TEAM ID- PNT2022TMID53509

Visualizing and Predicting Heart Diseases with an Interactive Dashboard

Heart Disease Prediction using Machine Learning Approach

Heart Disease (including Coronary Heart Disease, Hypertension, and Stroke) remains the No. 1 cause of death in the US.The Heart Disease and Stroke Statistics—2019 Update from the American Heart Association indicates that:

- 116.4 million, or 46% of US adults are estimated to have hypertension. These are findings related to the new 2017 Hypertension Clinical Practice Guidelines.
- On average, someone dies of CVD every 38 seconds. About 2,303 deaths from CVD each day, based on 2016 data.
- On average, someone dies of a stroke every 3.70 minutes. About 389.4 deaths from stroke each day, based on 2016 data.

In this machine learning project, we have collected the dataset from UCI (https://archive.ics.uci.edu/ml/datasets/statlog+(heart)) and we will be using Machine Learning to make predictions on whether a person is suffering from Heart Disease or not.

Problem Statement

- Complete analysis of Heart Disease UCI dataset.
- To predict whether a person has a heart disease or not based on the various biological and physical parameters.

Machine Learning Algorithms

- Random Forest Classifier
- K-Nearest Neighbors Classifier
- Decision Tree Classifier
- Naive Bayes Classifier

Import libraries

Let's first import all the necessary libraries. We will use `numpy` and `pandas` to start with. For visualization, we will use`pyplot` subpackage of `matplotlib`, use `rcParams` to add styling to the plots and `rainbow` for colors and `seaborn`. For implementing Machine Learning models and processing of data, we will use the `sklearn` library.

```
import pandas as pd
import numpy as np
```

```
import matplotlib.pyplot as plt
from matplotlib import rcParams
from matplotlib.cm import rainbow
import seaborn as sns
%matplotlib inline
```

For processing the data, we'll import a few libraries. To split the available dataset for testing and training, we'll use the `train_test_split` method. To scale the features, we are using `StandardScaler`.

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import LabelEncoder
from sklearn import tree
from warnings import filterwarnings
filterwarnings("ignore")
```

```
#model validation
from sklearn.metrics import
log_loss,roc_auc_score,precision_score,f1_score,recall_score,roc_curve
,auc,plot_roc_curve
from sklearn.metrics import classification_report,
confusion_matrix,accuracy_score,fbeta_score,matthews_corrcoef
from sklearn import metrics
from mlxtend.plotting import plot_confusion_matrix

----------------------------------------------------------------------
-----
ModuleNotFoundError                      Traceback (most recent call
last)
Input In [6], in <cell line: 5>()
      3 from sklearn.metrics import classification_report,
confusion_matrix,accuracy_score,fbeta_score,matthews_corrcoef
      4 from sklearn import metrics
----> 5 from mlxtend.plotting import plot_confusion_matrix

ModuleNotFoundError: No module named 'mlxtend'
```

For model validation, we'll import a few libraries.

```
#extra
from sklearn.pipeline import make_pipeline, make_union
from sklearn.preprocessing import PolynomialFeatures
from sklearn.feature_selection import SelectFwe, f_regression
```

Next, we will import all the Machine Learning algorithms

- K-Nearest Neighbors Classifier
- Random Forest Classifier
- Decision Tree Classifier
- Naive Bayes Classifier

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.naive_bayes import GaussianNB
```

Import dataset

Now that we have all the libraries we will need, we can import the dataset and take a look at it. The dataset is stored in the file `dataset.csv`. We'll use the pandas `read_csv` method to read the dataset.

```
dataset = pd.read_csv('dataset.csv',sep=',',encoding="utf-8")
```

Data Preparation and Data Exploration

```
type(dataset)
```

```
pandas.core.frame.DataFrame
```

```
dataset.shape
```

```
(270, 14)
```

The dataset is now loaded into the variable dataset. We'll just take a glimpse of the data using the `desribe()` and `info()` methods before we actually start processing and visualizing it.

```
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 270 entries, 0 to 269
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       270 non-null    int64  
 1   sex       270 non-null    int64  
 2   cp        270 non-null    int64  
 3   trestbps  270 non-null    int64  
 4   chol      270 non-null    int64  
 5   fbs       270 non-null    int64  
 6   restecg   270 non-null    int64  
 7   thalach   270 non-null    int64  
 8   exang     270 non-null    int64  
 9   oldpeak   270 non-null    float64
 10  slope     270 non-null    int64  
 11  ca        270 non-null    int64  
 12  thal      270 non-null    int64  
 13  target    270 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 29.7 KB
```

Looks like the dataset has a total of 270 rows and there are no missing values. There are a total of 13 features along with one target value which we wish to find.

```
dataset.columns
```

```
Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg',
'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

```
dataset.describe()
```

```
              age         sex          cp    trestbps        chol
fbs  \
count  270.000000  270.000000  270.000000  270.000000  270.000000
270.000000
mean    54.433333    0.677778    3.174074  131.344444  249.659259
0.148148
std      9.109067    0.468195    0.950090   17.861608   51.686237
0.355906
min     29.000000    0.000000    1.000000   94.000000  126.000000
0.000000
25%     48.000000    0.000000    3.000000  120.000000  213.000000
0.000000
50%     55.000000    1.000000    3.000000  130.000000  245.000000
0.000000
75%     61.000000    1.000000    4.000000  140.000000  280.000000
0.000000
max     77.000000    1.000000    4.000000  200.000000  564.000000
1.000000

          restecg     thalach       exang    oldpeak       slope
ca  \
count  270.000000  270.000000  270.000000  270.00000  270.000000
270.000000
mean     1.022222  149.677778    0.329630    1.05000    1.585185
0.670370
std      0.997891   23.165717    0.470952    1.14521    0.614390
0.943896
min      0.000000   71.000000    0.000000    0.00000    1.000000
0.000000
25%      0.000000  133.000000    0.000000    0.00000    1.000000
0.000000
50%      2.000000  153.500000    0.000000    0.80000    2.000000
0.000000
75%      2.000000  166.000000    1.000000    1.60000    2.000000
1.000000
max      2.000000  202.000000    1.000000    6.20000    3.000000
3.000000

             thal      target
count  270.000000  270.000000
mean     4.696296    1.444444
std      1.940659    0.497827
```

```
min      3.000000    1.000000
25%      3.000000    1.000000
50%      3.000000    1.000000
75%      7.000000    2.000000
max      7.000000    2.000000
```

The scale of each feature column is different and quite varied as well. While the maximum for age reaches 77, the maximum of chol (serum cholestoral) is 564.

```
dataset
```

```
     age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  
oldpeak  \
0     70    1   4       130   322    0        2      109      0      
2.4   
1     67    0   3       115   564    0        2      160      0      
1.6   
2     57    1   2       124   261    0        0      141      0      
0.3   
3     64    1   4       128   263    0        0      105      1      
0.2   
4     74    0   2       120   269    0        2      121      1      
0.2   
..   ...  ...  ..       ...   ...  ...      ...      ...    ...      .
..   
265   52    1   3       172   199    1        0      162      0      
0.5   
266   44    1   2       120   263    0        0      173      0      
0.0   
267   56    0   2       140   294    0        2      153      0      
1.3   
268   57    1   4       140   192    0        0      148      0      
0.4   
269   67    1   4       160   286    0        2      108      1      
1.5   

     slope  ca  thal  target  
0        2   3     3       2  
1        2   0     7       1  
2        1   0     7       2  
3        2   1     7       1  
4        1   1     3       1  
..     ...  ..   ...     ...  
265      1   0     7       1  
266      1   0     7       1  
267      2   0     3       1  
268      2   0     6       1  
269      2   3     3       2  

[270 rows x 14 columns]
```

```
dataset.head()
```

```
   age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak
slope  \
0   70    1   4       130   322    0        2      109      0      2.4
2
1   67    0   3       115   564    0        2      160      0      1.6
2
2   57    1   2       124   261    0        0      141      0      0.3
1
3   64    1   4       128   263    0        0      105      1      0.2
2
4   74    0   2       120   269    0        2      121      1      0.2
1

   ca  thal  target
0   3     3       2
1   0     7       1
2   0     7       2
3   1     7       1
4   1     3       1
```

```
dataset.isnull().sum()
```

```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

So, we have no missing values

```
dataset.apply(lambda x:len(x.unique()))
```

```
age          41
sex           2
cp            4
trestbps     47
chol        144
fbs           2
restecg       3
```

```
thalach      90
exang         2
oldpeak      39
slope         3
ca            4
thal          3
target        2
dtype: int64
```

```
print('cp ',dataset['cp'].unique())
print('fbs ',dataset['fbs'].unique())
print('restecg ',dataset['restecg'].unique())
print('exang ',dataset['exang'].unique())
print('slope ',dataset['slope'].unique())
print('ca ',dataset['ca'].unique())
print('thal ',dataset['thal'].unique())
```

```
cp  [4 3 2 1]
fbs  [0 1]
restecg  [2 0 1]
exang  [0 1]
slope  [2 1 3]
ca  [3 0 1 2]
thal  [3 7 6]
```

Dataset Description:

This dataset consists of 13 features and a target variable. The detailed description of all the features are as follows:

1. **Age**: Patients Age in years (Numeric)

---

1. **Sex**: Gender of patient (Male - 1, Female - 0)(Nominal)

---

1. **Chest Pain Type**: Type of chest pain experienced by patient categorized into : (Nominal)

- Value 1: Typical angina
- Value 2: Atypical angina
- Value 3: Non-anginal pain
- Value 4: Asymptomatic

(Angina: Angina is caused when there is not enough oxygen-rich blood flowing to a certain part of the heart. The arteries of the heart become narrow due to fatty deposits in the artery walls. The narrowing of arteries means that blood supply to the heart is reduced, causing angina.)

---

1. **resting bps**: Level of blood pressure at resting mode in mm/HG (Numerical)

---

1. **cholestrol**: Serum cholestrol in mg/dl (Numeric) (Cholesterol means the blockage for blood supply in the blood vessels)

---

1. **fasting blood sugar**: Blood sugar levels on fasting > 120 mg/dl represents as 1 in case of true and 0 as false (Nominal) (blood sugar taken after a long gap between a meal and the test. Typically, it's taken before any meal in the morning.)

---

1. **resting ecg**: Result of electrocardiogram while at rest are represented in 3 distinct values: (Nominal)

- Value 0: Normal
- Value 1: Having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV)
- Value 2: Showing probable or definite left ventricular hypertrophy by Estes' criteria.

(ECG values taken while person is on rest which means no exercise and normal functioning of heart is happening)

---

1. **oldpeak**: Exercise induced ST-depression in comparison with the state of rest (Numeric)

(ST Depression is the difference between value of ECG at rest and after exercise. An electrocardiogram records the electrical signals in your heart. It's a common and painless test used to quickly detect heart problems and monitor your heart's health. Electrocardiograms — also called ECGs or EKGs — are often done in a doctor's office, a clinic or a hospital room. ECG machines are standard equipment in operating rooms and ambulances. Some personal devices, such as smart watches.)

---

1. **ST slope**: ST segment measured in terms of slope during peak exercise (Nominal)

- Value 1: Upsloping
- Value 2: Flat
- Value 3: Downsloping

---

1. **ca**: Number of major blood vessels (0-3)(Numeric)

(Fluoroscopy is an imaging technique that uses X-rays to obtain real-time moving images of the interior of an object. In its primary application of medical imaging, a fluoroscope allows a physician to see the internal structure and function of a patient, so that the pumping action of the heart or the motion of swallowing, for example, can be watched)

---

1. **exang**: Exercise induced angina (1 = yes; 0 = no)

(is chest pain while exercising or doing any physical activity.)

---

1. **thal**: Thalium stress test

- Value 3: normal
- Value 6: fixed defect
- Value 7: reversibe defect

---

1. **thalach**: Maximum heart rate achieved in bpm(Numeric)

Target variable

1. **target**: It is the target variable which we have to predict 2 means patient is suffering from heart risk and 1 means patient is normal. (1 = no disease; 2 = disease)

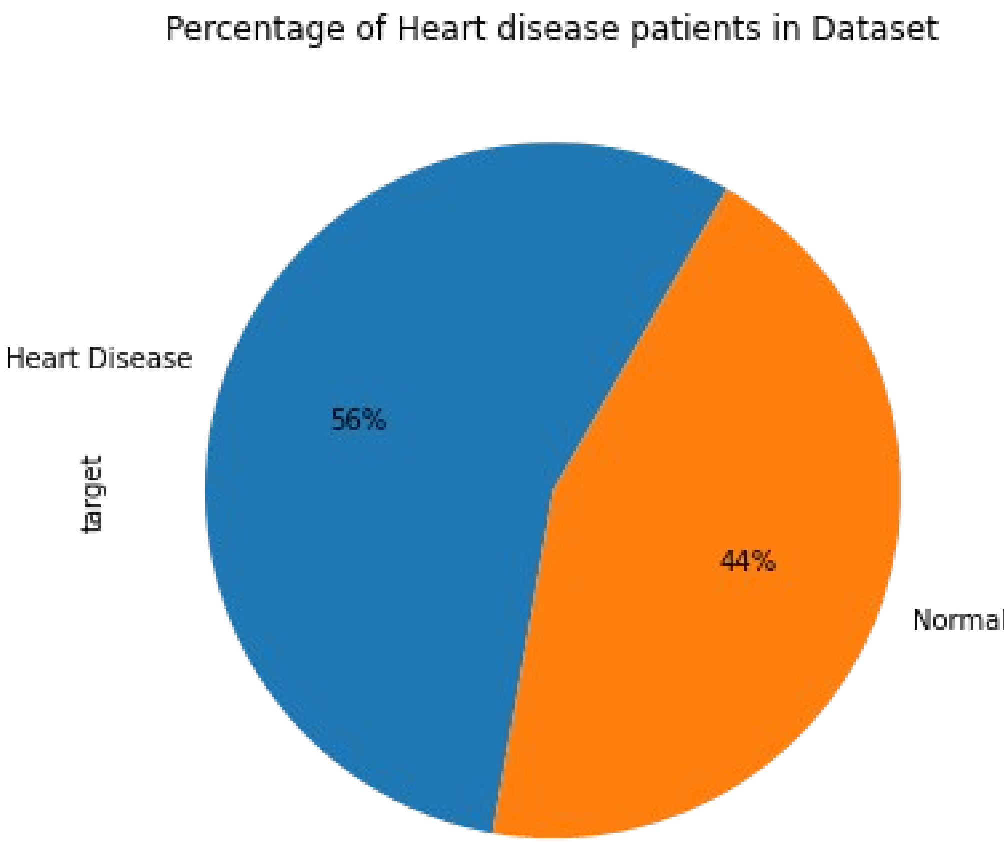
Data Visualization

Now let's see various visual representations of the data to understand more about relationship between various features.

