**DEEP LEARNING**

EXP NO : 1

AIM: : Verifying the performance of a linear regression by using choosen database with phython code

PROGRAM:

import numpy as np

import matplotlib.pyplot as plt

def estimate\_coef(x, y):

    # number of observations/points

    n = np.size(x)

    # mean of x and y vector

    m\_x = np.mean(x)

    m\_y = np.mean(y)

    # calculating cross-deviation and deviation about x

    SS\_xy = np.sum(y\*x) - n\*m\_y\*m\_x

    SS\_xx = np.sum(x\*x) - n\*m\_x\*m\_x

    # calculating regression coefficients

    b\_1 = SS\_xy / SS\_xx

    b\_0 = m\_y - b\_1\*m\_x

    return (b\_0, b\_1)

def plot\_regression\_line(x, y, b):

    # plotting the actual points as scatter plot

    plt.scatter(x, y, color = "r",

               marker = "o", s = 30)

    # predicted response vector

    y\_pred = b[0] + b[1]\*x

    # plotting the regression line

    plt.plot(x, y\_pred, color = "b")

    # putting labels

    plt.xlabel('x')

    plt.ylabel('y')

    # function to show plot

    plt.show()

def main():

    # observations / data

    x = np.array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])

    y = np.array([1, 3, 2, 5, 7, 8, 8, 9, 10, 12])

    # estimating coefficients

    b = estimate\_coef(x, y)

    print("Estimated coefficients:\nb\_0 = {}  \

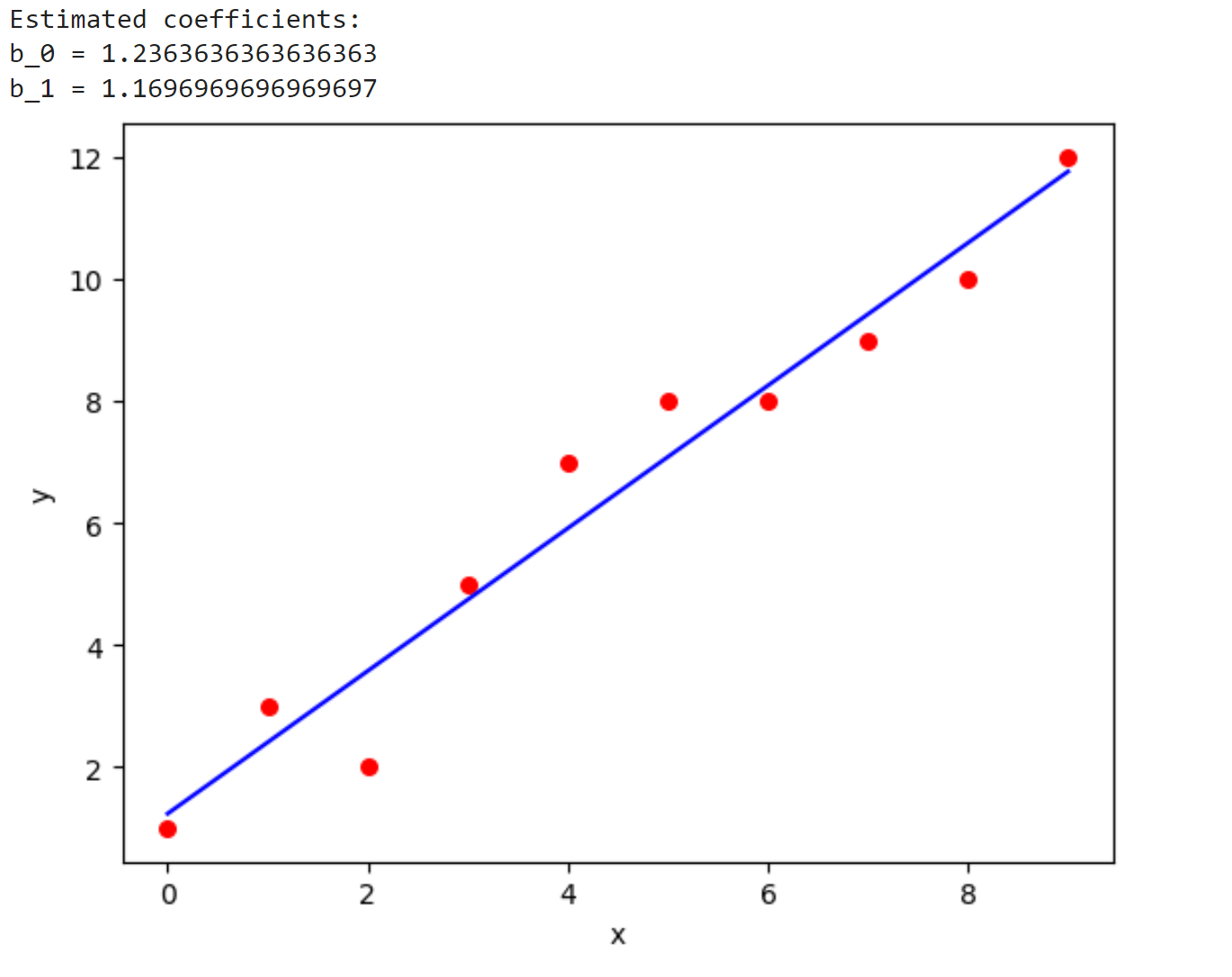
          \nb\_1 = {}".format(b[0], b[1]))

    # plotting regression line

    plot\_regression\_line(x, y, b)

if \_\_name\_\_ == "\_\_main\_\_":

    main()

OUTPUT: 

EXP NO :2

AIM: : Verifying the performance of a logistic regression by using choosen database with phython code

PROGRAM:

import numpy as np

import matplotlib.pyplot as plt

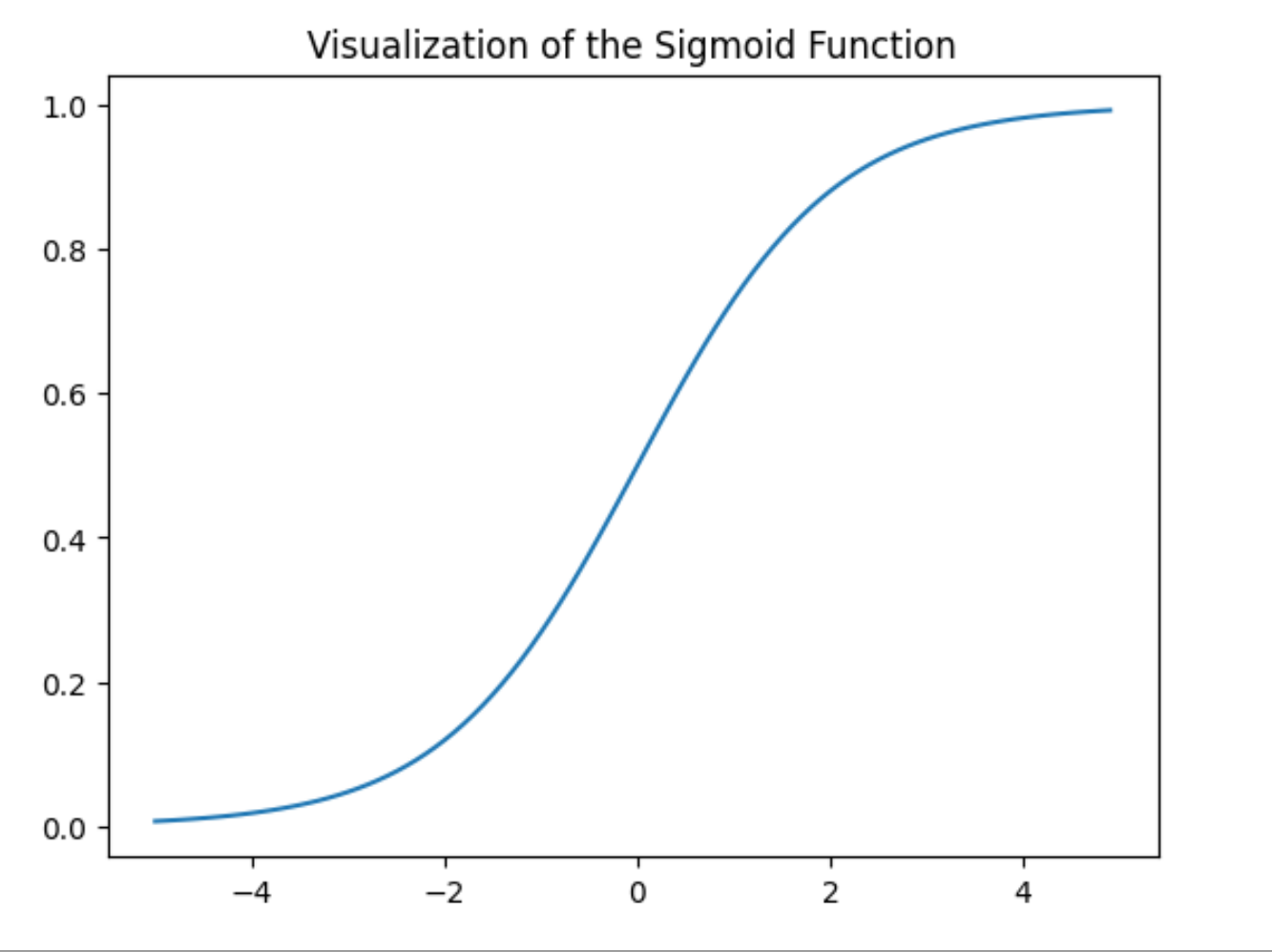
def sigmoid(z):

    return 1 / (1 + np.exp( - z))

plt.plot(np.arange(-5, 5, 0.1), sigmoid(np.arange(-5, 5, 0.1)))

plt.title('Visualization of the Sigmoid Function')

plt.show()

OUTPUT: 

EXP NO : 3

AIM: class confusion matrix

PROGRAM:

#Import the necessary libraries

import numpy as np

from sklearn.metrics import confusion\_matrix

import seaborn as sns

import matplotlib.pyplot as plt

#Create the NumPy array for actual and predicted labels.

actual    = np.array(

  ['Dog','Dog','Dog','Not Dog','Dog','Not Dog','Dog','Dog','Not Dog','Not Dog'])

predicted = np.array(

  ['Dog','Not Dog','Dog','Not Dog','Dog','Dog','Dog','Dog','Not Dog','Not Dog'])

#compute the confusion matrix.

cm = confusion\_matrix(actual,predicted)

#Plot the confusion matrix.

sns.heatmap(cm,

            annot=True,

            fmt='g',

            xticklabels=['Dog','Not Dog'],

            yticklabels=['Dog','Not Dog'])

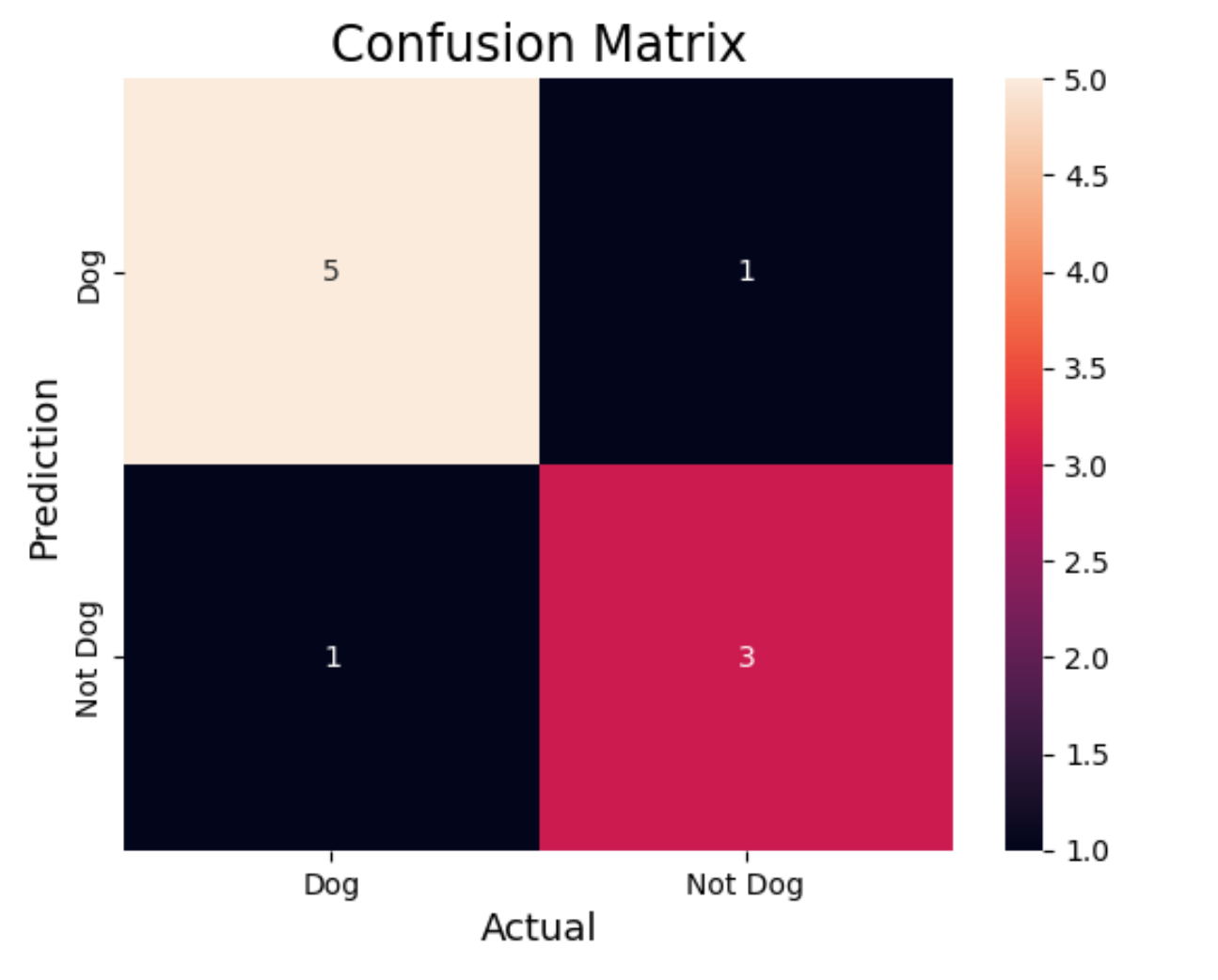
plt.ylabel('Prediction',fontsize=13)

plt.xlabel('Actual',fontsize=13)

plt.title('Confusion Matrix',fontsize=17)

plt.show()

