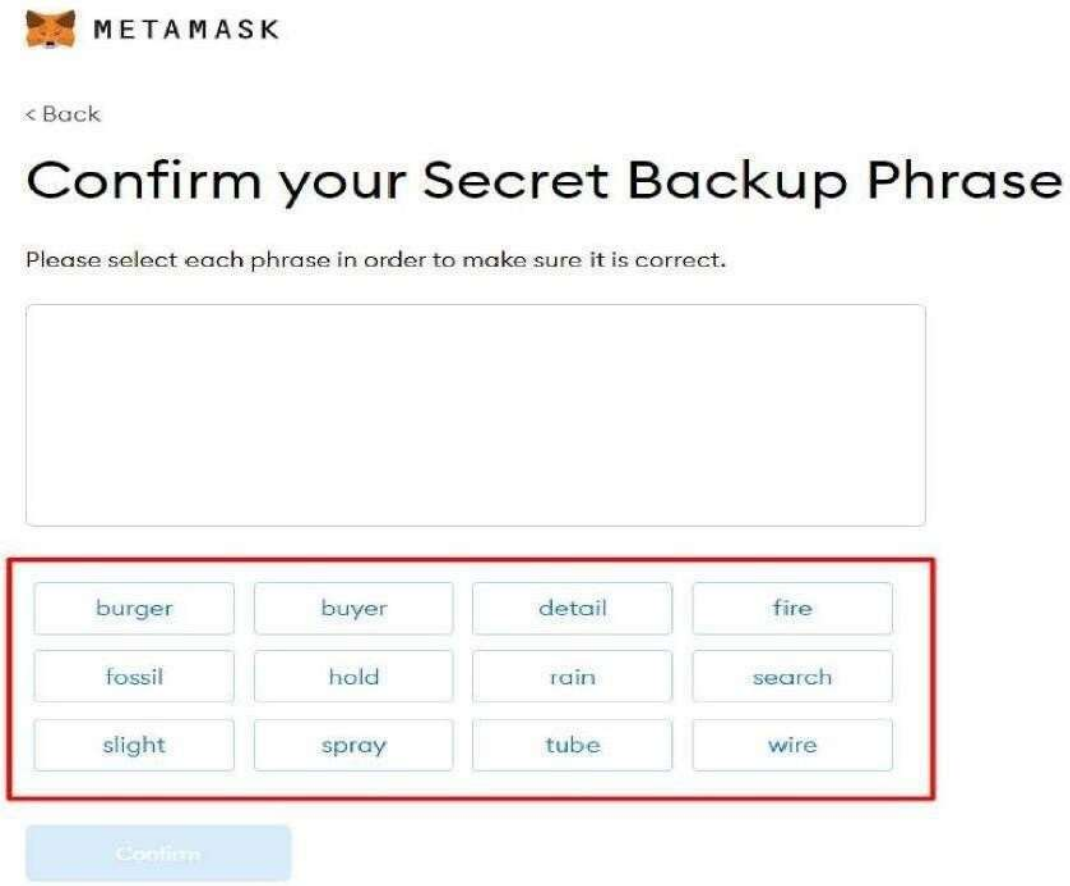


Step 5:

Securely store the seed phrase for your wallet Click on –Click here to reveal secret words‖ to show the seed phrase.

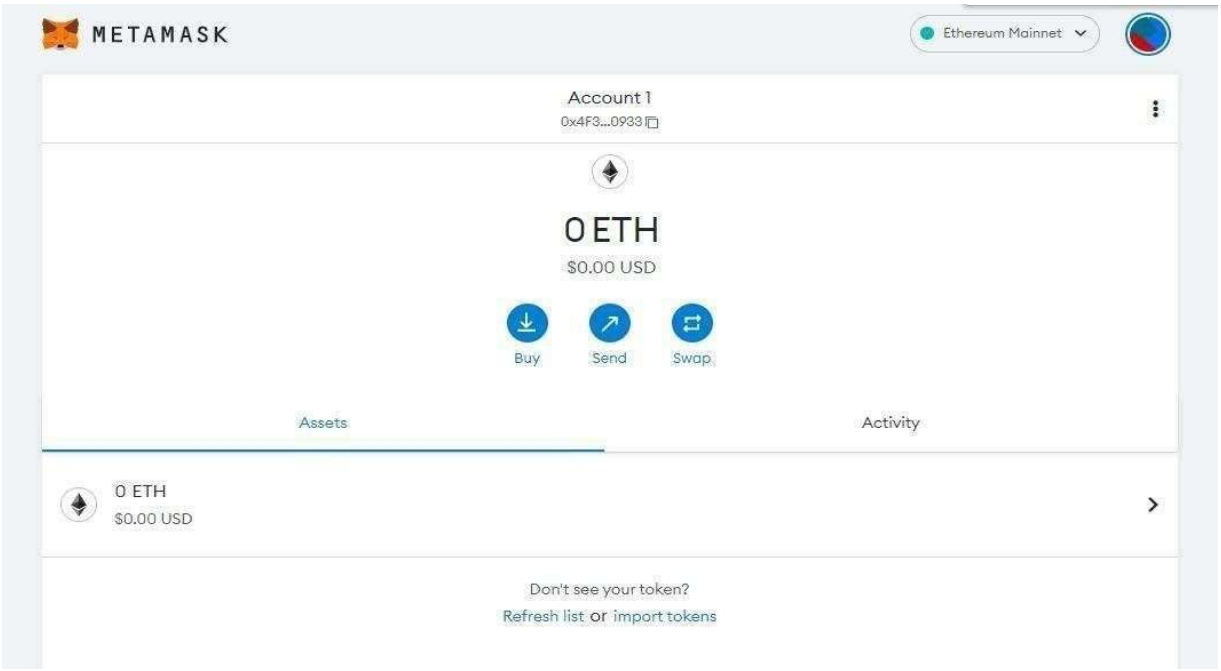
MetaMask requires that you store your seed phrase in a safe place. It is the only way to recover your funds should your device crash or your browser reset. We recommend you write it down. The most common method is to write your 12-word phrase on a piece of paper and store it safelyin a place where only you have access. Note: if you lose your seed phrase, MetaMask can‟t help you recover your wallet and your funds will be lost forever.

Never share your seed phrase or your private key to anyone or any site, unless you want them to have full control over your funds.



Step 6: Click the *Confirm* button. Please follow the tips mentioned.

Step 7: One can see the balance and copy the address of the account by clicking on the *Account 1* area.



Conclusion: Hence,we havestudiedto create a wallet using Meta

Assignment No. 3

Title: Write a smart contract on a test network for Bank account of a customer for following operations.

- Deposit Money
- Withdraw Money
- Show Balance

Objective: Understand and explore the working of Blockchain technology and its applications.

Course Outcome:

CO6:Interpret the basic concepts in Blockchain technology and its application.

