day86-88-heart-disease-prediction

January 18, 2024

Day 86-88 Heart Disease Prediction   By: Loga Aswin

[1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px


from sklearn.preprocessing import LabelEncoder, StandardScaler, MinMaxScaler,␣
 ↪OneHotEncoder
from sklearn.cluster import KMeans
```

[50]:
```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.metrics import accuracy_score, confusion_matrix
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
```

[2]:
```
df = pd.read_csv("/content/heart.csv")
```

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

[3]:
```
   age  sex  cp  trtbps  chol  fbs  restecg  thalachh  exng  oldpeak  slp  \
0   63    1   3     145   233    1        0       150     0      2.3    0
1   37    1   2     130   250    0        1       187     0      3.5    0
2   41    0   1     130   204    0        0       172     0      1.4    2
3   56    1   1     120   236    0        1       178     0      0.8    2
4   57    0   0     120   354    0        1       163     1      0.6    2

   caa  thall  output
0    0      1       1
```

```
1     0       2        1
2     0       2        1
3     0       2        1
4     0       2        1
```

[4]:
```
df.shape
```

[4]:
```
(303, 14)
```

[5]:
```
df.describe
```

[5]:
```
<bound method NDFrame.describe of      age  sex  cp  trtbps  chol  fbs  restecg
thalachh  exng  oldpeak  slp  \
0      63    1   3     145   233    1        0       150     0      2.3    0
1      37    1   2     130   250    0        1       187     0      3.5    0
2      41    0   1     130   204    0        0       172     0      1.4    2
3      56    1   1     120   236    0        1       178     0      0.8    2
4      57    0   0     120   354    0        1       163     1      0.6    2
..    …   …  ..     …    …   …       …      …    …      … …
298    57    0   0     140   241    0        1       123     1      0.2    1
299    45    1   3     110   264    0        1       132     0      1.2    1
300    68    1   0     144   193    1        1       141     0      3.4    1
301    57    1   0     130   131    0        1       115     1      1.2    1
302    57    0   1     130   236    0        0       174     0      0.0    1

     caa  thall  output
0      0      1       1
1      0      2       1
2      0      2       1
3      0      2       1
4      0      2       1
..   …    …     …
298    0      3       0
299    0      3       0
300    2      3       0
301    1      3       0
302    1      2       0

[303 rows x 14 columns]>
```

[6]:
```
# uniqueness
for column in df.columns:
  distinct_value = len(df[column].unique())
  print(f"{column}: {distinct_value} distinct values")
```

```
age: 41 distinct values
sex: 2 distinct values
```

```
cp: 4 distinct values
trtbps: 49 distinct values
chol: 152 distinct values
fbs: 2 distinct values
restecg: 3 distinct values
thalachh: 91 distinct values
exng: 2 distinct values
oldpeak: 40 distinct values
slp: 3 distinct values
caa: 5 distinct values
thall: 4 distinct values
output: 2 distinct values
```

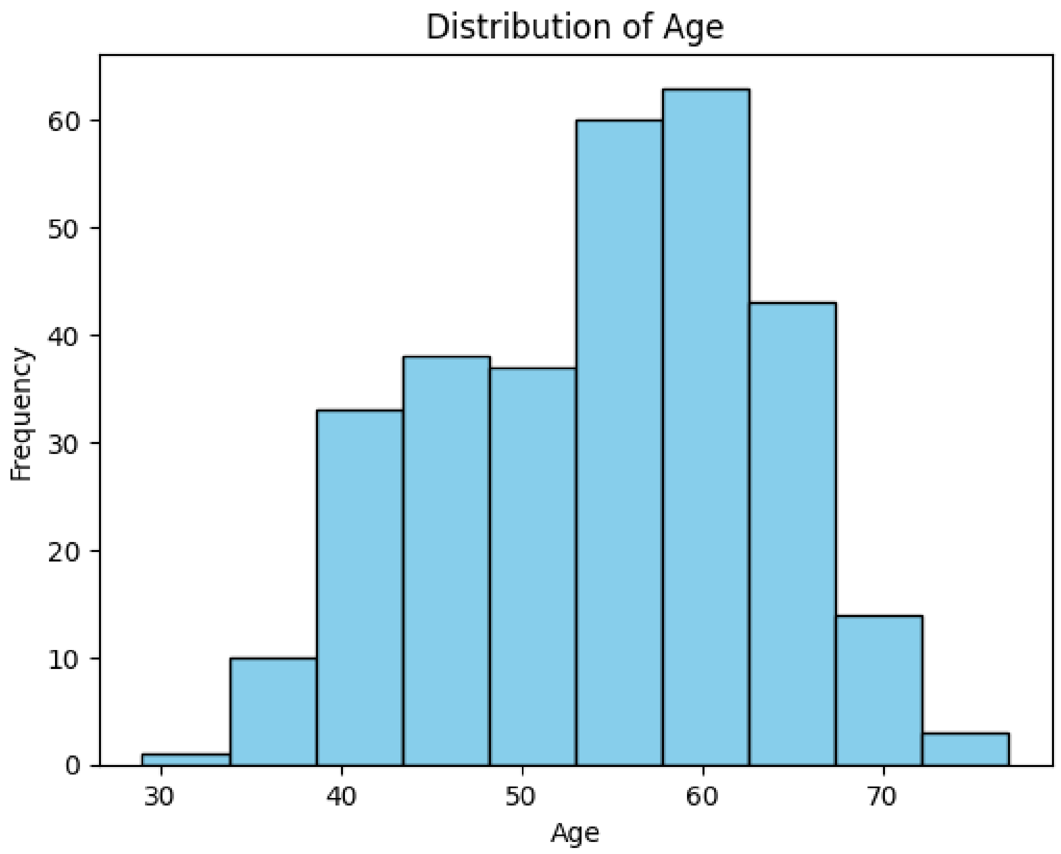
[7]:
```
duplicate_data = df[df.duplicated()]
print("No. of Duplicate Rows: ", duplicate_data)
```

```
No. of Duplicate Rows:        age  sex  cp  trtbps  chol  fbs  restecg  thalachh
exng  oldpeak  slp  \
164   38    1   2     138   175    0        1       173     0      0.0    2

     caa  thall  output
164    4      2       1
```

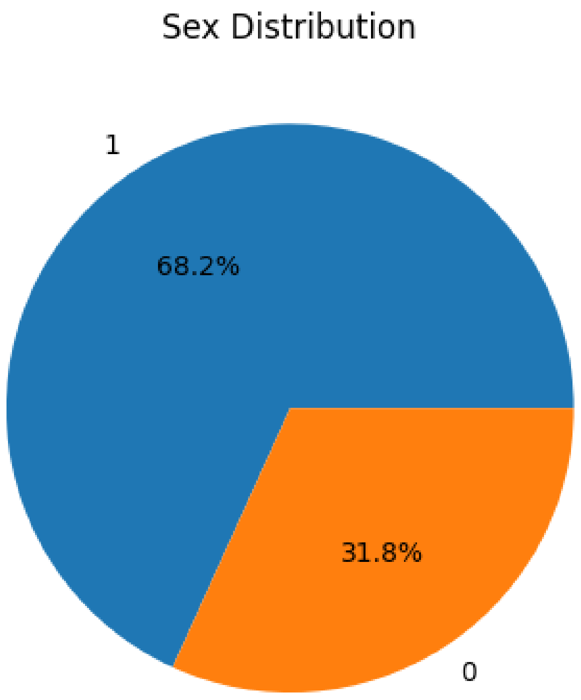
[8]:
```
df = df.drop_duplicates()
```

Univariate Analysis

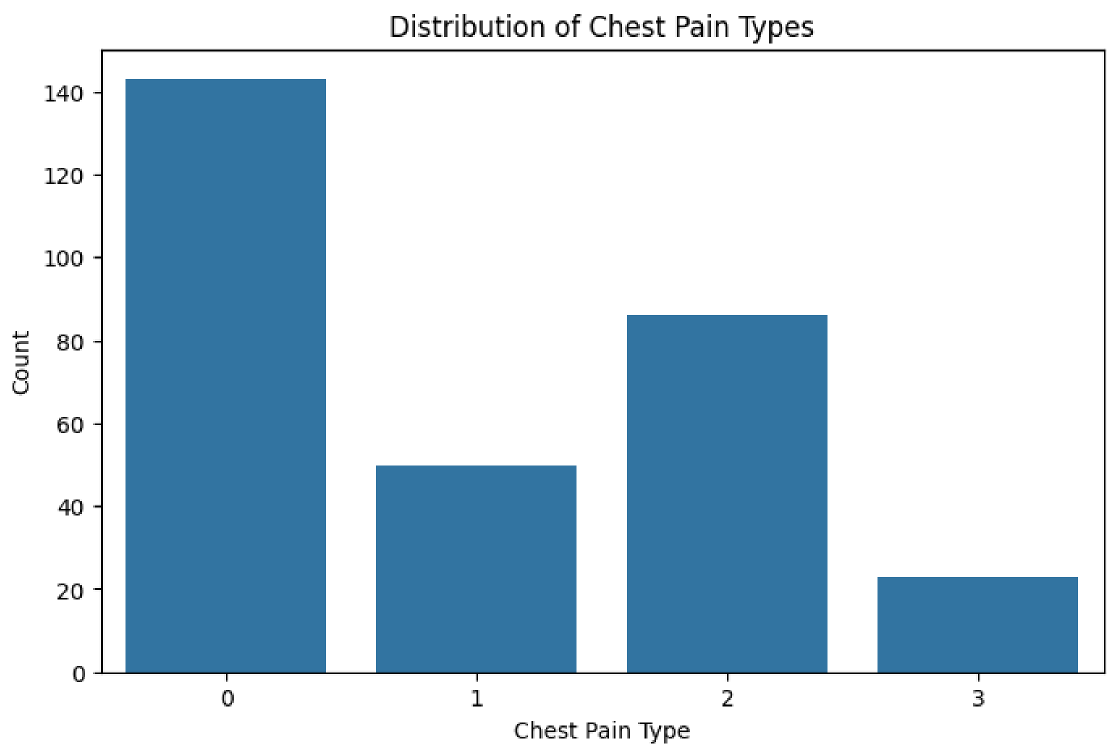
[9]:
```
plt.hist(df['age'], bins=10, color='skyblue', edgecolor='black')
plt.title('Distribution of Age')
plt.xlabel('Age')
plt.ylabel('Frequency')

