Program 01

1.Program on data wrangling: Combining and merging datasets, Reshaping and Pivoting

Source code:

```
# Import necessary libraries

import pandas as pd

importnumpy as np


# 1. Combining and Merging Datasets


# Create two sample DataFrames

sales_data_1 = pd.DataFrame({

   'OrderID': [1, 2, 3, 4],

   'Product': ['Laptop', 'Tablet', 'Smartphone', 'Headphones'],

   'Sales': [1200, 800, 1500, 300]

})


sales_data_2 = pd.DataFrame({

   'OrderID': [3, 4, 5, 6],

   'Product': ['Smartphone', 'Headphones', 'Smartwatch', 'Tablet'],

   'Sales': [1500, 300, 200, 900]

})


# Display the DataFrames

print("Sales Data 1:\n", sales_data_1)

print("\nSales Data 2:\n", sales_data_2)


# Merge DataFrames based on 'OrderID' using an inner join
```

```
merged_data = pd.merge(sales_data_1, sales_data_2, on='OrderID', how='inner',
suffixes=('_left', '_right'))
print("\nMerged Data (Inner Join):\n", merged_data)

# Concatenate the DataFrames vertically
combined_data = pd.concat([sales_data_1, sales_data_2], ignore_index=True)
print("\nCombined Data (Concatenated Vertically):\n", combined_data)

# 2. Reshaping Data with Melt

# Create a sample DataFrame for reshaping
reshaping_data = pd.DataFrame({
    'Month': ['Jan', 'Feb', 'Mar'],
    'Product_A': [100, 150, 130],
    'Product_B': [90, 80, 120]
})

print("\nReshaping Data (Original):\n", reshaping_data)

# Melt the DataFrame to reshape it from wide to long format
melted_data = pd.melt(reshaping_data, id_vars=['Month'], var_name='Product',
value_name='Sales')
print("\nMelted Data (Long Format):\n", melted_data)

# 3. Pivoting Data

# Create a sample DataFrame for pivoting
pivot_data = pd.DataFrame({
    'Month': ['Jan', 'Jan', 'Feb', 'Feb', 'Mar', 'Mar'],
    'Product': ['Product_A', 'Product_B', 'Product_A', 'Product_B', 'Product_A', 'Product_B'],
```

```
    'Sales': [100, 90, 150, 80, 130, 120]
})

print("\nPivot Data (Original):\n", pivot_data)

# Pivot the DataFrame to reshape it back to wide format
pivoted_data = pivot_data.pivot(index='Month', columns='Product', values='Sales')
print("\nPivoted Data (Wide Format):\n", pivoted_data)

# 4. Handling Missing Data

# Introduce some missing values
pivoted_data.loc['Feb', 'Product_A'] = np.nan
pivoted_data.loc['Mar', 'Product_B'] = np.nan
print("\nPivoted Data with Missing Values:\n", pivoted_data)

# Fill missing values with the mean of each column
filled_data = pivoted_data.fillna(pivoted_data.mean())
print("\nFilled Data (Missing Values Handled):\n", filled_data)

# 5. Summary Statistics
print("\nSummary Statistics of Filled Data:\n", filled_data.describe())
```

Sample output:

```
Sales Data 1:
OrderIDProduct  Sales
0       1       Laptop   1200
1       2       Tablet    800
```

2 3 Smartphone 1500

3 4 Headphones 300

Sales Data 2:

OrderIDProduct Sales

0 3 Smartphone 1500

1 4 Headphones 300

2 5 Smartwatch 200

3 6 Tablet 900

Merged Data (Inner Join):

OrderIDProduct_leftSales_leftProduct_rightSales_right

0 3 Smartphone 1500 Smartphone 1500

1 4 Headphones 300 Headphones 300

Combined Data (Concatenated Vertically):

OrderIDProduct Sales

0 1 Laptop 1200

1 2 Tablet 800

2 3 Smartphone 1500

3 4 Headphones 300

4 3 Smartphone 1500

5 4 Headphones 300

6 5 Smartwatch 200

7 6 Tablet 900

Reshaping Data (Original):

Month Product_AProduct_B

0 Jan 100 90

1 Feb 150 80

2 Mar 130 120

Melted Data (Long Format):

	Month	Product	Sales
0	Jan	Product_A	100
1	Feb	Product_A	150
2	Mar	Product_A	130
3	Jan	Product_B	90
4	Feb	Product_B	80
5	Mar	Product_B	120

Pivot Data (Original):

	Month	Product	Sales
0	Jan	Product_A	100
1	Jan	Product_B	90
2	Feb	Product_A	150
3	Feb	Product_B	80
4	Mar	Product_A	130
5	Mar	Product_B	120

Pivoted Data (Wide Format):

Product	Product_A	Product_B
Month		
Jan	100.0	90.0
Feb	150.0	80.0
Mar	130.0	120.0

Pivoted Data with Missing Values:

Product Product_AProduct_B

Month

Jan 100.0 90.0

Feb NaN 80.0

Mar 130.0 NaN

Filled Data (Missing Values Handled):

Product Product_AProduct_B

Month

Jan 100.0 90.0

Feb 126.7 80.0

Mar 130.0 110.0

Summary Statistics of Filled Data:

Product_AProduct_B

count 3.0 3.0

mean 118.9 93.3

std 15.6 15.3

min 100.0 80.0

25% 113.3 85.0

50% 126.7 90.0

75% 128.3 100.0

max 130.0 110.0

Explanation:

Combining: Joining data from multiple sources into one dataset.

Merging: Similar to SQL joins (e.g., inner, outer, left, right join).

Reshaping: Changing the layout of the data, e.g., from wide to long format or vice versa.

Pivoting: Rearranging data based on unique values of a column to create a summary table.

Program 02

2.a. Program on Data Transformation: String Manipulation.

Source code:

String Manipulation:

```
# Sample text to work with
text = "  Hello, World! Welcome to Python programming.  "

# 1. Strip leading and trailing spaces
clean_text = text.strip()
print(f"Original Text: '{text}'")
print(f"Text after stripping spaces: '{clean_text}'")

# 2. Convert the text to uppercase
upper_text = clean_text.upper()
print(f"\nText in uppercase: '{upper_text}'")

# 3. Convert the text to lowercase
lower_text = clean_text.lower()
print(f"\nText in lowercase: '{lower_text}'")

# 4. Count occurrences of a substring (e.g., "o")
count_o = clean_text.count("o")
print(f"\nNumber of occurrences of 'o': {count_o}")

# 5. Replace a word in the string
replaced_text = clean_text.replace("Python", "Data Science")
```

```
print(f"\nText after replacing 'Python' with 'Data Science': '{replaced_text}'")

# 6. Find the position of a word in the string
position_world = clean_text.find("World")
print(f"\nPosition of 'World' in the text: {position_world}")

# 7. Split the text into words (by default on spaces)
words = clean_text.split()
print(f"\nList of words in the text: {words}")

# 8. Join the words back into a single string
joined_text = " ".join(words)
print(f"\nText after joining words: '{joined_text}'")

# 9. Check if the text starts with "Hello"
starts_with_hello = clean_text.startswith("Hello")
print(f"\nDoes the text start with 'Hello'? {starts_with_hello}")

# 10. Check if the text ends with a specific word (e.g., "programming.")
ends_with_programming = clean_text.endswith("programming.")
print(f"\nDoes the text end with 'programming.'? {ends_with_programming}")
```

Sample output:

```
Original Text: '  Hello, World! Welcome to Python programming.  '
Text after stripping spaces: 'Hello, World! Welcome to Python programming.'

Text in uppercase: 'HELLO, WORLD! WELCOME TO PYTHON PROGRAMMING.'

Text in lowercase: 'hello, world! welcome to python programming.'
```

Number of occurrences of 'o': 5

Text after replacing 'Python' with 'Data Science': 'Hello, World! Welcome to Data Science programming.'

Position of 'World' in the text: 7

List of words in the text: ['Hello,', 'World!', 'Welcome', 'to', 'Python', 'programming.']

Text after joining words: 'Hello, World! Welcome to Python programming.'

Does the text start with 'Hello'? True

Does the text end with 'programming.'? True

Explanation:

Python program involves various string manipulation techniques using built-in string functions such as:

- Convert the string to uppercase.
- Convert the string to lowercase.
- Replace a specific substring with another.
- Split the string into a list of words.
- Reverse the string.
- Remove leading and trailing whitespaces.
- Check if the string starts with a specific substring.
- Count occurrences of a substring.
- Capitalize the first letter of the string.
- Find the position of a substring.

Python offers several built-in methods to manipulate strings, such as:

- **Splitting** (split()): Breaks a string into a list.
- **Joining** (join()): Combines a list of strings into a single string.