Description:

First of all, we need to understand the differences between a paper contract and a smart contract and the reason why smart contracts become increasingly popular and important in recent years. A contract, by definition, is a written or spoken (mostly written) law-enforced agreement containing the rights and duties of the parties. Because most of business contracts are complicated and tricky, the parties need to hire professional agents or lawyers for protecting their own rights. However, if we hire those professionals every time we sign contracts, it is going to be extremely costly and inefficient. Smart contracts perfectly solve this by working on „If-Then‟ principle and also as escrow services. All participants need to put their money, ownership rightor other tradable assets into smart contracts before any successful transaction. As long as all participating parties meet the requirement, smart contracts will simultaneously distribute stored assets to recipients and the distribution process will be witnessed and verified by the nodes on Ethereum network.

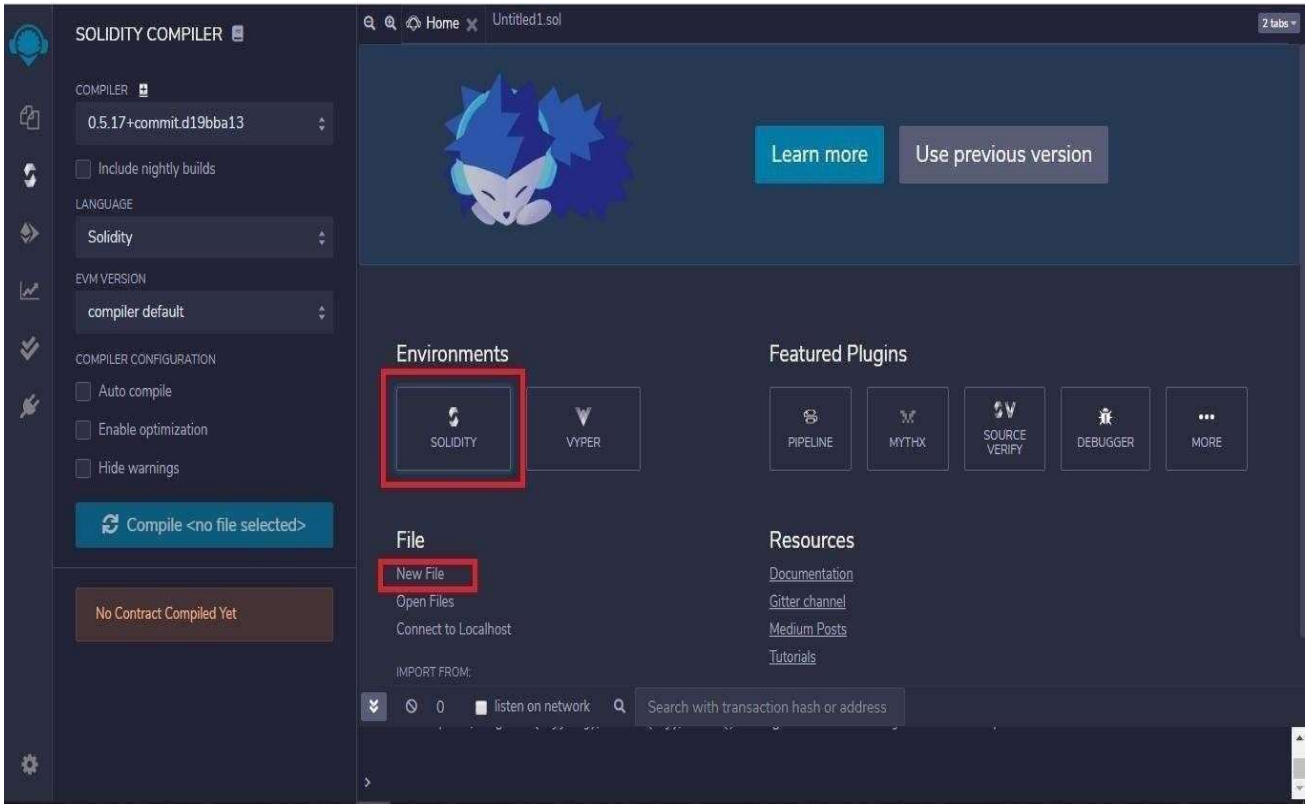
There are a couple of languages we can use to program smart contract. Solidity, an object-oriented and high-level language, is by far the most famous and well maintained one. We can use Solidity to create various smart contracts which can be used in different scenarios, including voting, blind auctions and safe remote purchase. In this lab, we will discuss the semantics and syntax of Solidity with specific explanation, examples and practices.

After deciding the coding language, we need to pick an appropriate compiler. Among various compilers like Visual Code Studio, we will use Remix IDE in this and following labs because it can be directly accessed from browser where we can test, debug and deploy smart contracts without any installation.

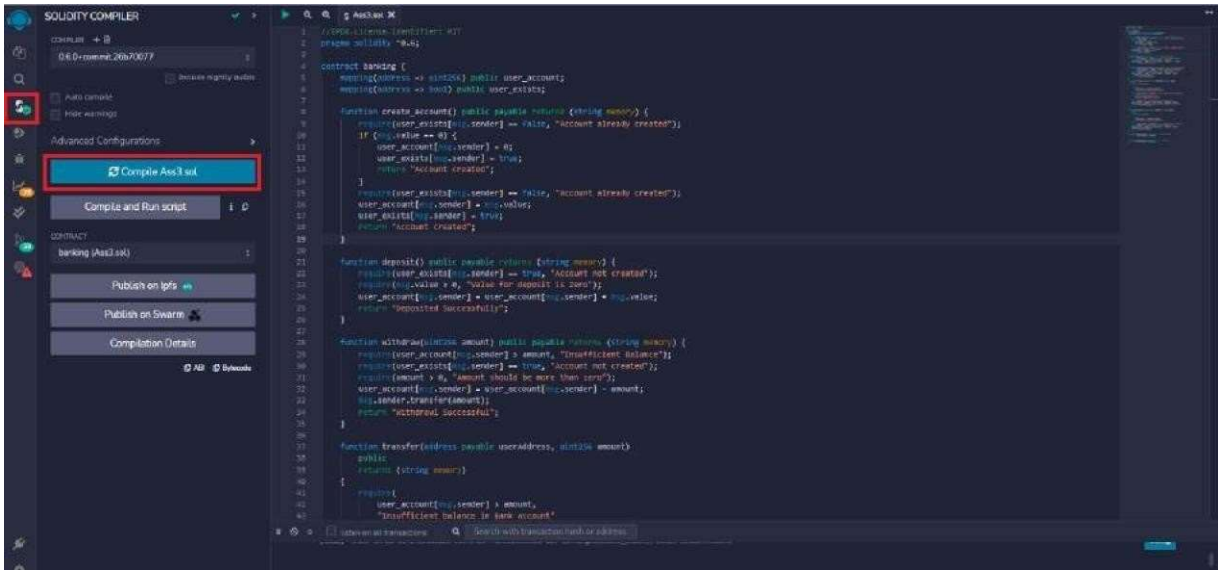
Steps to Execute Solidity Smart Contract using Remix IDE

Remix IDE is generally used to compile and run Solidity smart contracts. Below are the steps for the compilation, execution, and debugging of the smart contract.

