Analysis of Heat Disease Diagnostic

Introduction and defination of features in the dataset

- age: The patient's age. One major risk factor for heart disease is age.
- sex: The patient's gender (0 for female, 1 for male). There is a gender component to heart disease risk. As more cases have been reported related cardiovascular diseases in men.
- chest pain (cp): Type of chest pain (0-4). There are many kinds of chest discomfort that might signify different risk factors for heart disease.
- trestbps: Resting blood pressure: Measured in millimeter-Hg. One of the main risk factors for heart disease is high blood pressure.
- serum cholesterol (chol) mg/dl: Elevated cholesterol levels may result in atherosclerosis, hence elevating the risk of cardiovascular disease.
- fbs: Fasting blood sugar > 120 mg/dl (1 = true, 0 = false). Diabetes is a significant risk factor for heart disease.
- restecg: Resting electrocardiographic results (0-2).
  0: Normal
  1: Having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV)
  2: Showing probable or definite left ventricular hypertrophy by Estes' criteria
- thalach: Maximum heart rate achieved. Lower maximum heart rates can indicate poorer cardiovascular fitness.
- exang: Exercise-induced angina (1 = yes, 0 = no).
- oldpeak: ST depression induced by exercise relative to rest. This can indicate the severity of ischemia.
- slope: The slope of the peak exercise ST segment (0-2).
  0: Upsloping
  1: Flat
  2: Downsloping
- ca: Number of major vessels (0-4) colored by fluoroscopy.
- thal: Thalassemia (1-3).
  1: Normal
  2: Fixed defect
  3: Reversible defect
- target: Presence of heart disease (1 = yes, 0 = no). This is the outcome variable indicating whether the patient has heart disease.

In [1]:

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

In [2]:

```
data = pd.read_csv('Heart Disease data.csv')
```

In [3]:

```
data.head(10)
```

Out[3]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1.0	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0.0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0
5	58	0	0	100	248	0	0	122	0	1.0	1	0	2	1
6	58	1	0	114	318	0	2	140	0	4.4	0	3	1	0
7	55	1	0	160	289	0	0	145	1	0.8	1	1	3	0
8	46	1	0	120	249	0	0	144	0	0.8	2	0	3	0
9	54	1	0	122	286	0	0	116	1	3.2	1	2	2	0

In [4]:

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1025 entries, 0 to 1024
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       1025 non-null   int64  
 1   sex       1025 non-null   int64  
 2   cp        1025 non-null   int64  
 3   trestbps  1025 non-null   int64  
 4   chol      1025 non-null   int64  
 5   fbs       1025 non-null   int64  
 6   restecg   1025 non-null   int64  
 7   thalach   1025 non-null   int64  
 8   exang     1025 non-null   int64  
 9   oldpeak   1025 non-null   float64
 10  slope     1025 non-null   int64  
 11  ca        1025 non-null   int64  
 12  thal      1025 non-null   int64  
 13  target    1025 non-null   int64  
dtypes: float64(1), int64(13)
memory usage: 112.2 KB
```

In [5]:

```
data.shape
```

Out[5]:

```
(1025, 14)
```

Observations

There is 1025 records in the dataset
There are 14 features that are non-null in the dataset
All the features present in the dataset are numerical type

In [6]:

```
data.describe()
```

Out[6]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach
count	1025.000000	1025.000000	1025.000000	1025.000000	1025.00000	1025.000000	1025.000000	1025.000000
mean	54.434146	0.695610	0.942439	131.611707	246.00000	0.149268	0.529756	149.114146
std	9.072290	0.460373	1.029641	17.516718	51.59251	0.356527	0.527878	23.005724
min	29.000000	0.000000	0.000000	94.000000	126.00000	0.000000	0.000000	71.000000
25%	48.000000	0.000000	0.000000	120.000000	211.00000	0.000000	0.000000	132.000000
50%	56.000000	1.000000	1.000000	130.000000	240.00000	0.000000	1.000000	152.000000
75%	61.000000	1.000000	2.000000	140.000000	275.00000	0.000000	1.000000	166.000000
max	77.000000	1.000000	3.000000	200.000000	564.00000	1.000000	2.000000	202.000000

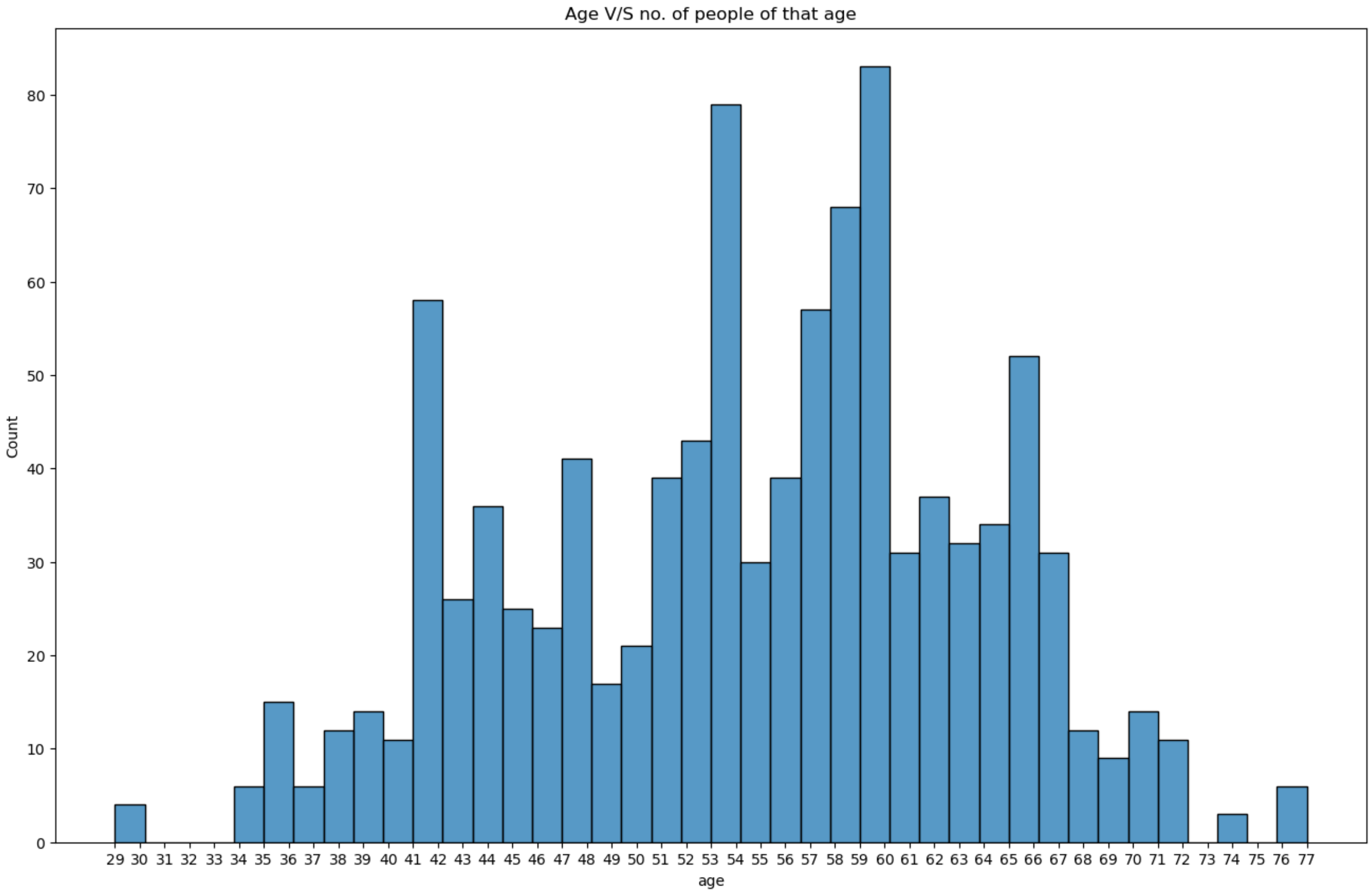
In [7]:

```
print(f"Youngest among the patients diagnosed: {data['age'].min()}")
print(f"Oldest among the patients diagnosed: {data['age'].max()}")
```

```
Youngest among the patients diagnosed: 29
Oldest among the patients diagnosed: 77
```

In [8]:

```
plt.figure(figsize=(16,10))
plt.title('Age V/S no. of people of that age')
plt.xticks(range(29,78))
sns.histplot(data = data, x = 'age', bins = 40)
plt.show()
```



In [9]:

```
data['sex'].value_counts()
```

Out[9]:

```
1    713
0    312
Name: sex, dtype: int64
```

Observation

The dataset includes the medical records of indiviuals from 29 to 77 of age
Among which 713 are male (assuming because men are generally more represented in cardiovascular datasets due to higher historical rates of heart disease in men compared to women) and 312 are females (assumption)

In [10]:

```
data['target'].value_counts()
```

Out[10]:

```
1    526
0    499
Name: target, dtype: int64
```

In [11]:

```
data['target'].value_counts(normalize=True)
```

Out[11]:

```
1    0.513171
0    0.486829
Name: target, dtype: float64
```

In [12]:

```
data.groupby('sex')['target'].value_counts(normalize=True)
```

Out[12]:

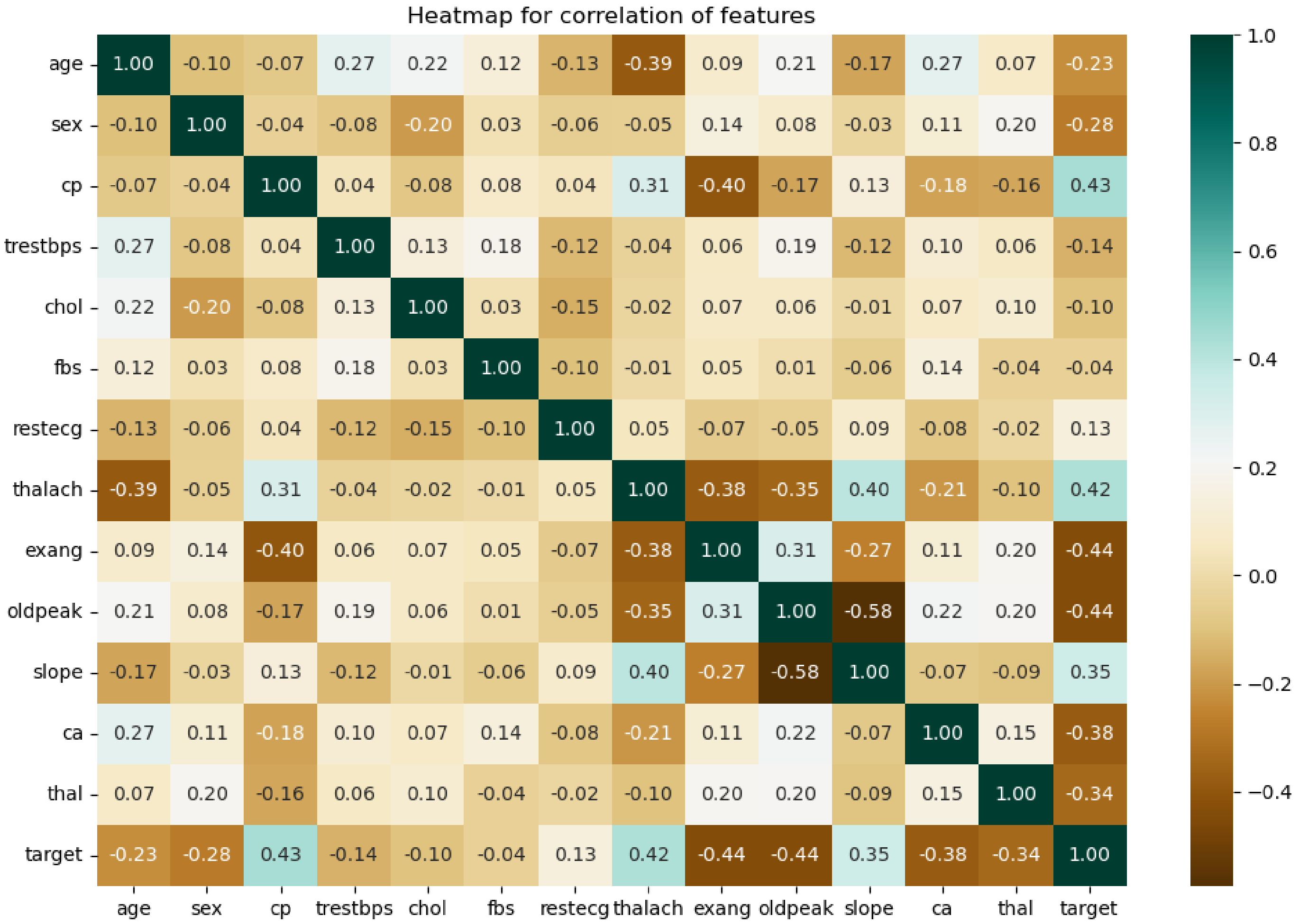
```
sex  target
0    1         0.724359
     0         0.275641
1    0         0.579243
     1         0.420757
Name: target, dtype: float64
```

Observation

The dataset contains medical records of individuals among which 51% individuals have been diagnosed with a heart disease and other 49%
This further confirms our assumption that men are diagnosed with cardiovascular diseases more often then women

In [13]:

```
plt.figure(figsize=(12,8))
plt.title('Heatmap for correlation of features')

sns.heatmap(data = data.corr(), cmap='BrBG', annot=True, fmt='.2f')
plt.show()
```



Checking columns for outlier (only those which have more than 4 unique values)

In [14]:

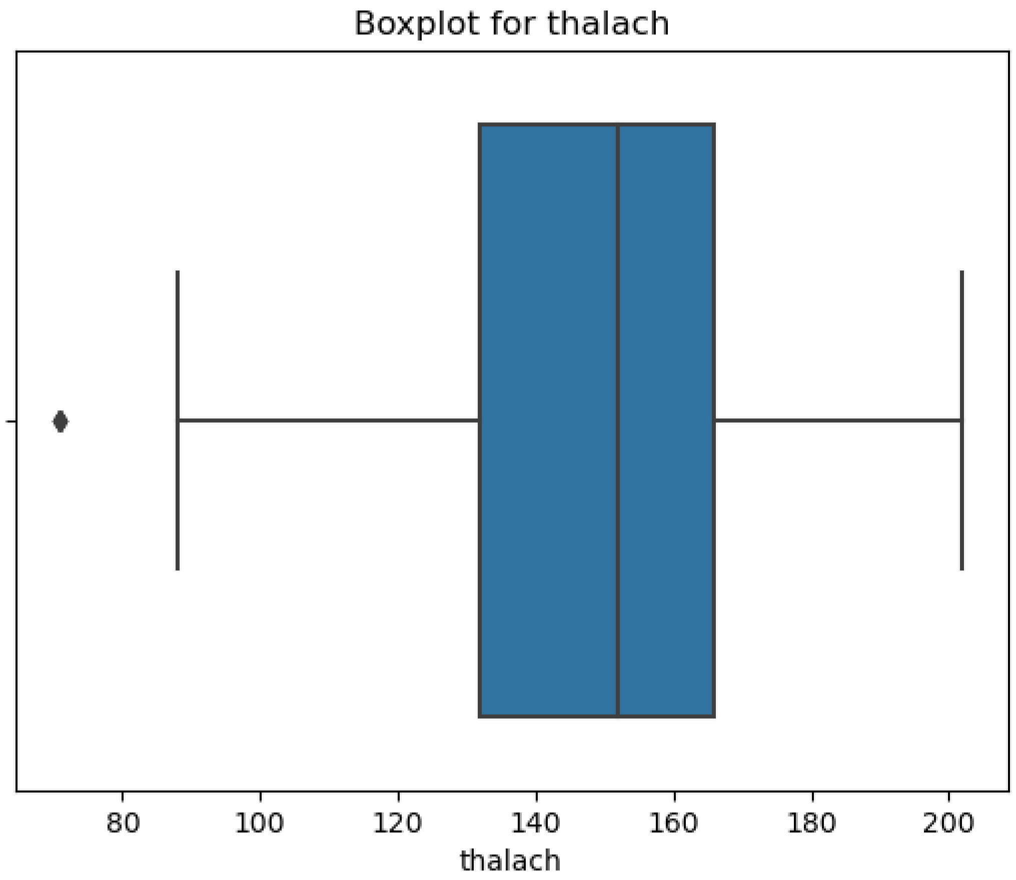
```
outlier_check_columns = [column for column in data.columns if len(data[column].value_cou
print(outlier_check_columns)
```

```
['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
```

Visualising outliers using boxplot in different features

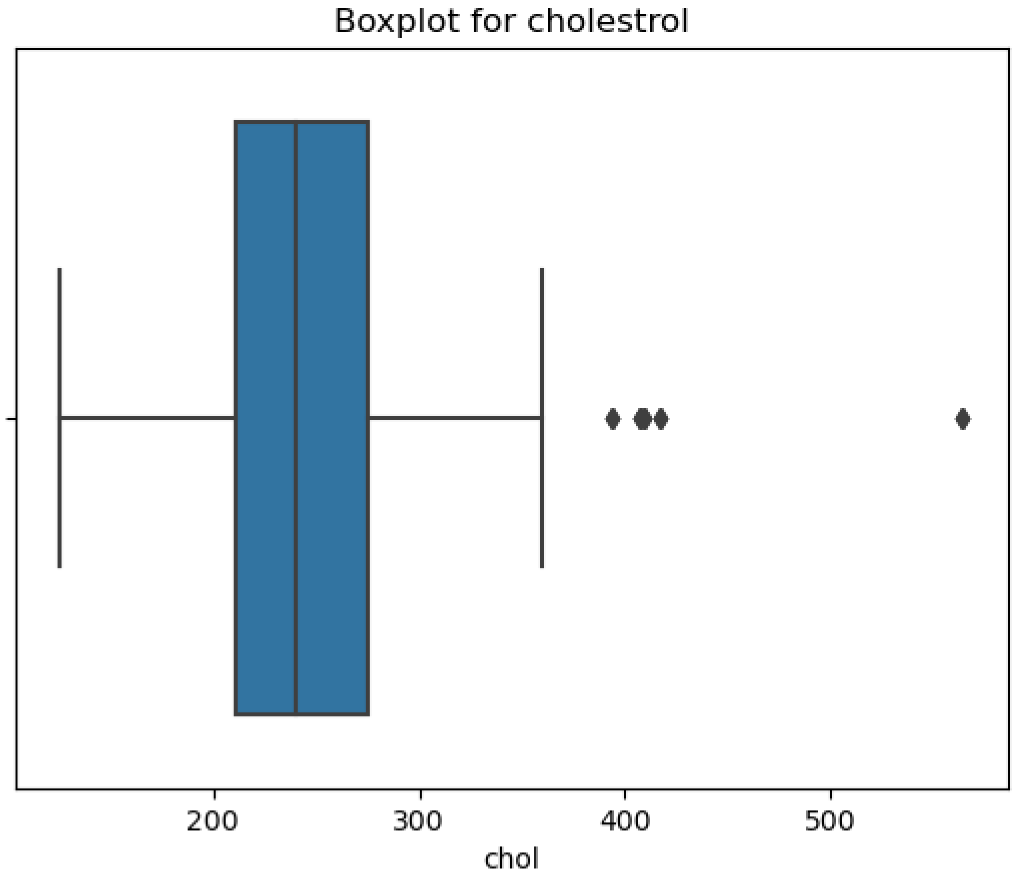
In [15]:

```
sns.boxplot(data = data, x='thalach')
plt.title('Boxplot for thalach')
plt.show()
```



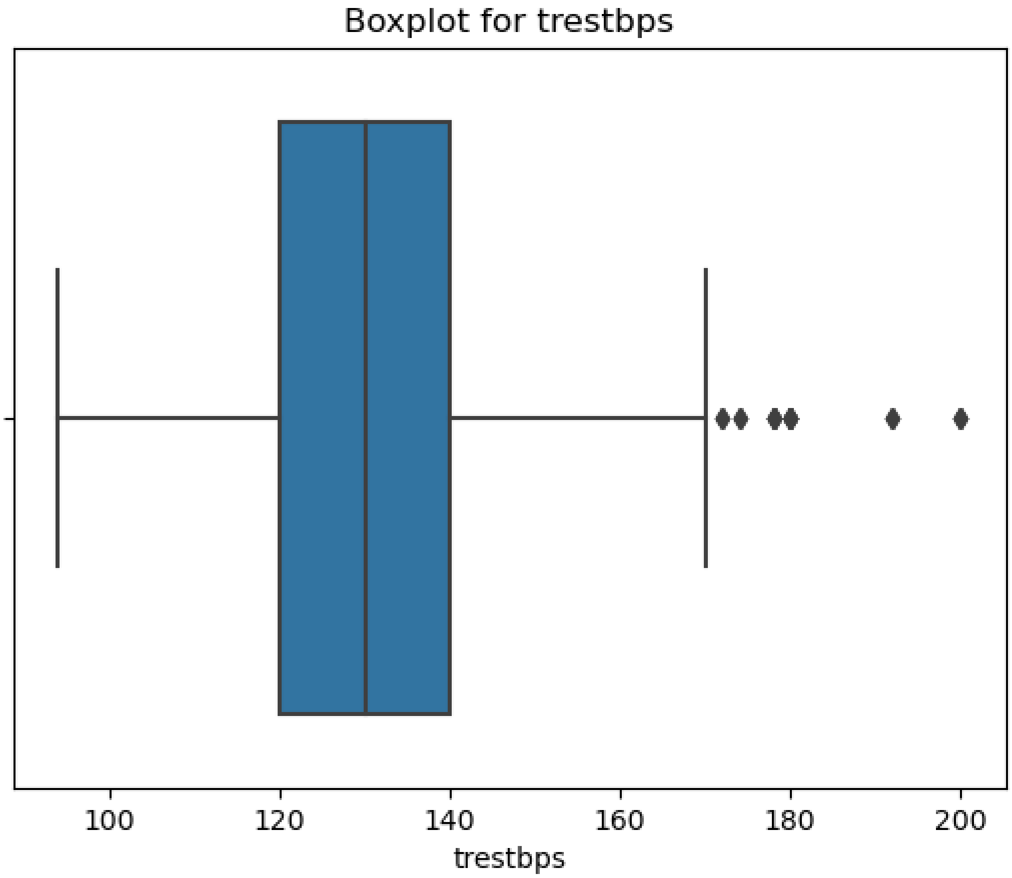
In [16]:

```python
sns.boxplot(data = data, x='chol')
plt.title('Boxplot for cholestrol')
plt.show()
```



In [17]:

```python
sns.boxplot(data = data, x='trestbps')
plt.title('Boxplot for trestbps')
plt.show()
```



Outlier detection using IQR

In [18]:
```
def outlier_detection(df):
    outliers = {}
    for column in df.columns:
        Q1 = df[column].quantile(0.25)
        Q3 = df[column].quantile(0.75)
        IQR = Q3 - Q1
        lower_bound = Q1 - 1.5 * IQR
        upper_bound = Q3 + 1.5 * IQR
        outliers.update({column : [value for value in df[column] if value <= lower_bound
    return outliers

data_outliers = outlier_detection(data[outlier_check_columns])
```

Removing features from outliers dictionary if they are empty

In [19]:
```
no_outlier_features = [feature for feature in data_outliers if len(data_outliers[feature

for feature in no_outlier_features:
    data_outliers.pop(feature)

data_outliers
```

Out[19]:
```
{'trestbps': [180,
  178,
  170,
  170,
  174,
  170,
  180,
  192,
  170,
  200,
  170,
  178,
  170,
  192,
  180,
  170,
  200,
  192,
  172,
  180,
  170,
  174,
  178,
  180,
  200,
  180,
  178,
  170,
  180,
  170,
  178,
  174,
  180,
  170,
  200,
  170,
  170,
  172,
  170,
  170,
  180,
  178,
  178,
  172,
  180],
 'chol': [417,
  564,
  409,
  564,
  394,
  407,
  564,
  407,
  394,
  394,
  409,
  417,
  407,
  407,
  417,
  409],
 'thalach': [71, 71, 71, 71],
 'oldpeak': [5.6, 5.6, 6.2, 6.2, 6.2, 5.6, 5.6]}
```

Removing duplicate values from the outliers dictionary

In [20]:

```
for key in data_outliers.keys():
    data_outliers.update({key: set(data_outliers[key])})
```

In [21]:
```
data_outliers
```

Out[21]:
```
{'trestbps': {170, 172, 174, 178, 180, 192, 200},
 'chol': {394, 407, 409, 417, 564},
 'thalach': {71},
 'oldpeak': {5.6, 6.2}}
```

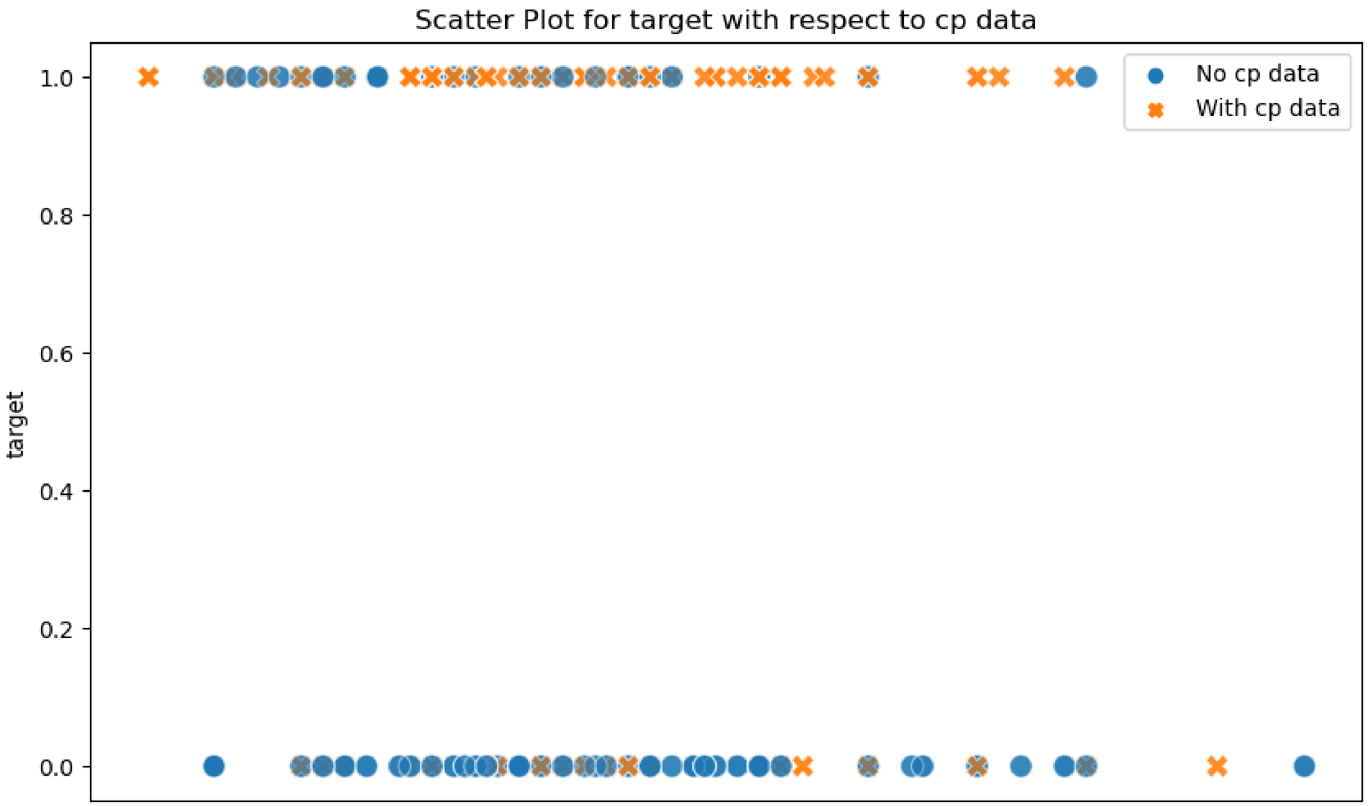
In [22]:
```
data.head(20)
```

Out[22]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1.0	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0.0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0
5	58	0	0	100	248	0	0	122	0	1.0	1	0	2	1
6	58	1	0	114	318	0	2	140	0	4.4	0	3	1	0
7	55	1	0	160	289	0	0	145	1	0.8	1	1	3	0
8	46	1	0	120	249	0	0	144	0	0.8	2	0	3	0
9	54	1	0	122	286	0	0	116	1	3.2	1	2	2	0
10	71	0	0	112	149	0	1	125	0	1.6	1	0	2	1
11	43	0	0	132	341	1	0	136	1	3.0	1	0	3	0
12	34	0	1	118	210	0	1	192	0	0.7	2	0	2	1
13	51	1	0	140	298	0	1	122	1	4.2	1	3	3	0
14	52	1	0	128	204	1	1	156	1	1.0	1	0	0	0
15	34	0	1	118	210	0	1	192	0	0.7	2	0	2	1
16	51	0	2	140	308	0	0	142	0	1.5	2	1	2	1
17	54	1	0	124	266	0	0	109	1	2.2	1	1	3	0
18	50	0	1	120	244	0	1	162	0	1.1	2	0	2	1
19	58	1	2	140	211	1	0	165	0	0.0	2	0	2	1

Scatterplot for cp

In [23]:
```
scatter_data = data.copy()

# Creating a new column to differentiate the points
scatter_data['highlighted'] = 'No cp data'

scatter_data.loc[scatter_data['cp'] > 0, 'highlighted'] = 'With cp data'

# Creating a scatter plot and adding the figure size
plt.figure(figsize=(10, 6))
sns.scatterplot(data=scatter_data, x='trestbps', y='target', hue='highlighted', style='h

plt.title('Scatter Plot for target with respect to cp data')
plt.xticks([])
plt.xlabel('')
plt.legend()
plt.show()
```



In [24]:
```
scatter_data['highlighted'].value_counts()
```

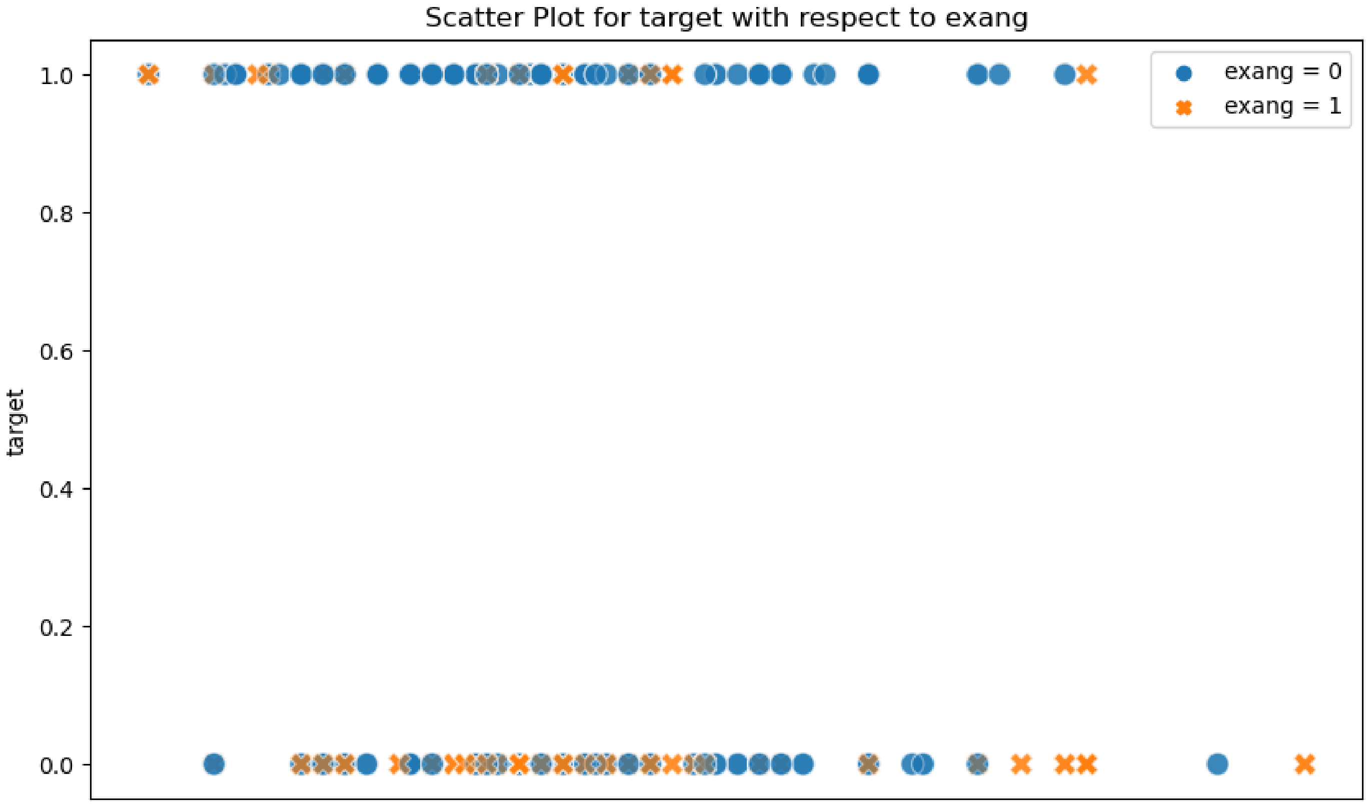
Out[24]:
```
With cp data    528
No cp data      497
Name: highlighted, dtype: int64
```

Observation

As can be seen in the above scatter plot, majority of the heart diseases are associated with chest pain as a symptom

Scatterplot for exang

In [25]:
```
scatter_data = data.copy()