- **Replacing** (replace()): Replaces a substring with another substring.
- **Case transformation** (lower(), upper()): Converts the string to lowercase or uppercase.
- **Slicing**: Extracting parts of strings by specifying start and end positions

2.b. Program on Data Transformation: Regular Expressions

Source code:

```
import re

# Sample text

text = """

John's email is [email protected]. He said, "Python is awesome!!"  It's a  great  language.

Another email: [email protected].

"""

# 1. Remove special characters except for spaces and email-related characters.

# Using regex to remove non-alphabetic characters and non-email symbols

clean_text = re.sub(r"[^a-zA-Z0-9@\.\s]", "", text)

print("Text after removing special characters:")

print(clean_text)


# 2. Convert the text to lowercase

clean_text = clean_text.lower()

print("\nText after converting to lowercase:")

print(clean_text)

# 3. Replace multiple spaces with a single space

clean_text = re.sub(r"\s+", " ", clean_text)

print("\nText after replacing multiple spaces:")

print(clean_text)


# 4. Extract all words starting with a vowel (a, e, i, o, u)
```

```
vowel_words = re.findall(r"\b[aeiouAEIOU]\w+", clean_text)

print("\nWords starting with a vowel:")

print(vowel_words)


# 5. Replace email addresses with '[email protected]'

masked_text = re.sub(r"\b[A-Za-z0-9._%+-]+@[A-Za-z0-9.-]+\.[A-Z|a-z]{2,}\b", "[email protected]", clean_text)

print("\nText after replacing emails:")

print(masked_text)
```

Explanation:

Regular Expressions:

- **Definition** A regular expression (RegEx) is a sequence of characters that defines a search pattern, mainly for matching strings.
- **Functionality** Python's `re` module allows you to check if a string matches a specific pattern defined by a regular expression, letting you find, replace, or split strings.
- **Usage** Regular expressions are powerful for pattern matching, enabling operations like validating email formats, searching for specific sequences, and more.

- **Searching**: Finding whether a pattern exists in a string (`re.search()`).
- **Matching**: Checking if a string fully matches a pattern (`re.match()`).
- **Finding all matches**: Extracting all occurrences of a pattern in a string (`re.findall()`).
- **Substituting**: Replacing parts of a string that match a pattern (`re.sub()`).

Sample Output:

```
Text after removing special characters:

johns email is john.doe@example.com. he said python is awesome its a great language another email jane@example.com
```

Text after converting to lowercase:

johns email is john.doe@example.com. he said python is awesome its a great language another email jane@example.com

Text after replacing multiple spaces:

johns email is john.doe@example.com. he said python is awesome its a great language another email jane@example.com

Words starting with a vowel:

['email', 'is', 'awesome', 'another', 'email']

Text after replacing emails:

johns email is . he said python is awesome its a great language another email

Explanation :

1. **Remove Special Characters**:
   - We use re.sub() to substitute all characters that are not alphabetic, numeric, or email-related symbols (like @ and .). The pattern [^a-zA-Z0-9@\.\s] matches any character not within the alphabet or specified symbols.
2. **Convert to Lowercase**:
   - The built-in method lower() is used to convert all characters to lowercase, standardizing the text for further processing.
3. **Replace Multiple Spaces**:
   - Regex \s+ matches one or more whitespace characters. We replace them with a single space, ensuring uniform spacing between words.
4. **Extract Words Starting with a Vowel**:
   - Using re.findall(), we search for all words starting with a vowel using the regex pattern \b[aeiouAEIOU]\w+. Here, \b ensures that we are matching the beginning of a word.
5. **Replace Email Addresses**:
   - The regex pattern \b[A-Za-z0-9._%+-]+@[A-Za-z0-9.-]+\.[A-Z|a-z]{2,}\b is designed to match email addresses. We replace any matches with the string .

Program 03

3.Program on Time series: GroupBy Mechanics to display in data vector, multivariate time series and forecasting formats

Source code:

```
import pandas as pd
importnumpy as np
importmatplotlib.pyplot as plt
fromstatsmodels.tsa.holtwinters import ExponentialSmoothing

# Create sample time series data
np.random.seed(42)
date_range = pd.date_range(start="2022-01-01", end="2023-01-01", freq="D")
data = pd.DataFrame({
    "Date": date_range,
    "Value_A": np.random.normal(100, 10, len(date_range)),
    "Value_B": np.random.normal(200, 20, len(date_range)),
})

# Set Date as the index
data.set_index("Date", inplace=True)

# GroupBy Mechanics
defgroupby_mechanics(data):
print("\n--- GroupBy Mechanics ---")
    # Group data by month and calculate mean
grouped = data.resample('M').mean()
print(grouped)
return grouped
```

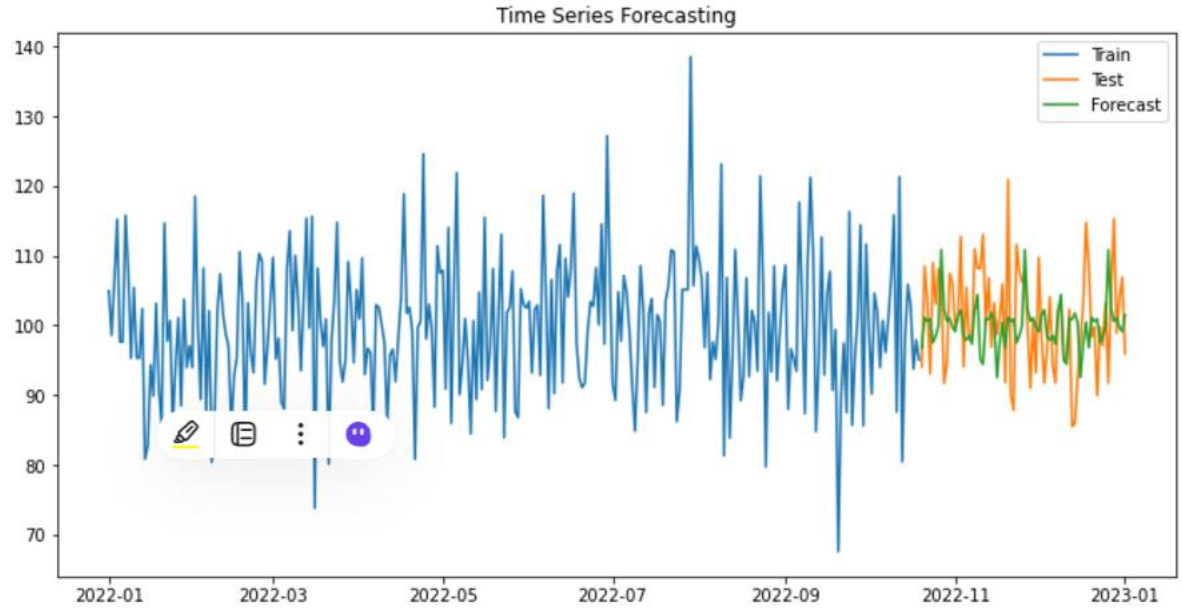
```
# Data Formats: Vector and Multivariate
defdata_formats(data):
print("\n--- Data Formats ---")
   # Display data as vector
print("\nVector Format:")
print(data["Value_A"].head())

   # Display multivariate time series
print("\nMultivariate Time Series:")
print(data.head())

# Forecasting Example
deftime_series_forecasting(data):
print("\n--- Forecasting ---")
   # Select a single column for forecasting
ts = data["Value_A"]

   # Train-Test Split
train = ts[:int(0.8 * len(ts))]
test = ts[int(0.8 * len(ts)):]

   # Fit the Holt-Winters Exponential Smoothing model
model = ExponentialSmoothing(train, seasonal="add", seasonal_periods=30).fit()

   # Forecast for the test period
forecast = model.forecast(len(test))

   # Plot results
plt.figure(figsize=(12, 6))
```

```
plt.plot(train, label="Train")
plt.plot(test, label="Test")
plt.plot(forecast, label="Forecast")
plt.legend()
plt.title("Time Series Forecasting")
plt.show()

# Main function
if __name__ == "__main__":
print("--- Time Series Data ---")
print(data.head())

   # Grouping Mechanics
monthly_data = groupby_mechanics(data)

   # Data Formats
data_formats(data)

   # Time Series Forecasting
time_series_forecasting(data)
```