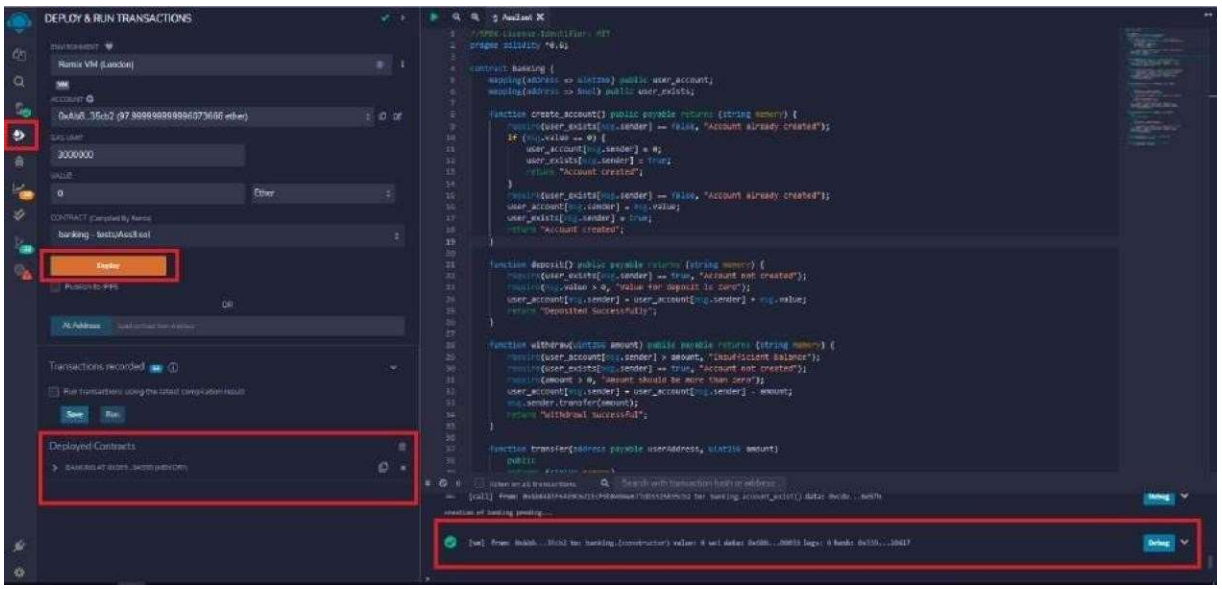
Step 1: Open Remix IDE on any of your browsers, select on the *New File* and click on *Solidity* to choose the environment.



Step 2: Write the Smart contract in the code section, and click the *Compile button* under the Compiler window to compile the contract.



Step 3: To execute the code, click on the *Deploy button* under Deploy and Run Transactions window. After deploying the code click on the drop-down on the console.



Code

```
//SPDX-License-Identifier: MIT
pragma solidity ^0.6;
```

```
contract banking
{
   mapping(address=>uint) public user_account;
   mapping(address=>bool) public user_exists;

   function create_account() public payable returns(string memory)
   {
      require(user_exists[msg.sender]==false,'Account already created');
      if(msg.value==0)
      {
user_account[msg.sender]=0;
user_exists[msg.sender]=true;
         return "Account created";
      }
      require(user_exists[msg.sender]==false,"Account already created");
user_account[msg.sender]=msg.value;
user_exists[msg.sender]=true;
      return "Account created";
   }

   function deposit() public payable returns(string memory)
   {
      require(user_exists[msg.sender]==true,"Account not created");
      require(msg.value>0,"Value for deposit is Zero");
user_account[msg.sender]=user_account[msg.sender]+msg.value;
      return "Deposited Successfully";
   }

   function withdraw(uint amount) public payable returns(string memory)
   {
```

```
        require(user_account[msg.sender]>amount,"Insufficient Balance");
        require(user_exists[msg.sender]==true,"Account not created");
        require(amount>0,"Amount should be more than zero");
user_account[msg.sender]=user_account[msg.sender]-amount;
msg.sender.transfer(amount);
        return "Withdrawl Successful";
    }

    function transfer(address payable userAddress, uint amount) public returns(string memory)
    {
        require(user_account[msg.sender]>amount,"Insufficient balance in Bank account");
        require(user_exists[msg.sender]==true,"Account is not created");
        require(user_exists[userAddress]==true,"Transfer account does not exist");
        require(amount>0,"Amount should be more than zero");
user_account[msg.sender]=user_account[msg.sender]-amount;
user_account[userAddress]=user_account[userAddress]+amount;
        return "Transfer Successful";
    }

    function send_amt(address payable toAddress, uint256 amount) public payable returns(string
memory)
    {
        require(user_account[msg.sender]>amount,"Insufficeint balance in Bank account");
        require(user_exists[msg.sender]==true,"Account is not created");
        require(amount>0,"Amount should be more than zero");
user_account[msg.sender]=user_account[msg.sender]-amount;
toAddress.transfer(amount);
        return "Transfer Success";
    }

    function user_balance() public view returns(uint)
```

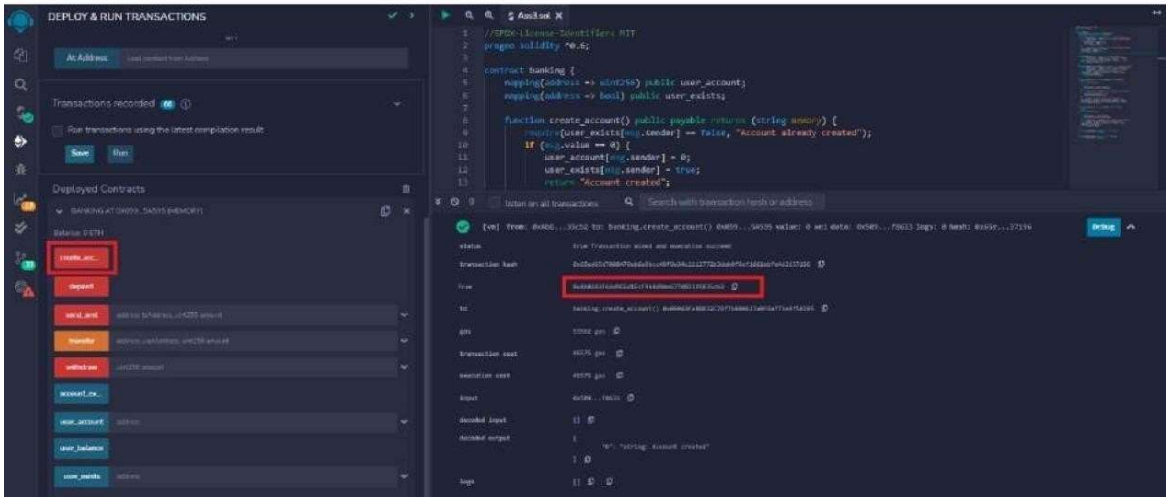
```
    {
        return user_account[msg.sender];
    }

    function account_exist() public view returns(bool)
    {
        return user_exists[msg.sender];
    }
}
```

