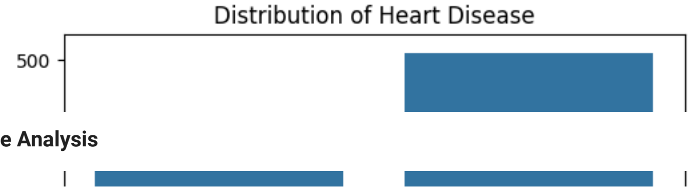
Exploratory Data Analysis (EDA)

Univariate Analysis

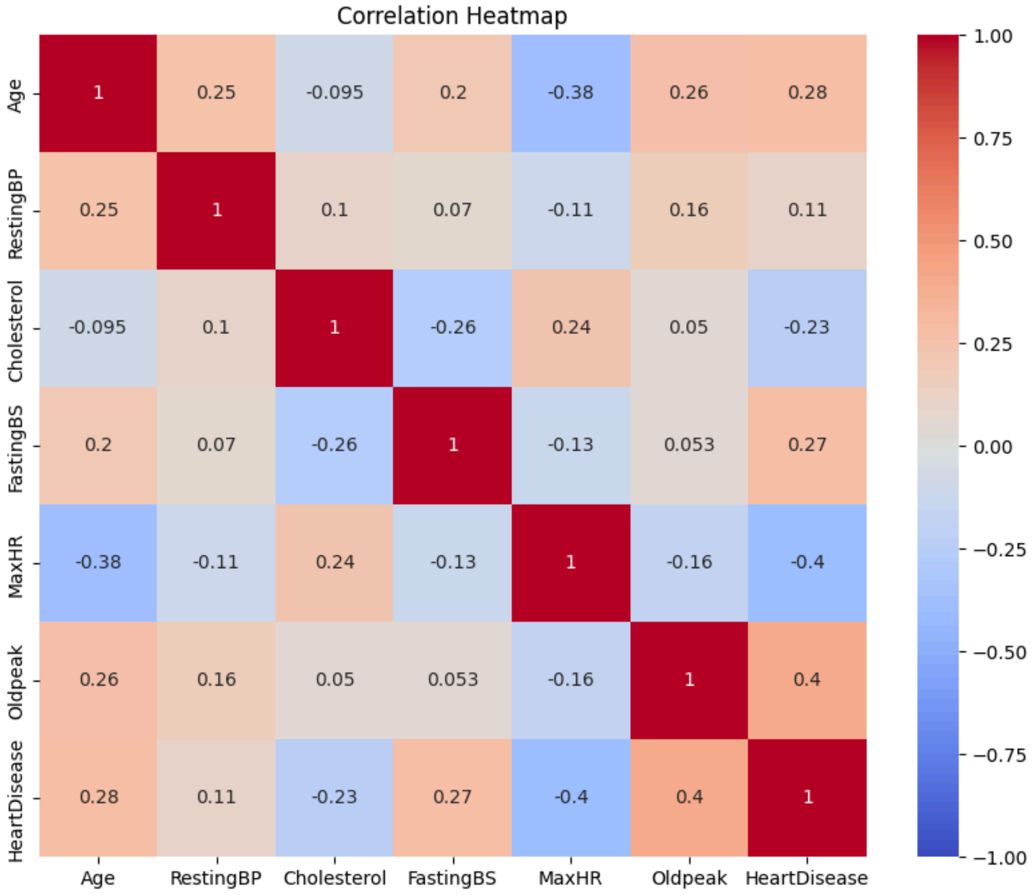
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np

# Load the dataset (replace with your file path)
data = pd.read_csv('/content/heart disease prediction.csv')

# Display basic information about the dataset
print(data.head())
print(data.info())
print(data.describe())

# Univariate Analysis
# Distribution of the target variable
plt.figure(figsize=(6, 4))
sns.countplot(x='HeartDisease', data=data)
plt.title('Distribution of Heart Disease')
plt.show()

