2024 - 2025

Machine Learning

Practical Report Msc.IT sem III
part II

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Practical 1a

Aim:- Design a simple machine learning model to train the training instances and test the same.

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Code:-

Practical 1b

Aim:- Implement and demonstrate the FIND-S algorithm for finding the most specific hypothesis based on a given set of training data samples. Read the training data from a .CSV file

Theory:-

Code:-

Output:-

Practical 1c

Aim:- Perform Data Loading, Feature selection (Principal Component analysis) and Feature Scoring and Ranking

Theory:-

In machine learning and data analysis, **data preprocessing** is a crucial step that involves preparing the raw data for model building. This often includes tasks like data loading, feature selection, and feature scoring. These processes ensure that only the most relevant and meaningful features are used, making the model more efficient and accurate.

Data loading refers to the process of bringing raw data into your system, typically from external sources like databases, CSV files, or APIs, for further processing.

Feature selection involves selecting the most relevant features (variables) from the dataset to improve model performance and reduce complexity. One common method for feature selection is **Principal Component Analysis (PCA)**.

Feature scoring and ranking are methods used to evaluate the importance of each feature in predicting the target variable. The most important features are ranked higher, and they can be used to improve the model's performance.

Code:-

```
from sklearn.feature_extraction.text import CountVectorizer

from sklearn.naive_bayes import MultinomialNB

from sklearn.model_selection import train_test_split

from sklearn.metrics import accuracy_score, classification_report


sms_data = [

    "Free entry in 2 a weekly competition to win FA Cup final tickets",

    "Hey, I will call you later. Don't forget to bring the document.",

    "Congratulations! You've won a free cruise to the Bahamas",

    "Hi there, can we meet tomorrow for lunch?",

    "URGENT! Your mobile number has won a $2000 prize!",
```

```
    "Reminder: Your appointment with the dentist is at 3 PM today.",
    "You have won a lottery! Claim your prize now by calling us.",
    "Are we still meeting at the coffee shop today?",
    "Exclusive deal just for you! Buy now and get 50% off!",
    "Can you send me the report by end of the day?"
]

sms_labels = [
    "spam", "ham", "spam", "ham", "spam",
    "ham", "spam", "ham", "spam", "ham"
]
vectorizer = CountVectorizer()
X = vectorizer.fit_transform(sms_data)

X_train, X_test, y_train, y_test = train_test_split(X, sms_labels, test_size=0.3, random_state=42)

classifier = MultinomialNB()
classifier.fit(X_train, y_train)

y_pred = classifier.predict(X_test)

accuracy = accuracy_score(y_test,y_pred)
report = classification_report(y_test, y_pred)

print("Test Data:")
for doc, actual, predicted in zip(sms_data[len(sms_data) - len(y_test):], y_test, y_pred):
```

```
print(f"Message: {doc}, Actual: {actual}, Predicted: {predicted}")


print(f"\nAccuracy: {accuracy:.2f}")
print(report)
print("Gayatri Kulkarni -53004230002")
```

Output:-

```
Test Data:
Message: Are we still meeting at the coffee shop today?, Actual: spam, Predicted: ham
Message: Exclusive deal just for you! Buy now and get 50% off!, Actual: ham, Predicted: ham
Message: Can you send me the report by end of the day?, Actual: ham, Predicted: ham

Accuracy: 0.67
              precision    recall  f1-score   support

         ham       0.67      1.00      0.80         2
        spam       0.00      0.00      0.00         1

    accuracy                           0.67         3
   macro avg       0.33      0.50      0.40         3
weighted avg       0.44      0.67      0.53         3

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```

Practical 1d

Aim:- 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.

Theory:-

Code:-

Output:-

Practical 2a

Aim:- 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.

Theory:-

The naïve Bayesian(or naïve Bayes) classifier is a simple probabilistic machine learning model based on Bayes' Theorem. It assumes that features (or predictors) are independent of each other, which is why it's called "naïve."

- Bayes' Theorem: It calculates the probability of a class given the features by combining the prior probability of the class with the likelihood of the features.

- Naïve independence assumption: It assumes that the features are conditionally independent of each other given the class.

- Despite the simplification, it often works surprisingly well in real-world applications, especially in text classification and spam filtering.

It's fast, easy to implement, and works well with large datasets.

$$P(C|X) = \frac{P(X|C) \cdot P(C)}{P(X)}$$

Where:

- P(C|X)= Posterior probability of class C given feature set X
- P(X|C) = Likelihood of feature set X given class C
- P(C) = Prior probability of class C
- P(X) = Probability of feature set X (this can be ignored in classification, as it is constant across classes)

For the **naïve** Bayes classifier, the assumption is that the features X1,X2,..., Xn are conditionally independent. So the likelihood P(X|C) becomes:

P(X|C)=P(X1|C)·P(X2|C)·...·P(Xn|C)

Thus, the **naïve Bayes formula** is:

$$P(C|X) \propto P(C) \cdot \prod_{i=1}^{n} P(X_i|C)$$

This is used to compute the probability for each class C, and the class with the highest probability is selected as the prediction.

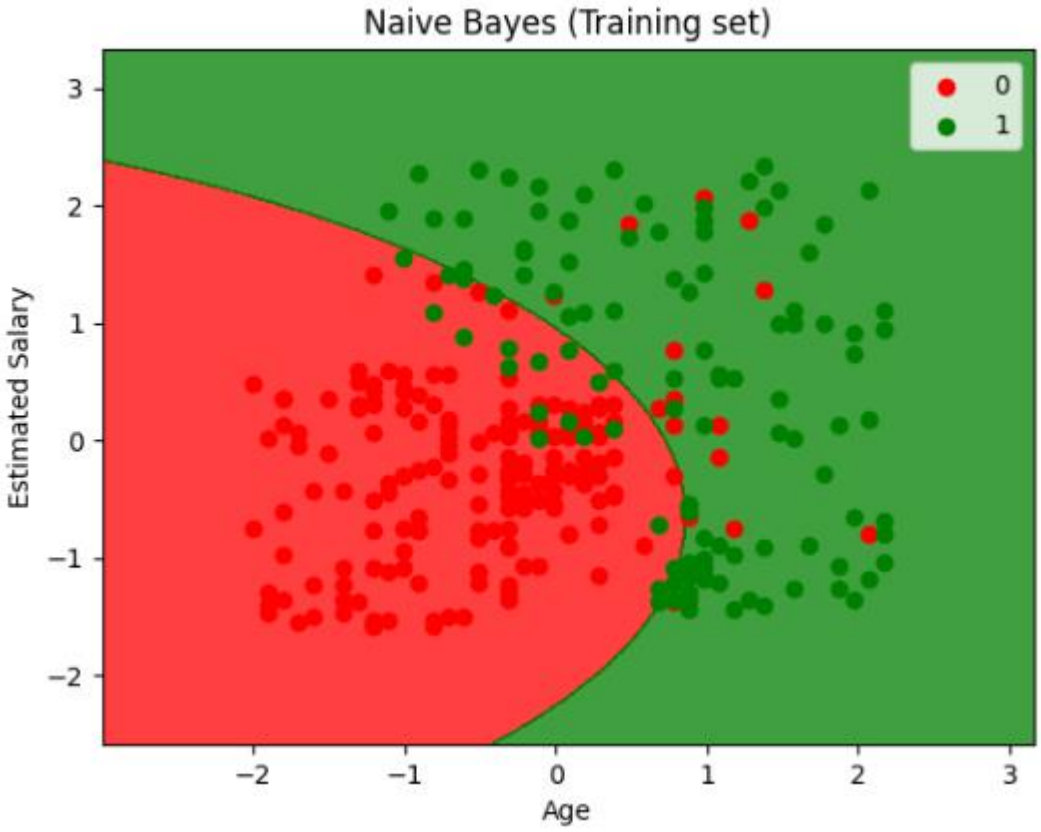
Code:-

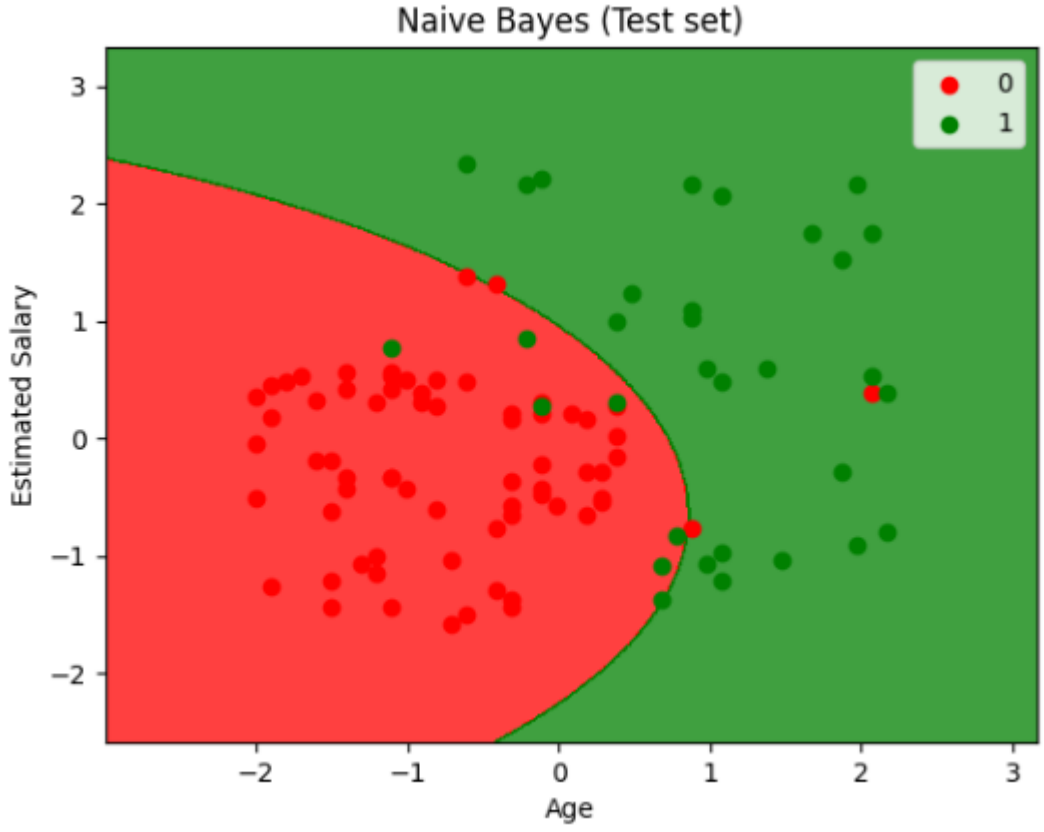
```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd


# Importing the dataset
dataset = pd.read_csv('Social_Network_Ads.csv')
X = dataset.iloc[:, [2, 3]].values
y = dataset.iloc[:, 4].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 = 0)


# Feature Scaling
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)


# Fitting classifier to the Training set
from sklearn.naive_bayes import GaussianNB
```

```
classifier = GaussianNB()
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
cm = confusion_matrix(y_test, y_pred)

# Visualising the Training set results
from matplotlib.colors import ListedColormap
X_set, y_set = X_train, y_train
X1, X2 = np.meshgrid(np.arange(start = X_set[:, 0].min() - 1, stop = X_set[:, 0].max() + 1, step = 0.01),
                     np.arange(start = X_set[:, 1].min() - 1, stop = X_set[:, 1].max() + 1, step = 0.01))
plt.contourf(X1, X2, classifier.predict(np.array([X1.ravel(), X2.ravel()]).T).reshape(X1.shape),
             alpha = 0.75, cmap = ListedColormap(('red', 'green')))
plt.xlim(X1.min(), X1.max())
plt.ylim(X2.min(), X2.max())
for i, j in enumerate(np.unique(y_set)):
    plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
                c = ListedColormap(('red', 'green'))(i), label = j)
plt.title('Naive Bayes (Training set)')
plt.xlabel('Age')
plt.ylabel('Estimated Salary')
```

```
plt.legend()
plt.show()


# Visualising the Test set results
from matplotlib.colors import ListedColormap
X_set, y_set = X_test, y_test
X1, X2 = np.meshgrid(np.arange(start = X_set[:, 0].min() - 1, stop = X_set[:, 0].max() + 1, step = 0.01),
                     np.arange(start = X_set[:, 1].min() - 1, stop = X_set[:, 1].max() + 1, step = 0.01))
plt.contourf(X1, X2, classifier.predict(np.array([X1.ravel(), X2.ravel()]).T).reshape(X1.shape),
             alpha = 0.75, cmap = ListedColormap(('red', 'green')))
plt.xlim(X1.min(), X1.max())
plt.ylim(X2.min(), X2.max())
for i, j in enumerate(np.unique(y_set)):
    plt.scatter(X_set[y_set == j, 0], X_set[y_set == j, 1],
                c = ListedColormap(('red', 'green'))(i), label = j)
plt.title('Naive Bayes (Test set)')
plt.xlabel('Age')
plt.ylabel('Estimated Salary')
plt.legend()
plt.show()
print('Gayatri Kulkarni - 53004230002')
```

Output:-





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Practical 2b

Aim:- Write a program to implement Decision Tree and Random forest with Prediction, Test Score and Confusion Matrix.

Theory:-

In machine learning, **Decision Trees** and **Random Forests** are two powerful and widely-used algorithms for both classification and regression tasks. They are based on tree structures, where decisions are made based on the value of input features.

A **Decision Tree** is a flowchart-like structure where each internal node represents a decision based on a feature, each branch represents the outcome of that decision, and each leaf node represents a class label or a continuous value (in case of regression).

-**Recursive Splitting**: The dataset is split based on certain feature conditions to create "branches."

-**Impurity Measures**: At each split, an impurity measure like **Gini Index** or **Entropy (Information Gain)** is used to determine the best split, i.e., the feature that best separates the data.

-**Leaf Nodes**: The final nodes represent the predicted outcome (class or value).

A **Random Forest** is an ensemble learning method that builds multiple decision trees and combines their predictions. It improves upon decision trees by reducing overfitting and increasing accuracy.

Once a model is trained using a decision tree or random forest, its performance is evaluated on test data. The most common evaluation metrics include **accuracy**, **confusion matrix**, and **other metrics** like precision and recall.

A **confusion matrix** is used to visualize the performance of a classification model by comparing the actual labels with predicted labels.

It consists of 4 key terms:

- **True Positive (TP)**: Correctly predicted positive class.
- **True Negative (TN)**: Correctly predicted negative class.
- **False Positive (FP)**: Incorrectly predicted as positive.

- **False Negative (FN)**: Incorrectly predicted as negative.

Code:-

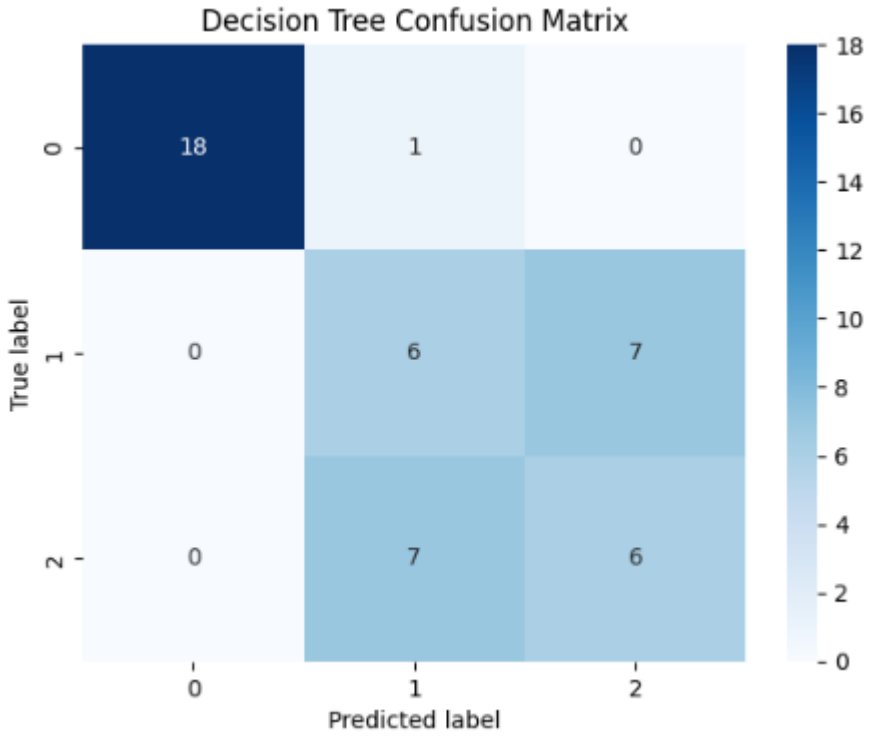
```
#Import necessary libraries

import pandas as pd

import numpy as np

from sklearn.model_selection import train_test_split

from sklearn.tree import DecisionTreeClassifier

from sklearn.ensemble import RandomForestClassifier

from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

import seaborn as sns

import matplotlib.pyplot as plt

from sklearn.datasets import load_iris


#Load the dataset into choose only two features for visualization (we'll use the first two)

iris = load_iris()