Sample Output

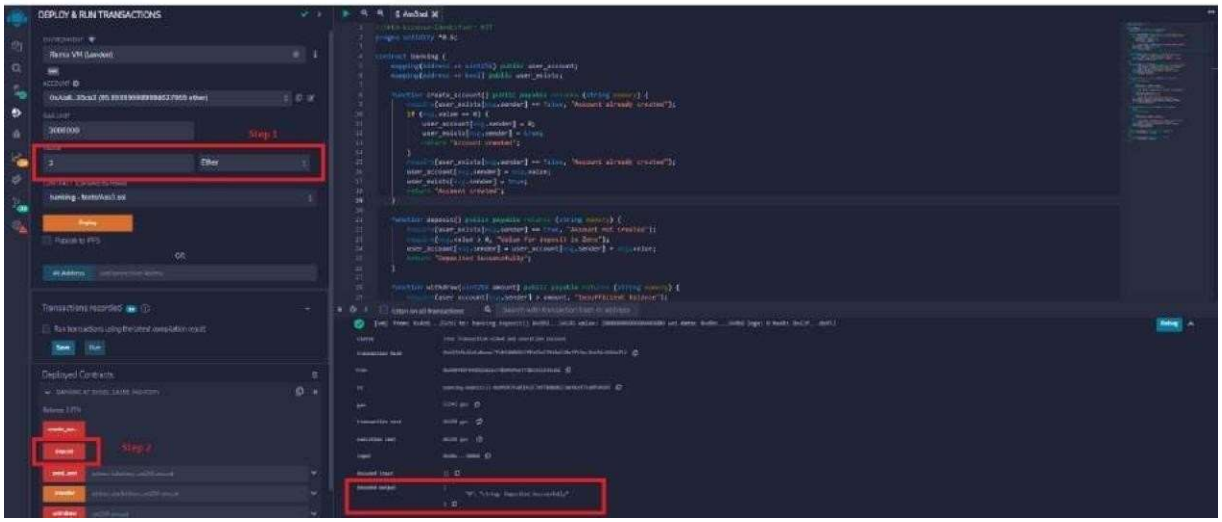
After deploying the contact successful you can observe following buttonscreate_account, deposit, send_amt, transfer, account_exist, user_account, user_balance and user_exists.