Distribution of Heart disease (target variable)

It's always a good practice to work with a dataset where the target classes are of approximately equal size. Thus, let's check for the same.

```
fig, (ax1) = plt.subplots(nrows=1, ncols=1, sharey=False,
figsize=(14,6))

ax1 = dataset['target'].value_counts().plot.pie( x="Heart disease" ,y
='no.of patients',
                   autopct = "%1.0f%%",labels=["Heart
Disease","Normal"], startangle = 60,ax=ax1);
ax1.set(title = 'Percentage of Heart disease patients in Dataset')
plt.show()
```

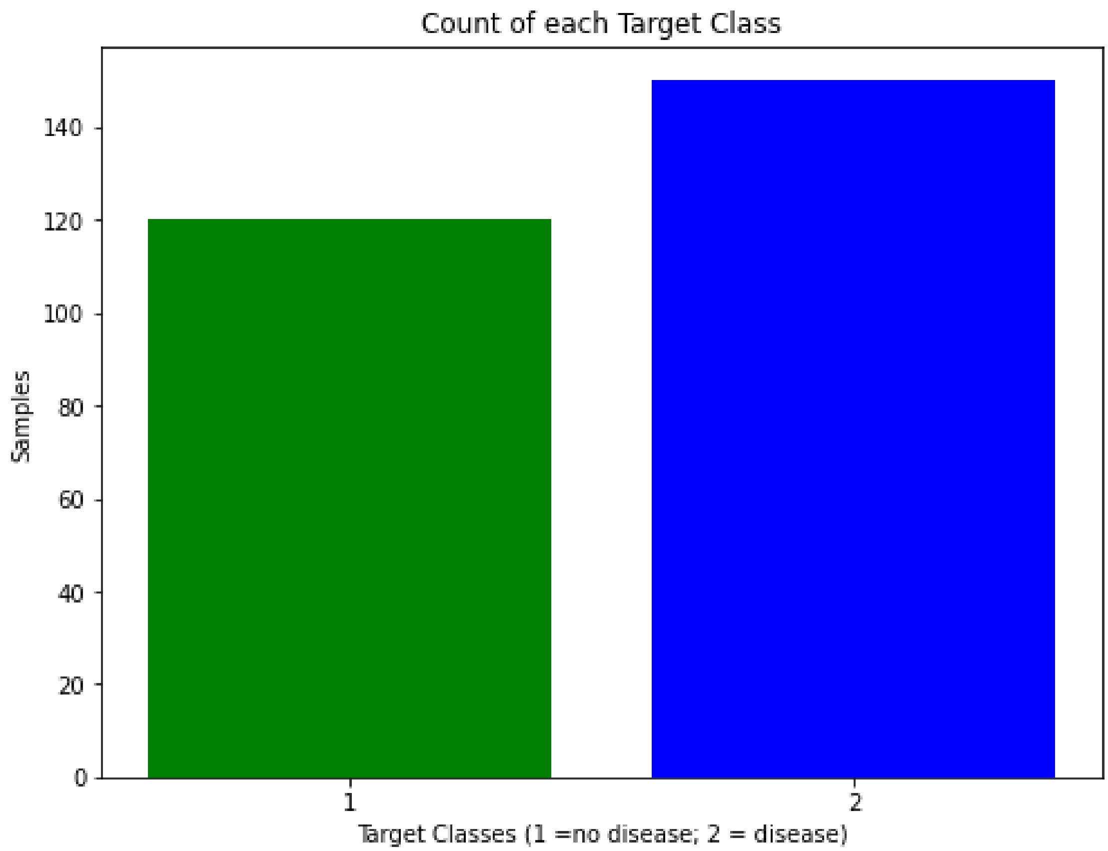


The two classes are not exactly 50% each but the ratio is good enough to continue without dropping/increasing our data.

```
y = dataset["target"]
```

```
rcParams['figure.figsize'] = 8,6
plt.bar(dataset['target'].unique(), dataset['target'].value_counts(),
color = ['blue', 'green'])
plt.xticks([1, 2])
plt.xlabel('Target Classes (1 =no disease; 2 = disease)')
plt.ylabel('Samples')
plt.title('Count of each Target Class')
target_temp = dataset.target.value_counts()
print(target_temp)
```

```
1    150
2    120
Name: target, dtype: int64
```

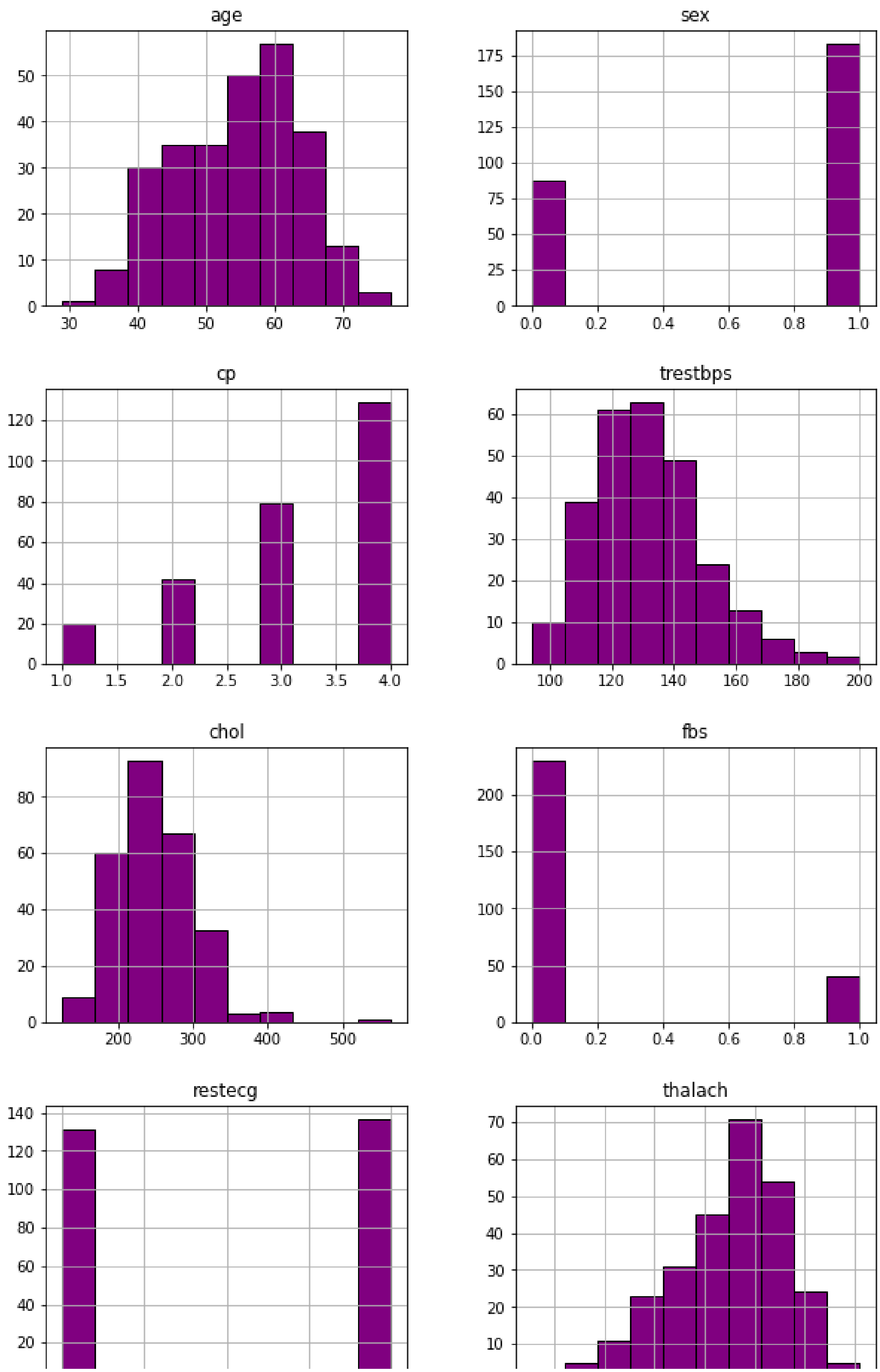


From the total dataset of 270 patients, 150 (56%) have a heart disease (target=2)

Next, we'll take a look at the histograms for each variable.

```
dataset.hist(edgecolor='black',layout = (7, 2),
            figsize = (10, 30),
            color=['purple'])
```

```
array([[<AxesSubplot:title={'center':'age'}>,
        <AxesSubplot:title={'center':'sex'}>],
       [<AxesSubplot:title={'center':'cp'}>,
        <AxesSubplot:title={'center':'trestbps'}>],
       [<AxesSubplot:title={'center':'chol'}>,
        <AxesSubplot:title={'center':'fbs'}>],
       [<AxesSubplot:title={'center':'restecg'}>,
        <AxesSubplot:title={'center':'thalach'}>],
       [<AxesSubplot:title={'center':'exang'}>,
        <AxesSubplot:title={'center':'oldpeak'}>],
       [<AxesSubplot:title={'center':'slope'}>,
        <AxesSubplot:title={'center':'ca'}>],
       [<AxesSubplot:title={'center':'thal'}>,
        <AxesSubplot:title={'center':'target'}>]], dtype=object)
```


age
0
10
20
30
40
50
30
40
50
60
70
sex
0
25
50
75
100
125
150
175
0.0
0.2
0.4
0.6
0.8
1.0
cp
0
20
40
60
80
100
120
1.0
1.5
2.0
2.5
3.0
3.5
4.0
trestbps
0
10
20
30
40
50
60
100
120
140
160
180
200
chol
0
20
40
60
80
200
300
400
500
fbs
0
50
100
150
200
0.0
0.2
0.4
0.6
0.8
1.0
restecg
20
40
60
80
100
120
140
thalach
10
20
30
40
50
60
70

Taking a look at the histograms above, I can see that each feature has a different range of distribution. Thus, using scaling before our predictions should be of great use. Also, the categorical features do stand out.

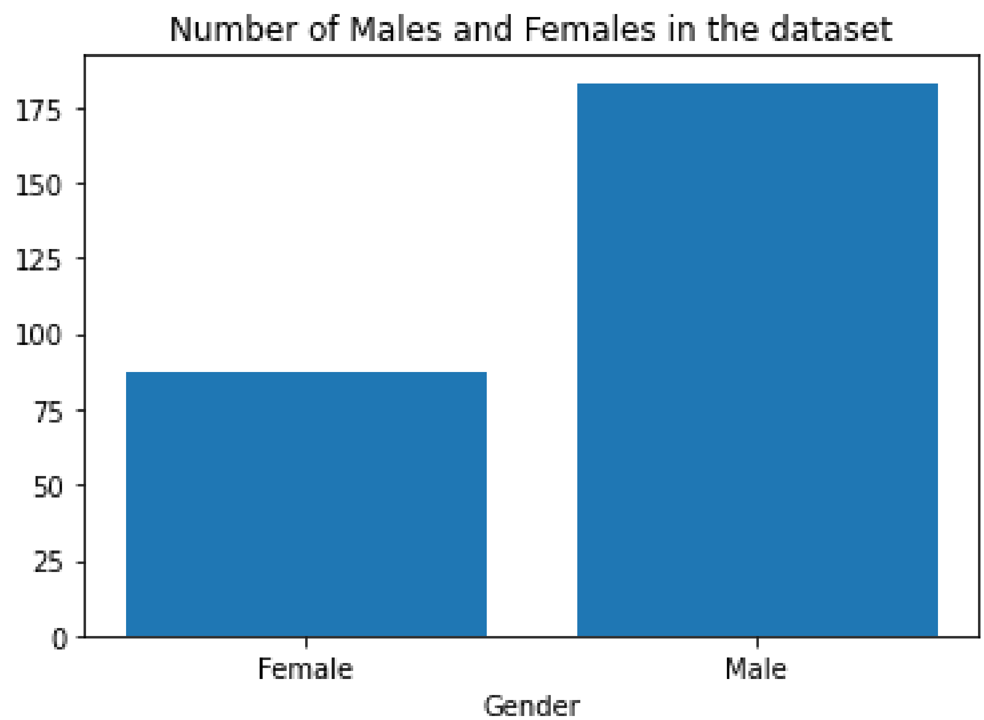
Exploratory Data Analysis (EDA)

Gender distribution based on heart disease

```
dataset["sex"].unique()
```

```
array([1, 0], dtype=int64)
```

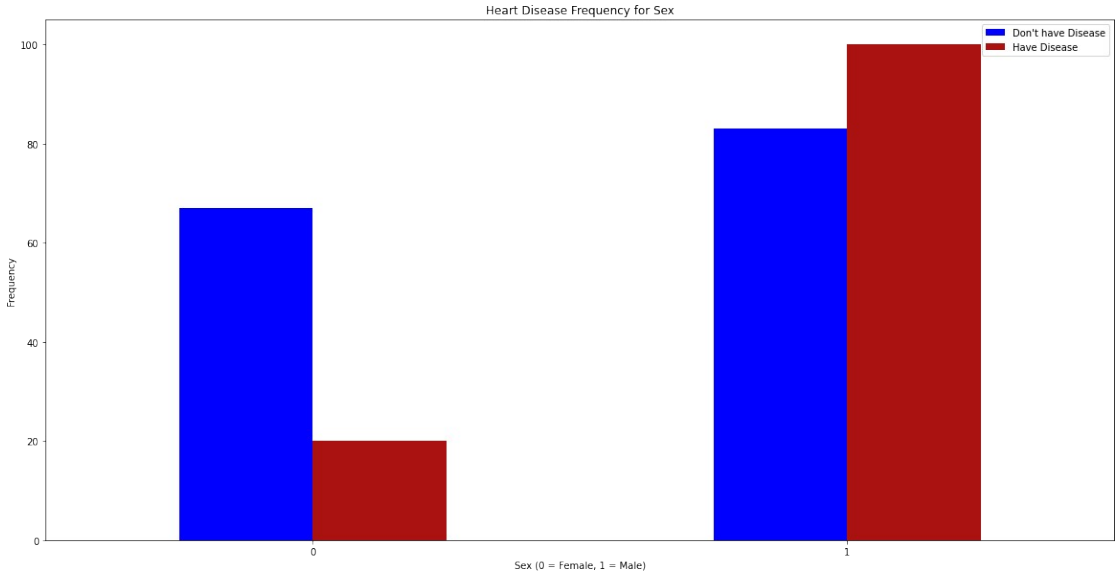
```
# Number of males and females
F = dataset[dataset["sex"] == 0].count()["target"]
M = dataset[dataset["sex"] == 1].count()["target"]

# Create a plot
figure, ax = plt.subplots(figsize = (6, 4))
ax.bar(x = ['Female', 'Male'], height = [F, M])
plt.xlabel('Gender')
plt.title('Number of Males and Females in the dataset')
plt.show()
```



Heart Disease frequency for gender

```
pd.crosstab(dataset.sex,dataset.target).plot(kind="bar",figsize=(20,10
),color=['blue','#AA1111' ])
plt.title('Heart Disease Frequency for Sex')
plt.xlabel('Sex (0 = Female, 1 = Male)')
```

```
plt.xticks(rotation=0)
plt.legend(["Don't have Disease", "Have Disease"])
plt.ylabel('Frequency')
plt.show()
```

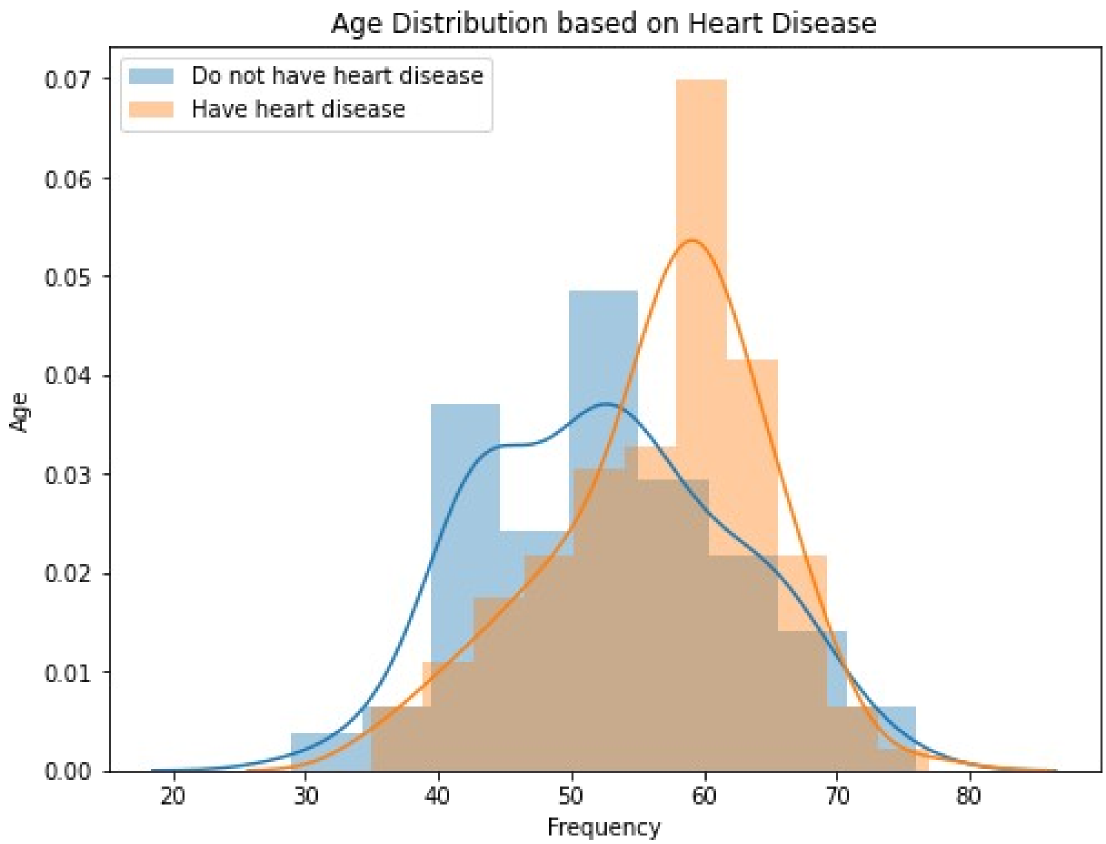



```
countFemale = len(dataset[dataset.sex == 0])
countMale = len(dataset[dataset.sex == 1])
print("Percentage of Female Patients:{:.2f}
%".format((countFemale)/(len(dataset.sex))*100))
print("Percentage of Male Patients:{:.2f}
%".format((countMale)/(len(dataset.sex))*100))
```

```
Percentage of Female Patients:32.22%
Percentage of Male Patients:67.78%
```

Age distribution based on heart disease

```
# Display age distribution based on heart disease
sns.distplot(dataset[dataset['target'] == 1]['age'], label='Do not
have heart disease')
sns.distplot(dataset[dataset['target'] == 2]['age'], label = 'Have
heart disease')
plt.xlabel('Frequency')
plt.ylabel('Age')
plt.title('Age Distribution based on Heart Disease')
plt.legend()
plt.show()
```



Get min, max and average of the age of the people do not have heart disease

```
print('Min age of people who do not have heart disease: ',
min(dataset[dataset['target'] == 1]['age']))
print('Max age of people who do not have heart disease: ',
max(dataset[dataset['target'] == 1]['age']))
print('Average age of people who do not have heart disease: ',
dataset[dataset['target'] == 1]['age'].mean())
```

```
Min age of people who do not have heart disease:  29
Max age of people who do not have heart disease:  76
Average age of people who do not have heart disease:
52.70666666666666
```

Get min, max and average of the age of the people have heart disease

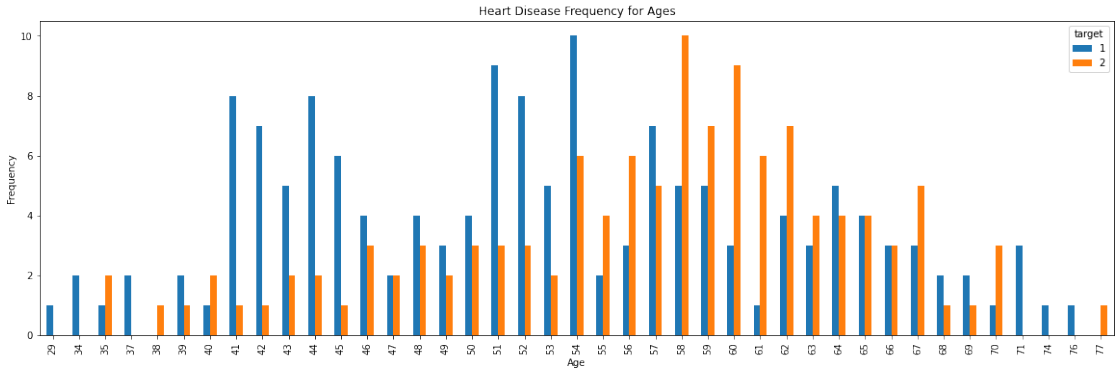
```
print('Min age of people who have heart disease: ',
min(dataset[dataset['target'] == 2]['age']))
print('Max age of people who have heart disease: ',
max(dataset[dataset['target'] == 2]['age']))
print('Average age of people who have heart disease: ',
dataset[dataset['target'] == 2]['age'].mean())
```

```
Min age of people who have heart disease:  35
Max age of people who have heart disease:  77
Average age of people who have heart disease:  56.59166666666667
```

From the data, we can say that the heart disease infects the old and young people, and the probability of the old people te be infected is higher than young people.