# Distribution of numerical features
data.hist(bins=30, figsize=(15, 10))
plt.show()
```

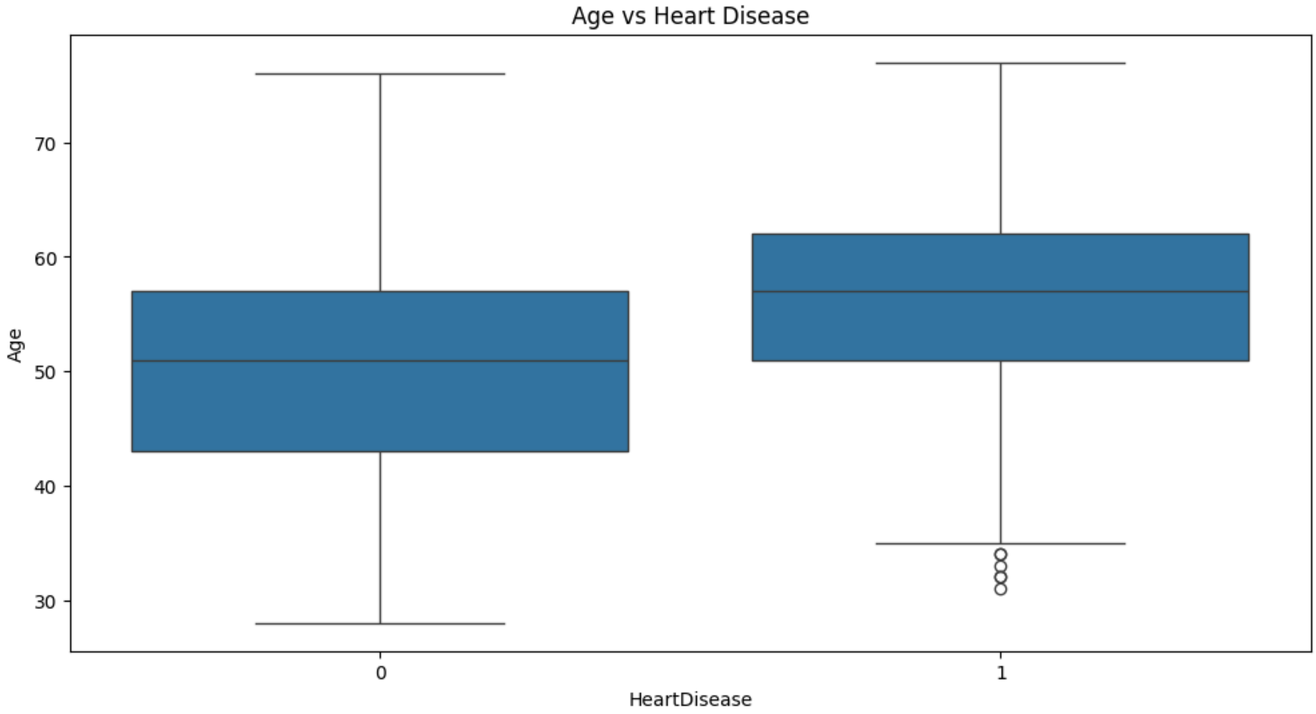
```
   Age Sex ChestPainType  RestingBP  Cholesterol  FastingBS RestingECG  MaxHR  \
0   40   M           ATA        140          289          0     Normal    172   
1   49   F           NAP        160          180          0     Normal    156   
2   37   M           ATA        130          283          0         ST     98   
3   48   F           ASY        138          214          0     Normal    108   
4   54   M           NAP        150          195          0     Normal    122   

  ExerciseAngina  Oldpeak ST_Slope  HeartDisease  
0              N      0.0       Up             0  
1              N      1.0     Flat             1  
2              N      0.0       Up             0  
3              Y      1.5     Flat             1  
4              N      0.0       Up             0  
<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
None
              Age   RestingBP  Cholesterol   FastingBS       MaxHR  \
count  918.000000  918.000000   918.000000  918.000000  918.000000   
mean    53.510893  132.396514   198.799564    0.233115  136.809368   
std      9.432617   18.514154   109.384145    0.423046   25.460334   
min     28.000000    0.000000     0.000000    0.000000   60.000000   
25%     47.000000  120.000000   173.250000    0.000000  120.000000   
50%     54.000000  130.000000   223.000000    0.000000  138.000000   
75%     60.000000  140.000000   267.000000    0.000000  156.000000   
max     77.000000  200.000000   603.000000    1.000000  202.000000   