Refer the following output

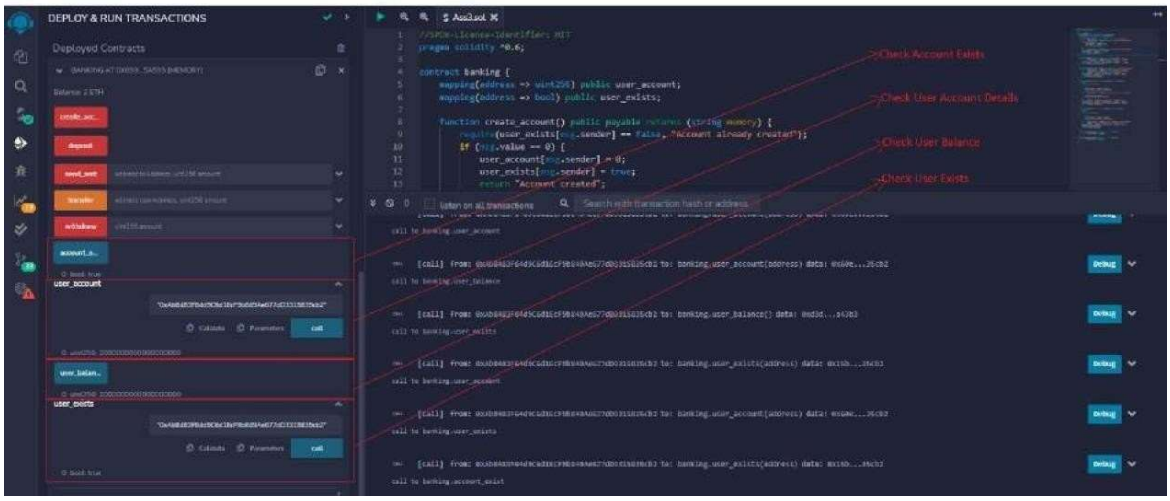
- Create account



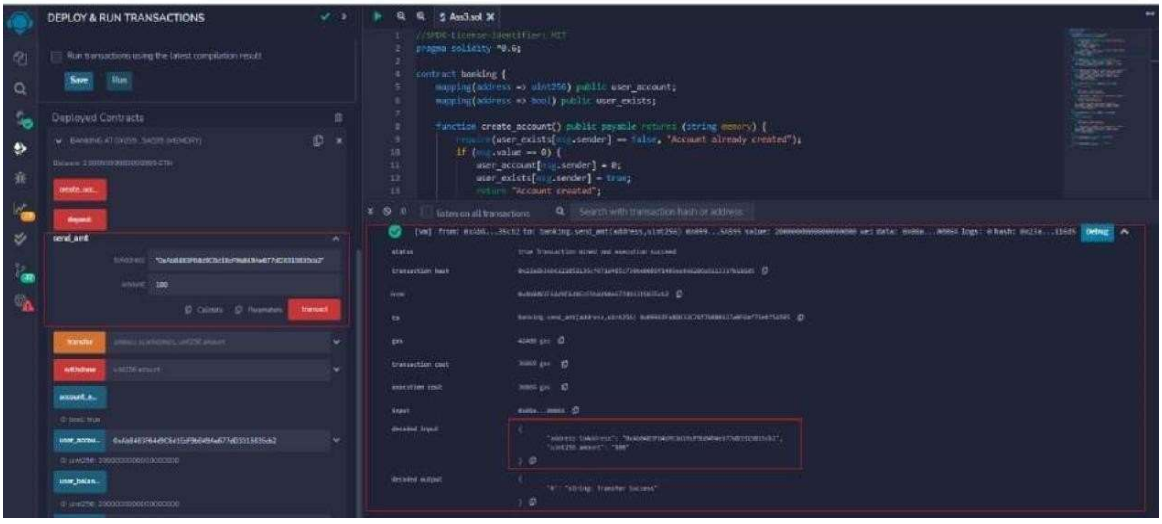
Deposit Amount



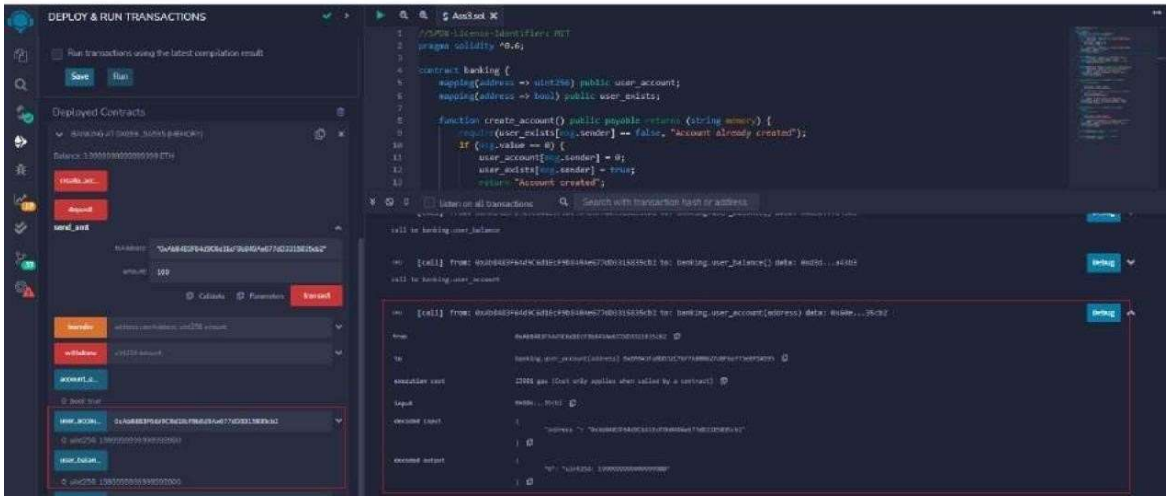
- Check Account Exists
- Check User Account Exists
- Check User Balance
- Check User Exists



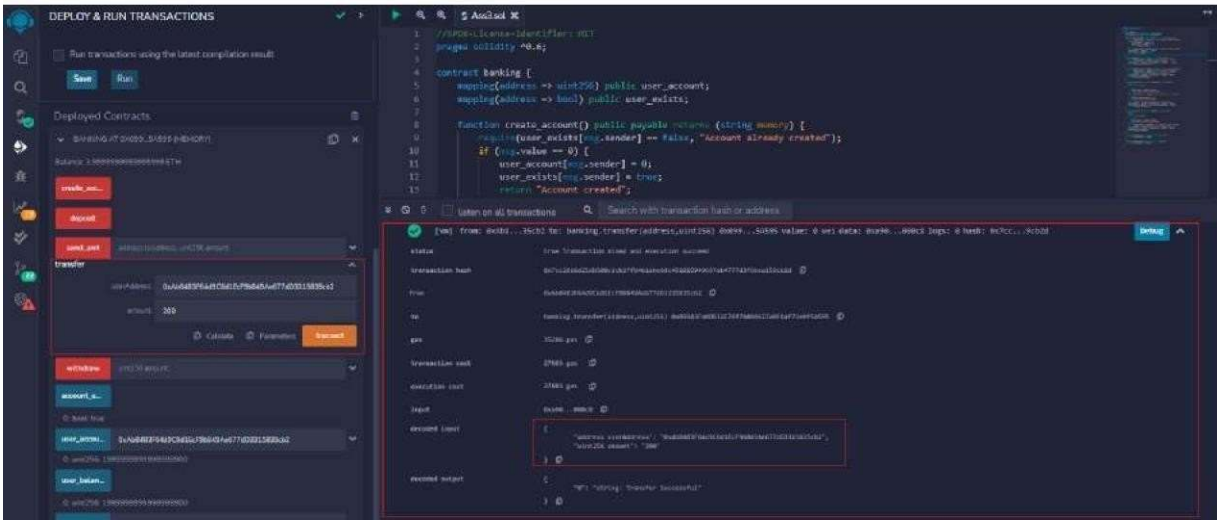
- Send Amount



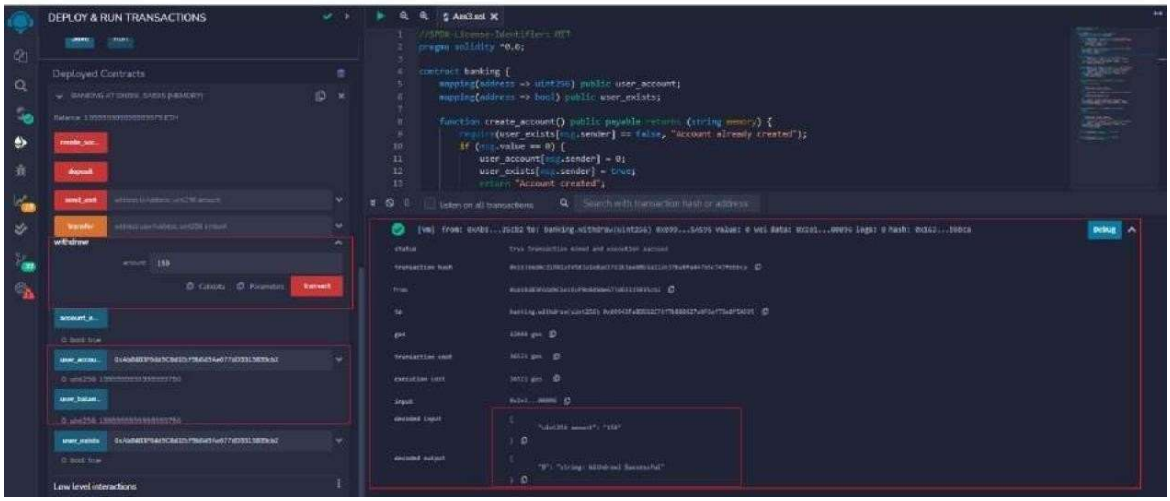
- Check User Account Balance



- Transfer Amount and Check User Account Balance



- Withdraw Amount and Check User Account Balance



Conclusion: Hence,wehave studied a smart contract on a test network for Bank account of a customer

Assignment No. 4

Title: Write a program in solidity to create Student data. Use the following constructs:

- Structures
- Arrays
- Fallback

Deploy this as smart contract on Ethereum and Observe the transaction fee and Gas value.