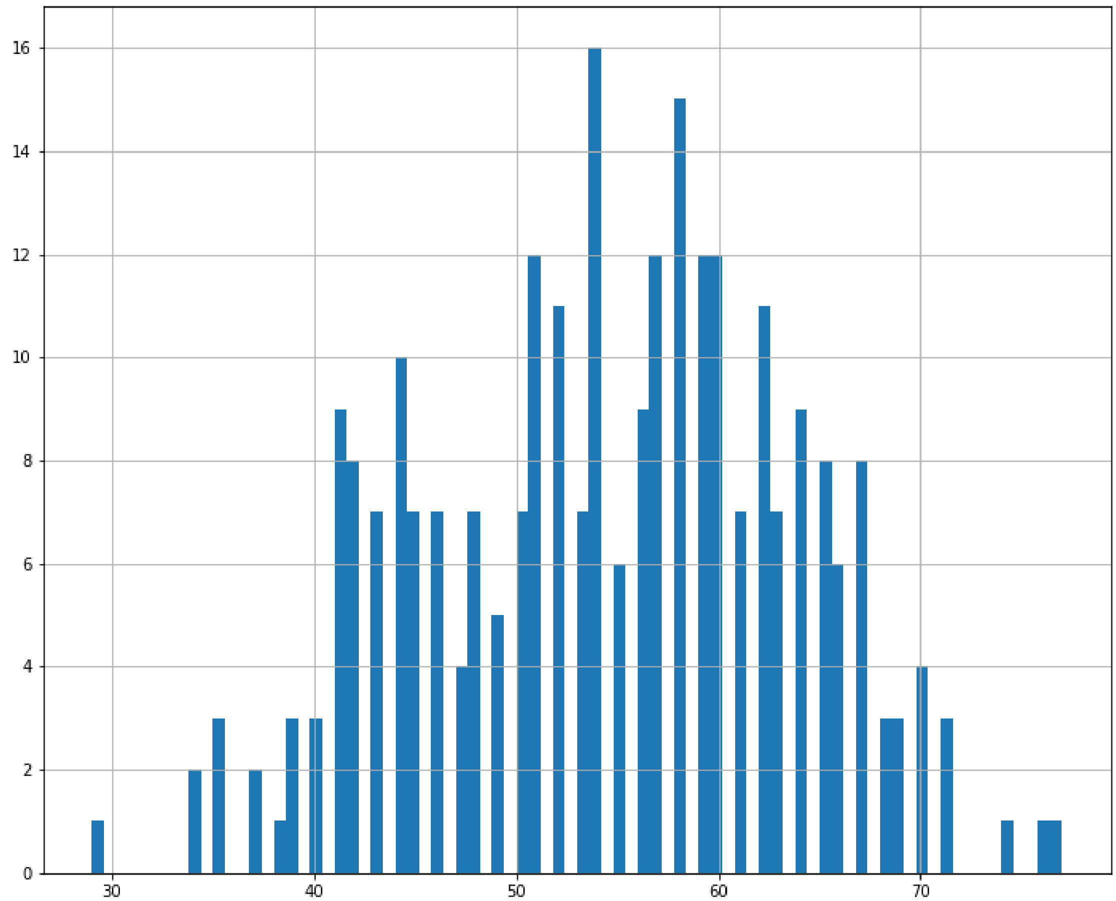
Heart Disease Frequency for ages

```
pd.crosstab(dataset.age,dataset.target).plot(kind="bar",figsize=(20,6)
)
plt.title('Heart Disease Frequency for Ages')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.savefig('heartDiseaseAndAges.png')
plt.show()
```




```
plt.figure(figsize=(12, 10))
dataset.age.hist(bins=80)
```

```
<AxesSubplot:>
```



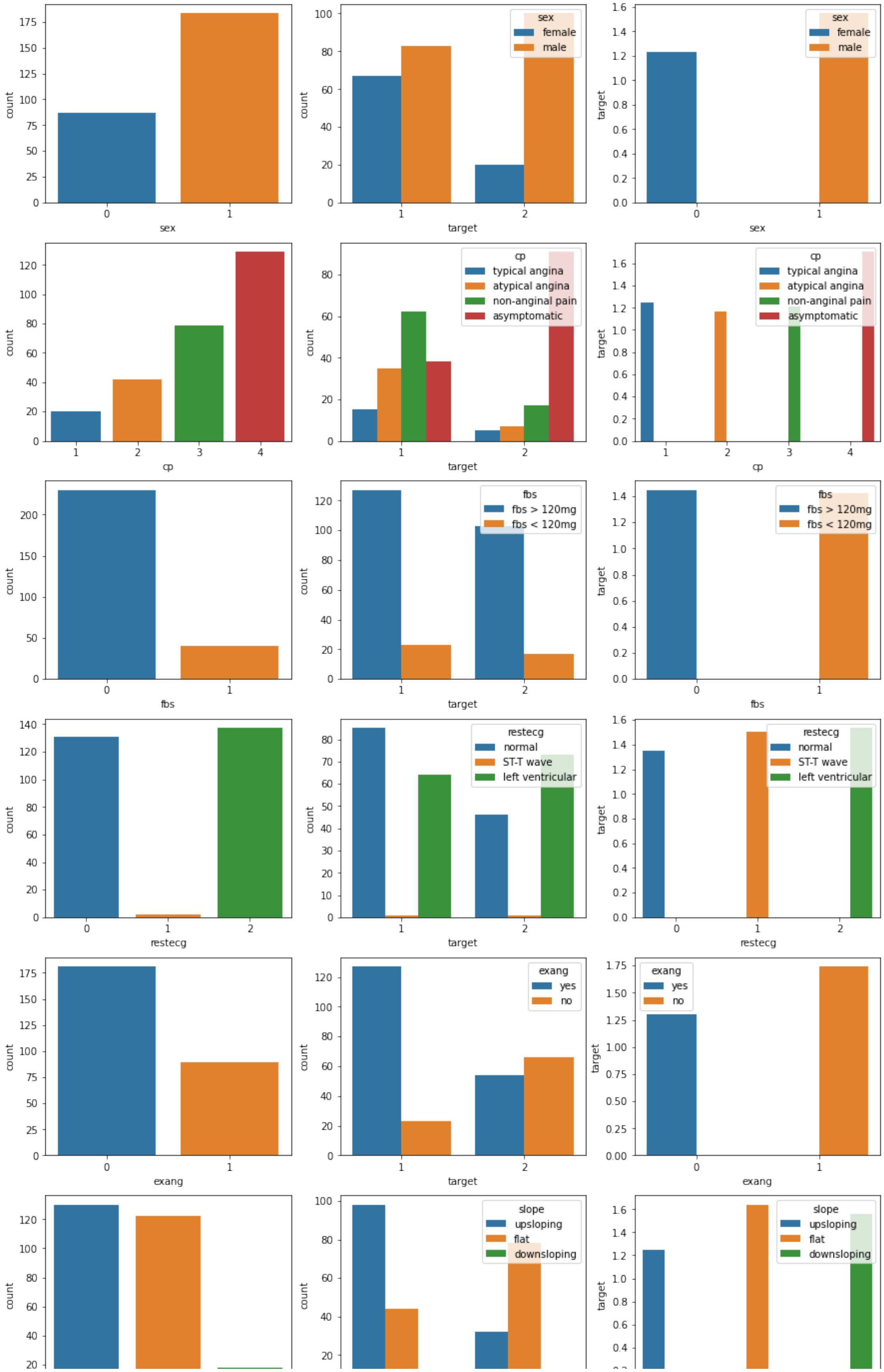

```
print(f"The most of the patients have a mean age of :
{dataset.age.mean()}")
```

```
The most of the patients have a mean age of : 54.43333333333333
```

Distribution of Categorial features

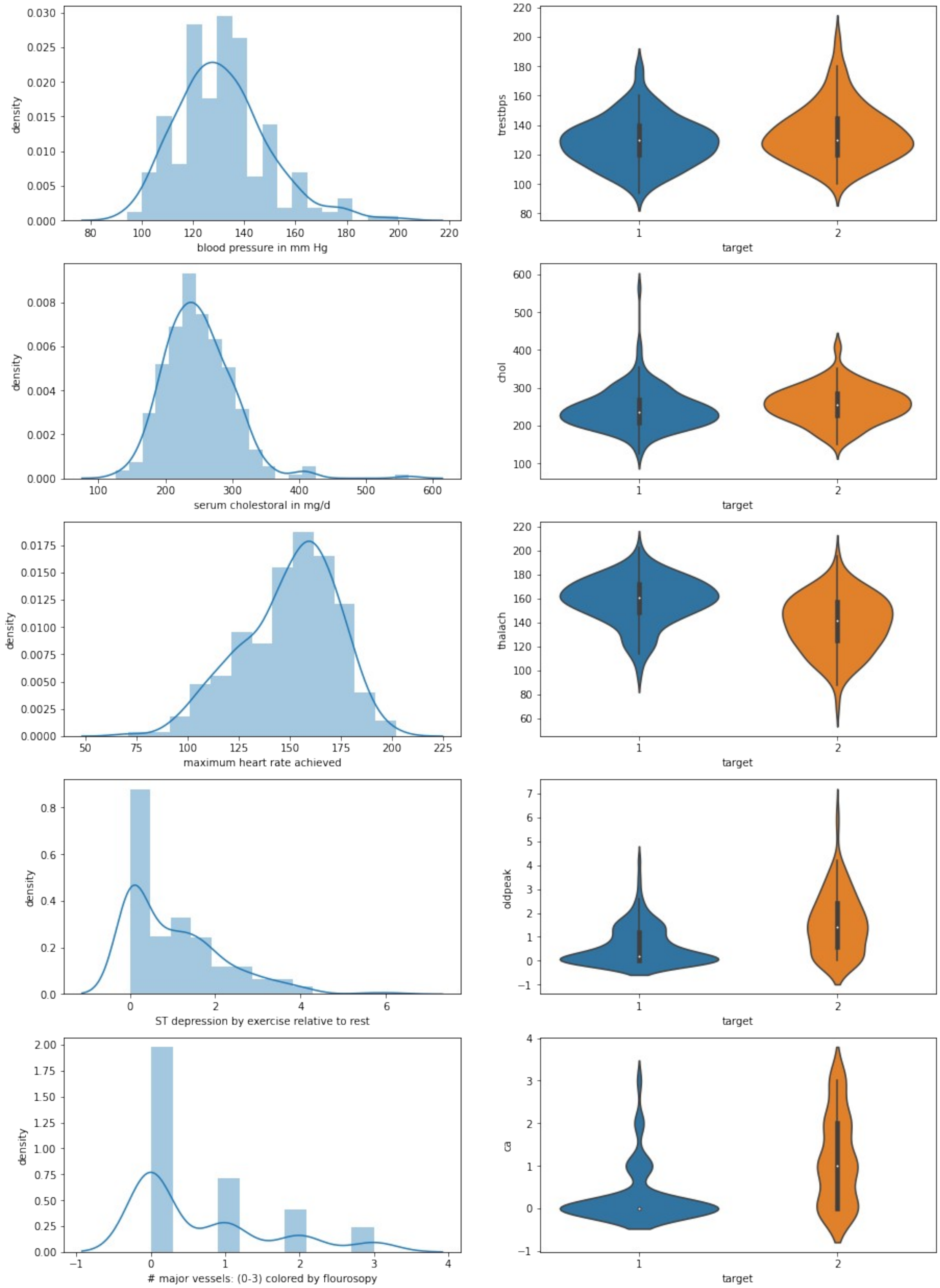
```
categorial = [('sex', ['female', 'male']),
              ('cp', ['typical angina', 'atypical angina', 'non-
anginal pain', 'asymptomatic']),
              ('fbs', ['fbs > 120mg', 'fbs < 120mg']),
              ('restecg', ['normal', 'ST-T wave', 'left
ventricular']),
              ('exang', ['yes', 'no']),
              ('slope', ['upsloping', 'flat', 'downsloping']),
              ('thal', ['normal', 'fixed defect', 'reversible
defect'])]

def plotGrid(isCategorial):
    if isCategorial:
        [plotCategorial(x[0], x[1], i) for i, x in
enumerate(categorial)]
    else:
```

```
        [plotContinuous(x[0], x[1], i) for i, x in
enumerate(continuous)]

def plotCategorial(attribute, labels, ax_index):
    sns.countplot(x=attribute, data=dataset, ax=axes[ax_index][0])
    sns.countplot(x='target', hue=attribute, data=dataset,
ax=axes[ax_index][1])
    avg = dataset[[attribute, 'target']].groupby([attribute],
as_index=False).mean()
    sns.barplot(x=attribute, y='target', hue=attribute, data=avg,
ax=axes[ax_index][2])

    for t, l in zip(axes[ax_index][1].get_legend().texts, labels):
        t.set_text(l)
    for t, l in zip(axes[ax_index][2].get_legend().texts, labels):
        t.set_text(l)

fig_categorial, axes = plt.subplots(nrows=len(categorial), ncols=3,
figsize=(15, 30))

plotGrid(True)
```


count
sex
count
target
sex
female
male
target
sex
sex
female
male
count
cp
count
target
cp
typical angina
atypical angina
non-anginal pain
asymptomatic
target
cp
cp
typical angina
atypical angina
non-anginal pain
asymptomatic
count
fbs
count
target
fbs
fbs > 120mg
fbs < 120mg
target
fbs
fbs
fbs > 120mg
fbs < 120mg
count
restecg
count
target
restecg
normal
ST-T wave
left ventricular
target
restecg
restecg
normal
ST-T wave
left ventricular
count
exang
count
target
exang
yes
no
target
exang
exang
yes
no
count
count
slope
upsloping
flat
downsloping
target
slope
upsloping
flat
downsloping

Distribution of Continuous features

```
continuous = [('trestbps', 'blood pressure in mm Hg'),
              ('chol', 'serum cholestoral in mg/d'),
              ('thalach', 'maximum heart rate achieved'),
              ('oldpeak', 'ST depression by exercise relative to 
rest'),
              ('ca', '# major vessels: (0-3) colored by flourosopy')]

def plotContinuous(attribute, xlabel, ax_index):
    sns.distplot(dataset[[attribute]], ax=axes[ax_index][0])
    axes[ax_index][0].set(xlabel=xlabel, ylabel='density')
    sns.violinplot(x='target', y=attribute, data=dataset, 
ax=axes[ax_index][1])

fig_continuous, axes = plt.subplots(nrows=len(continuous), ncols=2, 
figsize=(15, 22))

plotGrid(isCategorial=False)
```