OUTPUT:



Program :

#Import the necessary libraries

from sklearn.datasets import load\_breast\_cancer

from sklearn.model\_selection import train\_test\_split

from sklearn.tree import DecisionTreeClassifier

from sklearn.metrics import confusion\_matrix

import seaborn as sns

import matplotlib.pyplot as plt

from sklearn.metrics import accuracy\_score, precision\_score, recall\_score, f1\_score

# Load the breast cancer dataset

X, y= load\_breast\_cancer(return\_X\_y=True)

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y,test\_size=0.25)

# Train the model

tree = DecisionTreeClassifier(random\_state=23)

tree.fit(X\_train, y\_train)

# preduction

y\_pred = tree.predict(X\_test)

# compute the confusion matrix

cm = confusion\_matrix(y\_test,y\_pred)

#Plot the confusion matrix.

sns.heatmap(cm,

annot=True,

fmt='g',

xticklabels=['malignant', 'benign'],

yticklabels=['malignant', 'benign'])

plt.ylabel('Prediction',fontsize=13)

plt.xlabel('Actual',fontsize=13)

plt.title('Confusion Matrix',fontsize=17)

plt.show()

# Finding precision and recall

accuracy = accuracy\_score(y\_test, y\_pred)

print("Accuracy :", accuracy)

precision = precision\_score(y\_test, y\_pred)

print("Precision :", precision)

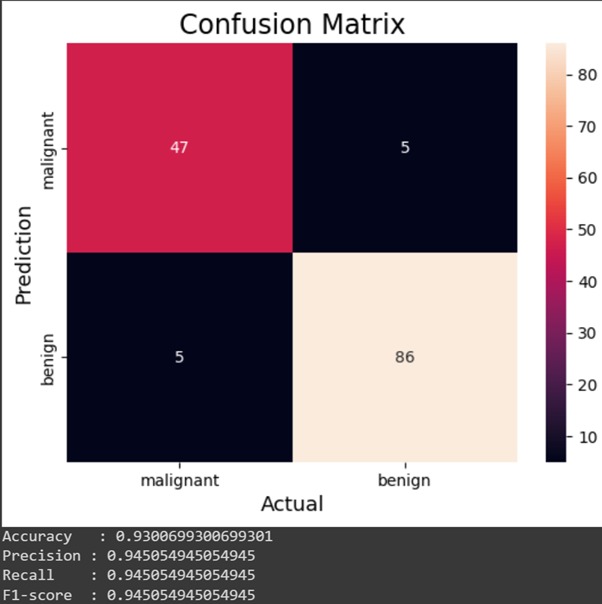
recall = recall\_score(y\_test, y\_pred)

print("Recall :", recall)

F1\_score = f1\_score(y\_test, y\_pred)

print("F1-score :", F1\_score)

output:



EXP NO :4

AIM: Verifying the performance of a multi class confusion matrix by using choosen database with phython code

PROGRAM:

#Import the necessary libraries

from sklearn.datasets import load\_digits

from sklearn.model\_selection import train\_test\_split

from sklearn.ensemble import RandomForestClassifier

from sklearn.metrics import confusion\_matrix

import seaborn as sns

import matplotlib.pyplot as plt

from sklearn.metrics import accuracy\_score, precision\_score, recall\_score, f1\_score

# Load the breast cancer dataset

X, y= load\_digits(return\_X\_y=True)

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y,test\_size=0.25)

# Train the model

clf = RandomForestClassifier(random\_state=23)

clf.fit(X\_train, y\_train)

# preduction

y\_pred = clf.predict(X\_test)

# compute the confusion matrix

cm = confusion\_matrix(y\_test,y\_pred)

#Plot the confusion matrix.

sns.heatmap(cm,

            annot=True,

            fmt='g')

plt.ylabel('Prediction',fontsize=13)

plt.xlabel('Actual',fontsize=13)

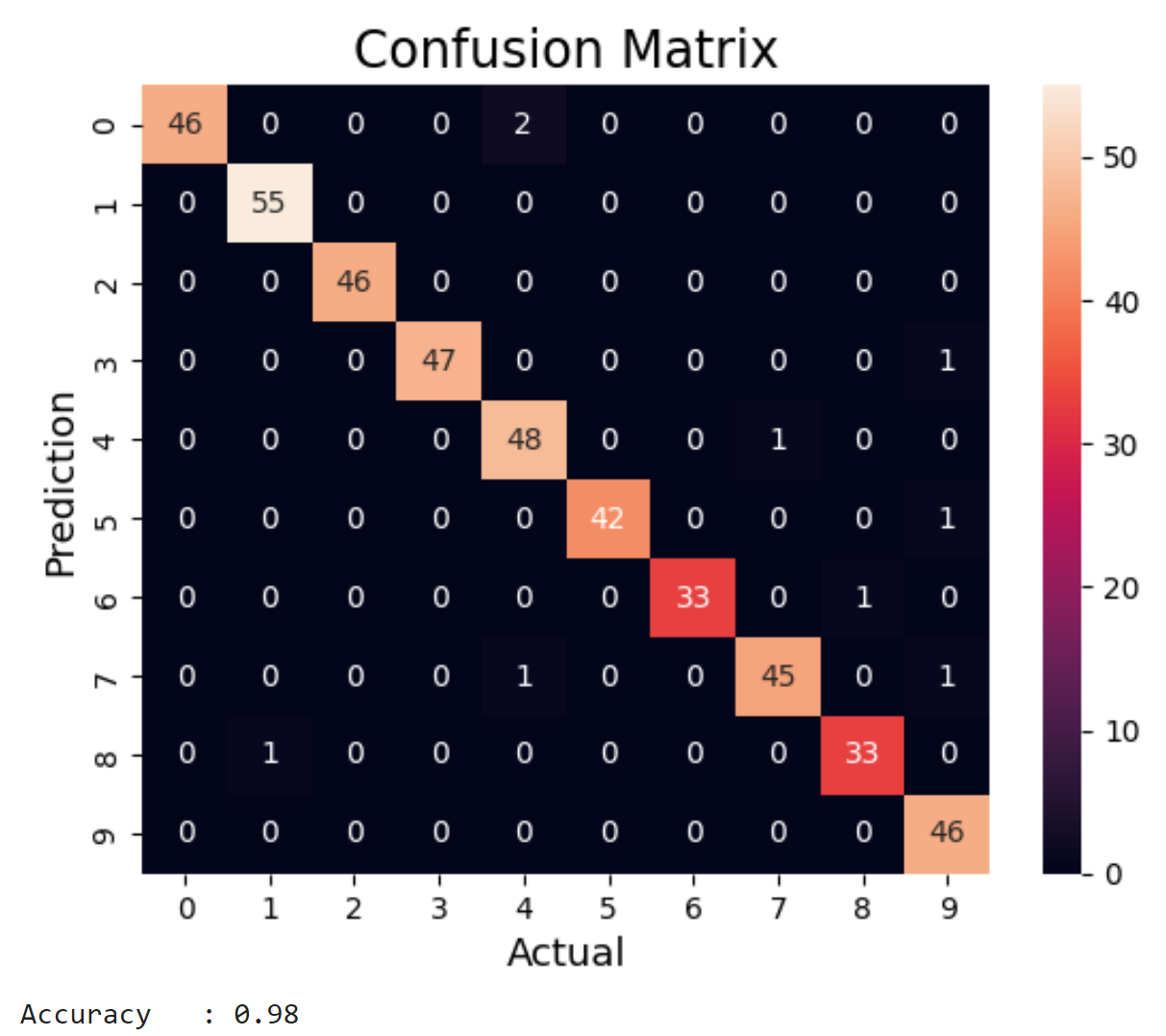
plt.title('Confusion Matrix',fontsize=17)

plt.show()