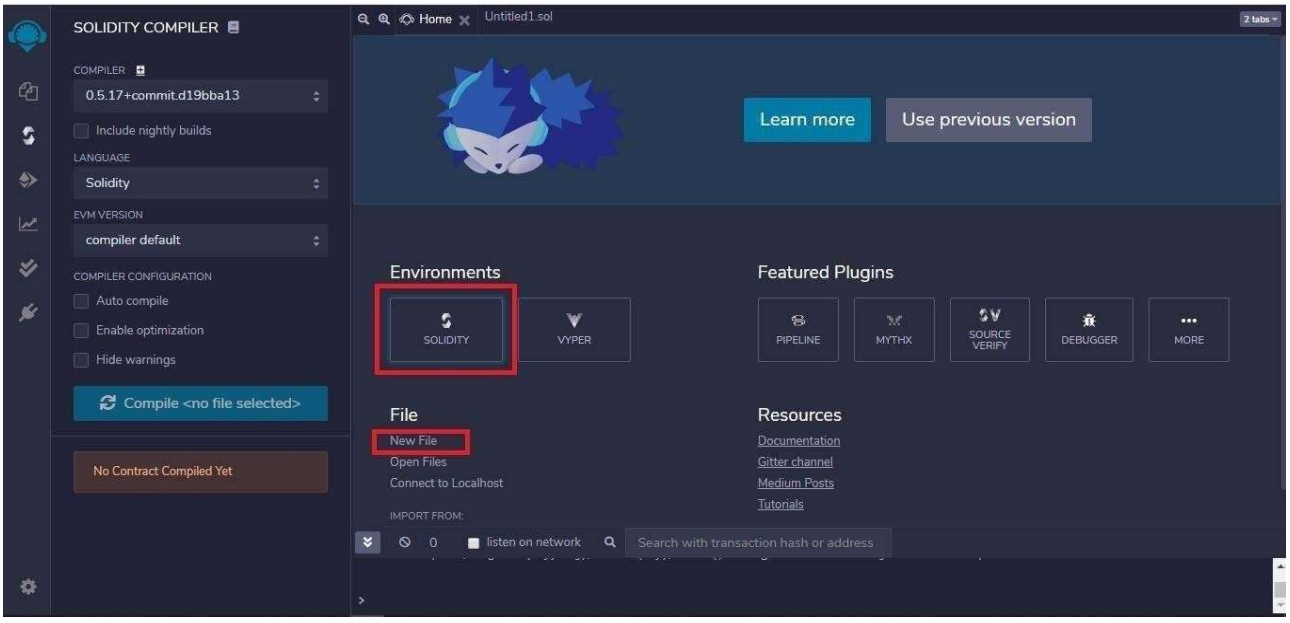
Objective: Understand and explore the working of Blockchain technology and its applications.

Course Outcome:

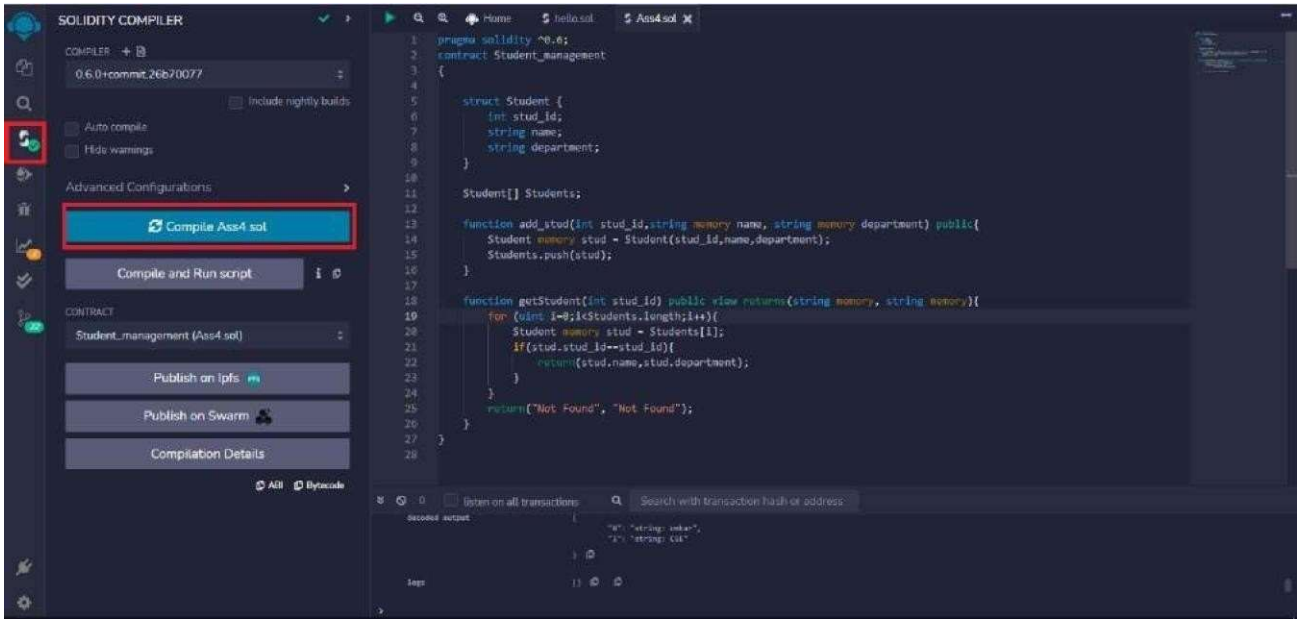
CO6:Interpret the basic concepts in Blockchain technology and its application.

Description:

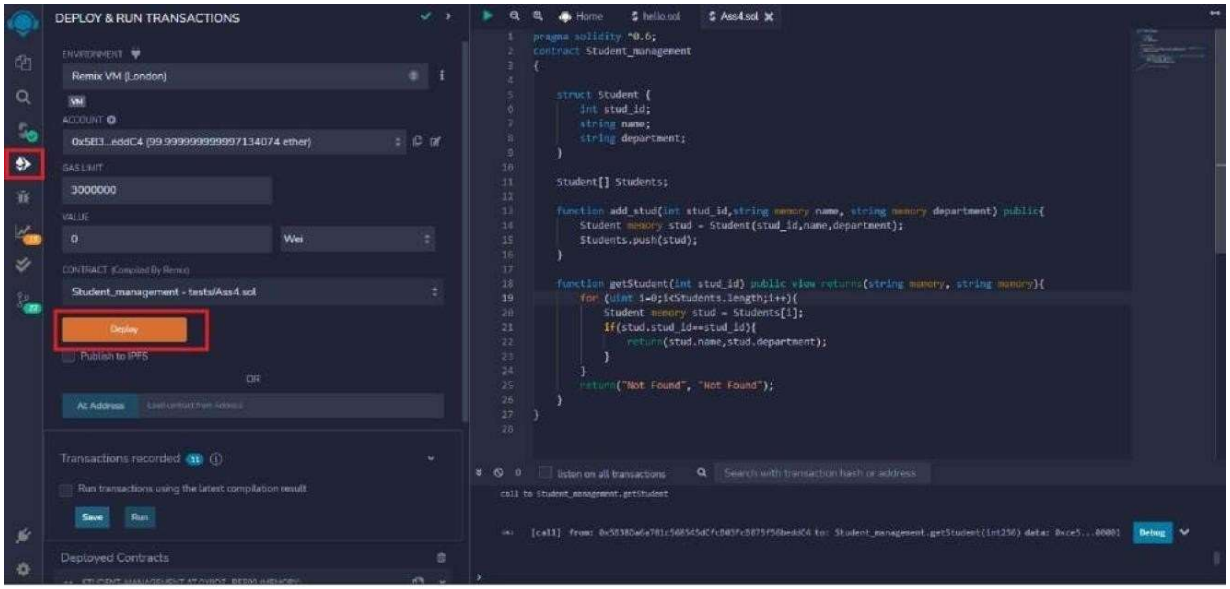
Step 1: Open Remix IDE on any of your browsers, select on the *New File* and click on *Solidity* to choose the environment.