X = pd.DataFrame(iris.data, columns=iris.feature_names).iloc[:, :2] #Only first two features

y = pd.DataFrame(iris.target, columns=['species'])


#Split the dataset into training and testing sets

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)


#Function to plot decision boundary

def plot_decision_boundary(clf, X, y, title):

    #Create a meshgrid
```

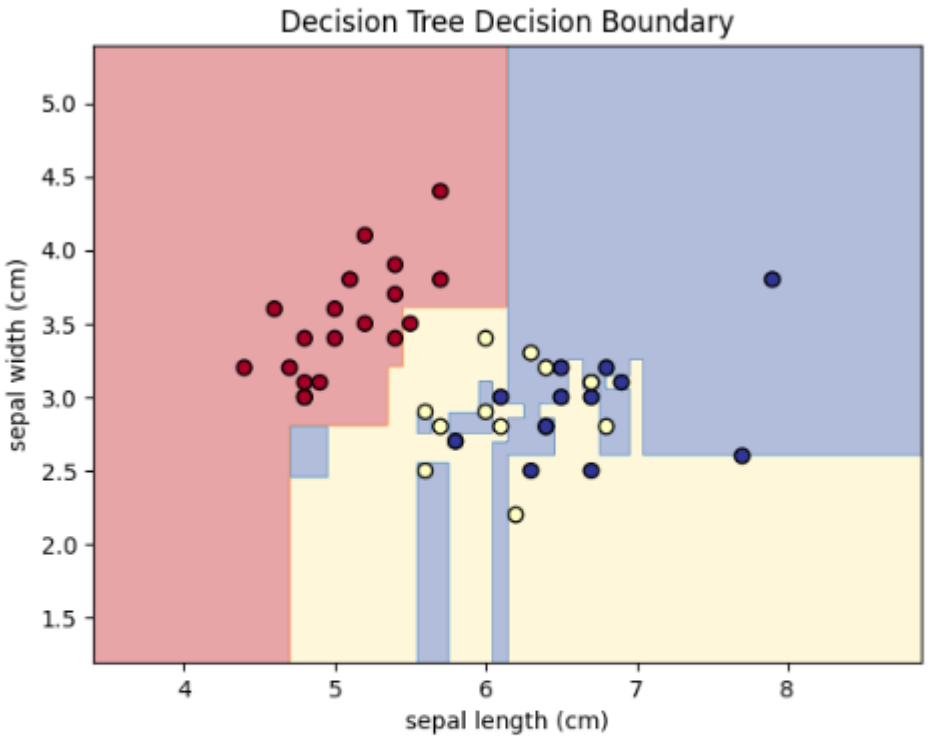
```
    x_min, x_max = X.iloc[:,0].min()-1,X.iloc[:,0].max() + 1
    y_min, y_max = X.iloc[:,1].min()-1,X.iloc[:,1].max() + 1
    xx, yy = np.meshgrid(np.arange(x_min, x_max, 0.01),
                         np.arange(y_min, y_max, 0.01))

    #Predict for the entire grid
    Z = clf.predict(np.c_[xx.ravel(), yy.ravel()])
    Z = Z.reshape(xx.shape)

    #Plot the contors and trainig points
    plt.contourf(xx, yy, Z, alpha=0.4, cmap=plt.cm.RdYlBu)

plt.scatter(X.iloc[:,0],X.iloc[:,1],c=y.values.ravel(),s=40,edgecolor='k',cmap=plt
.cm.RdYlBu)
    plt.title(title)
    plt.xlabel(iris.feature_names[0])
    plt.ylabel(iris.feature_names[1])
    plt.show()
#Desion tree classifier
dt_model = DecisionTreeClassifier(random_state=42)
dt_model.fit(X_train, y_train)

dt_predictions = dt_model.predict(X_test)
#Make predictions with Decision Tree
dt_accuracy = accuracy_score(y_test, dt_predictions)
dt_confusion_matrix = confusion_matrix(y_test, dt_predictions)

#Plot Confusion Matrix for Decision Tree
```

```
sns.heatmap(dt_confusion_matrix, annot=True, fmt='d', cmap='Blues')
plt.title('Decision Tree Confusion Matrix')
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

#Plot Decison Boundary for Decision Tree
plot_decision_boundary(dt_model,X_test,y_test,'Decision Tree Decision Boundary')

#Random Forest Classifier
rf_model = RandomForestClassifier(n_estimators=100, random_state=42)
rf_model.fit(X_train, y_train.values.ravel())

#Make predictions with Random Forest
rf_predictions = rf_model.predict(X_test)

rf_confusion_matrix = confusion_matrix(y_test, rf_predictions)
#Random Forest Accuracy and Confusion Matrix
rf_accuracy = accuracy_score(y_test, rf_predictions)

print(f"Random Forest Accuracy: {rf_accuracy}")
print("Random Forest Classification Report:")
print(classification_report(y_test, rf_predictions))

#PLot Confusion Matrix for Random Forest
sns.heatmap(rf_confusion_matrix, annot=True, fmt='d', cmap='Greens')
plt.title('Random Forest Confusion Matrix')
```

```
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()


#plot Descision Boundary for Random Forest
plot_decision_boundary(rf_model, X_test, y_test, "Random Forest Decision Boundary")
print('Gayatri Kulkarni - 53004230002')
```

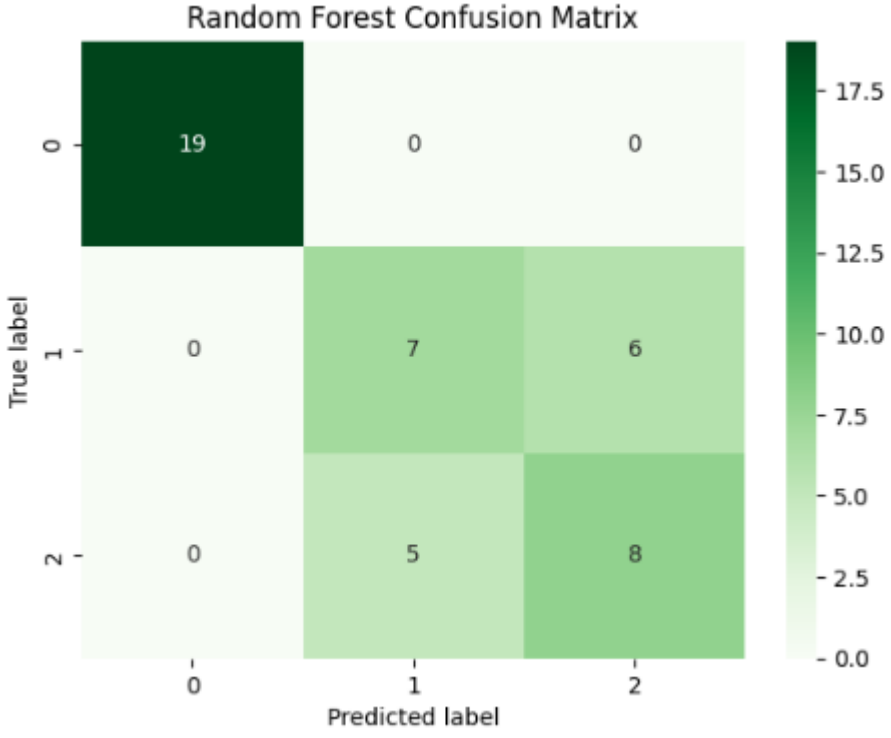
Output:-

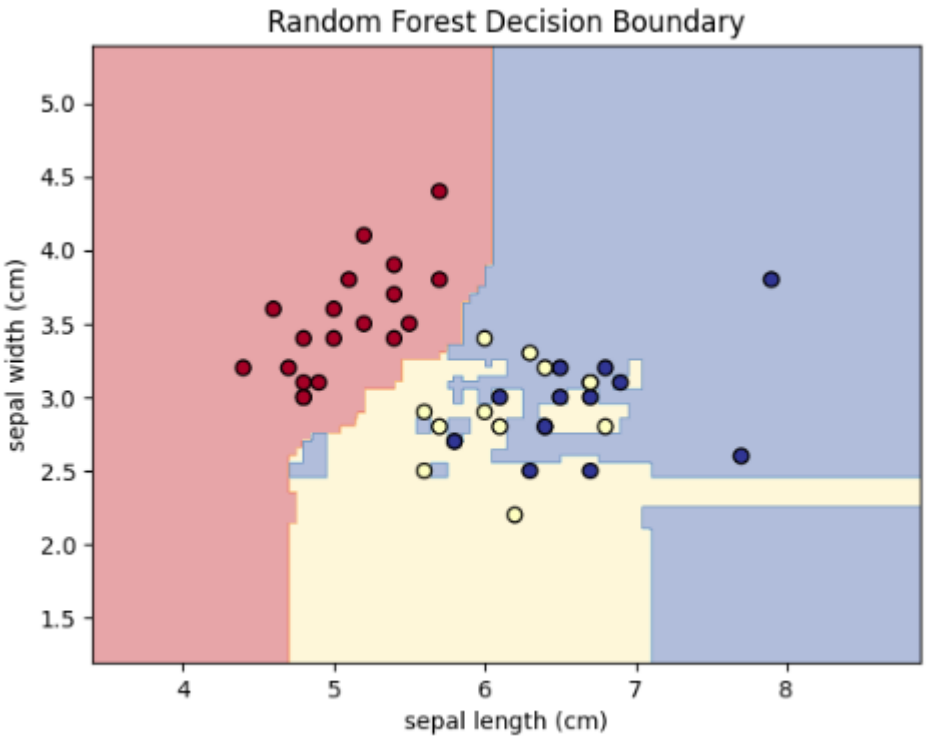




Random Forest Accuracy: 0.7555555555555555
Random Forest Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	19
1	0.58	0.54	0.56	13
2	0.57	0.62	0.59	13
accuracy			0.76	45
macro avg	0.72	0.72	0.72	45
weighted avg	0.76	0.76	0.76	45





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Practical 2c

Aim:- For a given set of training data examples stored in a .CSV file implement Least Square Regression algorithm.

Theory:-

The **Least Squares Regression** algorithm finds the line (or curve) that best represents the relationship between the variables by minimizing the sum of the squared differences (or residuals) between the observed values and the values predicted by the model. These residuals represent the errors between the actual values and the values predicted by the regression line.

Mathematical Formulation:

For a simple linear regression model with one predictor variable:

$y=\beta0+\beta1x+\epsilon$

Where:

- yis the dependent variable (target).
- x is the independent variable (predictor).
- β0 is the intercept of the regression line.
- β1 is the slope of the regression line.
- ϵ is the error term (residual).

The objective of least squares regression is to minimize the **sum of squared residuals**:

$$\min \sum_{i=1}^{n} (y_i - \hat{y}_i)^2$$

Where:

- yi is the actual value.
- yi^ is the predicted value.
- n is the number of data points.

This optimization problem gives us the values of β0 and β1that minimize the error. Steps followed are initialization, compute residuals, minimize sum of Squared Residuals, Prediction.

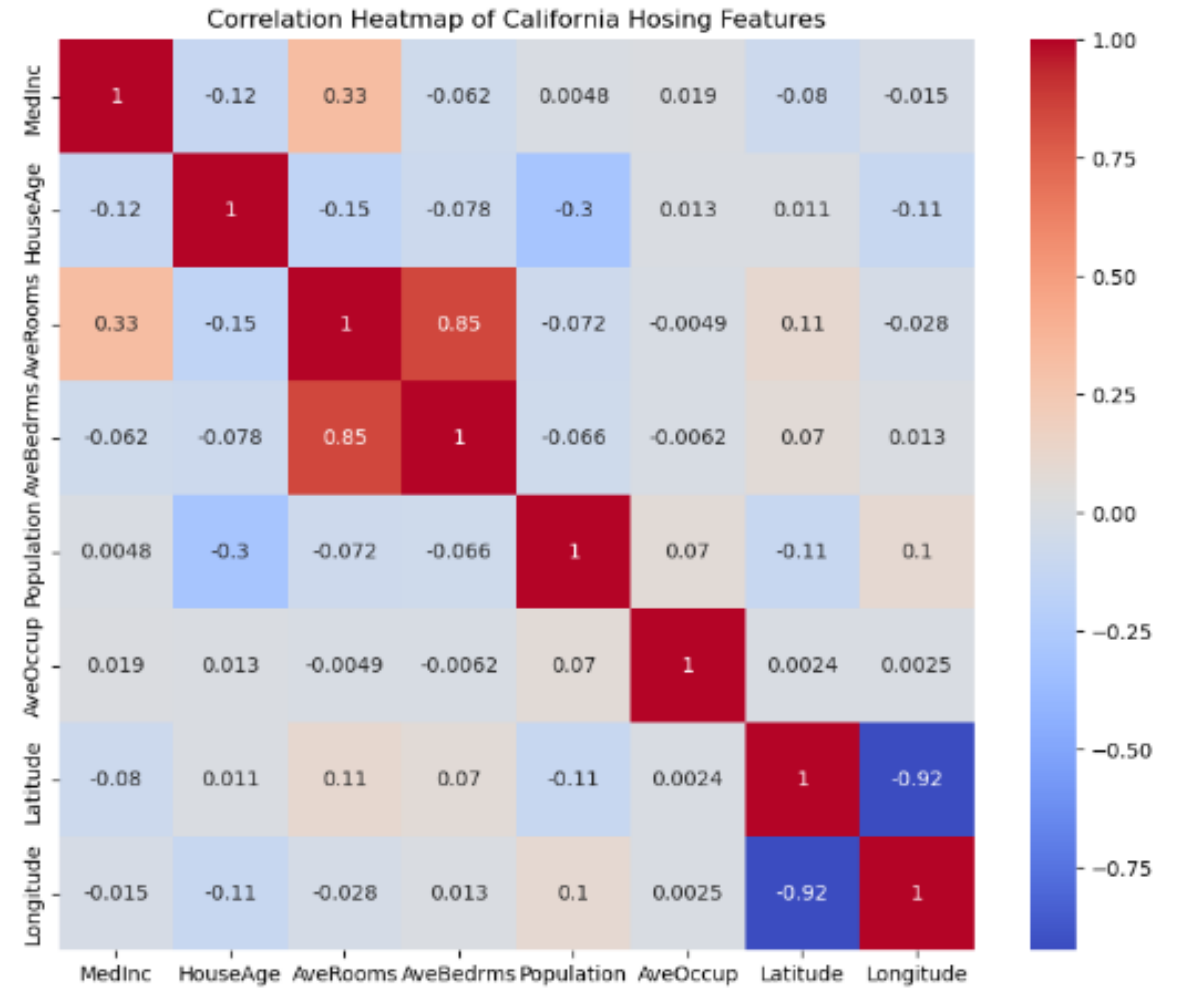
Code:-

