import matplotlib.pyplot as plt

import tensorflow as tf

import random

import os

from glob import glob

from matplotlib import pyplot

import cv2

import pandas as pd

import numpy as np

import matplotlib.gridspec as gridspec

import seaborn as sns

import itertools

import sklearn

import itertools

import scipy

import skimage

from skimage.transform import resize

import csv

from tqdm import tqdm

from sklearn import model\_selection

from sklearn.model\_selection import train\_test\_split, learning\_curve,KFold,cross\_val\_score,StratifiedKFold

from sklearn.metrics import confusion\_matrix

import keras

from keras.utils import np\_utils

from keras.utils.np\_utils import to\_categorical

from tensorflow.keras.preprocessing.image import load\_img,img\_to\_array

from keras.preprocessing.image import ImageDataGenerator

from keras import models, layers, optimizers

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

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

from keras.layers import Activation,Dense, Dropout, Flatten

from keras.models import Model

**EXPERIMENT:1(A)**

**AIM:** To demonstrate confusion matrix using python

**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'])

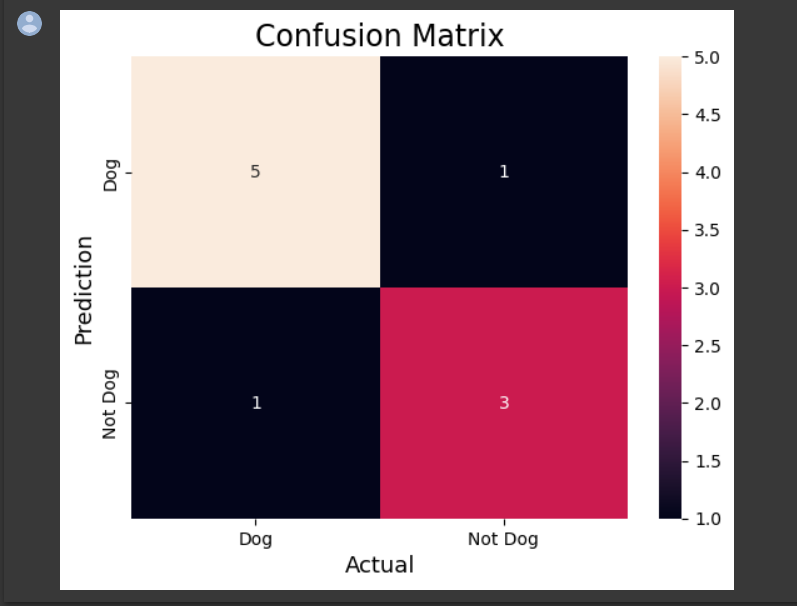
plt.ylabel('Prediction',fontsize=13)

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

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

plt.show()