Step 2: Write the Student Management code in the code section, and click the *Compile button* under the Compiler window to compile the contract.



Step 3: To execute the code, click on the *Deploy button* under Deploy and Run Transactions window. After deploying the code click on the drop-down on the console.



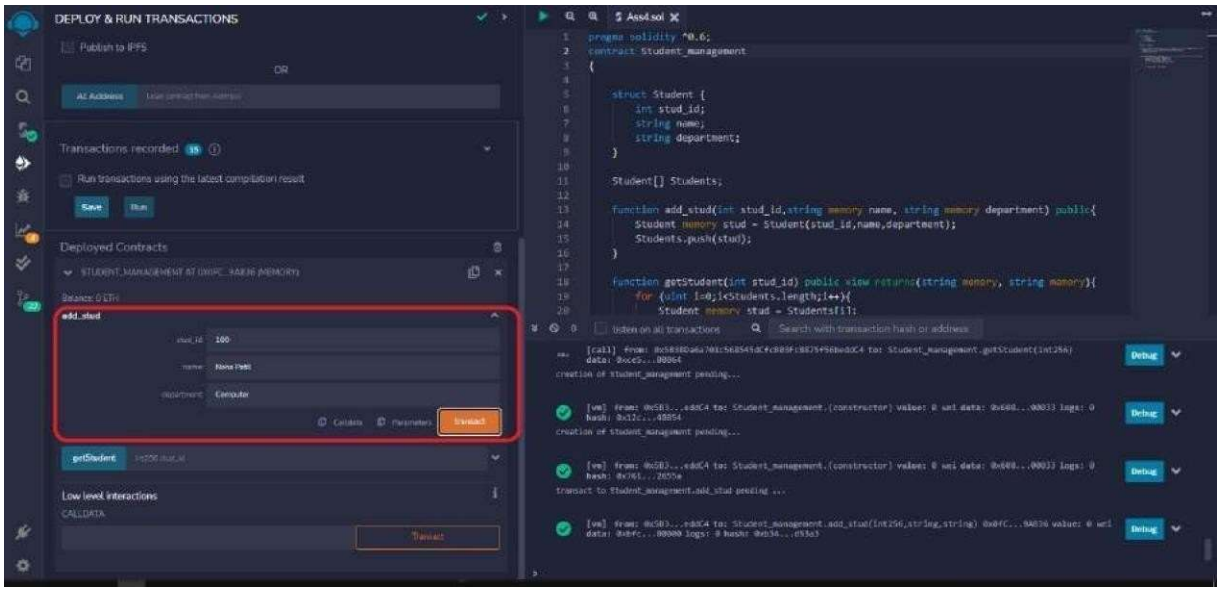
Code

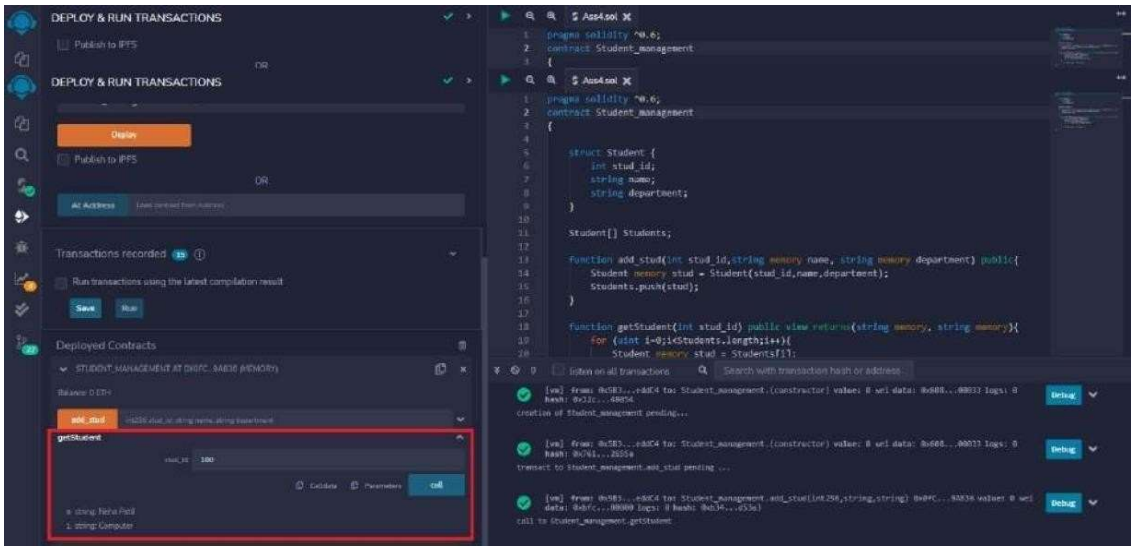
```
pragma solidity ^0.6;
contract Student_management
{

struct Student {
intstud_id;
        string name;
        string department;
    }

    Student[] Students;

    function add_stud(intstud_id,string memory name, string memory department) public{
        Student memory stud = Student(stud_id,name,department);
Students.push(stud);
    }

    function getStudent(intstud_id) public view returns(string memory, string memory){
        for (uinti=0;i<Students.length;i++){
            Student memory stud = Students[i];
            if(stud.stud_id==stud_id){
                return(stud.name,stud.department);
            }
        }
        return("Not Found", "Not Found");
    }
}
```

Sample Output

After deploying the contact successful you can observe two button add_stud and getStudents.Give the input stud_id, name dept and click on getStudents button, enter the stud_id which you have given as an Input and get the information of Students name and department

Refer the following output





Conclusion: Hence,wehave studieda program in solidity to create Student data.

Assignment No : 5

Title of the Assignment: Write a survey report on types of Blockchains and its real time use cases.

