Assignment 8-9:

Total Points: 2 points)

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Objective:

Use a real-world dataset to analyze and compare Decision Trees, Random Forest, Ensemble Models (Bagging and Boosting), Dimensionality Reduction (PCA), and Clustering (k-means). This assignment aims to explore the effectiveness of these methods, understand their strengths and limitations, and identify practical use cases.

Dataset:

Use the "Heart Disease Dataset" from Kaggle: https://www.kaggle.com/datasets/fedesoriano/heart-failure-prediction. This dataset contains health indicators such as age, cholesterol levels, and smoking habits, with the goal of predicting the likelihood of heart disease.

Instructions:

1. Dataset Preparation (0.5 points)

Download and explore the Heart Disease Dataset.

Preprocess the data:

Handle missing values (if any).

Normalize/standardize the numerical features.

Encode categorical variables.

Visualize key variables to understand relationships (e.g., age vs. cholesterol).

2. Task 1: Decision Trees and Random Forest (0.5 points)

Define a classification task, such as predicting whether a person has heart disease ("Yes" or "No").

Implement Decision Tree and Random Forest models.

Perform hyperparameter tuning for both models.

Record performance metrics such as accuracy, precision, recall, and F1-score.

Extract and visualize feature importance from both models.

Write a short analysis comparing Decision Tree and Random Forest, focusing on overfitting, interpretability, and predictive performance.

3. Task 2: Ensemble Models – Bagging and Boosting (0.5 points)

Implement Bagging and Boosting methods using:

Bagging: BaggingClassifier (e.g., with Decision Trees).

Boosting: AdaBoost or Gradient Boosting.

Evaluate and compare the performance of these models against Random Forest.

Discuss how Bagging and Boosting handle bias-variance trade-offs.

4. Task 3: Dimensionality Reduction and Clustering (0.5 points):

Dimensionality Reduction:

Apply PCA to the dataset and retain components that explain 80% of the variance.

Visualize the dataset in 2D using the top two principal components.

Clustering:

Perform k-means clustering on the dataset (or PCA-reduced data).

Determine the optimal number of clusters using the elbow method or silhouette analysis.

Compare the clusters to the actual heart disease labels and evaluate clustering performance using metrics like purity or Adjusted Rand Index.

Grading (2 Points Total)

Dataset Preparation and Visualization (0.5 points)

Thorough preprocessing and meaningful visualizations of relationships between features.

Implementation and Results (1 point):

Accurate implementation of all models and dimensionality reduction techniques.

Clear evaluation of results with metrics and visualizations.

Analysis and Comparison (0.5 points):

Insightful comparison of methods, highlighting trade-offs and practical recommendations.

In [1]:
```
import pandas as pd
```

In [2]:
```
df = pd.read_csv("C:\Users\Acer\Downloads\heart.csv")
```

In [3]:
```
df.head()
```

Out[3]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0

In [4]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   Age             918 non-null    int64  
 1   Sex             918 non-null    object 
 2   ChestPainType   918 non-null    object 
 3   RestingBP       918 non-null    int64  
 4   Cholesterol     918 non-null    int64  
 5   FastingBS       918 non-null    int64  
 6   RestingECG      918 non-null    object 
 7   MaxHR           918 non-null    int64  
 8   ExerciseAngina  918 non-null    object 
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    object 
 11  HeartDisease    918 non-null    int64  
dtypes: float64(1), int64(6), object(5)
memory usage: 86.2 KB
```

In [5]:
```
df.isnull().sum()
```

Out[5]:
```
Age               0
Sex               0
ChestPainType     0
RestingBP         0
Cholesterol       0
FastingBS         0
RestingECG        0
MaxHR             0
ExerciseAngina    0
Oldpeak           0
ST_Slope          0
HeartDisease      0
dtype: int64
```

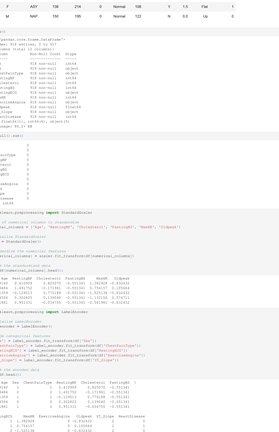
In [6]:
```
from sklearn.preprocessing import StandardScaler