# Creating a new column to differentiate the points
scatter_data['highlighted'] = 'exang = 1'

scatter_data.loc[scatter_data['exang'] == 0, 'highlighted'] = 'exang = 0'

# Creating a scatter plot and adding the figure size
plt.figure(figsize=(10, 6))
sns.scatterplot(data=scatter_data, x='trestbps', y='target', hue='highlighted', style='h

plt.title('Scatter Plot for target with respect to exang')
plt.xticks([])
plt.xlabel('')
plt.legend()
plt.show()
```



In [26]:
```
data.groupby('exang')['target'].value_counts()
```

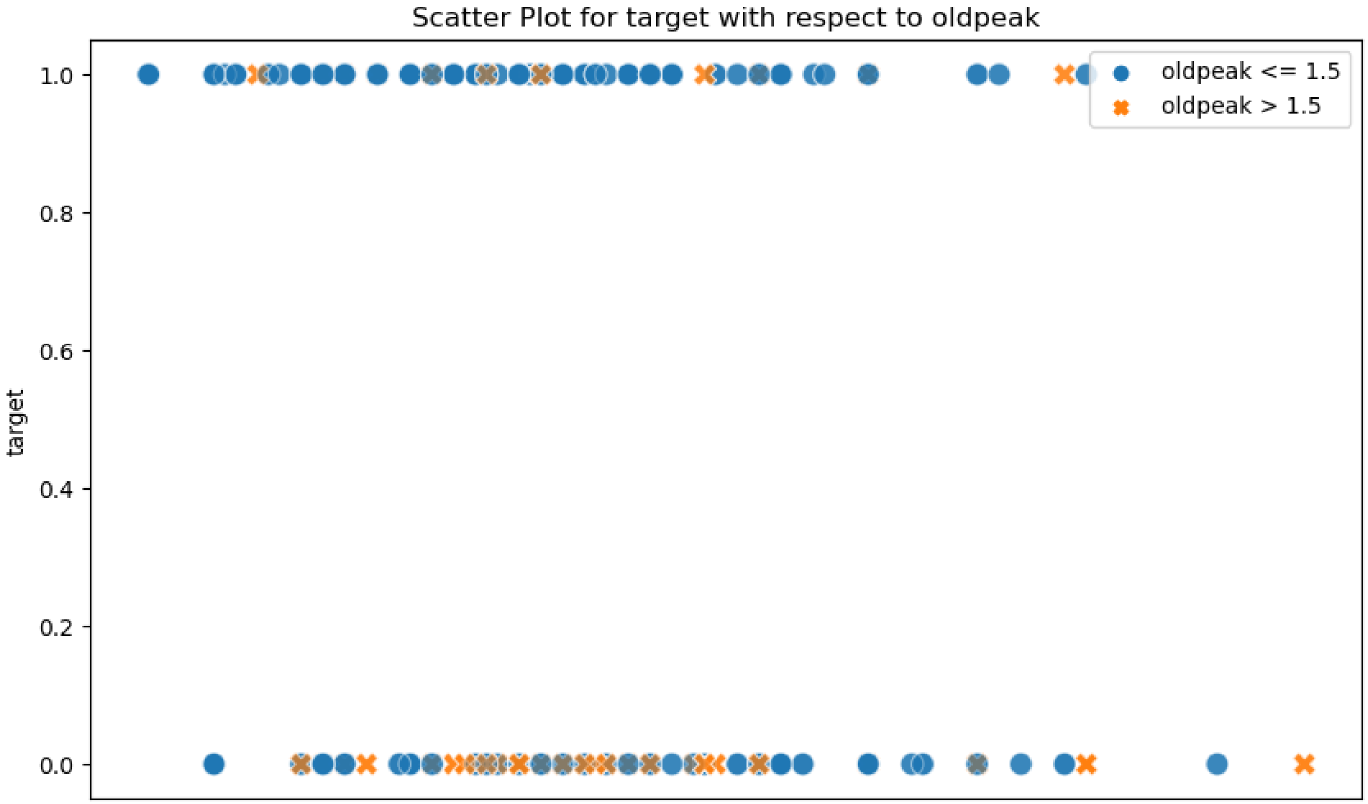
Out[26]:
```
exang  target
0      1         455
       0         225
1      0         274
       1          71
Name: target, dtype: int64
```

Observation

In the above plot we can see that records with exang = 0 have majority of target values as 1 which shows that there is higher chance of facing a heart disease if exang is not present

Scatterplot for oldpeak

In [27]:
```
scatter_data = data.copy()