```
#Import necessary libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error, r2_score
from sklearn.datasets import fetch_california_housing

#Load California Hosuing dataset
housing = fetch_california_housing()
X = pd.DataFrame(housing.data, columns=housing.feature_names)
y = pd.DataFrame(housing.target, columns=['MEDV'])

#Visualise dataset correlation heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(X.corr(), annot=True, cmap='coolwarm')
plt.title("Correlation Heatmap of California Hosing Features")
plt.show()

#Split the dataset into training and testingf sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)

#Implement Least Squares Regression (Linear Regression)
reg_model = LinearRegression()
```

```
reg_model.fit(X_train, y_train)



#Make predictions
y_train_pred = reg_model.predict(X_train)
y_test_pred = reg_model.predict(X_test)

#Generate relevant metrics
train_mse = mean_squared_error(y_train, y_train_pred)
test_mse = mean_squared_error(y_test, y_test_pred)
train_r2 = r2_score(y_train, y_train_pred)
test_r2 = r2_score(y_test, y_test_pred)

 #Print the results

print(f"Training Mean Squared Error: {train_mse}")
print(f"Test Mean Squared Error: {test_mse}")
print(f"Training R^2 Score: {train_r2}")
print(f"Test R^2 Score: {test_r2}")

# Visualise regression coefficients
coefficients = pd.DataFrame(reg_model.coef_.T, X.columns, columns=['Coefficient'])
print(coefficients)



#Plot predicted vs actual values for test set
plt.figure(figsize=(8,6))
plt.scatter(y_test, y_test_pred, c='blue')
plt.plot([y_test.min(), y_test.max()], [y_test.min(), y_test.max()], '--r', lw=3)
plt.xlabel("Actual Values")
```

```
plt.ylabel("Predicted Values")
plt.title("Actual vs Predicted Values (Test Set)")
plt.show()
print("Gayatri Kulkarni - 5300423002")
```

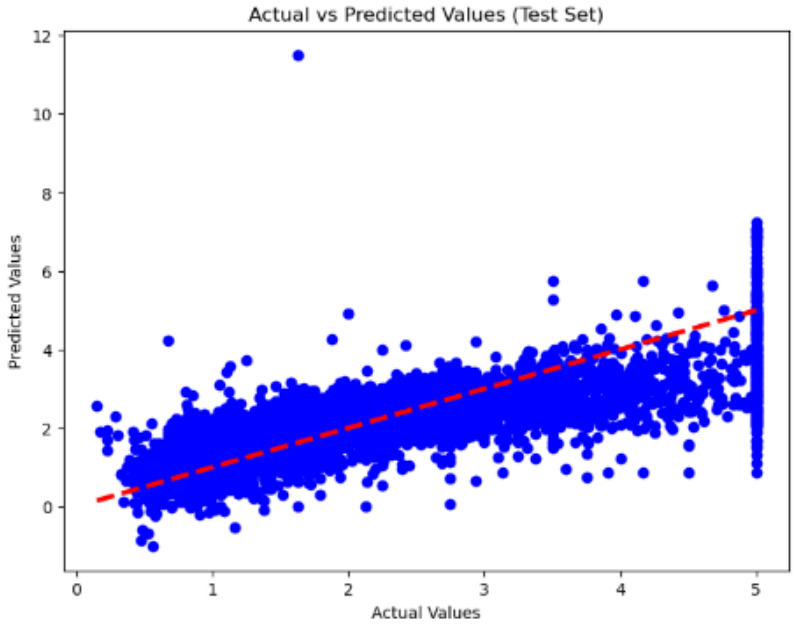
Output:-




```
Training Mean Squared Error: 0.5233576288267754
Test Mean Squared Error: 0.5305677824766757
Training R^2 Score: 0.609345972797216
Test R^2 Score: 0.595770232606166
              Coefficient
MedInc       4.458226e-01
HouseAge     9.681868e-03
AveRooms    -1.220951e-01
AveBedrms    7.785996e-01
Population  -7.757404e-07
AveOccup    -3.370027e-03
Latitude    -4.185367e-01
Longitude   -4.336880e-01
```

```
   MedInc  HouseAge  AveRooms  AveBedrms  Population  AveOccup  Latitude  Longitude
```

```
Training Mean Squared Error: 0.5233576288267754
Test Mean Squared Error: 0.5305677824766757
Training R^2 Score: 0.609345972797216
Test R^2 Score: 0.595770232606166
              Coefficient
MedInc       4.458226e-01
HouseAge     9.681868e-03
AveRooms    -1.220951e-01
AveBedrms    7.785996e-01
Population  -7.757404e-07
AveOccup    -3.370027e-03
Latitude    -4.185367e-01
Longitude   -4.336880e-01
```



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Practical 2d

Aim:- For a given set of training data examples stored in a .CSV file implement Logistic Regression algorithm.

Theory:-

Logistic regression models the probability that a given input belongs to a particular class. It estimates the **log odds** of the dependent variable being 1 (positive class) rather than 0 (negative class). The output of logistic regression is a probability value between 0 and 1, which is then used to classify the data points.

Logistic Function (Sigmoid Function):

The key to logistic regression is the **logistic function**, also known as the **sigmoid function**, which maps any real-valued number to the range (0, 1). The formula for the logistic function is:

$$f(z) = \frac{1}{1 + e^{-z}}$$

Where:

- z is the linear combination of the input features (like in linear regression), i.e., z= β0+β1x1+β2x2+...+βnxn.
- e is Euler's number (approximately 2.718).

This function ensures that the predicted value is between 0 and 1, representing a probability.**Logistic Regression** is a powerful, simple, and effective algorithm for binary and multi-class classification tasks. It models the relationship between input features and the probability of a particular outcome using the logistic (sigmoid) function. Despite its simplicity, it works well in many practical scenarios and serves as a good baseline model for classification tasks.

Code:-

```
#Import necessary libraries

import pandas as pd

import numpy as np

import matplotlib.pyplot as plt
```

```
import seaborn as sns

from sklearn.model_selection import train_test_split

from sklearn.linear_model import LogisticRegression

from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

from sklearn.datasets import load_breast_cancer


#Step 1: Load the inbulit Breast Cancer dataset

cancer_data = load_breast_cancer()

X = pd.DataFrame(cancer_data.data, columns=cancer_data.feature_names) #Feature

y = pd.DataFrame(cancer_data.target, columns=['target']) # Target


#Step 2: Explore the dataset

print("Dataset Head:")

print(X.head()) # Preview the first few rows of the feature set


print("\nTarget Distribution:")

print(y['target'].value_counts()) # Distribution of the target variable (0 = malignant 1= benign)


#Step 3: Split the databaset into traning and testing sets

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)


#Step 4 : Implement Logistic Regression

logreg = LogisticRegression(max_iter=10000, random_state=42) #Incresed max_itr to ensure convergence
```

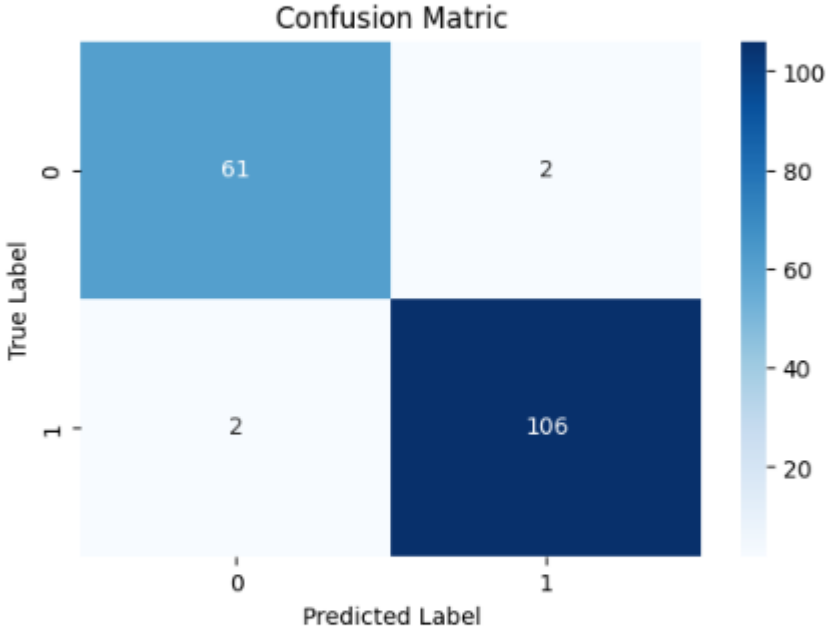
```
logreg.fit(X_train, y_train.values.ravel()) # y_train must be passed as a flat aaray


#Step 5 ; Make predictions on the test set
y_pred = logreg.predict(X_test)

#Step 6: Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)

print(f"\nAccuracy: {accuracy}")
print("\nConfusion Matrix:")
print(conf_matrix)
print("\nClassification Report:")
print(class_report)

# Step 7: Visualize the Confusion Matrix
plt.figure(figsize=(6,4))
sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues')
plt.title('Confusion Matric')
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()

#Step 8:Make a prediction on a  new input sample
#Example:Let's create a new sample input (using the mean of feature for simplicity)
```

```
#You can replace these values with actual feature values you'd like to predict for

new_input = np.array([X.mean().values])
# Ensure the new input has the correct shape (1, n_features)
print(f"\nNew Input for Prediction:\n{new_input}")

#Make a prediction on the new input
new_prediction = logreg.predict(new_input)

#Get the predictied class (0= malignant, 1=bening)
predicted_class = 'bening' if new_prediction == 1 else 'malignant'

print(f"\nPredited class for the new input: {predicted_class}")

#Step 9 : Visualise the Confusion Matrix for the test set
plt.figure(figsize=(6, 4))
sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues')
plt.title('Confusion Matrix- Test Set')
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()
print('Gayatri Kulkarni - 53004230002')
```

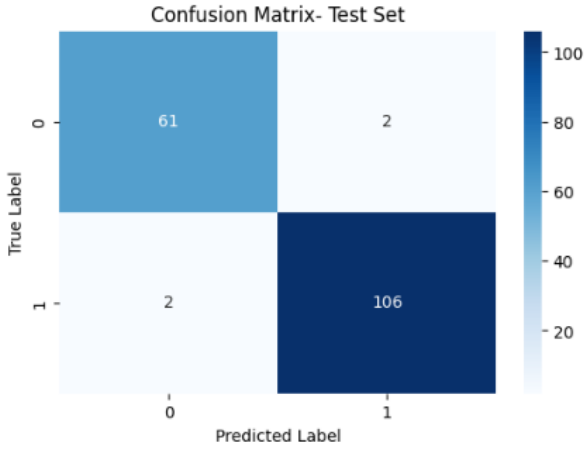
Output:-

```
Dataset Head:
   mean radius  mean texture  mean perimeter  mean area  mean smoothness  \
0        17.99         10.38          122.80     1001.0          0.11840
1        20.57         17.77          132.90     1326.0          0.08474
2        19.69         21.25          130.00     1203.0          0.10960
3        11.42         20.38           77.58      386.1          0.14250
4        20.29         14.34          135.10     1297.0          0.10030

   mean compactness  mean concavity  mean concave points  mean symmetry  \
0           0.27760          0.3001              0.14710         0.2419
1           0.07864          0.0869              0.07017         0.1812
2           0.15990          0.1974              0.12790         0.2069
3           0.28390          0.2414              0.10520         0.2597
4           0.13280          0.1980              0.10430         0.1809

   mean fractal dimension  ...  worst radius  worst texture  worst perimeter  \
0                 0.07871  ...         25.38          17.33           184.60
1                 0.05667  ...         24.99          23.41           158.80
2                 0.05999  ...         23.57          25.53           152.50
3                 0.09744  ...         14.91          26.50            98.87
4                 0.05883  ...         22.54          16.67           152.20

   worst area  worst smoothness  worst compactness  worst concavity  \
0      2019.0            0.1622             0.6656           0.7119
1      1956.0            0.1238             0.1866           0.2416
2      1709.0            0.1444             0.4245           0.4504
3       567.7            0.2098             0.8663           0.6869
4      1575.0            0.1374             0.2050           0.4000

   worst concave points  worst symmetry  worst fractal dimension
0                0.2654          0.4601                  0.11890
1                0.1860          0.2750                  0.08902
2                0.2430          0.3613                  0.08758
3                0.2575          0.6638                  0.17300
4                0.1625          0.2364                  0.07678

[5 rows x 30 columns]

Target Distribution:
target
1    357
0    212
Name: count, dtype: int64

Accuracy: 0.9766081871345029

Confusion Matrix:
[[ 61   2]
 [  2 106]]
```

```
Classification Report:
              precision    recall  f1-score   support

           0       0.97      0.97      0.97        63
           1       0.98      0.98      0.98       108

    accuracy                           0.98       171
   macro avg       0.97      0.97      0.97       171
weighted avg       0.98      0.98      0.98       171
```




```
New Input for Prediction:
[[1.41272917e+01 1.92896485e+01 9.19690334e+01 6.54889104e+02
  9.63602812e-02 1.04340984e-01 8.87993158e-02 4.89191459e-02
  1.81161863e-01 6.27976098e-02 4.05172056e-01 1.21685343e+00
  2.86605923e+00 4.03370791e+01 7.04097891e-03 2.54781388e-02
  3.18937163e-02 1.17961371e-02 2.05422988e-02 3.79490387e-03
  1.62691898e+01 2.56772232e+01 1.07261213e+02 8.80583128e+02
  1.32368594e-01 2.54265044e-01 2.72188483e-01 1.14606223e-01
  2.90075571e-01 8.39458172e-02]]