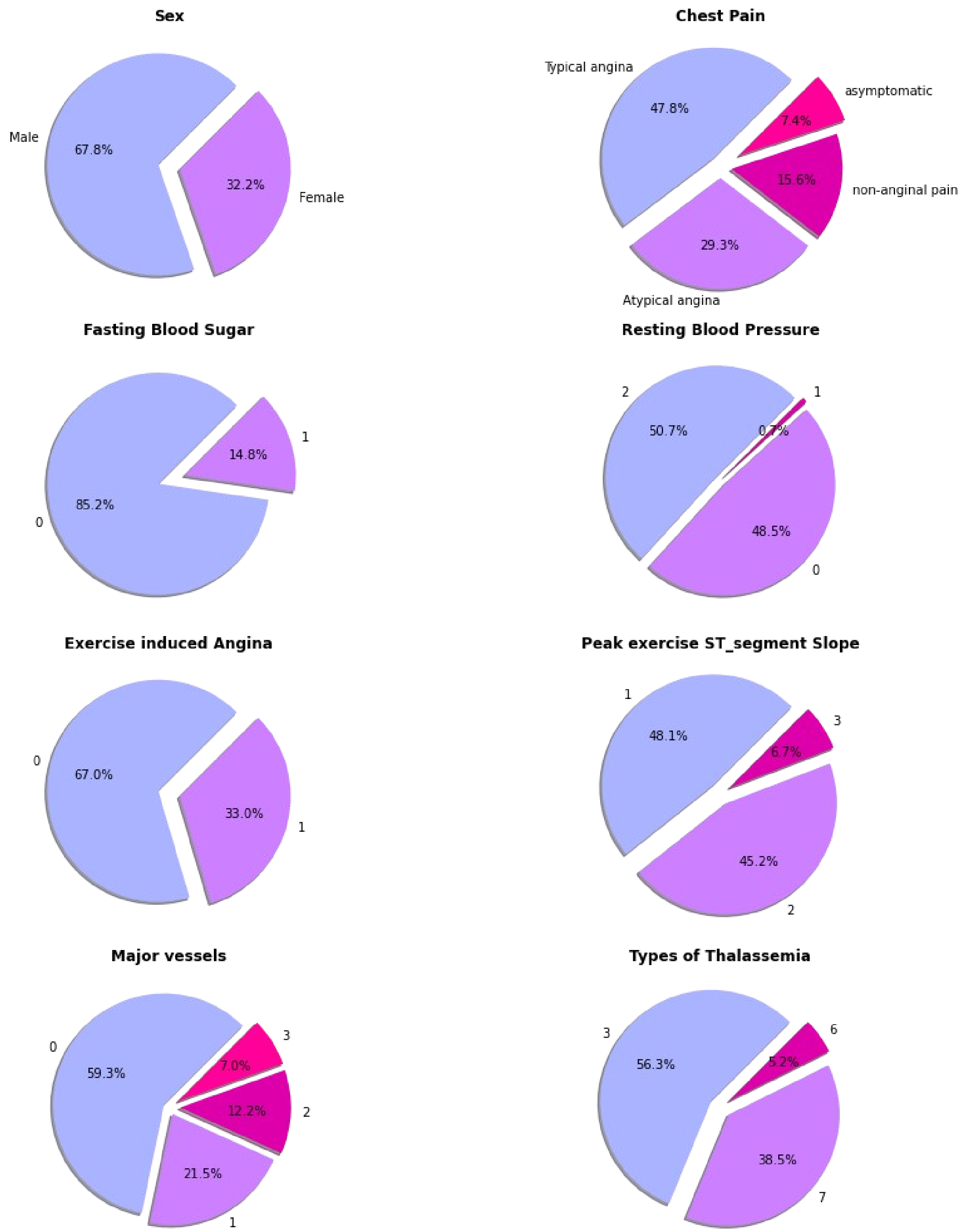


PiePlots

```
fig, ax = plt.subplots(4,2, figsize = (14,14))
((ax1, ax2), (ax3, ax4), (ax5, ax6), (ax7, ax8)) = ax
```

```
labels = ["Male", "Female"]
values = dataset['sex'].value_counts().tolist()[:2]
ax1.pie(x=values, labels=labels, autopct="%1.1f%
%",colors=['#AAb3ff','#CC80FF'],shadow=True,
startangle=45,explode=[0.1, 0.1])
ax1.set_title("Sex", fontdict={'fontsize': 12},fontweight ='bold')

labels = ["Typical angina", "Atypical angina","non-anginal
pain","asymptomatic"]
values = dataset['cp'].value_counts().tolist()
ax2.pie(x=values, labels=labels, autopct="%1.1f%
%",colors=['#AAb3ff','#CC80FF','#DD00AA','#FF0099'],shadow=True,starta
ngle=45,explode=[0.1, 0.1, 0.1, 0.2])
ax2.set_title("Chest Pain", fontdict={'fontsize': 12},fontweight
='bold')

labels = dataset['fbs'].value_counts().index.tolist()[:2]
values = dataset['fbs'].value_counts().tolist()
ax3.pie(x=values, labels=labels, autopct="%1.1f%
%",colors=['#AAb3ff','#CC80FF'],shadow=True,
startangle=45,explode=[0.1, 0.15])
ax3.set_title("Fasting Blood Sugar", fontdict={'fontsize':
12},fontweight ='bold')

labels = dataset['restecg'].value_counts().index.tolist()[:3]
values = dataset['restecg'].value_counts().tolist()
ax4.pie(x=values, labels=labels, autopct="%1.1f%%",
colors=['#AAb3ff','#CC80FF','#DD00AA'],shadow=True,startangle=45,explo
de=[ 0.05, 0.05, 0.05])
ax4.set_title("Resting Blood Pressure", fontdict={'fontsize':
12},fontweight ='bold')

labels = dataset['exang'].value_counts().index.tolist()[:2]
values = dataset['exang'].value_counts().tolist()
ax5.pie(x=values, labels=labels, autopct="%1.1f%%",
colors=['#AAb3ff','#CC80FF'],shadow=True, startangle=45,explode=[0.1,
0.1])
ax5.set_title("Exercise induced Angina", fontdict={'fontsize':
12},fontweight ='bold')

labels = dataset['slope'].value_counts().index.tolist()[:3]
values = dataset['slope'].value_counts().tolist()
ax6.pie(x=values, labels=labels, autopct="%1.1f%%",
colors=['#AAb3ff','#CC80FF','#DD00AA'],shadow=True,startangle=45,explo
de=[  0.1, 0.1, 0.1])
ax6.set_title("Peak exercise ST_segment Slope", fontdict={'fontsize':
12},fontweight ='bold')

labels = dataset['ca'].value_counts().index.tolist()[:4]
values = dataset['ca'].value_counts().tolist()
```

```
ax7.pie(x=values, labels=labels, autopct="%1.1f%%", shadow=True,
startangle=45,explode=[0.05, 0.07, 0.1,
0.1],colors=['#AAb3ff','#CC80FF','#DD00AA','#FF0099'])
ax7.set_title("Major vessels", fontdict={'fontsize': 12},fontweight
='bold')

labels = dataset['thal'].value_counts().index.tolist()[:3]
values = dataset['thal'].value_counts().tolist()
ax8.pie(x=values, labels=labels, autopct="%1.1f%%", shadow=True,
startangle=45,explode=[0.1, 0.1,
0.1],colors=['#AAb3ff','#CC80FF','#DD00AA'])
ax8.set_title("Types of Thalassemia", fontdict={'fontsize':
12},fontweight ='bold')

plt.tight_layout()
plt.show()

plt.savefig("PiePlots.png")
```

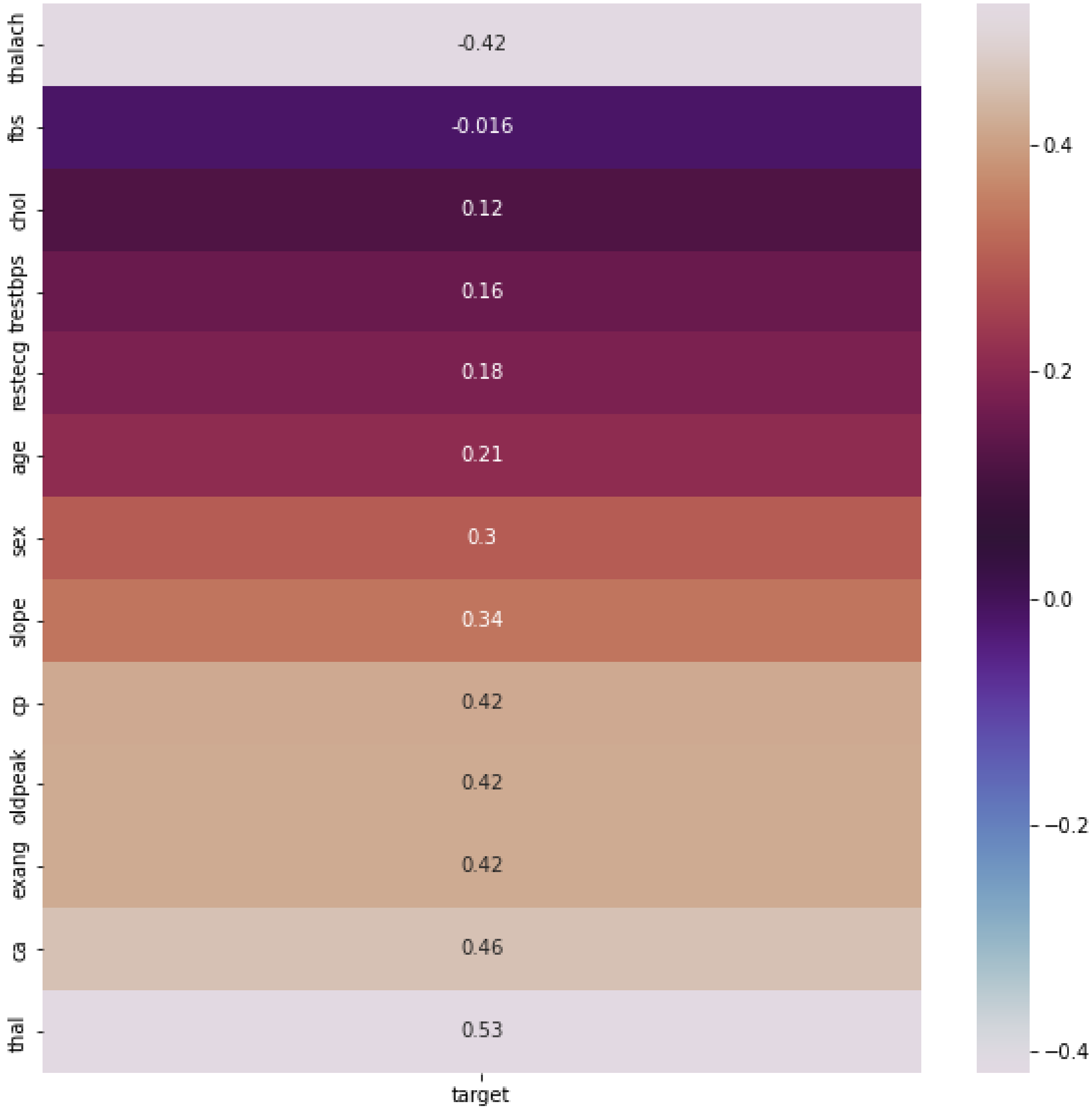



```
<Figure size 576x432 with 0 Axes>
```

Target Correlations

```
plt.figure(figsize=(10,10))
sns.heatmap(pd.DataFrame(dataset.corr()
['target']).sort_values(by='target').transpose().drop('target',axis=1)
```

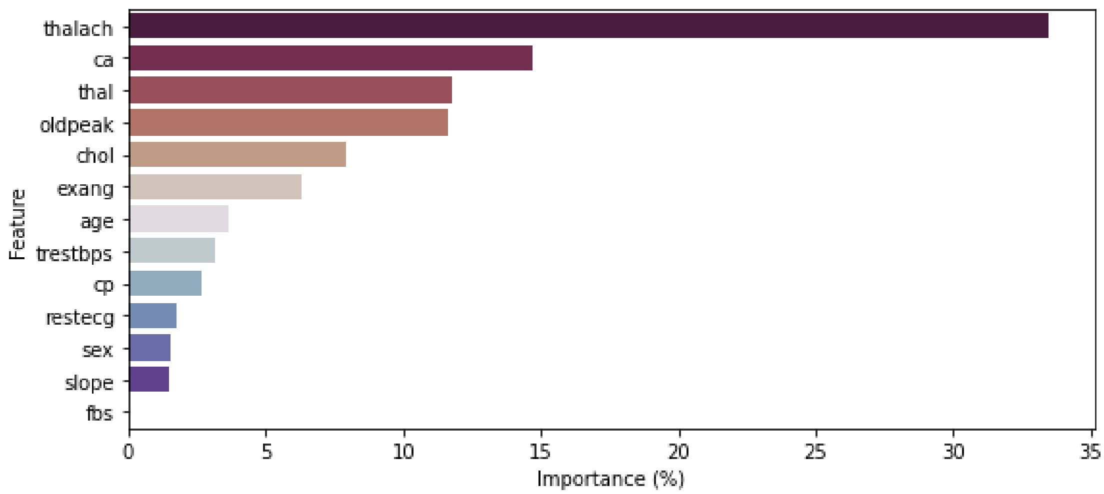
```
.transpose(),annot=True,cmap='twilight')
plt.savefig("TargetCorrelations.png")
```



Feature Importance

```
X = dataset.drop('target',axis=1)
Y = dataset['target']
from sklearn.feature_selection import SelectKBest, chi2
fs = SelectKBest(score_func=chi2, k='all')
fs.fit(X, Y)
per = []
for i in fs.scores_:
    per.append(round(((i/sum(fs.scores_))*100),3))

features_data =
pd.DataFrame({'Feature':X.columns,'Scores':fs.scores_,'Importance
(%)':per}).sort_values(by=['Scores'],ascending=False)
```

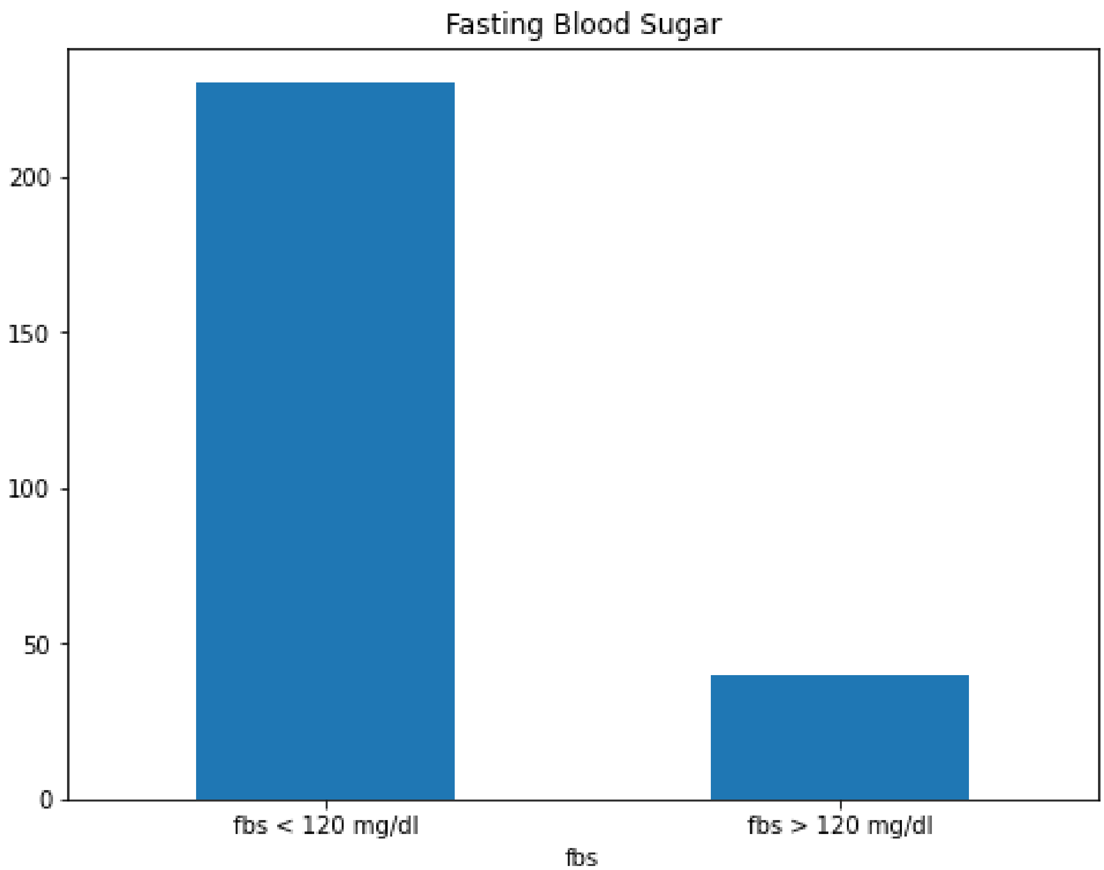
```python
plt.figure(figsize=(9,4))
sns.barplot( 'Importance (%)','Feature',orient='h',data=features_data,palette='twilight_shifted_r')
insignificant = features_data.loc[features_data['Importance (%)']<0.005]['Feature'].unique()
features_data = features_data.set_index('Feature')
features_data
plt.savefig("FeatureImportance.png")
```



Analysing Fasting Blood sugar [fbs]