# Finding precision and recall

accuracy = accuracy\_score(y\_test, y\_pred)

print("Accuracy   :", accuracy)

OUTPUT: 

EXP NO :5

AIM: : Verifying the performance of a over fitting by using choosen database with phython code

PROGRAM:

import numpy as np

import matplotlib.pyplot as plt

from sklearn.pipeline import Pipeline

from sklearn.preprocessing import PolynomialFeatures

from sklearn.linear\_model import LinearRegression

from sklearn.model\_selection import cross\_val\_score

def true\_fun(X):

    return np.cos(1.5 \* np.pi \* X)

np.random.seed(0)

n\_samples = 30

degrees = [1, 4, 15]

X = np.sort(np.random.rand(n\_samples))

y = true\_fun(X) + np.random.randn(n\_samples) \* 0.1

plt.figure(figsize=(14, 5))

for i in range(len(degrees)):

    ax = plt.subplot(1, len(degrees), i + 1)

    plt.setp(ax, xticks=(), yticks=())

    polynomial\_features = PolynomialFeatures(degree=degrees[i], include\_bias=False)

    linear\_regression = LinearRegression()

    pipeline = Pipeline(

        [

            ("polynomial\_features", polynomial\_features),

            ("linear\_regression", linear\_regression),

        ]

    )

    pipeline.fit(X[:, np.newaxis], y)

    # Evaluate the models using crossvalidation

    scores = cross\_val\_score(

        pipeline, X[:, np.newaxis], y, scoring="neg\_mean\_squared\_error", cv=10

    )

    X\_test = np.linspace(0, 1, 100)

    plt.plot(X\_test, pipeline.predict(X\_test[:, np.newaxis]), label="Model")

    plt.plot(X\_test, true\_fun(X\_test), label="True function")

    plt.scatter(X, y, edgecolor="b", s=20, label="Samples")

    plt.xlabel("x")

    plt.ylabel("y")

    plt.xlim((0, 1))

    plt.ylim((-2, 2))

    plt.legend(loc="best")

    plt.title(

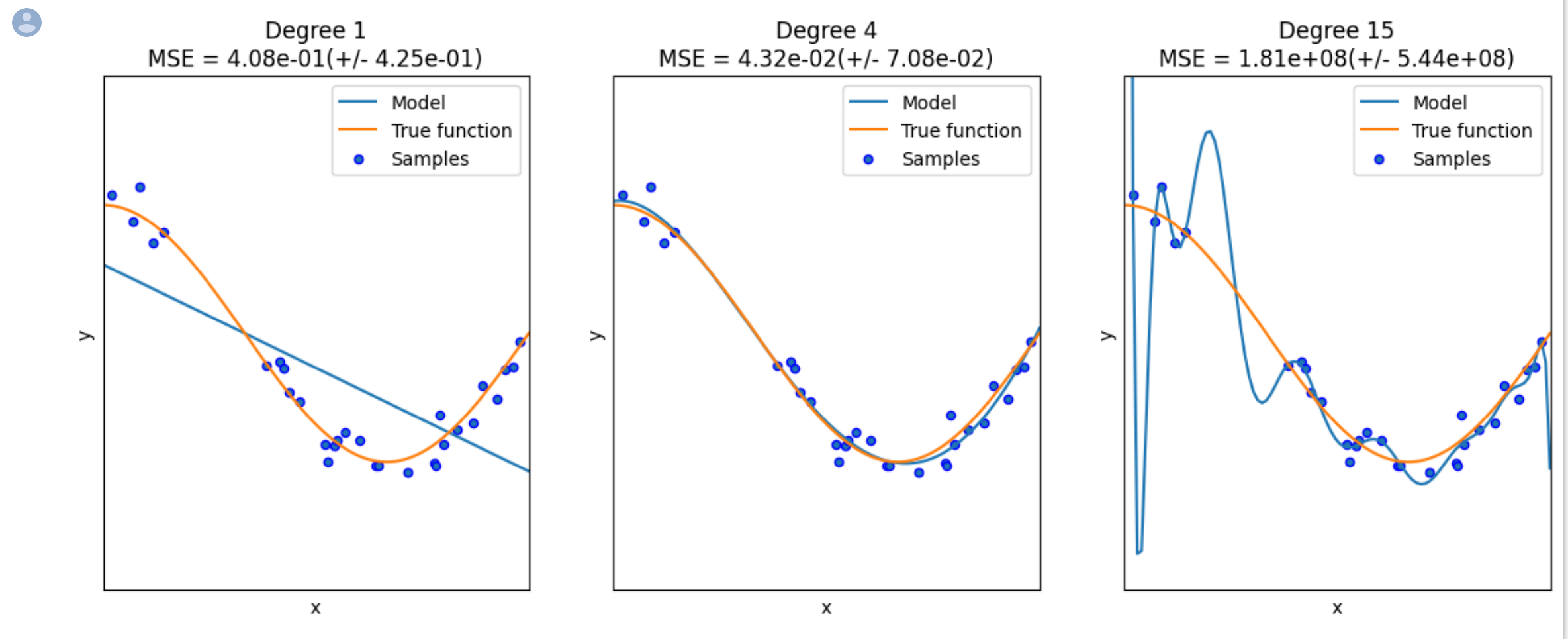
        "Degree {}\nMSE = {:.2e}(+/- {:.2e})".format(

            degrees[i], -scores.mean(), scores.std()

        )

    )

plt.show()

OUTPUT: 

EXP NO : 6

AIM: to find the accuracy by using these following algorithms

PROGRAM:

1.KNN

import numpy as np

import pandas as pd

dataset = pd.read\_csv("/content/breastcancer.csv")

"""

The breast cancer dataset has the following features: Sample code number, Clump Thickness, Uniformity of Cell Size,

Uniformity of Cell Shape, Marginal Adhesion, Single Epithelial Cell Size, Bare Nuclei, Bland Chromatin,

Normal Nucleoli, Mitosis, Class.

"""

X = dataset.iloc[:, :-1].values

y = dataset.iloc[:, -1].values

dataset.shape

#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 = 0.20, random\_state = 50)

#Feature Scaling

"""

Feature scaling is the process of converting the data into a given range.

In this case, the standard scalar technique is used.

"""

from sklearn.preprocessing import StandardScaler

sc = StandardScaler()

X\_train = sc.fit\_transform(X\_train)

X\_test = sc.transform(X\_test)

#Training the K-Nearest Neighbors (K-NN) Classification model on the Training set

"""

Once the dataset is scaled, next, the K-Nearest Neighbors (K-NN) classifier algorithm is used to create a model.

The hyperparameters such as n\_neighbors, metric, and p are set to 5, Minkowski, and 2 respectively.

The remaining hyperparameters are set to default values.