Predited class for the new input: malignant
```



Gayatri Kulkarni - 53004230002

Practical 3a

Aim:- 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.

Theory:-

ID3 is a decision tree-building algorithm that is based on the concept of **entropy** and **information gain** from information theory. It works by repeatedly splitting the dataset into smaller subsets based on the feature that provides the highest information gain until it reaches leaf nodes, which represent class labels.

At each node in the tree, ID3 selects the feature that best separates the data into the target classes. The algorithm continues this process recursively for each subset of the data, creating a tree structure that can be used for classification.

Entropy is a measure of the uncertainty or impurity in the data. It quantifies how mixed or homogeneous a set of classes is. If all examples in a subset belong to a single class, the entropy is 0 (pure), and if the examples are equally divided among classes, the entropy is 1 (maximum impurity).

$$\text{Entropy}(S) = -\sum_{i=1}^{k} p_i \log_2(p_i)$$

Where:

- pi is the proportion of examples in class iii.
- k is the total number of classes.

Information gain measures how much a feature reduces the entropy (impurity) in a dataset. ID3 chooses the feature with the highest information gain to split the data at each step.

The formula for information gain when splitting on feature A is:

$$\text{Gain}(S, A) = \text{Entropy}(S) - \sum_{v \in \text{Values}(A)} \frac{|S_v|}{|S|} \cdot \text{Entropy}(S_v)$$

Where:

- S is the original set.
- A is the feature being considered for the split.
- Sv is the subset of SSS where the feature A takes value v.
- | S_v|/||Sv| is the proportion of examples in subset Sv

The **ID3 algorithm** is a foundational decision tree algorithm that uses **entropy** and **information gain** to create decision trees for classification problems. By recursively splitting the dataset based on the most informative features, ID3 constructs a tree that can classify new data points. Although simple and easy to understand, ID3 can overfit and is sensitive to noise and features with many values. However, it remains a fundamental algorithm in machine learning and provides the basis for more advanced decision tree algorithms, such as C4.5 and CART.

Code:-

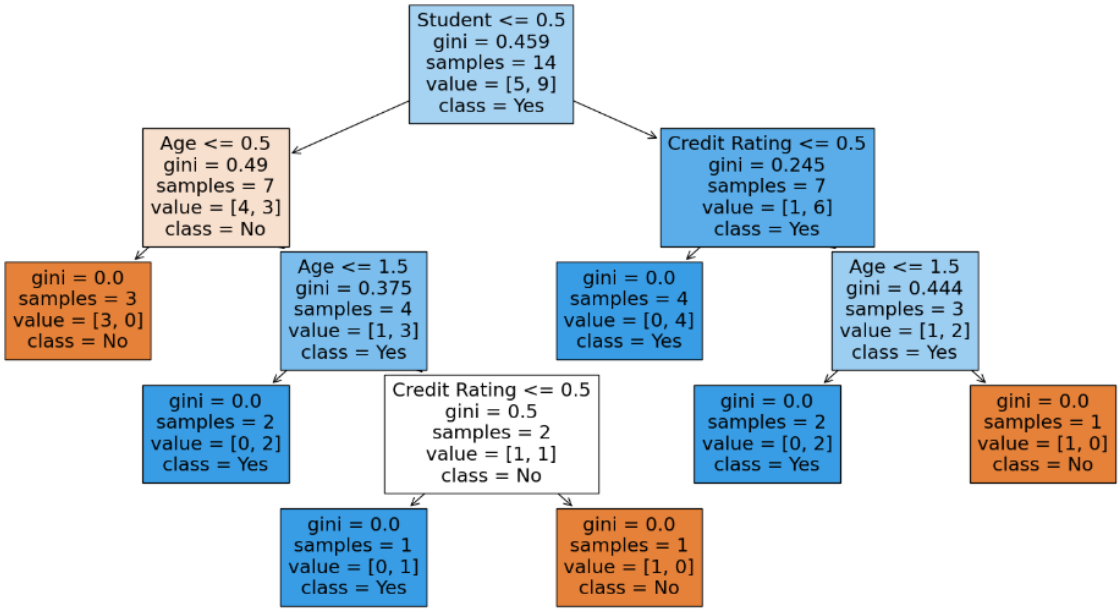
```
import pandas as pd

import numpy as np

import matplotlib.pyplot as plt

from sklearn import tree as sk_tree


# Step 1: Parse the dataset

data = {

    'Age': ['<=30', '<=30', '31-40', '>40', '>40', '>40', '31-40', '<=30', '<=30', '>40', '<=30', '31-40', '31-40', '>40'],

    'Income': ['High', 'High', 'High', 'Medium', 'Low', 'Low', 'Low', 'Medium', 'Low', 'Medium', 'Medium', 'Medium', 'High', 'Medium'],

    'Student': ['No', 'No', 'No', 'No', 'Yes', 'Yes', 'Yes', 'No', 'Yes', 'Yes', 'Yes', 'No', 'Yes', 'No'],

    'Credit Rating': ['Fair', 'Excellent', 'Fair', 'Fair', 'Fair', 'Excellent', 'Excellent', 'Fair', 'Fair', 'Fair', 'Excellent', 'Excellent', 'Fair', 'Excellent'],

    'Buys Computer': ['No', 'No', 'Yes', 'Yes', 'Yes', 'No', 'Yes', 'No', 'Yes', 'Yes', 'Yes', 'Yes', 'Yes', 'No']

}
```

```
df = pd.DataFrame(data)

# Encode the categorical variables
df_encoded = df.apply(lambda x: pd.factorize(x)[0])

# Fit the decision tree classifier using Gini impurity
clf_gini = sk_tree.DecisionTreeClassifier(criterion='gini')
clf_gini = clf_gini.fit(df_encoded.iloc[:, :-1], df_encoded['Buys Computer'])

# Convert the feature names from Index to list
feature_names = df.columns[:-1].tolist()

# Convert the class names to a list
class_names = df['Buys Computer'].unique().tolist()

# Plot the decision tree
plt.figure(figsize=(20,10))
sk_tree.plot_tree(clf_gini,feature_names=feature_names,class_names=class_names, filled=True)
plt.show()

# Function to print Gini impurity and chosen attribute at each split
def print_gini_and_splits(tree, feature_names):
    tree_ = tree.tree_
    feature_name = [
        feature_names[i] if i != sk_tree._tree.TREE_UNDEFINED else "undefined!"
```

```
        for i in tree_.feature
    ]

    print("Decision tree splits and Gini impurities:")
    for i in range(tree_.node_count):
        if tree_.children_left[i] != sk_tree._tree.TREE_LEAF:
            print(f"Node {i} (Gini: {tree_.impurity[i]:.4f}): split on feature '{feature_name[i]}'")
        else:
            print(f"Node {i} (Gini: {tree_.impurity[i]:.4f}): leaf node")

print_gini_and_splits(clf_gini, feature_names)

# Example test sample
test_sample = {
    'Age': '<=30',
    'Income': 'Medium',
    'Student': 'Yes',
    'Credit Rating': 'Fair'
}

# Encode the test sample
encoded_sample = pd.DataFrame([test_sample]).apply(lambda x: pd.factorize(df[x.name])[0][df[x.name].tolist().index(x[0])])

# Predict using sklearn decision tree
sklearn_prediction = clf_gini.predict([encoded_sample])
```

```
decoded_prediction = pd.factorize(df['Buys Computer'])[1][sklearn_prediction[0]]

print("Prediction for sklearn decision tree:", decoded_prediction)

print("Gayatri Kularni -53004230002")
```

Output:-




```
Decision tree splits and Gini impurities:
Node 0 (Gini: 0.4592): split on feature 'Student'
Node 1 (Gini: 0.4898): split on feature 'Age'
Node 2 (Gini: 0.0000): leaf node
Node 3 (Gini: 0.3750): split on feature 'Age'
Node 4 (Gini: 0.0000): leaf node
Node 5 (Gini: 0.5000): split on feature 'Credit Rating'
Node 6 (Gini: 0.0000): leaf node
Node 7 (Gini: 0.0000): leaf node
Node 8 (Gini: 0.2449): split on feature 'Credit Rating'
Node 9 (Gini: 0.0000): leaf node
Node 10 (Gini: 0.4444): split on feature 'Age'
Node 11 (Gini: 0.0000): leaf node
Node 12 (Gini: 0.0000): leaf node
Prediction for sklearn decision tree: Yes
Gayatri Kulkarni -53004230002
```

Practical 3b

Aim:- Write a program to implement k-Nearest Neighbour algorithm to classify the iris data set.

Theory:-

The **k-Nearest Neighbors (k-NN)** algorithm is a simple, non-parametric, and instance-based learning algorithm widely used for **classification** and **regression** tasks. It is one of the most straightforward machine learning algorithms, making decisions by looking at the **'k' closest data points** (neighbors) in the training set and using them to predict the outcome for a new data point.

The k-NN algorithm works by comparing a new data point with its nearest neighbors in the feature space, based on some distance metric, such as **Euclidean distance**. The class of the new point is then determined by the **majority class** of its neighbors (for classification) or by averaging the values of the neighbors (for regression).

The main idea is that **similar data points** (those close to each other) tend to have similar classifications or target values.

Here's a step-by-step process for how the k-NN algorithm works:

1. **Step 1: Choose the value of 'k'**:
    - The number kkk represents the number of nearest neighbors to consider when making a prediction. A small value of kkk can be more sensitive to noise, while a larger value smooths the decision boundary.
2. **Step 2: Calculate Distance**:
    - For each new data point, the algorithm calculates the distance between the new point and all points in the training dataset. Common distance metrics include:
        - **Euclidean Distance** (for continuous variables):

$$d(p,q) = \sqrt{\sum_{i=1}^{n}(p_i - q_i)^2}$$

        - **Manhattan Distance**: Measures distance as the sum of absolute differences across dimensions.

3. **Step 3: Identify Neighbors**:
    - The algorithm identifies the k data points in the training set that are closest to the new data point based on the calculated distances.
4. **Step 4: Voting (for Classification)**:
    - The algorithm assigns the new data point to the most common class among the k-nearest neighbors.
    - **Majority Voting**: If more neighbors belong to a particular class, the new point is assigned that class.

For Regression:

- The algorithm averages the target values of the k-nearest neighbors to predict a continuous value.

5. **Step 5: Make Prediction**:
    - Based on the voting (classification) or averaging (regression), the algorithm predicts the class label or continuous value for the new data point.

The **k-Nearest Neighbors (k-NN)** algorithm is a simple yet powerful machine learning method used for classification and regression tasks. By relying on the concept that similar data points tend to belong to the same class or have similar values, k-NN makes predictions by looking at the k-nearest data points. Although simple and effective for small datasets, k-NN can be computationally intensive for large datasets and sensitive to irrelevant features, which necessitates careful data preprocessing and selection of the appropriate value for k.

Code:-

```
# Step 1: Import necessary libraries

import pandas as pd

import matplotlib.pyplot as plt

import seaborn as sns

from sklearn.model_selection import train_test_split

from sklearn.preprocessing import StandardScaler
```

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score
from mpl_toolkits.mplot3d import Axes3D

# Step 2: Load and display the sample data
data = {
    'Age': [19, 21, 20, 23, 31, 22, 35, 25, 23, 64, 30, 67, 35, 58, 24],
    'Annual Income (k$)': [15, 15, 16, 16, 17, 17, 18, 18, 19, 19, 20, 20, 21, 21, 22],
    'Spending Score (1-100)': [39, 81, 6, 77, 40, 76, 6, 94, 3, 72, 79, 65, 76, 76, 94],
    'Segment': [0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1]  # 0: Low-value, 1: High-value
}

df = pd.DataFrame(data)
print("Sample Data:")
print(df.head())

# Step 3: Data Preprocessing
X = df[['Age', 'Annual Income (k$)', 'Spending Score (1-100)']]
y = df['Segment']

scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Step 4: Train-Test Split
```

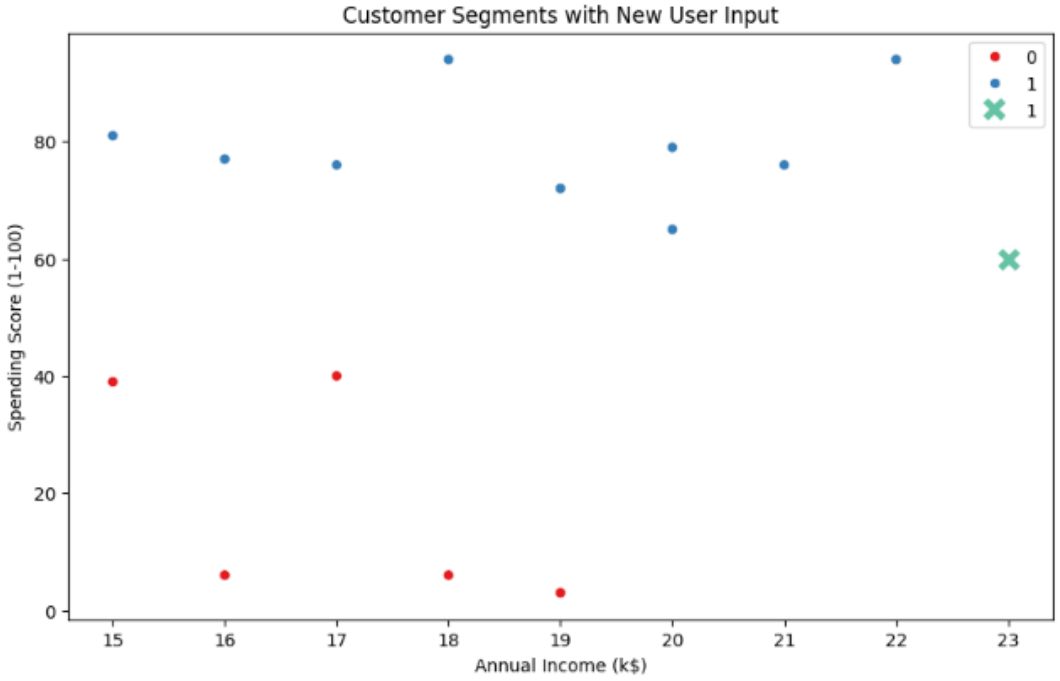
```
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.2, random_state=42)

# Step 5: Apply KNN Algorithm
knn = KNeighborsClassifier(n_neighbors=3)
knn.fit(X_train, y_train)
y_pred = knn.predict(X_test)

# Step 6: Evaluation
print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
print("\nClassification Report:")
print(classification_report(y_test, y_pred))
print("\nAccuracy Score:")
print(accuracy_score(y_test, y_pred))

# Step 7: Classify new user input
new_user_data = {'Age': [27], 'Annual Income (k$)': [23], 'Spending Score (1-100)': [60]}
new_user_df = pd.DataFrame(new_user_data)
new_user_scaled = scaler.transform(new_user_df)

new_user_segment = knn.predict(new_user_scaled)
new_user_df['Segment'] = new_user_segment
print("\nNew User Data Prediction:")
print(new_user_df)

# Visualization: Scatter plot of the customer segments
```