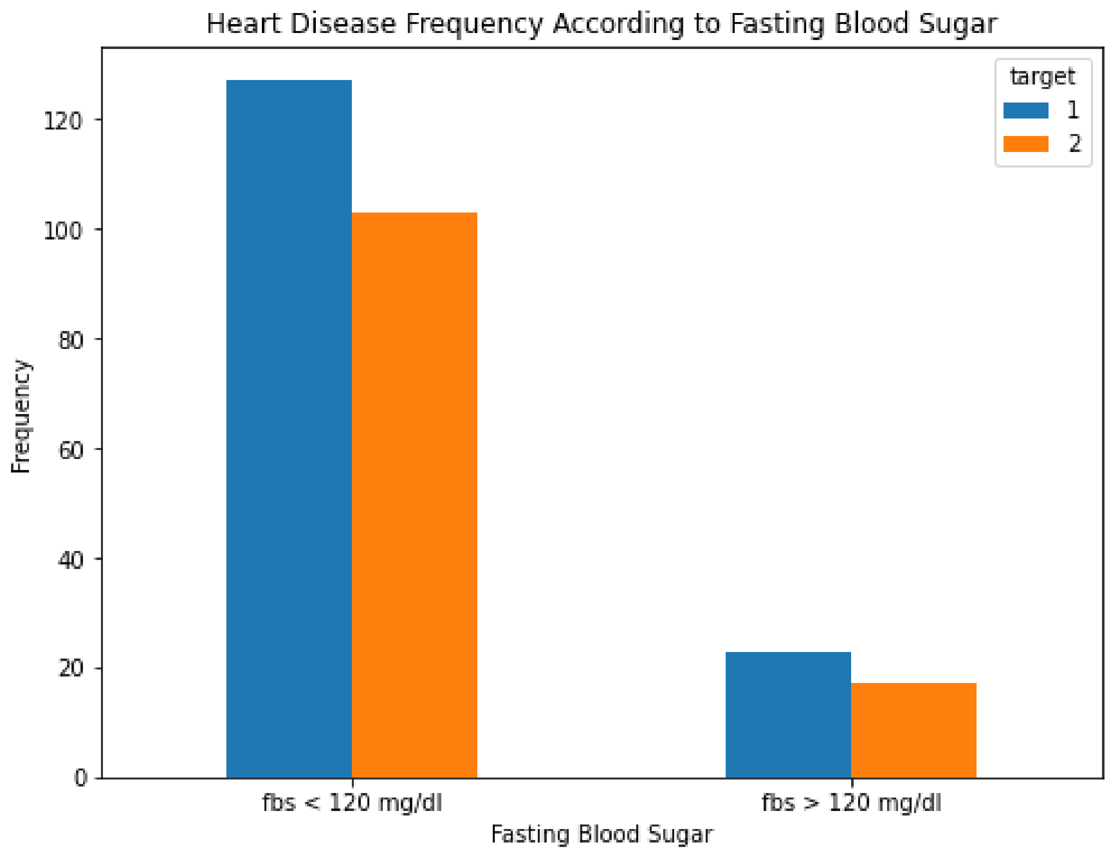
Heart disease according to Fasting Blood sugar

```python
# Display fasting blood sugar in bar chart
dataset.groupby(dataset['fbs']).count()['target'].plot(kind = 'bar', title = 'Fasting Blood Sugar', figsize = (8, 6))
plt.xticks(np.arange(2), ('fbs < 120 mg/dl', 'fbs > 120 mg/dl'), rotation = 0)
plt.show()
```



Display fasting blood sugar based on the target

```
pd.crosstab(dataset.fbs,dataset.target).plot(kind = "bar", figsize =
(8, 6))
plt.title('Heart Disease Frequency According to Fasting Blood Sugar')
plt.xlabel('Fasting Blood Sugar')
plt.xticks(np.arange(2), ('fbs < 120 mg/dl', 'fbs > 120 mg/dl'),
rotation = 0)
plt.ylabel('Frequency')
plt.show()
```



Analysing the Chest Pain [cp] (4 types of chest pain)

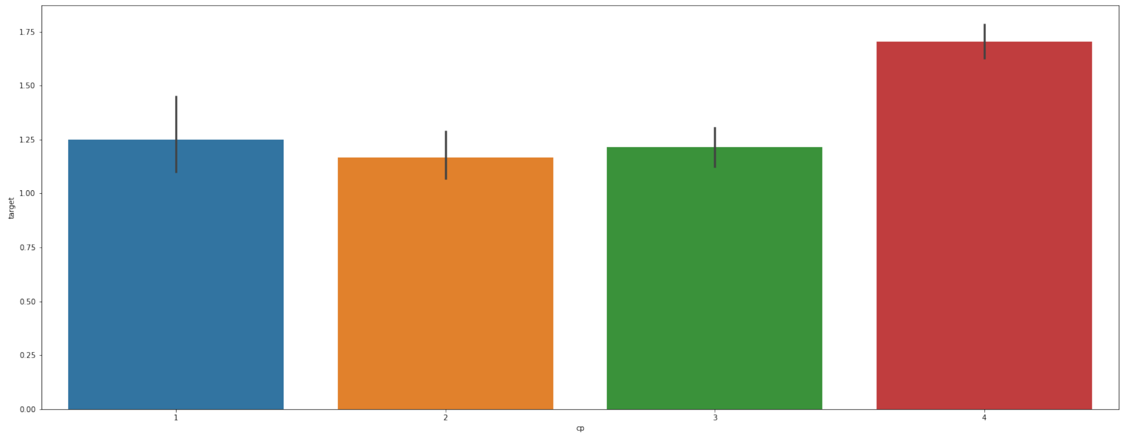
[Value 1: typical angina, Value 2: atypical angina, Value 3: non-anginal pain, Value 4: asymptomatic]

```
dataset["cp"].unique()
```

```
array([4, 3, 2, 1], dtype=int64)
```

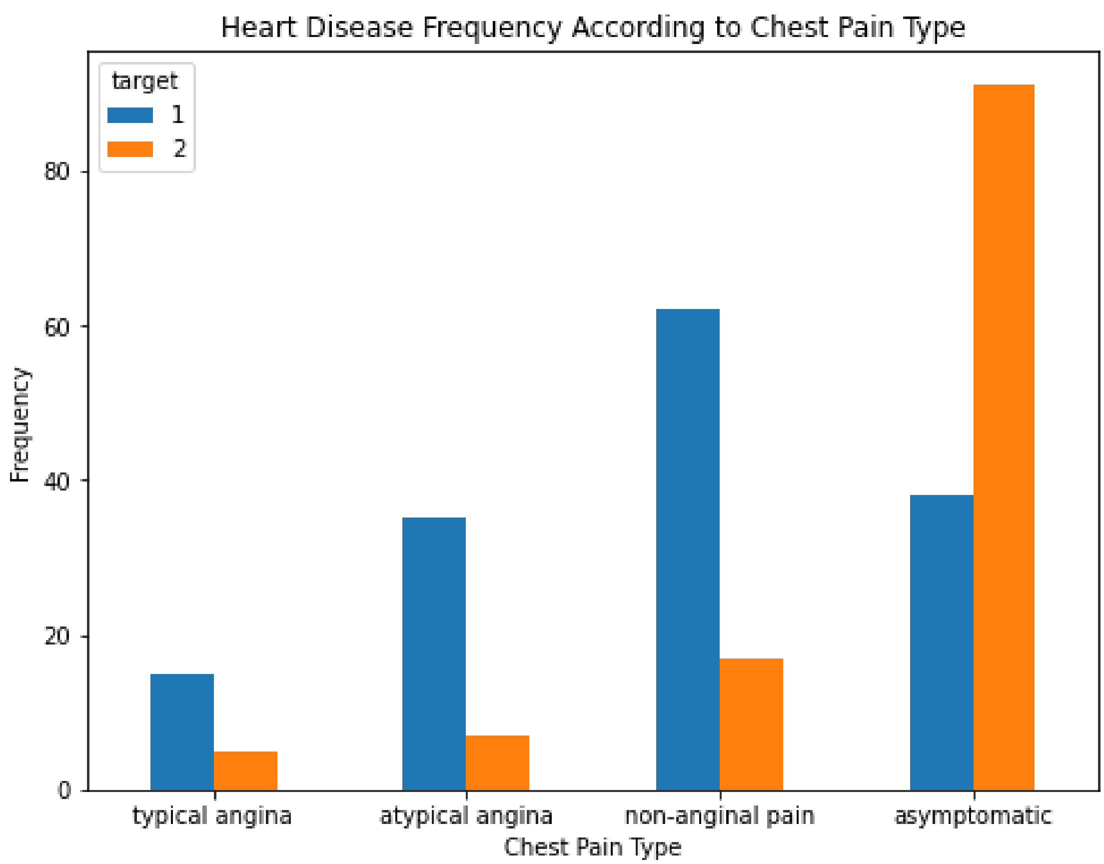
```
plt.figure(figsize=(26, 10))
sns.barplot(dataset["cp"],y)
```

```
<AxesSubplot:xlabel='cp', ylabel='target'>
```



Display chest pain types based on the target

```
pd.crosstab(dataset.cp,dataset.target).plot(kind = "bar", figsize =
(8, 6))
plt.title('Heart Disease Frequency According to Chest Pain Type')
plt.xlabel('Chest Pain Type')
plt.xticks(np.arange(4), ('typical angina', 'atypical angina', 'non-
anginal pain', 'asymptomatic'), rotation = 0)
plt.ylabel('Frequency')
plt.show()
```



Analysing Resting Blood Pressure [trestbps]

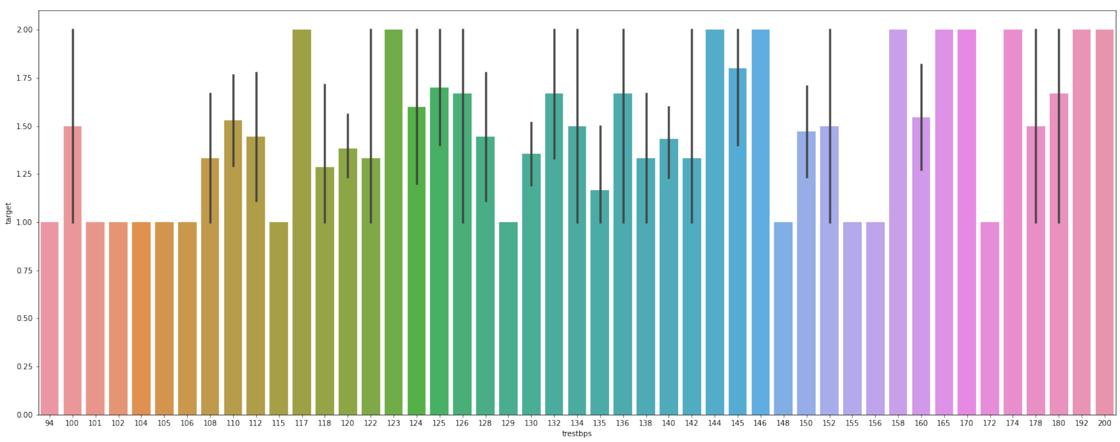
mm Hg on admission to the hospital

```
dataset["trestbps"].unique()
```

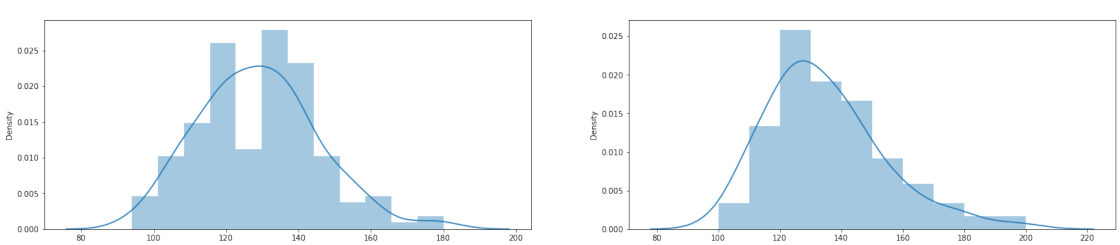
```
array([130, 115, 124, 128, 120, 110, 140, 150, 135, 142, 134, 112, 
132,
       138, 160, 170, 144, 122, 152, 101, 126, 118, 136, 105, 174, 
145,
       108, 156, 106, 104,  94, 146, 148, 178, 125, 100, 165, 180, 
158,
       200, 117, 192, 123, 129, 102, 155, 172], dtype=int64)
```

```
plt.figure(figsize=(26, 10))
sns.barplot(dataset["trestbps"],y)
```

```
<AxesSubplot:xlabel='trestbps', ylabel='target'>
```




```
fig, (axis1, axis2) = plt.subplots(1, 2,figsize=(25, 5))
ax = sns.distplot(dataset[dataset['target'] == 1]['trestbps'], 
label='Do not have heart disease', ax = axis1)
ax.set(xlabel='People Do Not Have Heart Disease')
ax = sns.distplot(dataset[dataset['target'] == 2]['trestbps'], label = 
'Have heart disease', ax = axis2)
ax.set(xlabel='People Have Heart Disease')
plt.show()
```




```
# Get min, max and average of the  blood pressure of the people do not 
have heart diseas
```

```
print('Min blood pressure of people who do not have heart disease: ', min(dataset[dataset['target'] == 1]['trestbps']))
print('Max blood pressure of people who do not have heart disease: ', max(dataset[dataset['target'] == 1]['trestbps']))
print('Average blood pressure of people who do not have heart disease: ', dataset[dataset['target'] == 1]['trestbps'].mean())
```

```
Min blood pressure of people who do not have heart disease:  94
Max blood pressure of people who do not have heart disease:  180
Average blood pressure of people who do not have heart disease:  128.86666666666667
```

```
# Get min, max and average of the blood pressure of the people have heart diseas
print('Min blood pressure of people who have heart disease: ', min(dataset[dataset['target'] == 2]['trestbps']))
print('Max blood pressure of people who have heart disease: ', max(dataset[dataset['target'] == 2]['trestbps']))
print('Average blood pressure of people who have heart disease: ', dataset[dataset['target'] == 2]['trestbps'].mean())
```

```
Min blood pressure of people who have heart disease:  100
Max blood pressure of people who have heart disease:  200
Average blood pressure of people who have heart disease:  134.44166666666666
```

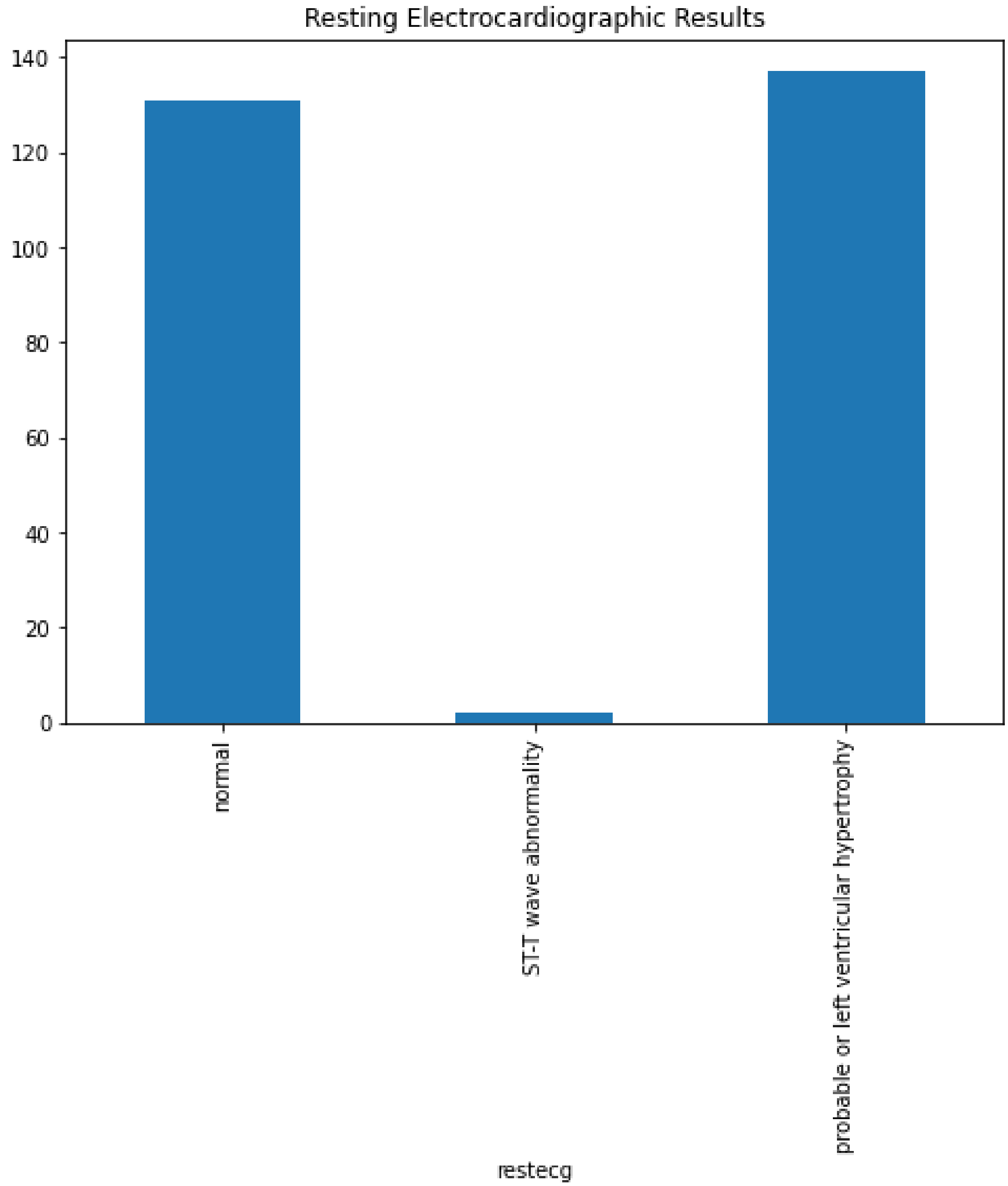
Analysing the Resting Electrocardiographic Measurement [restecg]