"""

from sklearn.neighbors import KNeighborsClassifier

classifier = KNeighborsClassifier(n\_neighbors = 5, metric = 'minkowski', p = 2)

classifier.fit(X\_train, y\_train)

"""

Display the results (confusion matrix and accuracy)

Here evaluation metrics such as confusion matrix and accuracy are used to evaluate the performance of the model built using a decision tree classifier.

"""

from sklearn.metrics import confusion\_matrix, accuracy\_score

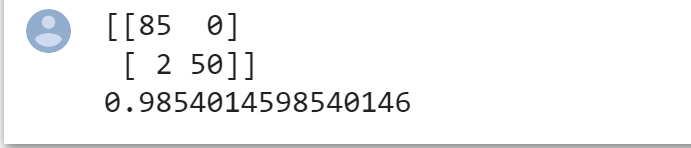
y\_pred = classifier.predict(X\_test)

cm = confusion\_matrix(y\_test, y\_pred)

print(cm)

accuracy\_score(y\_test, y\_pred)

OUTPUT:



3.LOGISTIC REGRESSION

import numpy as np

import pandas as pd

#"Importing the dataset

"""

After importing the necessary libraries, next, we import or read the dataset.

Click here to download the breast cancer dataset used in this implementation.

The breast cancer dataset has the following features:

Sample code number, Clump Thickness, Uniformity of Cell Size, Uniformity of Cell Shape, Marginal Adhesion,

Single Epithelial Cell Size, Bare Nuclei, Bland Chromatin, Normal Nucleoli, Mitosis, Class.

"""

# divide the dataset into concepts and targets. Store the concepts into X and targets into y.

dataset = pd.read\_csv("/content/breastcancer.csv")

X = dataset.iloc[:, :-1].values

y = dataset.iloc[:, -1].values

#Splitting the dataset into the Training set and Test

from sklearn.model\_selection import train\_test\_split

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size = 0.30, random\_state = 2)

#Feature Scaling

"""

Feature scaling is the process of converting the data into a given range. In this case, the standard scalar technique is used.

from sklearn.preprocessing import StandardScaler

"""

from sklearn.preprocessing import StandardScaler

sc = StandardScaler()

X\_train = sc.fit\_transform(X\_train)

X\_test = sc.transform(X\_test)

"""

Training the Logistic Regression (LR) Classification model on the Training set

Once the dataset is scaled, next, the Logistic Regression (LR) classifier algorithm is used to create a model.

The hyperparameters such as random\_state to 0 respectively.

The remaining hyperparameters Logistic Regression (LR) are set to default values.

"""

from sklearn.linear\_model import LogisticRegression

classifier = LogisticRegression(random\_state = 0)

classifier.fit(X\_train, y\_train)

#Logistic Regression (LR) classifier model

LogisticRegression(C=1.0, class\_weight=None, dual=False, fit\_intercept=True,

intercept\_scaling=1, l1\_ratio=None, max\_iter=100,

multi\_class='warn', n\_jobs=None, penalty='l2',

random\_state=32, solver='warn', tol=0.0001, verbose=0,

warm\_start=False)

#Display the results (confusion matrix and accuracy)

"""

Here evaluation metrics such as confusion matrix and accuracy are used to evaluate the performance of the model

built using a decision tree classifier.

"""

from sklearn.metrics import confusion\_matrix, accuracy\_score

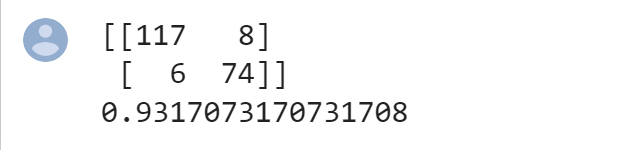
y\_pred = classifier.predict(X\_test)

cm = confusion\_matrix(y\_test, y\_pred)

print(cm)

accuracy\_score(y\_test, y\_pred)

OUTPUT:



3. LINEAR REGRESSION

import numpy as np

import pandas as pd

from sklearn.linear\_model import LinearRegression

from sklearn.metrics import r2\_score

from sklearn.model\_selection import train\_test\_split

from sklearn.preprocessing import StandardScaler

# read the data from the CSV file

data = pd.read\_csv("/content/breastcancer.csv")

# split the data into input features and target variable

X = data.iloc[:, :-1].values

y = data.iloc[:, -1].values

# split the data into training and testing sets

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size=0.2, random\_state=22)

# scale the input features using StandardScaler

sc = StandardScaler()

X\_train = sc.fit\_transform(X\_train)

X\_test = sc.transform(X\_test)

# create a Linear Regression model using scikit-learn

lr = LinearRegression()

# train the model

lr.fit(X\_train, y\_train)

# make predictions on the testing set

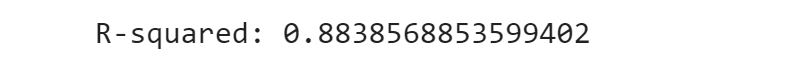
y\_pred = lr.predict(X\_test)

# calculate R-squared for the model

r2 = r2\_score(y\_test, y\_pred)

print("R-squared:", r2)

OUTPUT:



4. SVM

import numpy as np

import pandas as pd

# Importing the dataset

dataset = pd.read\_csv('/content/breastcancer.csv')

X = dataset.iloc[:, :-1].values

y = dataset.iloc[:, -1].values

# 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=0.25, random\_state=32)

# Feature Scaling

from sklearn.preprocessing import StandardScaler

sc = StandardScaler()

X\_train = sc.fit\_transform(X\_train)

X\_test = sc.transform(X\_test)

# Training the SVM model on the Training set

from sklearn.svm import SVC

classifier = SVC(kernel='linear', random\_state=0)

classifier.fit(X\_train, y\_train)

# Predicting the Test set results

y\_pred = classifier.predict(X\_test)

# Evaluating the performance of the model using confusion matrix and accuracy

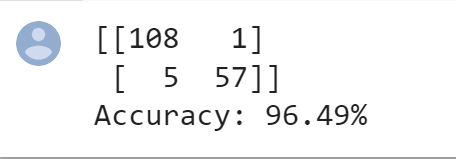
from sklearn.metrics import confusion\_matrix, accuracy\_score

cm = confusion\_matrix(y\_test, y\_pred)

print(cm)

print('Accuracy: {:.2f}%'.format(accuracy\_score(y\_test, y\_pred) \* 100))

OUTPUT:



5. NAÏVE BAYES

import numpy as np

import pandas as pd

#Importing the dataset

"""

Next, we import or read the dataset. Click here to download the breast cancer dataset used in this implementation.

After reading the dataset, divide the dataset into concepts and targets. Store the concepts into X and

targets into y.

"""

dataset = pd.read\_csv("/content/breastcancer.csv")

X = dataset.iloc[:, :-1].values

y = dataset.iloc[:, -1].values

"""

Splitting the dataset into the Training set and Test set

Once the dataset is read into the memory, next, divide the dataset into two parts, training and

testing using the train\_test\_split function from sklearn.

The test\_size and random\_state attributes are set to 0.25 and 0 respectively.

You can change these attributes as per your requirements.

"""

from sklearn.model\_selection import train\_test\_split

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size = 0.25, random\_state = 88)

#Feature Scaling

"""

Feature scaling is the process of converting the data into a min-max range. In this case,

the standard scalar method is used.