# List of numerical columns to standardize
numerical_columns = ['Age', 'RestingBP', 'Cholesterol', 'FastingBS', 'MaxHR', 'Oldpeak']

# Initialize StandardScaler
scaler = StandardScaler()

# Standardize the numerical features
df[numerical_columns] = scaler.fit_transform(df[numerical_columns])

# Check the standardized data
print(df[numerical_columns].head())
```

```
        Age  RestingBP  Cholesterol  FastingBS   MaxHR  Oldpeak
0 -1.431545  0.410909     0.825070  -0.551341  1.382928 -0.832432
1 -0.478484  1.491752    -0.171961  -0.551341  0.754157  0.105664
2 -1.751359 -0.129513     0.770188  -0.551341 -1.525138 -0.832432
3 -0.584556  0.302825     0.139040  -0.551341 -1.132156  0.574751
4  0.051881  0.951331    -0.034755  -0.551341 -0.581981 -0.832432
```

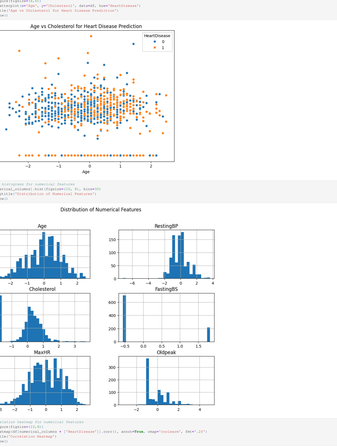
In [7]:
```
from sklearn.preprocessing import LabelEncoder

# Initialize LabelEncoder
label_encoder = LabelEncoder()

# Encode categorical features
df['Sex'] = label_encoder.fit_transform(df['Sex'])
df['ChestPainType'] = label_encoder.fit_transform(df['ChestPainType'])
df['RestingECG'] = label_encoder.fit_transform(df['RestingECG'])
df['ExerciseAngina'] = label_encoder.fit_transform(df['ExerciseAngina'])
df['ST_Slope'] = label_encoder.fit_transform(df['ST_Slope'])

# Check the encoded data
print(df.head())
```

```
        Age  Sex  ChestPainType  RestingBP  Cholesterol  FastingBS  \
0 -1.431545    1              1   0.410909     0.825070  -0.551341   
1 -0.478484    0              2   1.491752    -0.171961  -0.551341   
2 -1.751359    1              1  -0.129513     0.770188  -0.551341   
3 -0.584556    0              0   0.302825     0.139040  -0.551341   
4  0.051881    1              2   0.951331    -0.034755  -0.551341   

   RestingECG     MaxHR  ExerciseAngina   Oldpeak  ST_Slope  HeartDisease  
0           1  1.382928               0 -0.832432         2             0  
1           1  0.754157               0  0.105664         1             1  
2           2 -1.525138               0 -0.832432         2             0  
3           1 -1.132156               1  0.574751         1             1  
4           1 -0.581981               0 -0.832432         2             0  
```

In [8]:
```
import matplotlib.pyplot as plt
import seaborn as sns

# Scatter plot between Age and Cholesterol
# Assuming 'HeartDisease' is the target variable
sns.scatterplot(x="Age", y="Cholesterol", data=df, hue="HeartDisease")
plt.title("Age vs Cholesterol for Heart Disease Prediction")
plt.show()
```



In [9]:
```
# Plot histograms for numerical features
df[numerical_columns].hist(figsize=(15, 8), bins=20)
plt.suptitle('Distribution of Numerical Features')
plt.show()
```



In [10]:
```
# Visualize correlations between numerical features
plt.figure(figsize=(15,8))
sns.heatmap(df[numerical_columns + ['HeartDisease']].corr(), annot=True, cmap="coolwarm", fmt=".2f")
plt.title("Correlation Heatmap")
plt.show()
```

In [11]:
```
from sklearn.model_selection import train_test_split

# Define features (X) and target (y)
X = df.drop('HeartDisease', axis=1)  # Features
y = df['HeartDisease']  # Target variable

