

VISVESVARAYA TECHNOLOGICAL UNIVERSITY

“JnanaSangama”, Belgaum -590014, Karnataka.



LAB REPORT
on

Machine Learning

Submitted by

Arka Sinha (1BM19CS024)

in partial fulfillment for the award of the degree of
BACHELOR OF ENGINEERING

in
COMPUTER SCIENCE AND ENGINEERING



B.M.S. COLLEGE OF ENGINEERING

(Autonomous Institution under VTU)

BENGALURU-560019

Apr-2022 to Aug-2022

B. M. S. College of Engineering,
Bull Temple Road, Bangalore 560019
(Affiliated To Visvesvaraya Technological University, Belgaum)
Department of Computer Science and Engineering



CERTIFICATE

This is to certify that the Lab work entitled “**Machine Learning**” carried out by **Arka Sinha (1BM19CS024)**, who is a bonafide student of **B. M. S. College of Engineering**. It is in partial fulfillment for the award of **Bachelor of Engineering in Computer Science and Engineering** of the Visvesvaraya Technological University, Belgaum during the year 2022. The Lab report has been approved as it satisfies the academic requirements in respect of a **Machine Learning - (20CS6PCMAL)** work prescribed for the said degree.

Prof. Saritha A.N.
Assistant Professor
Department of CSE
BMSCE, Bengaluru

Dr. Jyothi S Nayak
Professor and Head
Department of CSE
BMSCE, Bengaluru

Index Sheet

Sl. No.	Experiment Title	Page No.
1.	Implement and demonstrate the FIND-S algorithm for finding the most specific hypothesis based on a given set of training data samples.	4
2.	For a given set of training data examples stored in a .CSV file, implement and demonstrate the Candidate-Elimination algorithm to output a description of the set of all hypotheses consistent with the training examples.	5
3.	Write a program to demonstrate the working of the Decision tree based ID3 algorithm. Use an appropriate data set for building the decision tree and apply this knowledge to classify a new sample	6
4.	Write a program to implement the Naïve Bayesian classifier for a sample training data set stored as a .CSV file. Compute the accuracy of the classifier, considering few test data sets	9
5.	Write a program to construct a Bayesian network considering training data. Use this model to make predictions.	11
6.	Apply k-Means algorithm to cluster a set of data stored in a .CSV file.	13
7.	Apply EM algorithm to cluster a set of data stored in a .CSV file. Compare the results of k-Means algorithm and EM algorithm.	18
8.	Implement the Linear Regression algorithm in order to fit data points. Select appropriate data set for your experiment and draw graphs.	19
9.	Write a program to implement k-Nearest Neighbour algorithm to classify the iris data set. Print both correct and wrong predictions.	20

Course Outcomes:

CO1	Ability to apply the different learning algorithms.
CO2	Ability to analyze the learning techniques for given dataset.
CO3	Ability to design a model using machine learning to solve a problem.
CO4	Ability to conduct practical experiments to solve problems using appropriate machine learning techniques.

1. Implement and demonstrate the FIND-S algorithm for finding the most specific hypothesis based on a given set of training data samples.

```
import pandas as pd
import numpy as np

#to read the data in the csv file
data = pd.read_csv("data.csv")
print(data,"n")

#making an array of all the attributes
d = np.array(data)[:,:-1]
print("n The attributes are: ",d)

#segragating the target that has positive and negative examples
target = np.array(data)[:,-1]
print("n The target is: ",target)

#training function to implement find-s algorithm
def train(c,t):
    for i, val in enumerate(t):
        if val == "yes":
            specific_hypothesis = c[i].copy()
            break

    for i, val in enumerate(c):
        if t[i] == "yes":
            for x in range(len(specific_hypothesis)):
                if val[x] != specific_hypothesis[x]:
                    specific_hypothesis[x] = '?'
            else:
                pass

    return specific_hypothesis

print("n The final hypothesis is:",train(d,target))
```

Output

	sky	air	temp	humidity	wind	water	forecast	enjoy	sport
0	sunny		warm	normal	strong	warm	same		yes
1	sunny		warm	high	strong	warm	same		yes
2	rainy		cold	high	strong	warm	change		no
3	sunny		warm	high	strong	cool	change		yes

```
n The attributes are: [['sunny' 'warm' 'normal' 'strong'
'warm' 'same']
['sunny' 'warm' 'high' 'strong' 'warm' 'same']
['rainy' 'cold' 'high' 'strong' 'warm' 'change']
['sunny' 'warm' 'high' 'strong' 'cool' 'change']]
n The target is: ['yes' 'yes' 'no' 'yes']
n The final hypothesis is: ['sunny' 'warm' '?' 'strong' '?' '?']
```

2. For a given set of training data examples stored in a .CSV file, implement and demonstrate the Candidate-Elimination algorithm to output a description of the set of all hypotheses consistent with the training examples.

```
import numpy as np
import pandas as pd
data = pd.read_csv('data.csv')
concepts = np.array(data.iloc[:,0:-1])
print("\nInstances:\n",concepts)
target = np.array(data.iloc[:,-1])
print("\nTarget Values: ",target)
def learn(concepts, target):
    sh = concepts[0].copy()
    print("\nInitialization of specific and general hypothesis")
    print("\nSpecific boundary: ", sh)
    gh = [["?" for i in range(len(sh))] for i in range(len(sh))]
    print("\nGeneric boundary: ",gh)
    for i, h in enumerate(concepts):
        print("\nInstance", i+1 , "is ", h)
        if target[i] == "yes":
            print("Instance is positive ")
            for x in range(len(sh)):
                if h[x] != sh[x]:
                    sh[x] = '?'
                    gh[x][x] = '?'
        if target[i] == "no":
            print("Instance is negative ")
            for x in range(len(sh)):
                if h[x] != sh[x]:
                    gh[x][x] = sh[x]
                else:
                    gh[x][x] = '?'
        print("Specific boundary after ", i+1, "instance is ", sh)
        print("Generic boundary after ", i+1, "instance is ", gh)
        print("\n")
    indices = [i for i, val in enumerate(gh) if val == ['?', '?', '?', '?', '?', '?']]
    for i in indices:
        gh.remove(['?', '?', '?', '?', '?', '?'])
    return sh, gh
```



```
print("Final specific hypothesis: ", sf,
      sep="\n") print("Final general hypothesis: ",
                      gf, sep="\n")
```

Output

Instances:

```
[['sunny' 'warm' 'normal' 'strong' 'warm' 'same']  
['sunny' 'warm' 'high' 'strong' 'warm' 'same']  
['rainy' 'cold' 'high' 'strong' 'warm' 'change']  
['sunny' 'warm' 'high' 'strong' 'cool' 'change']]
```

```
Target Values:  ['yes' 'yes' 'no' 'yes']
```

Initialization of specific and general hypothesis

```
Specific boundary: ['sunny' 'warm' 'normal' 'strong' 'warm' 'same']
```

```
Generic boundary: [['?', '?', '?', '?', '?', '?'], ['?', '?', '?', '?',  
                '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'],  
                ['?', '?', '?', '?', '?', '?']]
```

```
Instance 1 is ['sunny' 'warm' 'normal' 'strong' 'warm' 'same']
Instance is positive
Specific boundary after 1 instance is ['sunny' 'warm' 'normal' 'strong'
'warm' 'same']
Generic boundary after 1 instance is [['?', '?', '?', '?', '?', '?'],
['?', '?', '?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?',
'?',
'?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?', '?', '?', '?',
'?', '?']]
```

```
Instance 2 is ['sunny' 'warm' 'high' 'strong' 'warm'
'same'] Instance is positive
Specific boundary after 2 instance is ['sunny' 'warm' '?' 'strong' 'warm'
'same']
Generic boundary after 2 instance is [['?', '?', '?', '?', '?', '?'],
['?', '?', '?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?',
'?',
'?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?', '?', '?', '?',
'?', '?']]
```

```
Instance 3 is ['rainy' 'cold' 'high' 'strong' 'warm' 'change']
Instance is negative
Specific boundary after 3 instance is ['sunny' 'warm' '?' 'strong' 'warm'
'same']
Generic boundary after 3 instance is [['sunny', '?', '?', '?', '?', '?'],
['?', 'warm', '?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?',
'?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?', '?', '?',
'?', '?', 'same']]
```


Instance 4 is ['sunny' 'warm' 'high' 'strong' 'cool' 'change']
Instance is positive
Specific boundary after 4 instance is ['sunny' 'warm' '?' 'strong'
?' '?']
Generic boundary after 4 instance is [['sunny', '?', '?', '?', '?', '?'],
['?', 'warm', '?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?',
?', '?', '?', '?', '?'], ['?', '?', '?', '?', '?', '?'], ['?', '?', '?',
?', '?', '?']]

Final specific hypothesis:
['sunny' 'warm' '?' 'strong' '?' '?']
Final general hypothesis:
[['sunny', '?', '?', '?', '?', '?'], ['?', 'warm', '?', '?', '?', '?']]

3. Write a program to demonstrate the working of the Decision tree based ID3 algorithm. Use an appropriate data set for building the decision tree and apply this knowledge to classify a new sample

```
import pandas as pd
import math
import numpy as np
import pprint

data=pd.read_csv("tennis.csv")
print("\n Input Data Set is:\n", data)
features = [f for f in data]
features.remove("answer")

class Node:
    def __init__(self):
        self.children = []
        self.value = ""
        self.isLeaf = False
        self.pred = ""

def find_entropy(examples):
    pos = 0.0
    neg = 0.0
    for _, row in examples.iterrows():
        if row["answer"] == "yes":
            pos += 1
        else:
            neg += 1
    if pos == 0.0 or neg == 0.0:
        return 0.0
    else:
        p = pos / (pos + neg)
        n = neg / (pos + neg)
        return -(p * math.log(p, 2) + n * math.log(n, 2))

def info_gain(examples, attr):
    uniq = np.unique(examples[attr])
    gain = find_entropy(examples)
```

```

        for u in uniq:
            subdata = examples[examples[attr] == u]
            sub_e = find_entropy(subdata)
            gain -= (float(len(subdata)) / float(len(examples))) *
sub_e
        return gain

def id3(examples, attrs):
    root = Node()

    max_gain = 0
    max_feat = ""
    for feature in attrs:
        gain = info_gain(examples, feature)
        if gain > max_gain:
            max_gain = gain
            max_feat = feature
    root.value = max_feat
    uniq = np.unique(examples[max_feat])
    for u in uniq:
        subdata = examples[examples[max_feat] == u]
        if find_entropy(subdata) == 0.0:
            newNode = Node()
            newNode.isLeaf = True
            newNode.value = u
            newNode.pred = np.unique(subdata["answer"])
            root.children.append(newNode)
        else:
            tempNode = Node()
            tempNode.value = u
            new_attrs = attrs.copy()
            new_attrs.remove(max_feat)
            child = id3(subdata,
            new_attrs)
            tempNode.children.append(child
            )
            root.children.append(tempNode)
    return root

def printTree(root: Node, depth=0):
    for i in range(depth):
        print("\t", end="")

```



```

        print(" : ",
              root.pred) print()
    for child in root.children:
        printTree(child, depth +
                  1)

root = id3(data, features)
print("Final decision
tree:\n") printTree(root)