Sample output:

```
--- Time Series Data ---
Value_AValue_B
Date
2022-01-01  104.967142  204.481850
2022-01-02   98.617357  200.251848
2022-01-03  106.476885  201.953522
2022-01-04  115.230299  184.539804
2022-01-05   97.658466  200.490203
```

```
--- GroupBy Mechanics ---
Value_AValue_B
Date
2022-01-31   97.985125  202.137470
2022-02-28   98.568317  204.960833
2022-03-31  100.439383  194.956405
2022-04-30   99.797484  198.429574
2022-05-31   99.161855  199.020262
2022-06-30  102.912924  192.752508
2022-07-31  100.983406  199.844253
2022-08-31   99.784632  201.134556
2022-09-30   99.089296  203.720687
2022-10-31  100.649960  198.150774
2022-11-30  102.325711  199.427682
2022-12-31   99.467543  197.195680
2023-01-31   95.987795  180.432544

--- Data Formats ---

Vector Format:
Date
2022-01-01    104.967142
2022-01-02     98.617357
2022-01-03    106.476885
2022-01-04    115.230299
2022-01-05     97.658466
Name: Value_A, dtype: float64

Multivariate Time Series:
Value_AValue_B
Date
2022-01-01  104.967142  204.481850
2022-01-02   98.617357  200.251848
2022-01-03  106.476885  201.953522
2022-01-04  115.230299  184.539804
2022-01-05   97.658466  200.490203--- Forecasting ---
```


Time Series Forecasting
Train
Test
Forecast
140
130
120
110
100
90
80
70
2022-01
2022-03
2022-05
2022-07
2022-09
2022-11
2023-01

Program 04

4. Program to measure central tendency and measures of dispersion: Mean, Median, Mode, Standard Deviation, Variance, Mean deviation and Quartile deviation for a frequency distribution/data

Source code:

```
# Import necessary libraries
importnumpy as np
import pandas as pd

defcalculate_statistics(data, frequencies):
   # Create a DataFrame for the frequency distribution
df = pd.DataFrame({'Value': data, 'Frequency': frequencies})

   # Calculate the total number of observations
total = df['Frequency'].sum()

   # Calculate mean
df['Weighted_Value'] = df['Value'] * df['Frequency']
mean = df['Weighted_Value'].sum() / total

   # Calculate median
cumulative_frequency = df['Frequency'].cumsum()
median_index = cumulative_frequency.searchsorted(total / 2)
median = df['Value'][median_index]

   # Calculate mode
mode = df['Value'][df['Frequency'].idxmax()]
```

```
    # Calculate variance and standard deviation
variance = np.average((df['Value'] - mean) ** 2, weights=df['Frequency'])
std_deviation = np.sqrt(variance)

    # Calculate mean deviation
mean_deviation = np.average(np.abs(df['Value'] - mean), weights=df['Frequency'])

    # Calculate quartile deviation
    q1 = np.percentile(data, 25)
    q3 = np.percentile(data, 75)
quartile_deviation = (q3 - q1) / 2

return {
        'Mean': mean,
        'Median': median,
        'Mode': mode,
        'Variance': variance,
        'Standard Deviation': std_deviation,
        'Mean Deviation': mean_deviation,
        'Quartile Deviation': quartile_deviation
    }

# Get user input for data and frequencies
data_input = input("Enter the data values separated by commas (e.g., 10, 20, 30): ")
frequencies_input = input("Enter the corresponding frequencies separated by commas (e.g.,
1, 2, 3): ")

# Convert input strings to lists of integers
data = list(map(int, data_input.split(',')))
frequencies = list(map(int, frequencies_input.split(',')))
```

```
# Calculate statistics
statistics = calculate_statistics(data, frequencies)

# Display the results
for stat, value in statistics.items():
print(f"{stat}: {value:.2f}")
```

Sample output:

Data values: 10, 20, 20, 30, 30, 30, 40, 50, 50, 60
Frequencies: 1, 2, 3, 1, 1, 1, 1, 2, 2, 1

Mean:36.00

Median:30.00

Mode:30.00

Variance:167.78

Standard Deviation:12.93

Mean Deviation:11.70

Quartile Deviation:10.00

Explanation:

1. Mean (Average)

- **What it is**: The mean is what we usually call the average. It tells us what the "typical" number is when we have a bunch of numbers.
- **How to find it**: To find the mean, we add up all the numbers and then divide by how many numbers there are.
- **Example**: If you have 2 candies, 3 candies, and 5 candies, you first add them up (2 + 3 + 5 = 10) and then divide by how many groups of candies there are (3). So, the mean is 10÷3=3.3310 ÷ 3 = 3.3310÷3=3.33.

2. Median

- **What it is**: The median is the middle number in a list of numbers. If we lined up all our numbers from smallest to largest, the median would be the one right in the middle.
- **How to find it**: If there's an odd number of numbers, the median is the one in the middle. If there's an even number, we take the two middle numbers, add them together, and divide by 2.
- **Example**: For the numbers 2, 3, 5, the median is 3. For 2, 3, 4, 5, the median is (3+4)÷2=3.5 (3 + 4) ÷ 2 = 3.5(3+4)÷2=3.5.

3. Mode

- **What it is**: The mode is the number that appears the most in a list. It tells us which number is the most popular.
- **How to find it**: We look at our list of numbers and see which one shows up the most times.
- **Example**: If you have candies like this: 2, 2, 3, 4, the mode is 2 because it appears more times than any other number.

4. Variance

- **What it is**: Variance tells us how spread out the numbers are. If the numbers are all close to the mean, the variance is small. If they're very different from each other, the variance is big.
- **How to find it**: We calculate how far each number is from the mean, square those differences, and then average them.
- **Example**: If the numbers are 2, 3, and 4, they are all close to the mean (3), so the variance is small. If the numbers are 1, 5, and 10, they are more spread out, so the variance is larger.

5. Standard Deviation

- **What it is**: Standard deviation is just a fancy word for how much the numbers vary from the mean. It's like the square root of the variance.
- **How to find it**: We take the square root of the variance.
- **Example**: If the variance tells us how far apart the candies are from the average size, the standard deviation gives us a way to understand that distance in the same units as the candies.

6. Mean Deviation

- **What it is**: Mean deviation tells us, on average, how far each number is from the mean. It helps us see how different the numbers are from the average number.
- **How to find it**: We take the absolute value of the differences between each number and the mean, and then find the average of those differences.

- **Example**: If the mean is 3 and the numbers are 2, 3, and 4, the distances from the mean are 1 (for 2), 0 (for 3), and 1 (for 4). The mean deviation would be (1+0+1)÷3=0.67 (1 + 0 + 1) ÷ 3 = 0.67(1+0+1)÷3=0.67.

7. Quartile Deviation

- **What it is**: Quartile deviation measures how spread out the middle half of the data is. It uses the first quartile (Q1) and the third quartile (Q3) to find the "interquartile range."
- **How to find it**: We first find Q1 and Q3, then subtract Q1 from Q3, and divide by 2.
- **Example**: If Q1 is 2 and Q3 is 4, the quartile deviation is (4−2)÷2=1 (4 - 2) ÷ 2 = 1(4−2)÷2=1. This means the middle half of the candies is spread out over 1 candy.

Program 05

5.Program to perform cross validation for a given dataset to measure Root Mean Squared Error (RMSE), Mean Absolute Error (MAE) and R2 Error using Validation Set, Leave One Out Cross-Validation(LOOCV) and K-fold Cross-Validation approaches

Source code:

```
# Import necessary libraries
importnumpy as np
import pandas as pd
from sklearn.model_selection import train_test_split, KFold, LeaveOneOut
fromsklearn.metrics import mean_squared_error, mean_absolute_error, r2_score
from sklearn.linear_model import LinearRegression
fromsklearn.datasets import fetch_california_housing

# Load the California housing dataset
data = fetch_california_housing()
X = pd.DataFrame(data.data, columns=data.feature_names)
y = pd.Series(data.target)

# Function to calculate and display metrics
defdisplay_metrics(y_true, y_pred):
rmse = np.sqrt(mean_squared_error(y_true, y_pred))
mae = mean_absolute_error(y_true, y_pred)
   r2 = r2_score(y_true, y_pred)
print(f"Root Mean Squared Error (RMSE): {rmse:.4f}")
print(f"Mean Absolute Error (MAE): {mae:.4f}")
print(f"R² Score: {r2:.4f}")
returnrmse, mae, r2
```

```
# Validation Set Approach
defvalidation_set_approach(X, y):
print("Validation Set Approach:")
   # Split the dataset into training (80%) and validation (20%) sets
X_train, X_val, y_train, y_val = train_test_split(X, y, test_size=0.2, random_state=42)

   # Initialize and train the model
model = LinearRegression()
model.fit(X_train, y_train)

   # Make predictions on the validation set
y_pred = model.predict(X_val)

   # Display metrics
display_metrics(y_val, y_pred)

# Leave-One-Out Cross-Validation (LOOCV) Approach
defloocv_approach(X, y):
print("Leave-One-Out Cross-Validation (LOOCV):")
loo = LeaveOneOut()
y_true, y_pred = [], []

   # Loop through each sample using LOOCV
fortrain_index, test_index in loo.split(X):
X_train, X_test = X.iloc[train_index], X.iloc[test_index]
y_train, y_test = y.iloc[train_index], y.iloc[test_index]

      # Initialize and train the model
```

```
model = LinearRegression()
model.fit(X_train, y_train)

    # Make prediction for the single test sample
y_pred.append(model.predict(X_test)[0])
y_true.append(y_test.iloc[0])

  # Display metrics
display_metrics(y_true, y_pred)

# K-Fold Cross-Validation Approach
defkfold_approach(X, y, k=5):
print(f"{k}-Fold Cross-Validation Approach:")
kf = KFold(n_splits=k, shuffle=True, random_state=42)
y_true, y_pred = [], []

  # Loop through each fold
fortrain_index, test_index in kf.split(X):
X_train, X_test = X.iloc[train_index], X.iloc[test_index]
y_train, y_test = y.iloc[train_index], y.iloc[test_index]

    # Initialize and train the model
model = LinearRegression()
model.fit(X_train, y_train)

    # Make predictions on the test set
y_pred.extend(model.predict(X_test))
y_true.extend(y_test)
```

```
    # Display metrics
display_metrics(y_true, y_pred)


# Main function to run all approaches
def main():
print("Cross-Validation for RMSE, MAE, and R²:\n")
validation_set_approach(X, y)
print("\n")
loocv_approach(X, y)
print("\n")
kfold_approach(X, y, k=5)  # You can change k for different K-Fold Cross-Validation


# Execute the main function
if __name__ == "__main__":
main()
```