(0 = normal, 1 = having ST-T wave abnormality, 2 = showing probable or definite left ventricular hypertrophy by Estes' criteria)

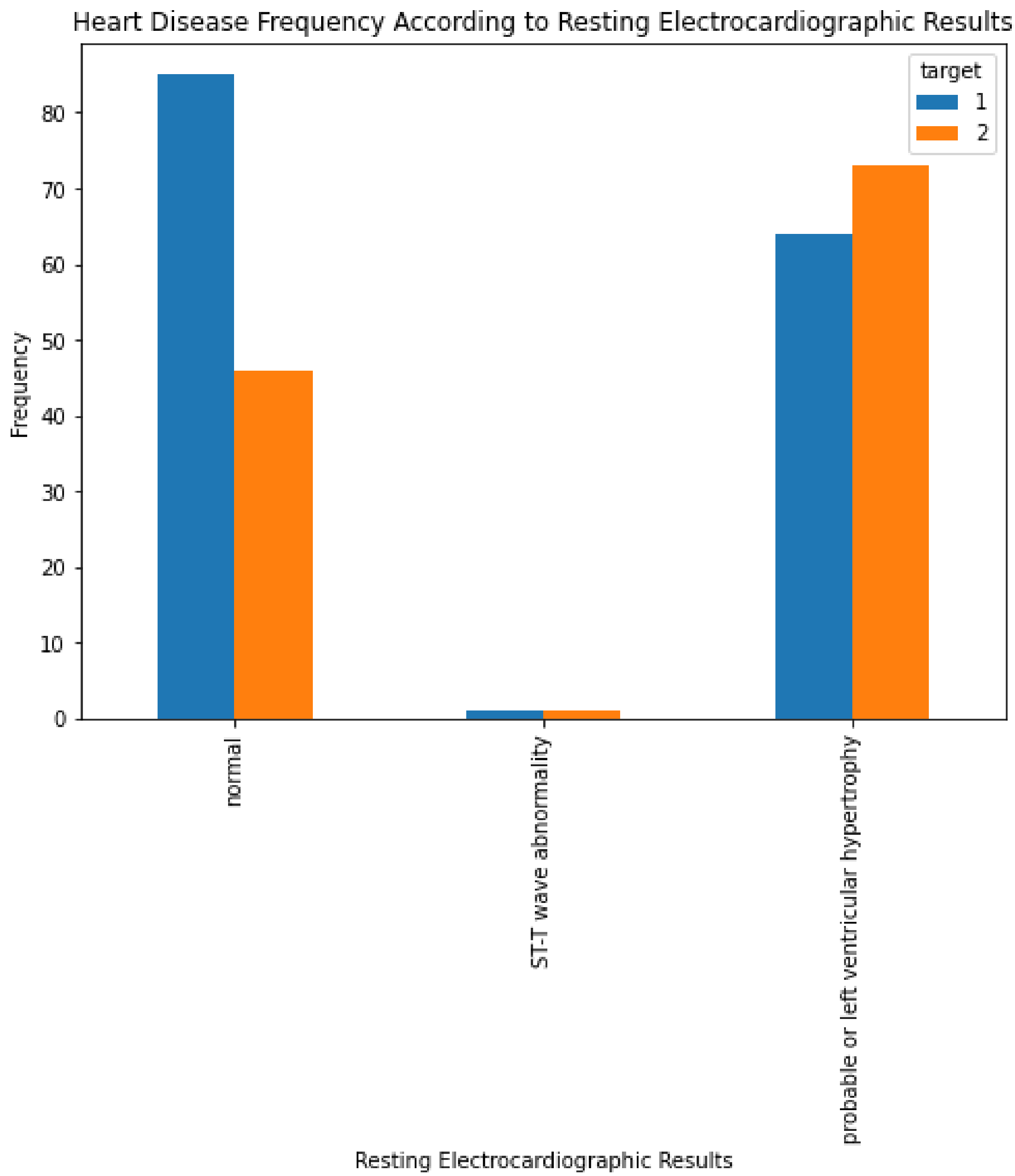
```
dataset["restecg"].unique()
```

```
array([2, 0, 1], dtype=int64)
```

```
# Display electrocardiographic results in bar chart
dataset.groupby(dataset['restecg']).count()['target'].plot(kind = 'bar', title = 'Resting Electrocardiographic Results', figsize = (8, 6))
plt.xticks(np.arange(3), ('normal', 'ST-T wave abnormality', 'probable or left ventricular hypertrophy'))
plt.show()
```




```
# Display resting electrocardiographic results based on the target
pd.crosstab(dataset.restecg,dataset.target).plot(kind = "bar", figsize
= (8, 6))
plt.title('Heart Disease Frequency According to Resting
Electrocardiographic Results')
plt.xticks(np.arange(3), ('normal', 'ST-T wave abnormality', 'probable
or left ventricular hypertrophy'))
plt.xlabel('Resting Electrocardiographic Results')
plt.ylabel('Frequency')
plt.show()
```



Usually the people who do not have heart disease have normal electrocardiographic, whereas the people who have heart disease have probable or left ventricular hypertrophy.

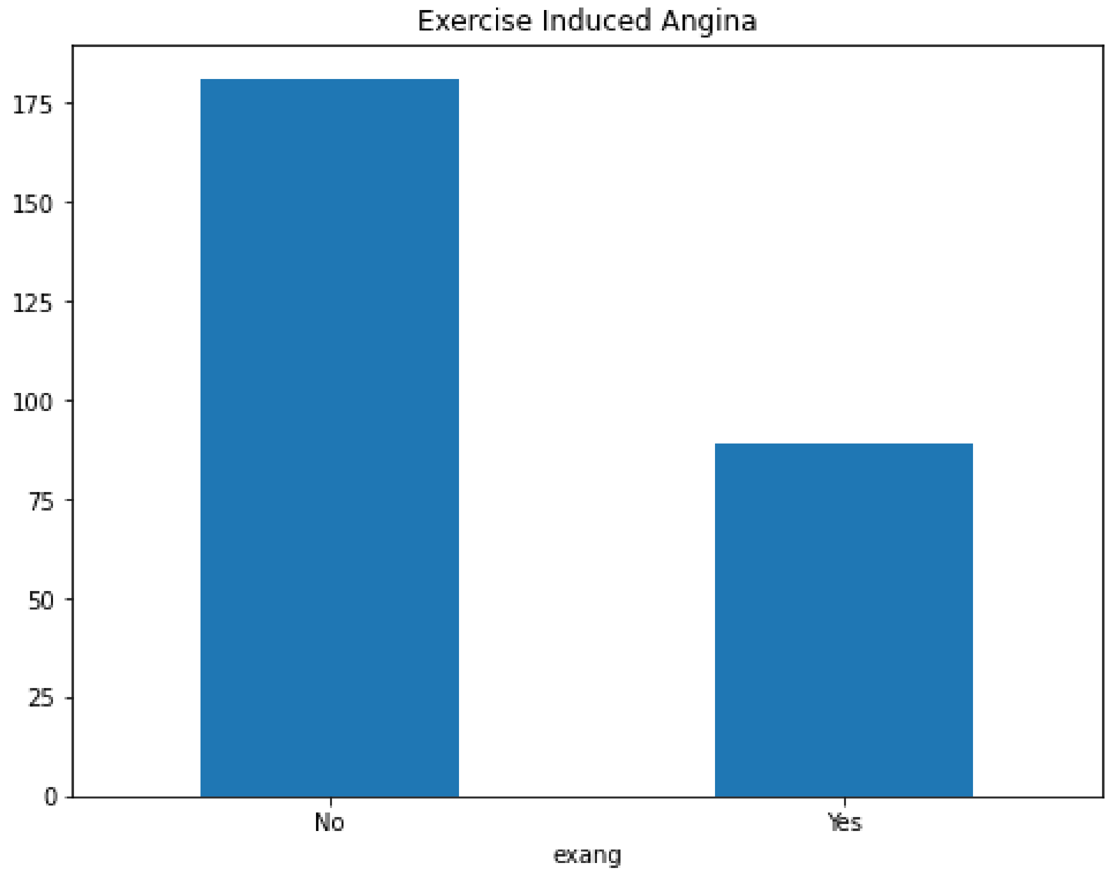
Analysing Exercise Induced Angina [exang]

(1 = yes; 0 = no)

```
dataset["exang"].unique()
```

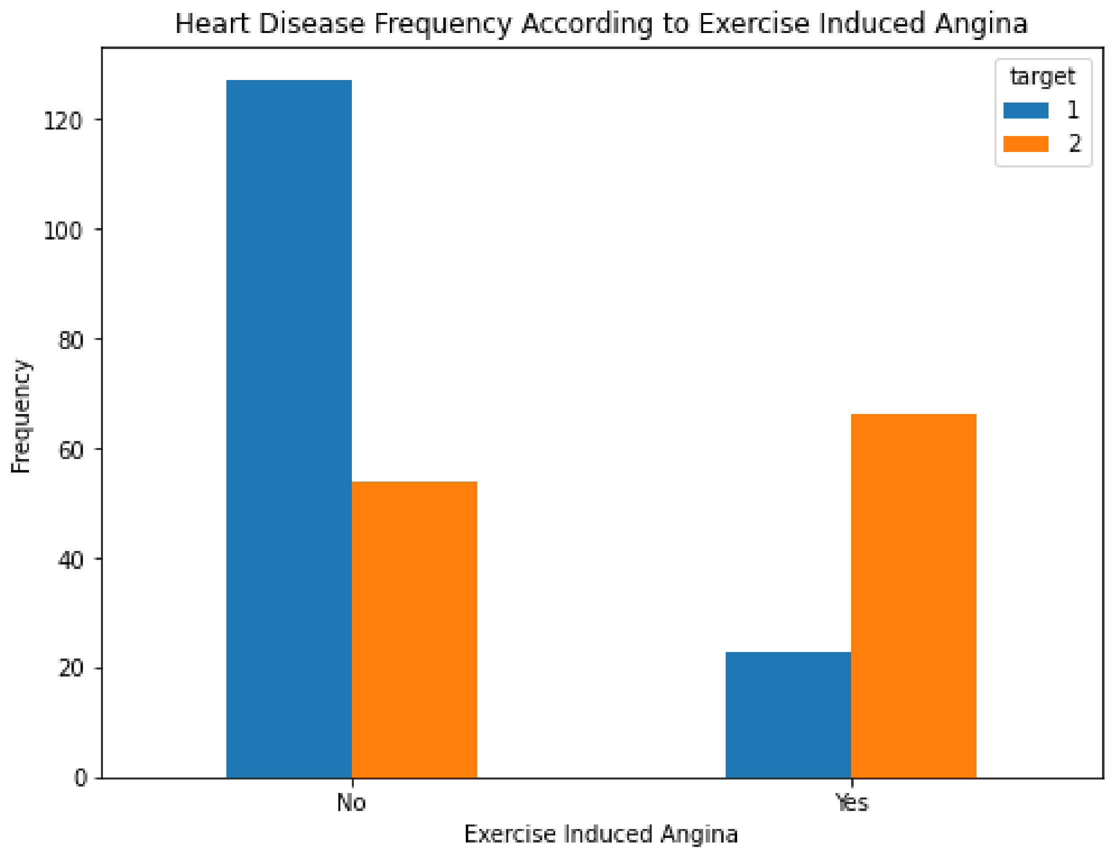
```
array([0, 1], dtype=int64)
```

```python
# Display exercise induced angina in bar chart
dataset.groupby(dataset['exang']).count()['target'].plot(kind = 'bar',
title = 'Exercise Induced Angina',  figsize = (8, 6))
plt.xticks(np.arange(2), ('No', 'Yes'), rotation = 0)
plt.show()
```



Display exercise induced angina based on the target

```python
pd.crosstab(dataset.exang,dataset.target).plot(kind = "bar", figsize =
(8, 6))
plt.title('Heart Disease Frequency According to Exercise Induced
Angina')
plt.xlabel('Exercise Induced Angina')
plt.xticks(np.arange(2), ('No', 'Yes'), rotation = 0)
plt.ylabel('Frequency')
plt.show()
```



The people who suffer from exercise induced angina are more likely to be infected with the heart disease.

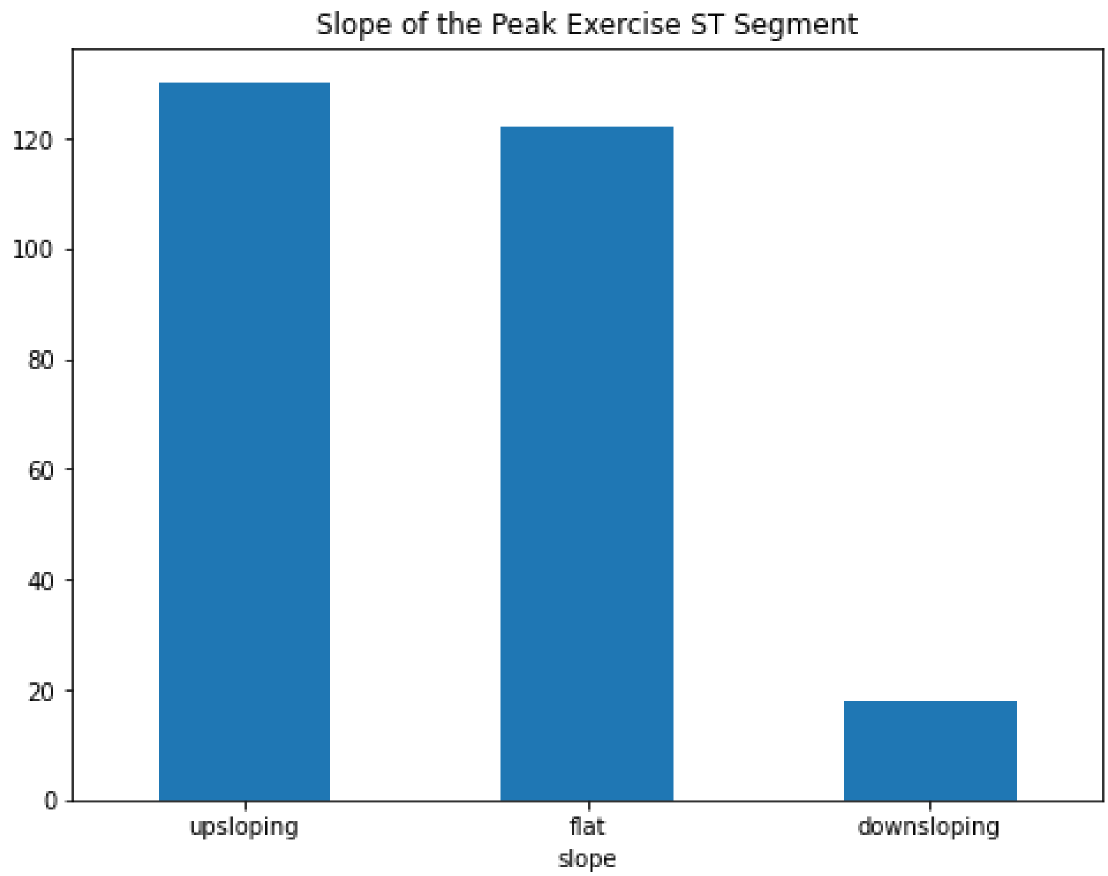
Analysing the Slope of the peak exercise ST segment [slope]

(Value 1: upsloping, Value 2: flat, Value 3: downsloping)

```
dataset["slope"].unique()
```