**OUTPUT:**



**EXPERIMENT:1(B)**

**AIM:** To demonstrate 2 class confusion matrix using python

**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)

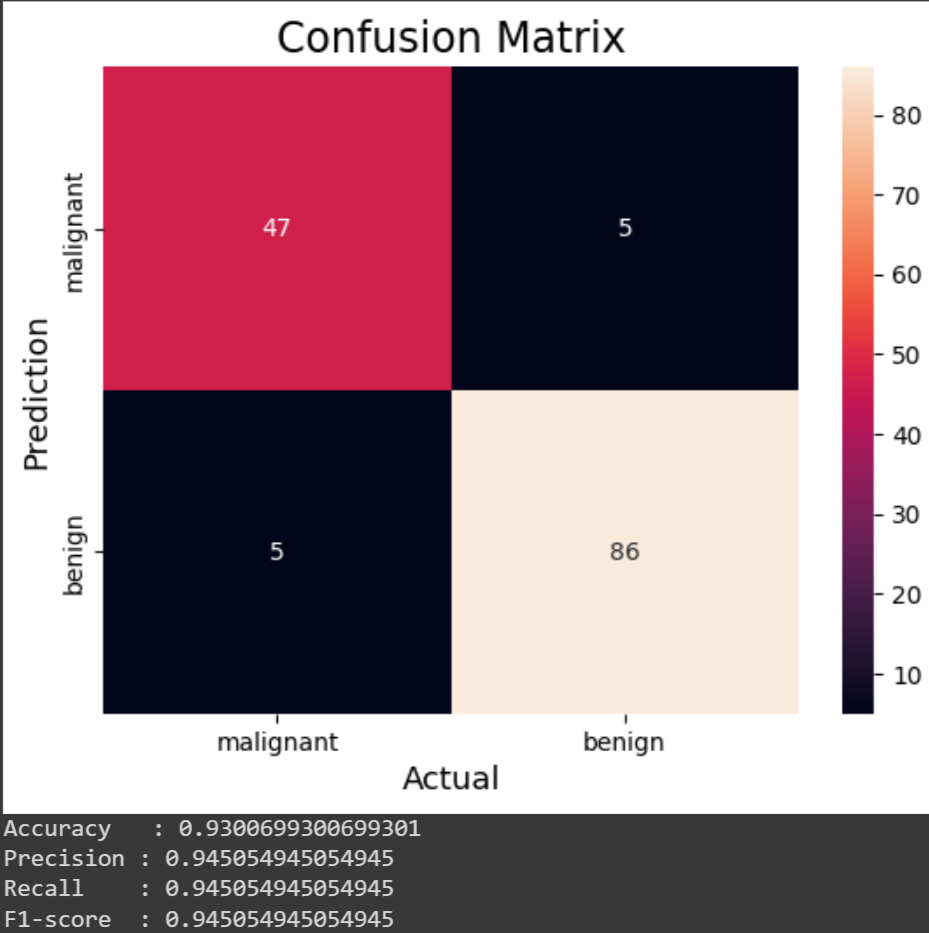
recall = recall\_score(y\_test, y\_pred)

print("Recall    :", recall)

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

print("F1-score  :", F1\_score)

**OUTPUT:**

****

**EXPERIMENT:2**

**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:**

****

**EXPERIMENT:3**

**AIM:** : Verifying the performance of a over fitting by using choosen database with python 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(

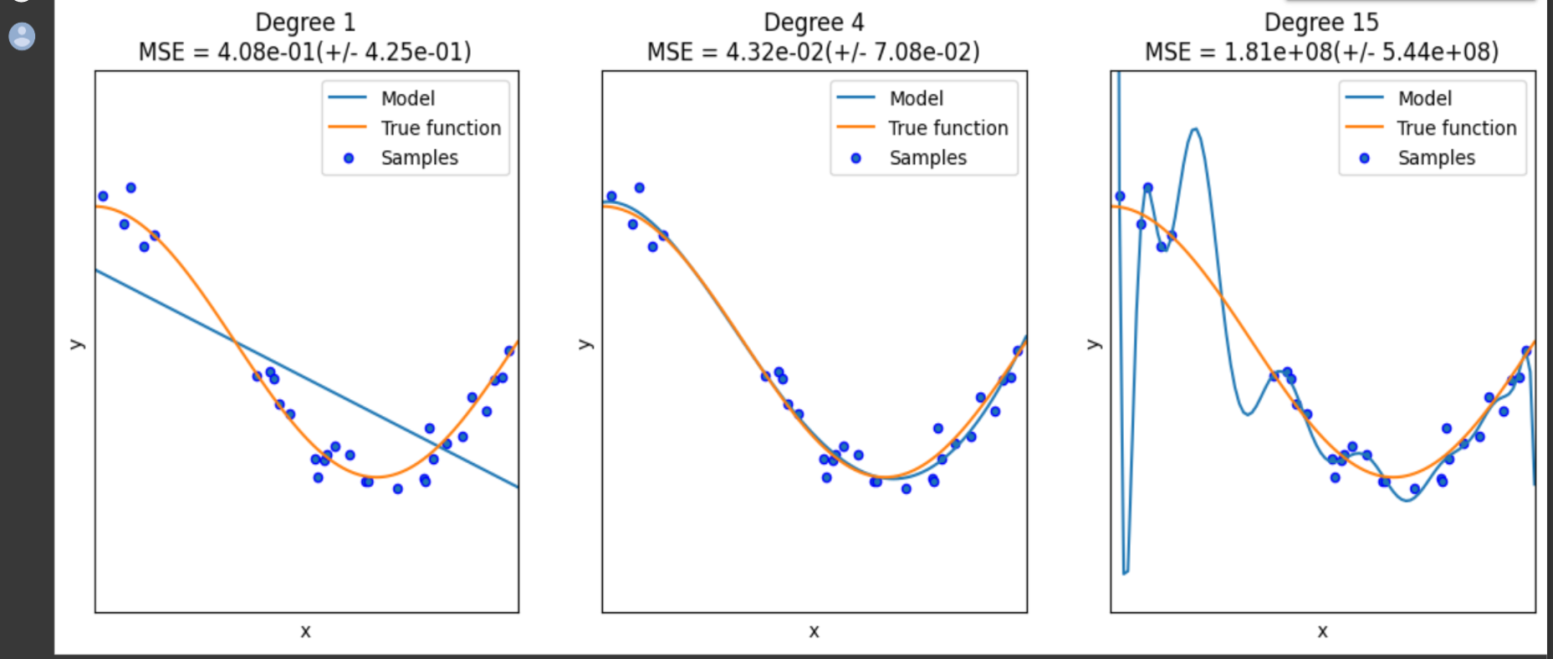
            degrees[i], -scores.mean(), scores.std()