"""

from sklearn.preprocessing import StandardScaler

sc = StandardScaler()

X\_train = sc.fit\_transform(X\_train)

X\_test = sc.transform(X\_test)

"""

Training the Naive Bayes Classification model on the Training set

Once the dataset is scaled, next, the Naive Bayes classifier algorithm is used to create a model.

The GaussianNB function is imported from sklearn.naive\_bayes library. The hyperparameters such as kernel,

and random\_state to linear, and 0 respectively. The remaining hyperparameters of the support vector machine

algorithm are set to default values.

"""

from sklearn.naive\_bayes import GaussianNB

classifier = GaussianNB()

classifier.fit(X\_train, y\_train)

#Naive Bayes classifier model

GaussianNB(priors=None, var\_smoothing=1e-09)

#Display the results (confusion matrix and accuracy)

"""

Here evaluation metrics such as confusion matrix and accuracy are used to evaluate the performance of

the model built using a decision tree classifier.

"""

from sklearn.metrics import confusion\_matrix, accuracy\_score

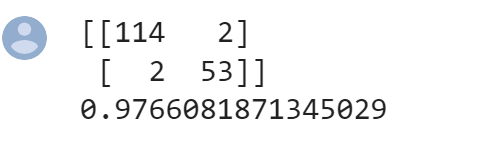
y\_pred = classifier.predict(X\_test)

cm = confusion\_matrix(y\_test, y\_pred)

print(cm)

accuracy\_score(y\_test, y\_pred)

OUTPUT:



6. RANDOM FOREST

import numpy as np

import pandas as pd

# Importing the dataset

dataset = pd.read\_csv('/content/breastcancer.csv')

X = dataset.iloc[:, :-1].values

y = dataset.iloc[:, -1].values

# 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=0.25, random\_state=39)

# Feature Scaling

from sklearn.preprocessing import StandardScaler

sc = StandardScaler()

X\_train = sc.fit\_transform(X\_train)

X\_test = sc.transform(X\_test)

# Training the Random Forest Classification model on the Training set

from sklearn.ensemble import RandomForestClassifier

classifier = RandomForestClassifier(n\_estimators=100, random\_state=42)

classifier.fit(X\_train, y\_train)

# Predicting the Test set results

y\_pred = classifier.predict(X\_test)

# Making the Confusion Matrix

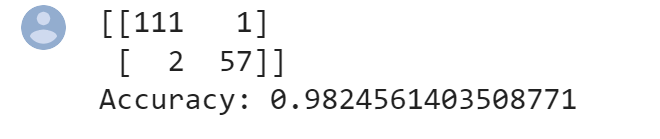
from sklearn.metrics import confusion\_matrix, accuracy\_score

cm = confusion\_matrix(y\_test, y\_pred)

print(cm)

print('Accuracy:', accuracy\_score(y\_test, y\_pred))

OUTPUT:



7. DECISION TREE

import numpy as np

import pandas as pd

# Importing the dataset

dataset = pd.read\_csv("/content/breastcancer.csv")

X = dataset.iloc[:, :-1].values

y = dataset.iloc[:, -1].values

# 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 = 0.25, random\_state = 8)

# Feature Scaling

from sklearn.preprocessing import StandardScaler

sc = StandardScaler()

X\_train = sc.fit\_transform(X\_train)

X\_test = sc.transform(X\_test)

# Training the Decision Tree Classification model on the Training set

from sklearn.tree import DecisionTreeClassifier

classifier = DecisionTreeClassifier(criterion = 'entropy', random\_state = 5)

classifier.fit(X\_train, y\_train)

# Display the Decision Tree

from sklearn.tree import plot\_tree

import matplotlib.pyplot as plt

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

plot\_tree(classifier, filled=True, rounded=True, feature\_names=dataset.columns[:-1])

plt.show()

# Predicting the Test set results

y\_pred = classifier.predict(X\_test)

# Display the results (confusion matrix and accuracy)

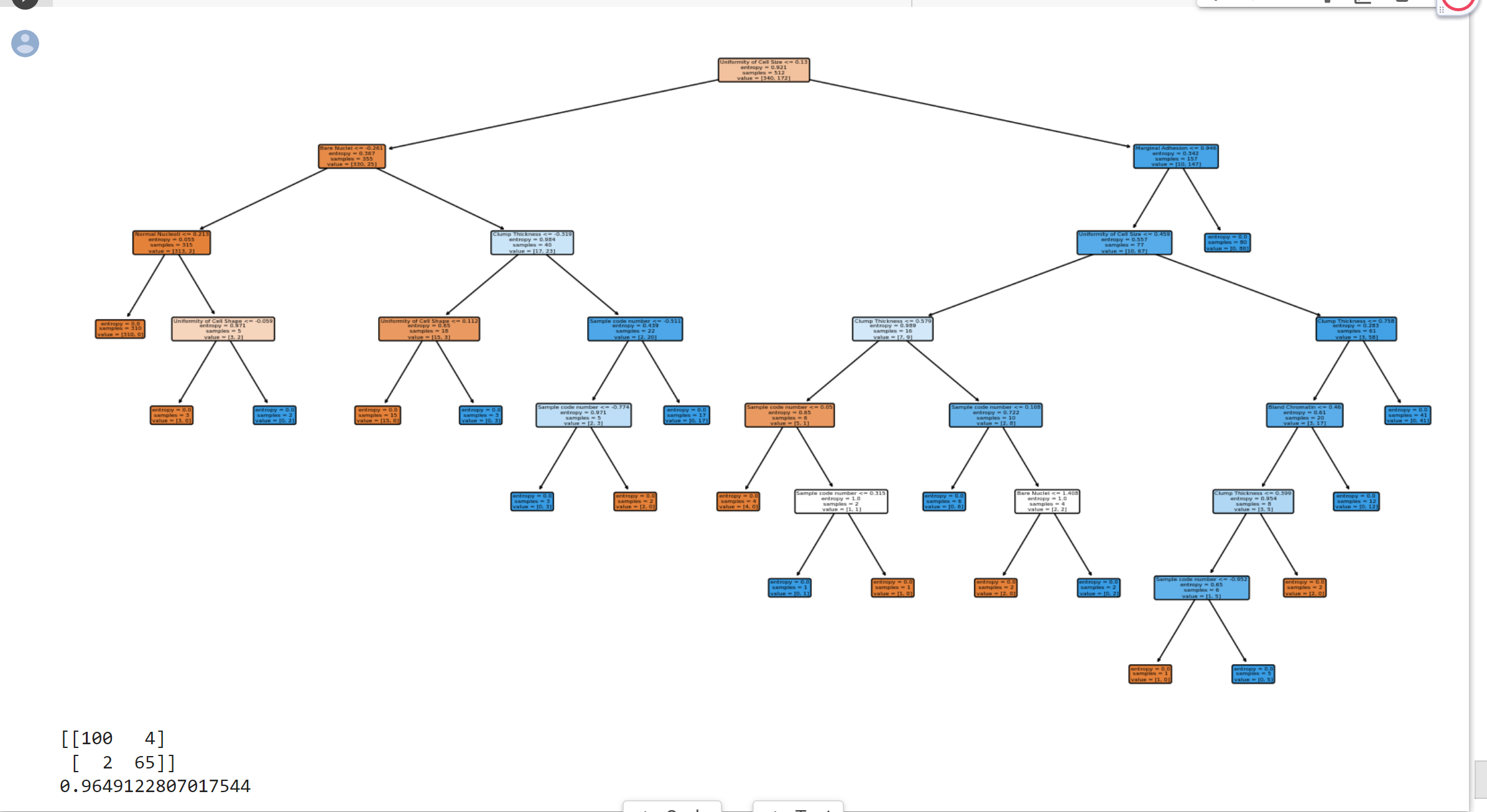
from sklearn.metrics import confusion\_matrix, accuracy\_score

cm = confusion\_matrix(y\_test, y\_pred)

print(cm)

accuracy\_score(y\_test, y\_pred)