# Creating a new column to differentiate the points
scatter_data['highlighted'] = 'oldpeak > 1.5'

scatter_data.loc[scatter_data['oldpeak'] <= 1.5, 'highlighted'] = 'oldpeak <= 1.5'

# Creating a scatter plot and adding the figure size
plt.figure(figsize=(10, 6))
sns.scatterplot(data=scatter_data, x='trestbps', y='target', hue='highlighted', style='h

plt.title('Scatter Plot for target with respect to oldpeak')
plt.xticks([])
plt.xlabel('')
plt.legend()
plt.show()
```



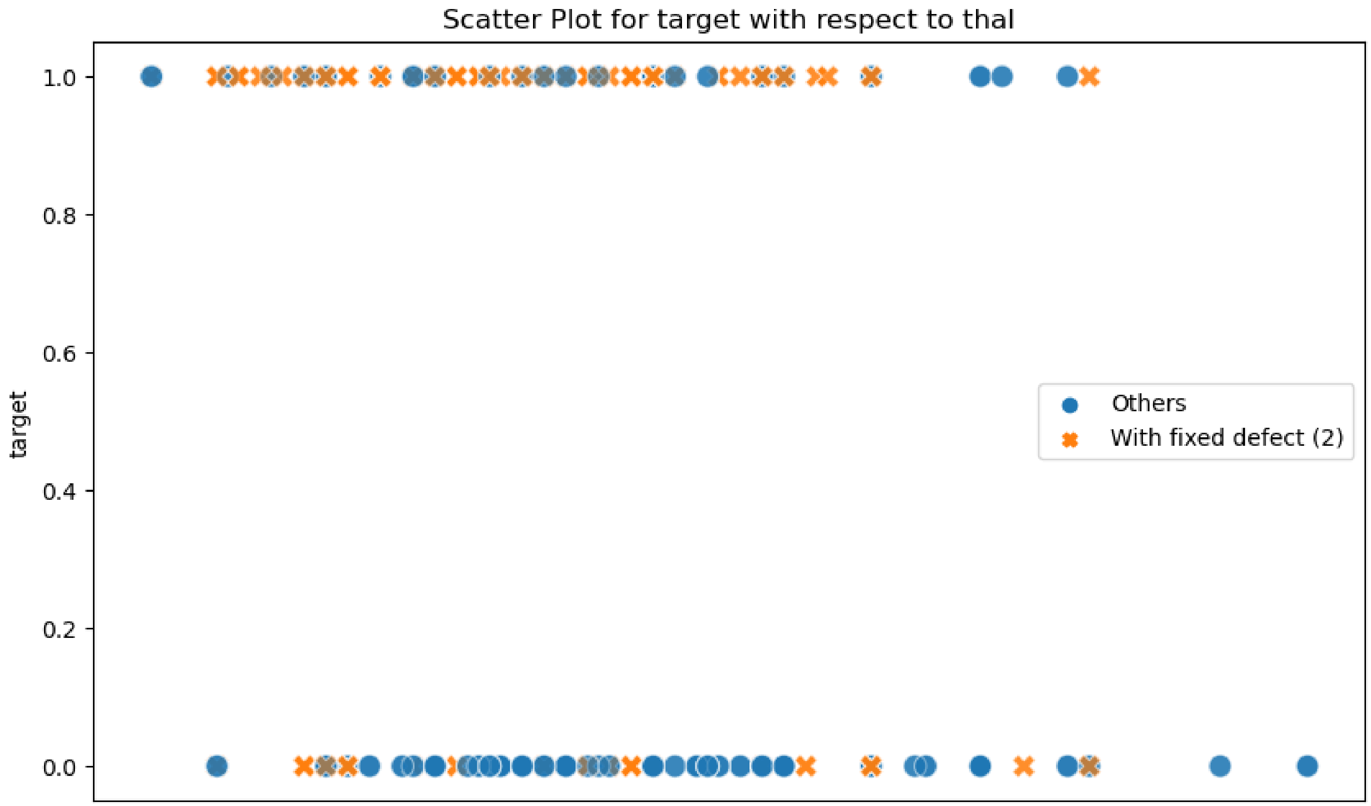
Observation

As can be seen in the above plot, values with <= 1.5 in oldpeak have higher chance of having a heart disease

Scatterplot for thal

In [28]:

```
scatter_data = data.copy()

# Creating a new column to differentiate the points
scatter_data['highlighted'] = 'Others'

scatter_data.loc[scatter_data['thal'] == 2, 'highlighted'] = 'With fixed defect (2)'

# Creating a scatter plot and adding the figure size
plt.figure(figsize=(10, 6))
sns.scatterplot(data=scatter_data, x='trestbps', y='target', hue='highlighted', style='h

plt.title('Scatter Plot for target with respect to thal')
plt.xticks([])
plt.xlabel('')
plt.legend()
plt.show()
```



In [29]:

```
scatter_data['highlighted'].value_counts()
```

Out[29]:

```
With fixed defect (2)    544
Others                   481
Name: highlighted, dtype: int64
```

Observation

In the above scatter plot one can see that many of the patients with thal value as 2 have been diagnosed to have heart diseases

Conclusion

So the final conclusion is that factors such as chest pain,old peak, exang, and thal act as the main indicators for detecting heart diseases

It is also true that other factors such cholestrol(chol) and fasting blood sugar(fbs) can also indicate heart diseases but we do not see much evidence of correlation of target with chol and fbs in our dataset

Using Logistic Regression to predict the values for target

In [30]:

```
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

X = data.drop(columns=['target', 'trestbps', 'fbs', 'restecg', 'chol'])
y = data['target']
```

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

# Initializing the logistic regression model
model = LogisticRegression(max_iter=1000)

# Training the model
model.fit(X_train, y_train)

# Using the model to make predictions
y_pred = model.predict(X_test)

# Evaluating the model
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)

print("Accuracy:", accuracy)
print("Confusion Matrix:\n", conf_matrix)
print("Classification Report:\n", class_report)
```

```
Accuracy: 0.8
Confusion Matrix:
 [[74 28]
 [13 90]]
Classification Report:
               precision    recall  f1-score   support

           0       0.85      0.73      0.78       102
           1       0.76      0.87      0.81       103

    accuracy                           0.80       205
   macro avg       0.81      0.80      0.80       205
weighted avg       0.81      0.80      0.80       205
```

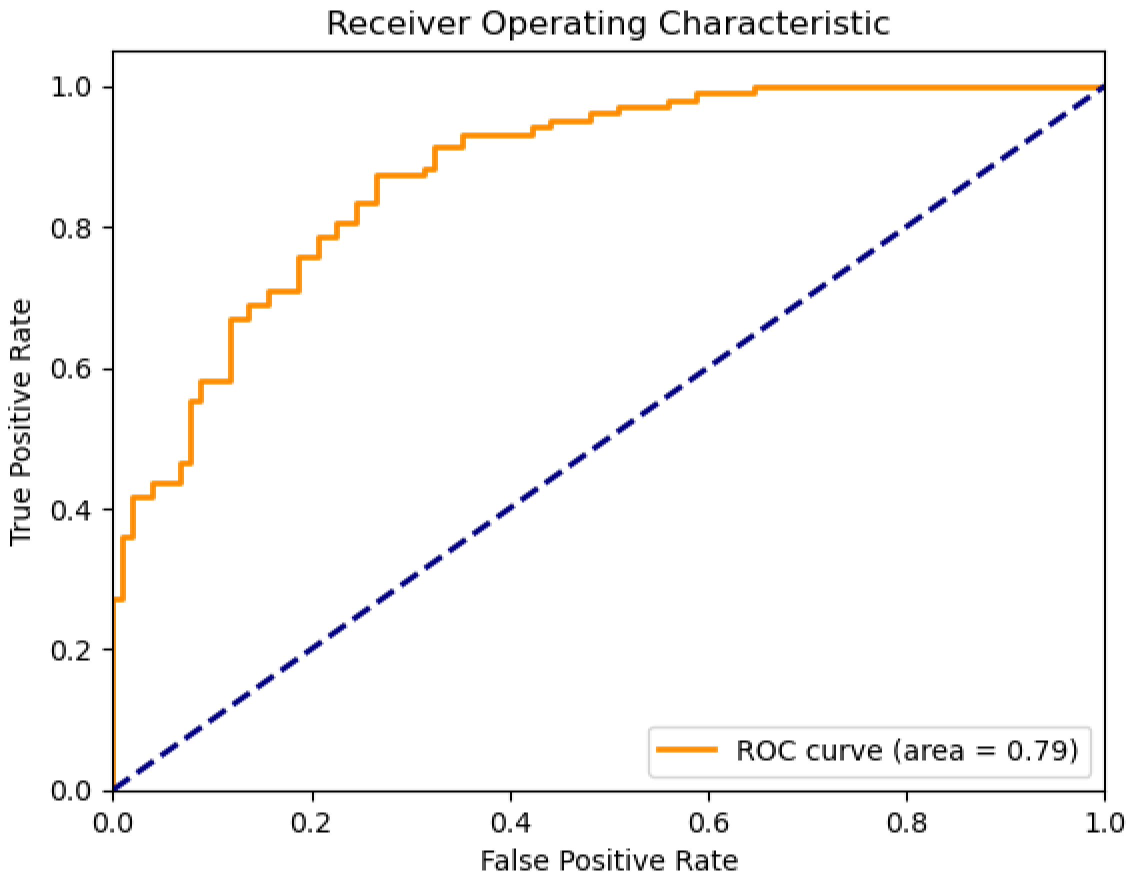
Using Logistic regression after applying standard scaler & hyperparameter tuning using Grid_SearchCV

In [35]:

```
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report, roc

X = data.drop(columns=['target'])
y = data['target']

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

scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

lr = LogisticRegression(random_state=42, solver='liblinear')

# Hyperparameter tuning using GridSearchCV
param_grid = {
    'C': [0.01, 0.1, 1, 10, 100],
    'penalty': ['l1', 'l2']
}
```

```
grid_search = GridSearchCV(estimator=lr, param_grid=param_grid, cv=5, scoring='accuracy'
grid_search.fit(X_train_scaled, y_train)

# Best hyperparameters
best_params = grid_search.best_params_
print("Best Parameters:", best_params)

# Training the best model
best_lr = grid_search.best_estimator_
best_lr.fit(X_train_scaled, y_train)

y_pred = best_lr.predict(X_test_scaled)

# Evaluating the model
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)
roc_auc = roc_auc_score(y_test, y_pred)

print("Accuracy:", accuracy)
print("Confusion Matrix:\n", conf_matrix)
print("Classification Report:\n", class_report)
print("ROC AUC Score:", roc_auc)

# ROC Curve
fpr, tpr, _ = roc_curve(y_test, best_lr.predict_proba(X_test_scaled)[:,1])
import matplotlib.pyplot as plt

plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic')
plt.legend(loc="lower right")
plt.show()
```

```
Best Parameters: {'C': 1, 'penalty': 'l1'}
Accuracy: 0.7951219512195122
Confusion Matrix:
 [[73 29]
 [13 90]]
Classification Report:
               precision    recall  f1-score   support

           0       0.85      0.72      0.78       102
           1       0.76      0.87      0.81       103

    accuracy                           0.80       205
   macro avg       0.80      0.79      0.79       205
weighted avg       0.80      0.80      0.79       205

ROC AUC Score: 0.7947363411383972
```



Observation

The accuracy is about 80 percent even after application of standardization and hyperparameter tuning in logistic regression

Using Random Forest Classifier for its robustness

In [32]:

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
from sklearn.model_selection import GridSearchCV

X = data.drop(columns=['target'])
y = data['target']

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

scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

rf = RandomForestClassifier(random_state=42)

param_grid = {
    'n_estimators': [100, 200, 300],
    'max_depth': [None, 10, 20, 30],
    'min_samples_split': [2, 10, 20],
    'min_samples_leaf': [1, 4, 8]
}
```

```
grid_search = GridSearchCV(estimator=rf, param_grid=param_grid, cv=5, scoring='accuracy'
grid_search.fit(X_train_scaled, y_train)

best_params = grid_search.best_params_
best_rf = grid_search.best_estimator_

y_pred = best_rf.predict(X_test_scaled)

accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)
```

In [33]:

```
print(f'''
best parameters: {best_params}


accuaracy: {accuracy}


confusion matrix:

{conf_matrix}


classification report:

{class_report}
''')
```

```
best parameters: {'max_depth': None, 'min_samples_leaf': 1, 'min_samples_split': 2, 'n_e
stimators': 100}


accuaracy: 0.9853658536585366


confusion matrix:

[[102   0]
 [  3 100]]


classification report:

              precision    recall  f1-score   support

           0       0.97      1.00      0.99       102
           1       1.00      0.97      0.99       103

    accuracy                           0.99       205
   macro avg       0.99      0.99      0.99       205
weighted avg       0.99      0.99      0.99       205
```