```

Output

```

Input Data Set is:
outlook temperature humidity    wind answer

```

```

Final decision tree:
outlook
  overcast :  ['yes']

```

```

    rain
      wind
        strong :  ['no']

```

```

        weak :  ['yes']

```

```

    sunny
      humidity
        high :  ['no']

```

```

        normal :  ['yes']

```

4. Write a program to implement the Naïve Bayesian classifier for a sample training data set stored as a .CSV file. Compute the accuracy of the classifier, considering few test data sets.

```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd

# Importing the dataset
#dataset =
pd.read_csv('181105_missing-data.csv') dataset =
pd.read_csv('salary.csv')
X = dataset.iloc[:, :-1].values #get a copy of dataset exclude last column
y = dataset.iloc[:, 1].values #get array of dataset in column 1st

# Splitting the dataset into the Training set and Test set
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=1/3,
random_state=0)

# Fitting Simple Linear Regression to the Training set
from sklearn.linear_model import LinearRegression
regressor = LinearRegression()
regressor.fit(X_train, y_train)

# Predicting the Test set results
y_pred =
regressor.predict(X_test)

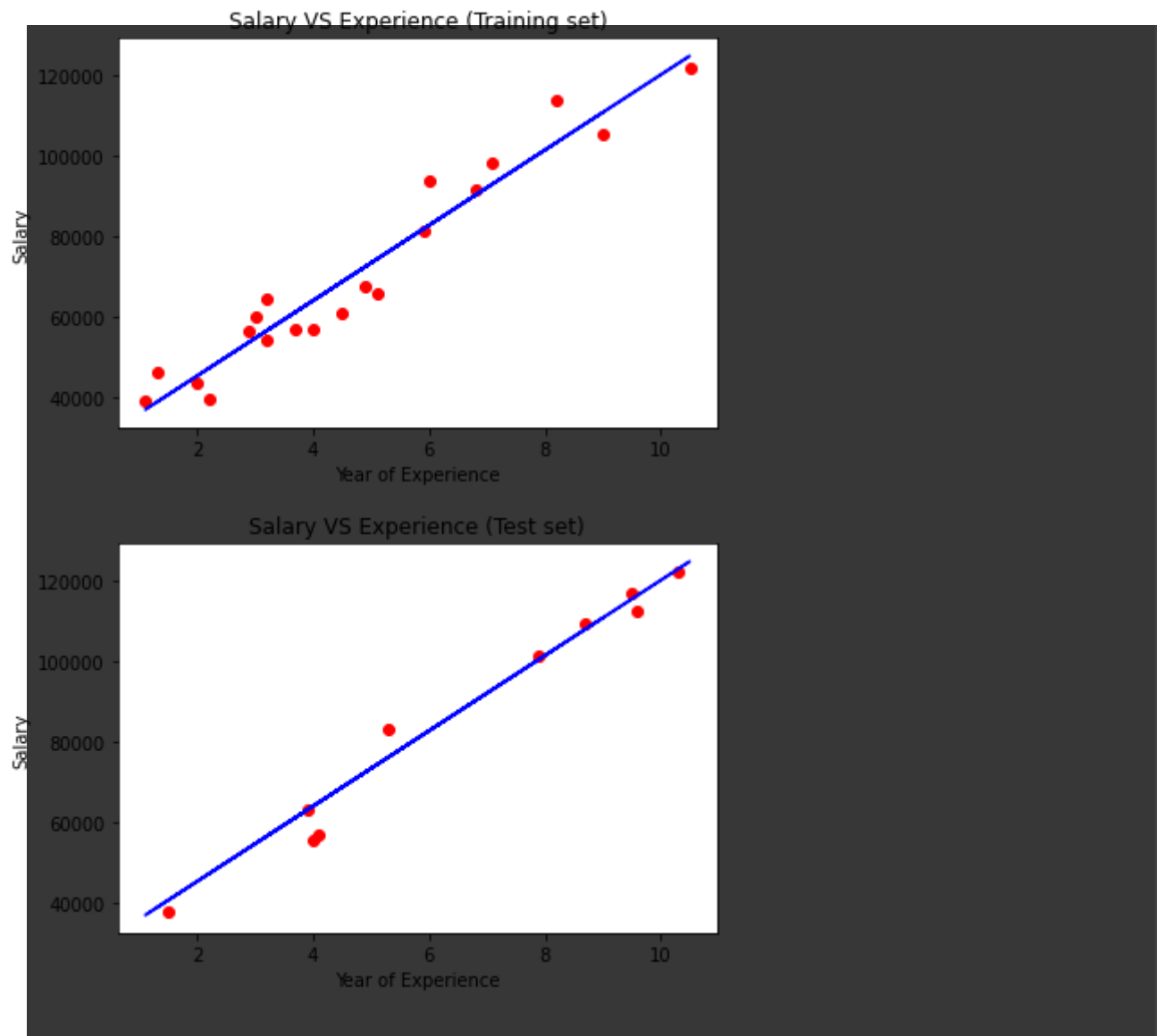
# Visualizing the Training set results
viz_train = plt
viz_train.scatter(X_train, y_train, color='red')
viz_train.plot(X_train, regressor.predict(X_train), color='blue')
viz_train.title('Salary VS Experience (Training set)')
viz_train.xlabel('Year of Experience')
viz_train.ylabel('Salary')
viz_train.show()

# Visualizing the Test set results
viz_test = plt
viz_test.scatter(X_test, y_test, color='red')
viz_test.plot(X_train, regressor.predict(X_train), color='blue')
viz_test.title('Salary VS Experience (Test set)')
```

```
viz_test.xlabel('Year of Experience')  
viz_test.ylabel('Salary')
```

```
viz_test.show()
```