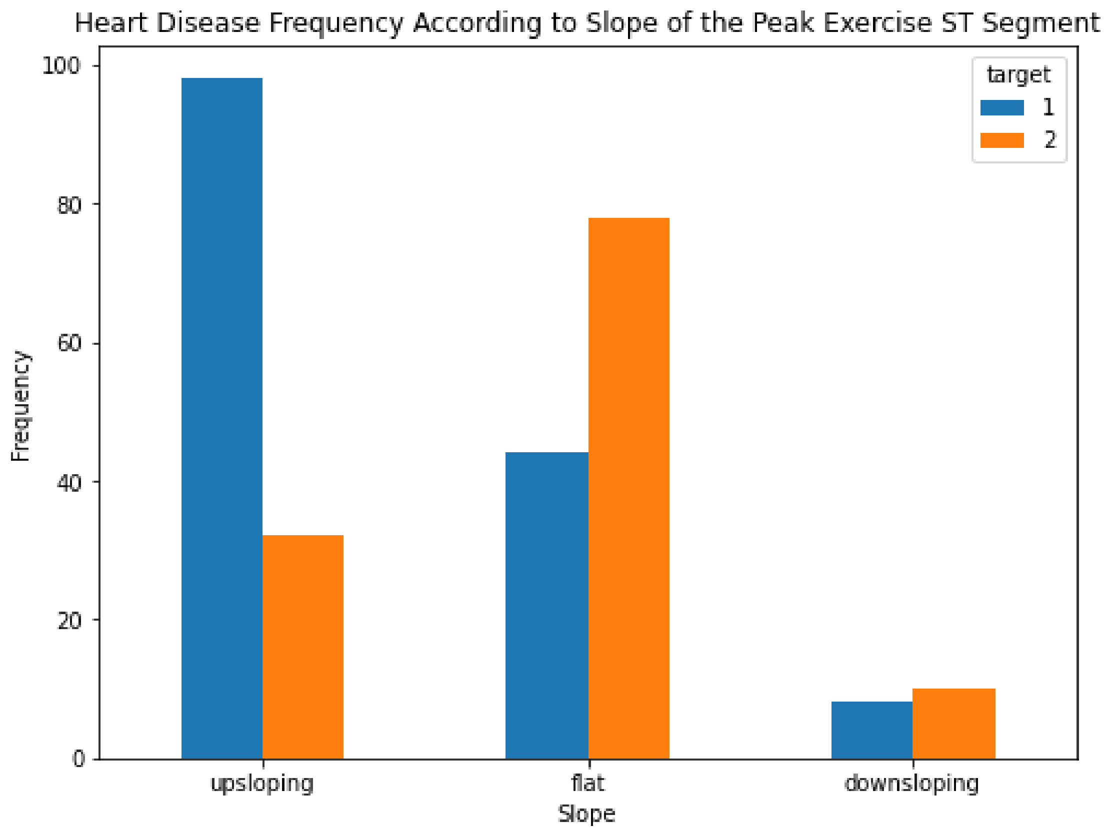
```
array([2, 1, 3], dtype=int64)
```

```
# Display slope of the peak exercise ST segment in bar chart
dataset.groupby(dataset['slope']).count()['target'].plot(kind = 'bar', title = 'Slope of the Peak Exercise ST Segment', figsize = (8, 6))
plt.xticks(np.arange(3), ('upsloping', 'flat', 'downsloping'), rotation = 0)
plt.show()
```



Display slope of the peak exercise ST segment based on the target

```
pd.crosstab(dataset.slope,dataset.target).plot(kind = "bar", figsize =
(8, 6))
plt.title('Heart Disease Frequency According to Slope of the Peak
Exercise ST Segment')
plt.xlabel('Slope')
plt.xticks(np.arange(3), ('upsloping', 'flat', 'downsloping'),
rotation = 0)
plt.ylabel('Frequency')
plt.show()
```



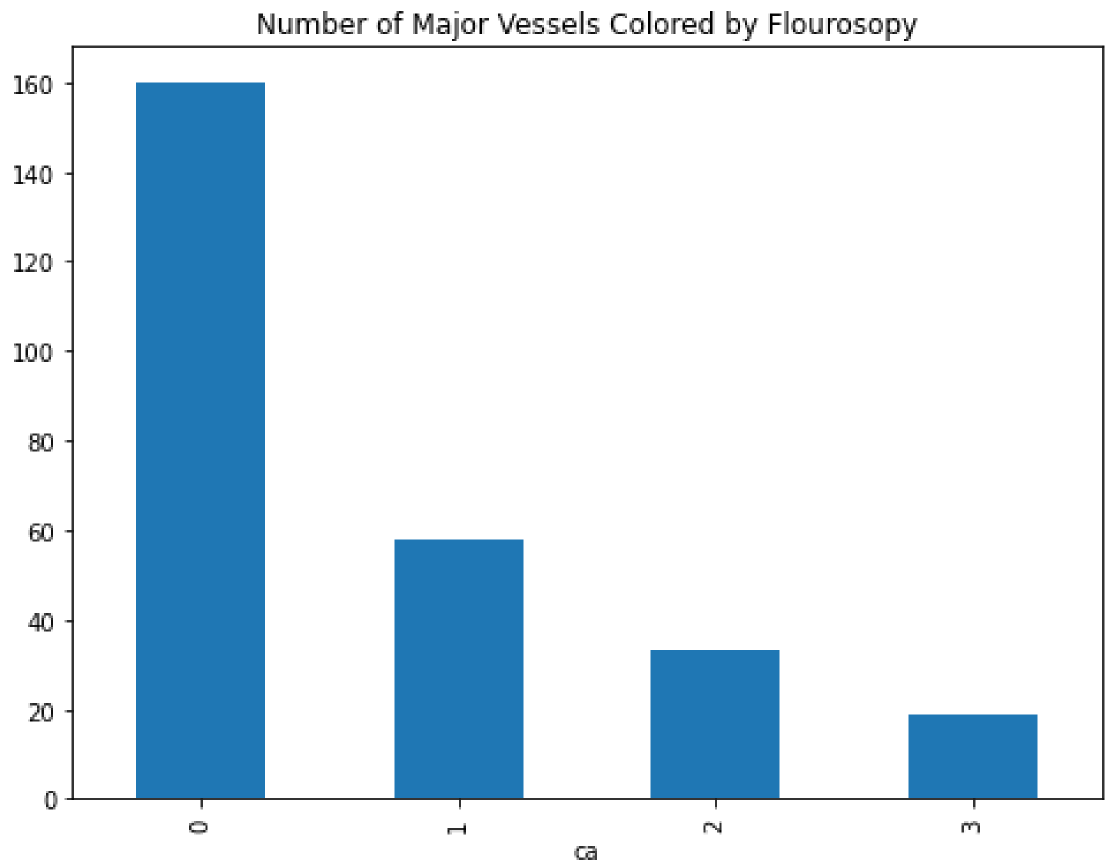
Analysing Number of Major Vessels (0-3) colored by flourosopy [ca]

```
dataset["ca"].unique()
```

```
array([3, 0, 1, 2], dtype=int64)
```

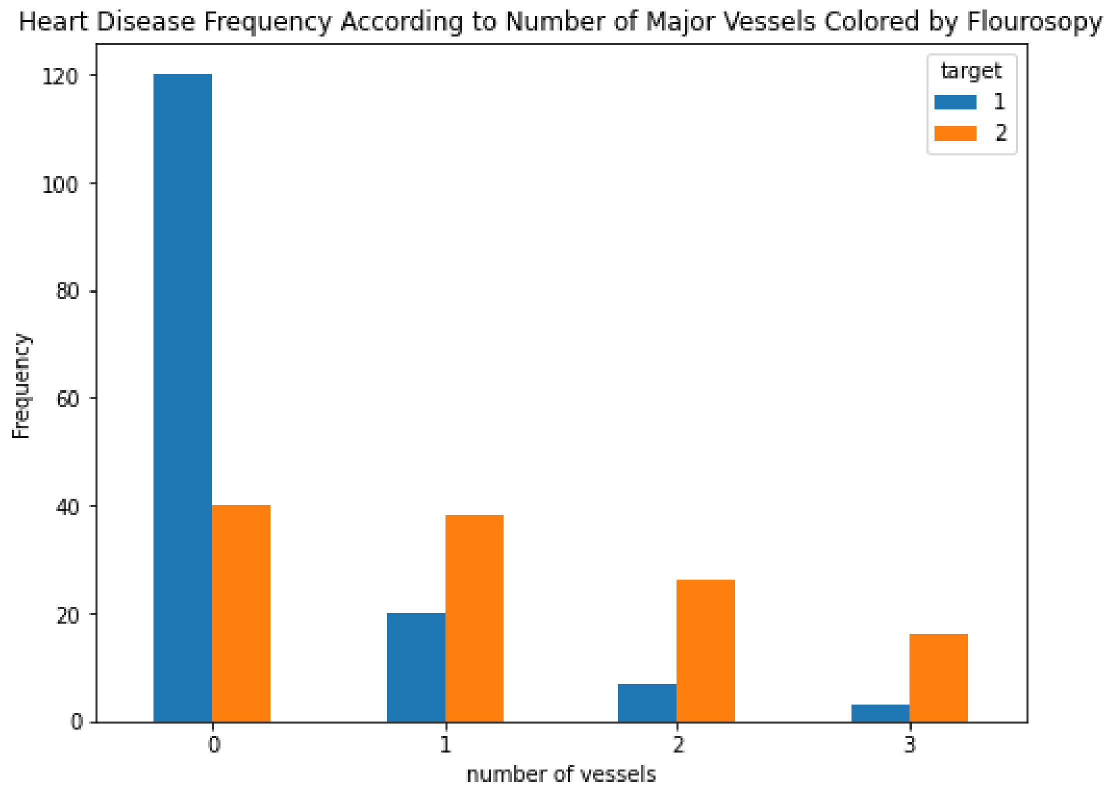
Display number of major vessels in bar chart

```
dataset.groupby(dataset['ca']).count()['target'].plot(kind = 'bar',
title = 'Number of Major Vessels Colored by Flourosopy',
                                                    figsize = (8, 6))
plt.show()
```



Display number of vessels based on the target

```
pd.crosstab(dataset.ca,dataset.target).plot(kind = "bar", figsize =
(8, 6))
plt.title('Heart Disease Frequency According to Number of Major
Vessels Colored by Flourosopy')
plt.xlabel('number of vessels')
plt.xticks(rotation = 0)
plt.ylabel('Frequency')
plt.show()
```



As it is clear, the people who do not have heart disease usually do not have major vessels colored by flourosopy.

Analysing a Blood Disorder called Thalassemia [thal]

(3 = normal ; 6 = fixed defect ; 7 = reversable defect)

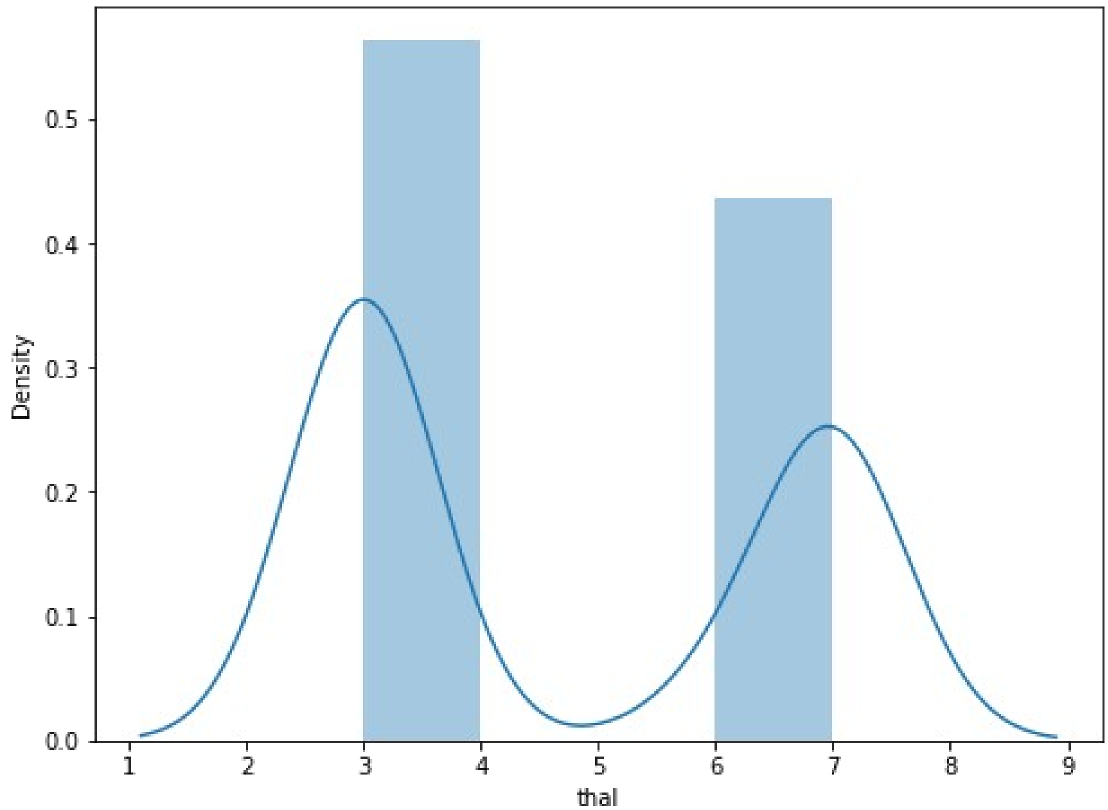
```
dataset["thal"].unique()
```

```
array([3, 7, 6], dtype=int64)
```

plotting the thalassemia distribution *(3,6,7)*

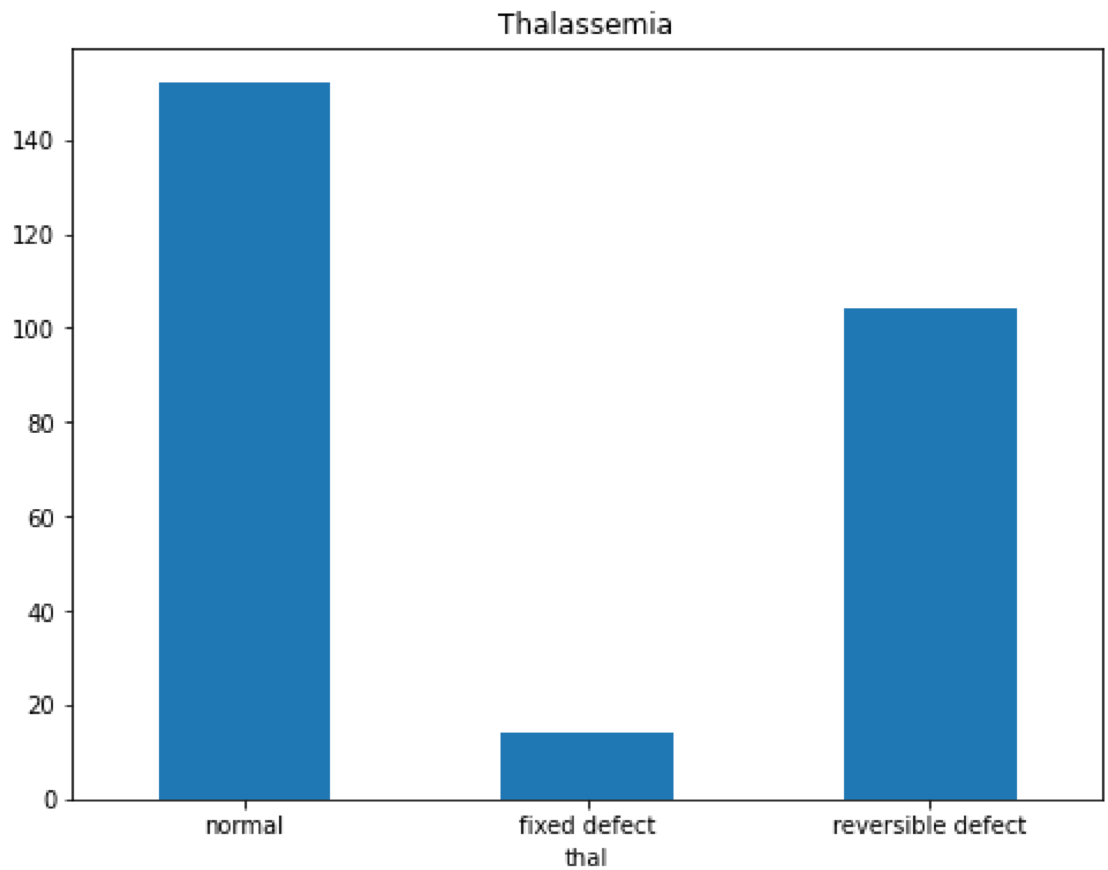
```
sns.distplot(dataset["thal"])
```

```
<AxesSubplot:xlabel='thal', ylabel='Density'>
```