OUTPUT:



EXP NO : 7

AIM: TO FIND THE GRADIENT DESENT FOR THE ACTUAL DATA

PROGRAM:

# Importing Libraries

import numpy as np

import matplotlib.pyplot as plt

def mean\_squared\_error(y\_true, y\_predicted):

    # Calculating the loss or cost

    cost = np.sum((y\_true-y\_predicted)\*\*2) / len(y\_true)

    return cost

# Gradient Descent Function

# Here iterations, learning\_rate, stopping\_threshold

# are hyperparameters that can be tuned

def gradient\_descent(x, y, iterations = 1000, learning\_rate = 0.0001,

                     stopping\_threshold = 1e-6):

    # Initializing weight, bias, learning rate and iterations

    current\_weight = 0.1

    current\_bias = 0.01

    iterations = iterations

    learning\_rate = learning\_rate

    n = float(len(x))

    costs = []

    weights = []

    previous\_cost = None

    # Estimation of optimal parameters

    for i in range(iterations):

        # Making predictions

        y\_predicted = (current\_weight \* x) + current\_bias

        # Calculating the current cost

        current\_cost = mean\_squared\_error(y, y\_predicted)

        # If the change in cost is less than or equal to

        # stopping\_threshold we stop the gradient descent

        if previous\_cost and abs(previous\_cost-current\_cost)<=stopping\_threshold:

            break

        previous\_cost = current\_cost

        costs.append(current\_cost)

        weights.append(current\_weight)

        # Calculating the gradients

        weight\_derivative = -(2/n) \* sum(x \* (y-y\_predicted))

        bias\_derivative = -(2/n) \* sum(y-y\_predicted)

        # Updating weights and bias

        current\_weight = current\_weight - (learning\_rate \* weight\_derivative)

        current\_bias = current\_bias - (learning\_rate \* bias\_derivative)

        # Printing the parameters for each 1000th iteration

        print(f"Iteration {i+1}: Cost {current\_cost}, Weight \

        {current\_weight}, Bias {current\_bias}")

    # Visualizing the weights and cost at for all iterations

    plt.figure(figsize = (8,6))

    plt.plot(weights, costs)

    plt.scatter(weights, costs, marker='o', color='red')

    plt.title("Cost vs Weights")

    plt.ylabel("Cost")

    plt.xlabel("Weight")

    plt.show()

    return current\_weight, current\_bias

def main():

    # Data

    X = np.array([32.50234527, 53.42680403, 61.53035803, 47.47563963, 59.81320787,

           55.14218841, 52.21179669, 39.29956669, 48.10504169, 52.55001444,

           45.41973014, 54.35163488, 44.1640495 , 58.16847072, 56.72720806,

           48.95588857, 44.68719623, 60.29732685, 45.61864377, 38.81681754])

    Y = np.array([31.70700585, 68.77759598, 62.5623823 , 71.54663223, 87.23092513,

           78.21151827, 79.64197305, 59.17148932, 75.3312423 , 71.30087989,

           55.16567715, 82.47884676, 62.00892325, 75.39287043, 81.43619216,

           60.72360244, 82.89250373, 97.37989686, 48.84715332, 56.87721319])

    # Estimating weight and bias using gradient descent

    estimated\_weight, estimated\_bias = gradient\_descent(X, Y, iterations=2000)

    print(f"Estimated Weight: {estimated\_weight}\nEstimated Bias: {estimated\_bias}")

    # Making predictions using estimated parameters

    Y\_pred = estimated\_weight\*X + estimated\_bias

    # Plotting the regression line

    plt.figure(figsize = (8,6))

    plt.scatter(X, Y, marker='o', color='red')

    plt.plot([min(X), max(X)], [min(Y\_pred), max(Y\_pred)], color='blue',markerfacecolor='red',

             markersize=10,linestyle='dashed')

    plt.xlabel("X")

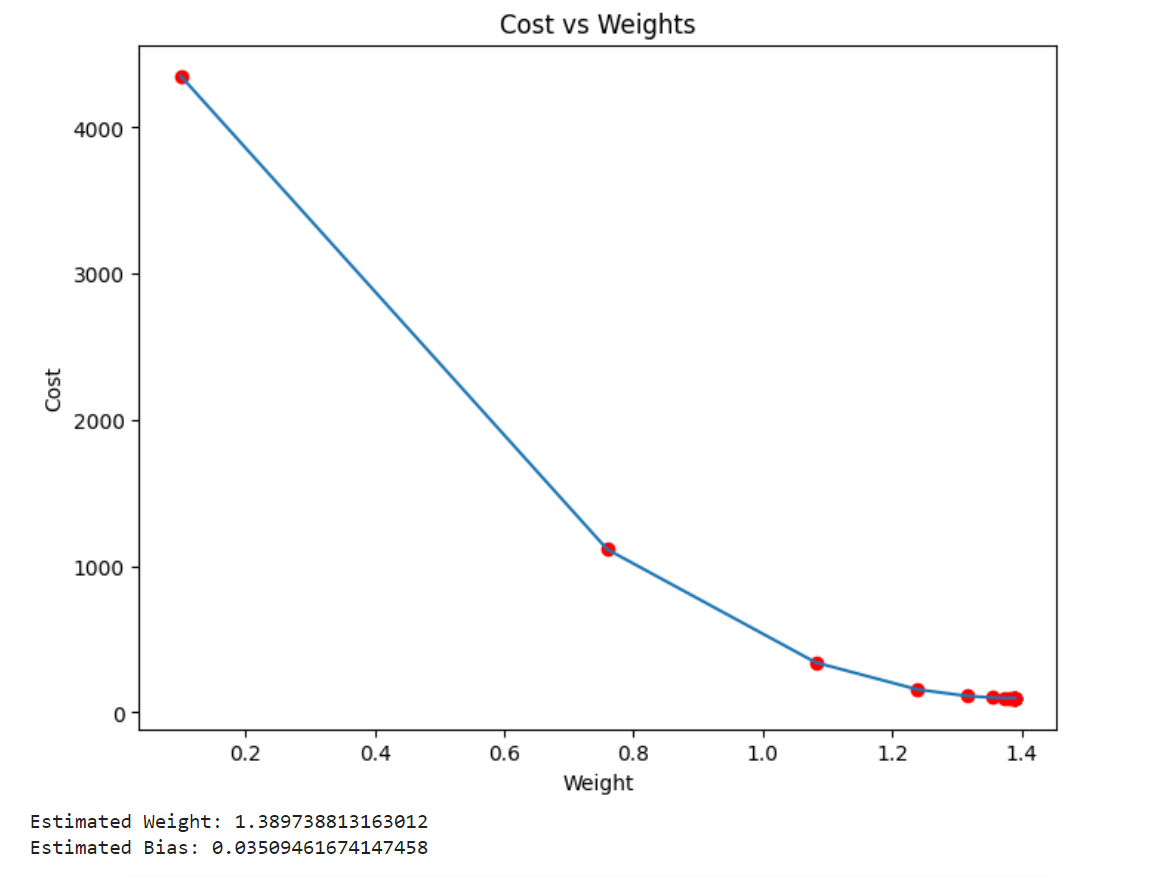
    plt.ylabel("Y")