Output



5. Write a program to construct a Bayesian network considering training data. Use this model to make predictions.

```
import csv
import random
import math
def loadcsv(filename):
    lines = csv.reader(open("naive.csv", "r"));
    dataset = list(lines)
    for i in range(len(dataset)):
        #converting strings into numbers for processing
        dataset[i] = [float(x) for x in dataset[i]]

    return dataset

def splitdataset(dataset, splitratio):
    #67% training size
    trainsize = int(len(dataset) * splitratio);
    trainset = []
    copy = list(dataset);
    while len(trainset) < trainsize:
        #generate indices for the dataset list randomly to pick ele for training
        data
        index = random.randrange(len(copy));
        trainset.append(copy.pop(index))
    return [trainset, copy]

def separatebyclass(dataset):
    separated = {} #dictionary of classes 1 and 0
    #creates a dictionary of classes 1 and 0 where the values are
    #the instances belonging to each class
    for i in range(len(dataset)):
        vector = dataset[i]
        if (vector[-1] not in separated):
            separated[vector[-1]] = []
        separated[vector[-1]].append(vector)
    return separated

def mean(numbers):
    return sum(numbers)/float(len(numbers))
```



```

    avg = mean(numbers)
    variance = sum([pow(x-avg,2) for x in numbers])/float(len(numbers)-1)
    return math.sqrt(variance)

def summarize(dataset): #creates a dictionary of classes
    summaries = [(mean(attribute), stdev(attribute)) for attribute in
zip(*dataset)];
    del summaries[-1] #excluding labels +ve or -ve
    return summaries

def summarizebyclass(dataset):
    separated = separatebyclass(dataset);
    #print(separated)
    summaries = {}
    for classvalue, instances in separated.items():
#for key,value in dic.items()
#summaries is a dic of tuples(mean,std) for each class value
        summaries[classvalue] = summarize(instances) #summarize is used to cal
to mean and std
    return summaries

def calculateprobability(x, mean, stdev):
    exponent = math.exp(-(math.pow(x-mean,2)/(2*math.pow(stdev,2))))
    return (1 / (math.sqrt(2*math.pi) * stdev)) * exponent

def calculateclassprobabilities(summaries, inputvector):
    probabilities = {} # probabilities contains the all prob of all class of
test data
    for classvalue, classsummaries in summaries.items():#class and attribute
information as mean and sd
        probabilities[classvalue] = 1
        for i in range(len(classsummaries)):
            mean, stdev = classsummaries[i] #take mean and sd of every attribute
for class 0 and 1 sepearely
            x = inputvector[i] #testvector's first attribute
            probabilities[classvalue] *= calculateprobability(x, mean,
stdev);#use normal dist
    return probabilities

def predict(summaries, inputvector): #training and test data is passed
    probabilities = calculateclassprobabilities(summaries, inputvector)
    bestLabel, bestProb = None, -1
    for classvalue, probability in probabilities.items():#assigns that class
which has he highest prob
        if bestLabel is None or probability > bestProb:

```

```

        bestProb = probability
        bestLabel = classvalue
    return bestLabel

def getpredictions(summaries, testset):
    predictions = []
    for i in range(len(testset)):
        result = predict(summaries, testset[i])
        predictions.append(result)
    return predictions

def getaccuracy(testset, predictions):
    correct = 0
    for i in range(len(testset)):
        if testset[i][-1] == predictions[i]:
            correct += 1
    return (correct/float(len(testset))) * 100.0

def main():
    filename = 'naivedata.csv'
    splitratio = 0.67
    dataset = loadcsv(filename);

    trainingset, testset = splitdataset(dataset, splitratio)
    print('Split {0} rows into train={1} and test={2}
rows'.format(len(dataset), len(trainingset), len(testset)))
    # prepare model
    summaries = summarizebyclass(trainingset);
    #print(summaries)
    # test model
    predictions = getpredictions(summaries, testset) #find the predictions of
test data with the training data
    accuracy = getaccuracy(testset, predictions)
    print('Accuracy of the classifier is : {0}%'.format(accuracy))

main()

```

Output

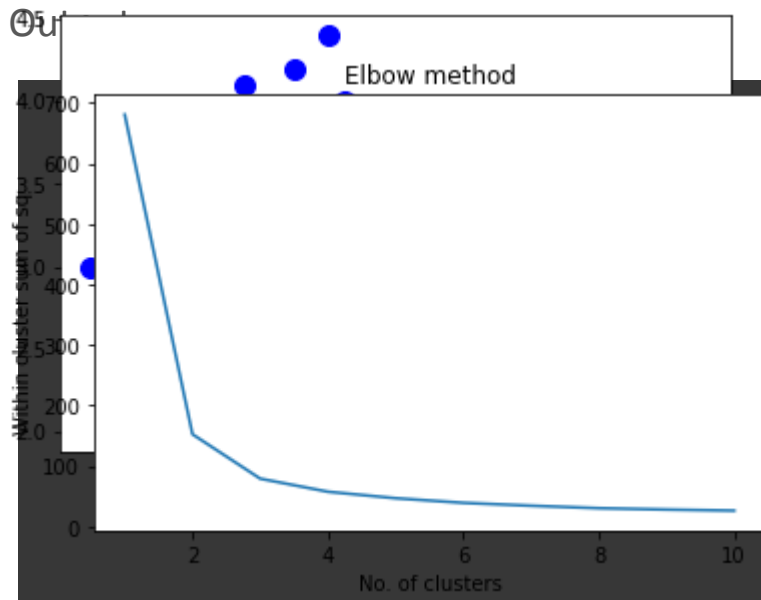
```

Split 767 rows into train=513 and test=254 rows
Accuracy of the classifier is : 74.80314960629921%