        )

    )

plt.show()

**OUTPUT:**

****

**EXPERIMENT:4**

**AIM:** To demonstrate the performance of a linear regression by using choosen database with python code

**PROGRAM: LINEAR REGRESSION**

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:**

****

**EXPERIMENT:5**

**AIM:** : To demonstrate the performance of a logistic regression by using choosen database with python code.

**PROGRAM:**

import numpy as np

import matplotlib.pyplot as plt

def sigmoid(z):

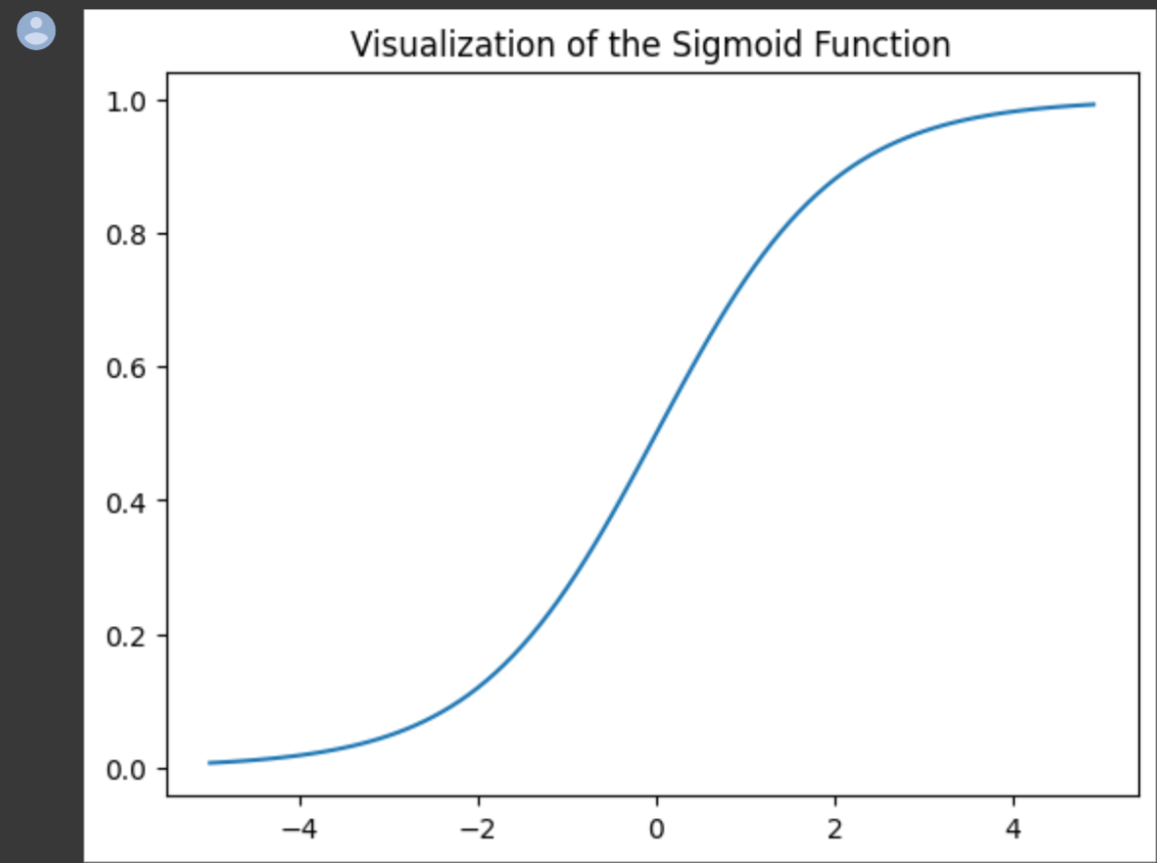
    return 1 / (1 + np.exp( - z))