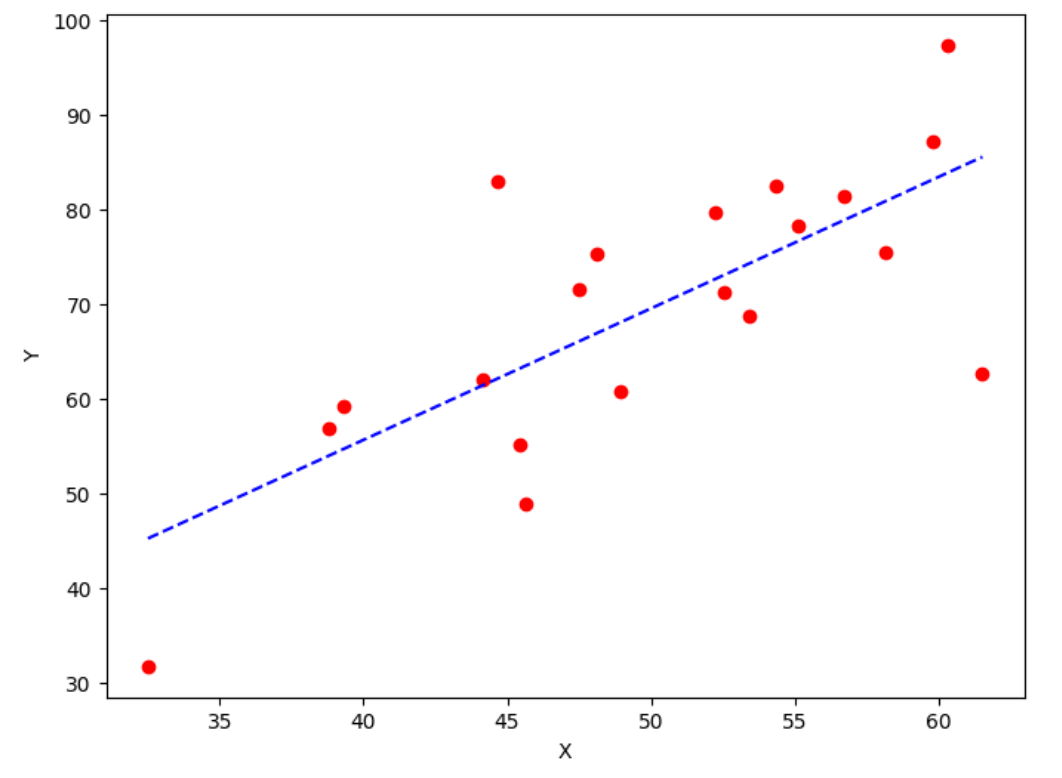
    plt.show()

if \_\_name\_\_=="\_\_main\_\_":

    main()

OUTPUT:





EXP NO :8

AIM: Verifying the performance of a image processing by using choosen database with phython code

PROGRAM:

import numpy as np

import cv2

from matplotlib import pyplot as plt

img = cv2.imread(r'C33P1thinF\_IMG\_20150619\_114756a\_cell\_181.png')

b,g,r = cv2.split(img)

rgb\_img = cv2.merge([r,g,b])

gray = cv2.cvtColor(img,cv2.COLOR\_BGR2GRAY)

ret, thresh = cv2.threshold(gray,0,255,cv2.THRESH\_BINARY\_INV+cv2.THRESH\_OTSU)

# noise removal

kernel = np.ones((2,2),np.uint8)

#opening = cv2.morphologyEx(thresh,cv2.MORPH\_OPEN,kernel, iterations = 2)

closing = cv2.morphologyEx(thresh,cv2.MORPH\_CLOSE,kernel, iterations = 2)

# sure background area

sure\_bg = cv2.dilate(closing,kernel,iterations=3)

# Finding sure foreground area

dist\_transform = cv2.distanceTransform(sure\_bg,cv2.DIST\_L2,3)

# Threshold

ret, sure\_fg = cv2.threshold(dist\_transform,0.1\*dist\_transform.max(),255,0)

# Finding unknown region

sure\_fg = np.uint8(sure\_fg)

unknown = cv2.subtract(sure\_bg,sure\_fg)

# Marker labelling

ret, markers = cv2.connectedComponents(sure\_fg)

# Add one to all labels so that sure background is not 0, but 1

markers = markers+1

# Now, mark the region of unknown with zero

markers[unknown==255] = 0

markers = cv2.watershed(img,markers)

img[markers == -1] = [255,0,0]

plt.subplot(211),plt.imshow(rgb\_img)

plt.title('Input Image'), plt.xticks([]), plt.yticks([])

plt.subplot(212),plt.imshow(thresh, 'gray')

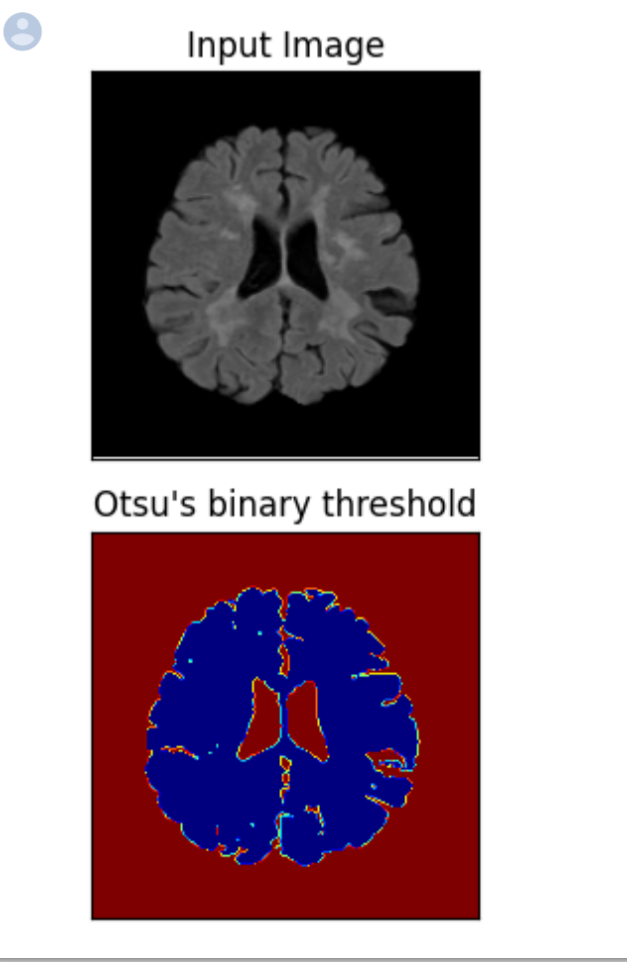
plt.imsave(r'thresh.png',thresh)

plt.title("Otsu's binary threshold"), plt.xticks([]), plt.yticks([])

plt.tight\_layout()

plt.show()

OUTPUT:



EXP NO :9

AIM:NEURAL NETWORK ANALYSIS

OUTPUT:

