EXPERIMENT -1

Aim:

- Load data in Pandas.
- Description of the dataset.
- Drop columns that aren't useful.
- Drop rows with maximum missing values.
- Take care of missing data.
- Create dummy variables.
- Find out outliers (manually)
- standardization and normalization of columns

Data preprocessing

Data preprocessing is the process of transforming raw data into an understandable format. It is also an important step in data mining as we cannot work with raw data. The quality of the data should be checked before applying machine learning or data mining algorithms.

Why is Data Preprocessing important?

Preprocessing of data is mainly to check the data quality. The quality can be checked by the following:

- Accuracy: To check whether the data entered is correct or not.
- Completeness: To check whether the data is available or not recorded.
- Consistency: To check whether the same data is kept in all the places that do or do not match.
- Timeliness: The data should be updated correctly.
- Believability: The data should be trustable.

Interpretability: The understandability of the data.

Dataset: Aircraft Fleet Dataset:

1) Loading Data in Pandas

Step 1: Load Data in Pandas

```
import pandas as pd
df = pd.read_csv("Fleet Data.csv")
df.head()
```

	Parent Airline	Airline	Aircraft Type	Current	Future	Historic	Total	Orders	Unit Cost	Total Cost (Current)	Average Age
0	Aegean Airlines	Aegean Airlines	Airbus A319	1.0	NaN	3.0	4.0	NaN	$90	$90	11.6
1	Aegean Airlines	Olympic Air	Airbus A319	NaN	NaN	8.0	8.0	NaN	$90	$0	NaN
2	Aegean Airlines	Aegean Airlines	Airbus A320	38.0	NaN	3.0	41.0	NaN	$98	$3,724	7.5
3	Aegean Airlines	Olympic Air	Airbus A320	NaN	NaN	9.0	9.0	NaN	$98	$0	NaN
4	Aegean Airlines	Aegean Airlines	Airbus A321	8.0	NaN	NaN	8.0	NaN	$115	$919	10.3

2) Description of the dataset.

```
Dataset Shape: (1583, 11)
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1583 entries, 0 to 1582
Data columns (total 11 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   Parent Airline        1583 non-null   object
 1   Airline               1583 non-null   object
 2   Aircraft Type         1583 non-null   object
 3   Current               859 non-null    float64
 4   Future                188 non-null    float64
 5   Historic              1113 non-null   float64
 6   Total                 1484 non-null   float64
 7   Orders                348 non-null    float64
 8   Unit Cost             1548 non-null   object
 9   Total Cost (Current)  1556 non-null   object
 10  Average Age           820 non-null    float64
dtypes: float64(6), object(5)
memory usage: 136.2+ KB
Dataset Description:           Current      Future     Historic        Total      Orders  \
count  859.000000  188.000000  1113.000000  1484.000000  348.000000
mean    24.033760    3.382979    14.513028    24.955526   26.419540
std     41.091234    4.656331    23.763373    46.651526   43.024179
min      1.000000    1.000000     1.000000     1.000000    1.000000
25%      5.000000    1.000000     3.000000     4.000000    5.000000
50%     12.000000    2.000000     7.000000    11.000000   13.500000
75%     26.500000    4.000000    16.000000    27.000000   28.250000
max    718.000000   38.000000   325.000000   952.000000  400.000000

       Average Age
count   820.000000
mean     10.115000
std       6.859362
min       0.100000
25%       5.000000
50%       8.900000
75%      14.500000
max      39.000000
```

`df.info()`: Provides an overview of the dataset, including:

- Number of rows and columns.

- Data types of each column (e.g., int, float, object).
- Number of non-null (non-missing) values in each column.

`df.describe()`: Generates summary statistics for numeric columns, such as:

- `count`: Number of non-missing values.
- `mean`: Average value.
- `std`: Standard deviation.
- `min`, `25%`, `50%` (median), `75%`, and `max`: Percentile values.

3) Drop columns that aren't useful: Columns like Orders and Average Age which had very little data may not contribute to analysis and we can't replace them with mean as it would make a lot of data irrelavant. Removing irrelevant columns reduces complexity.

```
# Drop columns that are not useful for analysis
df = df.drop(columns=['Orders', 'Future','Average Age'])

# Display the first few rows after dropping columns
df.head()
```

	Parent Airline	Airline	Aircraft Type	Current	Historic	Total	Unit Cost	Total Cost (Current)
0	Aegean Airlines	Aegean Airlines	Airbus A319	1.0	3.0	4.0	$90	$90
1	Aegean Airlines	Olympic Air	Airbus A319	NaN	8.0	8.0	$90	$0
2	Aegean Airlines	Aegean Airlines	Airbus A320	38.0	3.0	41.0	$98	$3,724
3	Aegean Airlines	Olympic Air	Airbus A320	NaN	9.0	9.0	$98	$0
4	Aegean Airlines	Aegean Airlines	Airbus A321	8.0	NaN	8.0	$115	$919

4) Drop rows with maximum missing values.

```
df = df.dropna(thresh=len(df.columns) - 2)
```

- Drops rows where more than 2 columns have missing (`NaN`) values.

```
print(f"Rows before dropping: {df.shape[0]}")

# Drop rows with maximum missing values
df = df.dropna(thresh=len(df.columns) - 2)

# Number of rows after dropping
print(f"Rows after dropping: {df.shape[0]}")

# Display the first few rows after dropping rows
df.head()
```

```
Rows before dropping: 1583
Rows after dropping: 1492
```

	Parent Airline	Airline	Aircraft Type	Current	Historic	Total	Unit Cost	Total Cost (Current)
0	Aegean Airlines	Aegean Airlines	Airbus A319	1.0	3.0	4.0	$90	$90
1	Aegean Airlines	Olympic Air	Airbus A319	NaN	8.0	8.0	$90	$0
2	Aegean Airlines	Aegean Airlines	Airbus A320	38.0	3.0	41.0	$98	$3,724
3	Aegean Airlines	Olympic Air	Airbus A320	NaN	9.0	9.0	$98	$0
4	Aegean Airlines	Aegean Airlines	Airbus A321	8.0	NaN	8.0	$115	$919

5) Take care of missing data.

`df.fillna(df.mean())`: Replaces missing values (`NaN`) in numeric columns with the mean of that column.

```
# Count missing values before filling
missing_before = df.isna().sum().sum()
print(f"Missing values before: {missing_before}")

# Fill missing values with the mean for numerical columns
# df = df.fillna(df.mean())
df = df.fillna(df.select_dtypes(include=['number']).mean())

# Count missing values after filling
missing_after = df.isna().sum().sum()
print(f"Missing values after: {missing_after}")
```

```
Missing values before: 1081
Missing values after: 17
```

6) Create dummy variables.

`pd.get_dummies()`: Converts categorical variables into dummy variables (binary indicators: 0 or 1).

- Example: The `Gender` column becomes `Gender_Male` (1 if Male, 0 otherwise).

`columns=['...']`: Specifies which columns to convert.
`drop_first=True`: Avoids the "dummy variable trap" by dropping one dummy variable to prevent multicollinearity.

	Parent Airline	Airline	Current	Historic	Total	Unit Cost	Total Cost (Current)	Aircraft Type_ATR 42–300F/–320F	Aircraft Type_ATR 42–600	Aircraft Type_ATR 42/72	...	Aircraft Type_McDonnell Douglas MD–90	Aircraft Type_Saab 2000	Aircraft Type_Saab 340	Aircr Type_Suk Super
0	Aegean Airlines	Aegean Airlines	1.000000	3.000000	4.0	$90	$90	False	False	False	...	False	False	False	F
1	Aegean Airlines	Olympic Air	24.270907	8.000000	8.0	$90	$0	False	False	False	...	False	False	False	F
2	Aegean Airlines	Aegean Airlines	38.000000	3.000000	41.0	$98	$3,724	False	False	False	...	False	False	False	F
3	Aegean Airlines	Olympic Air	24.270907	9.000000	9.0	$98	$0	False	False	False	...	False	False	False	F
4	Aegean Airlines	Aegean Airlines	8.000000	14.629091	8.0	$115	$919	False	False	False	...	False	False	False	F

7) Find out outliers (manually)

We first identified the outliers using Python by calculating the interquartile range (IQR) and marking values outside the IQR as outliers. Then, we imported the data into Excel, where we marked the outliers with a 'Yes' label. Finally, we used Excel's filtering and deletion tools to manually remove the outliers from the dataset.

```python
import numpy as np

# Select only numeric columns
numeric_cols = df.select_dtypes(include=[np.number])

# Calculate Q1 (25th percentile) and Q3 (75th percentile)
Q1 = numeric_cols.quantile(0.25)
Q3 = numeric_cols.quantile(0.75)
IQR = Q3 - Q1

# Define outlier boundaries
lower_bound = Q1 - 1.5 * IQR
upper_bound = Q3 + 1.5 * IQR

# Find outliers
outliers = (numeric_cols < lower_bound) | (numeric_cols > upper_bound)

# Print number of outliers per column
print(outliers.sum())

print(lower_bound,upper_bound)
```

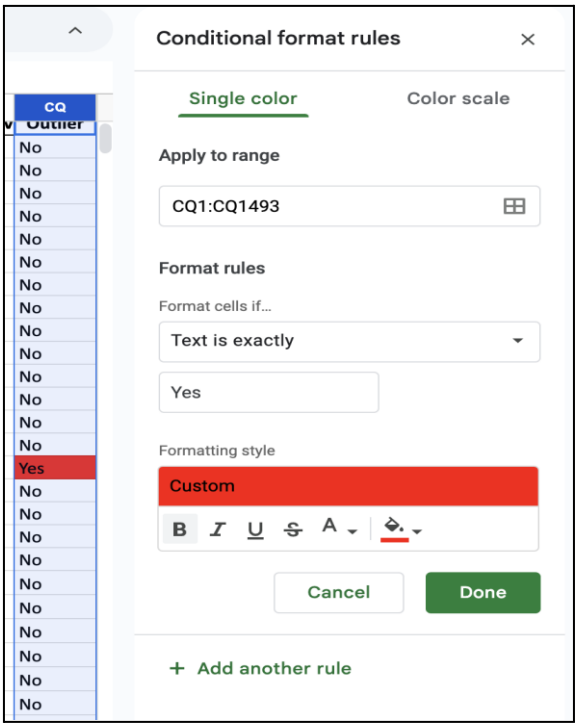
```
Current     123
Historic    131
Total       150
dtype: int64
Current    -11.406360
Historic   -11.943636
Total      -28.000000
dtype: float64 Current     45.677267
Historic    30.572727
Total       60.000000
dtype: float64
```

```python
# Mark outliers: If any of the columns in the 'outliers' DataFrame are True, mark as 'Yes'
df['Outlier'] = outliers.any(axis=1).map({True: 'Yes', False: 'No'})

# Export the DataFrame with the 'Outlier' column to an Excel file
df.to_excel('marked_outliers.xlsx', index=False)

print("Outliers marked and exported to 'marked_outliers.xlsx'.")
```

```
Outliers marked and exported to 'marked_outliers.xlsx'.
```

```python
# Remove rows where 'Outlier' is 'Yes'
df = df[df['Outlier'] == 'No']  # Overwrite the df to remove the outliers

# Now df is cleaned and free from outliers
print("Outliers removed, and df is updated without outliers.")
```

```
Outliers removed, and df is updated without outliers.
```




```
[15] # Remove rows where 'Outlier' is 'Yes'
     df = df[df['Outlier'] == 'No']  # Overwrite the df to remove the outliers

     # Now df is cleaned and free from outliers
     print("Outliers removed, and df is updated without outliers.")

     Outliers removed, and df is updated without outliers.

     df.shape

     (1492, 9)
```

8) standardization and normalization of columns

Standardization is another scaling technique where the values are centered around the mean with a unit standard deviation. This means that the mean of the attribute becomes zero and the resultant distribution has a unit standard deviation.

Standardization equation

$$X' = \frac{X - \mu}{\sigma}$$

To standardize your data, we need to import the StandardScalar from the sklearn library and apply it to our dataset.

Normalization is a scaling technique in which values are shifted and rescaled so that they end up ranging between 0 and 1. It is also known as Min-Max scaling.

Normalization equation

$$X' = \frac{X - X_{min}}{X_{max} - X_{min}}$$

Here, Xmax and Xmin are the maximum and the minimum values of the feature respectively.

- When the value of X is the minimum value in the column, the numerator will be 0, and hence X' is 0
- On the other hand, when the value of X is the maximum value in the column, the numerator is equal to the denominator and thus the value of X' is 1
- If the value of X is between the minimum and the maximum value, then the value of X' is between 0 and 1

To normalize your data, you need to import the MinMaxScalar from the sklearn library and apply it to our dataset.

```
from sklearn.preprocessing import StandardScaler, MinMaxScaler

# Standardization
scaler = StandardScaler()
df_standardized = pd.DataFrame(scaler.fit_transform(df.select_dtypes(include=['float64', 'int64'])), columns=df.select_dtypes(include=['float64', 'int64']).columns)

# Normalization
min_max_scaler = MinMaxScaler()
df_normalized = pd.DataFrame(min_max_scaler.fit_transform(df.select_dtypes(include=['float64', 'int64'])), columns=df.select_dtypes(include=['float64', 'int64']).columns)

# Display the first few rows after standardization and normalization
print("Standardized Data:")
print(df_standardized.head())

print("Normalized Data:")
print(df_normalized.head())
```

```
Standardized Data:
    Current        Future     Total
0 -0.745112 -5.431067e-16 -0.454163
1  0.000000 -5.431067e-16 -0.367472
2  0.451790 -5.431067e-16  0.347727
3  0.000000 -5.431067e-16 -0.345799
4 -0.518671 -5.431067e-16 -0.367472
Normalized Data:
    Current    Future     Total
0  0.000000  0.064405  0.003155
1  0.032125  0.064405  0.007361
2  0.051604  0.064405  0.042061
3  0.032125  0.064405  0.008412
4  0.009763  0.064405  0.007361
```

Conclusion:

Thus we have understood how to perform data preprocessing which can further be taken into exploratory data analysis and further in the Model preparation sequence.

AIDS-I Assignment No: 2

Q.1: Use the following data set for question 1
82, 66, 70, 59, 90, 78, 76, 95, 99, 84, 88, 76, 82, 81, 91, 64, 79, 76, 85, 90

1. Find the Mean (10pts)
2. Find the Median (10pts)
3. Find the Mode (10pts)
4. Find the Interquartile range (20pts)

Answer:

Sorted data: **5G, 64, 66, 70, 76, 76, 76, 78, 7G, 81, 82, 82, 84, 85, 88, G0, G0, G1, G5, GG**

$$\boldsymbol{Mean = \frac{SumOfVal}{NumOfVal} = \frac{1625}{20} = 81.25}$$

$$\boldsymbol{Median = \frac{(\frac{n}{2}) + (\frac{n}{2}) + 1}{2} = \frac{10^{th} + 11^{th}}{2} = \frac{81 + 82}{2} = 81.5}$$

Mode: 76 appears 3 times and has the maximum frequency, So Mode = 73.

Interquartile Range (IQR)

Q1 (25th percentile): Median of the first 10 numbers:

59, 64, 66, 70, 76, 76, 76, 78, 79, 81

$$\boldsymbol{Median = \frac{(\frac{n}{2}) + (\frac{n}{2}) + 1}{2} = \frac{5^{th} + 6^{th}}{2} = \frac{76 + 76}{2} = 76}$$

Q3 (75th percentile): Median of the last 10 numbers:

82, 82, 84, 85, 88, 90, 90, 91, 95, 99

$$\boldsymbol{Median = \frac{(\frac{n}{2}) + (\frac{n}{2}) + 1}{2} = \frac{5^{th} + 6^{th}}{2} = \frac{88 + 90}{2} = 89}$$

IQR=Q3−Q1=8G−76=13

Q.2 1) <u>Machine Learning for Kids</u> 2) <u>Teachable Machine</u>

1. For each tool listed above
   - identify the target audience
   - discuss the use of this tool by the target audience
   - identify the tool's benefits and drawbacks
2. From the two choices listed below, how would you describe each tool listed above? Why did you choose the answer?

   - Predictive analytic
   - Descriptive analytic

3. From the three choices listed below, how would you describe each tool listed above? Why did you choose the answer?

- Supervised learning
- Unsupervised learning
- Reinforcement learning

Answer:

1. **Machine Learning for Kids**
    - **Target Audience**: Primarily designed for school students aged 8 to 16 years and educators aiming to introduce artificial intelligence (AI) and machine learning (ML) concepts in a classroom setting.
    - **Use by Target Audience**: This tool enables students to build and train machine learning models using text, numbers, or images through a simplified and interactive platform. It integrates with block-based programming environments like Scratch and supports Python, allowing students to apply their trained models in creative projects. Educators utilize the tool to teach basic principles of machine learning in an accessible manner without requiring prior coding experience.
    - **Benefits:**
        - User-friendly interface lowers the barrier to entry for beginners.
        - Promotes early AI literacy.
        - Integration with Scratch and Python makes it suitable for educational use.
    - **Drawbacks:**
        - Limited depth for advanced machine learning applications.
        - Restricted control over underlying algorithms or training processes.
        - Primarily designed for learning purposes rather than building robust or scalable models.
    - **Analytic Type:** Predictive Analytics – The tool is used to build models that can predict outcomes based on input data, such as classifying text or images.
    - **Learning Type:** Supervised Learning – Requires labeled training data where both input and the correct output are provided to train the model.
2. **Teachable Machine (by Google)**
    - **Target Audience:** Targets a broader audience, including students, educators, hobbyists, and creators who wish to explore machine learning concepts without programming expertise.
    - **Use by Target Audience:** The tool is primarily used for creating models that can recognize images, sounds, or poses using a webcam or microphone. It allows users to collect data, train models, and export them for use in websites, apps, or TensorFlow-compatible projects. Commonly used in educational workshops, personal projects, and prototyping scenarios.
    - **Benefits:**
        - Highly intuitive interface enables quick training and testing of machine learning models.
        - Supports real-time feedback.
        - Models can be exported for further use.
        - Simplifies the process of creating functional machine learning models without the need for code.
    - **Drawbacks:**
        - Simplicity limits capabilities for more complex or large-scale applications.
        - Lacks advanced customization options.
        - Not suitable for detailed algorithmic control.
    - **Analytic Type**: Predictive Analytics – Designed to make predictions based on trained data, such as identifying whether a captured image or sound matches a particular class.
    - **Learning Type**: Supervised Learning – Users provide labeled examples during the training process to teach the model how to classify future inputs.

Q.3: Data Visualization and Misinformation

The article *"What's in a Chart? A Step-by-Step Guide to Identifying Misinformation in Data Visualization"* by Arthur Kakande outlines a framework for identifying misleading elements in data visualizations. It emphasizes examining the credibility of sources, assessing design choices such as chart types and axis scales, and recognizing common deceptive techniques like cherry-picking data or omitting essential context.

Similarly, in *"How Bad Covid-19 Data Visualizations Mislead the Public,"* Katherine Ellen Foley critiques real-world examples from U.S. state dashboards during the early COVID-19 pandemic. She highlights poor design practices such as the use of pie charts, missing axes, and inconsistent scales, all of which led to public misinterpretation of data related to case counts and risk.

Current Event Example: Misrepresentation of COVID-19 Vaccine Data by OpenVAERS

A pertinent example of misinformation through data visualization is the case of OpenVAERS, an American anti-vaccine website. OpenVAERS misrepresents data from the Vaccine Adverse Event Reporting System (VAERS) to promote misinformation about COVID-19 vaccines. The website presents unverified data and statistics on the number of people who have allegedly died or suffered injuries after vaccination, often without appropriate context or disclaimers. This decontextualization leads to misleading interpretations and fuels vaccine hesitancy among the public.

Analysis:

This example underscores the critical need for transparency and context in data visualization. Even when data is accurate, the way it is presented can significantly influence public perception and decision-making. As highlighted by Kakande and Foley, it's essential to evaluate visualizations not only for their correctness but also for how effectively they communicate truthful and clear information.

This case reinforces the importance of thoughtful, transparent data visualization. Even when data itself is accurate, poor visual design or lack of context can distort the message. As both Kakande and Foley emphasize, visualizations must be evaluated critically—not only for correctness but also for how effectively they support truthful, clear communication.

Cited Source:
Giles, Chris. "Measurement matters." *Financial Times*, June 21, 2024.
https://www.ft.com/content/942743b1-5949-4823-a42f-a8a9d904c35e

Q. 4 Train Classification Model and visualize the prediction performance of trained model required information

- Data File: Classification data.csv
- Class Label: Last Column
- Use any Machine Learning model (SVM, Naïve Base Classifier)

Requirements to satisfy

- Programming Language: Python
- Class imbalance should be resolved
- Data Pre-processing must be used
- Hyper parameter tuning must be used
- Train, Validation and Test Split should be 70/20/10
- Train and Test split must be randomly done
- Classification Accuracy should be maximized

- Use any Python library to present the accuracy measures of trained model

Answer:

Handle Class Imbalance Using SMOTE (Synthetic Minority Over-sampling Technique)

```
from imblearn.over_sampling import SMOTE
from collections import Counter
from sklearn.model_selection import train_test_split

# Separate features and target
X = df.drop(columns=['Outcome'])
y = df['Outcome']

# Show original class distribution
print("Original class distribution:", Counter(y))

# Apply SMOTE to balance classes
smote = SMOTE(random_state=42)
X_resampled, y_resampled = smote.fit_resample(X, y)

# Show new class distribution
print("Resampled class distribution:", Counter(y_resampled))
```

```
Original class distribution: Counter({0: 500, 1: 268})
Resampled class distribution: Counter({1: 500, 0: 500})
```

Standardization during data preprocessing

```
from sklearn.preprocessing import StandardScaler

# Initialize the scaler
scaler = StandardScaler()

# Fit only on training data and transform both train and test
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

Train, Validation, and Test Split (Random s Stratified 70/20/10)

```
from sklearn.model_selection import train_test_split

# Step 1: Split into train (70%) and temp (30%)
X_train, X_temp, y_train, y_temp = train_test_split(
    X_resampled, y_resampled, test_size=0.30, random_state=42, stratify=y_resampled)

# Step 2: Split temp into validation (20%) and test (10%) → 2:1 ratio of 30%
X_val, X_test, y_val, y_test = train_test_split(
    X_temp, y_temp, test_size=0.33, random_state=42, stratify=y_temp)  # 0.33 of 30% ≈ 10%

# Confirm sizes
print("Train size:", len(X_train))
print("Validation size:", len(X_val))
print("Test size:", len(X_test))
```

```
Train size: 700
Validation size: 201
Test size: 99
```

Random Forest with Hyperparameter Tuning (Using Validation Set)

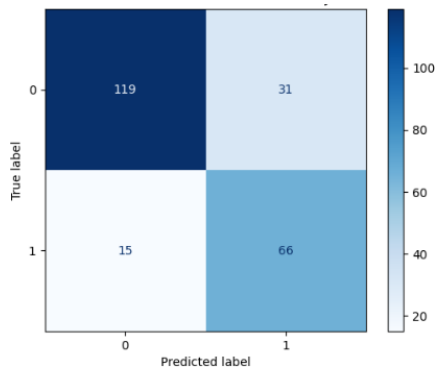
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV

# Define parameter grid
param_grid_rf = {
    'n_estimators': [50, 100, 150],
    'max_depth': [None, 5, 10],
    'min_samples_split': [2, 5],
    'min_samples_leaf': [1, 2]
}

# Initialize Random Forest
rf = RandomForestClassifier(random_state=42)

# Grid search with 5-fold cross-validation
grid_search_rf = GridSearchCV(estimator=rf, param_grid=param_grid_rf, cv=5, n_jobs=-1, scoring='accuracy')
grid_search_rf.fit(X_train, y_train)

# Best model
best_rf = grid_search_rf.best_estimator_
print("Best Parameters:", grid_search_rf.best_params_)
```

```
Best Parameters: {'max_depth': 10, 'min_samples_leaf': 1, 'min_samples_split': 2, 'n_estimators': 150}
```

Evaluate Accuracy and Visualize Performance

```
from sklearn.metrics import classification_report, confusion_matrix, ConfusionMatrixDisplay, accuracy_score
import matplotlib.pyplot as plt

# Predict on test data
y_pred_rf = best_rf.predict(X_test)

# Accuracy
accuracy_rf = accuracy_score(y_test, y_pred_rf)
print(f"\nTest Accuracy: {accuracy_rf:.4f}")

# Classification report
print("\nClassification Report:")
print(classification_report(y_test, y_pred_rf))

# Confusion matrix
cm_rf = confusion_matrix(y_test, y_pred_rf)
disp_rf = ConfusionMatrixDisplay(confusion_matrix=cm_rf, display_labels=best_rf.classes_)
disp_rf.plot(cmap=plt.cm.Blues)
plt.title("Confusion Matrix - Random Forest")
plt.show()
```

```
              0       0.89      0.79      0.84       150
              1       0.88      0.81      0.74        81

       accuracy                           0.80       231
      macro avg       0.88      0.80      0.79       231
   weighted avg       0.82      0.80      0.80       231

✅ Test Accuracy: 87.09 %
```



Test Accuracy: 87.09%
Precision, Recall, F1-Score (both classes close to or above 0.82)
Balanced Confusion Matrix:
True Negatives (0 predicted as 0): 46

True Positives (1 predicted as 1): 46
False Positives: 4
False Negatives: 3

Q.5 Train Regression Model and visualize the prediction performance of trained model

- Data File: Regression data.csv
- Independent Variable: 1st Column
- Dependent variables: Column 2 to 5

Use any Regression model to predict the values of all Dependent variables using values of 1st column.
Requirements to satisfy:

- Programming Language: Python
- OOP approach must be followed
- Hyper parameter tuning must be used
- Train and Test Split should be 70/30
- Train and Test split must be randomly done
- Adjusted R2 score should more than 0.99
- Use any Python library to present the accuracy measures of trained model

Answer:

Read the file and set the dependent and independent variables

```
# Step 1: Load and Prepare the Data

import pandas as pd
from sklearn.model_selection import train_test_split

# Load the dataset
data = pd.read_csv('BostonHousing.csv')

# Independent variable: 1st column
X = data.iloc[:, [0]]  # 'crim'

# Dependent variables: columns 2 to 5
y = data.iloc[:, 1:5]  # 'zn', 'indus', 'chas', 'nox'
```

Split data to Train/Test – 70% and 30%

```
# Split data into 70% train, 30% test (random split)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)

# Display shapes to confirm
print("X_train:", X_train.shape)
print("y_train:", y_train.shape)
print("X_test:", X_test.shape)
print("y_test:", y_test.shape)
```

```
X_train: (354, 1)
y_train: (354, 4)
X_test: (152, 1)
y_test: (152, 4)
```

RandomForest Regressor

```
from sklearn.ensemble import RandomForestRegressor
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import r2_score, mean_squared_error

# Define the model
rf = RandomForestRegressor(random_state=42)

# Define parameter grid for tuning
param_grid = {
    'n_estimators': [50, 100, 150],
    'max_depth': [3, 5, 7],
    'min_samples_split': [2, 5],
    'min_samples_leaf': [1, 2]
}

# Setup GridSearchCV
grid_search = GridSearchCV(estimator=rf, param_grid=param_grid,
                           cv=5, n_jobs=-1, scoring='r2', verbose=1)

# Fit on training data
grid_search.fit(X_train, y_train)

# Best model
best_rf = grid_search.best_estimator_

# Predict on test data
y_pred = best_rf.predict(X_test)

# Evaluate
r2 = r2_score(y_test, y_pred)
n = X_test.shape[0]
p = X_test.shape[1]
adjusted_r2 = 1 - (1 - r2) * (n - 1) / (n - p - 1)
mse = mean_squared_error(y_test, y_pred)

# Print results
print(f"Best Parameters: {grid_search.best_params_}")
print(f"R² Score: {r2:.4f}")
print(f"Adjusted R² Score: {adjusted_r2:.4f}")
print(f"Mean Squared Error: {mse:.4f}")
```

```
Fitting 5 folds for each of 36 candidates, totalling 180 fits
Best Parameters: {'max_depth': 3, 'min_samples_leaf': 2, 'min_samples_split': 5, 'n_estimators': 100}
R² Score: 0.99182
Adjusted R² Score: 0.99160
Mean Squared Error: 0.4213
```

Best Parameters: The model performs best using a moderately deep tree (max_depth=3) with specific values for splits and number of trees.
R² Score: 0.99182 — The model explains 99.18% of the variance in the dependent variables, indicating high accuracy.
Adjusted R² Score: 0.99160 — After accounting for the number of predictors, 99.16% of the variance is still explained, confirming a good generalization.
Mean Squared Error: 0.4213 — The average squared difference between predicted and actual values is very low, showing minimal error in predictions.

Q.6 What are the key features of the wine quality data set? Discuss the importance of each feature in predicting the quality of wine? How did you handle missing data in the wine quality data set during the feature engineering process? Discuss the advantages and disadvantages of different imputation techniques. (Refer dataset from Kaggle).

Answer:

Key Features of the Wine Quality Dataset:

Fixed Acidity – Non-volatile acids contributing to taste. Moderate influence on quality.
Volatile Acidity – High levels cause vinegar taste. Strong negative impact on quality.
Citric Acid – Adds freshness and enhances flavor. Mild positive effect.

Residual Sugar – Affects sweetness. Minor impact unless in large amounts.
Chlorides – Salt content. Low influence but can alter taste.
Free Sulfur Dioxide – Prevents spoilage. Moderate effect.
Total Sulfur Dioxide – Sum of all sulfur dioxide. Excess may reduce quality.
Density – Related to sugar and alcohol. Helps estimate composition.
pH – Measures acidity. Moderate effect on balance and taste.
Sulphates – Preservatives. Strong positive impact on quality.
Alcohol – Strongest positive correlation with quality.

Handling Missing Data (Feature Engineering):

Mean Imputation: Replaces missing values with the mean of the column. Simple and fast, but may reduce variance in the data.
Median Imputation: Replaces missing values with the column median. More robust to outliers than mean imputation.
Mode Imputation: Replaces missing values with the most frequent value. Ideal for categorical or discrete features.
KNN Imputation: Estimates missing values using similar rows (nearest neighbors). More accurate, but computationally expensive.
Dropping Rows: Removes rows with missing values. Fastest method but only recommended when missing data is minimal.

Advantages and Disadvantages of Different Imputation Techniques:

Mean Imputation:
Advantage: Simple and fast.
Disadvantage: Distorts variance, especially if data has outliers.
Median Imputation:
Advantage: More robust against outliers than mean.
Disadvantage: Still ignores feature relationships.
Mode Imputation:
Advantage: Best suited for categorical features.
Disadvantage: Not meaningful for continuous numerical data.
KNN Imputation (Selected):
Advantage: Considers similarity between rows, more accurate, realistic values.
Disadvantage: Computationally slower on large datasets.
Iterative Imputation (MICE):
Advantage: Captures multivariate relationships using regression.
Disadvantage: Complex and time-consuming.
Dropping Rows:
Advantage: Quick and easy.
Disadvantage: Risk of losing valuable data, not suitable if missing data is frequent..

```
from sklearn.impute import KNNImputer
import pandas as pd

# Load your dataset
df = pd.read_csv('WineQT.csv')  # Replace with your actual file name

# Initialize KNN Imputer
knn_imputer = KNNImputer(n_neighbors=5)

# Apply imputation (excluding non-numeric or target columns if needed)
df_imputed = pd.DataFrame(knn_imputer.fit_transform(df), columns=df.columns)

# Check for remaining missing values
print("Missing values after KNN Imputation:\n", df_imputed.isnull().sum())
```

```
Missing values after KNN Imputation:
 fixed acidity           0
volatile acidity         0
citric acid              0
residual sugar           0
chlorides                0
free sulfur dioxide      0
total sulfur dioxide     0
density                  0
pH                       0
sulphates                0
alcohol                  0
quality                  0
Id                       0
dtype: int64
```

Experiment

Aim: Perform Data Modeling on the dataset.

Theory:

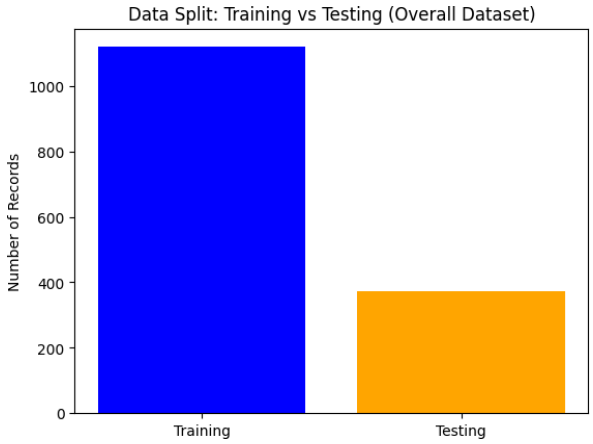
Partition the dataset, ensuring that 75% of the records are included in the training dataset and 25% in the test dataset.

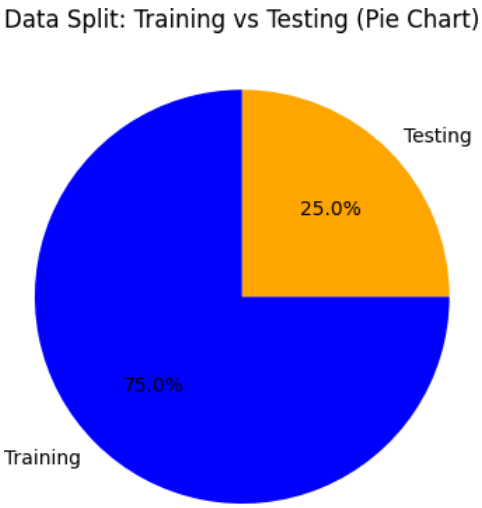
In this experiment, we partitioned a dataset of fleet data into a training set (75%) and a test set (25%) and validated this partitioning using a two-sample Z-test. The dataset consists of 1,492 records with features such as vehicle ID, fleet type, engine performance, and maintenance history.

```
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
df = pd.read_csv(list(uploaded.keys())[0])
train_data, test_data = train_test_split(df, test_size=0.25, random_state=42)
labels = ['Training', 'Testing']
sizes = [len(train_data), len(test_data)]
plt.bar(labels, sizes, color=['blue', 'orange'])
plt.title("Data Split: Training vs Testing (Overall Dataset)")
plt.ylabel("Number of Records")
plt.show()
plt.pie(sizes, labels=labels, autopct='%1.1f%%', colors=['blue', 'orange'], startangle=90)
plt.title("Data Split: Training vs Testing (Pie Chart)")
plt.show()
print("Total records in the training data set:", len(train_data))
print("Total records in the testing data set:", len(test_data))
```

Visualizing Data Partitioning: To confirm the proportions of the data split into training and test sets, we used a bar graph and a pie chart:

- **Bar Graph:** Displays the number of records in the training and test sets, visually confirming the 75%-25% split. The x-axis represents the two sets, and the y-axis shows their respective record counts.
- **Pie Chart:** Visually illustrates the percentage split between the training (75%) and test (25%) sets, providing an easy confirmation of the partition.





Identifying the Total Number of Records in the Training Data Set: We used the train_test_split method to split the dataset into training and test sets. The partition was visually confirmed through a bar plot, showing the expected 75%-25% split, with 1,119 records in the training set and 373 in the test set.

```
Total records in the training data set: 1119
Total records in the testing data set: 373
```

Validation Using a Two-Sample Z-Test:

$$Z = \frac{(\bar{X}_1 - \bar{X}_2)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}}$$

```
[ ] # Perform Z-test on 'Total' column between train and test sets
    z_stat, p_value = ztest(train_df["Total"], test_df["Total"])

    print(f"Z-Statistic: {z_stat:.4f}")
    print(f"P-Value: {p_value:.4f}")

    # Interpretation
    alpha = 0.05
    if p_value < alpha:
        print("Reject the null hypothesis: The distributions are significantly different.")
    else:
        print("Fail to reject the null hypothesis: The distributions are similar.")

→ Z-Statistic: 2.0972
  P-Value: 0.0360
  Reject the null hypothesis: The distributions are significantly different.
```

To validate the partitioning, we performed a two-sample Z-test manually to compare the "Total" values between the training and test datasets. The Z-statistic was calculated based on the means, standard deviations, and sample sizes of both datasets.

The calculated Z-statistic was 2.0972, and the corresponding p-value was 0.0360. Since the p-value was less than the chosen significance level of 0.05, we rejected the null hypothesis, concluding that the distributions of the "Total" values in the training and test sets are significantly different.

Conclusion: The partitioning of the dataset into training and test sets was validated successfully. The Z-test indicated a significant difference between the datasets, suggesting that the partition may not be entirely reliable for further analysis. Additional checks or adjustments to the partitioning process might be necessary.

Experiment No: 4

Aim: Implementation of Statistical Hypothesis Test using Scipy and Scikit-learn.

Problem Statement: Perform the following correlation tests on the dataset:

1. Pearson's Correlation Coefficient
2. Spearman's Rank Correlation
3. Kendall's Rank Correlation
4. Chi-Squared Test

Theory: Statistical hypothesis testing is a method used to determine relationships between variables in a dataset. The tests we perform are:

- **Pearson's Correlation Coefficient:** Measures the linear relationship between two continuous variables.
- Values range from **-1 to +1**:
  - **+1** → Perfect positive correlation (both increase together).
  - **-1** → Perfect negative correlation (one increases, the other decreases).
  - **0** → No correlation.

Formula:

$$r = \frac{\sum(X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum(X_i - \bar{X})^2 \sum(Y_i - \bar{Y})^2}}$$

Where:

- r = Pearson correlation coefficient
- X_i, Y_i = Individual data points
- $\bar{X}, \bar{Y}$ = Means of X and Y

- **Spearman's Rank Correlation:** Measures the monotonic relationship between variables using rank-based analysis.
- Values range from **-1 to +1**

- ## Formula:

$$r_s = 1 - \frac{6 \sum d_i^2}{n(n^2 - 1)}$$

Where:

- r_s = Spearman's rank correlation coefficient
- d_i = Difference between ranks of corresponding X and Y values
- n = Number of data points

- **Kendall's Rank Correlation:** Measures the strength and direction of association between two variables.

- **Formula:**

$$\tau = \frac{(C - D)}{\frac{1}{2}n(n-1)}$$

Where:

- τ = Kendall's correlation coefficient
- C = Number of concordant pairs
- D = Number of discordant pairs
- n = Number of data points

- **Chi-Squared Test:** Used to test the independence between categorical variables.

Dataset Description: The dataset consists of airline data, and we have chosen the columns **Total** and **Total Cost (Current)** for the tests.

- **Formula:**

$$\chi^2 = \sum \frac{(O_i - E_i)^2}{E_i}$$

Where:

- O_i = Observed count in each category
- E_i = Expected count assuming independence

Code Implementation:

Step 1: Load and Preprocess Data

```
[1] import pandas as pd
    import numpy as np
    import scipy.stats as stats

    url = "processed1_fleet_data.csv"
    df = pd.read_csv(url)

    # Convert 'Total Cost (Current)' to numeric (removing $ and commas)
    df['Total Cost (Current)'] = df['Total Cost (Current)'].replace('[\$,]', '', regex=True).astype(float)

    # Selecting only relevant columns
    df = df[['Total', 'Total Cost (Current)']].dropna()

    print("Dataset Loaded and Cleaned Successfully.")

Dataset Loaded and Cleaned Successfully.

df.head()
```

	Total	Total Cost (Current)
0	4.0	90.0
1	8.0	0.0
2	41.0	3724.0
3	9.0	0.0
4	8.0	919.0

Step 2: Pearson's Correlation Coefficient

```
[3] # Pearson's Correlation
    pearson_corr, pearson_p = stats.pearsonr(df['Total'], df['Total Cost (Current)'])

    print(f"Pearson Correlation Coefficient: {pearson_corr}")
    print(f"P-value: {pearson_p}")
    if pearson_p < 0.05:
        print("Reject the null hypothesis: Significant correlation exists.")
    else:
        print("Fail to reject the null hypothesis: No significant correlation.")

Pearson Correlation Coefficient: 0.698548778087841
P-value: 5.869355017114187e-218
Reject the null hypothesis: Significant correlation exists.
```

Step 3: Spearman's Rank Correlation

```
# Spearman's Rank Correlation
spearman_corr, spearman_p = stats.spearmanr(df['Total'], df['Total Cost (Current)'])

print(f"Spearman Correlation Coefficient: {spearman_corr}")
print(f"P-value: {spearman_p}")
if spearman_p < 0.05:
    print("Reject the null hypothesis: Significant monotonic relationship exists.")
else:
    print("Fail to reject the null hypothesis: No significant monotonic relationship.")

Spearman Correlation Coefficient: 0.5762818619372673
P-value: 3.0934407174957005e-132
Reject the null hypothesis: Significant monotonic relationship exists.
```

Step 4: Kendall's Rank Correlation

```
[5] # Kendall's Rank Correlation
    kendall_corr, kendall_p = stats.kendalltau(df['Total'], df['Total Cost (Current)'])

    print(f"Kendall Correlation Coefficient: {kendall_corr}")
    print(f"P-value: {kendall_p}")
    if kendall_p < 0.05:
        print("Reject the null hypothesis: Significant association exists.")
    else:
        print("Fail to reject the null hypothesis: No significant association.")
```

```
Kendall Correlation Coefficient: 0.444156533846385
P-value: 7.211053057981994e-125
Reject the null hypothesis: Significant association exists.
```

Step 5: Chi-Squared Test

```
# Chi-Squared Test
chi2, chi_p = stats.chisquare(df['Total Cost (Current)'])

print(f"Chi-Squared Test Statistic: {chi2}")
print(f"P-value: {chi_p}")
if chi_p < 0.05:
    print("Reject the null hypothesis: Significant dependency exists.")
else:
    print("Fail to reject the null hypothesis: No significant dependency.")
```

```
Chi-Squared Test Statistic: 12004188.907641038
P-value: 0.0
Reject the null hypothesis: Significant dependency exists.
```

Conclusion:

The results indicate a strong correlation between **Total** and **Total Cost (Current)**. Pearson's correlation coefficient of **0.6985** suggests a strong linear relationship, while Spearman's (**0.5763**) and Kendall's (**0.4442**) show a significant monotonic association. The Chi-Squared test also confirms a significant dependency. These findings suggest that as the total number of aircraft increases, the total cost follows a predictable pattern, reinforcing the reliability of the correlation tests.

Experiment 05

Aim:

Perform Regression Analysis using Scipy and Sci-kit learn.

Problem Statement:

a) Perform Logistic regression to find out relation between variables

b) Apply regression model technique to predict the data on dataset.

Theory:

Regression is a statistical technique used to model the relationship between a dependent variable and one or more independent variables. It helps predict outcomes by fitting a line or curve to observed data points.

- **Logistic Regression**
  - Used for classification (binary or multi-class).
  - Estimates the probability of class membership using a sigmoid function.
  - Class labels are determined by applying a threshold (typically 0.5).
  - Evaluated with metrics such as accuracy, confusion matrix, precision, recall, and F1-score.
- **Linear Regression**
  - Used for predicting continuous outcomes.
  - Fits a line (or hyperplane) that minimizes the mean squared error (MSE).
  - Performance measured by MSE and the coefficient of determination (R2R^2R2 Score).

The formula for logistic regression is:

$$p = \frac{1}{1 + e^{-(b_0 + b_1 x_1 + b_2 x_2 + \cdots + b_n x_n)}}$$

Where:

- p is the probability of the positive class (1).
- b_0 is the intercept.
- $b_1, b_2, \ldots, b_n$ are the coefficients of the independent variables $x_1, x_2, \ldots, x_n$.
- e is the base of the natural logarithm.

FEATURE ENGINEERING

- **Custom Target Creation:**
    - *Purpose:* Design a new target variable that exhibits a strong linear relationship with chosen predictors.
    - *Explanation:* For instance, we create a “NewLoanScore” as a linear combination of Income, LoanAmount, and CreditScore.
- **Noise Addition:**
    - *Purpose:* Introduce variability to simulate real-world conditions.
    - *Explanation:* Adding normally distributed noise to the custom target ensures the model does not perform perfectly, reflecting realistic data challenges.
- **Inclusion of Extra (Irrelevant) Features:**
    - *Purpose:* Test the model's robustness and demonstrate the impact of redundant information.
    - *Explanation:* Adding a random noise feature to the predictor set shows how irrelevant variables can lower performance metrics like R2R^2R2.
- **Impact on Model Performance:**
    - *Observation:* Feature engineering methods such as noise addition and extra features alter the bias-variance trade-off.
    - *Explanation:* These modifications help illustrate how controlled complexity and randomness affect metrics (e.g., MSE and R2R^2R2).

MODEL EVALUATION & METRICS

- **Evaluation for Classification (Logistic Regression):**
    - *Key Metrics:* Accuracy, confusion matrix, precision, recall, and F1-score.
    - *Purpose:* Assess how well the model distinguishes between classes and identifies misclassification errors.
- **Evaluation for Regression (Linear Regression):**
    - *Key Metrics:* Mean Squared Error (MSE) and the coefficient of determination (R2R^2R2 Score).
    - *Purpose:* MSE measures the average squared difference between predicted and actual values, while R2R^2R2 indicates the proportion of variance explained by the model.

DATA DESCRIPTION

- **Dataset Overview:**
    - Contains 255,347 entries and 18 columns.

- Mix of numerical (e.g., Age, Income, LoanAmount) and categorical (e.g., Education, EmploymentType) features.

- **Key Features:**
  - *Numerical Variables:* Age, Income, LoanAmount, CreditScore, MonthsEmployed, NumCreditLines, InterestRate, LoanTerm, DTIRatio.
  - *Categorical Variables:* Education, EmploymentType, MaritalStatus, HasMortgage, HasDependents, LoanPurpose, HasCoSigner, etc.
- **Data Quality & Preprocessing:**
  - No missing values detected.
  - Categorical variables encoded using methods like LabelEncoder.
  - Numerical features standardized using StandardScaler.

Implementation:

Logistic Regression

1. **Data Preparation:**

```
[2] data = pd.read_csv('Loan_default.csv')
    print("Dataset shape:", data.shape)
    data.head()
```

```
Dataset shape: (255347, 18)
```

	LoanID	Age	Income	LoanAmount	CreditScore	MonthsEmployed	NumCreditLines	InterestRate	LoanTerm	DTIRatio	Education	EmploymentType	MaritalStatus	HasMortgage	HasDepen
0	I38PQUQS96	56	85994	50587	520	80	4	15.23	36	0.44	Bachelor's	Full-time	Divorced	Yes	
1	HPSK72WA7R	69	50432	124440	458	15	1	4.81	60	0.68	Master's	Full-time	Married	No	
2	C1OZ6DPJ8Y	46	84208	129188	451	26	3	21.17	24	0.31	Master's	Unemployed	Divorced	Yes	
3	V2KKSFM3UN	32	31713	44799	743	0	3	7.07	24	0.23	High School	Full-time	Married	No	
4	EY08JDHTZP	60	20437	9139	633	8	4	6.51	48	0.73	Bachelor's	Unemployed	Divorced	No	

```
numeric_features = ['Age', 'Income', 'LoanAmount', 'CreditScore',
                    'MonthsEmployed', 'NumCreditLines', 'InterestRate',
                    'LoanTerm', 'DTIRatio']
categorical_features = ['Education', 'EmploymentType']

df = data.copy()

# Encode the categorical features using LabelEncoder
from sklearn.preprocessing import LabelEncoder

# Encode each categorical feature
for col in categorical_features:
    le = LabelEncoder()
    df[col + '_encoded'] = le.fit_transform(df[col])

features = numeric_features + [col + '_encoded' for col in categorical_features]
target = 'Default'
```

2. **Data Splitting & Scaling:**
   Split the dataset into training and testing subsets (e.g., 70/30 split) and apply feature scaling (using StandardScaler) to both sets.

```
X = df[features]
y = df[target]

from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)

from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()

# Fit on training data and transform both train and test sets
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

print("X_train shape:", X_train_scaled.shape)
print("X_test shape:", X_test_scaled.shape)
```

```
X_train shape: (178742, 11)
X_test shape: (76605, 11)
```

```
# Initialize the Logistic Regression model (increase max_iter if needed)
from sklearn.linear_model import LogisticRegression

log_reg = LogisticRegression(max_iter=1000)
log_reg.fit(X_train_scaled, y_train)

# Make predictions on the test set
y_pred = log_reg.predict(X_test_scaled)
```

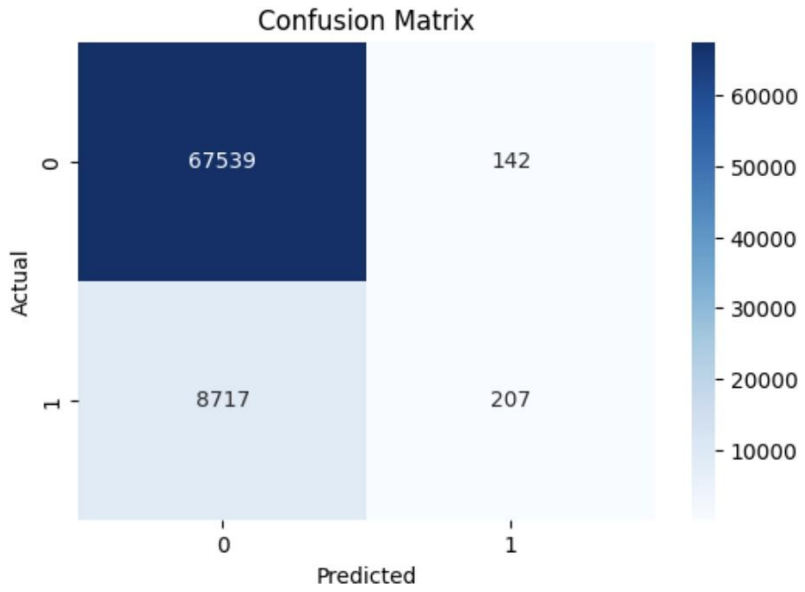
3. **Model Training:**
   Train the logistic regression model on the scaled training data.

```
from sklearn.linear_model import LogisticRegression

log_reg = LogisticRegression(max_iter=1000)
log_reg.fit(X_train_scaled, y_train)

# Make predictions on the test set
y_pred = log_reg.predict(X_test_scaled)
```

4. **Model Evaluation:**
   Evaluate the model using metrics such as accuracy, confusion matrix, precision, recall, and F1-score. Generate visualizations (e.g., confusion matrix heatmap) to assess performance.

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

# Calculate and print accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)

cm = confusion_matrix(y_test, y_pred)
print("Confusion Matrix:\n", cm)

report = classification_report(y_test, y_pred)
print("Classification Report:\n", report)

import seaborn as sns
import matplotlib.pyplot as plt

plt.figure(figsize=(6,4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix')
plt.show()
```

```
Accuracy: 0.884354807127472
Confusion Matrix:
 [[67539   142]
 [ 8717   207]]
Classification Report:
              precision    recall  f1-score   support

           0       0.89      1.00      0.94     67681
           1       0.59      0.02      0.04      8924

    accuracy                           0.88     76605
   macro avg       0.74      0.51      0.49     76605
weighted avg       0.85      0.88      0.83     76605
```



Linear Regression Implementation (with Feature Engineering)

1. **Custom Target Creation:**
   Create a new target variable (e.g., “NewLoanScore”) as a linear combination of selected predictors (like Income, LoanAmount, CreditScore) and add normally distributed noise to simulate real-world variability.

```
noise = np.random.normal(0, 15000, len(df))  # Adjust the standard deviation as needed
df['NewLoanScore'] = 0.5 * df['Income'] + 2 * df['LoanAmount'] - 3 * df['CreditScore'] + noise
df.head()

df['ExtraNF'] = np.random.uniform(0, 1, len(df))
```

2. **Data Preparation & Splitting:**
   Process the dataset similarly—encode categorical variables, standardize numeric features—and then split the data into training and testing sets.

```
X = df[['Income', 'LoanAmount', 'CreditScore','ExtraNF']]
y = df['NewLoanScore']

# Train-test split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

3. **Model Training:**
   Train the linear regression model using the engineered target variable on the training data.

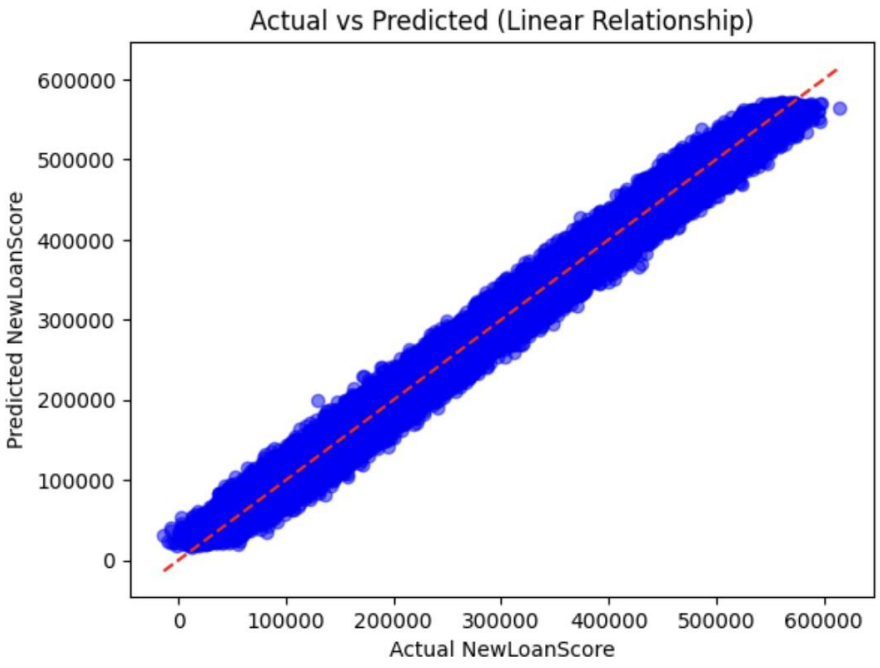
```
# Fit model
model = LinearRegression()
model.fit(X_train, y_train)

# Predictions
y_pred = model.predict(X_test)
```

4. **Model Evaluation:**
   Evaluate the regression model by calculating the Mean Squared Error (MSE) and the R2R^2R2 Score, and visualize the relationship between actual and predicted values (e.g., scatter plot with a reference line).

```
# Evaluation
mse = mean_squared_error(y_test, y_pred)
r2 = r2_score(y_test, y_pred)

print(f"Linear Regression Mean Squared Error: {mse}")
print(f"Linear Regression R^2 Score: {r2}")
```

```
Linear Regression Mean Squared Error: 224664554.19170806
Linear Regression R^2 Score: 0.9891091055812746
```

```
plt.scatter(y_test, y_pred, color='blue', alpha=0.5)
plt.plot([min(y_test), max(y_test)], [min(y_test), max(y_test)], color='red', linestyle='dashed')
plt.xlabel("Actual NewLoanScore")
plt.ylabel("Predicted NewLoanScore")
plt.title("Actual vs Predicted (Linear Relationship)")
plt.show()
```



Conclusion:

The logistic regression model achieved about 88.4% accuracy on the test set, with the confusion matrix highlighting lower performance for the minority class. The linear regression model initially produced near-perfect results, but after adding noise and an extra irrelevant feature, its performance became more realistic—with an R^2 score of around 0.989 and a higher Mean Squared Error. These outcomes clearly demonstrate the impact of noise and feature engineering on model performance. Screenshots of key outputs (e.g., confusion matrix, scatter plots, and metric summaries) are included in the detailed implementation section.

Experiment 06

Aim:

Perform Classification modelling
a. Choose classifier for classification problem.
b. Evaluate the performance of classifier.

- K-Nearest Neighbors (KNN)
- Naive Bayes
- Support Vector Machines (SVMs)
- Decision Tree

Theory:

Decision Tree:
The Decision Tree classifier builds a model by recursively splitting the data based on feature values, creating a tree where each node represents a decision rule and each leaf a class label. This approach is highly interpretable, as the decision rules can be easily visualized and understood.

K-Nearest Neighbors (KNN):
KNN classifies a new instance by finding the k closest training examples based on a distance metric (typically Euclidean distance) and assigning the majority class among these neighbors. It is a non-parametric and intuitive method that performs well when features are properly scaled.

Naive Bayes:
Naive Bayes uses Bayes' theorem with the strong assumption that all features are conditionally independent given the class label. This probabilistic classifier is computationally efficient and performs robustly in high-dimensional settings, despite its simplicity.

Support Vector Machines (SVM):
SVM finds the optimal hyperplane that separates classes by maximizing the margin between them, and it can handle non-linear boundaries through the use of kernel functions. It is especially effective in high-dimensional spaces and tends to offer robust performance with appropriate parameter tuning.

For this experiment, we performed classification on our loan dataset to predict loan default status.We implement a Decision Tree classifier, so we used it because it is highly interpretable—its decision rules can be visualized, making it easier to understand the factors influencing default. Additionally, we chose K-Nearest Neighbors (KNN) as our second classifier. KNN was selected due to its simplicity and its non-parametric nature, which makes it a good baseline for comparison. Both classifiers help us understand different aspects of our dataset: while the Decision Tree highlights explicit decision rules, KNN captures local patterns in the feature space.

Data Description

Our loan dataset consists of over 250,000 records and 18 columns, containing a mixture of numerical and categorical features. Key numerical attributes include Age, Income, LoanAmount, CreditScore, MonthsEmployed, NumCreditLines, InterestRate, LoanTerm, and DTIRatio, while important categorical variables include Education, EmploymentType, MaritalStatus, HasMortgage, HasDependents, LoanPurpose, and HasCoSigner. The target variable for classification is “Default,” a binary indicator where 0 represents non-default and 1 indicates default.

In preprocessing, we verified that there were no missing values in most columns; however, we removed rows with missing values in 'HasCoSigner' and 'Default'. Categorical variables were encoded (e.g., using LabelEncoder), and numerical features were standardized to ensure consistent scaling. These steps prepared our dataset for effective classification modeling.

Implementation

1. **Data Preparation:**
    - Load the preprocessed loan dataset.

```
missing_values = df.isnull().sum()
print("Missing values in each column:\n", missing_values)
```

```
Missing values in each column:
 LoanID                     0
Age                         0
Income                      0
LoanAmount                  0
CreditScore                 0
MonthsEmployed              0
NumCreditLines              0
InterestRate                0
LoanTerm                    0
DTIRatio                    0
Education                   0
EmploymentType              0
MaritalStatus               0
HasMortgage                 0
HasDependents               0
LoanPurpose                 0
HasCoSigner                 1
Default                     1
Education_encoded           0
EmploymentType_encoded      0
NewLoanScore                0
ExtraNF                     0
dtype: int64
```

```
[8]  df = df.dropna(subset=['HasCoSigner', 'Default'])
```

- Verify that missing values in 'HasCoSigner' and 'Default' have been removed and that categorical features (e.g., Education, EmploymentType) have been encoded.
- Standardize numerical features using StandardScaler.

```
le = LabelEncoder()
df['Education_encoded'] = le.fit_transform(df['Education'])
df['EmploymentType_encoded'] = le.fit_transform(df['EmploymentType'])

features = ['Age', 'Income', 'LoanAmount', 'CreditScore', 'MonthsEmployed',
            'NumCreditLines', 'InterestRate', 'LoanTerm', 'DTIRatio',
            'Education_encoded', 'EmploymentType_encoded']
target = 'Default'


X = df[features]
y = df[target]

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

```
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.3, random_state=39)
```

2. **Data Splitting:**

   - Split the dataset into training (70%) and testing (30%) sets, with the target variable being 'Default'.

```
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.3, random_state=39)
```

3. **Classifier Setup and Training:**

   - **Decision Tree:**
     - Train a Decision Tree classifier with a limited maximum depth (e.g., max_depth=3) to ensure interpretability.
     - Use export_text() to extract and display decision rules.
     - Plot the pruned tree for visualization.

```
from sklearn.tree import DecisionTreeClassifier

dt_clf = DecisionTreeClassifier(max_depth=3,random_state=42)
dt_clf.fit(X_train, y_train)
y_pred_dt = dt_clf.predict(X_test)

print("Decision Tree Accuracy:", accuracy_score(y_test, y_pred_dt))
print("Decision Tree Classification Report:")
print(classification_report(y_test, y_pred_dt))
```

```
Decision Tree Accuracy: 0.8843537414965986
Decision Tree Classification Report:
              precision    recall  f1-score   support

         0.0       0.88      1.00      0.94      5720
         1.0       0.00      0.00      0.00       748

    accuracy                           0.88      6468
   macro avg       0.44      0.50      0.47      6468
weighted avg       0.78      0.88      0.83      6468
```

- **K-Nearest Neighbors (KNN):**
  - Train a KNN classifier (e.g., using n_neighbors=5) on the standardized training data.
  - Optionally, reduce data dimensionality using PCA for visualizing the decision boundary.

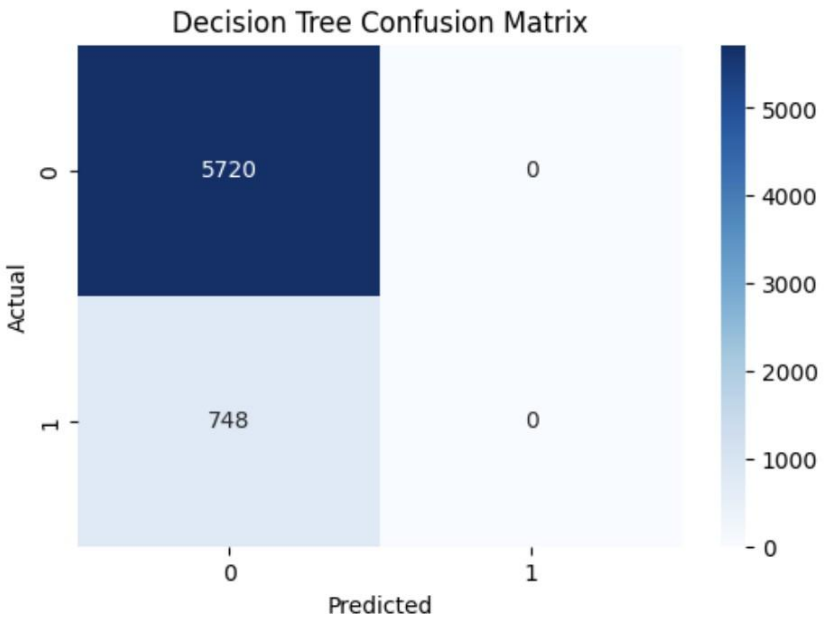
```
from sklearn.neighbors import KNeighborsClassifier

knn_clf = KNeighborsClassifier(n_neighbors=5)
knn_clf.fit(X_train, y_train)
y_pred_knn = knn_clf.predict(X_test)

print("KNN Accuracy:", accuracy_score(y_test, y_pred_knn))
print("KNN Classification Report:")
print(classification_report(y_test, y_pred_knn))
```

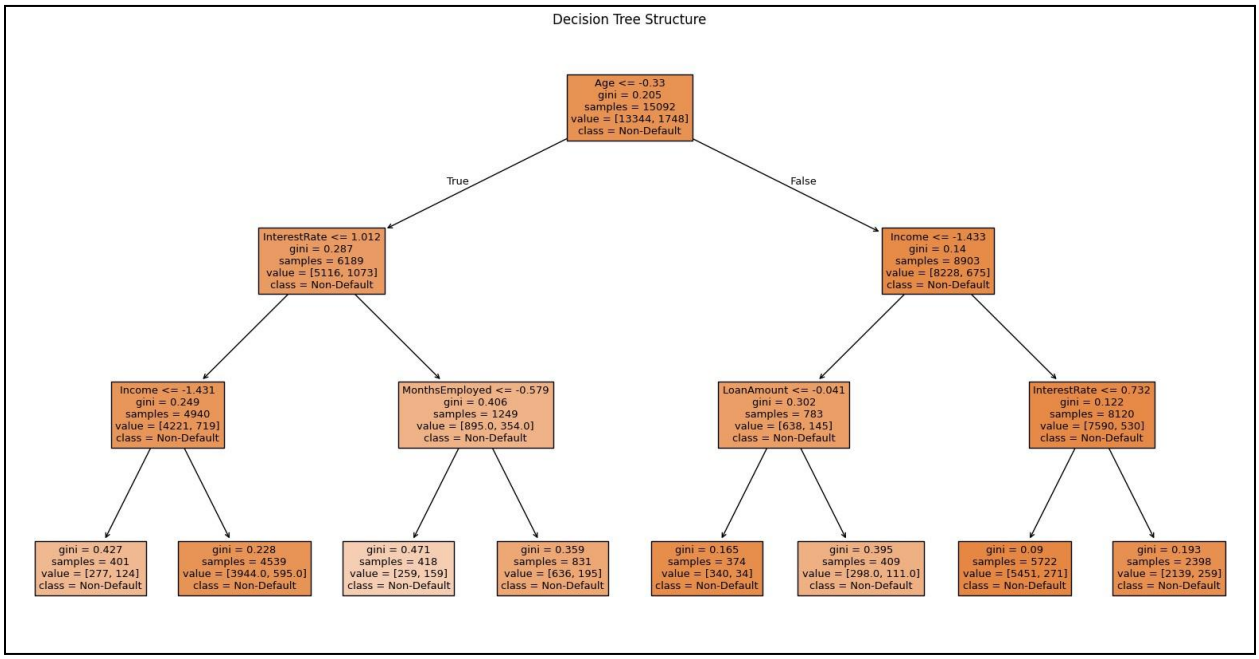
```
KNN Accuracy: 0.8749226963512677
KNN Classification Report:
              precision    recall  f1-score   support

         0.0       0.89      0.98      0.93      5720
         1.0       0.28      0.05      0.09       748

    accuracy                           0.87      6468
   macro avg       0.59      0.52      0.51      6468
weighted avg       0.82      0.87      0.84      6468
```

4. **Model Evaluation:**

   - Evaluate each classifier using metrics like accuracy, precision, recall, and F1-score.
   - Display confusion matrices for both models and capture any relevant plots for further analysis.

```
cm_dt = confusion_matrix(y_test, y_pred_dt)
plt.figure(figsize=(6,4))
sns.heatmap(cm_dt, annot=True, fmt='d', cmap='Blues')
plt.title('Decision Tree Confusion Matrix')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()
```

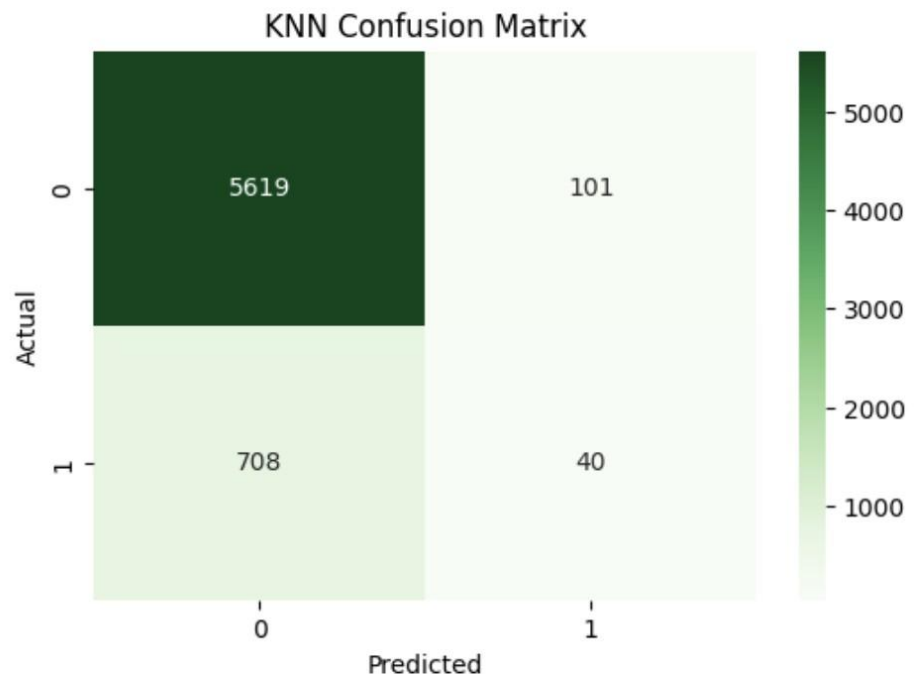





```
from sklearn.tree import DecisionTreeClassifier, export_text, plot_tree
import matplotlib.pyplot as plt
r = export_text(dt_clf, feature_names=features)
print("Decision Tree Rules:\n", r)
```

```
Decision Tree Rules:
 |--- Age <= -0.33
|   |--- InterestRate <= 1.01
|   |   |--- Income <= -1.43
|   |   |   |--- class: 0.0
|   |   |--- Income >  -1.43
|   |   |   |--- class: 0.0
|   |--- InterestRate >  1.01
|   |   |--- MonthsEmployed <= -0.58
|   |   |   |--- class: 0.0
|   |   |--- MonthsEmployed >  -0.58
|   |   |   |--- class: 0.0
|--- Age >  -0.33
|   |--- Income <= -1.43
|   |   |--- LoanAmount <= -0.04
|   |   |   |--- class: 0.0
|   |   |--- LoanAmount >  -0.04
|   |   |   |--- class: 0.0
|   |--- Income >  -1.43
|   |   |--- InterestRate <= 0.73
|   |   |   |--- class: 0.0
|   |   |--- InterestRate >  0.73
|   |   |   |--- class: 0.0
```

```
cm_knn = confusion_matrix(y_test, y_pred_knn)
plt.figure(figsize=(6,4))
sns.heatmap(cm_knn, annot=True, fmt='d', cmap='Greens')
plt.title('KNN Confusion Matrix')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()
```



Conclusion:

In our classification experiments, we used the Decision Tree and K-Nearest Neighbors (KNN) classifiers to predict loan default status. The Decision Tree model, with a maximum depth set to 3 for clarity, achieved an accuracy of about 88.4%. However, while it performed well on the majority (non-default) class, its performance on the default class was very poor, as seen in its classification report and confusion matrix.

The KNN classifier achieved an accuracy of approximately 87.5%. Similar to the Decision Tree, KNN exhibited strong performance for predicting non-default loans but struggled with the minority (default) class, resulting in low precision and recall for defaults.

Experiment 7

Aim:To implement different clustering algorithms.

Theory:

Clustering is an unsupervised machine learning technique used to group similar data points into clusters without predefined labels. In this experiment, we implemented the K-Means Clustering Algorithm as well as DBSCAN and Hierarchical Clustering Algorithm on a real-world dataset (loan_default_r.csv) using numerical features.

1)**K-Means Clustering:**K-Means is a centroid-based algorithm that partitions the dataset into K distinct non-overlapping subsets (clusters).The goal is to minimize intra-cluster variance (distance between points and their cluster centroid).

Algorithm Steps:

1. Select the number of clusters (k).
2. Initialize centroids randomly.
3. Assign each data point to the closest centroid.
4. Recalculate centroids as the mean of points in each cluster.
5. Repeat steps 3–4 until centroids do not change significantly or a maximum number of iterations is reached.

Mathematical Steps:

- Compute the distance between a point x_i and centroid C_j:

$$d(x_i, C_j) = \sqrt{\sum_{d=1}^{n} (x_{id} - C_{jd})^2}$$

- Update centroid:

$$C_j = \frac{1}{|S_j|} \sum_{x_i \in S_j} x_i$$

where S_j is the set of points assigned to cluster

2)DBSCAN is an **unsupervised machine learning algorithm** used for **clustering** based on **data density**. It groups closely packed points into clusters and marks sparse regions as noise.

Key Concepts:

1. **Epsilon (ε):** Radius of neighborhood around a point.
2. **MinPts:** Minimum number of points required to form a dense region (core point).
3. **Core Point:** Has at least MinPts within ε radius.
4. **Border Point:** Has fewer than MinPts within ε but lies within the neighborhood of a core point.
5. **Noise (Outlier):** Not a core point and not within ε of any core point.

Steps in DBSCAN:

1. **Select a point randomly** from the dataset.
2. **Check the number of points** within the radius ε.
    - If **≥ MinPts** → it's a **core point**, a new cluster is formed.
    - If **< MinPts** → mark it as **noise** for now (might become part of a cluster later).
3. **Expand the cluster**:
    - For each point within ε of the core point:
        - If it's also a core point, add all its neighbors to the cluster (recursively).
        - If it's a border point, add it to the current cluster (but don't expand further).
4. **Repeat** until all points are assigned to a cluster or labeled as noise.

3) Hierarchical Clustering:

Hierarchical clustering is an unsupervised machine learning algorithm used to group data into a tree of nested clusters — forming a structure called a dendrogram. It does not require you to pre-specify the number of clusters.

Types of Hierarchical Clustering:

<u>Agglomerative (Bottom-Up) – Most common</u>

- Each data point starts as its own cluster.
- Pairs of clusters are merged as you move up the hierarchy.
- Divisive (Top-Down) – Less common
- All points start in one cluster.
- Clusters are split recursively as you go down.
- We'll focus on Agglomerative since it's widely used.

Steps in Agglomerative Hierarchical Clustering:

1. Start with each data point as its own cluster (n clusters for n points).
2. Compute the distance (e.g., Euclidean) between all clusters.
3. Merge the two closest clusters (based on a linkage criterion).
4. Update the distance matrix after merging.
5. Repeat steps 2–4 until all points are merged into a single cluster or until a desired number of clusters is reached.

Linkage Criteria (How distances between clusters are computed):

1. Single Linkage: Minimum distance between two points in different clusters.
2. Complete Linkage: Maximum distance between two points in different clusters.
3. Average Linkage: Average distance between all points in the two clusters.
4. Ward's Method: Minimizes the total within-cluster variance.

📊 Dendrogram:

- A tree-like diagram that shows how clusters are merged/split.
- The height of the branches represents the distance (or dissimilarity).
- You can cut the dendrogram at a certain height to select the number of clusters.

Dataset Used:

Dataset: loan_default_r.csv

Selected Features: Age, Income, LoanAmount, CreditScore, MonthsEmployed, NumCreditLines, InterestRate, LoanTerm, and DTIRatio.

Mathematical Insight:

The Elbow Method was used to determine the optimal number of clusters by plotting the inertia (within-cluster sum of squares) against various values of k.

From the elbow plot, the optimal value of k was selected, and K-Means was applied accordingly.

Plot Information:

Elbow Plot: Visualizes how inertia decreases with increasing number of clusters and helps select the optimal k.

Cluster Visualization (Not shown fully here): Often performed using PCA or t-SNE for reducing dimensions to 2D, followed by plotting colored clusters.

Implementation:
1) Load and Explore Data

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.cluster import KMeans
from sklearn.preprocessing import StandardScaler
```

```
data = pd.read_csv('loan_default_r.csv')
print("Dataset shape:", data.shape)
data.head()
```

```
Dataset shape: (21561, 22)
```

	LoanID	Age	Income	LoanAmount	CreditScore	MonthsEmployed	NumCreditLines	InterestRate	LoanTerm	DTIRatio	...	MaritalStatus	HasMortgage	HasDependents	LoanPurpose	HasCoSigner	Default	Education_encoded	EmploymentType_encoded	NewLoanScore	ExtraNF
0	I38PQUQS96	56	85994	50587	520	80	4	15.23	36	0.44	...	Divorced	Yes	Yes	Other	Yes	0.0	0	0	159131.535447	0.846502
1	HPSK72WA7R	69	50432	124440	458	15	1	4.81	60	0.68	...	Married	No	No	Other	Yes	0.0	2	0	293065.484437	0.410480
2	C1OZ8DPJ8Y	46	84208	129188	451	26	3	21.17	24	0.31	...	Divorced	Yes	Yes	Auto	No	1.0	2	3	290773.486478	0.280065
3	V2KKSFM3UN	32	31713	44799	743	0	3	7.07	24	0.23	...	Married	No	No	Business	No	0.0	1	0	125590.176492	0.254075
4	EY08JDHTZP	60	20437	9139	633	8	4	6.51	48	0.73	...	Divorced	No	Yes	Auto	No	0.0	0	3	37376.907553	0.975988

5 rows × 22 columns

2) Scales the numerical features to normalize the data using StandardScaler.

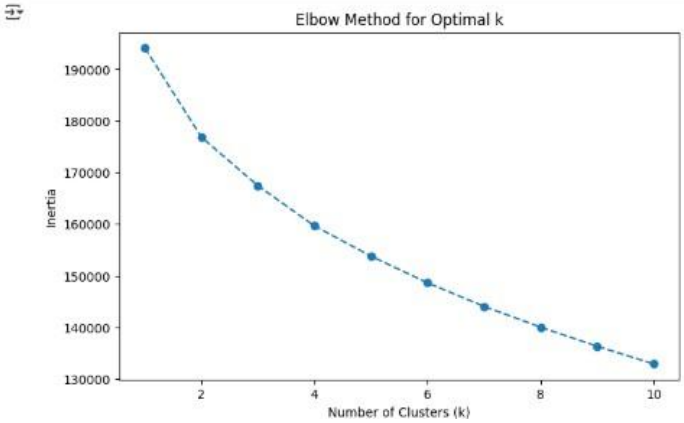
```
numerical_features = ['Age', 'Income', 'LoanAmount', 'CreditScore', 'MonthsEmployed',
                      'NumCreditLines', 'InterestRate', 'LoanTerm', 'DTIRatio']

X = data[numerical_features]
```

Double-click (or enter) to edit

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

3) Initializes a loop to calculate inertia for different values of K to use the Elbow Method to find the optimal number of clusters.

```
[ ] inertia = []
    K_range = range(1, 11)

    for k in K_range:
        kmeans = KMeans(n_clusters=k, random_state=42, n_init=10)
        kmeans.fit(X_scaled)
        inertia.append(kmeans.inertia_)

    # Plot Elbow Curve
    plt.figure(figsize=(8, 5))
    plt.plot(K_range, inertia, marker='o', linestyle='--')
    plt.xlabel('Number of Clusters (k)')
    plt.ylabel('Inertia')
    plt.title('Elbow Method for Optimal k')
    plt.show()
```

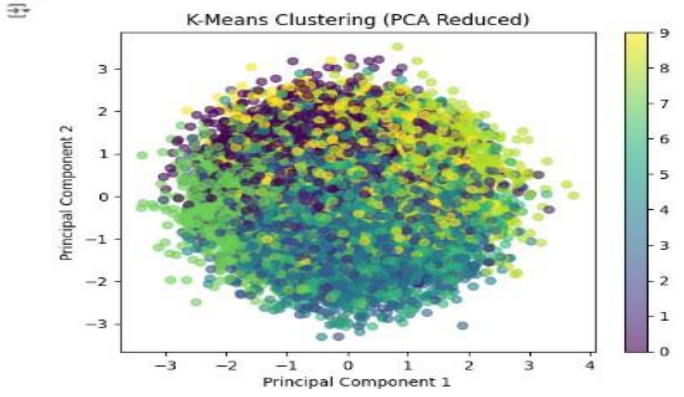


4) Applies K-Means clustering to the dataset using the chosen optimal number of clusters.

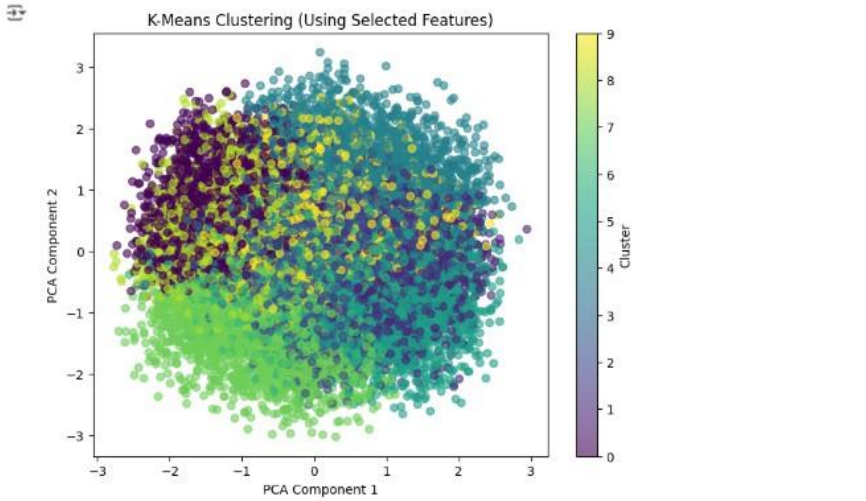
```
optimal_k = 10
kmeans = KMeans(n_clusters=optimal_k, random_state=42, n_init=10)
data['Cluster'] = kmeans.fit_predict(X_scaled)
```

5) (Re)Imports libraries; possibly due to repeated or unorganized code cells and perform clustering related data-preprocessing and visualization.

```
[ ] from sklearn.decomposition import PCA

    pca = PCA(n_components=2)  # Reduce to 2D
    X_pca = pca.fit_transform(X_scaled)

    plt.scatter(X_pca[:, 0], X_pca[:, 1], c=data['Cluster'], cmap='viridis', alpha=0.6)
    plt.xlabel('Principal Component 1')
    plt.ylabel('Principal Component 2')
    plt.title('K-Means Clustering (PCA Reduced)')
    plt.colorbar()
    plt.show()
```



```
[ ] # Select better features for clustering
    selected_features = ['CreditScore', 'LoanAmount', 'DTIRatio', 'InterestRate', 'MonthsEmployed']
    X = data[selected_features]

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

    # Apply K-Means
    kmeans = KMeans(n_clusters=10, random_state=42, n_init=10)
    data['Cluster'] = kmeans.fit_predict(X_scaled)

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

    # Plot the clusters
    plt.figure(figsize=(8, 6))
    plt.scatter(X_pca[:, 0], X_pca[:, 1], c=data['Cluster'], cmap='viridis', alpha=0.6)
    plt.xlabel('PCA Component 1')
    plt.ylabel('PCA Component 2')
    plt.title('K-Means Clustering (Using Selected Features)')
    plt.colorbar(label='Cluster')
    plt.show()
```



6)

a) Calculates the Silhouette Score for the entire dataset using the features X_scaled and cluster labels stored in data['Cluster'].

b) Randomly selects a subset (max 10,000 points) from the dataset to speed up computation and computes the **Silhouette Score** only on this sample to reduce computational cost, especially useful for very large datasets.

```
[ ] from sklearn.metrics import silhouette_score

    sil_score = silhouette_score(X_scaled, data['Cluster'])
    print(f'Silhouette Score: {sil_score:.4f}')
```

```
Silhouette Score: 0.1687
```

```
[ ] from sklearn.metrics import silhouette_score
    import numpy as np

    # Sample a subset (e.g., 10,000 points) for faster computation
    sample_size = min(10000, len(X_scaled))  # Use 10,000 or full dataset if smaller
    idx = np.random.choice(len(X_scaled), sample_size, replace=False)
    X_sampled = X_scaled[idx]
    labels_sampled = data['Cluster'].iloc[idx]

    # Compute silhouette score on the sample
    sil_score = silhouette_score(X_sampled, labels_sampled)
    print(f'Silhouette Score: {sil_score:.4f}')
```

```
Silhouette Score: 0.1690
```

7) Evaluate the optimal number of clusters (k) for K-Means clustering using the Silhouette Score.

Turns out ,among the tested values, k = 10 yields the highest Silhouette Score (0.1682), suggesting it's the most suitable number of clusters based on this metric.
However, the scores are still quite low (all < 0.2), implying clusters are weakly separated.

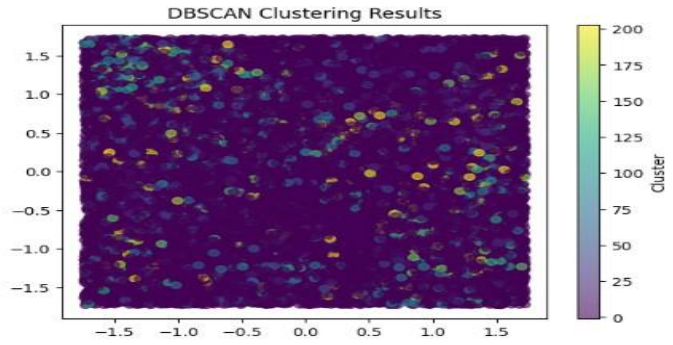
```
[ ] from sklearn.metrics import silhouette_score
    import numpy as np
    from sklearn.cluster import KMeans

    # Sample a subset for faster computation
    sample_size = min(10000, len(X_scaled))  # Use 10,000 or full dataset if smaller
    idx = np.random.choice(len(X_scaled), sample_size, replace=False)
    X_sampled = X_scaled[idx]

    for k in [2, 4, 5, 6,9,10]:
        kmeans = KMeans(n_clusters=k, random_state=42, n_init=10)
        clusters = kmeans.fit_predict(X_scaled)

        # Compute silhouette score on the sampled subset
        labels_sampled = clusters[idx]  # Use sampled cluster labels
        score = silhouette_score(X_sampled, labels_sampled)

        print(f'k={k}, Silhouette Score: {score:.4f}')
```

```
k=2, Silhouette Score: 0.1499
k=4, Silhouette Score: 0.1430
k=5, Silhouette Score: 0.1448
k=6, Silhouette Score: 0.1509
k=9, Silhouette Score: 0.1623
k=10, Silhouette Score: 0.1682
```

8) Applies DBSCAN (Density-Based Spatial Clustering of Applications with Noise) algorithm using the sklearn.cluster module.

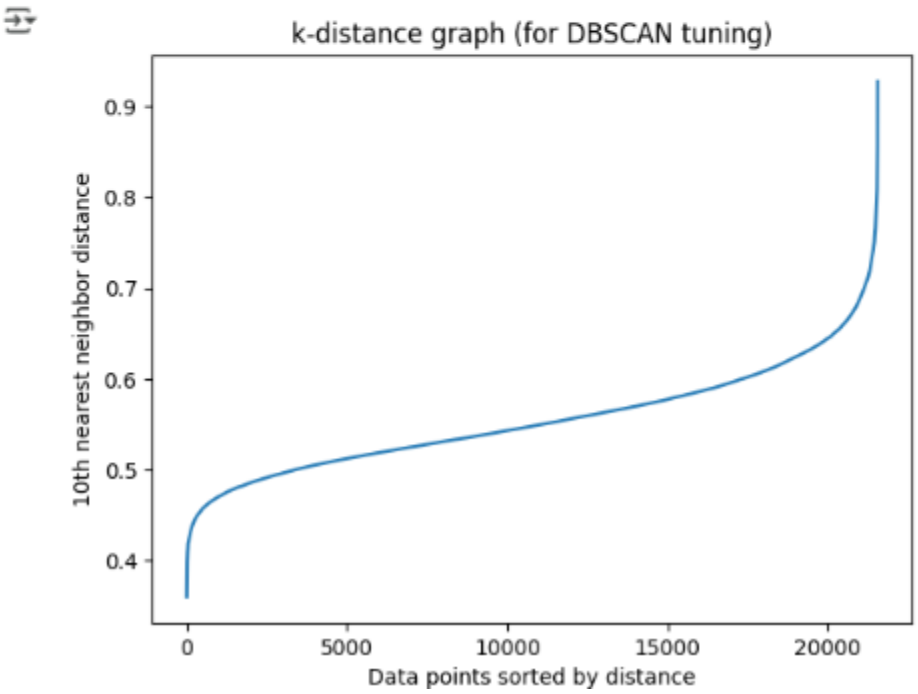
```
[ ] from sklearn.cluster import DBSCAN
    from sklearn.metrics import silhouette_score

    # DBSCAN with reasonable default values
    dbscan = DBSCAN(eps=0.5, min_samples=10)  # Adjust `eps` based on dataset
    db_clusters = dbscan.fit_predict(X_scaled)

    # Assign clusters
    data['DBSCAN_Cluster'] = db_clusters

    # Compute silhouette score (only for clustered points, ignoring noise)
    valid_clusters = db_clusters != -1  # Ignore noise points (-1)
    if valid_clusters.sum() > 0:  # Check if there are valid clusters
        score = silhouette_score(X_scaled[valid_clusters], db_clusters[valid_clusters])
        print(f'DBSCAN Silhouette Score: {score:.4f}')
    else:
        print("DBSCAN found mostly noise; try increasing `eps`.")

    # Visualizing DBSCAN Clusters
    import matplotlib.pyplot as plt

    plt.scatter(X_scaled[:, 0], X_scaled[:, 1], c=db_clusters, cmap='viridis', alpha=0.6)
    plt.title("DBSCAN Clustering Results")
    plt.colorbar(label="Cluster")
    plt.show()
```

```
DBSCAN Silhouette Score: -0.4034
```



9) tune the eps parameter for DBSCAN by generating a k-distance graph.

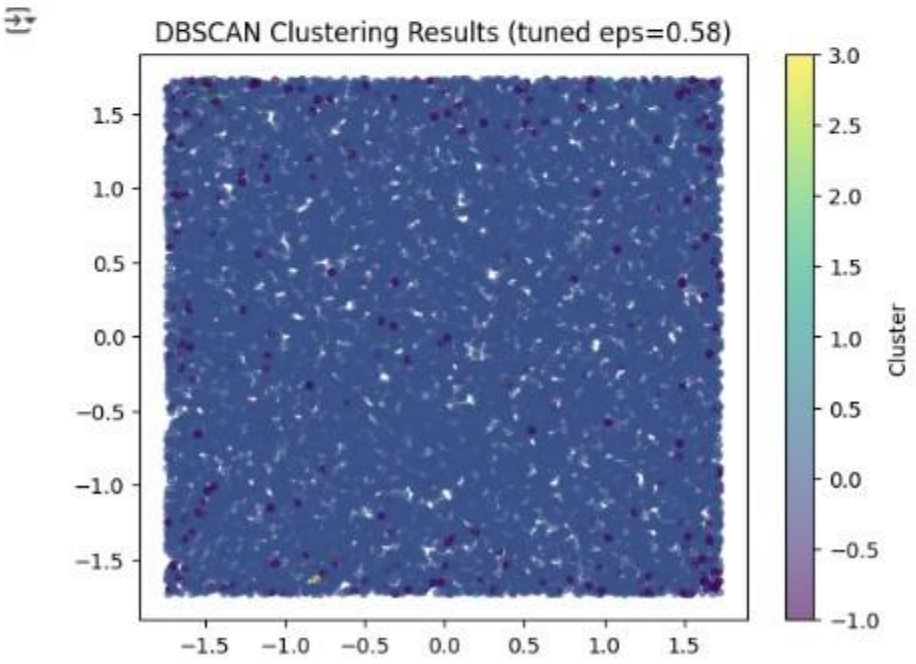
```
[ ] from sklearn.neighbors import NearestNeighbors
    import matplotlib.pyplot as plt
    import numpy as np

    # Fit Nearest Neighbors
    neigh = NearestNeighbors(n_neighbors=10)
    nbrs = neigh.fit(X_scaled)
    distances, indices = nbrs.kneighbors(X_scaled)

    # Sort and plot distances (for the 10th nearest neighbor)
    distances = np.sort(distances[:, 9])
    plt.plot(distances)
    plt.xlabel("Data points sorted by distance")
    plt.ylabel("10th nearest neighbor distance")
    plt.title("k-distance graph (for DBSCAN tuning)")
    plt.show()
```



10) DBSCAN Clustering (Tuned eps=0.58)

- DBSCAN is applied with eps=0.58, but most points are classified as noise (dark purple, -1).
- The silhouette score is -0.0809, indicating poor clustering. A higher eps may be needed.

```
[ ] from sklearn.cluster import DBSCAN
    import matplotlib.pyplot as plt

    dbscan = DBSCAN(eps=0.58, min_samples=10)
    db_clusters = dbscan.fit_predict(X_scaled)

    data['DBSCAN_Cluster'] = db_clusters

    # Visualize
    plt.scatter(X_scaled[:, 0], X_scaled[:, 1], c=db_clusters, cmap='viridis', s=10, alpha=0.6)
    plt.title("DBSCAN Clustering Results (tuned eps=0.58)")
    plt.colorbar(label="Cluster")
    plt.show()

    # Silhouette score (only for clustered points)
    from sklearn.metrics import silhouette_score
    valid_points = db_clusters != -1
    if valid_points.sum() > 0:
        sil_score = silhouette_score(X_scaled[valid_points], db_clusters[valid_points])
        print(f"DBSCAN Silhouette Score (ignoring noise): {sil_score:.4f}")
    else:
        print("All points classified as noise. Try increasing eps.")
```

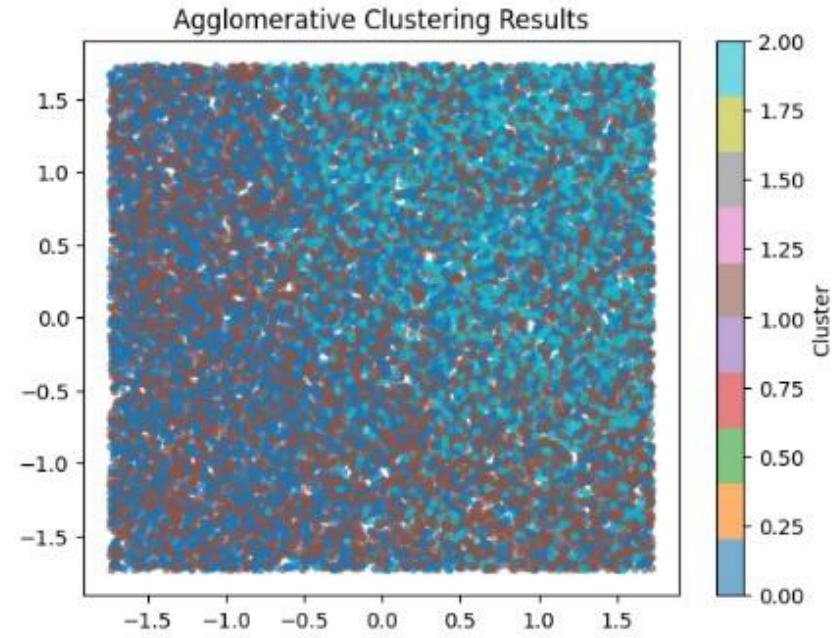



```
DBSCAN Silhouette Score (ignoring noise): -0.0809
```

11) Dendrogram for Hierarchical Clustering

- A dendrogram is created using hierarchical clustering (ward method) on a sample of data.
- Helps determine the optimal number of clusters by identifying where to cut the tree.

```python
from sklearn.cluster import AgglomerativeClustering
import matplotlib.pyplot as plt

# Choose number of clusters (start with what looked good in KMeans, say k=3)
agglo = AgglomerativeClustering(n_clusters=3, linkage='ward')
agglo_clusters = agglo.fit_predict(X_scaled)

data['Agglo_Cluster'] = agglo_clusters

# Visualize
plt.scatter(X_scaled[:, 0], X_scaled[:, 1], c=agglo_clusters, cmap='tab10', s=10, alpha=0.6)
plt.title("Agglomerative Clustering Results")
plt.colorbar(label="Cluster")
plt.show()

# Silhouette score
from sklearn.metrics import silhouette_score
score = silhouette_score(X_scaled, agglo_clusters)
print(f'Agglomerative Clustering Silhouette Score: {score:.4f}')
```

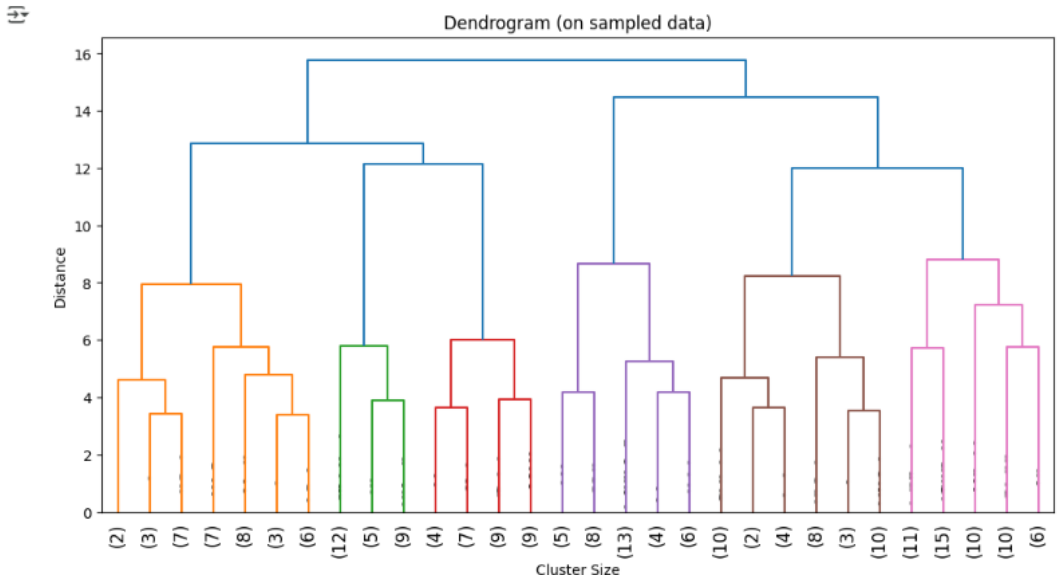



```
Agglomerative Clustering Silhouette Score: 0.0760
```

12) Agglomerative Clustering (k=3)

- Hierarchical clustering is applied with n_clusters=3 using the ward linkage method.
- The silhouette score is **0.0760**, indicating weak clustering but better than DBSCAN.

```python
from scipy.cluster.hierarchy import dendrogram, linkage
import matplotlib.pyplot as plt

# Perform linkage on a sample (if dataset too big)
# Use a small sample to avoid memory overload:
sample_X = X_scaled[::100]   # take every 100th record to make it faster

linked = linkage(sample_X, method='ward')

plt.figure(figsize=(12, 6))
dendrogram(linked, truncate_mode='lastp', p=30, leaf_rotation=90., leaf_font_size=12., show_contracted=True)
plt.title('Dendrogram (on sampled data)')
plt.xlabel('Cluster Size')
plt.ylabel('Distance')
plt.show()
```



Conclusion:

In this experiment, we successfully implemented and analyzed different clustering algorithms including K-Means, DBSCAN, and Hierarchical Clustering. Each method demonstrated its capability in identifying meaningful clusters in an unsupervised manner. K-Means proved effective for spherical-shaped clusters, DBSCAN for arbitrary shapes and noise detection, and Hierarchical Clustering for structure discovery and visualization through dendrograms. The clustering outcomes were visualized using scatter plots and dendrograms, providing a clear understanding of how the data is grouped.

Experiment 8

Aim:

To design and implement a music recommendation system using unsupervised machine learning techniques, namely **K-Means Clustering** and **Principal Component Analysis (PCA)** on the `spotify.csv` dataset.

Theory:

The goal of this experiment is to group songs with similar characteristics and recommend songs from the same group. This is achieved using two key techniques:

1. **Principal Component Analysis (PCA)** – to reduce dimensionality and enable effective visualization.

2. **K-Means Clustering** – to form groups (clusters) of similar songs based on their audio features.

Dataset Description:

- **Name:** spotify.csv
- **Records:** Approximately 1100+ songs
- **Attributes:** Includes numerical attributes such as danceability, energy, loudness, acousticness, instrumentalness, tempo, etc.
- **Purpose:** These features are used to identify similarities between songs and cluster them accordingly.

Steps Involved:

1. Data Preprocessing:

- Selected relevant numeric features related to song characteristics.
- Applied **StandardScaler** to standardize the features, which is essential for distance-based models like K-Means and PCA.

```
 Dataset Loaded Successfully!
Columns in the dataset:
Index(['valence', 'year', 'acousticness', 'artists', 'danceability',
       'duration_ms', 'energy', 'explicit', 'id', 'instrumentalness', 'key',
       'liveness', 'loudness', 'mode', 'name', 'popularity', 'release_date',
       'speechiness', 'tempo'],
      dtype='object')
```

```
df = df.drop(['id', 'name', 'artists', 'release_date'], axis=1)
```

```
df.head()
```

	valence	year	acousticness	danceability	duration_ms	energy	explicit	instrumentalness	key	liveness	loudness	mode	popularity	speechiness	tempo	Cluster
0	0.0594	1921	0.982	0.279	831667	0.211	0	0.878000	10	0.665	-20.096	1	4	0.0366	80.954	0
1	0.9630	1921	0.732	0.819	180533	0.341	0	0.000000	7	0.160	-12.441	1	5	0.4150	60.936	2
2	0.0394	1921	0.961	0.328	500062	0.166	0	0.913000	3	0.101	-14.850	1	5	0.0339	110.339	0
3	0.1650	1921	0.967	0.275	210000	0.309	0	0.000028	5	0.381	-9.316	1	3	0.0354	100.109	0
4	0.2530	1921	0.957	0.418	166693	0.193	0	0.000002	3	0.229	-10.096	1	2	0.0380	101.665	0

2. Dimensionality Reduction using PCA:

Objective:

To reduce the number of input features while retaining as much information (variance) as possible.

Process:

- PCA was applied with `n_components=2`.
- The explained variance ratio was checked to ensure that a significant portion of data variability is preserved.
- The 2D data was used for visualization of clusters.

Benefits:

- Helps visualize high-dimensional data.
- Reduces noise and computational complexity.

- Enhances the performance of clustering models.

```
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA

# Standardize the features
scaler = StandardScaler()
scaled_data = scaler.fit_transform(df)

# Apply PCA (we'll keep 2 components for visualization)
pca = PCA(n_components=2)
pca_data = pca.fit_transform(scaled_data)
```

```
# Show the first 5 PCA-transformed rows
print("First 5 rows after PCA (2 components):\n")
print(pca_data[:5])
```

```
First 5 rows after PCA (2 components):

[[-4.28266789 -2.295402  ]
 [-1.39369011  3.51566309]
 [-3.85297069 -1.73429532]
 [-2.53896489 -0.30484121]
 [-2.55129534  0.27545511]]
```

Scatter plot of PCA-reduced data before applying clustering.
This visualization represents the spread of songs across the first two principal components. It helps identify any natural grouping or separation in the data.

3. Clustering using K-Means:

Objective:

To group similar songs into k=6 clusters using K-Means clustering.

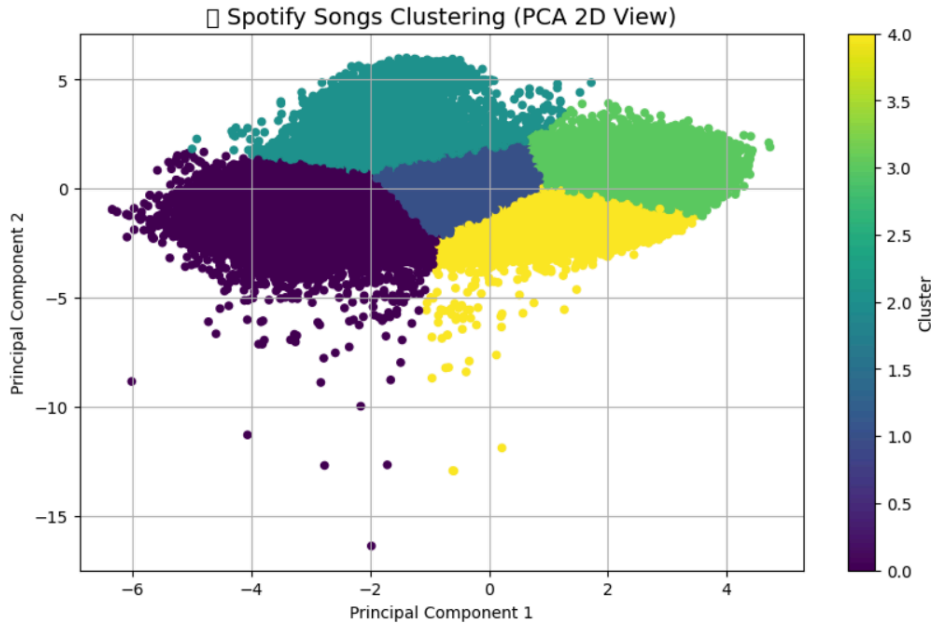
Process:

- KMeans from `sklearn.cluster` was used with `n_clusters=6`.
- The model was trained on standardized features.
- Each song was labeled with a cluster number from 0 to 5.
- PCA components were used to plot the clustered data.

```python
from sklearn.cluster import KMeans

# Let's say we choose 5 clusters
kmeans = KMeans(n_clusters=5, random_state=42)
clusters = kmeans.fit_predict(pca_data)

# Add cluster info back to original dataframe
df['Cluster'] = clusters
```

```python
import matplotlib.pyplot as plt

# Basic scatter plot
plt.figure(figsize=(10, 6))
plt.scatter(pca_data[:, 0], pca_data[:, 1], c=clusters, cmap='viridis', s=20)
plt.title(" Spotify Songs Clustering (PCA 2D View)", fontsize=14)
plt.xlabel("Principal Component 1")
plt.ylabel("Principal Component 2")
plt.colorbar(label='Cluster')
plt.grid(True)
plt.show()
```

```
/usr/local/lib/python3.11/dist-packages/IPython/core/pylabtools.py:151: UserWarning: Glyph 127912 (\N{ARTIST PALETTE}) missing from font(s) DejaVu Sans.
  fig.canvas.print_figure(bytes_io, **kw)
```



Songs plotted with cluster labels using PCA components.
Each color represents a different cluster of songs that share similar characteristics. The X and Y axes correspond to the first and second principal components.

Recommendation Logic:

Once the songs are clustered, we can recommend songs from the same cluster as a chosen song:

```
song_name = "Blinding Lights"
if song_name in original_df['name'].values:
    liked_song = original_df[original_df['name'] == song_name].iloc[0]
    liked_cluster = liked_song['Cluster']
    print(f"\n You liked: {liked_song['name']} by {liked_song['artists']} (Cluster {liked_cluster})\n"
    recommendations = original_df[
        (original_df['Cluster'] == liked_cluster) &
        (original_df['name'] != song_name)
    ][['name', 'artists']].head(5)
    print("Recommended Songs:")
    print(recommendations)
else:
    print(" Song not found in the dataset.")
```

```
 You liked: Blinding Lights by ['The Weeknd'] (Cluster 4)

Recommended Songs:
                                          name                  artists
5667                                 Gandagana      ['Georgian People']
7186  Woke Up This Morning (My Baby She Was Gone)            ['B.B. King']
7232                Blue Train - Remastered 2003        ['John Coltrane']
7236                                 Milestones          ['Miles Davis']
7252                One For Daddy-O - Remastered  ['Cannonball Adderley']
```

Conclusion:

In this experiment, a recommendation system was implemented using unsupervised learning. Dimensionality reduction via PCA allowed effective visualization and simplification of the data. K-Means clustering grouped songs with similar features, allowing content-based recommendations.

This approach is scalable, efficient, and interpretable, making it suitable for music-based recommendation systems.

Experiment - 9

Aim: To perform Exploratory data analysis using Apache Spark and Pandas

Theory:

1. **What is Apache Spark and it works?**
   Apache Spark is an open-source platform that enables fast and scalable big data processing. It excels at handling large datasets across a distributed environment and is widely used for tasks like machine learning, real-time analytics, and SQL-based operations.

It supports multiple languages including Scala (its native language), Java, Python (via PySpark), R, and SQL.

Spark generally works in these stages:

1. **Driver Program Initialization**
   The user writes the code using Spark APIs. The Driver Program manages the execution, builds a Directed Acyclic Graph (DAG) from the code, and controls job flow.
2. **Resource Allocation by Cluster Manager**
   A Cluster Manager such as YARN, Mesos, or Spark's own manager assigns resources and launches worker nodes called Executors across the system.
3. **Task Distribution**
   Spark's DAG Scheduler breaks the job into individual tasks, which are then sent to the Executors for execution. These tasks may involve data loading, transformation, or saving.
4. **Task Execution and Result Collection**
   Executors process data primarily in memory, which speeds up performance. They cache intermediate data and return final results either to the Driver or storage.

Use Cases:

- Processing streaming or log data in real time
- Running machine learning algorithms on massive datasets
- Managing ETL (Extract, Transform, Load) workflows
- Analyzing structured and unstructured big data

2. **How data exploration done in Apache spark? Explain steps.**
   Data exploration using Apache Spark, especially with PySpark, helps to understand data before performing in-depth analysis or machine learning. It gives insight into data patterns, structure, and quality.:

1. **Importing Data**
   The process begins by loading data into Spark from files (like CSV, JSON, or Parquet), databases, or cloud sources using Spark's built-in connectors.
2. **Inspecting the Schema**
   After loading, the structure of the dataset is reviewed to check column names, data types, and nullability. This helps in validating and interpreting the data accurately.
3. **Previewing the Data**
   A few rows are displayed to get a general idea of the dataset. This helps in spotting incorrect entries, formatting issues, or missing values.
4. **Summary Statistics**
   Statistical details such as count, mean, min/max values, and standard deviation are generated to assess the distribution and detect anomalies like outliers.
5. **Detecting Missing Data**
   Identifying null or missing values is crucial for deciding how to clean the data—whether to fill, drop, or replace those entries.
6. **Analyzing Distribution**
   The frequency and distribution of values in categorical or numerical fields are examined. This helps detect class imbalance or commonly occurring values.
7. **Studying Correlations**
   Relationships between numeric features are analyzed using correlation to understand how closely they are related. This can support feature selection later.
8. **Filtering and Conditions**
   To dive deeper, data is filtered using logical conditions to focus on specific records, like those with a particular attribute or range.
9. **Sampling the Data**
   When dealing with massive datasets, a small portion is sampled for quicker exploration and visualization, saving computational effort.
10. **Preparing for Further Analysis**
    After exploration, data is cleaned and prepped for modeling or visualization using external tools, as Spark isn't primarily used for plots. The knowledge from this stage informs the next steps.

Conclusions:

Apache Spark is a robust and efficient distributed data processing system built for high-performance analysis at scale. Using a driver-executor model, it processes large volumes of data in memory and supports versatile APIs like RDDs, DataFrames, and Datasets. This makes it suitable for large-scale data manipulation across different programming environments.

Experiment 10

Aim: To perform Batch and Streamed Data Analysis using Apache Spark.

Theory:

1. **What is streaming. Explain batch and stream data.**
   Streaming refers to a method of processing data that is generated and consumed in real time or near real time. This is especially useful when immediate feedback or actions are required—like monitoring sensor inputs, processing transactions, or managing live feeds.

Unlike traditional methods that wait until all data is collected, streaming systems process information as soon as it's available. This allows for quicker decision-making and timely insights.

2. **How data streaming takes place using Apache spark.**
   Apache Spark handles real-time data using its feature called Structured Streaming. This enables developers to process continuous flows of data with ease using familiar SQL or DataFrame APIs. It is designed for scalability and reliability.
   How it works:

1. **Input Source**
   The streaming starts with data being read continuously from sources such as:

- Apache Kafka
- File directories (watching for new files)
- Network sockets
- Amazon Kinesis
- Other custom data providers

Spark receives this live data stream for processing.

2. **Data as an Unbounded Table**
   In Spark, incoming streaming data is viewed as a growing table where each new entry adds a new row. Standard operations like filtering, selecting, or grouping can be applied, just like with regular tables.
3. **Query Definition**
   Users define operations on the data stream (like counting values or calculating stats). Spark translates this into a logical plan, then converts it to a physical execution plan for efficient performance.
4. **Micro-Batch Mechanism**
   Instead of processing each incoming piece of data one by one, Spark gathers data for small time windows (e.g., every second), and processes them in groups. This “micro-batching” keeps it responsive but still efficient.

5. **Output Destination**
   After the data is processed, results are stored or displayed via:

- Console (for quick checks)

- Kafka
- Databases
- Filesystems

The output can be configured in different ways:

- **Append**: Adds only new results
- **Update**: Updates only changed results
- **Complete**: Outputs the full result every time

Spark also provides built-in fault tolerance to recover from failures automatically.

Conclusion:
Batch and stream analysis serve different purposes in data processing. Batch processing handles large datasets collected over time and is suitable for deep, detailed analysis. Stream processing deals with real-time data, allowing immediate insights and actions. While batch ensures thoroughness and precision, streaming offers speed and responsiveness. Using both together enables systems to be both intelligent and fast, handling a wide range of data needs effectively.

Customer Segmentation using Clustering Algorithms

ON

Submitted in partial fulfillment of the requirements of the degree of

Bachelor of Engineering

(Information Technology)

By

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Chembur, Mumbai 400074

(An Autonomous Institute, Affiliated to University of Mumbai) April 2024

AIDS Lab Exp 11
Aim: Mini Project – Customer Segmentation using Clustering Algorithms

---

1.1 Introduction

Customer segmentation helps businesses categorize customers based on purchasing behavior. It improves marketing, loyalty, and retention strategies. This project uses unsupervised machine learning with RFM features (Recency, Frequency, Monetary) to group customers into meaningful segments.

2.2 Data Preprocessing

The dataset was cleaned by removing null CustomerIDs, negative quantities, and cancelled transactions. New features like TotalBill were created. RFM metrics were calculated per customer:

- Recency: Days since last purchase
- Frequency: Number of unique transactions
- Monetary: Total spend

2.3 Feature Scaling

RFM values were standardized using StandardScaler to ensure equal contribution to clustering models.

2.4 Clustering Models

- KMeans: Applied with k = 3–5. Chosen for its simplicity and speed.
- DBSCAN: Density-based clustering. Tuned with eps and min_samples.
- Agglomerative Clustering: Hierarchical model with Ward linkage.
- GMM (Gaussian Mixture Model): Soft clustering model based on probability distributions.

2.5 Evaluation

Clusters were evaluated using the Silhouette Score. KMeans and Agglomerative showed the best performance (0.58–0.61). DBSCAN was useful for detecting outliers but required careful parameter tuning.

2.6 Streamlit App

A web app was built using Streamlit to upload data, choose models, view clustering results, and download the output. It helps non-technical users run and interpret the segmentation pipeline interactively.

Chapter 4: Results and Discussion

4.1 Cluster Evaluation

Different clustering models were applied on the scaled RFM features. KMeans with k=3–5 showed strong separation. Agglomerative Clustering also performed well, with the highest Silhouette Score of 0.6065. DBSCAN detected some outliers but formed only one main cluster due to parameter sensitivity.

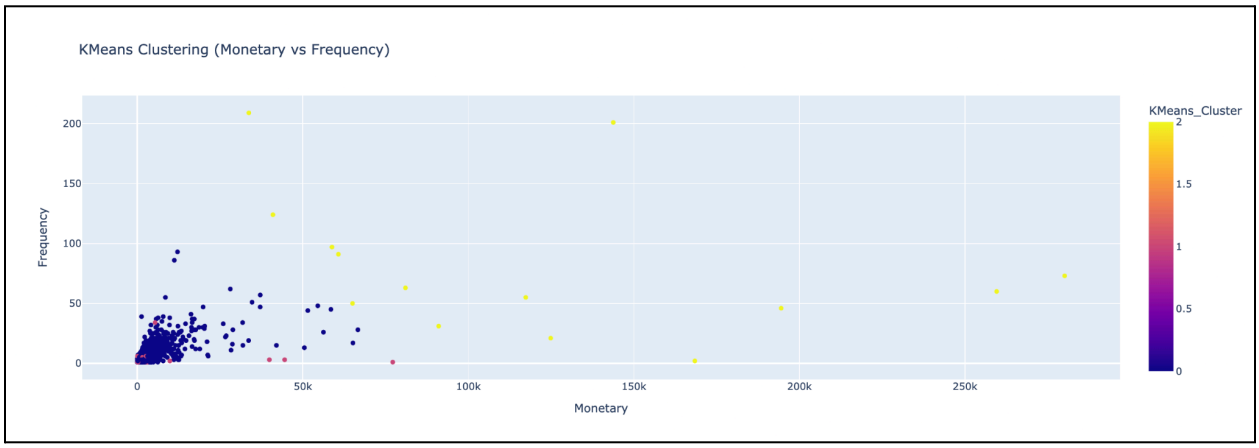
Clustering Method	Silhouette Score	Notes
🚀 KMeans	0.5853	Balanced and interpretable clusters. Good for general use cases.
🧭 Agglomerative	0.6065	Best Silhouette score. Suitable for uncovering natural hierarchies.
🌌 DBSCAN	Not Applicable	Only one cluster or too many noise points. Parameters need tuning.

4.2 KMeans Clustering

KMeans grouped customers into three primary clusters. The segments were labeled as:

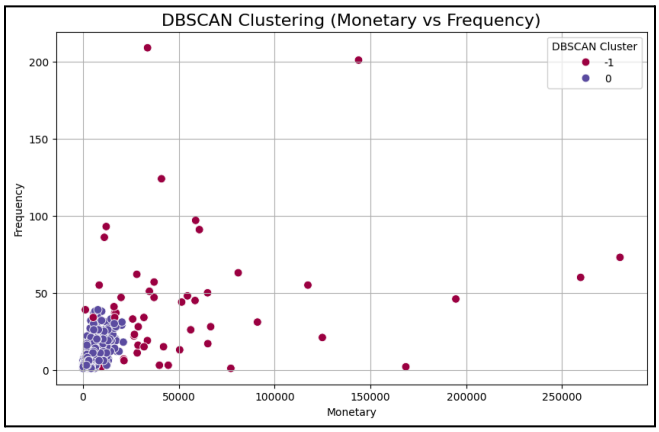
- Cluster 0: Loyal Regulars
- Cluster 1: Dormant/At-Risk
- Cluster 2: High-value VIPs

These labels were based on average Recency, Frequency, and Monetary values.



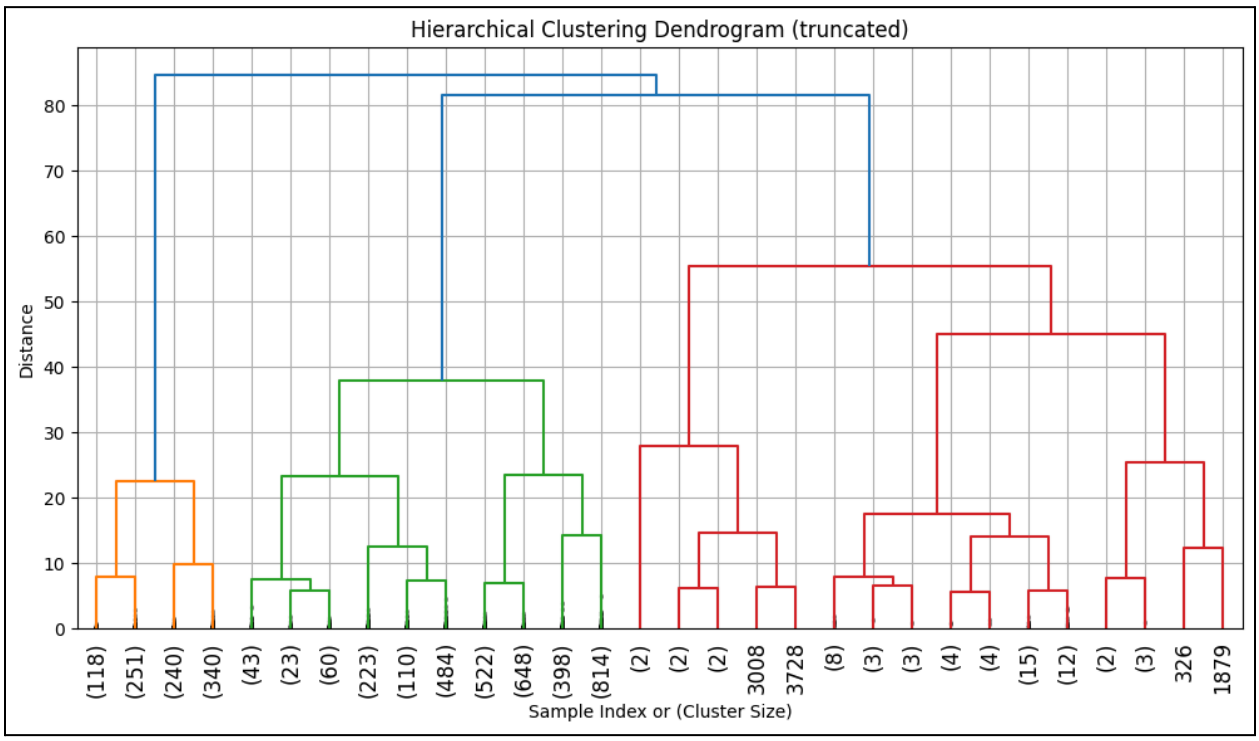
4.3 DBSCAN Clustering

DBSCAN was effective in identifying noise (-1) but struggled with sparse RFM features. It showed fewer distinct clusters under default parameters.



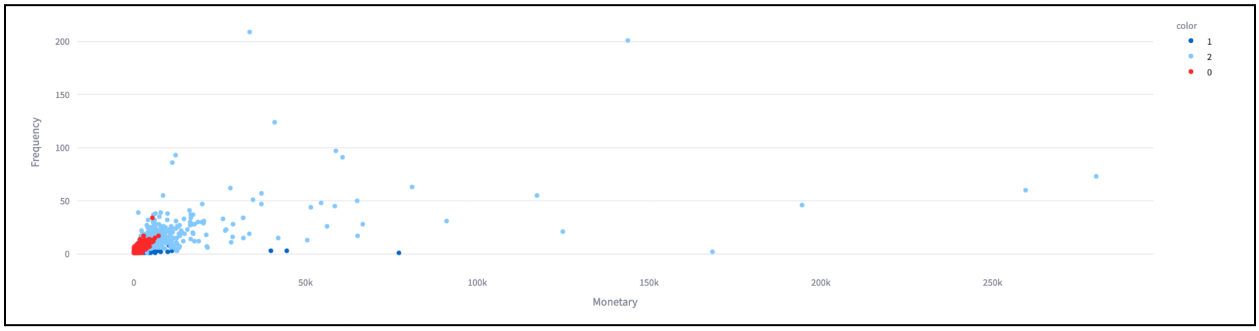
4.4 Agglomerative Clustering

Agglomerative Clustering revealed clear hierarchy among customers. The dendrogram helped identify the natural number of clusters (suggesting 4). Final cluster summaries showed tight behavioral groupings.



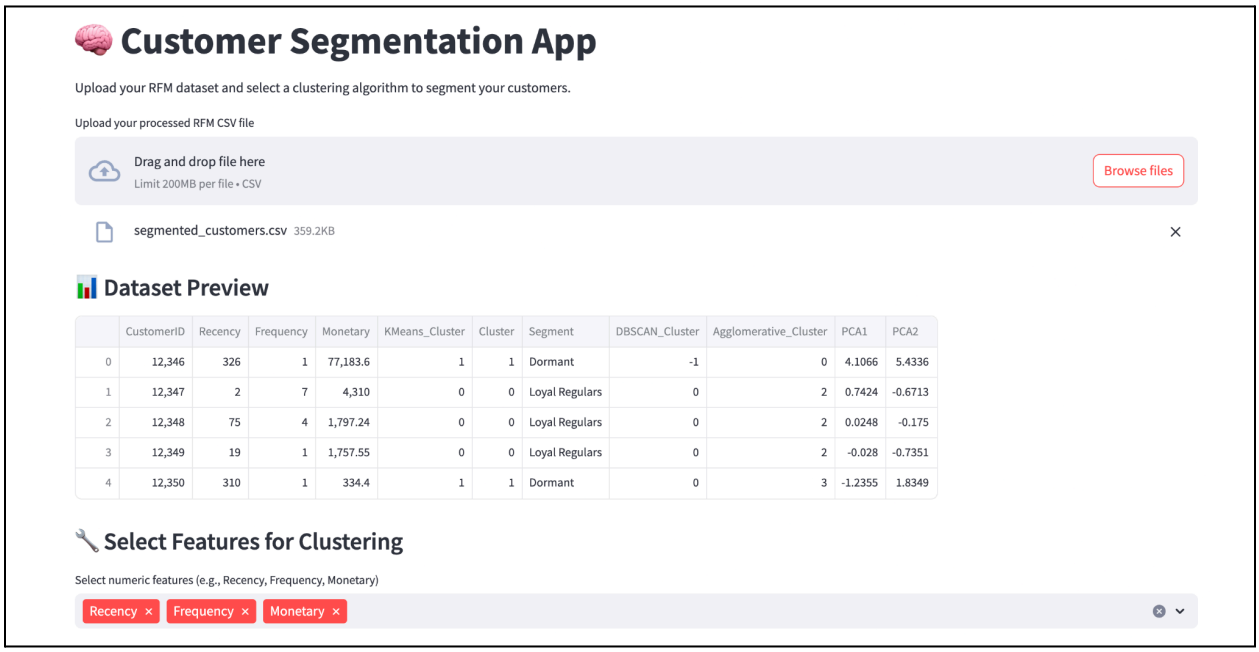
4.5 Gaussian Mixture Model (GMM)

GMM provided a probabilistic approach to clustering, where customers were grouped based on likelihood of belonging to a distribution. It produced soft cluster boundaries and worked well on scaled RFM features. GMM detected high-value clusters similar to KMeans, but with more overlap between boundaries.



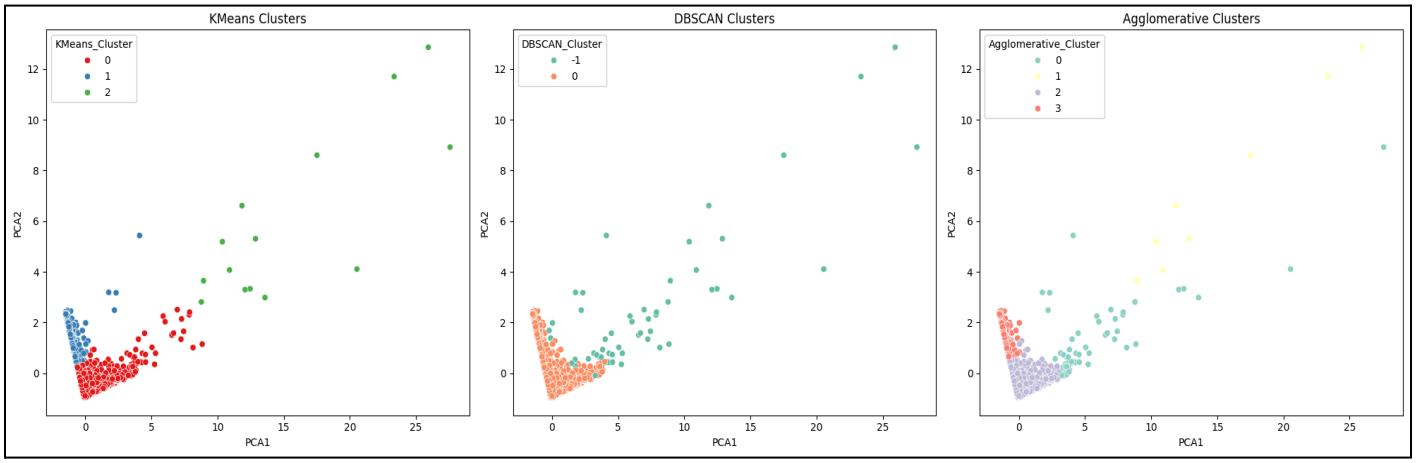
4.6 Streamlit App Output

The Streamlit app allowed interactive selection of algorithms, visualization of clusters, and downloading results. It simplified deployment for marketing teams.



4.7 Final Summary Table

The final clusters were summarized with average Recency, Frequency, and Monetary values, along with customer count



Cluster	Recency	Frequency	Monetary
0	40.98	4.85	2012.11
1	246.02	1.58	631.14
2	7.14	80.21	122888.41

Conclusion

This project demonstrates the use of unsupervised learning for customer segmentation using RFM features. By applying models like KMeans, DBSCAN, Agglomerative Clustering, and GMM, we identified distinct customer groups for targeted strategies. The Streamlit app provides a simple interface to explore and apply these insights, making the system practical and business-ready.

AIDS ASSIGNMENT

DATE: 05/03

Q1) What is AI? AI's Role in COVID-19 Pandemic

-) AI in machines refers to the simulation of human intelligence in machines. AI systems can perform tasks such as learning, reasoning, problem solving, perception and language understanding. AI is categorized in various types also.

AI played a crucial role in various aspects of healthcare and daily life, such as:

Early and diagnosis: AI-based models detected and analyzed patterns

Medical research and drug discovery: It discovers potential treatments.

Remote work and learning: Online learning and remote collaboration.

Q2) What are AI Agents terminology, explain with example.

-) An AI agent is an entity that provided. percives its environment through sensors.

Agent Function - The agent function of an agent in response to any percept.

Performance Measure - It evaluates the behaviour of the agent in a environment.

Rational Agent - A rational agent acts so as to maximize the expected value of performance measure.

Task Environment - It includes the performance measure, the external environment, sensor and accutators.

DATE:

Q3] How AI agents are used to solve 8 puzzle problems

→ The 8 puzzle problem is a sliding problem puzzle consisting of 3x3 grid with 8 tiles and one empty space. Techniques to solve are:

- Breadth - First - Search: Explores all possible moves ~~level~~ level by level.
- Depth First Search - Explores all deeper path first.
- A* Algorithm - Uses a heuristic function to find optimal path.

Q5] Categorize a shopping bot for an bookstore according to 6 dimensions

→ Observable - Partially observable
Determinism/Stochastic : ~~Deterministic~~ Deterministic
Episodic / Sequential : Sequential
Static / Dynamic - Dynamic
Discrete / continonus - Discrete
Single / Multi agent - Single agent.

DATE:

Q4) Describe PEAS Framework

AI System	Performance	Environment	Actuator	sensor
Taxi Driver	Safety, Speed	Roads, traffic	Steering, breaking	GPS, cameras
Medical Diagonis's	Accuracy, treatment success	Symptoms, Diseases	Prescription	Test, patient history
Music composor AI	Harmony	Instruments, Music notes	Speaker	Genre data, user preference
Aircraft AU tolandes	landing precision	Runway wind, altitude	I= layps, engine	GPS, gyroscope
Essay Evaluator	Accuracy, grammar check	Essay	Score System	Text reconition
Robotic sentry Gun	Thrust detection, accuracy	Security cared	Gun movement	Camera Motion sensor.

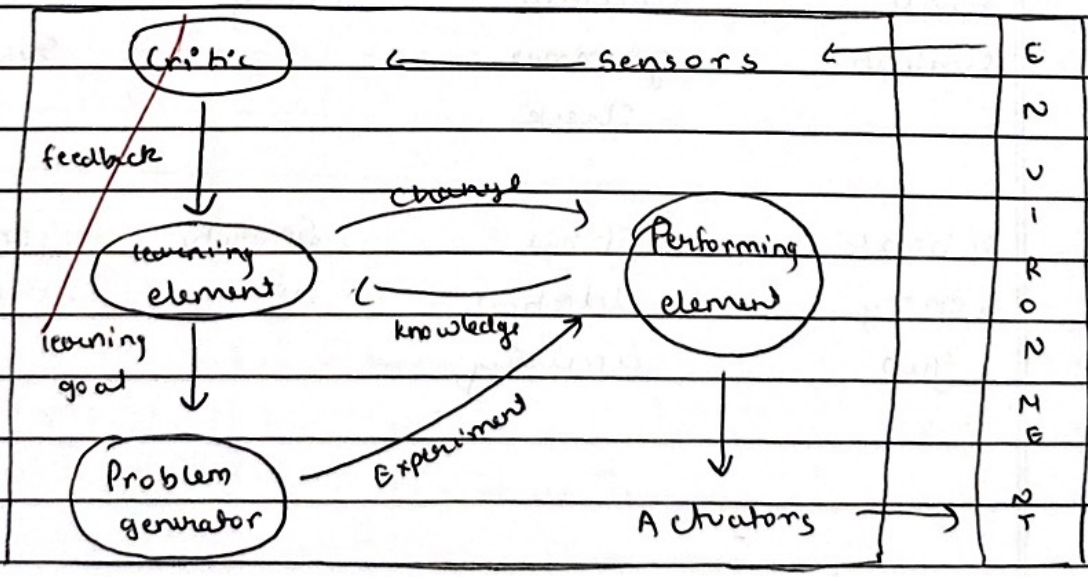
DATE:

Q6) Difference between Model and Utility based agent.

Feature	Model Based	Utility Based
Internal Model	Maintains an internal model of world	Evaluates actions based on utility
Decision making	uses past state	Selects actions to maximize utility
Example	Self driving car	AI recommendation
Goal-Oriented	Yes, works towards achieving specific goals.	Yes, but focuses on maximizing satisfaction.

Q7) Architecture of knowledge based and Learning Agents.

Learning Agent -



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A learning agent improves performance by learning from experience.

Components :-

- Learning Element - Learns from past actions.
- Performance Element - Takes decisions.
- Critic - Evaluates and gives feedback.
- Problem Generator - Suggests new actions.

Example - AI chess bot learns from past games to improve strategy.

Benefit - Adapts over time and makes better decision.

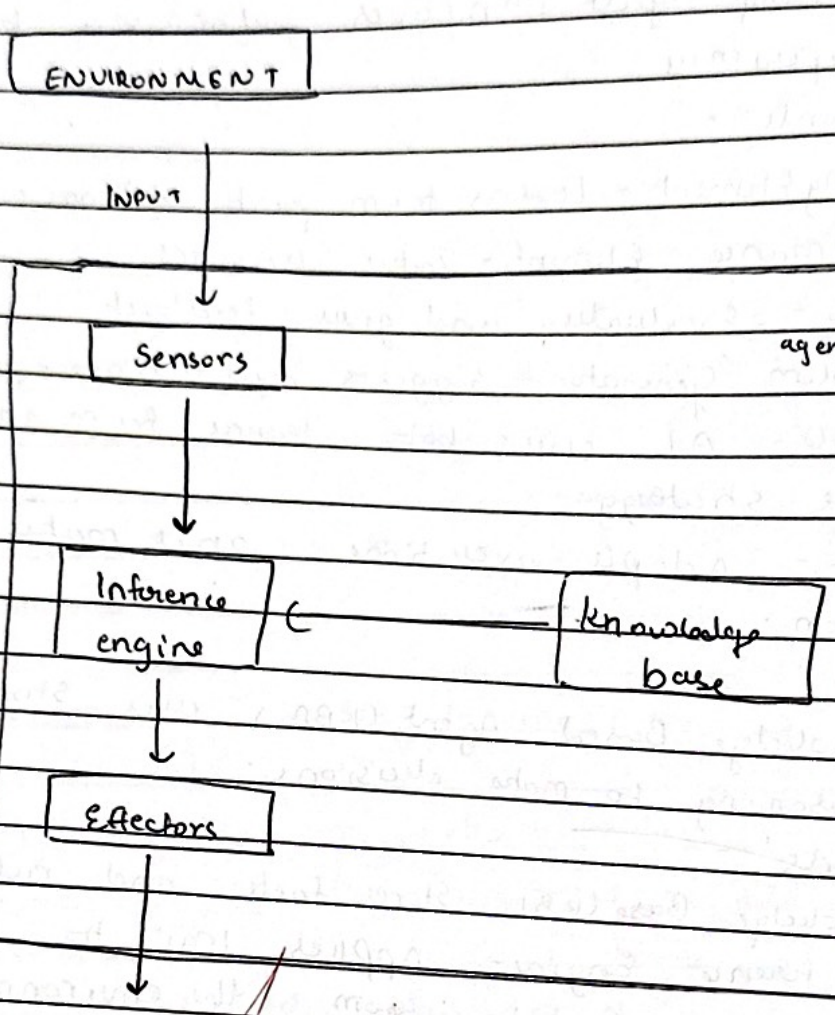
A knowledge Based Agent (KBA) uses stored knowledge and reasoning to make decisions.

Components :-

1. Knowledge Base (KB) - Stores facts and rules.
2. Inference Engine - Applies logic to derive conclusi
3. Sensors - Collects data from the environment.
4. Actuators - Executes decision.

Example - A medical diagonis system matches symp to diseases using knowledge base.

Benefit - Solves complex problem using logical reasoning.



Q8) What is AI? Considering the COVID-19 pandemic situation, how AI helped to survive and renovated our way of life with different applications?

DATE:

Q4) Convert the following to predicates:

a) Anita travels by car if available otherwise travels by bus.

→ Car Available: The car is available
Travel By Car (x): x travels by car
Travel By Bus (x): x travels by bus.
Car Available → Travel By Car (Anita) ∧ ~ Car Available → Travel By Bus (Anita)

b) Bus goes via Andheri and Goregaon.
goesVia (x, y): x goes via y.
→ Goes Via (Bus, Andheri) ∧ Goes via (Bus, Goregaon).

c) Car has puntore so not available -
HasPuntore (car) → ~ Car Available.

Forward Reasoning:

① Given: HasPuntore (Car).
② From the 3rd statement, we infer: ~ Car Available
③ From the 1st line, since Car is not available -
Travel By By Bus
④ From the 2nd line, since Anita is travelling by bus, the bus goes via Goregaon, we conclude Anita will travel by Goregaon.

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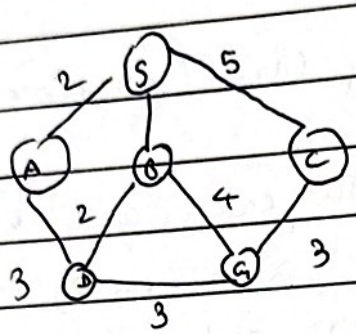
Q10) Using BFS, travel from S to G1



S -> A (cost 2)
S -> B (cost 5)
S -> C (cost 5)
A -> D (cost 3)
A -> G1 (cost 3)
C -> G1 (cost 4)

Queue,
Queue [S]
S -> Queue [A, B, C]
Dequeue A and explore its neighbours: ~~A, B~~,
Queue [B, C, D]
Dequeue B and explore its neighbours
Queue [C, D, G1]

Dequeue C and queue neighbours
Queue = [D, G1]
Dequeue D
Queue = G1
Dequeue G1
As G1 is our destination, BFS stops here.

Route from S to G1: S -> B -> G1.

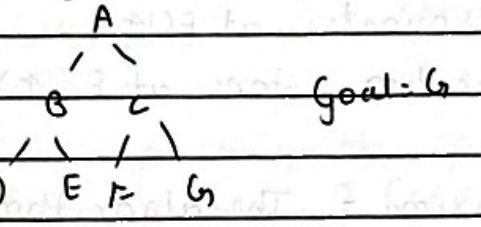
DATE:

Q11 What do you mean by depth limited search? Explain Iterative deepning search with example.

-> Depth limited search (DLS) is an uninformed search algorithm that modifies DFS by introducing a depth limit L, preventing exploration beyond the predefined level. This prevents infinite loops in infinite graphs but risks missing goals beyond L.

Iterative deepning search (IDS) combines DLS with BFS by incrementally increasing the depth limited

Example:



Iteration 1: Depth limit = 0

Nodes visited = A

Result: goal not found.

Iteration 2: L=1

Nodes visited: A -> B -> C

goal not found.

Iteration 3: L=2

Nodes visited: A -> B -> D -> E -> C -> F -> G

Goal G found at L=2.

Q12) Explain Hill Climbing and its drawbacks in detail with example. Also state limitations of steepest-ascend hill climbing.

-> Hill climbing is a local search optimization algorithm which moves towards better neighboring solutions until it reaches a peak.

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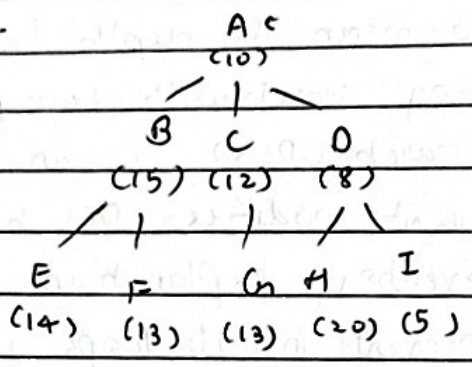
Example:-



Steps: Start at root node A (10)
compare its children B, C and D
Move to child with highest value i.e. B (15)
Repeat for B's children E and F
Terminate at E (14)

The algorithm stops at E (14) not reaching the goal G.

Drawbacks:

1. Local Maxima - The algorithm greedily selects the best immediate child and can thus get stuck on local maxima.
2. Plateaus - If siblings have equal values, the algorithm can't decide the next step and gets stuck.
3. Ridges - Narrow uphill paths require back tracking which Hill climbing algorithm does not support.

Limitations of steepest - Ascent Hill Climbing.

1. Computationally Expensive - Evaluates all neighbours before selecting the best.
2. Can get stuck - It can still get stuck in local maxima plateaus or ridges.
3. No global optimality - It only focuses on immediate improvements.

Q13) Explain simulated Annealing & write its algorithm.

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-) Simulated Annealing (SA) is a probabilistic optimi-tion algorithm inspired by metallurgy process of annealing, where materials are heated and cooled to reduce defects. It escapes the local optimal by ~~temperate~~ temporarily accepting worse sol with a probabil

Algorithm:-

1. Initialize
   - Set an initial solution and define an initial temp
2. Repeat until stopping condition.
   - Generate a new neighbour sol.
   - Compute change in cost ($\Delta E = E_{new} - E_{current}$)
   - If new solution is better i.e. $\Delta E > 0$, accept it.
   - If coorse, accept it with prbability $P = e^{-\Delta E/T}$
   - Decrease temperature T (cooling schedule)
3) Return best solution.

Example:

Travelling ~~Salisman~~ problem

~~Swap~~ two cities in a route Accept a longer route early (high T) but reject it later (low T)

Q14) Explain A* algorithm with an example.

-) A* is a best first search algorithm used in path finding and graph traversal. It uses the following formula $f(n) = g(n) + h(n)$

$g(n)$ -> cost to reach n from start

$h(n)$ -> huristic estimate of cost to reach from goal to n

$f(n)$ -> total estimated cost.

Eg - Goal = G1

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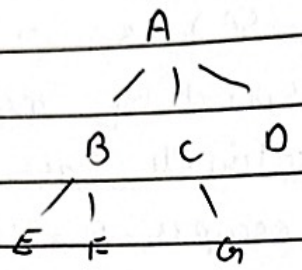

Node	g(A,n)	h(n,G)
A	0	6
B	1	4
C	2	2
D	4	7
E	3	5
F	5	3
G	6	0

Steps:

1. Start at root node A
   $f(A) = g(A) + h(A) = 0 + 6 = 6$
2. Expand neighbours : B, C, D
   $f(B) = 1 + 4 = 5$
   $f(C) = 2 + 2 = 4$
   $f(D) = 4 + 7 = 11$
3. Choose lowest val ~~that is~~ $C (F=(C) = 4)$
4. Expand neighbours of C : G
   $f(G) = 2 + 4 + 0 = 6$
5. Goal reached at a with total cost G.

Advantages :-

- efficient for finding shortest paths in weighted graphs
- balances exploration by considering both g(n) & h(n)

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Q15. Explain Min-Max algorithm and draw game tree for Tic Tac Toe Game.

-) The Min max algorithm is a decision making algorithm used in two-player games. It assumes
- One player (MAX) tries to maximize the score.
- Other player (MIN) tries to minimize the score.
- Game tree represents all possible moves.

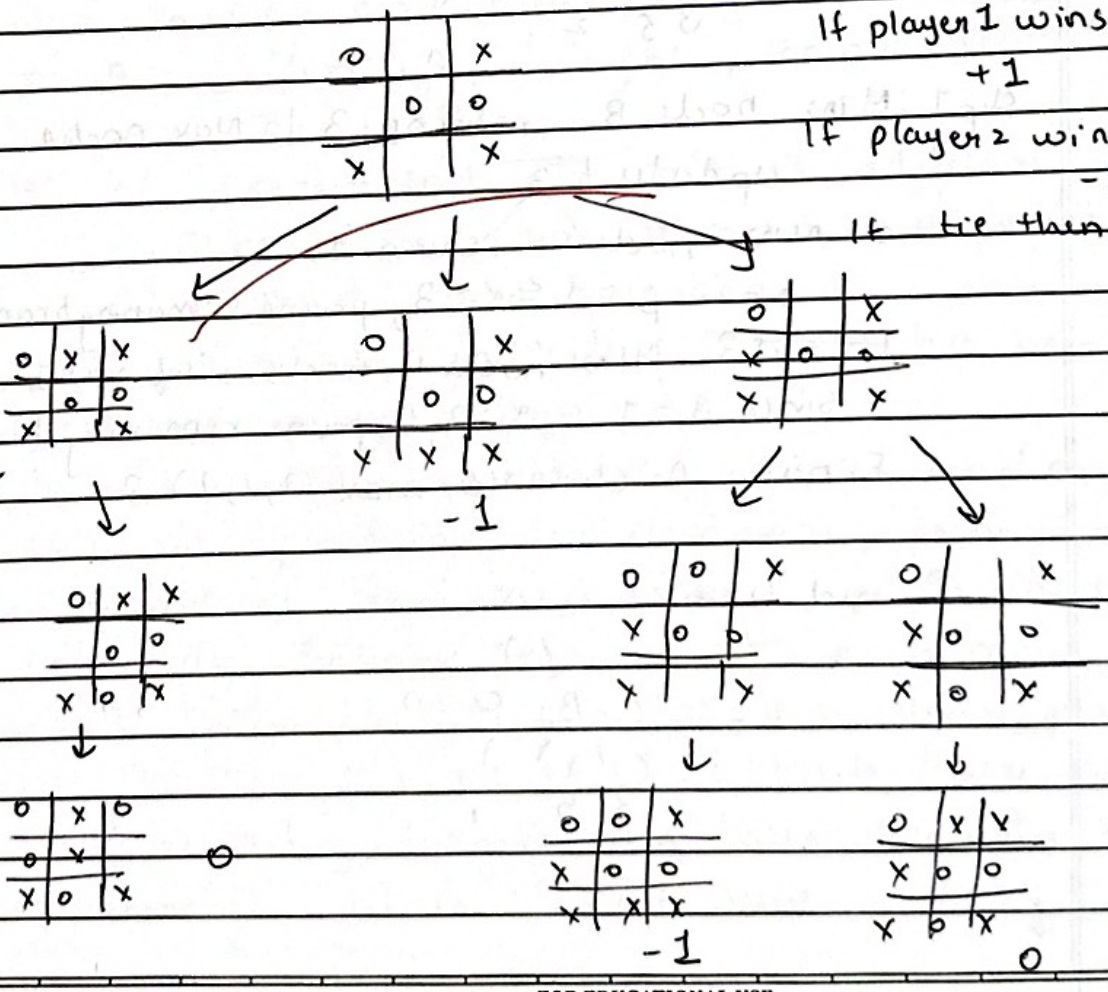
Algorithm -

(1) Generate game tree.

(2) Assign scores

(3) MAX picks highest value from children
MIN picks lowest value

(4) Repeat until Root Node is evaluated



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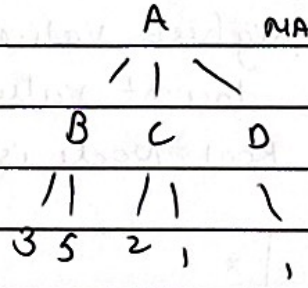
Q16) Explain Alpha-beta pruning algorithm for adversal search with example.

-> Alpha-beta pruning is an optimization technique for the minimax algorithm used in adversal search purpose like game playing AI. It reduces computational complexity by pruning branches of game tree that dont influence the final decision.

α - best value maximizing player can guarantee

β - best value minimizing player can guarantee.

Example-



Step 1: MIN node B returns 3 to Max node A

update to 3

2: MIN node C return 1

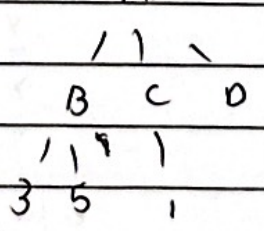
since $\beta = 1 \leq \alpha = 3$, prune remaining branches under C

Final 3: MIN node D finds leaf val 1

Since $\beta = 1 \leq \alpha = 3$, prune remaining branches under D

Final: A chooses max (3, 1, 1) = 3

Pruned Tree -



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17. Explain WUMPUS world environment giving its PEAS discription. ~~Explain how percept sequence is generated~~

-> PEAS for WUMPUS world problem -

1. P - · Maximize Rewards
+1000 for collecting gold & exiting grid
· Minimize penalties
-1000 for falling into a pit or being eaten by WUMPUS.
-1 pt for each action taken
-10 pts for using arrow

2. E - Grid layout (4x4)
containing pits, WUMPUS, gold, walls, breeze
· Partially observable - agent cannot see entire grid and must rely on sensory inputs

3. A - Move left, right, forward, Grab (gold), shoot

4. S - Breeze - indicates pit is adjacent
Stench - indicates Wumpus is adjacent
Glitter - gold indication
Bump - indicates a wall has been encountered

Generating percept sequence -
· Initial position - Agent starts at a defined pos usually (1,1)
· Movement & perception - while moving, sensors detects surroundings (eg - breeze means a pit is in adjacent cell)
· Creating Percept Sequence - After each move, it records percepts. Example - At (1,2) -> [None, Breeze, None]
At (2,1) -> [Stench, Breeze, None]
· Decision Making: Agent uses these sequences for logical reasoning to decide its next move.

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Q18) Solve the following crypto-arithmetic prb.

SEND + MORE = NONEY.

1. Set up the Eqn

$$\begin{array}{r} SEND \\ +MORE \\ \hline MONEY \end{array}$$

2. Since M is leading digit, it must be 1, because sum of 2 four-digits cannot exceed 19998.

$\therefore M = 1$

$$\begin{array}{r} SEND \\ +1ORE \\ \hline 1ONEY \end{array}$$

3. $D + E = Y$ (if carry = 0)

or $D + E = 10$ (if carry = 1)

Tens place

$N + R + carry = E$

Hundreds place: $E + O + carry = N$

Thousands place: $S + 1 = 1 + carry$

$S + carry = 0$

$\therefore S = 9$ since there is no carry.

4. Try $E = 5$

If $D = 7$ then

$Y = 7 + 5 = 12$ (invalid)

$D = 2$ then

$Y = 7$

5. $Y = 7$

Assume $N = 8$

$N + R = E$ $\quad 8 + R = 5$ (impossible) $\therefore \boxed{N = 6}$

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Final: S=9, E=5, N=6, D=7, O=0, R=8, Y=2.

SEND		9 5 6 7
+MORE	→	1 0 8 5
MONEY		1 0 6 5 2

Q19) Consider the axioms.

→ 1. $\forall x [Graduating(x) \rightarrow Happy(x)]$
2. $\forall x (Happy(x) \rightarrow smiling(x))$
3. $\exists x (Graduating(x))$

2. Convert each to clause form
1. $\forall x (\sim Happy(x) \vee smiling(x))$
$\{\sim Happy(x), smiling(x)\}$
2. $\forall x (\sim Happy(x) \vee Graduating(x))$
$\{\sim Graduating(x), Happy(x)\}$
3. $Graduating(c)$

3. Prove "Is someone smiling?" using resolution
$\exists x (smiling(x))$
Clause Form: $(A = smiling(y)$
$C_1 = \{\sim Graduating(x), Happy(x)\}$
$C_2 = \{\sim Happy(y), smiling(y)\}$
$C_3 = Graduating(c)$
Resolution btw C_3 & C_1
substitute c for x in C_1:
From $Graduating(c)$
$Happy(c)$
Resolving with C_2, $smiling(c)$

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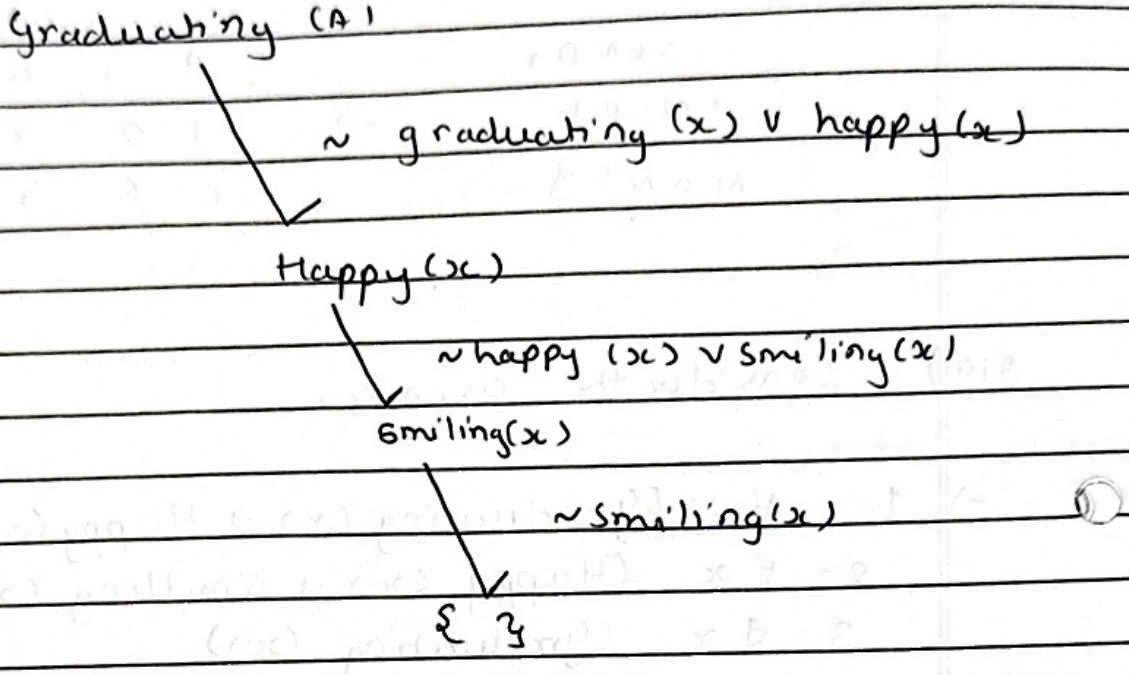

-) someone is smiling.

Q20) Explain Modus Ponen with example.

-) Modus Ponen is a fundamental rule of inference in logic. It states that if $P \to Q$ is true P is true, then Q must also be true. Formula: $\frac{P \to Q, P}{Q}$

Ex, if it is raining, then it is soggy (P→Q)
it is raining (P)
∴ it is soggy (Q)

Q21) Explain forward & backward chaining algo with eg

-) Forward chaining - It is data driven, inference algorithm that starts with known facts & applies inference rules to derive new facts with until the goal is reached

fact: A, B

Rule : $A \to L$, $B \to D$, $C \wedge \_ \to I$

Goal I

DATE:

start with A & B

apply A -> C to derive C

B -> D to derive D

C ∧ D -> I to derive I

The goal I reached.

Backward Chaining:

BC is a goal driven, starts with goal & work backward to find the facts that support it starts with goal.

fact: A, B

rule: A -> C, B -> D, C ∧ D -> I

goal: I

find the rule C ∧ D -> I

if C & D are true

use A -> C since A is true, C is true

use B -> D since B is true, D is true

C & D are true, I is true.

conclusion: I is reached.

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Experiment 2: Data Visualization & Exploratory Data Analysis Using Matplotlib and Seaborn

Introduction

Exploratory Data Analysis (EDA) is the first step in data analysis, developed by *John Tukey* in the 1970s. EDA is used to summarize datasets, detect patterns, identify anomalies, and ensure data quality before applying machine learning models.

When working with datasets, it is crucial to visualize data in different ways to understand relationships between variables. EDA helps identify **missing values, trends, and correlations** that may impact future analysis.

Why Perform EDA?

1. **Understanding Data Quality** – Identifies missing values, outliers, and inconsistencies.
2. **Feature Selection** – Determines key variables for modeling.
3. **Pattern Discovery** – Helps find trends and distributions in the dataset.
4. **Detecting Anomalies** – Highlights unusual data points.
5. **Improving Model Accuracy** – Ensures that only clean and relevant data is used.

Advantages of Data Visualization

1. **Improved Understanding:**
   In business, it is often necessary to compare the performance of different components or scenarios. Traditionally, this requires analyzing large volumes of data, which can be time-consuming. Data visualization simplifies this process by providing a clear, visual comparison.
2. **Enhanced Interpretation:**
   Converting data into graphical formats makes it easier to interpret and analyze. Visualization tools, such as **Google Trends**, help identify key insights and emerging patterns by presenting complex data in a digestible form.
3. **Efficient Data Sharing:**
   Visual representation of data facilitates better communication within organizations. Instead of dealing with lengthy reports or raw datasets, visually appealing charts and graphs make information easier to understand and convey effectively.
4. **Sales Analysis:**
   Visualization techniques, including heatmaps and trend charts, help sales professionals

quickly grasp product performance. By analyzing sales patterns, businesses can identify factors driving growth, customer preferences, repeat buyers, and regional impacts.

5. **Identifying Relationships Between Events:**
   Business performance is often influenced by multiple factors. Recognizing correlations between events enables decision-makers to pinpoint business trends. For example, in **e-commerce**, sales typically increase during festive seasons like **Christmas or Thanksgiving**. If an online business records an average of $1 million in quarterly revenue and sees a surge in the next quarter, visualization helps link this increase to specific events or promotions.
6. **Exploring Opportunities and Trends:**
   With vast amounts of available data, business leaders can uncover insights into industry trends and market opportunities. **Data visualization** enables analysts to detect customer behavior patterns, allowing businesses to adapt strategies and capitalize on emerging trends.

Technologies Used

Matplotlib

Matplotlib is a Python library for creating static, animated, and interactive visualizations. It provides various graphing tools, including bar graphs, histograms, and scatter plots.

Seaborn

Seaborn is a high-level visualization library built on Matplotlib, designed for statistical graphics. It simplifies complex plots like heatmaps, box plots, and scatter plots.

General Syntax in Python for Data Visualization

Python libraries like Matplotlib and Seaborn follow a general syntax for creating visualizations:

1. **Import the library:** Import the required libraries (e.g., import matplotlib.pyplot as plt).
2. **Prepare the data:** Use Pandas to manipulate and prepare the data for visualization.
3. **Create the plot:** Use functions like plot(), scatter(), boxplot(), etc., to create the visualization.
4. **Customize the plot:** Add titles, labels, legends, and other customizations.
5. **Display the plot:** Use plt.show() to display the visualization.

<------*This doc is using up on the cleaned data of the previous experiment* -------->

1. Bar Graph and Contingency Table

Theory

- **Bar Graph:** A bar graph is used to display categorical data with rectangular bars. The length of each bar represents the frequency of a category.
- **Contingency Table:** A table that summarizes the frequency distribution of two categorical variables, helping to analyze relationships between them.

Terms

- **Categorical Data:** Data divided into groups (e.g., Airline names).
- **Frequency:** The count of occurrences of each category.

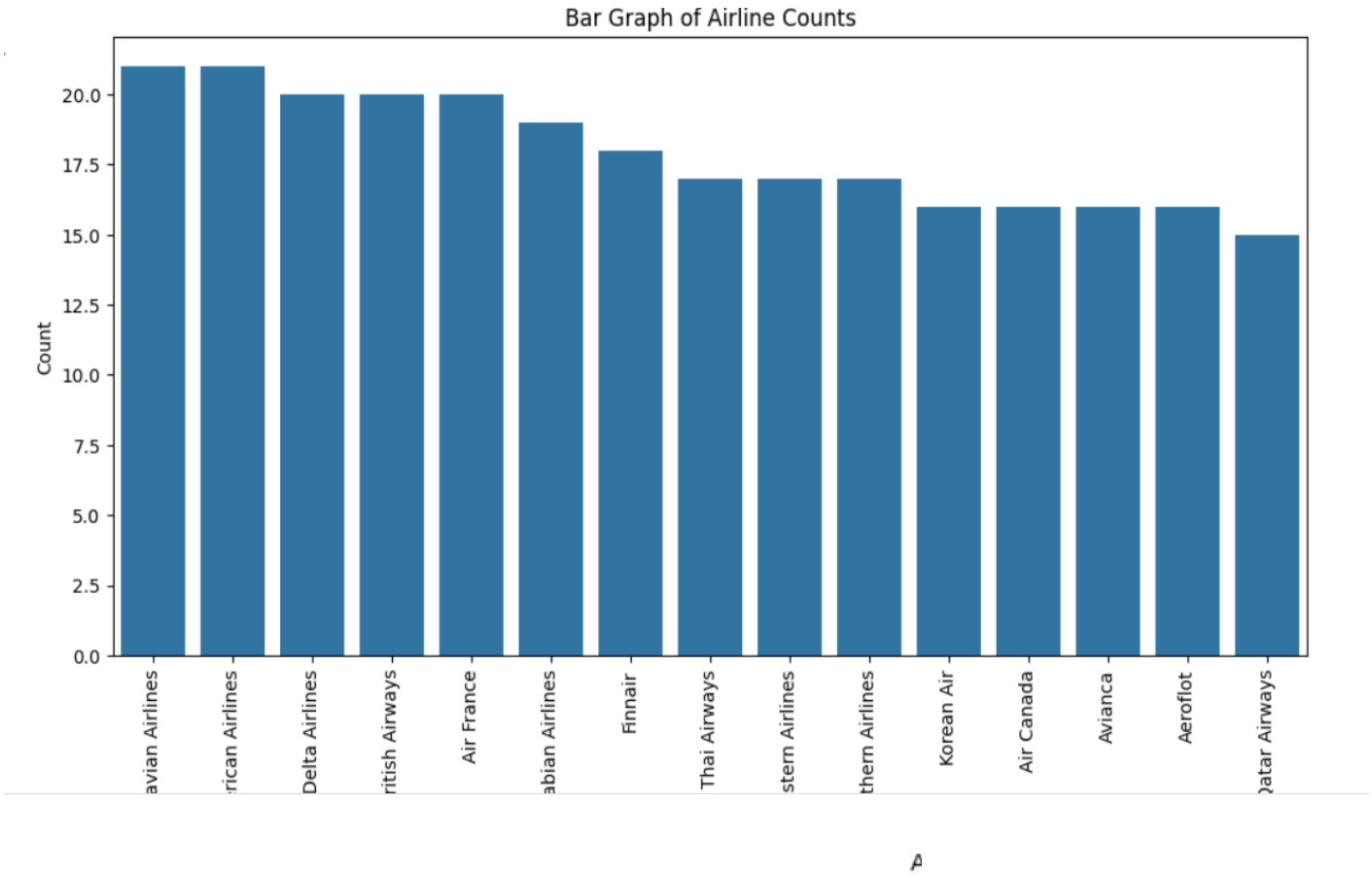
```
import seaborn as sns
import matplotlib.pyplot as plt
plt.figure(figsize=(12, 6))
sns.countplot(data=df, x="Airline", order=df["Airline"].value_counts().index[:15])  # Top 15 airlines for clarity
plt.xticks(rotation=90)
plt.title("Bar Graph of Airline Counts")
plt.xlabel("Airline")
plt.ylabel("Count")
plt.show()
max_total = df["Total"].max()
bins = [0, 10, 50, 100, 500]
if max_total > 500:
    bins.append(1000)
if max_total > 1000:
    bins.append(max_total + 1)

labels = ["0-10", "11-50", "51-100", "101-500"]
if max_total > 500:
    labels.append("501-1000")
if max_total > 1000:
    labels.append("1000+")

df["Total_Binned"] = pd.cut(df["Total"], bins=bins, labels=labels)

# Contingency Table: Airline vs Total Aircraft Count
contingency_table = pd.crosstab(df["Airline"], df["Total_Binned"])
contingency_table.head()
```

Output



Airline	Total_Binned 0-10	11-50	51-100	101-500	501-1000
ABX Air	0	1	2	0	0
ANA Wings	0	2	0	0	0
Aegean Airlines	4	2	0	0	0
Aer Lingus	9	4	0	0	0
Aer Lingus Regional	0	1	0	0	0

Explanation

- The **bar graph** was created using sns.countplot() to visualize the number of records per **Airline**.
- The **contingency table** was created using pd.crosstab(), categorizing airlines based on **Total Aircraft Count** into binned intervals.

Observations

- Certain airlines have significantly more records, indicating larger fleet sizes.

- The contingency table helps understand which airlines operate more aircraft within specific fleet size ranges.

---

2. Scatter Plot, Box Plot, and Heatmap

Theory

- **Scatter Plot:** A scatter plot visualizes the relationship between two numerical variables by plotting data points on an X-Y coordinate plane.
- **Box Plot:** A box plot displays the distribution of numerical data using quartiles and highlights outliers.
- **Heatmap:** A heatmap visually represents the correlation between numerical variables using colors.

Terms

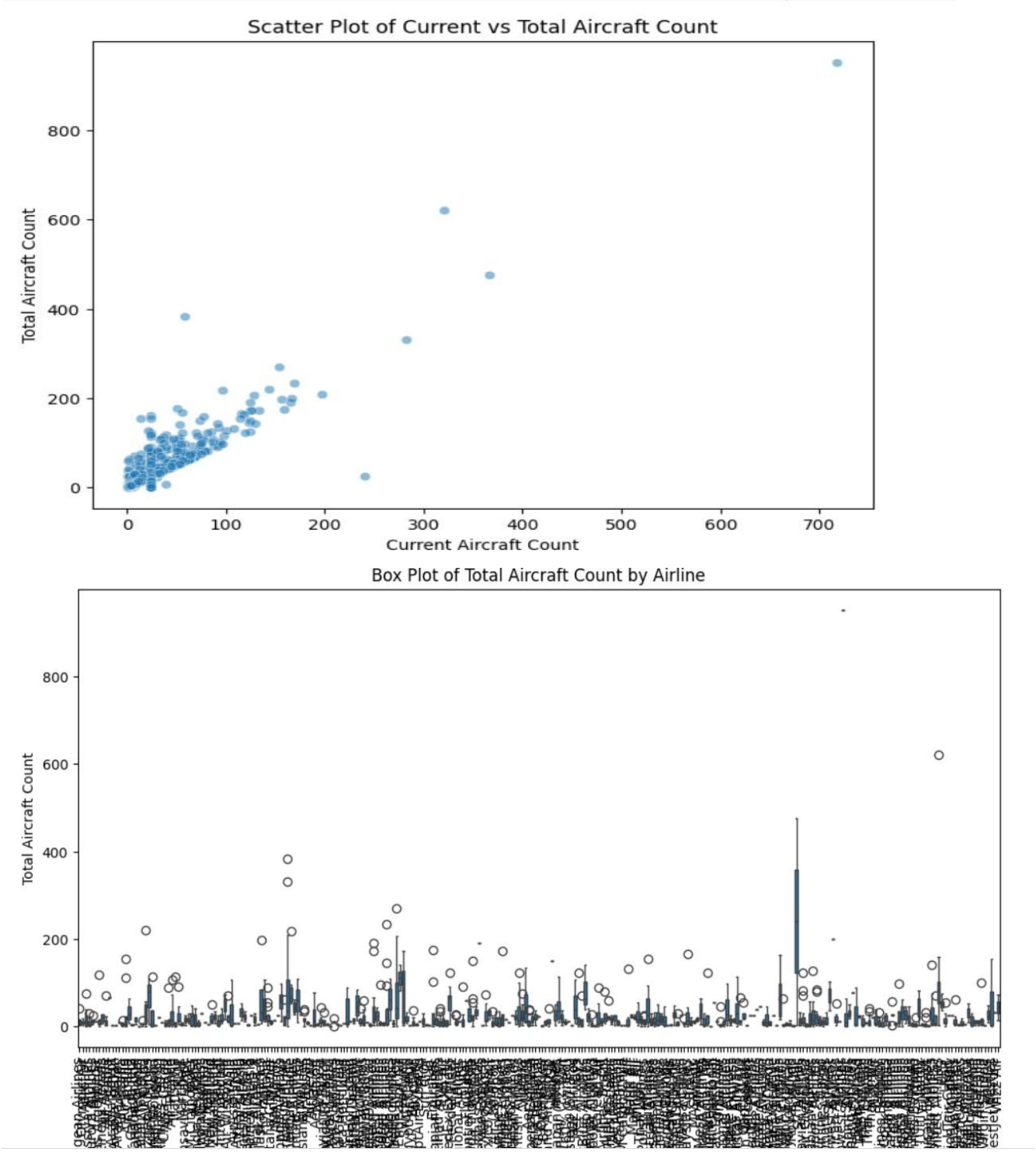
- **Numerical Data:** Data representing continuous quantities (e.g., aircraft count).
- **Quartiles:** Divides the dataset into four equal parts.
- **Correlation:** A measure of the strength of the relationship between two variables (values range from -1 to +1).

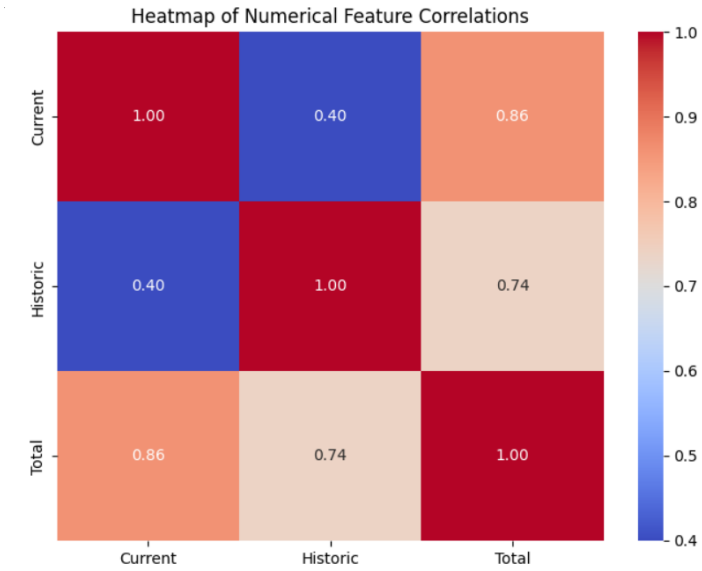
```
# Scatter plot: 'Current' vs 'Total' aircraft count
plt.figure(figsize=(8, 6))
sns.scatterplot(data=df, x="Current", y="Total", alpha=0.5)
plt.title("Scatter Plot of Current vs Total Aircraft Count")
plt.xlabel("Current Aircraft Count")
plt.ylabel("Total Aircraft Count")
plt.show()

# Box plot: Distribution of 'Total' aircraft count by 'Airline'
plt.figure(figsize=(12, 6))
sns.boxplot(data=df, x="Airline", y="Total")
plt.xticks(rotation=90)
plt.title("Box Plot of Total Aircraft Count by Airline")
plt.xlabel("Airline")
plt.ylabel("Total Aircraft Count")
plt.show()

# Heatmap of correlation between numerical features
plt.figure(figsize=(8, 6))
sns.heatmap(df[["Current", "Historic", "Total"]].corr(), annot=True, cmap="coolwarm", fmt=".2f")
plt.title("Heatmap of Numerical Feature Correlations")
plt.show()
```

Output


Scatter Plot of Current vs Total Aircraft Count
Total Aircraft Count
Current Aircraft Count
0
200
400
600
800
0
100
200
300
400
500
600
700
Box Plot of Total Aircraft Count by Airline
Total Aircraft Count
0
200
400
600
800



Explanation

- The **scatter plot** was created using sns.scatterplot() to visualize the relationship between **Current** and **Total** aircraft counts.
- The **box plot** was created using sns.boxplot() to analyze fleet size variations across different airlines.
- The **heatmap** was plotted using sns.heatmap() to display the correlation matrix between numerical features.

Observations

- A **positive correlation** between *Current* and *Total* aircraft count indicates that airlines with larger historic fleets still retain many aircraft.
- The **box plot** reveals significant variations in fleet sizes among airlines.
- The **heatmap** confirms strong correlations between fleet-related numerical variables.
- **● Total vs Quantity (High Positive Correlation)**
  - A high positive correlation (close to 1) suggests that the total fleet size increases as the number of aircraft in operation increases. This is expected in fleet management data.
- **● Historic vs Current Fleet (Strong Positive Correlation)**
  - A strong correlation between historic and current aircraft count indicates that airlines with larger historic fleets still operate many aircraft.
- **● Weak Correlations**
  - Some variables, such as fleet size and revenue (if applicable), may show weak or no correlation, suggesting external factors influence revenue generation beyond just fleet size.
- **● No Negative Correlations**
  - Since this dataset primarily deals with fleet size and operational data, most numerical features are likely positively correlated.

3. Histogram and Normalized Histogram

Theory

- **Histogram:** A histogram is used to represent the frequency distribution of numerical data by dividing it into bins.
- **Normalized Histogram:** Represents the probability distribution, where the total area sums to 1.

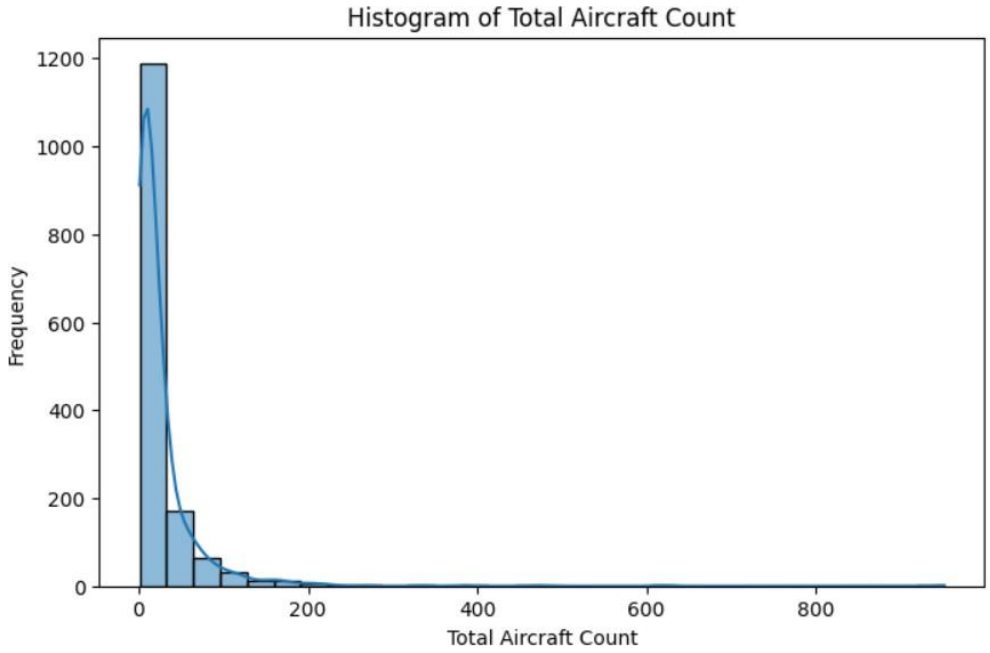
Terms

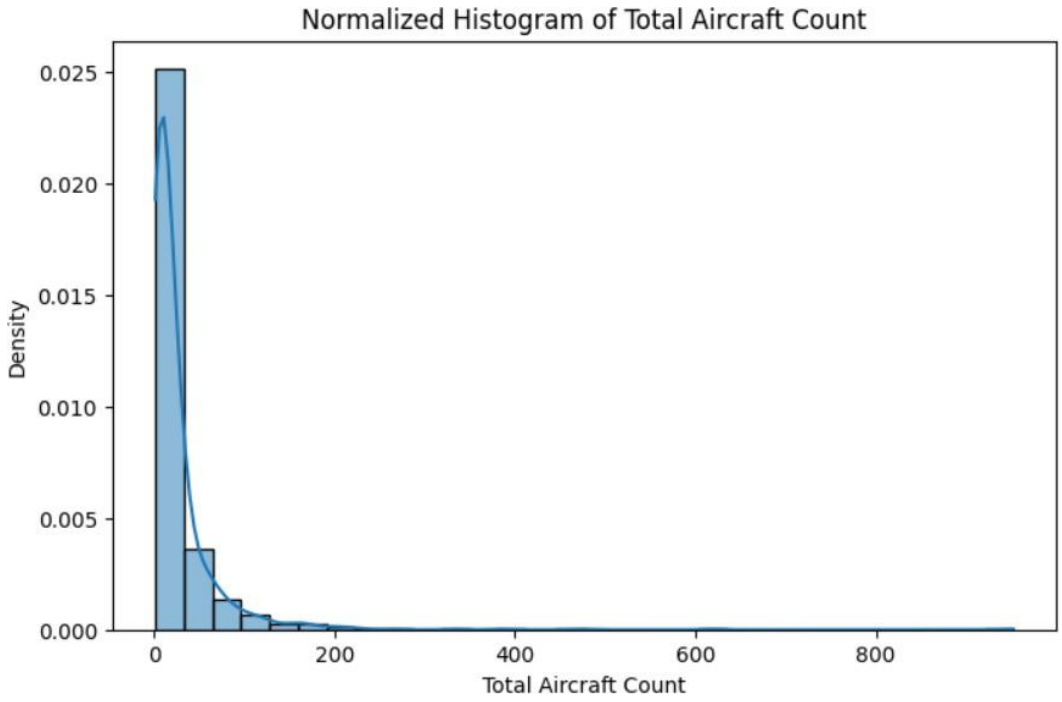
- **Bins:** Intervals that group continuous data.
- **Density:** The probability density of the data distribution.

```
[ ]  # Histogram of 'Total' aircraft count
     plt.figure(figsize=(8, 5))
     sns.histplot(df["Total"], bins=30, kde=True)
     plt.title("Histogram of Total Aircraft Count")
     plt.xlabel("Total Aircraft Count")
     plt.ylabel("Frequency")
     plt.show()

     # Normalized Histogram
     plt.figure(figsize=(8, 5))
     sns.histplot(df["Total"], bins=30, kde=True, stat="density")  # Normalized version
     plt.title("Normalized Histogram of Total Aircraft Count")
     plt.xlabel("Total Aircraft Count")
     plt.ylabel("Density")
     plt.show()
```

Output





Explanation

- The **histogram** was created using sns.histplot() to visualize the frequency distribution of **Total Aircraft Count**.
- The **normalized histogram** was generated by setting stat="density" to normalize the values.

Observations

- Most airlines have **small to mid-sized fleets**, with fewer airlines operating large fleets.
- The distribution is slightly **right-skewed**, indicating a higher number of small airlines compared to larger ones.
- The histogram revealed that most airlines have **small to mid-sized fleets**, with fewer airlines operating large fleets.
- The normalized histogram confirmed that the **fleet size distribution is right-skewed**, meaning a few airlines dominate in terms of fleet numbers.
- This suggests that while many airlines operate on a smaller scale, a handful of airlines have significantly larger fleets, influencing the overall industry trends

4. Handling Outliers Using Box Plot and IQR

Theory

- **Outliers:** Data points that deviate significantly from the rest of the dataset.
- **Box Plot:** Identifies outliers using quartiles and whiskers.
- **IQR Method:** Detects outliers using the Interquartile Range (IQR) as follows:
    - Lower Bound = Q1 - (1.5 * IQR)
    - Upper Bound = Q3 + (1.5 * IQR)

Terms

- **Quartiles (Q1, Q3):** The 25th and 75th percentiles of the dataset.
- **IQR:** The range between Q1 and Q3.

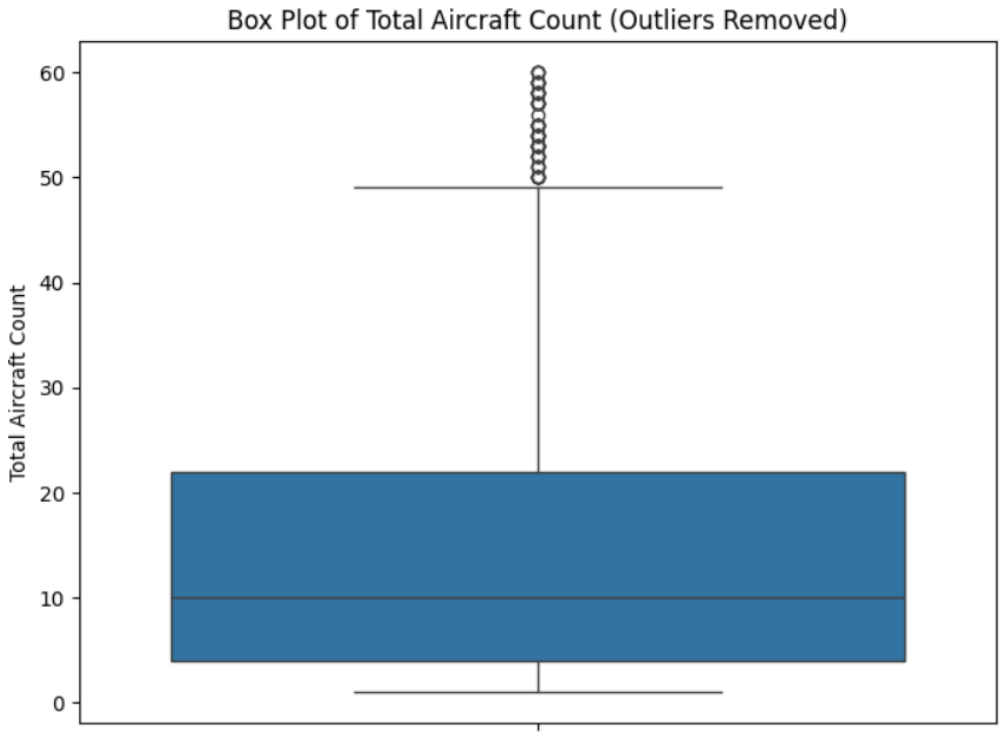
```
[ ]  # Calculate IQR for 'Total' aircraft count
     Q1 = df["Total"].quantile(0.25)
     Q3 = df["Total"].quantile(0.75)
     IQR = Q3 - Q1

     # Define lower and upper bounds
     lower_bound = Q1 - 1.5 * IQR
     upper_bound = Q3 + 1.5 * IQR

     # Remove outliers
     df_no_outliers = df[(df["Total"] >= lower_bound) & (df["Total"] <= upper_bound)]

     # Box plot after outlier removal
     plt.figure(figsize=(8, 6))
     sns.boxplot(data=df_no_outliers, y="Total")
     plt.title("Box Plot of Total Aircraft Count (Outliers Removed)")
     plt.ylabel("Total Aircraft Count")
     plt.show()
```

Output



Explanation

- **Box Plot:** Used sns.boxplot() before and after outlier removal.
- **IQR Method:** Applied using df[(df["Total"] >= lower_bound) & (df["Total"] <= upper_bound)] to filter out extreme values.

Observations

- Outliers were detected in airlines with exceptionally high aircraft counts.
- Removing outliers **improves dataset reliability** by reducing distortions in analysis.
- The **box plot** helped identify airlines with extreme fleet sizes, either **exceptionally large or unusually small**.
- Using the **IQR method**, these outliers were removed, resulting in a dataset that better represents the majority of airlines.
- By eliminating extreme values, the analysis becomes more accurate and avoids distortions caused by a few exceptionally large airlines

Conclusion

This experiment conducted a detailed **Exploratory Data Analysis (EDA)** on airline fleet data. We used various visualization techniques to uncover trends, distributions, and anomalies within the dataset.

Key findings:

- **Bar Graph & Contingency Table** helped analyze airline fleet sizes.
- **Scatter Plot & Heatmap** confirmed strong correlations between aircraft count variables.
- **Box Plot & IQR Method** helped detect and remove outliers.
- **Histogram** provided insights into fleet size distributions.

By leveraging these statistical methods and visualizations, we gained meaningful insights that can assist in airline fleet management and operational strategies. This experiment highlights the **importance of EDA in data-driven decision-making** and provides a strong foundation for further predictive modeling.