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:**

****

**EXPERIMENT:6(a)KNN**

**AIM:** Finding accuracy value of iris data set using KNN algorithm

**PROGRAM:**

**Mainfileupload\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

from google.colab import files

uploaded = files.upload()

import numpy as np

import pandas as pd

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

"""

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 = 42)

#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:**



**EXPERIMENT:6(B)NAVIE**

**AIM: :** finding accuracy value of iris data set using NAVIE BAYES algorithm

**PROGRAM:**

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.xls")

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

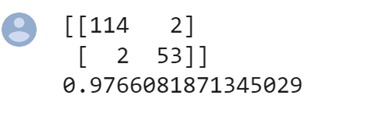
X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size = 0.25, random\_state = 0)

#Feature Scaling

"""

Feature scaling is the process of converting the

**OUTPUT:**



**EXPERIMENT:6(C)LOGISTIC**

**AIM: :** finding accuracy value of iris data set using LOGISTIC REGRESSION algorithm

**PROGRAM:**

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.xls")

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 = 0)

#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

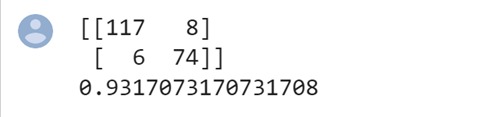
y\_pred = classifier.predict(X\_test)

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

print(cm)

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

**OUTPUT:**

****

**EXPERIMENT:6(D)DECISION**

**AIM: :** finding accuracy value of iris data set using DECISION TREE algorithm

**PROGRAM:**

import numpy as np

import pandas as pd

# Importing the dataset

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

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)

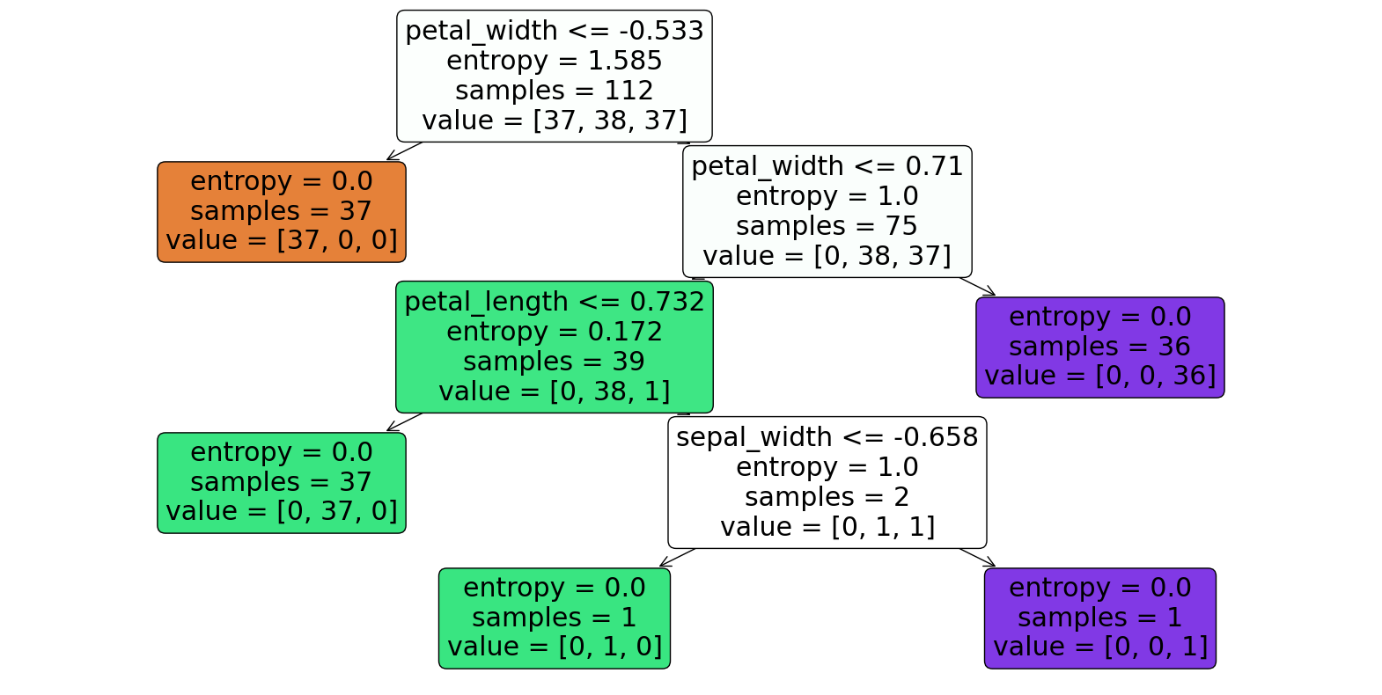
from sklearn.metrics import confusion\_matrix, accuracy\_score