```

6. Apply k-Means algorithm to cluster a set of data stored in a .CSV file

```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
dataset = pd.read_csv('iris.csv')
x = dataset.iloc[:, [1, 2, 3, 4]].values
from sklearn.cluster import KMeans
wcss = []
for i in range(1, 11):
    kmeans = KMeans(n_clusters = i, init = 'k-means++', max_iter = 300,
n_init = 10, random_state = 0)
    kmeans.fit(x)
    wcss.append(kmeans.inertia_)
plt.plot(range(1, 11), wcss)
plt.title('Elbow method')
plt.xlabel('No. of clusters')
plt.ylabel('Within cluster sum of sq')
plt.show()
kmeans = KMeans(n_clusters = 3, init = 'k-means++', max_iter = 300, n_init =
10, random_state = 0)
y_kmeans = kmeans.fit_predict(x)
plt.scatter(x[y_kmeans == 0, 0], x[y_kmeans == 0, 1], s = 100, c = 'red',
label = 'Iris-setosa')
plt.scatter(x[y_kmeans == 1, 0], x[y_kmeans == 1, 1], s = 100, c = 'blue',
label = 'Iris-versicolour')
plt.scatter(x[y_kmeans == 2, 0], x[y_kmeans == 2, 1], s = 100, c = 'green',
label = 'Iris-virginica')
plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:,1], s =
100, c = 'yellow', label = 'Centroids')
plt.legend()
```



<matplotlib.legend.Legend at 0x7fc6098efad0>

7. Apply EM algorithm to cluster a set of data stored in a .CSV file. Compare the results of k-Means algorithm and EM algorithms.

```
!pip install pgmpy
from pgmpy.models import BayesianModel
from pgmpy.factors.discrete import TabularCPD
from pgmpy.inference import
VariableElimination
cancer_model = BayesianModel([('Pollution', 'Cancer'),
                              ('Smoker', 'Cancer'),
                              ('Cancer', 'Xray'),
                              ('Cancer', 'Dyspnoea')])

print('Bayesian network nodes:')
print('\t', cancer_model.nodes())
print('Bayesian network edges:')
print('\t', cancer_model.edges())

cpd_poll = TabularCPD(variable='Pollution', variable_card=2,
                      values=[[0.9], [0.1]])
cpd_smoke = TabularCPD(variable='Smoker', variable_card=2,
                      values=[[0.3], [0.7]])
cpd_cancer = TabularCPD(variable='Cancer', variable_card=2,
                      values=[[0.03, 0.05, 0.001, 0.02],
                              [0.97, 0.95, 0.999, 0.98]],
                      evidence=['Smoker', 'Pollution'],
                      evidence_card=[2, 2])
cpd_xray = TabularCPD(variable='Xray', variable_card=2,
                      values=[[0.9, 0.2], [0.1, 0.8]],
                      evidence=['Cancer'], evidence_card=[2])
cpd_dysp = TabularCPD(variable='Dyspnoea', variable_card=2,
                      values=[[0.65, 0.3], [0.35, 0.7]],
                      evidence=['Cancer'], evidence_card=[2])
cancer_model.add_cpds(cpd_poll, cpd_smoke, cpd_cancer, cpd_xray,
cpd_dysp)
print('Model generated bt adding conditional probability
distribution(cpds)')
print('Checking for Correctness of model:', end='')
print(cancer_model.check_model())
'''print('All local dependencies are as
follows') cancer_model.get_independencies()
'''
```

```

print('Displaying CPDs')
print(cancer_model.get_cpds('Pollution'))
print(cancer_model.get_cpds('Smoker'))
print(cancer_model.get_cpds('Cancer'))
print(cancer_model.get_cpds('Xray'))
print(cancer_model.get_cpds('Dyspnoea'))
cancer_infer =
VariableElimination(cancer_model)
print('\nInferencing with Bayesian Network')
print('\nProbability of Cancer given Smoker')
q = cancer_infer.query(variables=['Cancer'],
evidence={'Smoker': 1})
print(q)
print('\nProbability of Cancer given Smoker, Pollution')
q = cancer_infer.query(variables=['Cancer'],
evidence={'Smoker': 1, 'Pollution': 1})
print(q)

```

Output

Looking in indexes: <https://pypi.org/simple>,

<https://us-python.pkg.dev/colab-wheels/public/simple/>

Collecting pgmpy

Downloading pgmpy-0.1.19-py3-none-any.whl (1.9 MB)

 1.9 MB 5.0 MB/s

Requirement already satisfied: joblib in /usr/local/lib/python3.7/dist-packages (from pgmpy) (1.1.0)

Requirement already satisfied: pandas in /usr/local/lib/python3.7/dist-packages (from pgmpy) (1.3.5)

Requirement already satisfied: pyparsing in /usr/local/lib/python3.7/dist-packages (from pgmpy) (3.0.9)

Requirement already satisfied: scikit-learn in /usr/local/lib/python3.7/dist-packages (from pgmpy) (1.0.2)

Requirement already satisfied: numpy in /usr/local/lib/python3.7/dist-packages (from pgmpy) (1.21.6)

Requirement already satisfied: torch in /usr/local/lib/python3.7/dist-packages (from pgmpy) (1.11.0+cu113)

Requirement already satisfied: tqdm in /usr/local/lib/python3.7/dist-packages (from pgmpy) (4.64.0)

Requirement already satisfied: networkx in /usr/local/lib/python3.7/dist-packages (from pgmpy) (2.6.3)

Requirement already satisfied: scipy in /usr/local/lib/python3.7/dist-packages (from pgmpy) (1.4.1)