          Oldpeak  HeartDisease  
count  918.000000    918.000000  
mean     0.887364      0.553377  
std      1.066570      0.497414  
min     -2.600000      0.000000  
25%      0.000000      0.000000  
50%      0.600000      1.000000  
75%      1.500000      1.000000  
max      6.200000      1.000000  
```



Bivariate Analysis

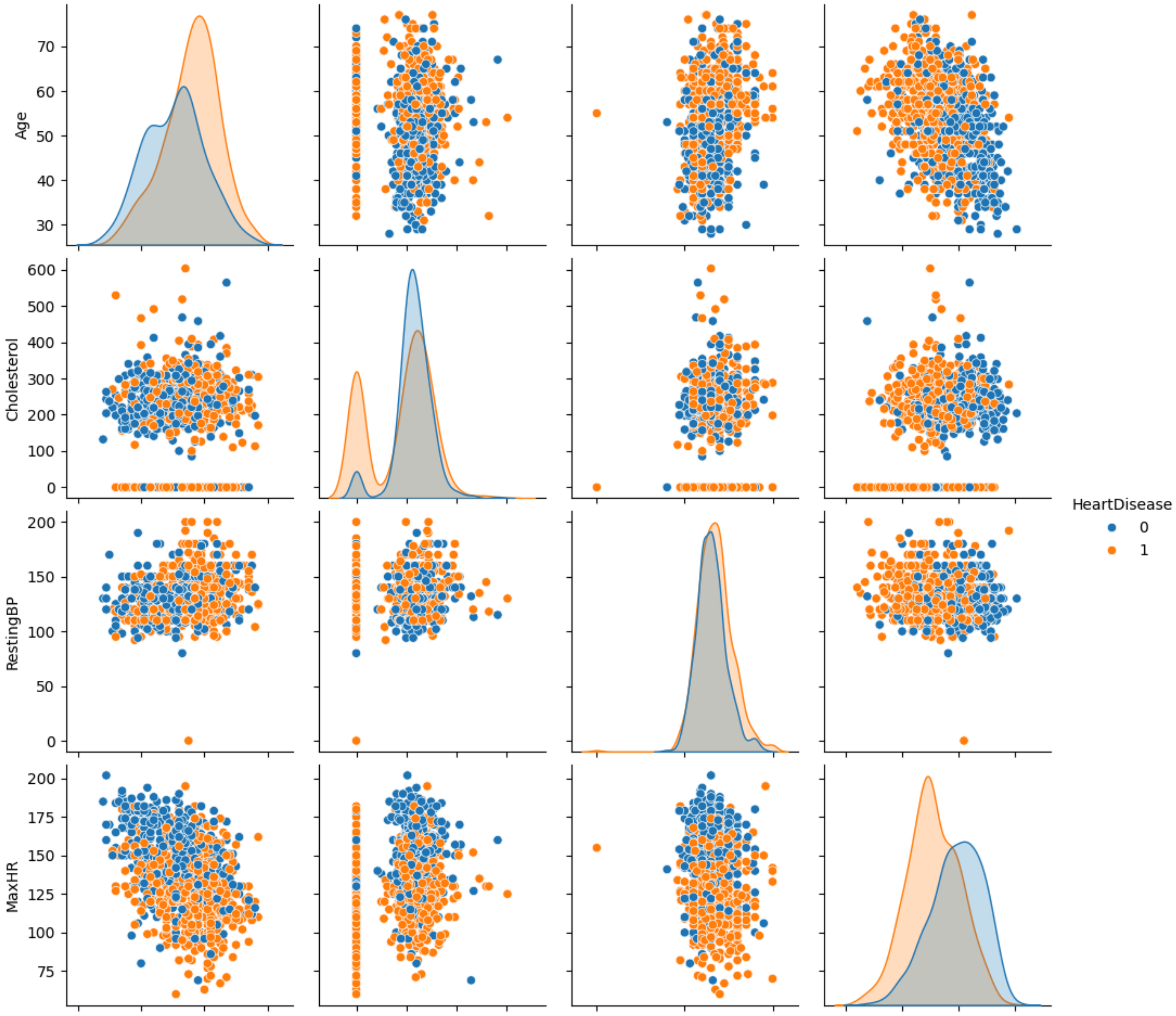
```
# Correlation heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(data.select_dtypes(include=np.number).corr(), annot=True, cmap='coolwarm', vmin=-1, vmax=1) # Select only numerical columns f
plt.title('Correlation Heatmap')
plt.show()

# Boxplot for numerical features by target
plt.figure(figsize=(12, 6))
sns.boxplot(x='HeartDisease', y='Age', data=data)
plt.title('Age vs Heart Disease')
plt.show()
```





Multivariate Analysis

```
# Pairplot for selected features
sns.pairplot(data, hue='HeartDisease', vars=['Age', 'Cholesterol', 'RestingBP', 'MaxHR'])
plt.show()
```



Data Preprocessing

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.impute import SimpleImputer
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, accuracy_score
import joblib

# Preprocessing
# Handle missing values and encode categorical variables
features = data.drop(columns=['HeartDisease'])
target = data['HeartDisease']

# Identify categorical and numerical columns
categorical_features = features.select_dtypes(include=['object']).columns
numerical_features = features.select_dtypes(exclude=['object']).columns

# Define preprocessing for numerical and categorical data
numerical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler())])

categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='most_frequent')),
    ('onehot', OneHotEncoder(handle_unknown='ignore'))])

preprocessor = ColumnTransformer(
    transformers=[
        ('num', numerical_transformer, numerical_features),
        ('cat', categorical_transformer, categorical_features)])

# Split data
```

```
X_train, X_test, y_train, y_test = train_test_split(features, target, test_size=0.2, random_state=42)

# Define model
model = Pipeline(steps=[('preprocessor', preprocessor),
                        ('classifier', RandomForestClassifier(random_state=42))])

# Train model
model.fit(X_train, y_train)

# Predict and evaluate
y_pred = model.predict(X_test)
print("Train Accuracy:", accuracy_score(y_train, model.predict(X_train)))
print("Test Accuracy:", accuracy_score(y_test, y_pred))
print(classification_report(y_test, y_pred))
```

```
Train Accuracy: 1.0
Test Accuracy: 0.8804347826086957
              precision    recall  f1-score   support

           0       0.85      0.87      0.86        77
           1       0.90      0.89      0.90       107
```