# Show the plot
plt.show()
```



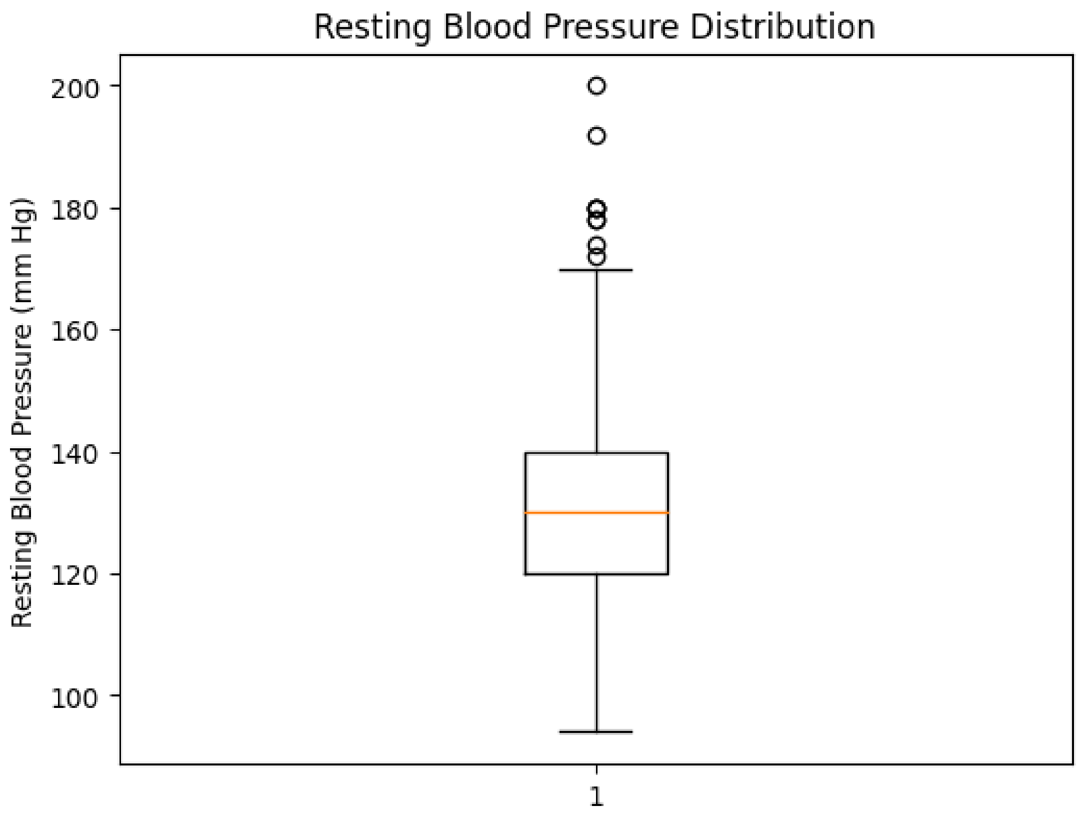
[10]:
```
sex_count = df['sex'].value_counts()
plt.pie(sex_count, labels=sex_count.index, autopct='%1.1f%%')
plt.title('Sex Distribution')
plt.show()
```



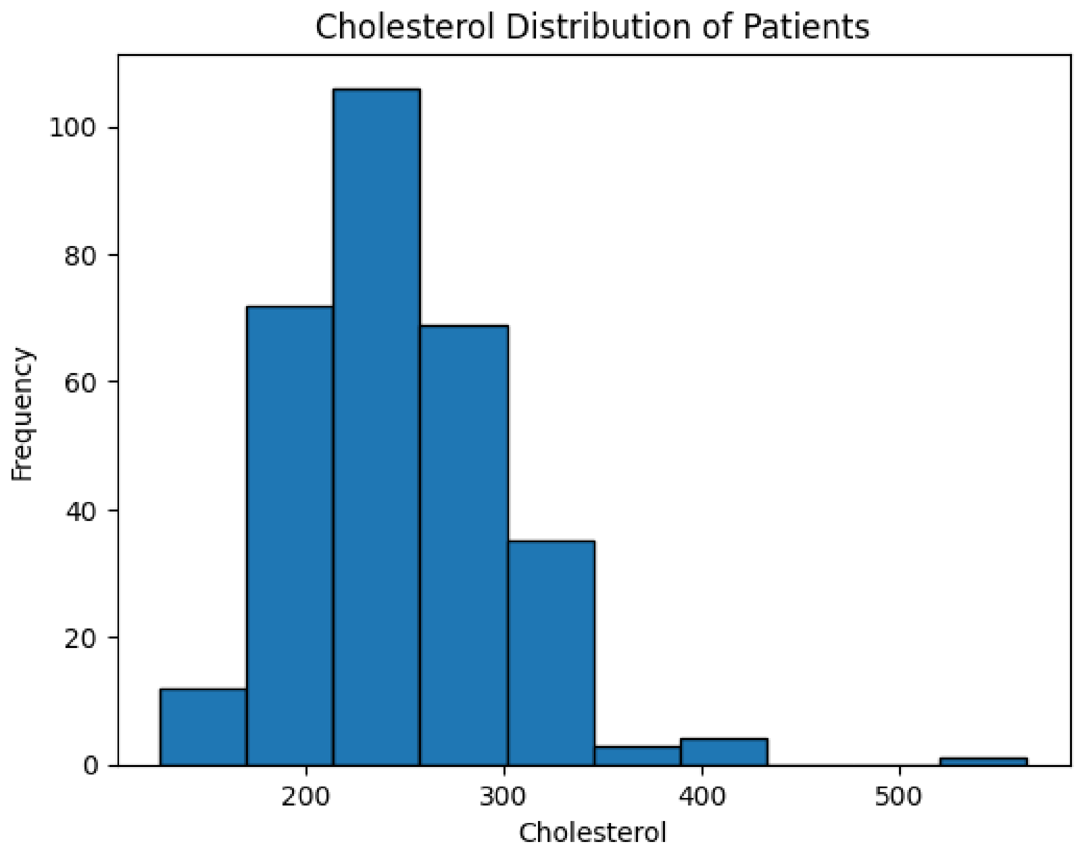
[11]:
```
plt.figure(figsize=(8, 5))
sns.countplot(x='cp', data=df)
plt.title('Distribution of Chest Pain Types')
plt.xlabel('Chest Pain Type')
plt.ylabel('Count')
plt.show()
```



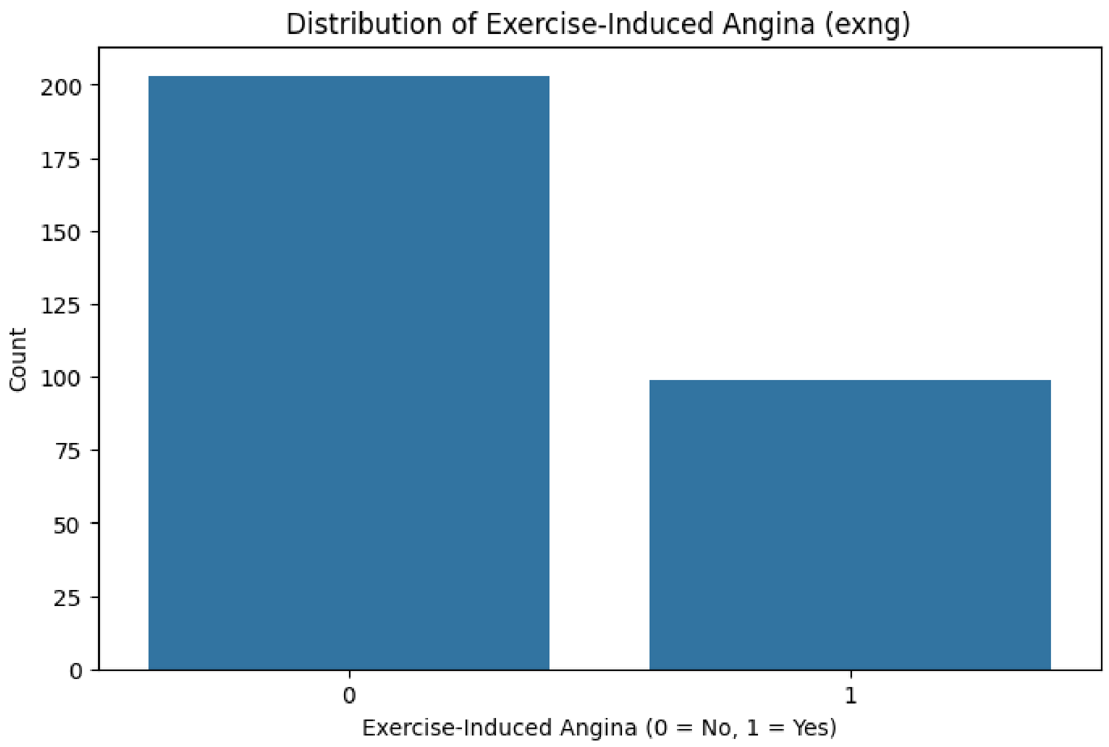
```
[12]: plt.boxplot(df['trtbps'])
      plt.title('Resting Blood Pressure Distribution')
      plt.ylabel('Resting Blood Pressure (mm Hg)')
      plt.show()
```



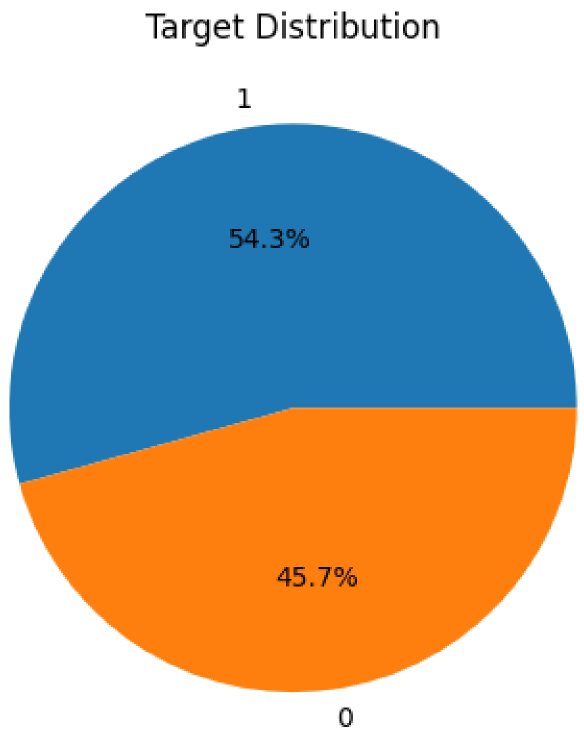
```
[13]: plt.hist(df['chol'], bins=10, edgecolor='black')
      plt.title('Cholesterol Distribution of Patients')
      plt.xlabel('Cholesterol')
      plt.ylabel('Frequency')
      plt.show()
```



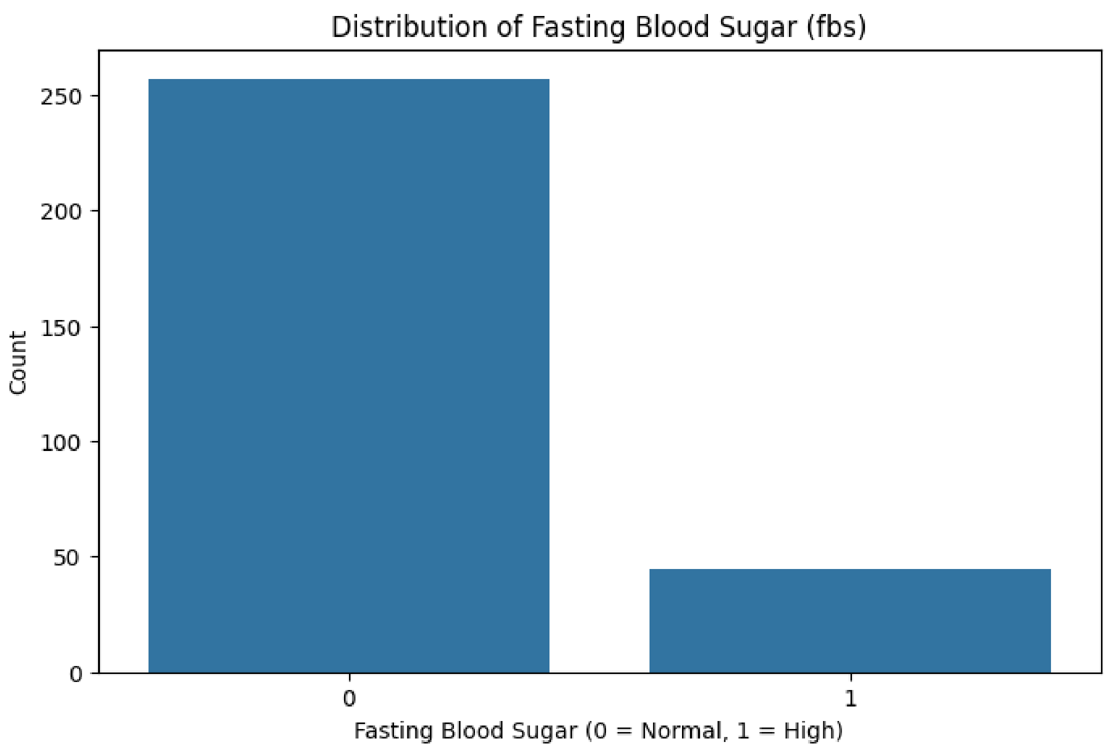
[14]:
```
plt.figure(figsize=(8, 5))
sns.countplot(x='exng', data=df)
plt.title('Distribution of Exercise-Induced Angina (exng)')
plt.xlabel('Exercise-Induced Angina (0 = No, 1 = Yes)')
plt.ylabel('Count')
plt.show()
```



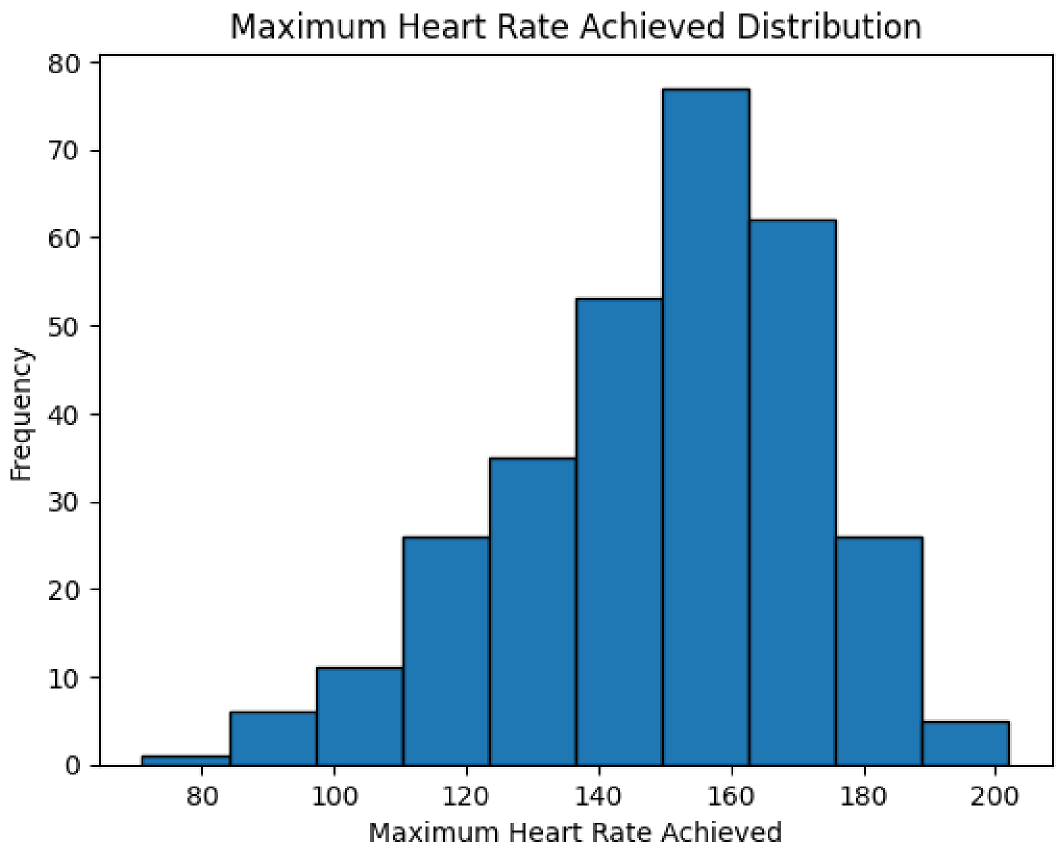
[15]:
```
target_count = df['output'].value_counts()
plt.pie(target_count, labels=target_count.index, autopct='%1.1f%%')
plt.title('Target Distribution')
plt.show()
```