Requirement already satisfied: statsmodels in /usr/local/lib/python3.7/dist-packages


```

(from pgmpy) (0.10.2)
Requirement already satisfied: python-dateutil>=2.7.3 in
/usr/local/lib/python3.7/dist-packages (from pandas->pgmpy) (2.8.2)
Requirement already satisfied: pytz>=2017.3 in /usr/local/lib/python3.7/dist-packages
(from pandas->pgmpy) (2022.1)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.7/dist-packages
(from python-dateutil>=2.7.3->pandas->pgmpy) (1.15.0)
Requirement already satisfied: threadpoolctl>=2.0.0 in
/usr/local/lib/python3.7/dist-packages (from scikit-learn->pgmpy) (3.1.0)
Requirement already satisfied: patsy>=0.4.0 in
/usr/local/lib/python3.7/dist-packages (from statsmodels->pgmpy) (0.5.2)
Requirement already satisfied: typing-extensions in
/usr/local/lib/python3.7/dist-packages (from torch->pgmpy) (4.1.1)
Installing collected packages: pgmpy
Successfully installed pgmpy-0.1.19
/usr/local/lib/python3.7/dist-packages/statsmodels/tools/_testing.py:19:
FutureWarning: pandas.util.testing is deprecated. Use the functions in the public API at
pandas.testing instead.
    import pandas.util.testing as
tm Bayesian network nodes:
    ['Pollution', 'Cancer', 'Smoker', 'Xray', 'Dyspnoea']
Bayesian network edges:
    [('Pollution', 'Cancer'), ('Cancer', 'Xray'), ('Cancer', 'Dyspnoea'), ('Smoker', 'Cancer')]
Model generated bt adding conditional probability distribution(cpd)
Checking for Correctness of
model:True Displaying CPDs
+-----+-----+
| Pollution(0) | 0.9 |
+-----+-----+
| Pollution(1) | 0.1 |
+-----+-----+
+-----+-----+
+-----+-----+
| Smoker(0) | 0.3 |
+-----+-----+
+-----+-----+
| Smoker(1) | 0.7 |
+-----+-----+
+-----+-----+-----+-----+-----+-----+
| Smoker | Smoker(0) | Smoker(0) | Smoker(1) | Smoker(1) |
+-----+-----+-----+-----+-----+-----+
| Pollution | Pollution(0) | Pollution(1) | Pollution(0) | Pollution(1) |
+-----+-----+-----+-----+-----+-----+
| Cancer(0) | 0.03 | 0.05 | 0.001 | 0.02 |
+-----+-----+-----+-----+-----+-----+
| Cancer(1) | 0.97 | 0.95 | 0.999 | 0.98 |
+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+
| Cancer | Cancer(0) | Cancer(1) |
+-----+-----+-----+
| Xray(0) | 0.9 | 0.2 |

```

```

+-----+-----+-----+
| Xray(1) | 0.1    | 0.8    |
+-----+-----+-----+
+-----+-----+-----+
| Cancer  | Cancer(0) | Cancer(1) |
+-----+-----+-----+
| Dyspnoea(0) | 0.65    | 0.3     |
+-----+-----+-----+
| Dyspnoea(1) | 0.35    | 0.7     |
+-----+-----+-----+

```

Inferencing with Bayesian Network
Probability of Cancer given Smoker

/usr/local/lib/python3.7/dist-packages/pgmpy/models/BayesianModel.py:10:
FutureWarning: BayesianModel has been renamed to BayesianNetwork. Please use
BayesianNetwork class, BayesianModel will be removed in future.
FutureWarning,

```

Finding Elimination Order: : 100%
1/1 [00:00<00:00, 8.95it/s]
Eliminating: Pollution: 100%
1/1 [00:00<00:00, 14.21it/s]

```

```

+-----+-----+
| Cancer | phi(Cancer) |
+=====+=====+
| Cancer(0) | 0.0029 |
+-----+-----+
| Cancer(1) | 0.9971 |
+-----+-----+

```

Probability of Cancer given Smoker, Pollution

```

Finding Elimination Order: :
0/0 [00:00<?, ?it/s]
0/0 [00:00<?, ?it/s]

```

```

+-----+-----+
| Cancer | phi(Cancer) |
+=====+=====+
| Cancer(0) | 0.0200 |
+-----+-----+
| Cancer(1) | 0.9800 |
+-----+-----+

```

8. Implement the Linear Regression algorithm in order to fit data points. Select appropriate data set for your experiment and draw graphs.

```
import matplotlib.pyplot as plt
import seaborn as sns
sns.set_style("white")
%matplotlib inline
#for matrix math
import numpy as np
#for normalization + probability density function computation
from scipy import stats
#for data preprocessing
import pandas as pd
from math import sqrt, log, exp, pi
from random import uniform
random_seed=36788765
np.random.seed(random_seed)

Mean1 = 2.0 # Input parameter, mean of first normal probability
distribution
Standard_dev1 = 4.0 #@param {type:"number"}
Mean2 = 9.0 # Input parameter, mean of second normal
probability distribution
Standard_dev2 = 2.0 #@param {type:"number"}

# generate data
y1 = np.random.normal(Mean1, Standard_dev1, 1000)
y2 = np.random.normal(Mean2, Standard_dev2, 500)
data=np.append(y1,y2)

# For data visualisation calculate left and right of the graph
Min_graph = min(data)
Max_graph = max(data)

x = np.linspace(Min_graph, Max_graph, 2000) # to plot the data
```

```

print('Input Gaussian {:}:  $\mu = {:.2}$ ,  $\sigma = {:.2}$ '.format("1", Mean1,
Standard_dev1))
print('Input Gaussian {:}:  $\mu = {:.2}$ ,  $\sigma = {:.2}$ '.format("2", Mean2,
Standard_dev2))
sns.distplot(data, bins=20, kde=False);

from sklearn.mixture import GaussianMixture
gmm = GaussianMixture(n_components = 2, tol=0.000001)
gmm.fit(np.expand_dims(data, 1)) # Parameters: array-like, shape
(n_samples, n_features), 1 dimension dataset so 1 feature
Gaussian_nr = 1
print('Input Gaussian {:}:  $\mu = {:.2}$ ,  $\sigma = {:.2}$ '.format("1", Mean1,
Standard_dev1))
print('Input Gaussian {:}:  $\mu = {:.2}$ ,  $\sigma = {:.2}$ '.format("2", Mean2,
Standard_dev2))
for mu, sd, p in zip(gmm.means_.flatten(),
np.sqrt(gmm.covariances_.flatten()),
gmm.weights_):
    print('Gaussian {:}:  $\mu = {:.2}$ ,  $\sigma = {:.2}$ , weight =
{:.2}'.format(Gaussian_nr, mu, sd, p))
    g_s = stats.norm(mu, sd).pdf(x) * p
    plt.plot(x, g_s, label='gaussian sklearn');
    Gaussian_nr += 1
sns.distplot(data, bins=20, kde=False, norm_hist=True)
gmm_sum = np.exp([gmm.score_samples(e.reshape(-1, 1)) for e in x])
#gmm gives log probability, hence the exp() function
plt.plot(x, gmm_sum, label='gaussian mixture');
plt.legend();

```

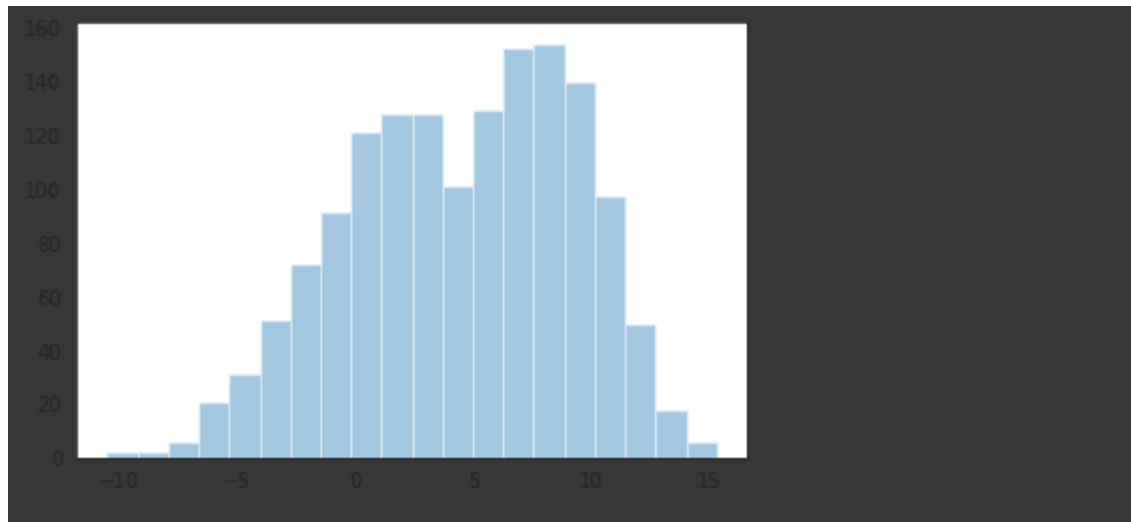
Output

Input Gaussian 1: $\mu = 2.0$, $\sigma = 4.0$

Input Gaussian 2: $\mu = 9.0$, $\sigma = 2.0$

/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please adapt
your code to use either `displot` (a figure-level function with similar flexibility) or `histplot`
(an axes-level function for histograms).

warnings.warn(msg, FutureWarning)



Input Gaussian 1: $\mu = 2.0$, $\sigma = 4.0$

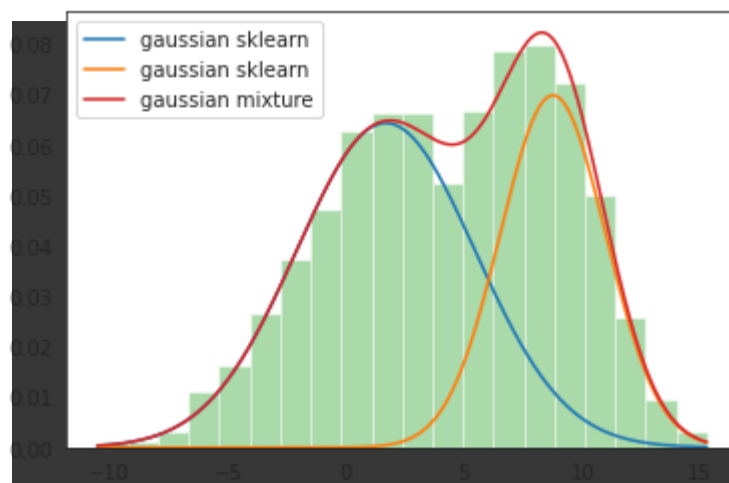
Input Gaussian 2: $\mu = 9.0$, $\sigma = 2.0$

Gaussian 1: $\mu = 1.7$, $\sigma = 3.8$, weight = 0.61

Gaussian 2: $\mu = 8.8$, $\sigma = 2.2$, weight = 0.39

/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureWarning: ``distplot`` is a deprecated function and will be removed in a future version. Please adapt your code to use either ``displot`` (a figure-level function with similar flexibility) or ``histplot`` (an axes-level function for histograms).

warnings.warn(msg, FutureWarning)