Sample output:

Cross-Validation for RMSE, MAE, and R²:

Validation Set Approach:
Root Mean Squared Error (RMSE): 0.7456
Mean Absolute Error (MAE): 0.5332
R² Score: 0.5758

Leave-One-Out Cross-Validation (LOOCV):
Root Mean Squared Error (RMSE): 0.7268
Mean Absolute Error (MAE): 0.5317
R² Score: 0.6033

5-Fold Cross-Validation Approach:
Root Mean Squared Error (RMSE): 0.7284
Mean Absolute Error (MAE): 0.5317
R² Score: 0.6015

Program 06

6.Program to display Normal, Binomial Poisson, Bernoulli disrtibutions for a given frequency distribution

Source code:

```
Import numpy as np

Import mat plotlib.pyplot as plt

From scipy.stats import norm, binom, poisson, bernoulli


defget_user_data():

   # Get the frequency distribution input from the user

data_input = input("Enter the data values separated by commas (e.g., 10, 20, 30): ")

frequencies_input = input("Enter the corresponding frequencies separated by commas (e.g., 2, 3, 4): ")


   # Convert the inputs into lists of integers

data = list(map(int, data_input.split(',')))

frequencies = list(map(int, frequencies_input.split(',')))


return data, frequencies


defplot_normal_distribution(data, frequencies):

   # Fit and plot Normal distribution

mean = np.mean(data)

std_dev = np.std(data)


   x = np.linspace(min(data), max(data), 100)

pdf = norm.pdf(x, mean, std_dev)
```

```
plt.plot(x, pdf, 'r-', lw=2, label='Normal Distribution')
plt.title('Normal Distribution')
plt.xlabel('Value')
plt.ylabel('Probability Density')
plt.show()

defplot_binomial_distribution(data, frequencies):
    # Fit and plot Binomial distribution (assuming n is max(data) and p is mean/len(data))
    n = max(data)
    p = np.mean(data) / n

    x = np.arange(0, n+1)
pmf = binom.pmf(x, n, p)

plt.bar(x, pmf, alpha=0.7, color='b', label='Binomial Distribution')
plt.title('Binomial Distribution')
plt.xlabel('Value')
plt.ylabel('Probability')
plt.show()

defplot_poisson_distribution(data, frequencies):
    # Fit and plot Poisson distribution (lambda is the mean of the data)
lam = np.mean(data)

    x = np.arange(0, max(data)+1)
pmf = poisson.pmf(x, lam)

plt.bar(x, pmf, alpha=0.7, color='g', label='Poisson Distribution')
plt.title('Poisson Distribution')
```

```
plt.xlabel('Value')
plt.ylabel('Probability')
plt.show()

defplot_bernoulli_distribution(data, frequencies):
   # Assuming binary outcome for Bernoulli
success_prob = np.mean(data) / max(data)

   x = [0, 1]
pmf = bernoulli.pmf(x, success_prob)

plt.bar(x, pmf, alpha=0.7, color='purple', label='Bernoulli Distribution')
plt.title('Bernoulli Distribution')
plt.xlabel('Value')
plt.ylabel('Probability')
plt.show()

defanalyze_distributions(data, frequencies):
print("Analyzing Normal Distribution:")
plot_normal_distribution(data, frequencies)

print("Analyzing Binomial Distribution:")
plot_binomial_distribution(data, frequencies)

print("Analyzing Poisson Distribution:")
plot_poisson_distribution(data, frequencies)

print("Analyzing Bernoulli Distribution:")
plot_bernoulli_distribution(data, frequencies)
```

```
# Main program

data, frequencies = get_user_data()

analyze_distributions(data, frequencies)
```

Explanation:

1. Normal Distribution

- **What it is**: The Normal distribution (also called the Gaussian distribution) is the most common probability distribution. It looks like a bell-shaped curve and is symmetrical around the mean.
- **Real-world analogy**: Imagine you're measuring the height of a group of people. Most people will have heights around the average (mean), and fewer people will be much taller or much shorter. The majority of the data clusters around the average with fewer extreme values on either side.
- **Key Points**:
    - Symmetrical bell curve.
    - Mean = Median = Mode.
    - Many natural phenomena, like people's heights, shoe sizes, or IQ scores, follow a Normal distribution.

2. Binomial Distribution

- **What it is**: The Binomial distribution is used to model the number of successful outcomes in a fixed number of independent trials, where each trial has two possible outcomes (like flipping a coin: heads or tails).
- **Real-world analogy**: Imagine you flip a coin 10 times. If you're trying to figure out how many heads you'll get, the Binomial distribution helps you calculate the probability of getting 0 heads, 1 head, 2 heads, all the way up to 10 heads.
- **Key Points**:
    - Two possible outcomes: success or failure (like heads or tails).
    - Fixed number of trials (e.g., flipping a coin 10 times).
    - Probability of success (like getting heads) stays the same for each trial.

3. Poisson Distribution

- **What it is**: The Poisson distribution is used to model the probability of a given number of events happening in a fixed interval of time or space, where these events occur independently of each other.
- **Real-world analogy**: Imagine you're running a bakery, and you want to know the probability of a certain number of customers arriving in the next hour. The Poisson

distribution can help you predict this based on the average number of customers you usually get in an hour.

- **Key Points**:
  - The events are random and independent.
  - It's used when you're counting the number of occurrences over a fixed period or space (e.g., customers arriving, phone calls received).
  - Average rate of occurrence (λ or lambda) is constant.

4. Bernoulli Distribution

- **What it is**: The Bernoulli distribution models the probability of a single trial with two possible outcomes, typically referred to as success (1) or failure (0).
- **Real-world analogy**: Suppose you're tossing a coin one time. The outcome can only be heads or tails (success or failure). The Bernoulli distribution helps model this scenario.
- **Key Points**:
  - There is just one trial (e.g., one coin flip).
  - The probability of success is constant.
  - The result is binary: either success (1) or failure (0).

Key Differences:

- **Normal Distribution**: Continuous and symmetrical. It models things like people's heights, weights, and test scores where the data is spread around the mean in a bell-shaped curve.
- **Binomial Distribution**: Discrete. It models how many times a success happens out of a fixed number of trials, such as how many heads you get when you flip a coin 10 times.
- **Poisson Distribution**: Discrete. It models how many times an event happens in a fixed amount of time or space (e.g., the number of cars passing by in an hour or phone calls received).
- **Bernoulli Distribution**: Discrete and binary. It models a single yes/no outcome (success or failure) for one event, such as one coin flip.

Visualizing Distributions:

- **Normal Distribution**: Think of a bell curve. Most values are clustered around the mean, and fewer values are farther away.
- **Binomial Distribution**: The histogram of outcomes peaks around the most likely number of successes (like getting 5 heads out of 10 coin flips).
- **Poisson Distribution**: It shows how the likelihood of different numbers of events drops off quickly (e.g., it's rare to get 10 customers in 5 minutes, but more common to get 1 or 2).
- **Bernoulli Distribution**: It's simple and binary, like flipping a coin. The bar chart has just two bars: one for success (1) and one for failure (0).

Program 07

7.Program to implement one sample, two sample and paired sample t-tests for sample data and analyzethe results.

Source code:

```
# Import necessary libraries
importnumpy as np
import pandas as pd
fromscipy import stats

# Sample data for demonstration
# One-sample test: A group of exam scores
exam_scores = np.array([85, 87, 90, 78, 88, 95, 82, 79, 94, 91])

# Two-sample test: Scores of two different groups
group_A = np.array([85, 89, 88, 90, 93, 85, 84, 79, 90, 87])
group_B = np.array([82, 86, 85, 87, 92, 80, 81, 78, 89, 85])

# Paired-sample test: Before and after treatment scores of the same group
before_treatment = np.array([82, 84, 88, 78, 80, 85, 90, 79, 87, 83])
after_treatment = np.array([85, 87, 89, 81, 83, 88, 92, 82, 89, 86])

# Function to perform one-sample t-test
defone_sample_ttest(data, population_mean):
t_stat, p_value = stats.ttest_1samp(data, population_mean)
returnt_stat, p_value

# Function to perform two-sample t-test (independent samples)
deftwo_sample_ttest(group1, group2):
```

```
t_stat, p_value = stats.ttest_ind(group1, group2)
returnt_stat, p_value

# Function to perform paired-sample t-test
defpaired_sample_ttest(before, after):
t_stat, p_value = stats.ttest_rel(before, after)
returnt_stat, p_value

# Analyze results of the t-tests
defanalyze_ttest_results(t_stat, p_value, alpha=0.05):
print(f"T-statistic: {t_stat}")
print(f"P-value: {p_value}")
ifp_value< alpha:
print("Result: The null hypothesis is rejected (statistically significant difference).")
else:
print("Result: The null hypothesis cannot be rejected (no statistically significant
difference).")

# One-sample t-test: Compare exam scores with a population mean (e.g., 85)
print("One-Sample T-Test:")
t_stat, p_value = one_sample_ttest(exam_scores, 85)
analyze_ttest_results(t_stat, p_value)
print()

# Two-sample t-test: Compare the means of two independent groups
print("Two-Sample T-Test:")
t_stat, p_value = two_sample_ttest(group_A, group_B)
analyze_ttest_results(t_stat, p_value)
print()
```

```
# Paired-sample t-test: Compare before and after treatment of the same group
print("Paired-Sample T-Test:")
t_stat, p_value = paired_sample_ttest(before_treatment, after_treatment)
analyze_ttest_results(t_stat, p_value)
```

Sample Output:

```
One-Sample T-Test:
T-statistic: 1.0189950494649807
P-value: 0.3348142605778697
Result: The null hypothesis cannot be rejected (no statistically significant difference).

Two-Sample T-Test:
T-statistic: 1.3547090246981803
P-value: 0.19227122007981406
Result: The null hypothesis cannot be rejected (no statistically significant difference).

Paired-Sample T-Test:
T-statistic: -11.758942438532781
P-value: 9.151111215642479e-07
Result: The null hypothesis is rejected (statistically significant difference).
```

Program 08

8.Program to implement One-way and Two-way ANOVA tests and analyze the results

Source code:

```
importnumpy as np
import pandas as pd
fromscipy.stats import f_oneway
importstatsmodels.api as sm
fromstatsmodels.formula.api import ols

# Function for One-way ANOVA
defone_way_anova(data, groups, response):
    """
    Perform one-way ANOVA.
:param data: DataFrame containing the dataset
:param groups: Column name for grouping variable
:param response: Column name for response variable
    """
grouped_data = [group[response].values for _, group in data.groupby(groups)]
f_stat, p_value = f_oneway(*grouped_data)
print("\nOne-way ANOVA Results:")
print(f"F-statistic: {f_stat:.4f}, p-value: {p_value:.4f}")
ifp_value< 0.05:
print("Reject the null hypothesis: Significant difference among group means.")
else:
print("Fail to reject the null hypothesis: No significant difference among group means.")
```

```
# Function for Two-way ANOVA
deftwo_way_anova(data, response, factor1, factor2):
    """
    Perform two-way ANOVA.
:param data: DataFrame containing the dataset
:param response: Column name for response variable
:param factor1: Column name for first factor
:param factor2: Column name for second factor
    """
    formula = f"{response} ~ C({factor1}) + C({factor2}) + C({factor1}):C({factor2})"
model = ols(formula, data).fit()
anova_table = sm.stats.anova_lm(model, typ=2)  # Type II ANOVA
print("\nTwo-way ANOVA Results:")
print(anova_table)

# Example usage
if __name__ == "__main__":
    # Example dataset for One-way ANOVA
data_one_way = pd.DataFrame({
        "Group": np.repeat(['A', 'B', 'C'], 10),
        "Score": np.concatenate([
np.random.normal(loc=50, scale=5, size=10),
np.random.normal(loc=55, scale=5, size=10),
np.random.normal(loc=60, scale=5, size=10)
        ])
    })

    # Perform One-way ANOVA
one_way_anova(data_one_way, groups="Group", response="Score")
```

```
   # Example dataset for Two-way ANOVA
data_two_way = pd.DataFrame({
      "Factor1": np.repeat(['Low', 'Medium', 'High'], 6),
      "Factor2": np.tile(['Type1', 'Type2'], 9),
      "Response": np.concatenate([
np.random.normal(loc=50, scale=5, size=6),
np.random.normal(loc=55, scale=5, size=6),
np.random.normal(loc=60, scale=5, size=6)
      ])
   })

   # Perform Two-way ANOVA
two_way_anova(data_two_way, response="Response", factor1="Factor1",
factor2="Factor2")
```

Sample output:

```
One-way ANOVA Results:
F-statistic: 25.1121, p-value: 0.0000
Reject the null hypothesis: Significant difference among group means.

Two-way ANOVA Results:
sum_sqdf        F    PR(>F)
C(Factor1)          159.837203   2.0  2.086902  0.166807
C(Factor2)           56.395083   1.0  1.472636  0.248276
C(Factor1):C(Factor2)   39.362026   2.0  0.513927  0.610731
Residual            459.544039  12.0NaNNaN
```

Program 09

9.Program to implement correlation, rank correlation and regression and plot x-y plot and heat maps of correlation matrices.

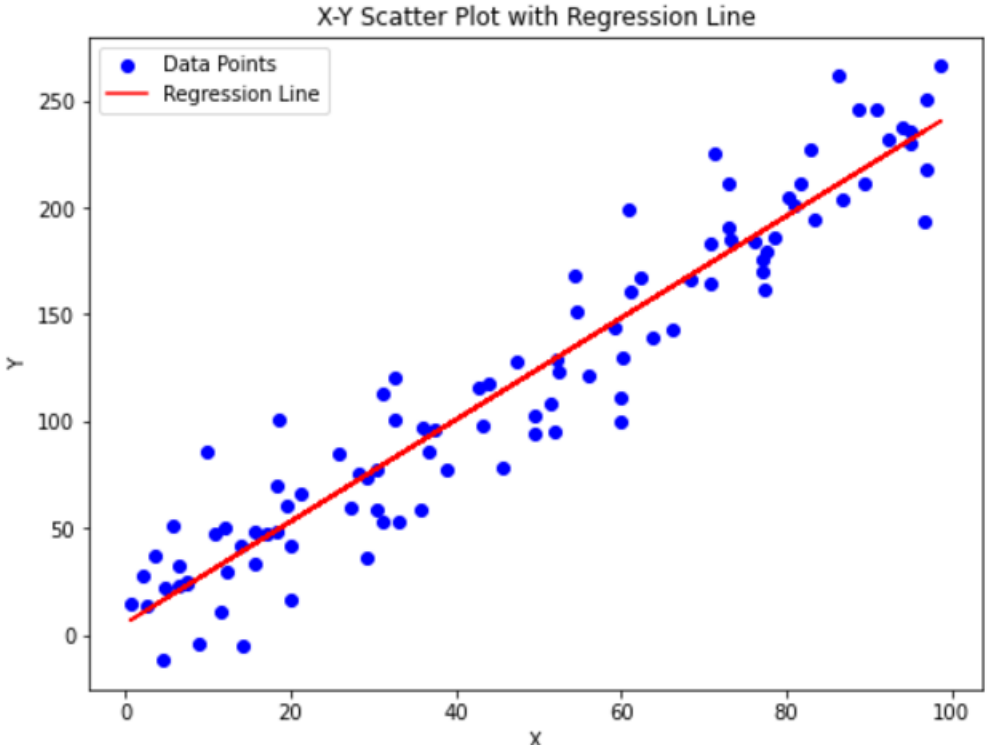
Source code:

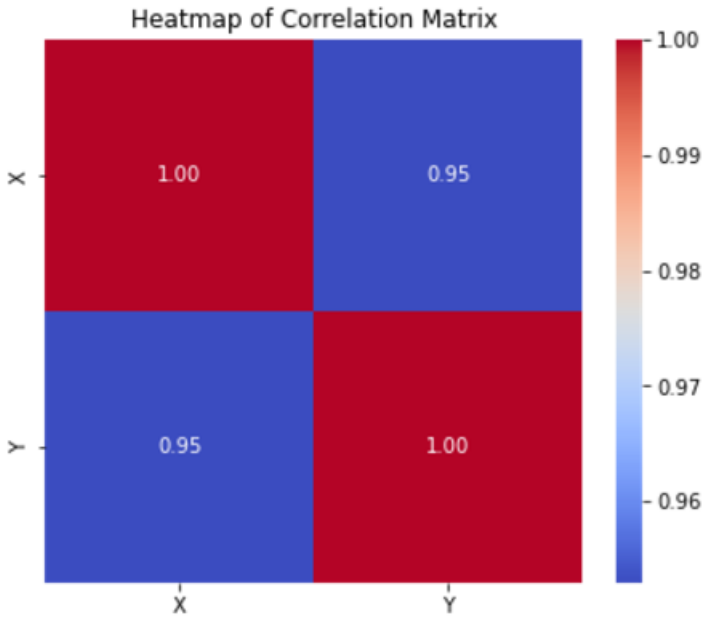
```
# Import required libraries
importnumpy as np
import pandas as pd
importseaborn as sns
importmatplotlib.pyplot as plt
fromscipy.stats import spearmanr
from sklearn.linear_model import LinearRegression
fromsklearn.metrics import mean_squared_error

# Generate sample data (or load your dataset here)
np.random.seed(42)  # For reproducibility
x = np.random.rand(100) * 100  # Random values for x
y = 2.5 * x + np.random.normal(0, 25, 100)  # Linear relation with noise

# Convert data into a DataFrame
data = pd.DataFrame({'X': x, 'Y': y})

# Compute Correlation
pearson_corr = data.corr(method='pearson')  # Pearson Correlation
spearman_corr, _ = spearmanr(data['X'], data['Y'])  # Spearman Rank Correlation

# Linear Regression
X = data['X'].values.reshape(-1, 1)  # Reshape for sklearn
Y = data['Y'].values
```

```
model = LinearRegression()
model.fit(X, Y)
Y_pred = model.predict(X)
regression_coeff = model.coef_[0]  # Slope
regression_intercept = model.intercept_  # Intercept
mse = mean_squared_error(Y, Y_pred)

# Print statistical results
print("Pearson Correlation Coefficient Matrix:")
print(pearson_corr)
print("\nSpearman Rank Correlation Coefficient:", spearman_corr)
print("\nLinear Regression Equation: Y = {:.2f}X + {:.2f}".format(regression_coeff,
regression_intercept))
print("Mean Squared Error (MSE):", mse)

# Plot X-Y scatter plot with regression line
plt.figure(figsize=(8, 6))
plt.scatter(data['X'], data['Y'], color='blue', label='Data Points')
plt.plot(data['X'], Y_pred, color='red', label='Regression Line')
plt.title('X-Y Scatter Plot with Regression Line')
plt.xlabel('X')
plt.ylabel('Y')
plt.legend()
plt.show()

# Plot heatmap of correlation matrix
plt.figure(figsize=(6, 5))
sns.heatmap(pearson_corr, annot=True, cmap='coolwarm', fmt='.2f')
plt.title('Heatmap of Correlation Matrix')
plt.show()
```

Note: To use this script with a custom dataset, replace the sample data generation section with loading your dataset using pandas (e.g., pd.read_csv).

```
Pearson Correlation Coefficient Matrix:
          X         Y
X  1.000000  0.952966
Y  0.952966  1.000000

Spearman Rank Correlation Coefficient: 0.9519351935193517

Linear Regression Equation: Y = 2.39X + 5.38
Mean Squared Error (MSE): 504.11535247940856
```




Heatmap of Correlation Matrix
1.00
0.95
0.95
1.00
X
Y
X
Y
1.00
0.99
0.98
0.97
0.96

Program 10

10.**Program to implement PCA for Wisconsin dataset, visualize and analyze the results**.

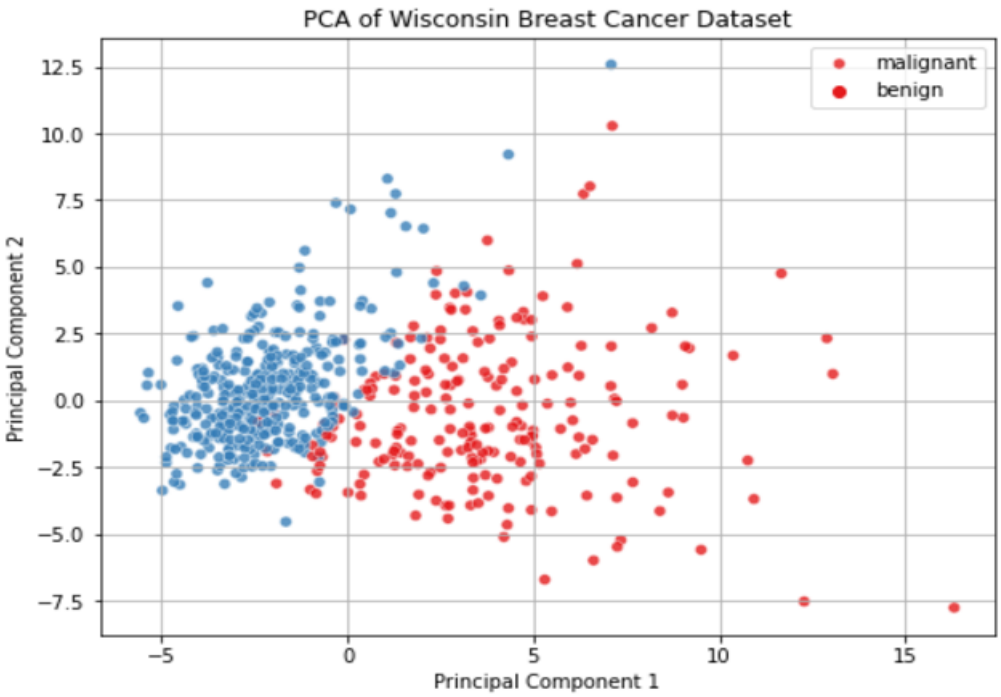
Source code:

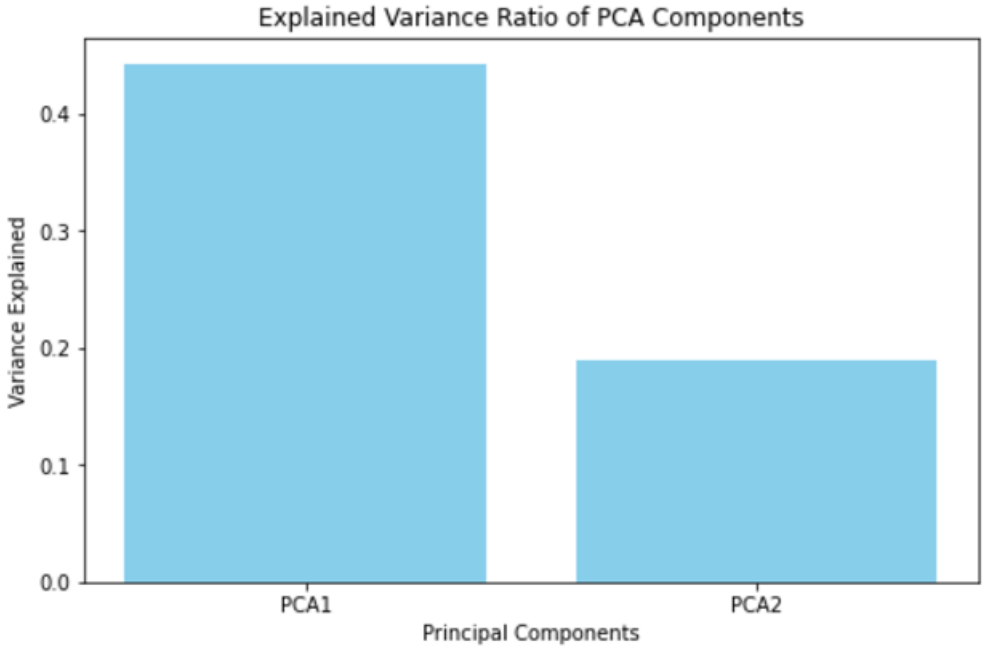
```
# Import necessary libraries
importnumpy as np
import pandas as pd
importmatplotlib.pyplot as plt
importseaborn as sns
fromsklearn.datasets import load_breast_cancer
fromsklearn.decomposition import PCA
fromsklearn.preprocessing import StandardScaler

# Load the Wisconsin Breast Cancer dataset
data = load_breast_cancer()
X = data.data  # Features
y = data.target  # Target variable (0 = malignant, 1 = benign)
feature_names = data.feature_names
target_names = data.target_names

# Standardize the data (important for PCA)
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Apply PCA
pca = PCA(n_components=2)  # Reduce to 2 dimensions for visualization
X_pca = pca.fit_transform(X_scaled)

# Get explained variance ratio for each component
```

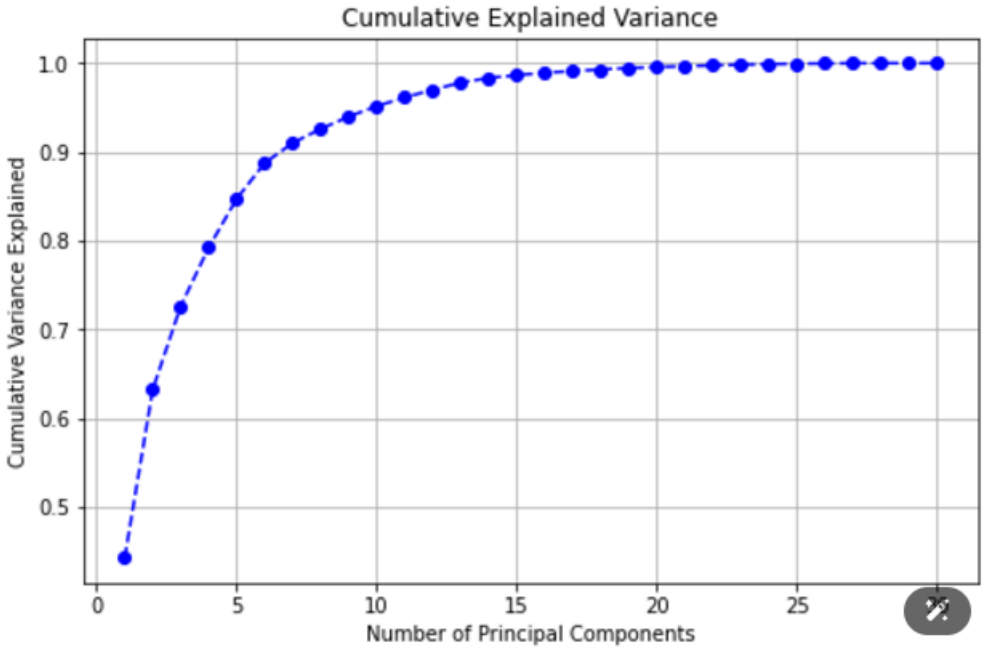
```
explained_variance_ratio = pca.explained_variance_ratio_

# Create a DataFrame for visualization
pca_df = pd.DataFrame(X_pca, columns=['PCA1', 'PCA2'])
pca_df['Target'] = y

# Plot the PCA results
plt.figure(figsize=(8, 6))
sns.scatterplot(data=pca_df, x='PCA1', y='PCA2', hue='Target', palette='Set1', alpha=0.8)
plt.title('PCA of Wisconsin Breast Cancer Dataset')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.legend(target_names)
plt.grid()
plt.show()

# Plot explained variance ratio
plt.figure(figsize=(8, 5))
plt.bar(range(1, 3), explained_variance_ratio, tick_label=['PCA1', 'PCA2'], color='skyblue')
plt.title('Explained Variance Ratio of PCA Components')
plt.xlabel('Principal Components')
plt.ylabel('Variance Explained')
plt.show()

# Full PCA with all components for analysis
pca_full = PCA()
X_pca_full = pca_full.fit_transform(X_scaled)
cumulative_variance = np.cumsum(pca_full.explained_variance_ratio_)
```

```
# Plot cumulative explained variance
plt.figure(figsize=(8, 5))
plt.plot(range(1, len(cumulative_variance) + 1), cumulative_variance, marker='o', linestyle='-', color='b')
plt.title('Cumulative Explained Variance')
plt.xlabel('Number of Principal Components')
plt.ylabel('Cumulative Variance Explained')
plt.grid()
plt.show()

# Print key insights
print("PCA Analysis of Wisconsin Breast Cancer Dataset")
print("-------------------------------------------------")
print(f"Explained Variance (PCA1): {explained_variance_ratio[0]:.4f}")
print(f"Explained Variance (PCA2): {explained_variance_ratio[1]:.4f}")
print("Cumulative Variance Explained by All Components:")
fori, cum_var in enumerate(cumulative_variance, start=1):
print(f"  Component {i}: {cum_var:.4f}")
```

Sample Output:


PCA of Wisconsin Breast Cancer Dataset
malignant
benign
Principal Component 2
Principal Component 1
12.5
10.0
7.5
5.0
2.5
0.0
−2.5
−5.0
−7.5
−5
0
5
10
15


Explained Variance Ratio of PCA Components
Variance Explained
Principal Components
PCA1
PCA2
0.4
0.3
0.2
0.1
0.0



PCA Analysis of Wisconsin Breast Cancer Dataset

Explained Variance (PCA1): 0.4427
Explained Variance (PCA2): 0.1897
Cumulative Variance Explained by All Components:
Component 1: 0.4427
Component 2: 0.6324
Component 3: 0.7264
Component 4: 0.7924
Component 5: 0.8473
Component 6: 0.8876
Component 7: 0.9101
Component 8: 0.9260
Component 9: 0.9399
Component 10: 0.9516
Component 11: 0.9614
Component 12: 0.9701
Component 13: 0.9781
Component 14: 0.9834
Component 15: 0.9865
Component 16: 0.9892
Component 17: 0.9911
Component 18: 0.9929
Component 19: 0.9945
Component 20: 0.9956
Component 21: 0.9966
Component 22: 0.9975
Component 23: 0.9983
Component 24: 0.9989
Component 25: 0.9994

Program 11

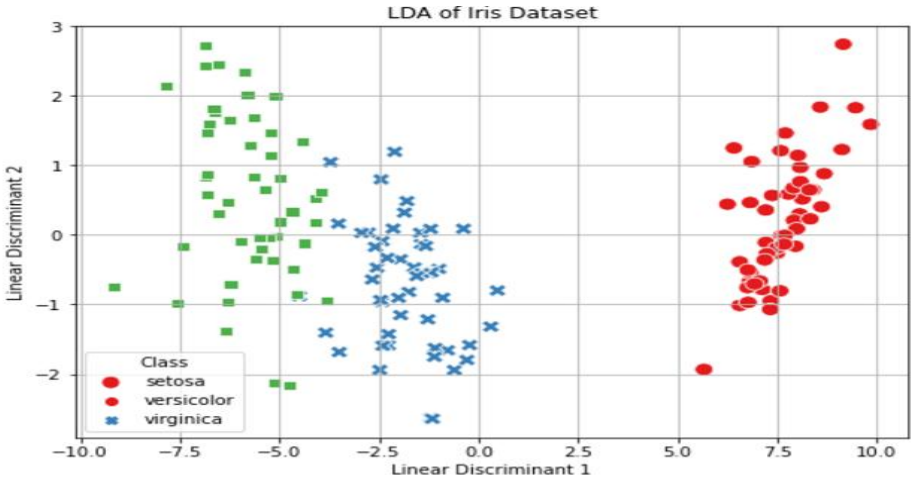
11.Program to implement the working of linear discriminant analysis using iris dataset and visualize the results.

Source code:

```
# Import necessary libraries
importnumpy as np
import pandas as pd
importmatplotlib.pyplot as plt
importseaborn as sns
fromsklearn.datasets import load_iris
fromsklearn.discriminant_analysis import LinearDiscriminantAnalysis
fromsklearn.preprocessing import StandardScaler

# Load the Iris dataset
data = load_iris()
X = data.data  # Features
y = data.target  # Target variable (0, 1, 2)
target_names = data.target_names  # Class names

# Standardize the data (LDA benefits from scaling)
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Apply Linear Discriminant Analysis (LDA)
lda = LinearDiscriminantAnalysis(n_components=2)  # Reduce to 2 components for visualization
X_lda = lda.fit_transform(X_scaled, y)
```

```
# Create a DataFrame for LDA-transformed data
lda_df = pd.DataFrame(X_lda, columns=['LDA1', 'LDA2'])
lda_df['Target'] = y

# Plot the LDA results in 2D space
plt.figure(figsize=(8, 6))
sns.scatterplot(data=lda_df, x='LDA1', y='LDA2', hue='Target', palette='Set1', style='Target', s=100)
plt.title('LDA of Iris Dataset')
plt.xlabel('Linear Discriminant 1')
plt.ylabel('Linear Discriminant 2')
plt.legend(title='Class', labels=target_names)
plt.grid()
plt.show()

# Print key insights
print("Linear Discriminant Analysis (LDA) Results")
print("-------------------------------------------------")
print("Explained Variance Ratio by LDA Components:")
fori, ratio in enumerate(lda.explained_variance_ratio_, start=1):
print(f"  LDA{i}: {ratio:.4f}")
```

Sample Output:




```
Linear Discriminant Analysis (LDA) Results
------------------------------------------------------
Explained Variance Ratio by LDA Components:
  LDA1: 0.9912
  LDA2: 0.0088
```

Program 12

12.Program to Implement multiple linear regression using iris dataset, visualize and analyse the results.