```
[16]: plt.figure(figsize=(8, 5))
      sns.countplot(x='fbs', data=df)
      plt.title('Distribution of Fasting Blood Sugar (fbs)')
      plt.xlabel('Fasting Blood Sugar (0 = Normal, 1 = High)')
      plt.ylabel('Count')
      plt.show()
```

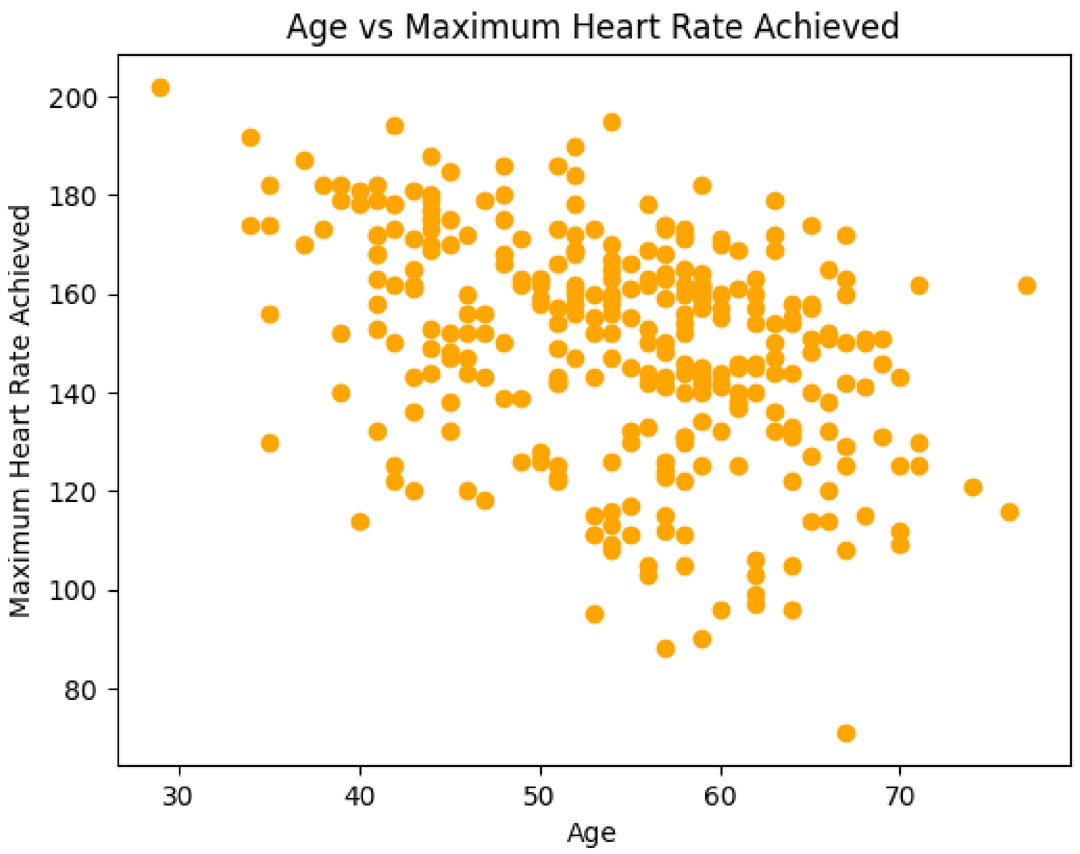


[17]:
```
plt.hist(df['thalachh'], bins=10, edgecolor='black')
plt.title('Maximum Heart Rate Achieved Distribution')
plt.xlabel('Maximum Heart Rate Achieved')
plt.ylabel('Frequency')
plt.show()
```

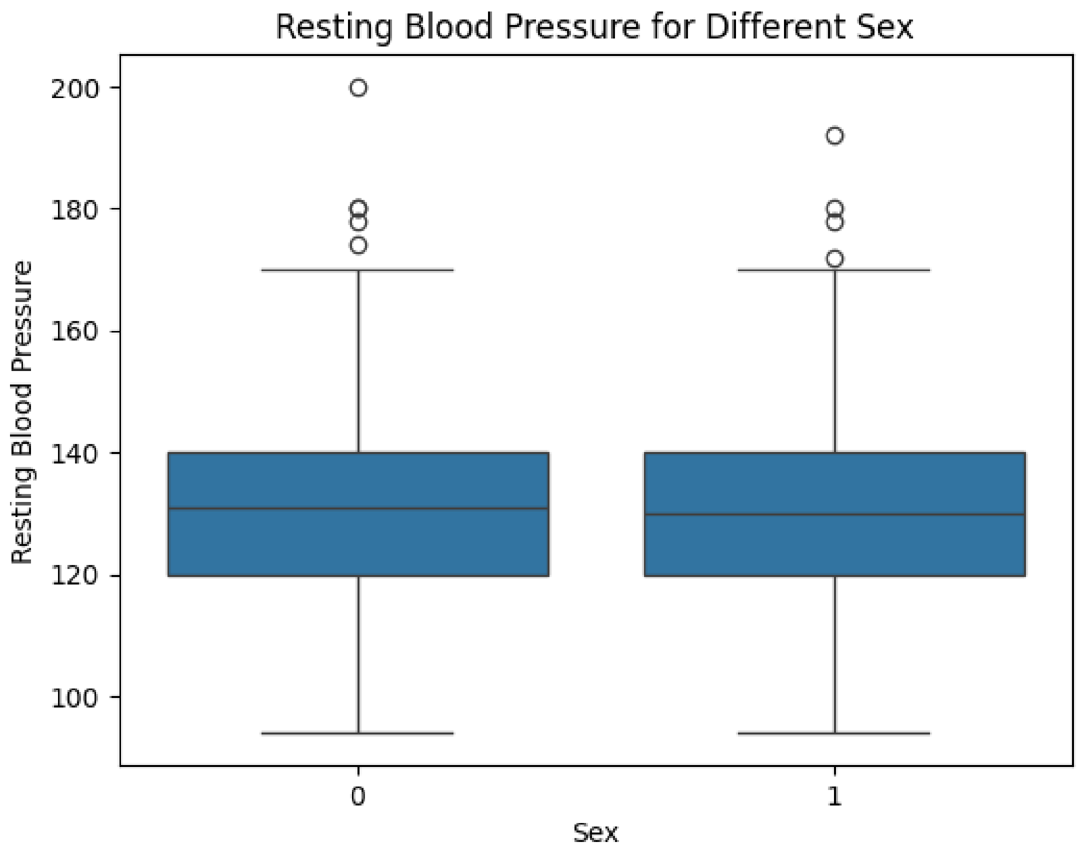


Bivarate Analysis:

```
[18]: plt.scatter(df['age'], df['thalachh'], color='orange')
      plt.title('Age vs Maximum Heart Rate Achieved')
      plt.xlabel('Age')
      plt.ylabel('Maximum Heart Rate Achieved')
      plt.show()
```

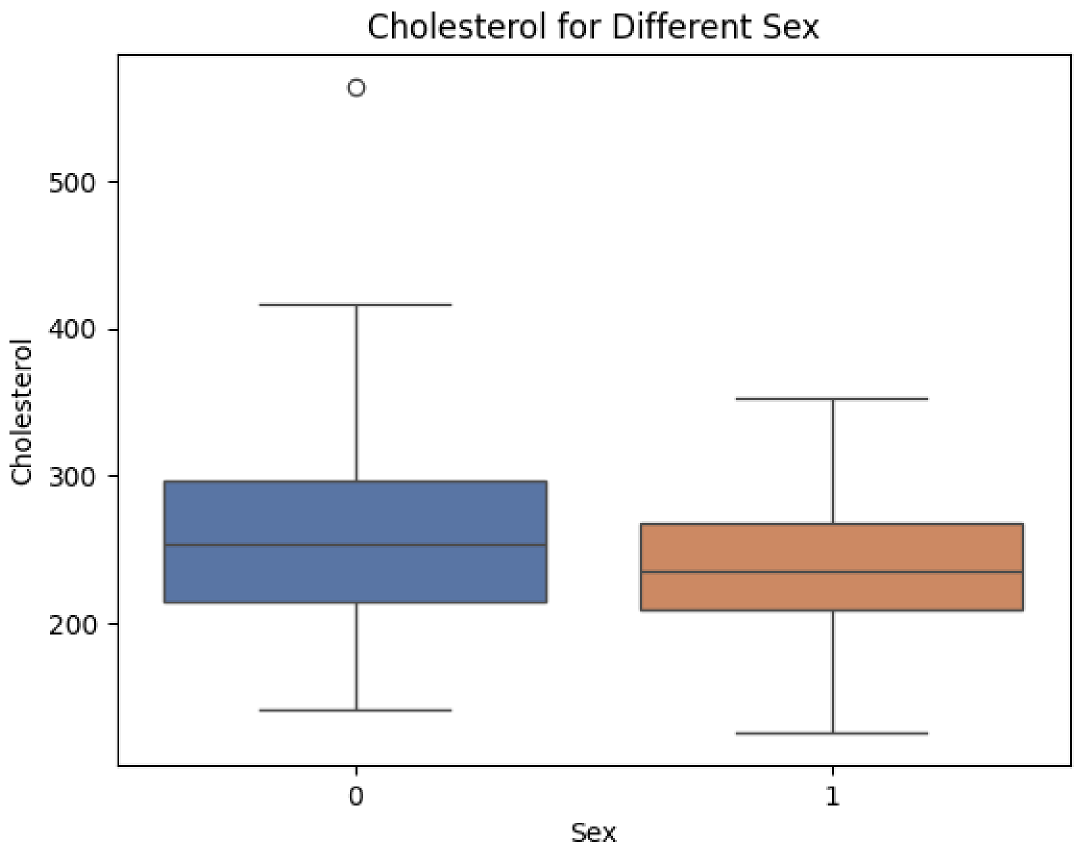


[19]:
```
sns.boxplot(x='sex', y='trtbps', data=df)
plt.title('Resting Blood Pressure for Different Sex')
plt.xlabel('Sex')
plt.ylabel('Resting Blood Pressure')
plt.show()
```



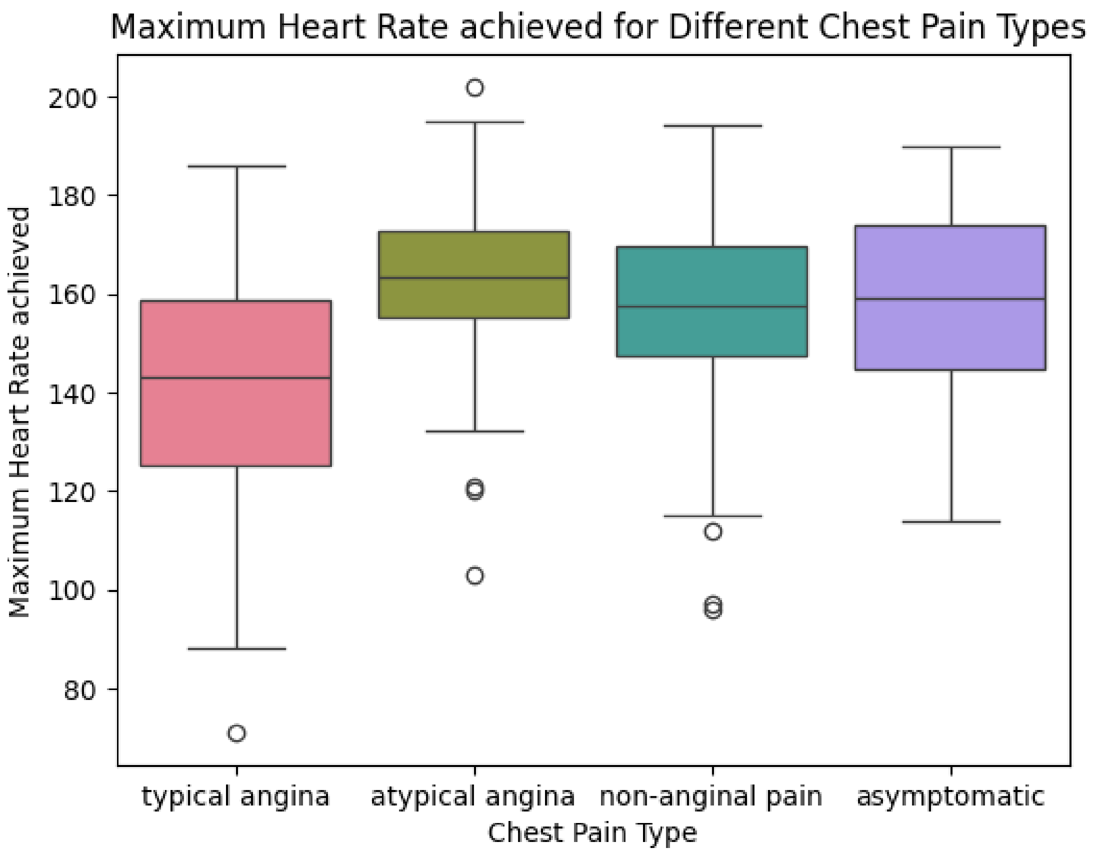
```
[20]: sns.boxplot(x='sex', y='chol', data=df, palette='deep')
      plt.title('Cholesterol for Different Sex')
      plt.xlabel('Sex')
      plt.ylabel('Cholesterol')
      plt.show()
```

```
<ipython-input-20-816911c146db>:1: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.boxplot(x='sex', y='chol', data=df, palette='deep')
```



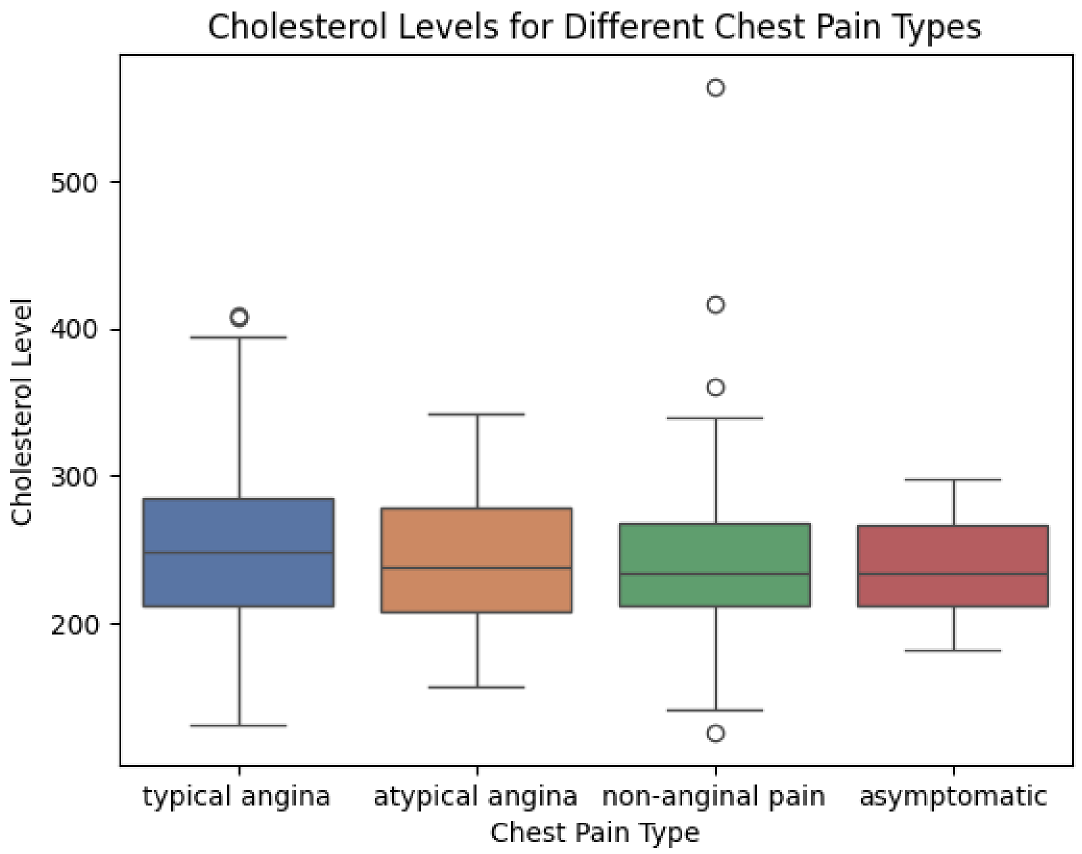
[21]:
```
sns.boxplot(x='cp', y='thalachh', data=df, palette='husl')
plt.title(' Maximum Heart Rate achieved for Different Chest Pain Types')
plt.xlabel('Chest Pain Type')
plt.ylabel('Maximum Heart Rate achieved')
plt.xticks(ticks=[0,1,2,3], labels=['typical angina', 'atypical angina',␣
 ↪'non-anginal pain', 'asymptomatic'])
plt.show()
```