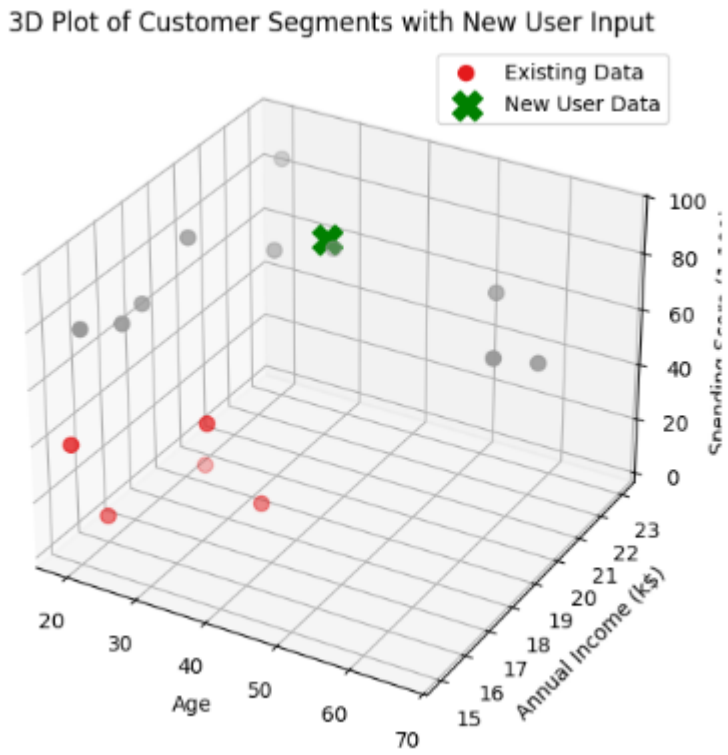
```
plt.figure(figsize=(10, 6))

sns.scatterplot(x='Annual Income (k$)', y='Spending Score (1-100)', hue='Segment', data=df, palette='Set1', marker='o')#, label='Existing Data'

sns.scatterplot(x='Annual Income (k$)', y='Spending Score (1-100)', hue='Segment', data=new_user_df, palette='Set2', marker='X', s=200)#, label='New User Data'

plt.title('Customer Segments with New User Input')

plt.xlabel('Annual Income (k$)')

plt.ylabel('Spending Score (1-100)')

plt.legend()

plt.show()


# Visualization: 3D plot for KNN decision boundaries and customer segments including new user input

fig = plt.figure(figsize=(10, 6))

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


# Plot the existing data with original values

ax.scatter(X['Age'], X['Annual Income (k$)'], X['Spending Score (1-100)'], c=y, cmap='Set1', s=50, label='Existing Data')


# Plot the new user input with original values

ax.scatter(new_user_df['Age'], new_user_df['Annual Income (k$)'], new_user_df['Spending Score (1-100)'], c='green', marker='X', s=200, label='New User Data')

ax.set_xlabel('Age')

ax.set_ylabel('Annual Income (k$)')

ax.set_zlabel('Spending Score (1-100)')

plt.title('3D Plot of Customer Segments with New User Input')

ax.legend()
```

```
plt.show()

print("Gayatri Kulkarni  53004230002")
```

Output:-

```
Sample Data:
   Age  Annual Income (k$)  Spending Score (1-100)  Segment
0   19                  15                      39        0
1   21                  15                      81        1
2   20                  16                       6        0
3   23                  16                      77        1
4   31                  17                      40        0

Confusion Matrix:
[[1 0]
 [0 2]]

Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00         1
           1       1.00      1.00      1.00         2

    accuracy                           1.00         3
   macro avg       1.00      1.00      1.00         3
weighted avg       1.00      1.00      1.00         3


Accuracy Score:
1.0

New User Data Prediction:
   Age  Annual Income (k$)  Spending Score (1-100)  Segment
0   27                  23                      60        1
```





Gayatri Kulkarni 53004230002

Practical 3c

Aim:- Implement the different Distance methods (Euclidean) with Prediction, Test Score and Confusion Matrix.

Theory:-

In machine learning, particularly for algorithms like **k-Nearest Neighbors (k-NN)**, **Clustering** (e.g., k-means), and **distance-based anomaly detection**, the choice of distance metrics is critical. The distance metric determines how "close" or "far" two data points are from each other, influencing the model's predictions.

Different tasks and types of data require different distance measures, and the **Euclidean distance** is one of the most commonly used, but it is not always the best. In this introduction, we'll explore **Euclidean distance**, as well as other commonly used distance methods such as **Manhattan**, **Minkowski**, and **Cosine Similarity**.

Euclidean distance is the most widely used distance metric, particularly for continuous, real-valued data. It represents the straight-line (or shortest) distance between two points in a multi-dimensional space.

The formula for **Euclidean Distance** between two points p=(p1,p2,...,pn)p = and q=(q1,q2,...,qn) in an n-dimensional space is:

$$d(p,q) = \sqrt{\sum_{i=1}^{n}(p_i - q_i)^2}$$

From the confusion matrix, we can calculate the following metrics:

- **Accuracy** = $\frac{TP+TN}{TP+TN+FP+FN}$
- **Precision** = $\frac{TP}{TP+FP}$
- **Recall** (Sensitivity) = $\frac{TP}{TP+FN}$
- **F1 Score** = Harmonic mean of precision and recall: $2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$

Code:-

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import classification_report,confusion_matrix

# Load the Iris dataset
iris = load_iris()
X = iris.data[:, :2]  # Select only the first two features (sepal length and sepal width)
y = iris.target

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)
# Initialize k-NN classifier with different distance metrics
k = 3

# List of distance metrics to test
distance_metrics = ['euclidean', 'manhattan', 'chebyshev']

# Create subplots for each distance metric
fig, axes = plt.subplots(1, len(distance_metrics), figsize=(15, 5))
for i, metric in enumerate(distance_metrics):
    knn_classifier = KNeighborsClassifier(n_neighbors=k, metric=metric)
```

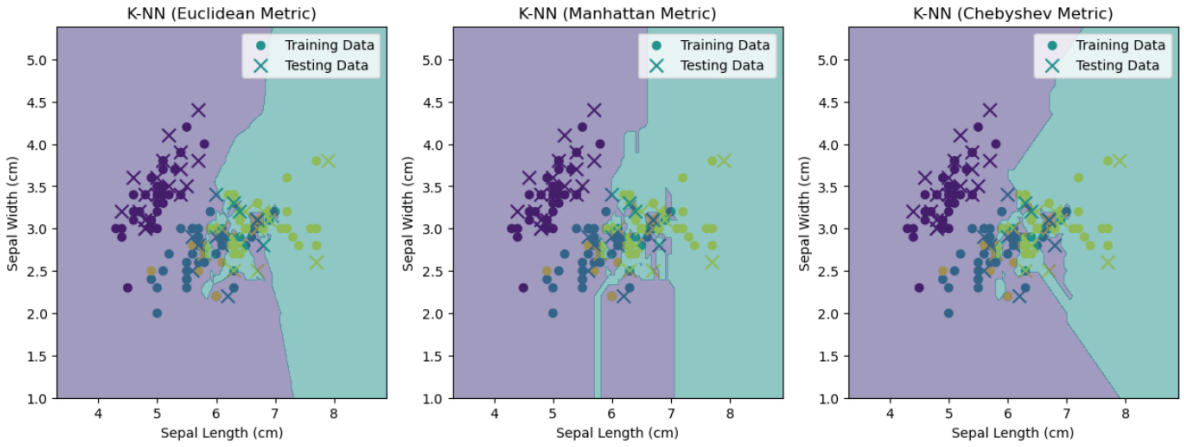
```
    # Fit the classifier to the training data
    knn_classifier.fit(X_train, y_train)
    # Make predictions on the test data
    y_pred = knn_classifier.predict(X_test)
    # Evaluate the classifier's performance
    print(f"Distance Metric: {metric}")
    print("Confusion Matrix:")
    print(confusion_matrix(y_test, y_pred))
    print("\nClassification Report:")
    print(classification_report(y_test, y_pred))
    print("\n")

    # Visualize the dataset and decision boundaries for the current metric
    ax = axes[i]
# Plot the training data points
    ax.scatter(X_train[:, 0], X_train[:, 1], c=y_train, cmap='viridis', label='Training Data')

    # Plot the testing data points
    ax.scatter(X_test[:, 0], X_test[:, 1], c=y_test, cmap='viridis', marker='x', s=100, label='Testing Data')
# Plot decision boundaries using the current metric
    knn_classifier = KNeighborsClassifier(n_neighbors=k, metric=metric)
    knn_classifier.fit(X, y)
    x_min, x_max = X[:, 0].min() - 1, X[:, 0].max() + 1
    y_min, y_max = X[:, 1].min() - 1, X[:, 1].max() + 1
    xx, yy = np.meshgrid(np.arange(x_min, x_max, 0.01), np.arange(y_min, y_max, 0.01))
```

```
    Z = knn_classifier.predict(np.c_[xx.ravel(), yy.ravel()])
    Z = Z.reshape(xx.shape)
ax.contourf(xx, yy, Z, cmap='viridis', alpha=0.5, levels=range(4))
    ax.set_title(f'K-NN ({metric.capitalize()} Metric)')
    ax.set_xlabel('Sepal Length (cm)')
    ax.set_ylabel('Sepal Width (cm)')
    ax.legend()

plt.show()
```

Output:-

```
Distance Metric: euclidean
Confusion Matrix:
[[19  0  0]
 [ 0  7  6]
 [ 0  5  8]]

Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        19
           1       0.58      0.54      0.56        13
           2       0.57      0.62      0.59        13

    accuracy                           0.76        45
   macro avg       0.72      0.72      0.72        45
weighted avg       0.76      0.76      0.76        45



Distance Metric: manhattan
Confusion Matrix:
[[19  0  0]
 [ 0  7  6]
 [ 0  5  8]]

Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        19
           1       0.58      0.54      0.56        13
           2       0.57      0.62      0.59        13

    accuracy                           0.76        45
   macro avg       0.72      0.72      0.72        45
weighted avg       0.76      0.76      0.76        45
```

```
Distance Metric: chebyshev
Confusion Matrix:
[[19  0  0]
 [ 0  8  5]
 [ 0  7  6]]

Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        19
           1       0.53      0.62      0.57        13
           2       0.55      0.46      0.50        13

    accuracy                           0.73        45
   macro avg       0.69      0.69      0.69        45
weighted avg       0.73      0.73      0.73        45
```



Gayatri Kulkarni -53004230002

Practical 3d

Aim:- Implement the classification model using clustering for the following techniques with K means clustering with Prediction, Test Score and Confusion Matrix

Theory:-

K-Means clustering works by minimizing the **intra-cluster variance** (distance between the points within a cluster) and maximizing the **inter-cluster variance** (distance between the centroids of different clusters). Each data point is assigned to the cluster whose centroid is closest to it, based on some distance metric (usually **Euclidean distance**).

Code:-

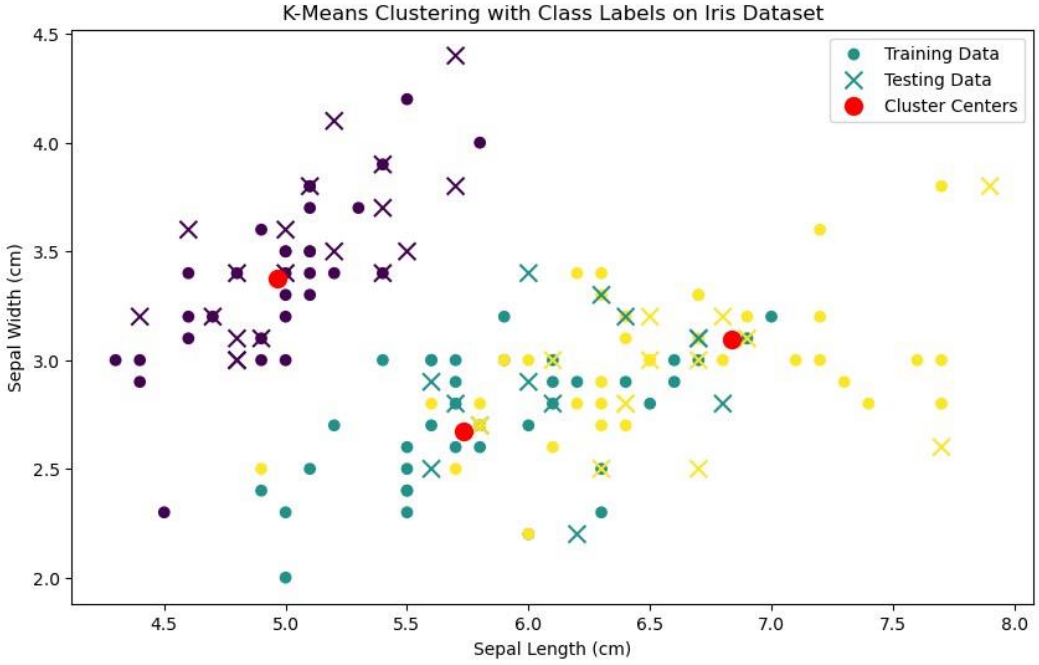
```
import numpy as np

import pandas as pd

import matplotlib.pyplot as plt

from sklearn.datasets import load_iris

from sklearn.model_selection import train_test_split

from sklearn.cluster import KMeans

from sklearn.metrics import classification_report, confusion_matrix


#Load the Iris dataset

iris = load_iris()

X = iris.data[:, :2] #Select only the features (sepal lengthy and sepal width)

y = iris.target


#Split database into traini9ng and testing

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)
```

```
#Initalize K-Means clustering with the number of clusters equal to the number of classes
n_clusters = len(np.unique(y))
kmeans = KMeans(n_clusters=n_clusters, random_state=42)

#Fit K-Means clustering to the training data
kmeans.fit(X_train)

#Assign cluster labels to data points in test set
cluster_labels = kmeans.predict(X_test)

#Assign class labels to clusters based on thge most frequent class label in each cluster
cluster_class_labels = []
for i in range(n_clusters):
    cluster_indices = np.where(cluster_labels ==i)[0]
    cluster_class_labels.append(np.bincount(y_test[cluster_indices]).argmax())

#Assign cluster class labels to data points in the test set
y_pred = np.array([cluster_class_labels[cluster_labels[i]] for i in range(len(X_test))])

#Evaluate the classifier's performance
print("Confusion Matrix:")
print(confusion_matrix(y_test, y_pred))
print("\nClassification Report:")
print(classification_report(y_test, y_pred))
```

```
#Visualize the dataset and cluster cemters

plt.figure(figsize=(10, 6))


#Plot the training data points

plt.scatter(X_train[:, 0], X_train[:, 1], c=y_train, cmap='viridis', label='Training Data')


#Plot testing data

plt.scatter(X_test[:, 0], X_test[:, 1], c=y_test, cmap='viridis', marker='x', s=100, label='Testing Data')


#plt cluster centers

plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:, 1], c='red', marker='o', s=100, label='Cluster Centers')


plt.xlabel('Sepal Length (cm)')

plt.ylabel('Sepal Width (cm)')

plt.title('K-Means Clustering with Class Labels on Iris Dataset')

plt.legend()

plt.show()

print("Gayatri Kulkarni- 5300423002")
```

Output:-

```
Confusion Matrix:
[[19  0  0]
 [ 0  8  5]
 [ 0  3 10]]

Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        19
           1       0.73      0.62      0.67        13
           2       0.67      0.77      0.71        13

    accuracy                           0.82        45
   macro avg       0.80      0.79      0.79        45
weighted avg       0.82      0.82      0.82        45
```



Gayatri Kulkarni- 5300423002

Practical 4a

Aim:- Implement the classification model using clustering for the following techniques with hierarchical clustering with Prediction, Test Score and Confusion Matrix

Theory:-

Hierarchical Clustering is a popular **unsupervised machine learning** technique used to group similar data points into clusters based on their distances from each other. Unlike K-Means clustering, which requires the number of clusters to be specified in advance, hierarchical clustering builds a hierarchy of clusters that can be represented in a **dendrogram** (a tree-like diagram), allowing users to determine the number of clusters by cutting the tree at a desired level.

Agglomerative Clustering:

- This is a bottom-up approach where each data point starts as its own cluster, and pairs of clusters are merged as one moves up the hierarchy.
- The steps are as follows:
    1. Start with each data point as its own cluster.
    2. Compute the proximity (or distance) between each pair of clusters.
    3. Merge the two closest clusters.
    4. Repeat steps 2-3 until all points are merged into a single cluster or a desired number of clusters is reached.

Divisive Clustering:

- This is a top-down approach where all data points start in a single cluster, and splits are performed recursively to divide the clusters into smaller ones.
- It is less commonly used than agglomerative clustering due to its computational complexity

A **dendrogram** is a visual representation of the hierarchical clustering process. It illustrates the arrangement of clusters and the distances at which clusters are merged. Each leaf node represents an individual data point, and the branches represent merges. The height at which two clusters are merged indicates the distance between them.

Hierarchical clustering is a versatile and intuitive method for grouping similar data points without requiring prior knowledge of the number of clusters. Its ability to provide a detailed visual representation of cluster relationships through dendrograms makes it a valuable tool in exploratory data analysis. While it has certain limitations, such as computational complexity and sensitivity to noise, it remains widely used in various fields for its interpretability and flexibility.

Code:-