Source code:

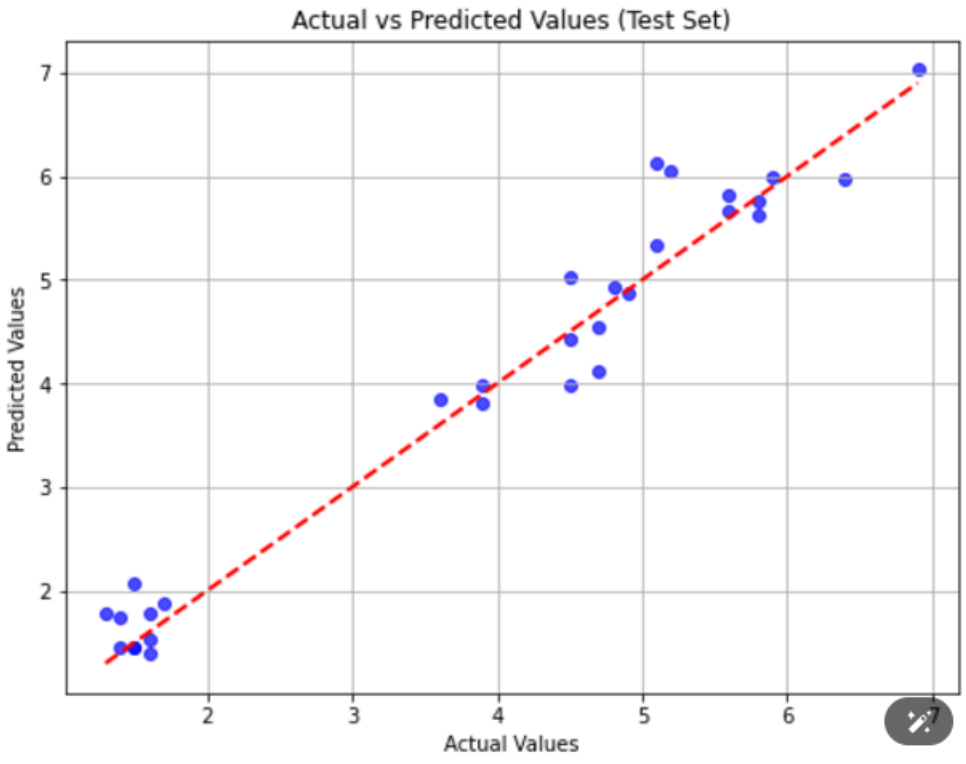
```
# Import necessary libraries

Import numpy as np

import pandas as pd

import matplotlib.pyplot as plt

import seaborn as sns

from sklearn.datasets import load_iris

from sklearn.model_selection import train_test_split

from sklearn.linear_model import Linear Regression

from sklearn.metrics import mean_squared_error, r2_score


# Load the Iris dataset

data = load_iris()

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

y = X['petal length (cm)']  # Let's predict 'petal length' as the dependent variable

X = X.drop(columns=['petal length (cm)'])  # Remove 'petal length' from independent variables


# Split the dataset into training and testing sets

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


# Apply Multiple Linear Regression

model = LinearRegression()

model.fit(X_train, y_train)  # Train the model
```

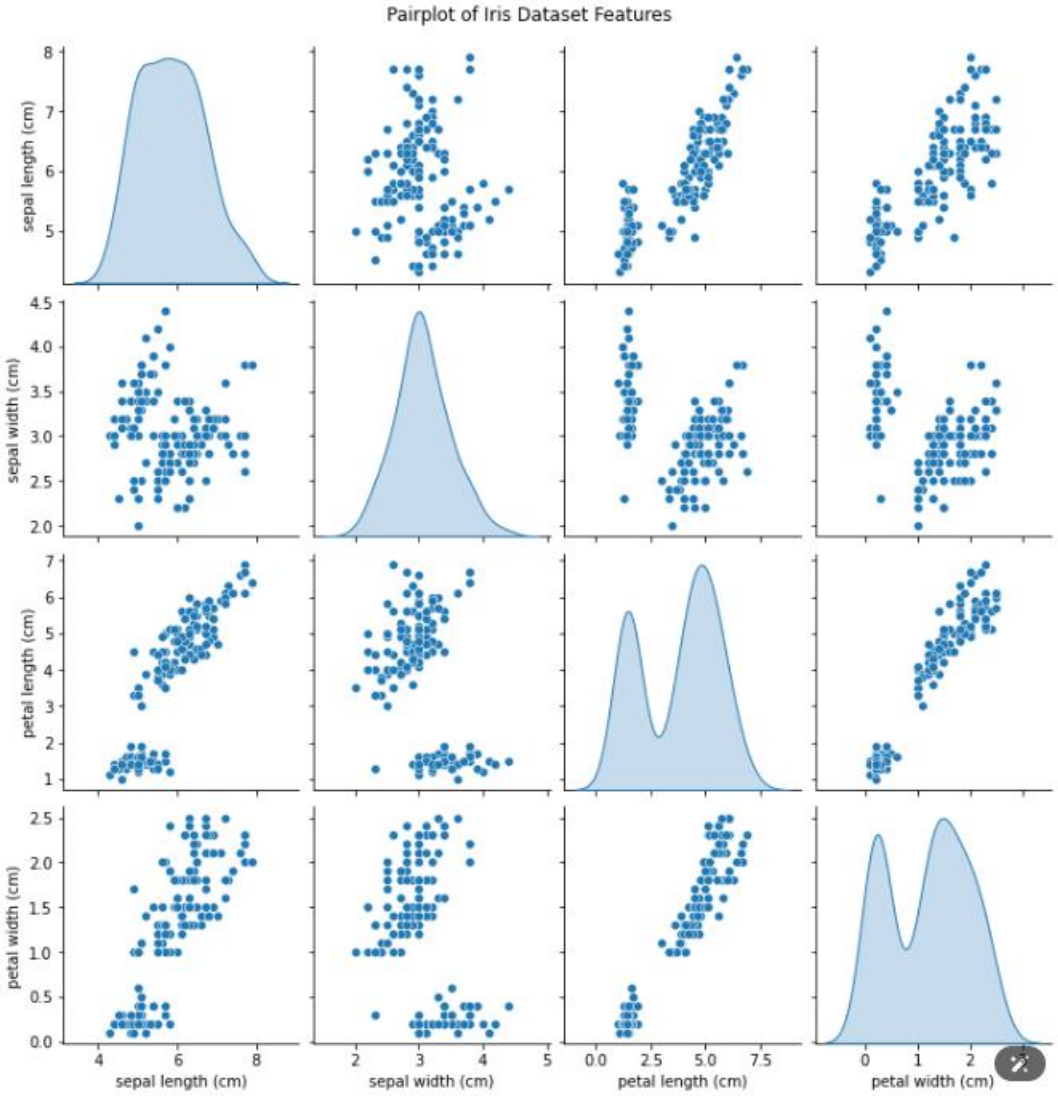
```
# Predict on the test set
y_pred = model.predict(X_test)

# Evaluate the model
mse = mean_squared_error(y_test, y_pred)
r2 = r2_score(y_test, y_pred)

# Print model performance metrics
print("Multiple Linear Regression Results")
print("----------------------------------")
print(f"Mean Squared Error (MSE): {mse:.4f}")
print(f"R-squared (R²): {r2:.4f}")
print("\nModel Coefficients:")
for feature, coef in zip(X.columns, model.coef_):
print(f"  {feature}: {coef:.4f}")
print(f"Intercept: {model.intercept_:.4f}")

# Visualize actual vs predicted values
plt.figure(figsize=(8, 6))
plt.scatter(y_test, y_pred, color='blue', alpha=0.7)
plt.plot([y_test.min(), y_test.max()], [y_test.min(), y_test.max()], color='red', linewidth=2,
linestyle='--')
plt.title('Actual vs Predicted Values (Test Set)')
plt.xlabel('Actual Values')
plt.ylabel('Predicted Values')
plt.grid()
plt.show()
```

```
# Pair plot to explore relationships in the dataset
sns.pairplot(pd.DataFrame(data.data, columns=data.feature_names), diag_kind='kde')
plt.suptitle('Pairplot of Iris Dataset Features', y=1.02)
plt.show()
```

Sample Output:

```
Multiple Linear Regression Results
----------------------------------
Mean Squared Error (MSE): 0.1300
R-squared (R²): 0.9603

Model Coefficients:
  sepal length (cm): 0.7228
  sepal width (cm): -0.6358
  petal width (cm): 1.4675
Intercept: -0.2622
```




Pairplot of Iris Dataset Features
sepal length (cm)
sepal width (cm)
petal length (cm)
petal width (cm)