```
<ipython-input-21-4c36d0afed2c>:1: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.boxplot(x='cp', y='thalachh', data=df, palette='husl')
```



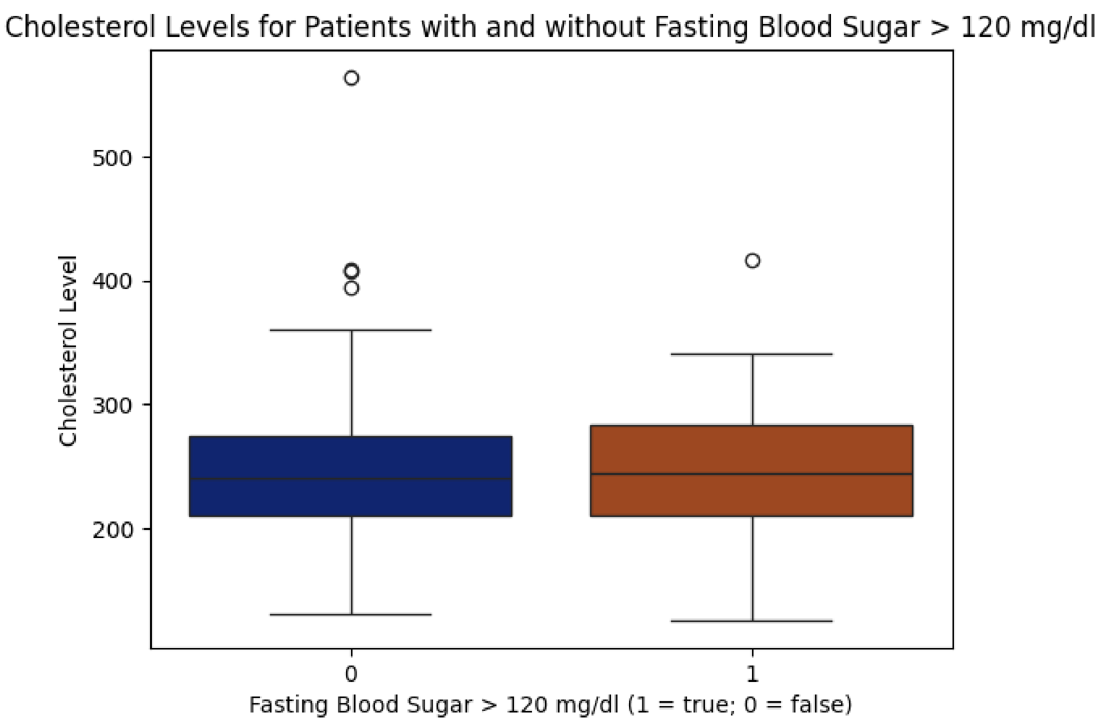
[22]:
```python
sns.boxplot(x='cp', y='chol', data=df, palette='deep')
plt.title('Cholesterol Levels for Different Chest Pain Types')
plt.xlabel('Chest Pain Type')
plt.ylabel('Cholesterol Level')
plt.xticks(ticks=[0,1,2,3], labels=['typical angina', 'atypical angina',␣
 ↪'non-anginal pain', 'asymptomatic'])
plt.show()
```

```
<ipython-input-22-aa5cd0b28f72>:1: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.boxplot(x='cp', y='chol', data=df, palette='deep')
```

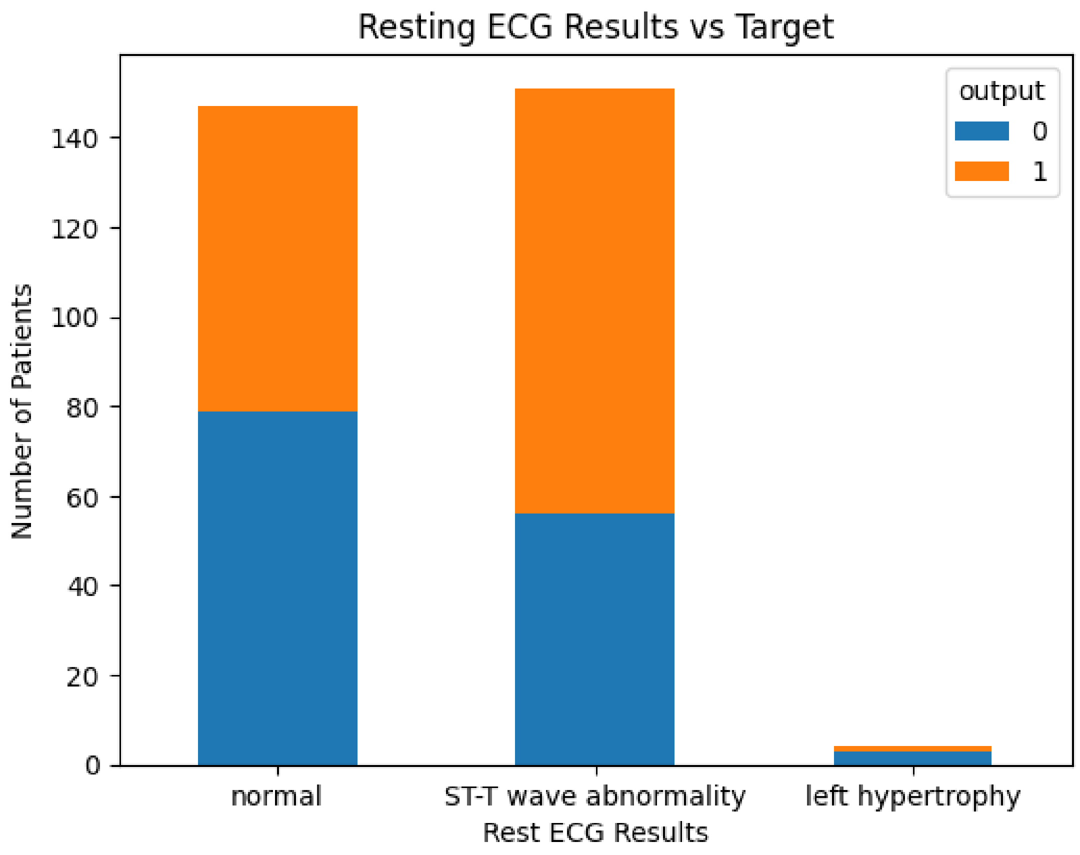