9. Write a program to implement k-Nearest Neighbour algorithm to classify the iris data set. Print both correct and wrong predictions.

```
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import classification_report, confusion_matrix
from sklearn import datasets

iris=datasets.load_iris()

x = iris.data
y = iris.target

# print ('sepal-length', 'sepal-width', 'petal-length', 'petal-width')
# print(x)
# print('class: 0-Iris-Setosa, 1- Iris-Versicolour, 2- Iris-Virginica')
# print(y)

x_train, x_test, y_train, y_test = train_test_split(x,y,test_size=0.3)

#To Training the model and Nearest nighbors K=5
classifier = KNeighborsClassifier(n_neighbors=5)
classifier.fit(x_train, y_train)

#To make predictions on our test data
y_pred=classifier.predict(x_test)

print('Confusion Matrix')
print(confusion_matrix(y_test,y_pred))
print('Accuracy Metrics')
print(classification_report(y_test,y_pred))
```

Output

Confusion Matrix



[0 2 18]]

Accuracy Metrics

	precision	recall	f1-score	support
0	1.00	1.00	1.00	14
1	0.83	0.91	0.87	11
2	0.95	0.90	0.92	20
accuracy			0.93	45
macro avg	0.93	0.94	0.93	45
weighted avg	0.94	0.93	0.93	45

10. Implement the non-parametric Locally Weighted Regression algorithm in order to fit data points. Select appropriate data set for your experiment and draw graphs.

```
from numpy import *
from os import listdir
import matplotlib
import matplotlib.pyplot as plt
import pandas as pd
import numpy as npl
import numpy.linalg as np
from scipy.stats.stats import pearsonr

def kernel(point,xmat, k):
    m,n = npl.shape(xmat)
    weights = npl.mat(npl.eye((m)))
    for j in range(m):
        diff = point - X[j]
        weights[j,j] = npl.exp(diff*diff.T/(-2.0*k**2))
    return weights

def localWeight(point,xmat,ymat,k):
    wei = kernel(point,xmat,k)
    W = (X.T*(wei*X)).I*(X.T*(wei*ymat.T))
    return W

def localWeightRegression(xmat,ymat,k):
    m,n = npl.shape(xmat)
    ypred = npl.zeros(m)
    for i in range(m):
        ypred[i] = xmat[i]*localWeight(xmat[i],xmat,ymat,k)
    return ypred

# load data points
data = pd.read_csv('/content/tips.csv')
bill = npl.array(data.total_bill)
tip = npl.array(data.tip)

#preparing and add 1 in bill
mbill = npl.mat(bill)
mtip = npl.mat(tip) # mat is used to convert to n dimesiona to 2
dimensional array form
```

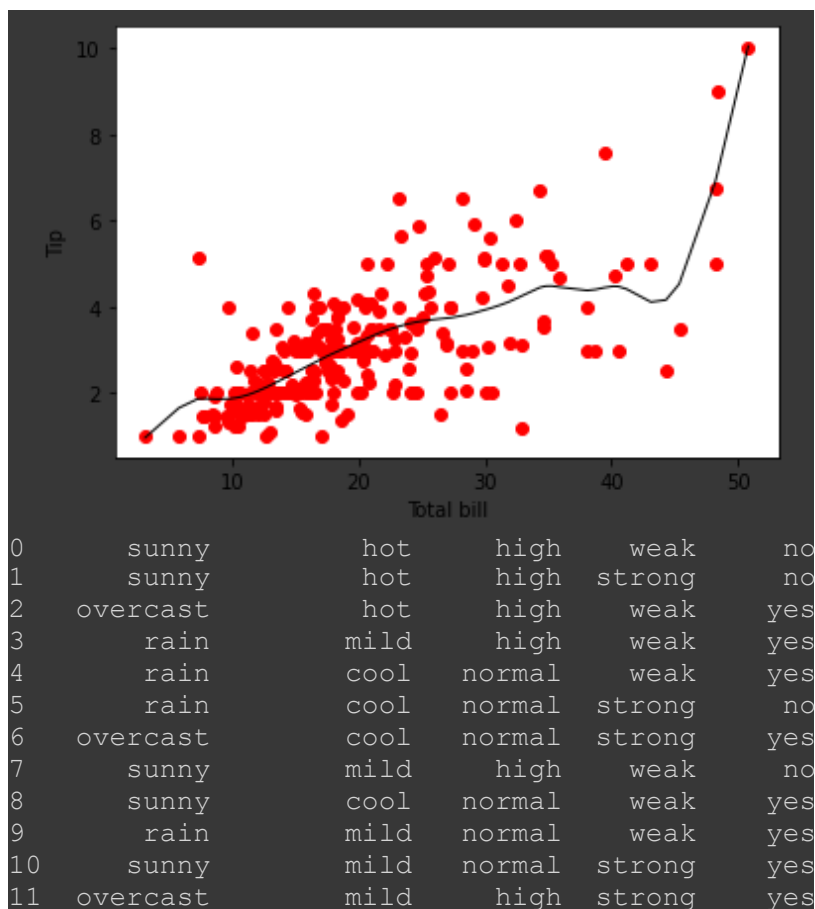


```

X= np.hstack((one.T,mbill.T)) # create a stack of bill from
ONE #print(X)
#set k here
ypred =
localWeightRegression(X,mtip,2)
SortIndex = X[:,1].argsort(0)
xsort =
X[SortIndex][:,0] fig =
plt.figure()
ax = fig.add_subplot(1,1,1)
ax.scatter(bill,tip,
color='red')
ax.plot(xsort[:,1],ypred[SortIndex], color = 'black',
linewidth=1) plt.xlabel('Total bill')
plt.ylabel('Tip
') plt.show()

```

Output



12	overcast	hot	normal	weak	yes
13	rain	mild	high	strong	no