```
import pandas as pd

import numpy as np

from sklearn.cluster import AgglomerativeClustering

from sklearn.model_selection import train_test_split

from sklearn.ensemble import RandomForestClassifier

from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

from sklearn.datasets import load_iris

import matplotlib.pyplot as plt

from scipy.cluster.hierarchy import dendrogram, linkage


#Load the Iris dataset

iris = load_iris()

X = iris.data

y = iris.target


#Step 1: Hierarchical Clustering with different Linkage Methods and Draw denograms

n_clusters = 3 # Number of clusters

linkage_methods = ['ward', 'single', 'complete'] # Different Linkage methods

cluster_labels = []
```

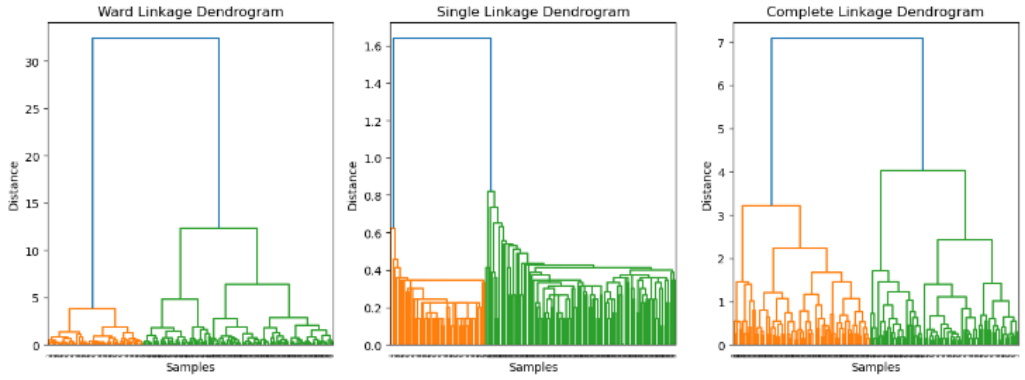
```
#Define figure and axes for dendrograms
plt.figure(figsize=(15, 5))
dendrogram_axes = []

for i, linkage_method in enumerate(linkage_methods):
        labels = AgglomerativeClustering(n_clusters=n_clusters, linkage=linkage_method).fit_predict(X)
    cluster_labels.append(labels)

#Create  a dendrgram for the current linkage method
    dendrogram_data = linkage(X, method=linkage_method)
    dendrogram_axes.append(plt.subplot(1, len(linkage_methods), i+1))
    dendrogram(dendrogram_data, orientation='top', labels=labels)
    plt.title(f"{linkage_method.capitalize()} Linkage Dendrogram")
    plt.xlabel('Samples')
    plt.ylabel('Distance')

#Plot clustering results for different linkage methods
plt.figure(figsize=(15, 5))
for i, linkage_method in enumerate(linkage_methods):
    plt.subplot(1, len(linkage_methods), i + 1)
    scatter = plt.scatter(X[:, 0], X[:, 1], c=cluster_labels[i], cmap='viridis',
                label=f'Clusters ({linkage_method.capitalize()} Linkage)')
    plt.title(f"{linkage_method.capitalize()} Linkage")
#Add legend to scatter plots
plt.legend(handles=scatter.legend_elements()[0], labels=[f'Cluster {i}' for i in range(n_clusters)])
```

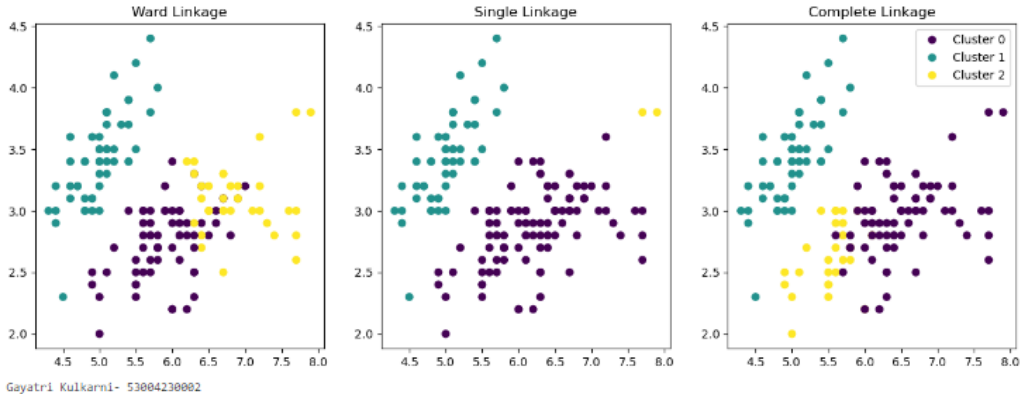
```
#sTEP 2 :fEATURE ENGINEERING (uSING CLUSTER ASSIGNMENT AS A feature)
X_with_cluster = np.column_stack((X, cluster_labels[-1])) # using complete linkage


#Step 3: Classification
X_train, X_test, y_train, y_test = train_test_split(X_with_cluster, y, test_size=0.2, random_state=42)
classifier = RandomForestClassifier(n_estimators=100, random_state=42)
classifier.fit(X_train, y_train)


#Step 4: Prediction
y_pred = classifier.predict(X_test)


#Step 5 : Test Score and Confusion Matrix
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)


#Genrate classification report with zero_division parametrs
classification_rep = classification_report(y_test, y_pred, zero_division=0)


#Print cluster description
cluster_descriptions = {
    'ward': 'Clusters based on Ward linkage interpretation.',
    'single': 'Cluster based on Single linkage interpretation.',
    'complete': 'Clusters based on Complete linkage interpretation.'
}
```

```
for method in linkage_methods:
    print(f"Cluster Descriptions ({method.capitalize()} Linkage):")
    print(cluster_descriptions[method.lower()])  # Convert to lowercase for dictionary access
# Print accuracy, confusion matrix, and classification report
print("Accuracy:", accuracy)
print("Confusion Matrix:\n", conf_matrix)
print("Classification Report:\n", classification_rep)
plt.show()
print("Gayatri Kulkarni- 53004230002")
```

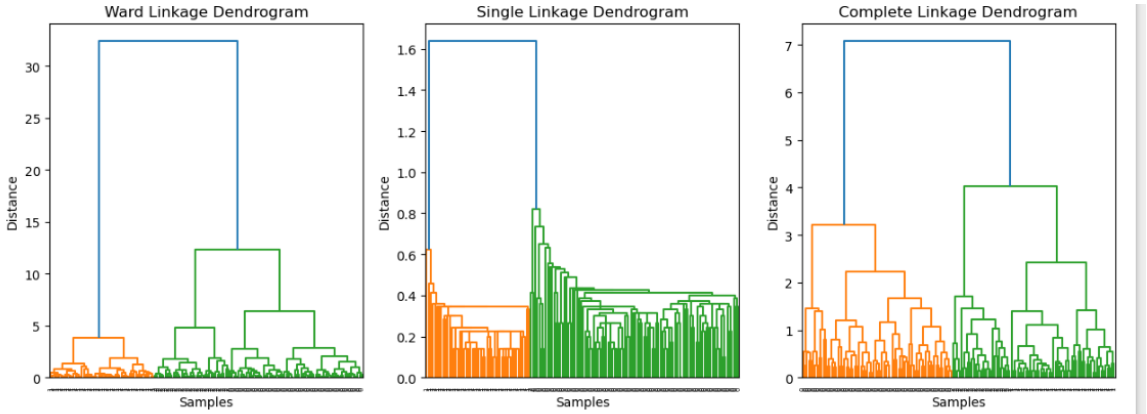
Output:-

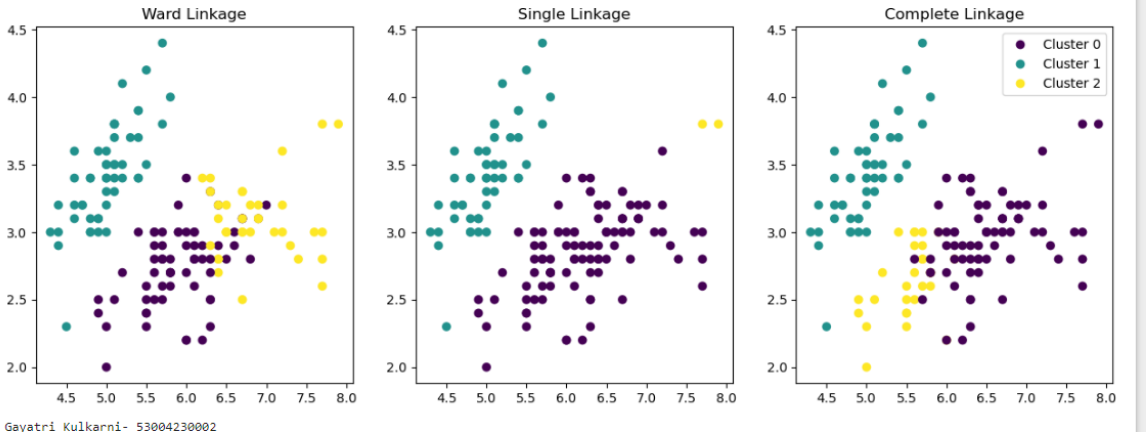
```
Cluster Descriptions (Ward Linkage):
Clusters based on Ward linkage interpretation.
Cluster Descriptions (Single Linkage):
Cluster based on Single linkage interpretation.
Cluster Descriptions (Complete Linkage):
Clusters based on Complete linkage interpretation.
Accuracy: 1.0
Confusion Matrix:
 [[10  0  0]
 [ 0  9  0]
 [ 0  0 11]]
Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        10
           1       1.00      1.00      1.00         9
           2       1.00      1.00      1.00        11

    accuracy                           1.00        30
   macro avg       1.00      1.00      1.00        30
weighted avg       1.00      1.00      1.00        30
```






```
Gayatri Kulkarni- 53004230002
```





Gayatri Kulkarni- 53004230002

Practical 4b

Aim:- Implement the Rule based method and test the same.

Theory:-

Rule-Based Methods are a type of artificial intelligence and machine learning approach that uses a set of "if-then" rules to make decisions, classify data, or derive insights from datasets. These methods are particularly useful in applications where human expertise can be encoded into a systematic approach, making them highly interpretable and easy to understand.

Rules: The fundamental building blocks of rule-based systems. A rule typically consists of two parts:

- **Condition (Antecedent)**: The "if" part of the rule, specifying a condition that must be satisfied.
- **Conclusion (Consequent)**: The "then" part of the rule, specifying the action to be taken or the result to be achieved if the condition is met.

 For example:

- **Rule**: If a customer's age is greater than 30 and their income is above $50,000, then classify them as a "high-income customer."

Knowledge Base: A collection of rules that govern the decision-making process. This knowledge base can be created through domain expertise or learned from data using various algorithms.

Inference Engine: The component that applies the rules to the knowledge base and makes decisions or classifications based on the given input data. It evaluates the rules and determines which ones are applicable.

Explanation Facility: This provides insight into how a decision was made based on the rules applied. It enhances the interpretability of the system and helps users understand the reasoning behind specific outcomes.

Code:-

```
import numpy as np

from sklearn.datasets import load_iris

from sklearn.model_selection import train_test_split
```

```
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report


#Load the Iris dataset
iris = load_iris()
X = iris.data
y = iris.target


#Split the data for testing
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)


#Define a simple rule-based classifier function
def rule_based_classifier(x):
    if x[2] < 2.0:
        rule = "If feature 2 < 2.0, assign to Classd 0"
        return 0 # Class 0
    elif x[3] > 1.5:
        rule = "If feature 2 >= 2.0 and feature 3 > 1.5, assign to Class 2"
        return 2 # Class 2
    else:
        rule = "If feature 2 >= 2.0 and feature 3 <=1.5, assign to Class 1"
        return 1 # Class 1
    print("Rule:", rule)


# Apply the rule-based classifier to make predictions on the test set
y_pred = [rule_based_classifier(x) for x in X_test]
```

```
# Calculate accuracy, confusion matrix, and classification report
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
classification_rep = classification_report(y_test, y_pred, target_names=iris.target_names)

# Print the results
print("Accuracy:", accuracy)
print("Confusion Matrix:\n", conf_matrix)
print("Classification Report:\n", classification_rep)
print("Gayatri Kulkarni - 53004230002")
```

Output:-

```
Accuracy: 0.9666666666666667
Confusion Matrix:
 [[10  0  0]
 [ 0  8  1]
 [ 0  0 11]]
Classification Report:
              precision    recall  f1-score   support

      setosa       1.00      1.00      1.00        10
  versicolor       1.00      0.89      0.94         9
   virginica       0.92      1.00      0.96        11

    accuracy                           0.97        30
   macro avg       0.97      0.96      0.97        30
weighted avg       0.97      0.97      0.97        30