```
[23]: sns.boxplot(x='fbs', y='chol', data=df, palette='dark')
      plt.title('Cholesterol Levels for Patients with and without Fasting Blood Sugar␣
       ↪> 120 mg/dl')
      plt.xlabel('Fasting Blood Sugar > 120 mg/dl (1 = true; 0 = false)')
      plt.ylabel('Cholesterol Level')
      plt.show()
```

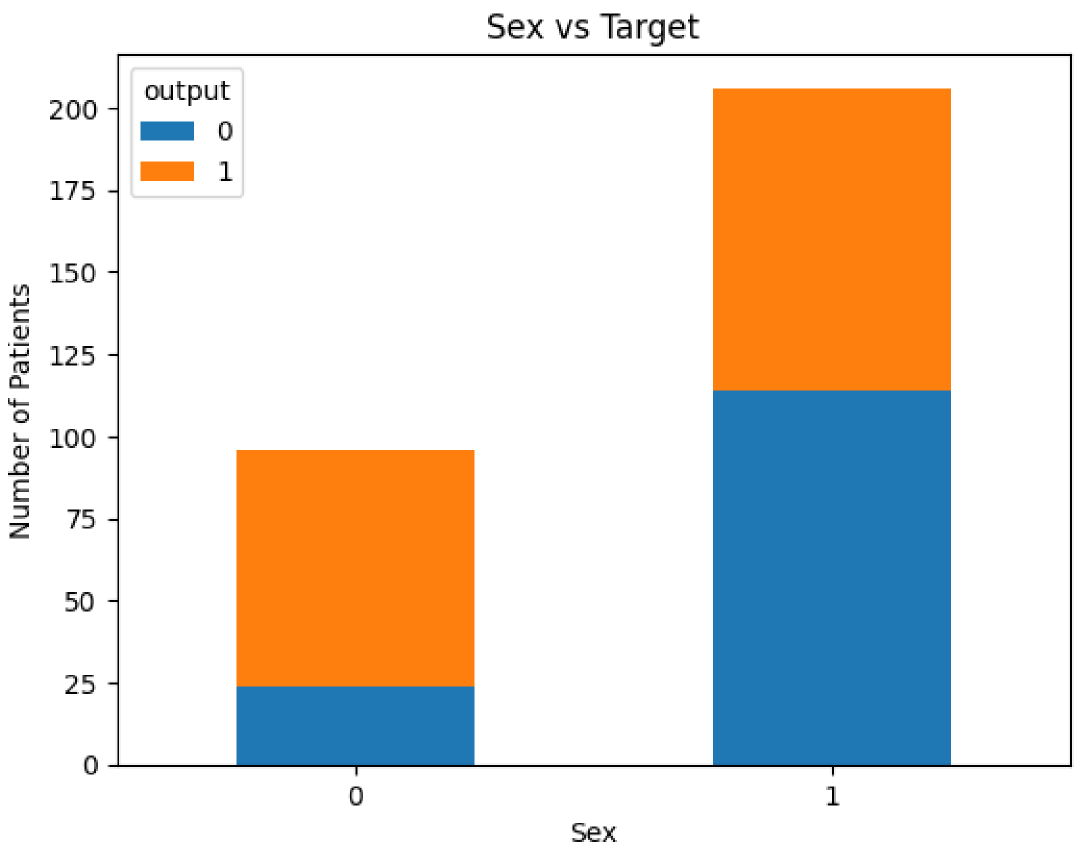
```
<ipython-input-23-17e263b47a3e>:1: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.boxplot(x='fbs', y='chol', data=df, palette='dark')
```



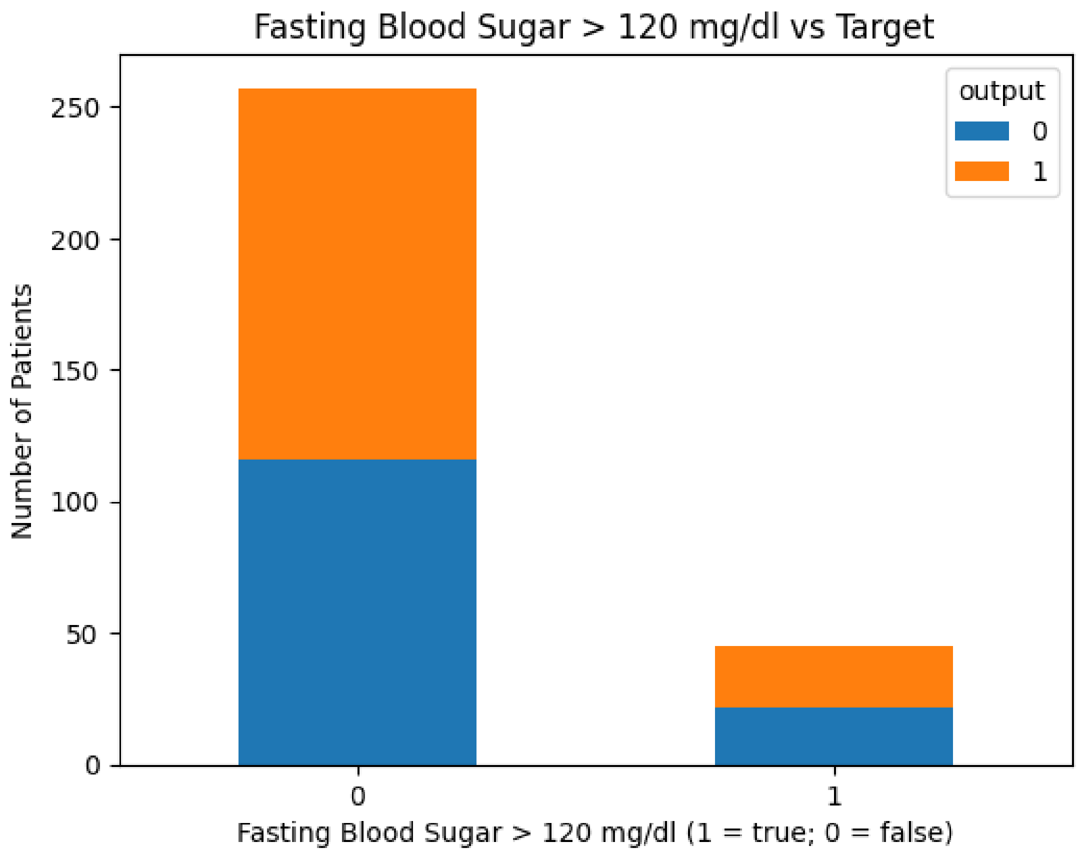
[24]:
```
restecg_target = df.groupby(['restecg', 'output']).size().unstack().fillna(0)
restecg_target.plot(kind='bar', stacked=True)
plt.title('Resting ECG Results vs Target')
plt.xlabel('Rest ECG Results')
plt.ylabel('Number of Patients')
plt.xticks(ticks=[0,1,2], labels=['normal', 'ST-T wave abnormality', 'left␣
 ↪hypertrophy'], rotation=0)
plt.show()
```



[25]:
```
sex_target = df.groupby(['sex', 'output']).size().unstack().fillna(0)
sex_target.plot(kind='bar', stacked=True)
plt.title('Sex vs Target')
plt.xlabel('Sex')
plt.ylabel('Number of Patients')
plt.xticks(rotation=0)
plt.show()
```

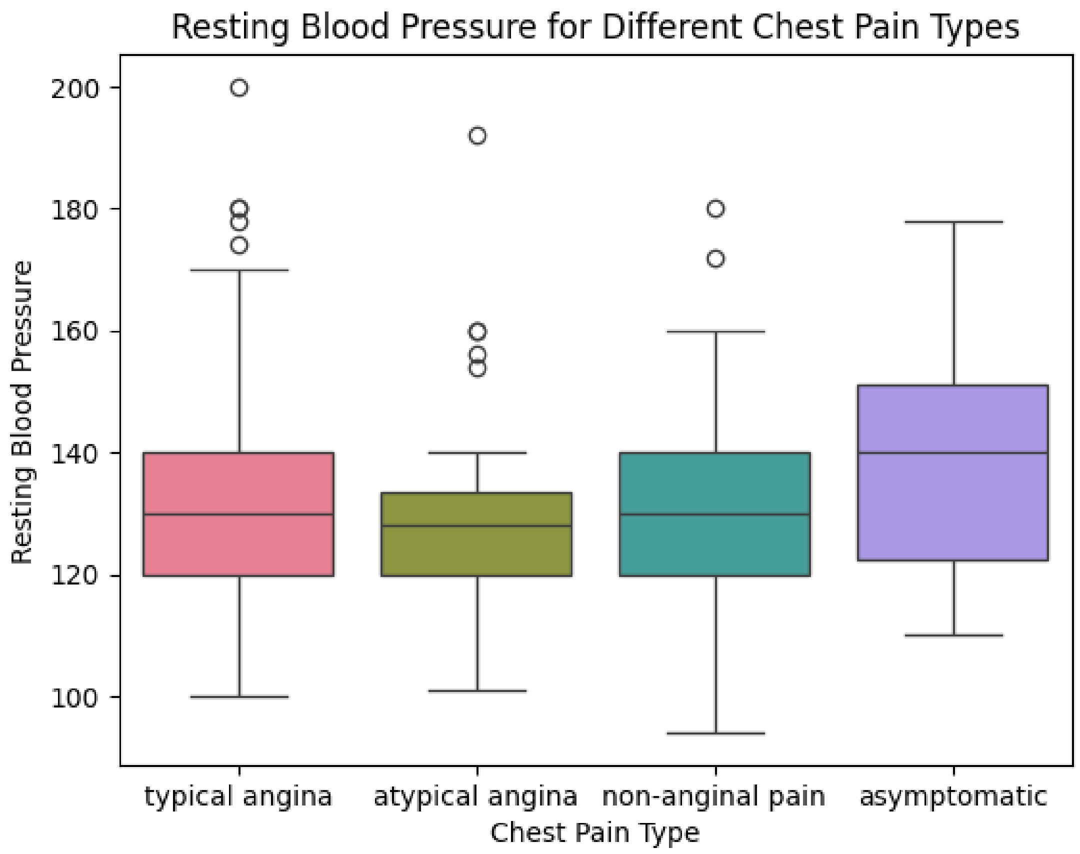


[26]:
```
fbs_target = df.groupby(['fbs', 'output']).size().unstack().fillna(0)
fbs_target.plot(kind='bar', stacked=True)
plt.title('Fasting Blood Sugar > 120 mg/dl vs Target')
plt.xlabel('Fasting Blood Sugar > 120 mg/dl (1 = true; 0 = false)')
plt.ylabel('Number of Patients')
plt.xticks(rotation=0)
plt.show()
```



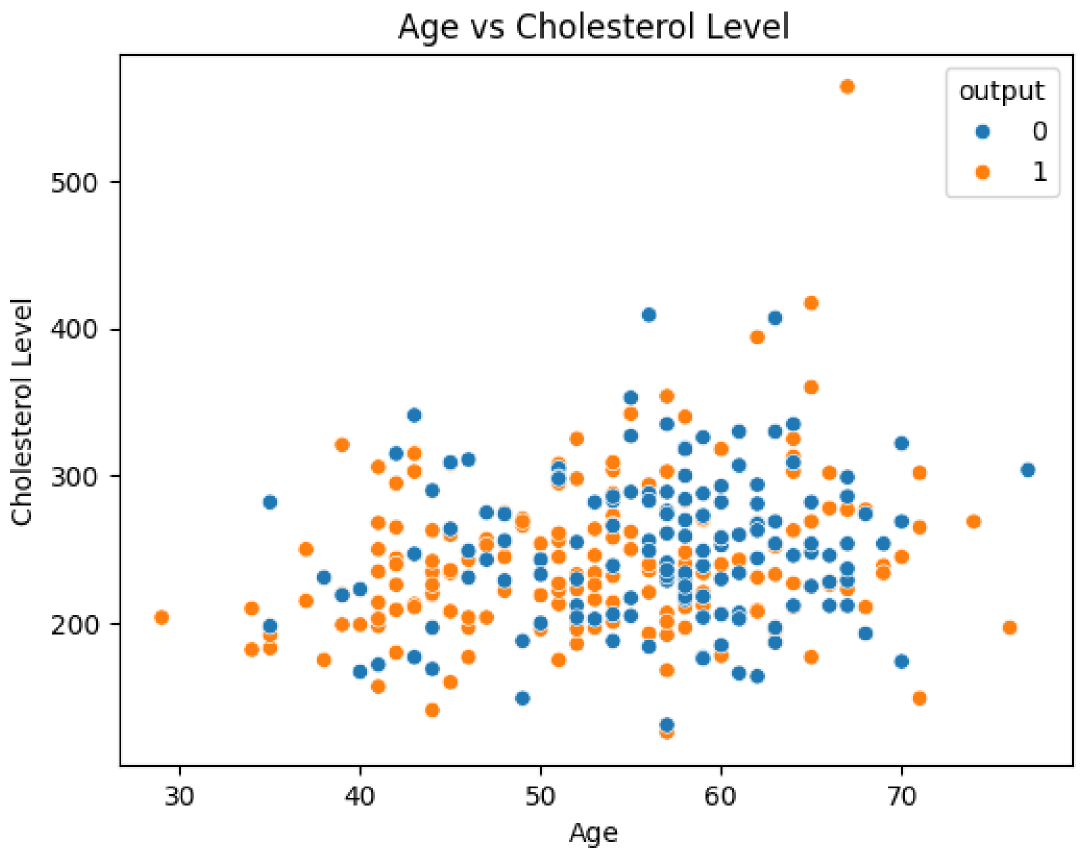
[27]:
```
sns.boxplot(x='cp', y='trtbps', data=df, palette='husl')
plt.title('Resting Blood Pressure for Different Chest Pain Types')
plt.xlabel('Chest Pain Type')
plt.ylabel('Resting Blood Pressure')
plt.xticks(ticks=[0,1,2,3], labels=['typical angina', 'atypical angina',␣
 ↪'non-anginal pain', 'asymptomatic'])
plt.show()
```

```
<ipython-input-27-337686c96ad5>:1: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.boxplot(x='cp', y='trtbps', data=df, palette='husl')
```

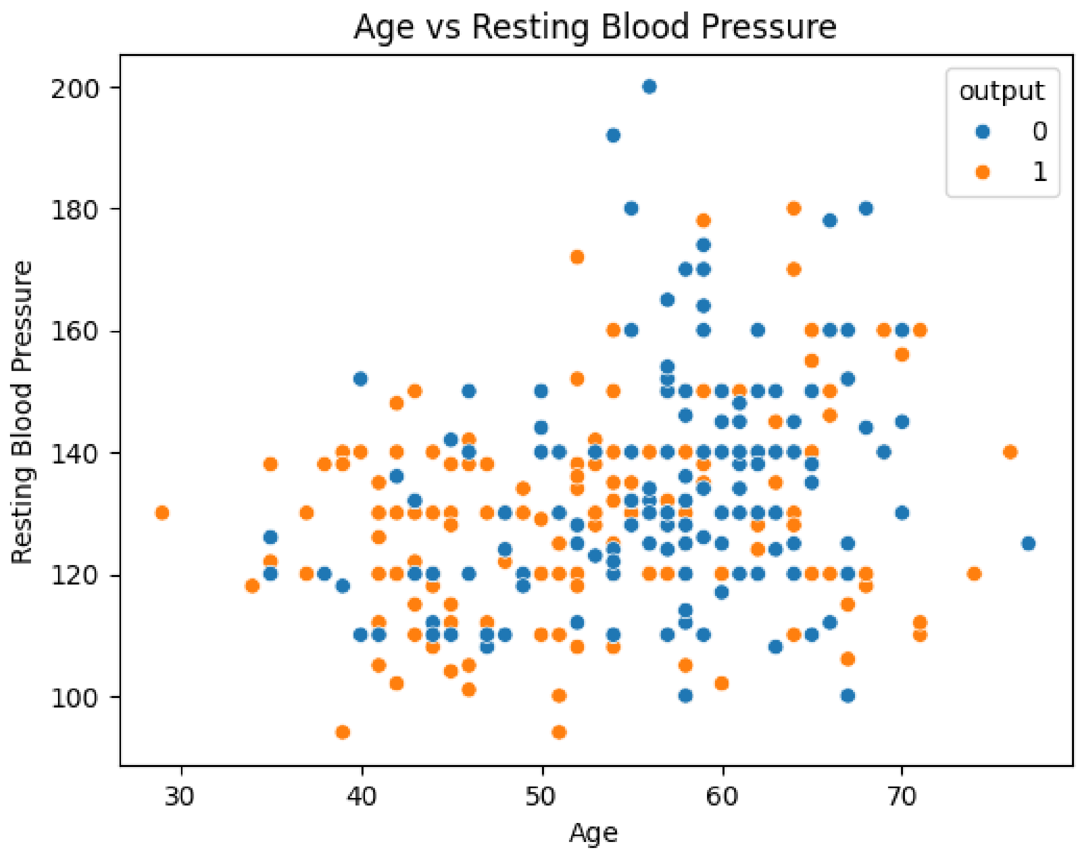


Multivariate Analysis:

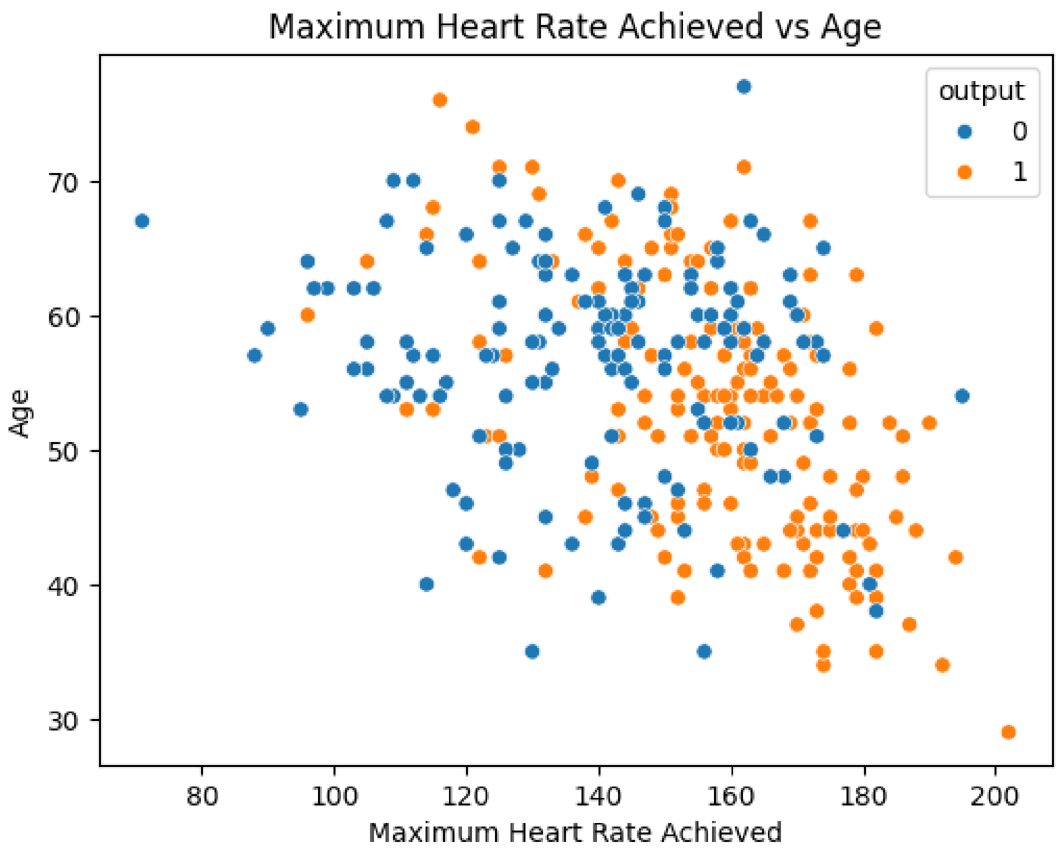
[28]:
```
sns.scatterplot(x='age', y='chol', hue='output', data=df)
plt.title('Age vs Cholesterol Level')
plt.xlabel('Age')
plt.ylabel('Cholesterol Level')
plt.show()
```



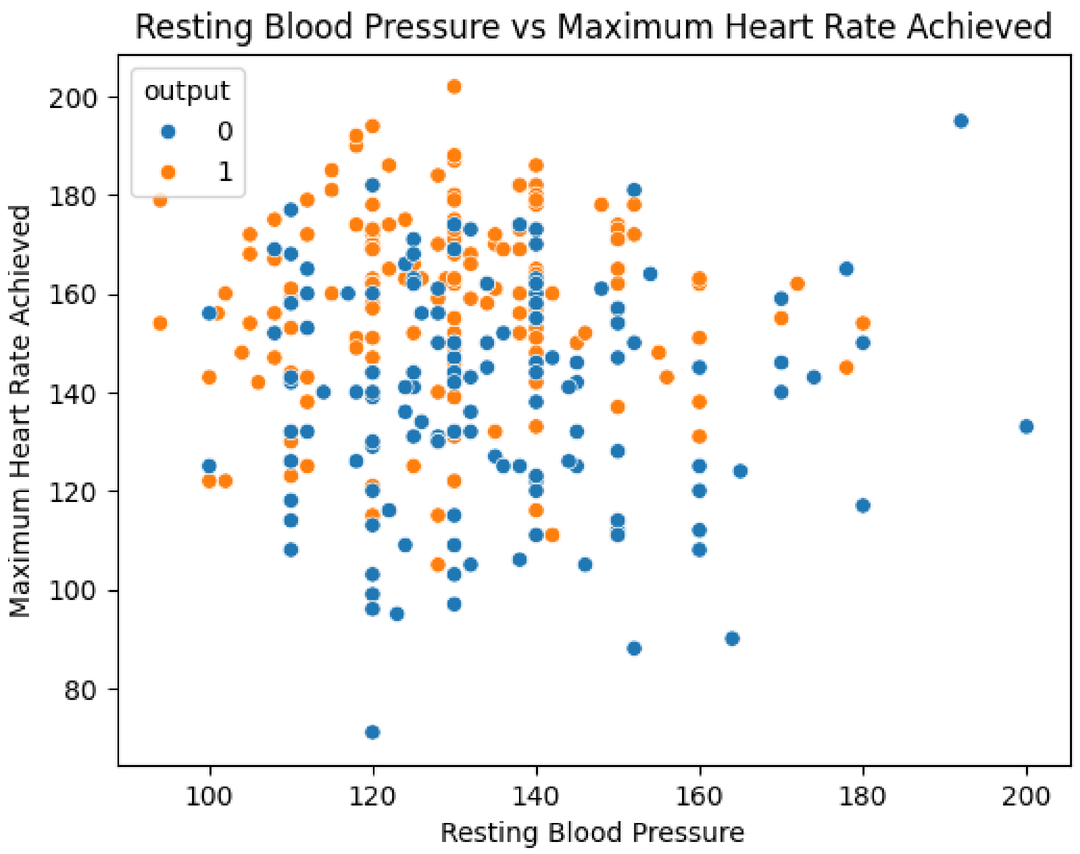
[29]:
```
sns.scatterplot(x='age', y='trtbps', hue='output', data=df)
plt.title('Age vs Resting Blood Pressure')
plt.xlabel('Age')
plt.ylabel('Resting Blood Pressure')
plt.show()
```



[30]:
```
sns.scatterplot(x='thalachh', y='age', hue='output', data=df)
plt.title('Maximum Heart Rate Achieved vs Age')
plt.xlabel('Maximum Heart Rate Achieved')
plt.ylabel('Age')
plt.show()
```



[31]:
```
sns.scatterplot(x='trtbps', y='thalachh', hue='output', data=df)
plt.title('Resting Blood Pressure vs Maximum Heart Rate Achieved')
plt.xlabel('Resting Blood Pressure')
plt.ylabel('Maximum Heart Rate Achieved')
plt.show()
```



Working with Categorical and Numerical Column:

```
[32]: categorical_columns = ['sex','cp','restecg','slp','thall']
      numerical_columns =␣
       ↪['age','trtbps','chol','fbs','thalachh','exng','oldpeak','caa','output']
      dummy_variables = pd.get_dummies(df, columns=categorical_columns,␣
       ↪drop_first=False)
```

Preprocessing and scaling data

```
[33]: scaler = StandardScaler()

      # Scale the numerical columns
      scaled_numerical = scaler.fit_transform(df[numerical_columns])

      # Convert the scaled numerical columns
      scaled_numerical_df = pd.DataFrame(scaled_numerical, columns=numerical_columns)
```

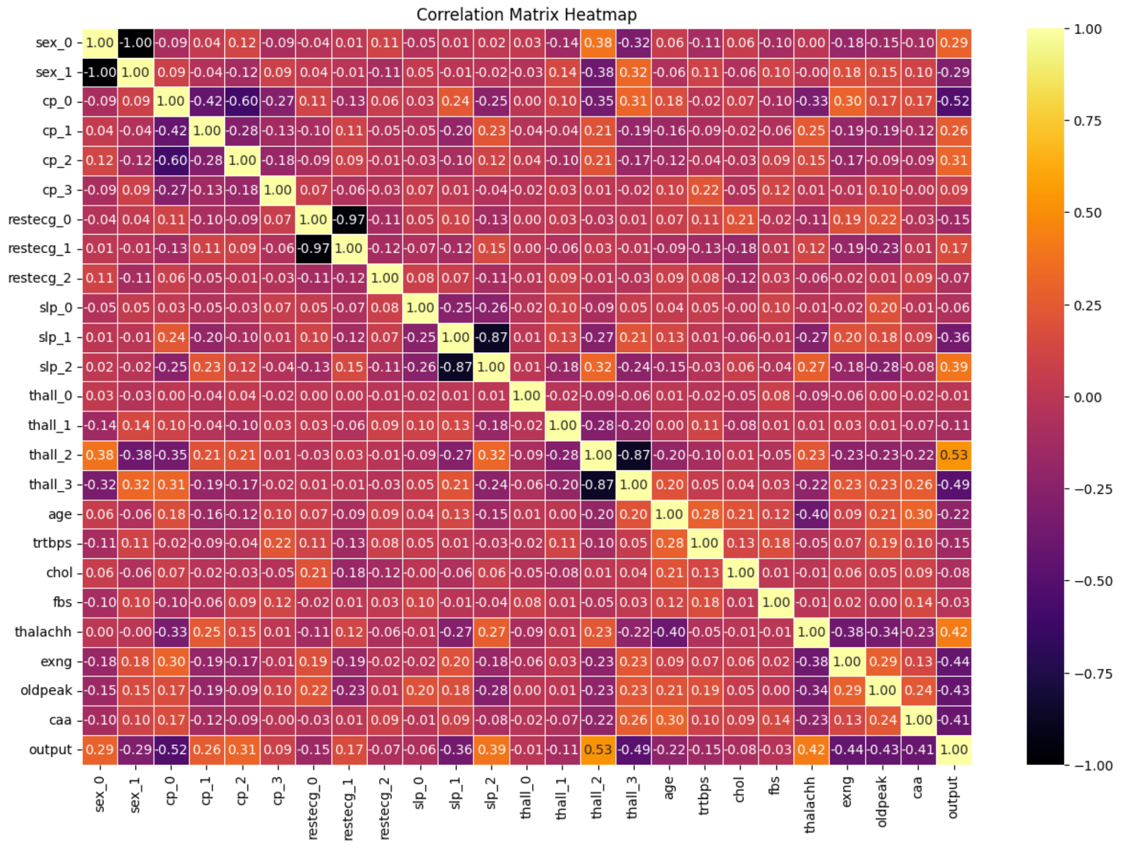
```
[34]: # Drop the original numerical columns
      dummy_variables = dummy_variables.drop(numerical_columns, axis=1)
```

```
# Concatenate the dummy variables and scaled numerical columns
processed_df = pd.concat([dummy_variables, scaled_numerical_df], axis=1)
```

Correlation matrix with dummy variables

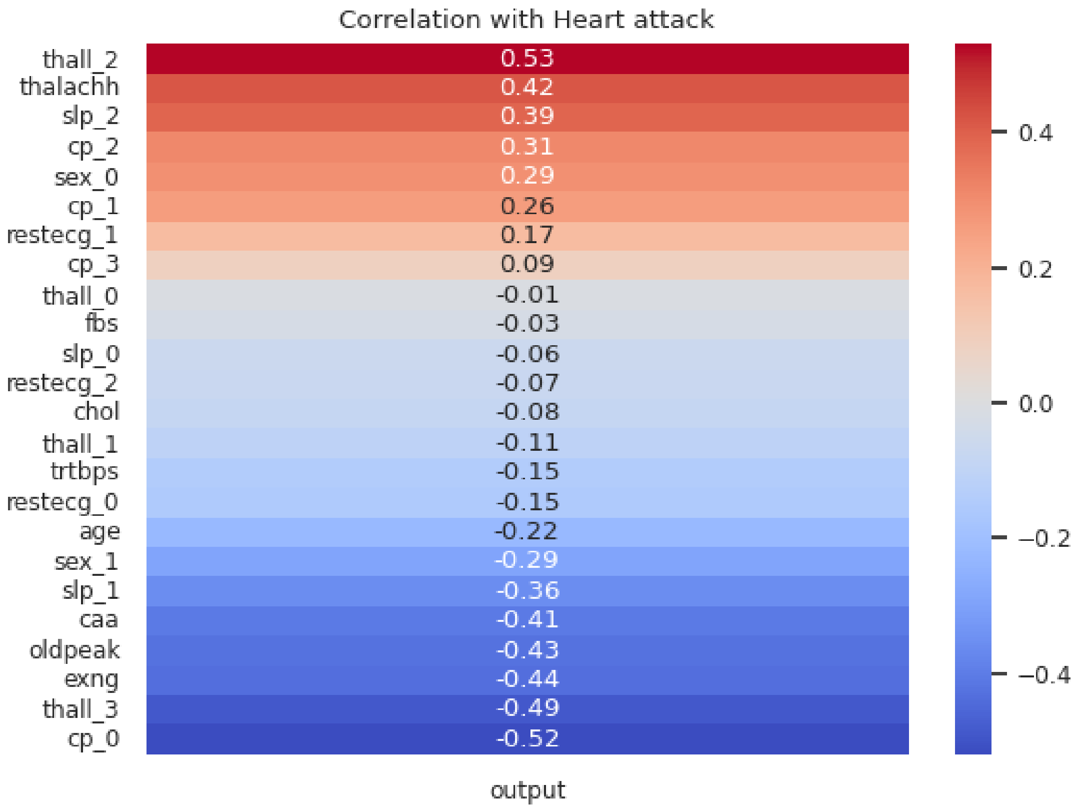
[35]:
```
correlation_matrix = processed_df.corr()
```

[36]:
```
#Graph 1
plt.figure(figsize=(15, 10))
sns.heatmap(correlation_matrix, annot=True, cmap='inferno', linewidths=0.5,␣
  ↪fmt='.2f')
plt.title("Correlation Matrix Heatmap")
plt.show()
```



[37]:
```
corr = processed_df.corr()
target_corr = corr['output'].drop('output')

# Sort correlation values in descending order
target_corr_sorted = target_corr.sort_values(ascending=False)
```

```
[38]: #Graph 2
      sns.set(font_scale=0.8)
      sns.set_style("white")
      sns.set_palette("dark")
      sns.heatmap(target_corr_sorted.to_frame(), cmap="coolwarm", annot=True, fmt='.
        ↪2f')
      plt.title('Correlation with Heart attack')
      plt.show()
```



Cluster Analysis

Preprocessing

```
[ ]: le = LabelEncoder()

     for col in ['sex','cp','restecg','slp','thall']:
         df[col] = le.fit_transform(df[col])

     # Scale numerical features
     scaler = StandardScaler()

     for col in ['age','trtbps','chol','fbs','thalachh','exng','oldpeak','caa']:
```

```
    df[col] = scaler.fit_transform(df[col].values.reshape(-1, 1))
```

[40]:
```
from sklearn.decomposition import PCA

X = df.drop('output', axis=1).values  # dropping the target column
y = df['output'].values

pca = PCA(n_components=2, random_state=42)
X_pca = pca.fit_transform(X)

#Create new dataframe
df_pca = pd.DataFrame(data=X_pca, columns=['Principal Component 1', 'Principal␣
 ↪Component 2'])
df_pca['Target'] = y

# Visualize with Plotly
fig_pca = px.scatter(df_pca, x='Principal Component 1', y='Principal Component␣
 ↪2', color='Target',
                      title='2 Component PCA', template='plotly')
fig_pca.show()
```

The selected text is interpreting the results of a plot:

- **Clusters**: The plot shows distinct clusters, suggesting groups of patients with similar characteristics. These characteristics could be a combination of various health factors.
- **Color Gradient**: The color gradient represents the diagnosis of heart disease and shows a clear pattern across the clusters. This suggests varying diagnoses within each cluster, indicating different risk groups for heart disease.
- **Outliers**: It's hard to determine any clear outliers from the image. Outliers would be patients with unique characteristics.
- **Axes in PCA plot**: The axes in our PCA plot don't correspond to specific variables, so it's not straightforward to define each cluster's characteristics. Further analysis would be needed.

Data Preprocessing:

[41]:
```
categorical_columns = ['sex','cp','restecg','slp','thall']
numerical_columns =␣
 ↪['age','trtbps','chol','fbs','thalachh','exng','oldpeak','caa']
```

[42]:
```
# Split data
X = df.drop('output', axis=1)
y = df['output']
```

Splitting into Data

[43]:
```
# Split data into train and test
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
 ↪random_state=42)
```

```
# define preprocessor
preprocessor = ColumnTransformer(
    transformers=[
        ('num', StandardScaler(), numerical_columns),
        ('cat', OneHotEncoder(), categorical_columns)])