Objective of the Assignment: Students should be able to learn new technology such as metamask.Its application and implementations

Prerequisite:

1. Basic knowledge of cryptocurrency
2. Basic knowledge of distributed computing concept
3. Working of blockchain

Contents for Theory:

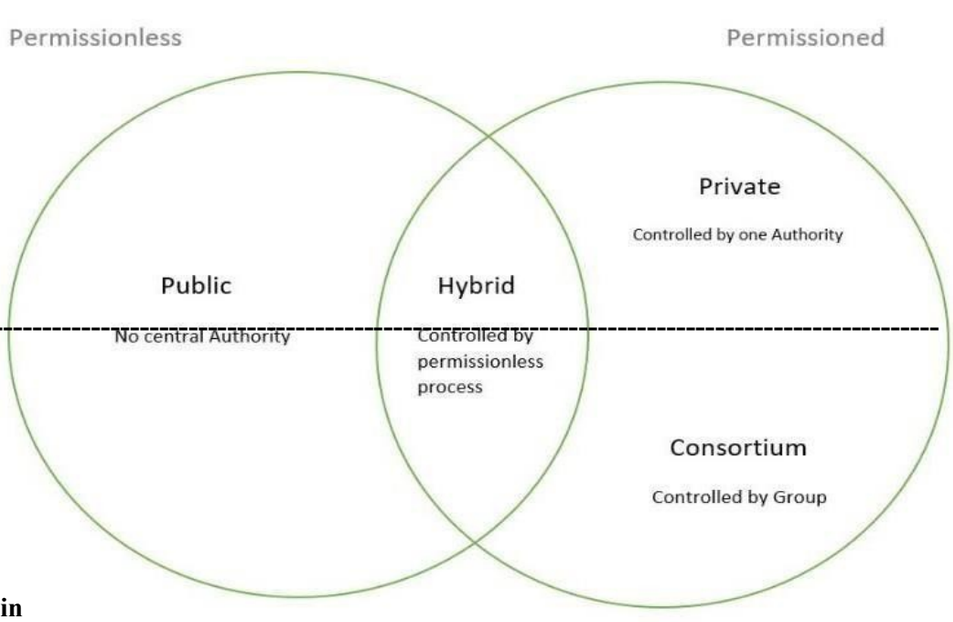
There are 4 types of blockchain:

Public Blockchain.

Private Blockchain.

Hybrid Blockchain.

Consortium Blockchain



1. Public Blockchain

These blockchains are completely open to following the idea of decentralization. They don‘t have any restrictions, anyone having a computer and internet can participate in the network.

As the name is public this blockchain is open to the public, which means it is not owned by anyone. Anyone having internet and a computer with good hardware can participate in this public blockchain. All the computer in the network hold the copy of other nodes or block present in the network
In this public blockchain, we can also perform verification of transactions or records Advantages:

Trustable: There are algorithms to detect no fraud. Participants need not worry about the other nodes in the network
Secure: This blockchain is large in size as it is open to the public. In a large size, there is greater distribution of records
Anonymous Nature: It is a secure platform to make your transaction properly at the same time, you are not required to reveal your name and identity in order to participate.
Decentralized: There is no single platform that maintains the network, instead every user has a copy of the ledger.
Disadvantages:

Processing: The rate of the transaction process is very slow, due to its large size. Verification of each node is a very time-consuming process.
Energy Consumption: Proof of work is high energy-consuming. It requires good computer hardware to participate in the network
Acceptance: No central authority is there so governments are facing the issue to implement the technology faster.
Use Cases: Public Blockchain is secured with proof of work or proof of stake they can be used to displace traditional financial systems. The more advanced side of this blockchain is the smart contract that enabled this blockchain to support decentralization. Examples of public blockchain are Bitcoin, Ethereum.

2. Private Blockchain
These blockchains are not as decentralized as the public blockchain only selected nodes can participate in the process, making it more secure than the others.

These are not as open as a public blockchain. They are
open to some authorized users only.
These blockchains are operated in a closed network.
In this few people are allowed to participate in a network within a company/organization.
Advantages:

Speed: The rate of the transaction is high, due to its small size. Verification of each node is less time- consuming.
Scalability: We can modify the scalability. The size of the network can be decided manually. Privacy: It has increased the level of privacy for confidentiality reasons as the businesses required.
Balanced: It is more balanced as only some user has the access to the transaction which improves the performance of the network.
Disadvantages:

Security- The number of nodes in this type is limited so chances of manipulation are there. These blockchains are more vulnerable.
Centralized- Trust building is one of the main disadvantages due to its central nature. Organizations can use this for malpractices.
Count- Since there are few nodes if nodes go offline the entire system of blockchain can be endangered. Use Cases: With proper security and maintenance, this blockchain is a great asset to secure information without exposing it to the public eye. Therefore companies use them for internal auditing, voting, and asset management. An example of private blockchains is Hyperledger, Corda.

3. Hybrid Blockchain
It is the mixed content of the private and public blockchain, where some part is controlled by some organization and other makes are made visible as a public blockchain.

It is a combination of both public and private blockchain.
Permission-based and permissionless systems are used. User
access information via smart contracts
Even a primary entity owns a hybrid blockchain it cannot alter the transaction Advantages:

Ecosystem: Most advantageous thing about this blockchain is its hybrid nature. It cannot be hacked as 51% of users don‘t have access to the network
Cost: Transactions are cheap as only a few nodes verify the transaction. All the nodes don‘t carry the verification hence less computational cost.
Architecture: It is highly customizable and still maintains integrity, security, and transparency. Operations: It can choose the participants in the blockchain and decide which transaction can be made public.

Disadvantages:

Efficiency: Not everyone is in the position to implement a hybrid Blockchain. The organization also faces

some difficulty in terms of efficiency in maintenance.
Transparency: There is a possibility that someone can hide information from the user. If someone wants to get access through a hybrid blockchain it depends on the organization whether they will give or not. Ecosystem: Due to its closed ecosystem this blockchain lacks the incentives for network participation. Use Case: It provides a greater solution to the health care industry, government, real estate, and financial companies. It provides a remedy where data is to be accessed publicly but needs to be shielded privately. Examples of Hybrid Blockchain are Ripple network and XRP token.

4. Consortium Blockchain
It is a creative approach that solves the needs of the organization. This blockchain validates the transaction and also initiates or receives transactions.

Also known as Federated Blockchain.
This is an innovative method to solve the organization‘s needs. Some part
is public and some part is private.
In this type, more than one organization manages the blockchain.
Advantages:

Speed: A limited number of users make verification fast. The high speed makes this more usable for organizations.
Authority: Multiple organizations can take part and make it decentralized at every level. Decentralized authority, makes it more secure.
Privacy: The information of the checked blocks is unknown to the public view. but any member belonging to the blockchain can access it.
Flexible: There is much divergence in the flexibility of the blockchain. Since it is not a very large decision can be taken faster.
Disadvantages:

Approval: All the members approve the protocol making it less flexible. Since one or more organizations are involved there can be differences in the vision of interest.
Transparency: It can be hacked if the organization becomes corrupt. Organizations may hide information from the users.
Vulnerability: If few nodes are getting compromised there is a greater chance of vulnerability in this blockchain
Use Cases: It has high potential in businesses, banks, and other payment processors. Food tracking of the organizations frequently collaborates with their sectors making it a federated solution ideal for their use. Examples of consortium Blockchain are Tendermint and Multichain.

Conclusion-In this way we have explored types of blockchain and its applications in real tim