Gayatri Kulkarni - 53004230002
```

Practical 4c

Aim:- Write a program to construct a Bayesian network considering medical data. Use this model to demonstrate the diagnosis of heart patients using standard Heart Disease Data Set.

Theory:-

Bayesian Networks (also known as **Bayesian Belief Networks** or **Bayesian Models**) are probabilistic graphical models that represent a set of variables and their conditional dependencies using a directed acyclic graph (DAG). These networks allow for the representation of complex relationships between random variables, making them useful in various fields such as machine learning, artificial intelligence, decision-making, and data analysis.

- **Nodes**: Each node in the graph represents a random variable, which can be discrete or continuous. The variable can represent observable quantities, latent variables, or even hypotheses.

- **Edges**: Directed edges between nodes indicate a probabilistic relationship, showing how one variable influences another. An edge from node A to node B implies that A is a parent of B, suggesting that the probability of B depends on the state of A.

- **Conditional Probability Distributions**: Each node has an associated conditional probability distribution (CPD) that quantifies the effect of its parent nodes on the node itself. For a node with no parents, the CPD is simply the prior probability of that node.

- **Directed Acyclic Graph (DAG)**: The structure of a Bayesian Network is represented as a DAG, ensuring that there are no cycles. This property guarantees that the dependencies between variables are well-defined.

Bayesian Networks offer a powerful framework for modeling uncertainty and making probabilistic inferences in complex systems. Their ability to represent relationships between variables through a directed acyclic graph makes them valuable in a wide range of applications. Despite some challenges in structure learning and scalability, Bayesian Networks remain a fundamental tool in data-driven decision-making and artificial intelligence.

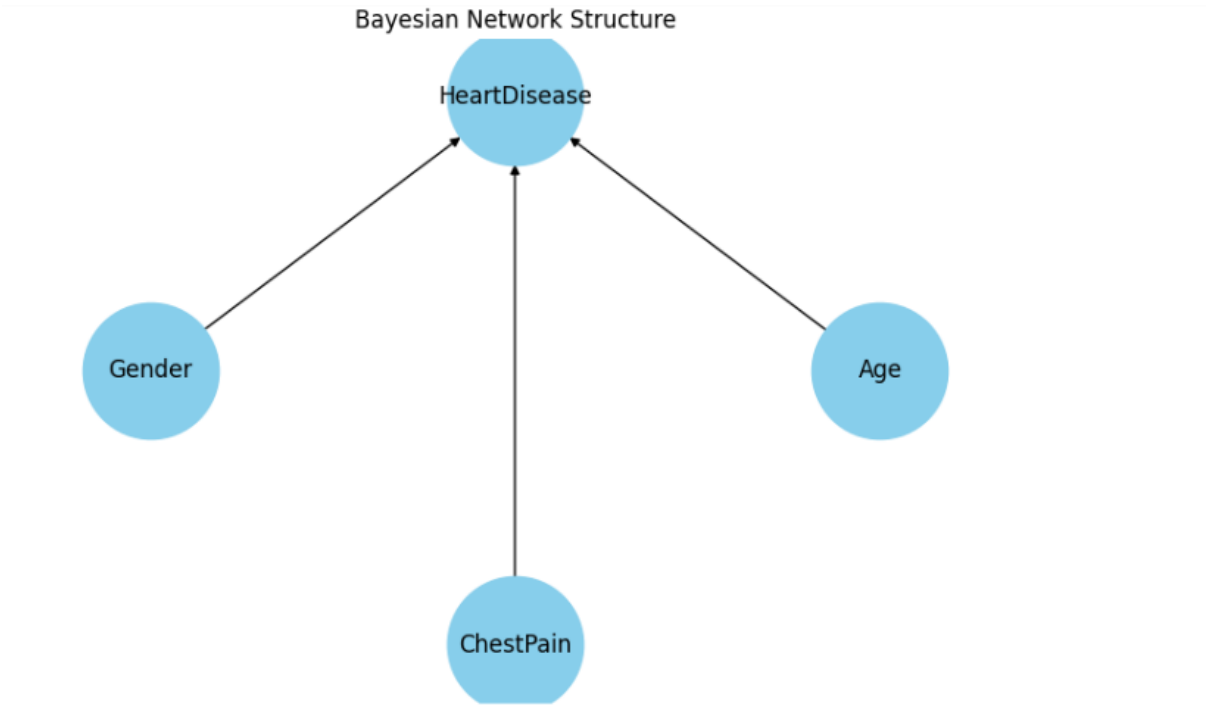
Code:-

```
import numpy as np
import pandas as pd
from pgmpy.models import BayesianNetwork
from pgmpy.estimators import ParameterEstimator, MaximumLikelihoodEstimator
from pgmpy.inference import VariableElimination
import networkx as nx
import matplotlib.pyplot as plt

data = pd.DataFrame (data={'Age': [30, 40, 50, 60, 70],
                    'Gender': ['Male', 'Female', 'Male', 'Female', 'Male'],
                    'ChestPain': ['Typical', 'Atypical', 'Typical', 'Atypical', 'Typical'],
                    'HeartDisease': ['Yes', 'No', 'Yes', 'No', 'Yes']})
model = BayesianNetwork([('Age', 'HeartDisease'),
                    ('Gender', 'HeartDisease'),
                    ('ChestPain', 'HeartDisease')])

model.fit(data, estimator=MaximumLikelihoodEstimator)

pos = nx.circular_layout(model)
nx.draw(model, pos, with_labels=True, node_size=5000, node_color="skyblue", font_size=12, font_color="black")
plt.title("Bayesian Network Structure")
plt.show()

for cpd in model.get_cpds():
```

```
print("CPD of", cpd.variable)
print(cpd)
```

```
inference = VariableElimination(model)
query = inference.query(variables=['HeartDisease'], evidence={'Age':50, 'Gender': 'Male', 'ChestPain': 'Typical'})
print(query)
print("Gayatri Kulkarni -53004230002")
```

Output:-




```
CPD of Age
+---------+-----+
| Age(30) | 0.2 |
+---------+-----+
| Age(40) | 0.2 |
+---------+-----+
| Age(50) | 0.2 |
+---------+-----+
| Age(60) | 0.2 |
+---------+-----+
| Age(70) | 0.2 |
+---------+-----+
```

CPD of HeartDisease

Age	Age(30)	...	Age(70)	Age(70)
ChestPain	ChestPain(Atypical)	...	ChestPain(Typical)	ChestPain(Typical)
Gender	Gender(Female)	...	Gender(Female)	Gender(Male)
HeartDisease(No)	0.5	...	0.5	0.0
HeartDisease(Yes)	0.5	...	0.5	1.0

CPD of Gender

Gender(Female)	0.4
Gender(Male)	0.6

CPD of ChestPain

ChestPain(Atypical)	0.4
ChestPain(Typical)	0.6

HeartDisease	phi(HeartDisease)
HeartDisease(No)	0.0000
HeartDisease(Yes)	1.0000

Gayatri Kulkarni -53004230002

Practical 4d

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

Theory:-

Locally Weighted Regression (LWR), also known as **Locally Weighted Scatterplot Smoothing (LOWESS)** or **LOESS**, is a non-parametric regression technique that fits multiple regressions in localized subsets of the data to create a smooth curve through a scatterplot of the data. This approach is particularly useful when the relationship between the independent and dependent variables is complex and cannot be adequately captured by traditional parametric models.

- **Non-Parametric Nature**: Unlike parametric methods that assume a specific functional form for the relationship between variables (e.g., linear, quadratic), non-parametric methods like LWR do not assume any global structure. Instead, they focus on local relationships, making them flexible for capturing intricate patterns in data.

- **Locally Weighted**: LWR fits a separate regression line to a subset of data points that are near the target point (the point where the prediction is being made). The weight assigned to each data point is based on its distance from the target point, with closer points receiving higher weights. This local approach allows LWR to adapt to changes in the underlying data structure.

- **Kernel Function**: The weighting is often done using a kernel function, such as the **Gaussian kernel**, which assigns weights that decrease with distance. The bandwidth (or the width of the kernel) controls how many points influence the estimate and how localized the fit is. A smaller bandwidth results in a more sensitive fit, while a larger bandwidth yields a smoother curve.

The process of Locally Weighted Regression can be summarized in the following steps:

1. **Select a Point**: Choose the point xxx at which you want to predict the value of the dependent variable.
2. **Calculate Weights**: For each data point (xi,yi) in the dataset, calculate the weight wi using a kernel function:

$wi=K(x,xi, \tau)$

where K is the kernel function, and τ is the bandwidth parameter.

3. **Fit Local Model**: Fit a weighted linear regression model using the weights calculated in the previous step. This involves minimizing the weighted sum of squared errors:

$$\hat{y}(x) = \arg\min_{\beta} \sum_{i=1}^{n} w_i (y_i - \beta^T x_i)^2$$

4. **Make Prediction**: Use the fitted model to predict the value of the dependent variable at the point xxx.
5. **Repeat**: Repeat the process for each point of interest to construct the overall fitted curve.

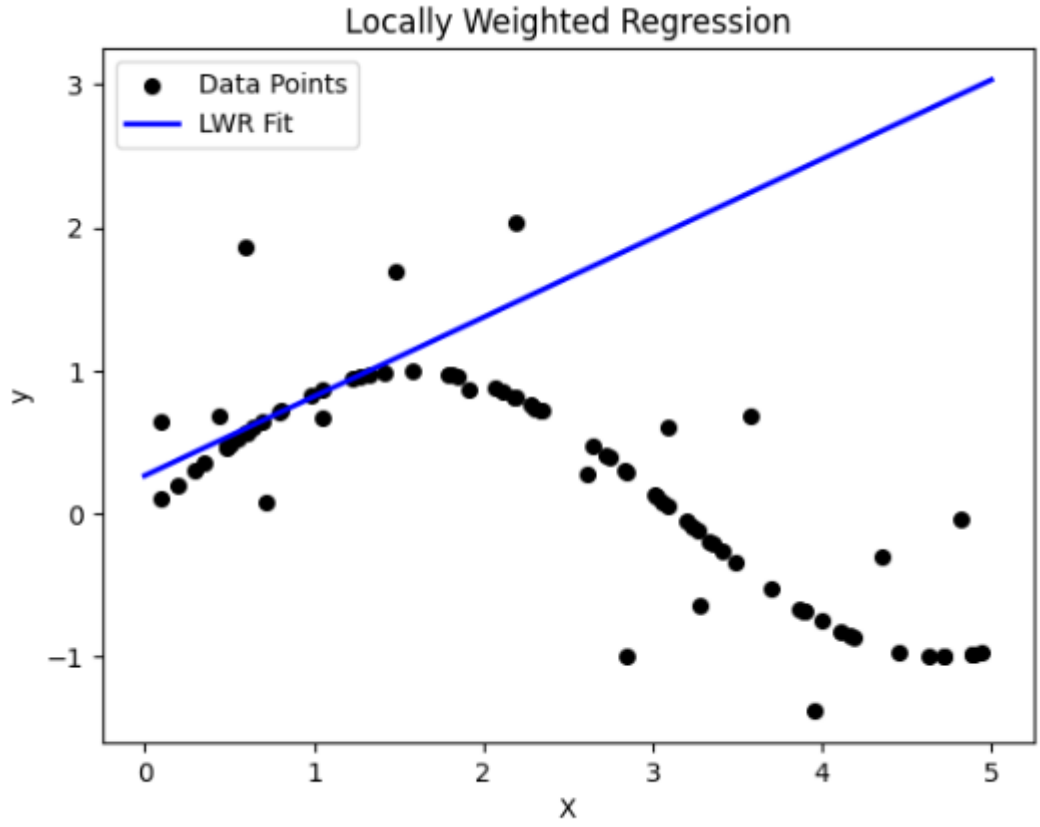
Code:-

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


# Seed for reproducibility
np.random.seed(0)


# Generate random dataset
X = np.sort(5 * np.random.rand(80, 1), axis=0)
y = np.sin(X).ravel()
y[::5] += 3 * (0.5 - np.random.rand(16))


# Locally Weighted Regression function
def locally_weighted_regression(query_point, X, y, tau=0.1):
    m = X.shape[0]
    # Calculate weights
    weights = np.exp(-((X - query_point) * 2).sum(axis=1) / (2 * tau * 2))
    W = np.diag(weights)
```

```
    # Add bias term to X
    X_bias = np.c_[np.ones((m, 1)), X]

    # Calculate theta using weighted least squares
    theta = np.linalg.inv(X_bias.T.dot(W).dot(X_bias)).dot(X_bias.T).dot(W).dot(y)

    # Predict for query_point
    x_query = np.array([1, query_point])
    prediction = x_query.dot(theta)
    return prediction

# Generate test points
X_test = np.linspace(0, 5, 100)

# Predict using locally weighted regression
predictions = [locally_weighted_regression(query_point, X, y, tau=0.1) for query_point in X_test]

# Plot results
plt.scatter(X, y, color='black', s=30, marker='o', label='Data Points')
plt.plot(X_test, predictions, color='blue', linewidth=2, label='LWR Fit')
plt.xlabel('X')
plt.ylabel('y')
plt.title('Locally Weighted Regression')
plt.legend()
plt.show()
```

print('Gayatri Kulkarni- 53004230002')

Output:-




```
Gayatri Kulkarni- 53004230002
```

Practical 1 EXTRA

Aim:- XOR NEURAL NETWORKS

Theory:-

Code:-

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


# Sigmoid activation function and its derivative
def sigmoid(x):
    return 1 / (1 + np.exp(-x))
```

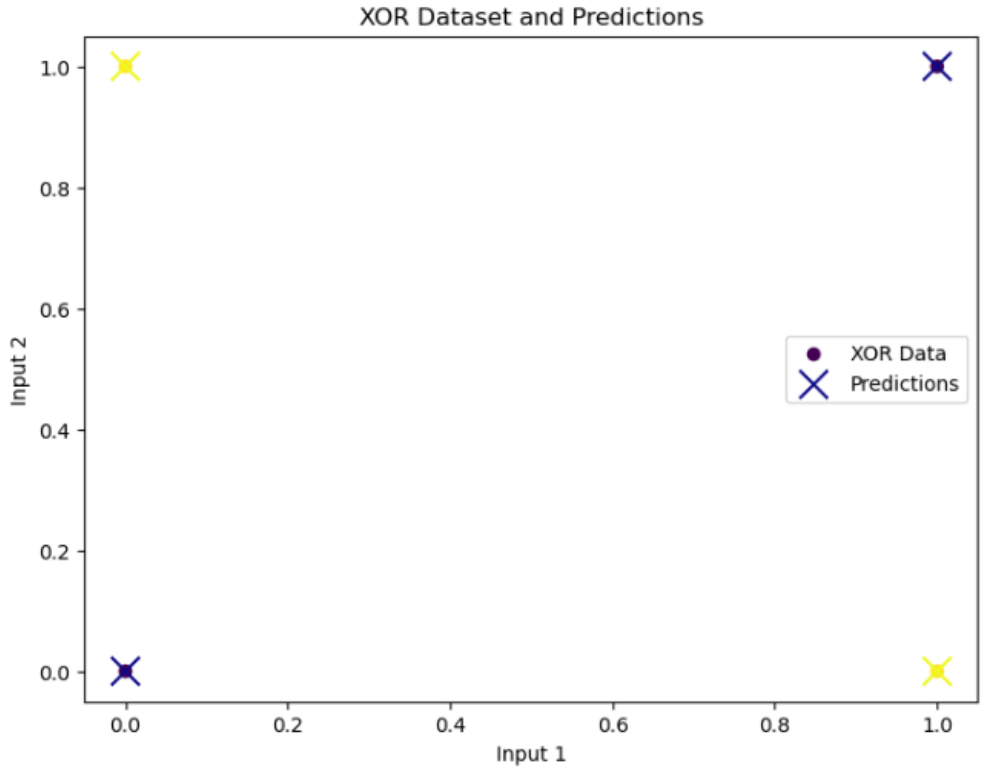
```
def sigmoid_derivative(x):
    return x * (1 - x)