# fit and transform training data
X_train = preprocessor.fit_transform(X_train)
X_test = preprocessor.transform(X_test)
```

[44]:
```
def evaluate_model(model, X_train, y_train, X_test, y_test):
    model.fit(X_train, y_train)
    train_pred = model.predict(X_train)
    test_pred = model.predict(X_test)
    train_acc = accuracy_score(y_train, train_pred)
    test_acc = accuracy_score(y_test, test_pred)
    return train_acc, test_acc, test_pred
```

[45]:
```
def plot_confusion_matrix(cm, classes, normalize=False, title='Confusion␣
 ↪matrix', cmap=plt.cm.Blues):
    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.title(title)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    if normalize:
        cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]

    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, cm[i, j], horizontalalignment="center", color="white" if␣
 ↪cm[i, j] > thresh else "black")

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

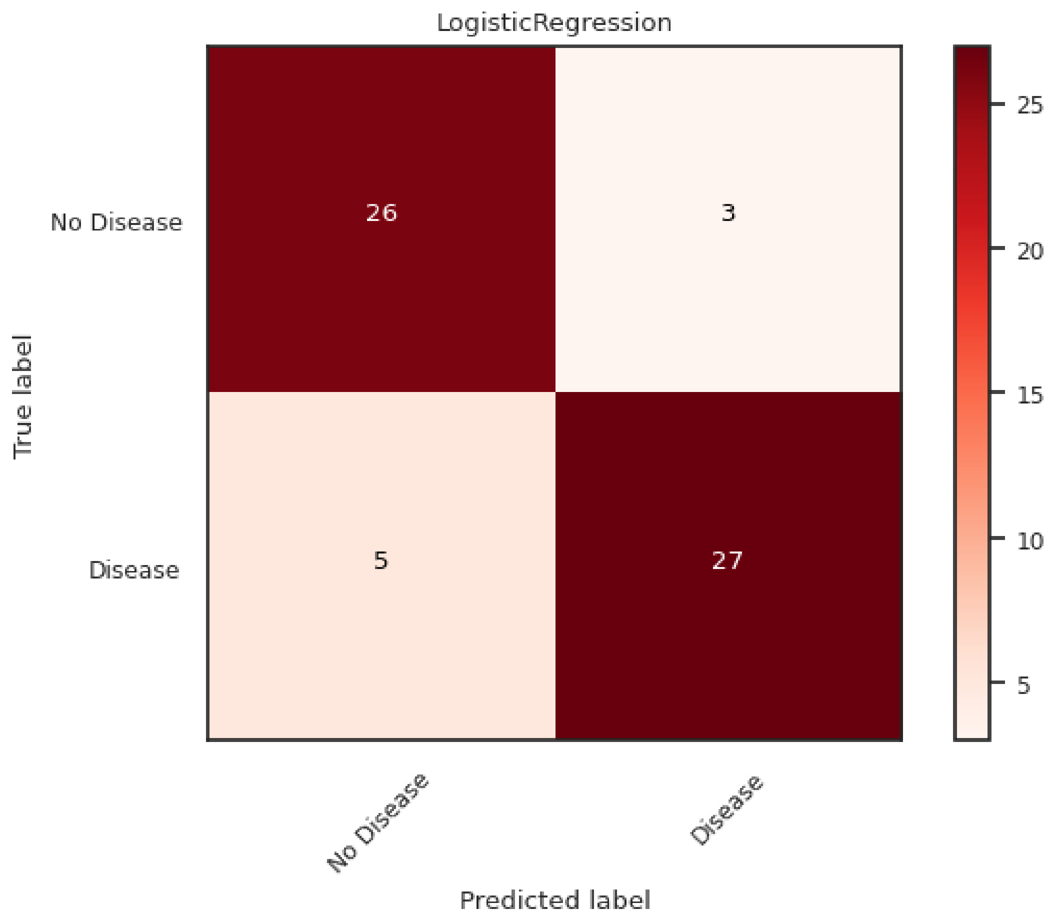
Model Training

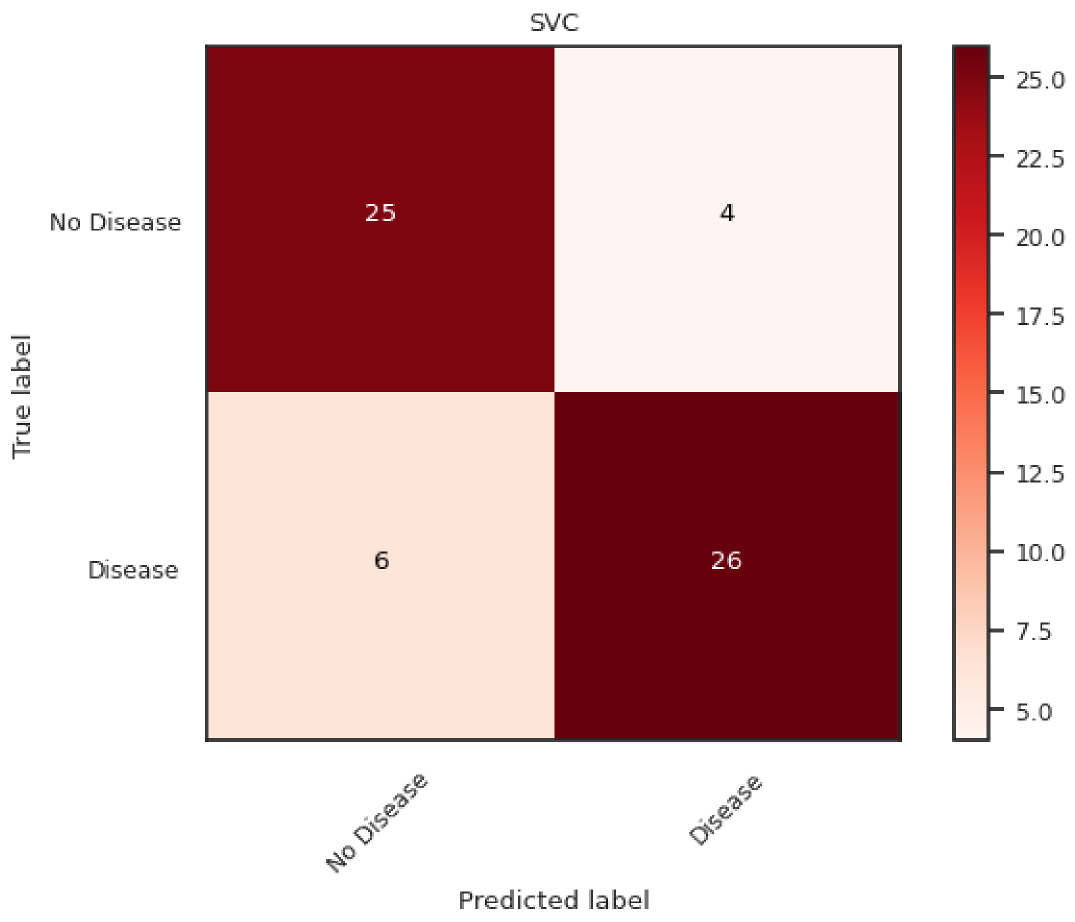
[46]:
```
models = [
    LogisticRegression(),
    SVC(),
    DecisionTreeClassifier(),
    RandomForestClassifier(),
    GradientBoostingClassifier(),
    KNeighborsClassifier(),
    GaussianNB()
]
```

```
[47]: model_names = ["Logistic Regression", "SVC", "Decision Trees", "Random Forest",␣
      ↪"Gradient Boosting", "KNN", "Naive Bayes"]

      train_results = []
      test_results = []
```

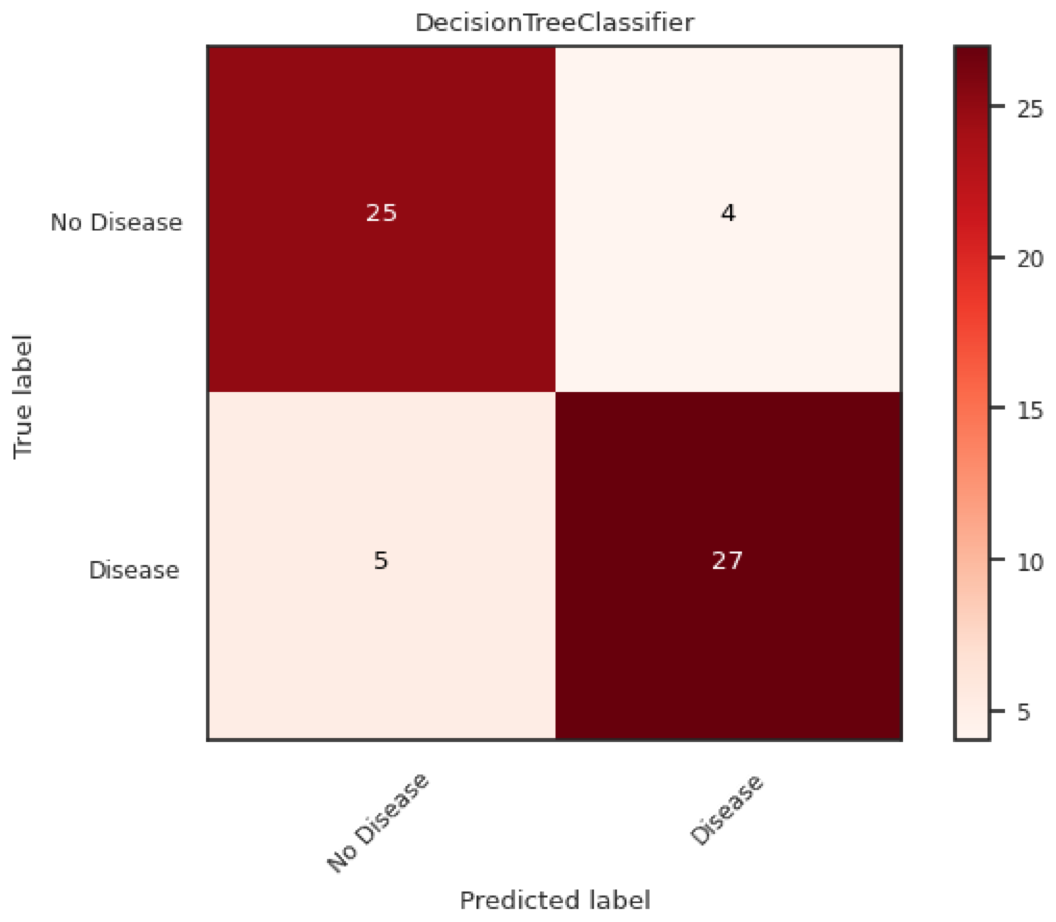
Model Evaluation:

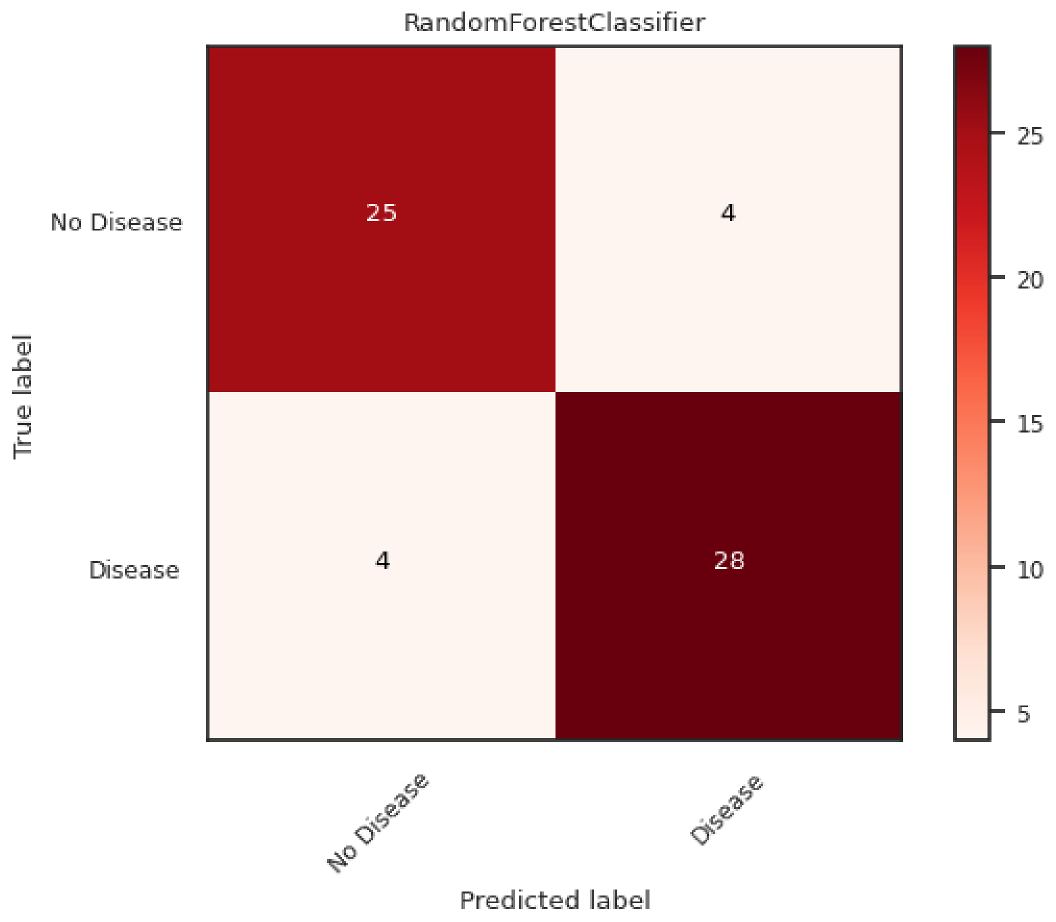
```
[48]: for model in models:
          train_acc, test_acc, y_pred = evaluate_model(model, X_train, y_train,␣
      ↪X_test, y_test)
          train_results.append(train_acc)
          test_results.append(test_acc)
          cm = confusion_matrix(y_test, y_pred)
          plot_confusion_matrix(cm, classes=['No Disease', 'Disease'], title=model.
      ↪__class__.__name__, cmap=plt.cm.Reds)
          plt.show()
```