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

print(cm)

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

**output:**

****

0.8947368421052632

[[13 0 0]

[ 0 11 1]

[ 0 3 10]]

**EXPERIMENT:6(E)SVM**

**AIM: :** finding accuracy value of iris data set using SVM algorithm

**PROGRAM:**

import numpy as np

import pandas as pd

# Importing the dataset

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

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:**

****

**EXPERIMENT:6(F)RANDOM**

**AIM: :** finding accuracy value of iris data set using RANDOM FOREST algorithm

**PROGRAM:**

import numpy as np

import pandas as pd

# Importing the dataset

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

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:**

****

**EXPERIMENT:7(A)**

**AIM:** To demonstrate gradient descent using python(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:**







**Experiment:7(b)**

**AIM:** To demonstrate gradient descent using python( modified data)

**PROGRAM:**

import numpy as np

import matplotlib.pyplot as plt

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

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

    return cost

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

                     stopping\_threshold=1e-6):

    current\_weight = 0.1

    current\_bias = 0.01

    iterations = iterations

    learning\_rate = learning\_rate

    n = float(len(x))

    costs = []

    weights = []

    previous\_cost = None

    for i in range(iterations):

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

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

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

            break

        previous\_cost = current\_cost

        costs.append(current\_cost)

        weights.append(current\_weight)

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

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

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

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

        if (i + 1) % 1000 == 0:

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

    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():

    X = np.array([1, 2, 3, 4, 5])  # Replace with your data

    Y = np.array([2, 3, 4, 5, 6])  # Replace with your data

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

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

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

    plt.figure(figsize=(8, 6))

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

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

    plt.xlabel("X")

    plt.ylabel("Y")

    plt.show()

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

    main()

**OUTPUT:**







**EXPERIMENT:8(A)SEGMENTATION**

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

**PROGRAM:**

**Mainimageupload\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

from google.colab import files

uploaded = files.upload()

# SEGMENTATION

import numpy as np

import cv2

from matplotlib import pyplot as plt

img = cv2.imread(r'apple.jpeg')

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:**



**EXPERIMENT:8(B)**

**AIM:** : Verifying the performance of a image processing by using water shed database with python code

**PROGRAM:**

# SEGMENTATION

import numpy as np

import cv2

from matplotlib import pyplot as plt

img = cv2.imread(r'apple.jpeg')

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)

plt.subplot(211),plt.imshow(closing, 'gray')

plt.title("morphologyEx:Closing:2x2"), plt.xticks([]), plt.yticks([])

plt.subplot(212),plt.imshow(sure\_bg, 'gray')

plt.imsave(r'dilation.png',sure\_bg)

plt.title("Dilation"), plt.xticks([]), plt.yticks([])

plt.tight\_layout()

plt.show()

**OUTPUT:**

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**EXPERIMENT:9 (a) TANH**

**AIM:** Neural network analysis using TANH activation

**OUTPUT:**

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**EXPERIMENT:9(B) SIGMIOD**

**AIM:** Neural network analysis using SIGMOID activation

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**EXPERIMENT:9(C) LINEAR**

**AIM:** Neural network analysis using LINEAR activation

**OUTPUT: **

**EXPERIMENT:9(D)RELU**

**AIM:** Neural network analysis using ReLU activation

**OUTPUT:**



**EXPERIMENT:10**

**AIM:** To demonstrate linear separability using python 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:**

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