# Define the neuralNetwork class
class NeuralNetwork:
    def __init__(self, input_size, hidden_size, output_size):
        #Initialize weights with random values
        self.weights_input_hidden = np.random.uniform(size=(input_size, hidden_size))
        self.weights_hidden_output = np.random.uniform(size=(hidden_size, output_size))

    def forward(self, X):
        #Forward propagation
        self.hidden_input = np.dot(X, self.weights_input_hidden)
        self.hidden_output = sigmoid(self.hidden_input)
        self.output = sigmoid(np.dot(self.hidden_output, self.weights_hidden_output))
        return self.output

    def backward(self, X, y, learning_rate):
        #Backpropagation
        error_output = y-self.output
        delta_output = error_output * sigmoid_derivative(self.output)

        error_hidden = delta_output.dot(self.weights_hidden_output.T)
        delta_hidden = error_hidden * sigmoid_derivative(self.hidden_output)
```

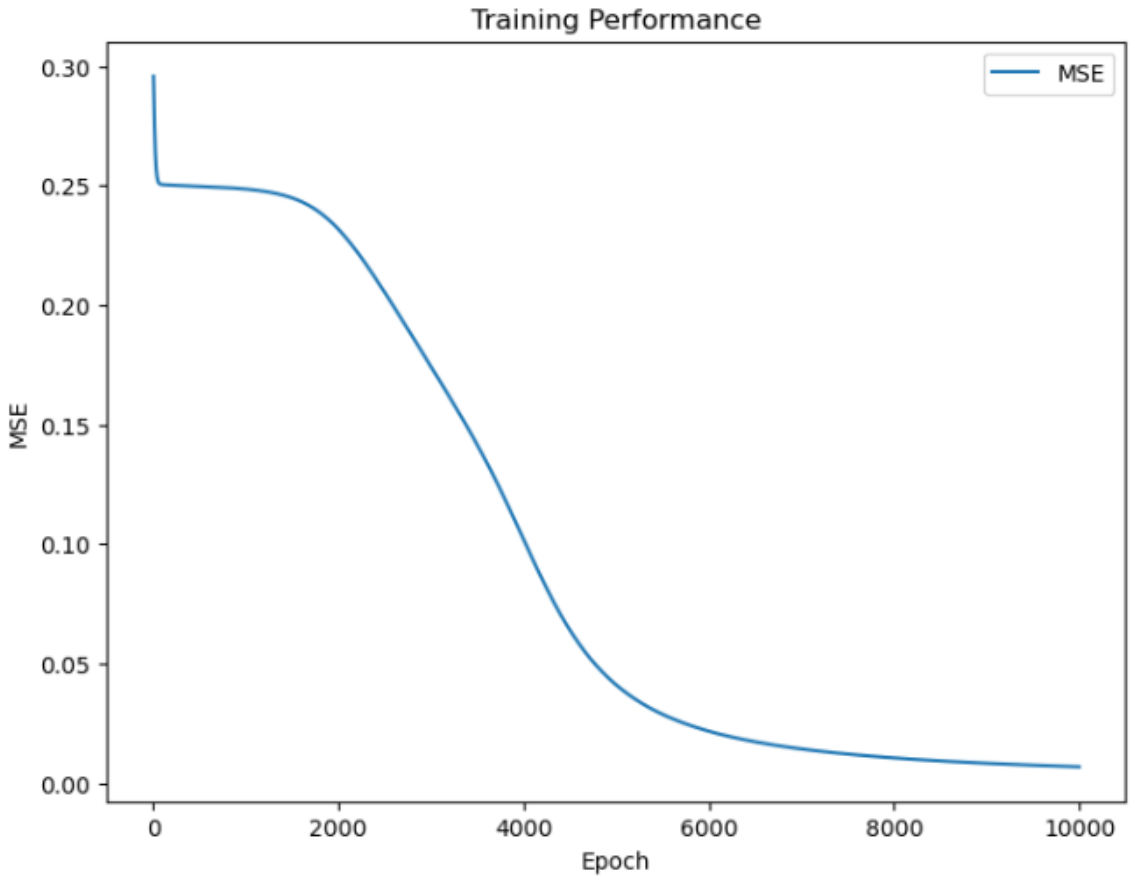
```
        self.weights_hidden_output += self.hidden_output.T.dot(delta_output) *
learning_rate
        self.weights_input_hidden += X.T.dot(delta_hidden) * learning_rate

    def train(self, X, y, learning_rate, epochs):
        self.loss_history = [] #Track loss dusring training
        for _ in range(epochs):
            output = self.forward(X)
            error = y-output
            self.loss_history.append(np.mean(error**2)) #Track MSE
            self.backward(X, y, learning_rate)

    def predict(self, X):
        return self.forward(X)

#XOR dataset
X = np.array([[0, 0], [0, 1], [1, 0],[1, 1]])
y = np.array([[0], [1], [1], [0]])

#Initalize and train the neural network
input_size = 2
hidden_size = 4
output_size = 1
learning_rate = 0.1
epochs = 10000

nn = NeuralNetwork(input_size, hidden_size, output_size)
nn.train(X, y, learning_rate, epochs)
```

```
#Make predictions
predictions = nn.predict(X)

#Plot the XOR dataset and predictions
plt.figure(figsize=(8, 6))
plt.scatter(X[:,0], X[:,1], c=y, cmap='viridis', label='XOR Data')
plt.scatter(X[:,0], X[:,1], c=np.round(predictions), cmap='plasma', marker='x', s=200, label='Predictions')
plt.title('XOR Dataset and Predictions')
plt.xlabel('Input 1')
plt.ylabel('Input 2')
plt.legend()

#PLot the performance (MSE) during training
plt.figure(figsize=(8,6))
plt.plot(nn.loss_history, label='MSE')
plt.title('Training Performance')
plt.xlabel('Epoch')
plt.ylabel('MSE')
plt.legend()

# Print predictions and actual values
for i in range(len(X)):
    print(f"Input: {X[i]}, Actual: {y[i]}, Predicted: {np.round(predictions[i])}")

plt.show()
print("Gayatri Kulkarni -53004230002")
```

Output:-

```
Input: [0 0], Actual: [0], Predicted: [0.]
Input: [0 1], Actual: [1], Predicted: [1.]
Input: [1 0], Actual: [1], Predicted: [1.]
Input: [1 1], Actual: [0], Predicted: [0.]
```





Gayatri Kulkarni -53004230002

Practical 2 Extra

Aim:- Linear Regression

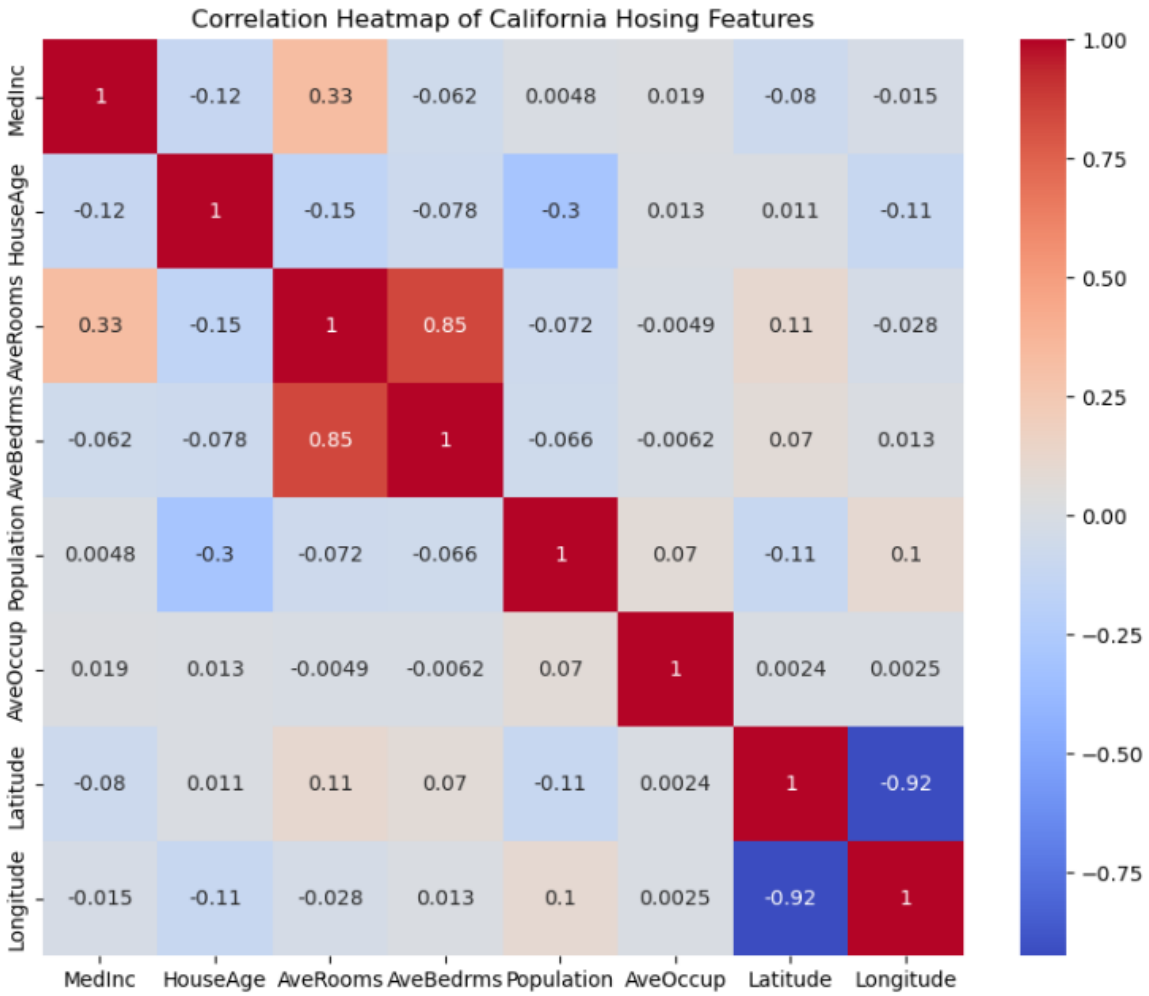
Theory:-

Code:-

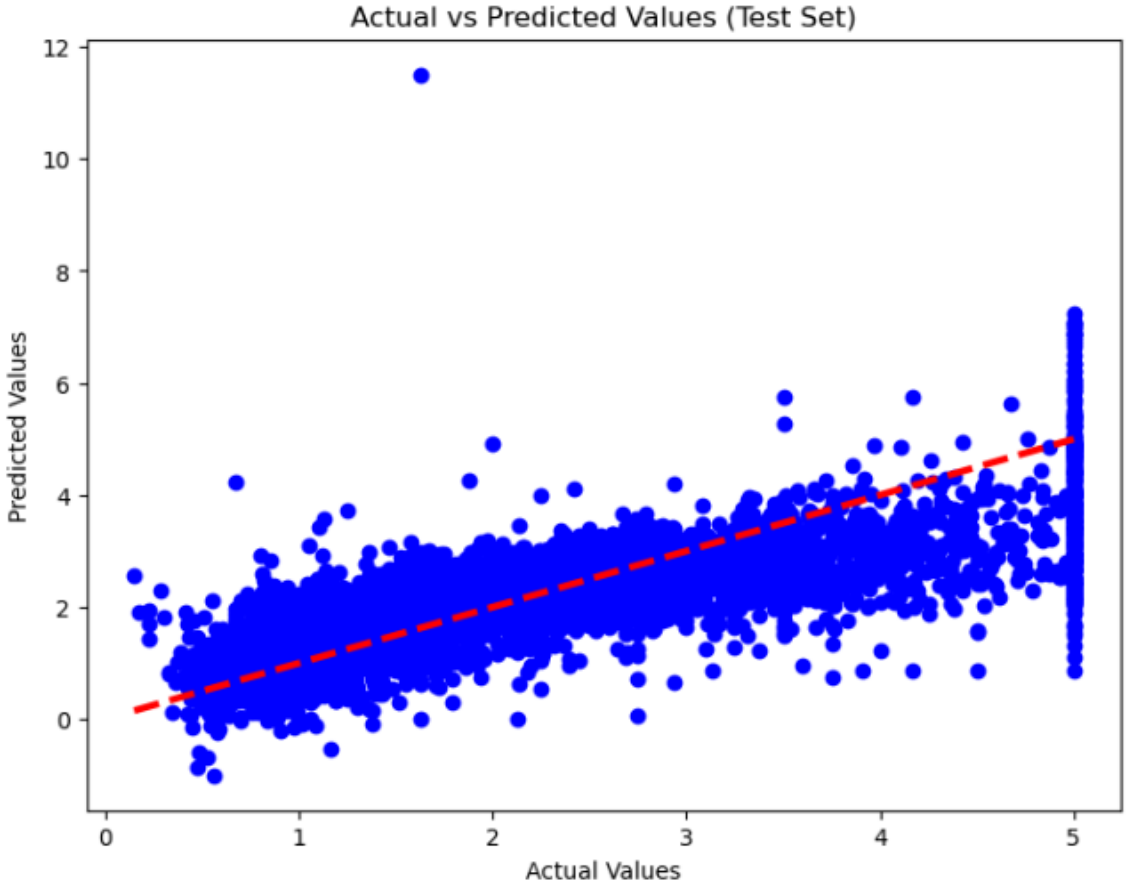
```
#Import necessary libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error, r2_score
```

```
from sklearn.datasets import fetch_california_housing

#Load California Hosuing dataset
housing = fetch_california_housing()
X = pd.DataFrame(housing.data, columns=housing.feature_names)
y = pd.DataFrame(housing.target, columns=['MEDV'])

#Visualise dataset correlation heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(X.corr(), annot=True, cmap='coolwarm')
plt.title("Correlation Heatmap of California Hosing Features")
plt.show()

#Split the dataset into training and testingf sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,
random_state=42)

#Implement Least Squares Regression (Linear Regression)
reg_model = LinearRegression()
reg_model.fit(X_train, y_train)


#Make predictions
y_train_pred = reg_model.predict(X_train)
y_test_pred = reg_model.predict(X_test)

#Generate relevant metrics
train_mse = mean_squared_error(y_train, y_train_pred)
```

```
test_mse = mean_squared_error(y_test, y_test_pred)
train_r2 = r2_score(y_train, y_train_pred)
test_r2 = r2_score(y_test, y_test_pred)

 #Print the results

print(f"Training Mean Squared Error: {train_mse}")
print(f"Test Mean Squared Error: {test_mse}")
print(f"Training R^2 Score: {train_r2}")
print(f"Test R^2 Score: {test_r2}")

# Visualise regression coefficients
coefficients = pd.DataFrame(reg_model.coef_.T, X.columns,
columns=['Coefficient'])
print(coefficients)



#Plot predicted vs actual values for test set
plt.figure(figsize=(8,6))
plt.scatter(y_test, y_test_pred, c='blue')
plt.plot([y_test.min(), y_test.max()], [y_test.min(), y_test.max()], '--r', lw=3)
plt.xlabel("Actual Values")
plt.ylabel("Predicted Values")
plt.title("Actual vs Predicted Values (Test Set)")
plt.show()
print("Gayatri Kulkarni - 5300423002")
```


Correlation Heatmap of California Hosing Features
MedInc
HouseAge
AveRooms
AveBedrms
Population
AveOccup
Latitude
Longitude
1 -0.12 0.33 -0.062 0.0048 0.019 -0.08 -0.015
-0.12 1 -0.15 -0.078 -0.3 0.013 0.011 -0.11
0.33 -0.15 1 0.85 -0.072 -0.0049 0.11 -0.028
-0.062 -0.078 0.85 1 -0.066 -0.0062 0.07 0.013
0.0048 -0.3 -0.072 -0.066 1 0.07 -0.11 0.1
0.019 0.013 -0.0049 -0.0062 0.07 1 0.0024 0.0025
-0.08 0.011 0.11 0.07 -0.11 0.0024 1 -0.92
-0.015 -0.11 -0.028 0.013 0.1 0.0025 -0.92 1
MedInc
HouseAge
AveRooms
AveBedrms
Population
AveOccup
Latitude
Longitude
1.00
0.75
0.50
0.25
0.00
−0.25
−0.50
−0.75

```
Training Mean Squared Error: 0.5233576288267755
Test Mean Squared Error: 0.5305677824766752
Training R^2 Score: 0.6093459727972159
Test R^2 Score: 0.5957702326061665
              Coefficient
MedInc       4.458226e-01
HouseAge     9.681868e-03
AveRooms    -1.220951e-01
AveBedrms    7.785996e-01
Population -7.757404e-07
AveOccup    -3.370027e-03
Latitude    -4.185367e-01
Longitude   -4.336880e-01
```



Gayatri Kulkarni - 5300423002