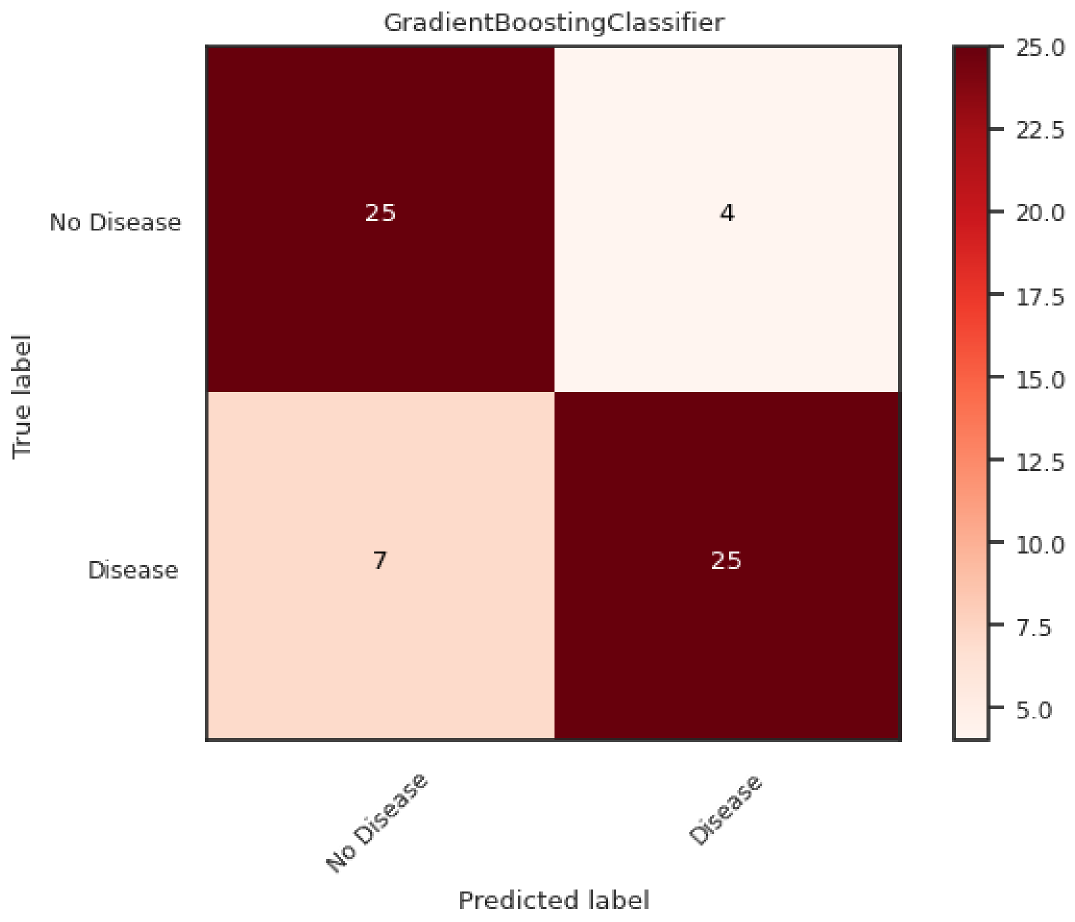

LogisticRegression
True label
No Disease
Disease
26
3
5
27
Predicted label
No Disease
Disease
25
20
15
10
5

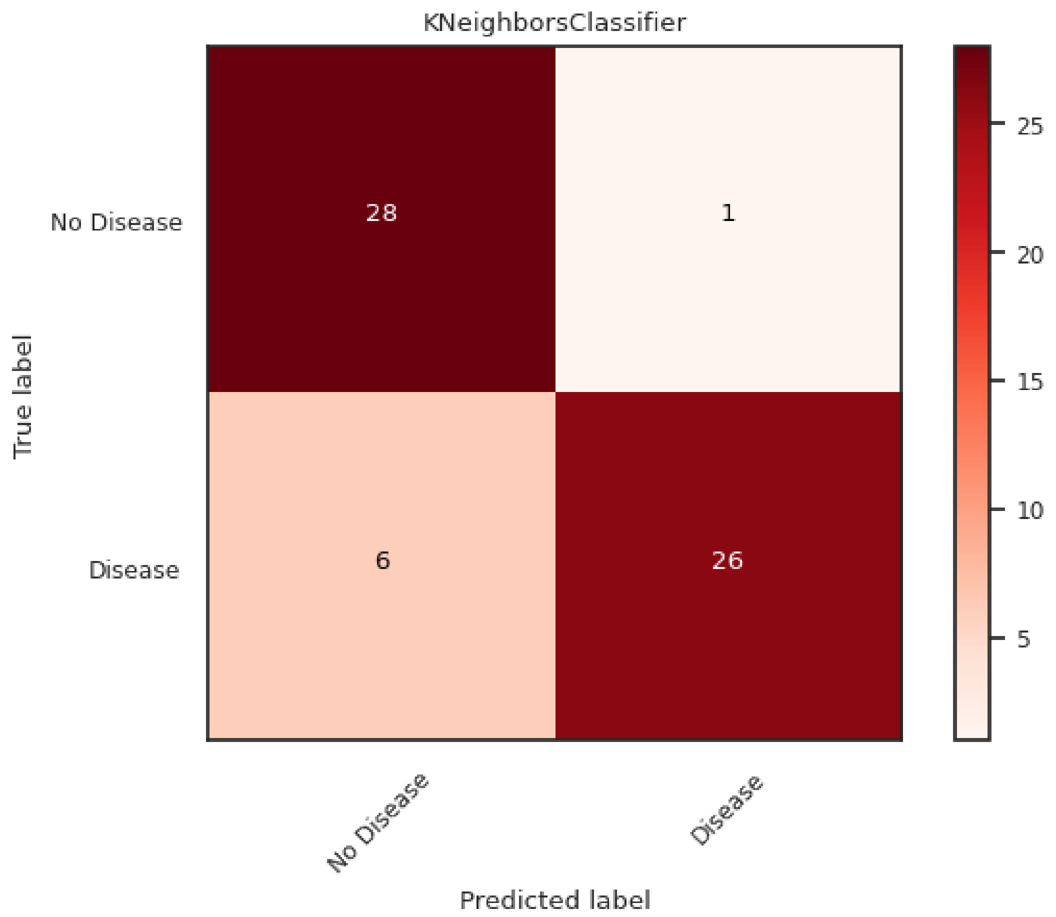


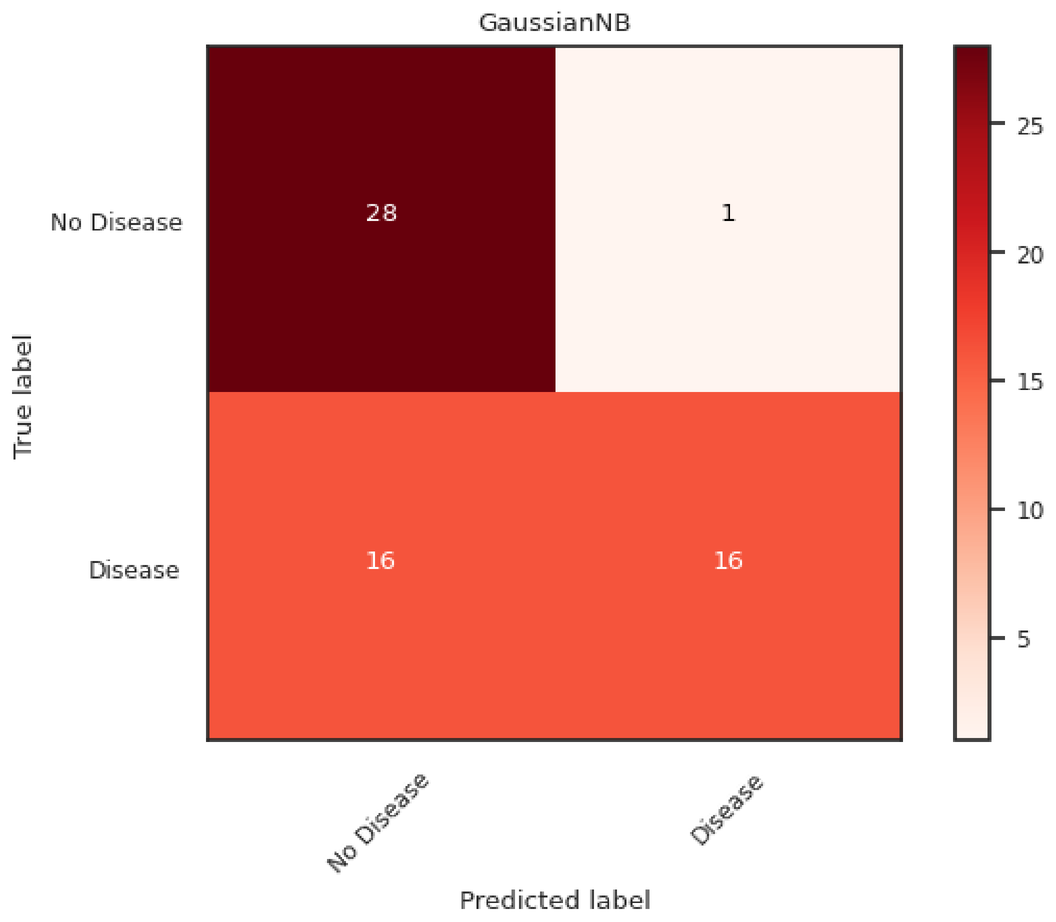
SVC
No Disease
Disease
True label
25
4
6
26
No Disease
Disease
Predicted label
25.0
22.5
20.0
17.5
15.0
12.5
10.0
7.5
5.0


DecisionTreeClassifier
True label
No Disease
Disease
25
4
5
27
Predicted label
No Disease
Disease
25
20
15
10
5

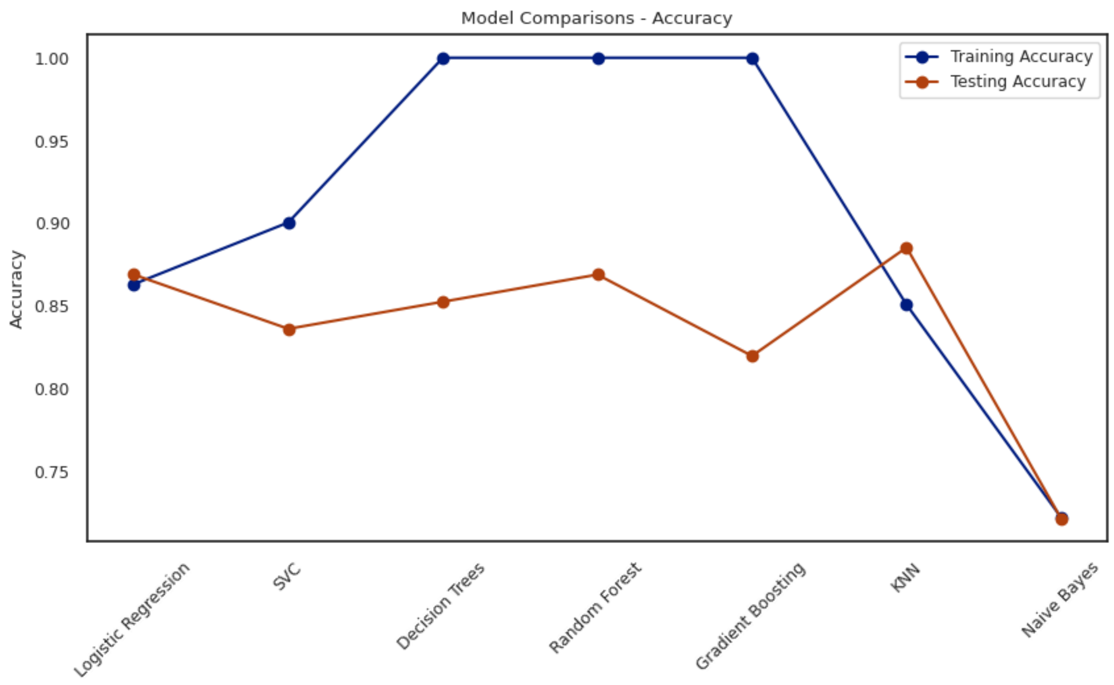

RandomForestClassifier
True label
No Disease
Disease
25
4
4
28
Predicted label
No Disease
Disease
25
20
15
10
5


GradientBoostingClassifier
No Disease
Disease
True label
25
4
7
25
No Disease
Disease
Predicted label
25.0
22.5
20.0
17.5
15.0
12.5
10.0
7.5
5.0


KNeighborsClassifier
True label
No Disease
Disease
Predicted label
No Disease
Disease
28
1
6
26
25
20
15
10
5



```
[49]: # plot model performance
      plt.figure(figsize=(10,5))
      plt.plot(model_names, train_results, 'o-', label="Training Accuracy")
      plt.plot(model_names, test_results, 'o-', label="Testing Accuracy")
      plt.ylabel("Accuracy")
      plt.xticks(rotation=45)
      plt.legend()
      plt.title("Model Comparisons - Accuracy")
      plt.show()
```



Here is our summary of the model comparison graph:

- Our graph shows the **training and testing accuracy** of seven different machine learning models for predicting heart disease.
- The models are **Logistic Regression, SVC, Decision Trees, Random Forest, Gradient Boosting, KNN, and Naive Bayes**.
- The **best performing model** on the testing data is **Gradient Boosting**, with an accuracy of **0.87**.
- The **worst performing model** on the testing data is **Naive Bayes**, with an accuracy of **0.74**.
- The **most overfitting model** is **Decision Trees**, which has a high training accuracy of **1.0** but a low testing accuracy of **0.77**.

In practical scenarios, it is advantageous to conduct additional analyses, including the optimization of hyperparameters and the implementation of techniques like cross-validation to validate the outcomes.

In Summary,

EDA - A crucial step in data science project and helped us identify trends, anomalies, patterns, and relationships within the data.

Next We performed **Correlation Analysis** where our **heatmap visualization** of the correlation matrix provided us insights into which features were positively or negatively correlated with each other and with the target variable 'output'.

further we performed **cluster analysis**, and finally **machine learning prediction**, where we applied seven ml model for heart disease prediction and evaluated their performance in terms of their accuracy, Where **GradientBoosting** has highest test accuracy.