# Split the data into training and testing sets (80% train, 20% test)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Check the shapes of the resulting splits
print(X_train.shape, X_test.shape)
```

```
(734, 11) (184, 11)
```

2. Implement Decision Tree and Random Forest Models:

In [12]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score
import matplotlib.pyplot as plt
import seaborn as sns
```

In [13]:
```
# Initialize Tree model
dt = DecisionTreeClassifier(random_state=42)

# Define the hyperparameters grid for tuning
param_grid_dt = {
    'max_depth': [None, 10, 20, 30],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4]
}

# Perform GridSearchCV
grid_search_dt = GridSearchCV(estimator=dt, param_grid=param_grid_dt, cv=5, scoring='accuracy', n_jobs=-1)
grid_search_dt.fit(X_train, y_train)

# Best parameters for Decision Tree
print("Best parameters for Decision Tree:", grid_search_dt.best_params_)

# Get the best Decision Tree model
best_dt = grid_search_dt.best_estimator_

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

```
Best parameters for Decision Tree: {'max_depth': 10, 'min_samples_leaf': 4, 'min_samples_split': 2}
```

Out[13]:
```
DecisionTreeClassifier(max_depth=10, min_samples_leaf=4, random_state=42)
```

In [14]:
```
# Random Forest Model
rf = RandomForestClassifier(random_state=42)

# Define the hyperparameter grid for tuning
param_grid_rf = {
    'n_estimators': [50, 100, 200],
    'max_depth': [None, 10, 20, 30],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4]
}

# Perform GridSearchCV
grid_search_rf = GridSearchCV(estimator=rf, param_grid=param_grid_rf, cv=5, scoring='accuracy', n_jobs=-1)
grid_search_rf.fit(X_train, y_train)

# Best parameters for Random Forest
print("Best parameters for Random Forest:", grid_search_rf.best_params_)

# Get the best Random Forest model
best_rf = grid_search_rf.best_estimator_

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

```
Best parameters for Random Forest: {'max_depth': 10, 'min_samples_leaf': 4, 'min_samples_split': 10, 'n_estimators': 200}
```

Out[14]:
```
RandomForestClassifier(max_depth=10, min_samples_leaf=4, min_samples_split=10,
                       n_estimators=200, random_state=42)
```

In [15]:
```
# Predict with Decision Tree
y_pred_dt = best_dt.predict(X_test)

# Predict with Random Forest
y_pred_rf = best_rf.predict(X_test)

# Calculate performance metrics for Decision Tree
accuracy_dt = accuracy_score(y_test, y_pred_dt)
precision_dt = precision_score(y_test, y_pred_dt)
recall_dt = recall_score(y_test, y_pred_dt)
f1_dt = f1_score(y_test, y_pred_dt)

# Calculate performance metrics for Random Forest
accuracy_rf = accuracy_score(y_test, y_pred_rf)
precision_rf = precision_score(y_test, y_pred_rf)
recall_rf = recall_score(y_test, y_pred_rf)
f1_rf = f1_score(y_test, y_pred_rf)

# Print out the metrics
print("Decision Tree - Accuracy:", accuracy_dt, "Precision:", precision_dt, "Recall:", recall_dt, "F1-Score:", f1_dt)
print("Random Forest - Accuracy:", accuracy_rf, "Precision:", precision_rf, "Recall:", recall_rf, "F1-Score:", f1_rf)
```

```
Decision Tree - Accuracy: 0.8043478260869565 Precision: 0.8461538461538461 Recall: 0.7857142857142857 F1-Score: 0.8148148148148148
Random Forest - Accuracy: 0.8858695652173914 Precision: 0.8571428571428571 Recall: 0.9107142857142857 F1-Score: 0.8831168831168831
```

In [16]:
```
# Plot feature importances for Decision Tree
plt.figure(figsize=(12, 6))
sns.barplot(x=best_dt.feature_importances_, y=X.columns)
plt.title("Feature Importances - Decision Tree")
plt.show()

# Plot feature importances for Random Forest
plt.figure(figsize=(12, 6))
sns.barplot(x=best_rf.feature_importances_, y=X.columns)
plt.title("Feature Importances - Random Forest")
plt.show()
```