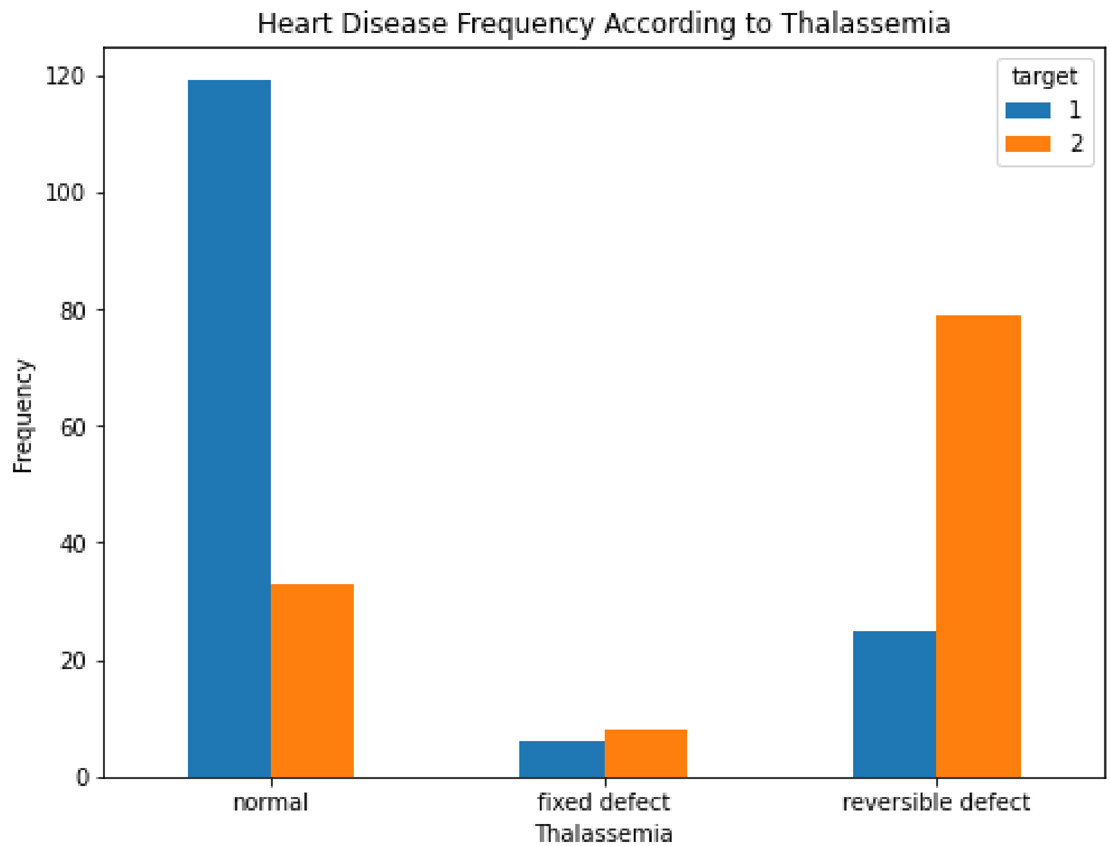
Display thalassemia in bar chart

```
dataset.groupby(dataset['thal']).count()['target'].plot(kind = 'bar',
title = 'Thalassemia')
plt.xticks(np.arange(3), ('normal', 'fixed defect', 'reversible
defect'), rotation = 0)
plt.show()
```



Thalassemia compared with target

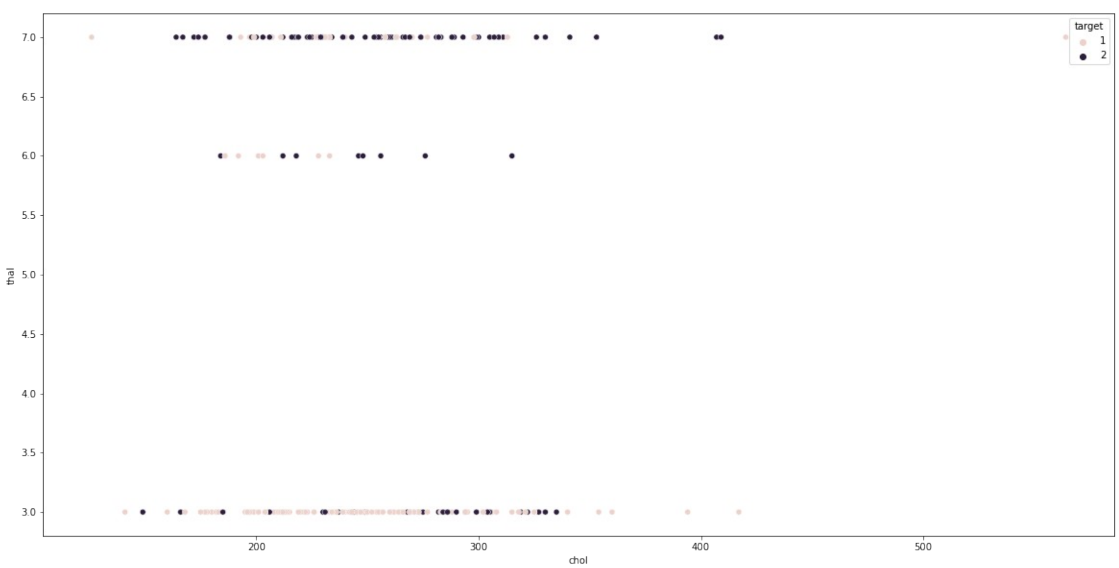
```
pd.crosstab(dataset.thal,dataset.target).plot(kind = "bar", figsize =
(8, 6))
plt.title('Heart Disease Frequency According to Thalassemia')
plt.xlabel('Thalassemia')
plt.xticks(np.arange(3), ('normal', 'fixed defect', 'reversible
defect'), rotation = 0)
plt.ylabel('Frequency')
plt.show()
```



As it is clear, the people with reversible defect are likely to have heart disease.

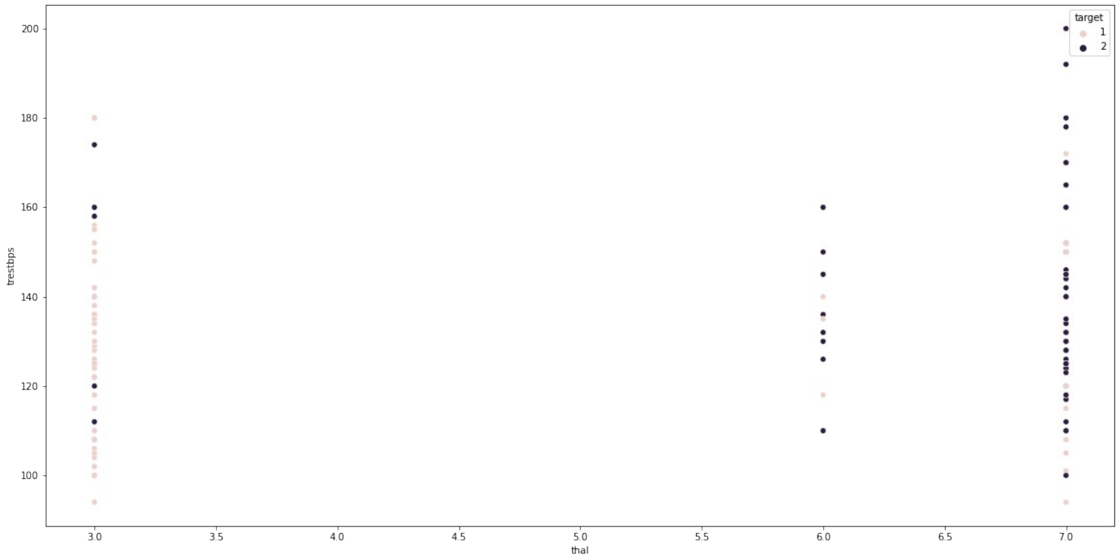
Thalassemia vs Cholesterol Scatterplot

```
plt.figure(figsize=(20,10))
sns.scatterplot(x='chol',y='thal',data=dataset,hue='target')
plt.show()
```



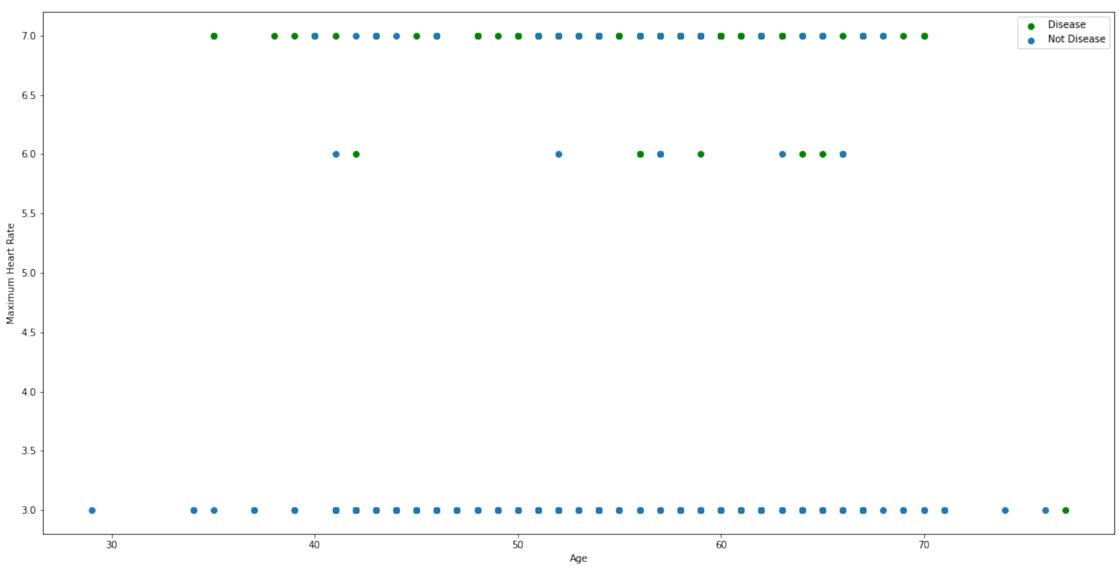
Thalassemia vs Resting blood pressure Scatterplot

```
plt.figure(figsize=(20,10))
sns.scatterplot(x='thal',y='trestbps',data=dataset,hue='target')
plt.show()
```



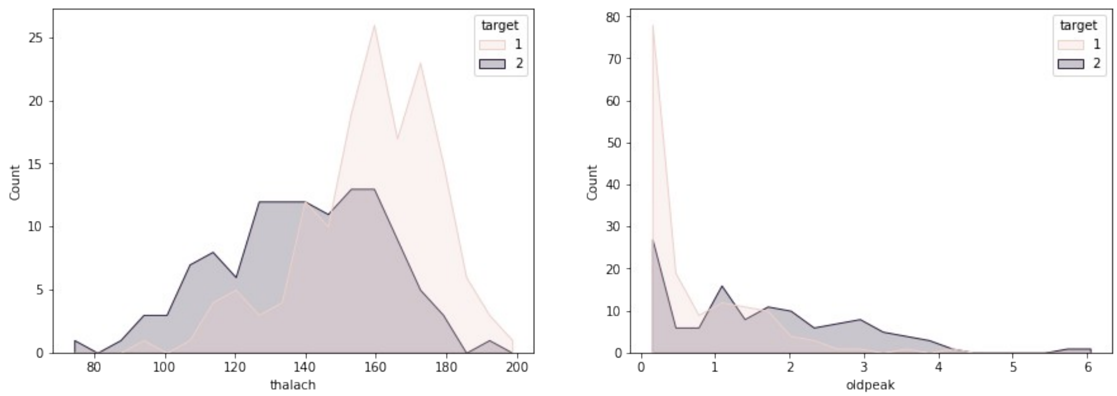
Thalassemia vs Age Scatterplot

```
plt.figure(figsize=(20, 10))
plt.scatter(x=dataset.age[dataset.target==2],
y=dataset.thal[(dataset.target==2)], c="green")
plt.scatter(x=dataset.age[dataset.target==1],
y=dataset.thal[(dataset.target==1)])
plt.legend(["Disease", "Not Disease"])
plt.xlabel("Age")
plt.ylabel("Maximum Heart Rate")
plt.show()
```



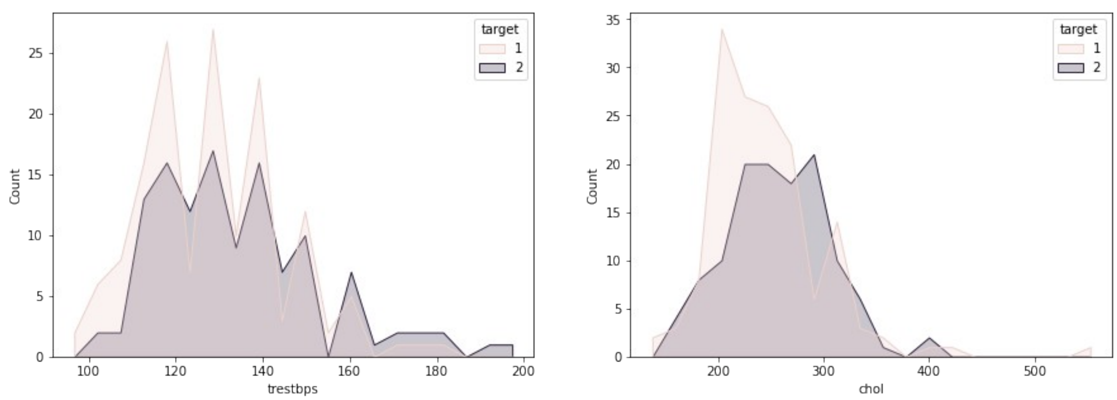
Maximum Heart Rate vs Oldpeak(Exercise induced ST-depression in comparison with the state of rest)

```
plt.figure(figsize=(15,5))
plt.subplot(1,2,1)
sns.histplot(data=dataset,hue='target',x='thalach',bins=20,element='po
ly')
plt.subplot(1,2,2)
sns.histplot(data=dataset,hue='target',x='oldpeak',bins=20,element='po
ly')
plt.savefig("Thalach&oldpeak_Histplot.png")
```



Resting Blood Pressure vs Cholestrol

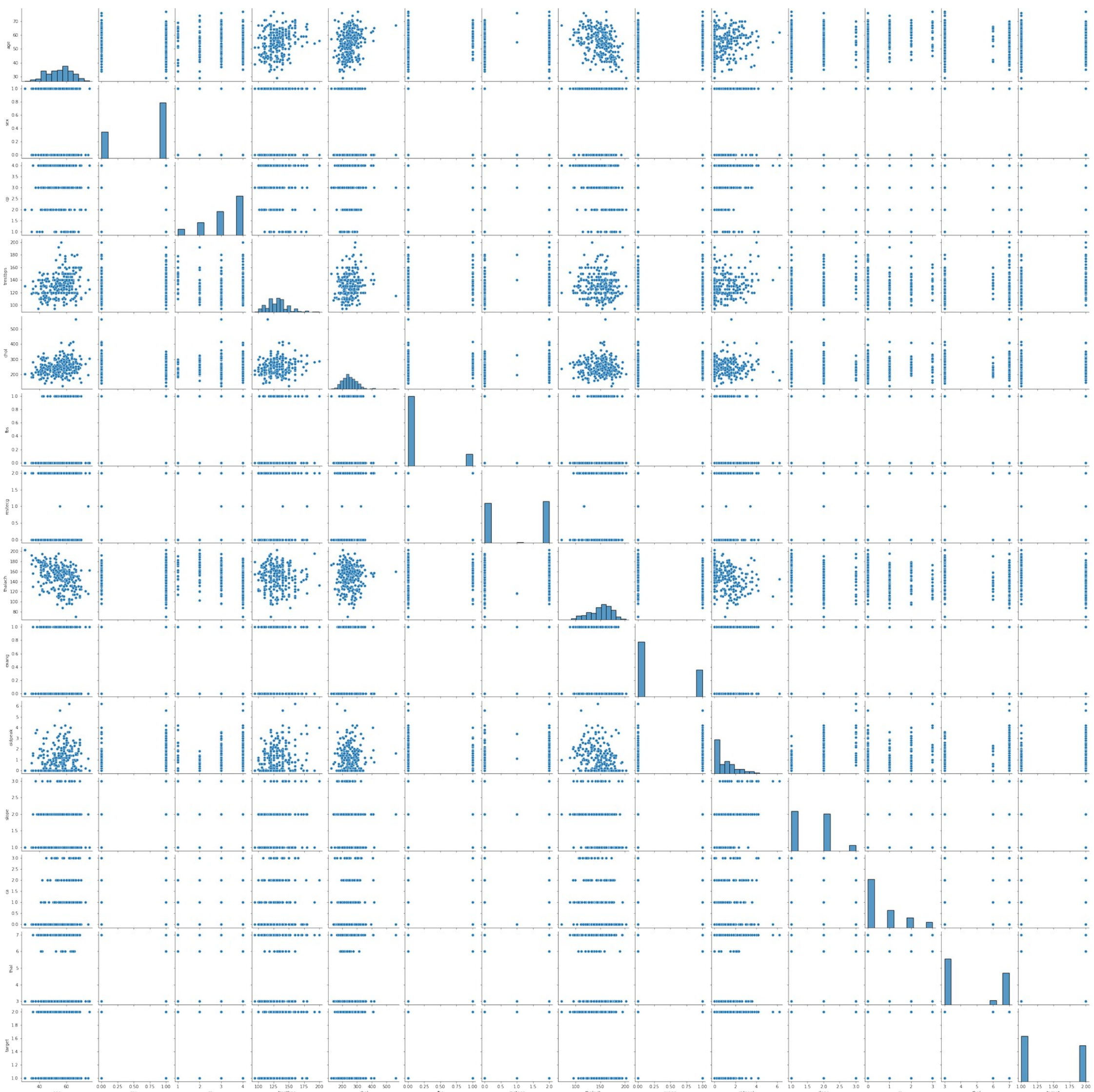
```
plt.figure(figsize=(15,5))
plt.subplot(1,2,1)
sns.histplot(data=dataset,hue='target',x='trestbps',bins=20,element='p
oly')
plt.subplot(1,2,2)
sns.histplot(data=dataset,hue='target',x='chol',bins=20,element='poly'
)
plt.savefig("Resting_blood_pressure&chol_Histplot.png")
```



Pair Plots

```
sns.pairplot(data=dataset)
```

```
<seaborn.axisgrid.PairGrid at 0x17e93d63730>
```

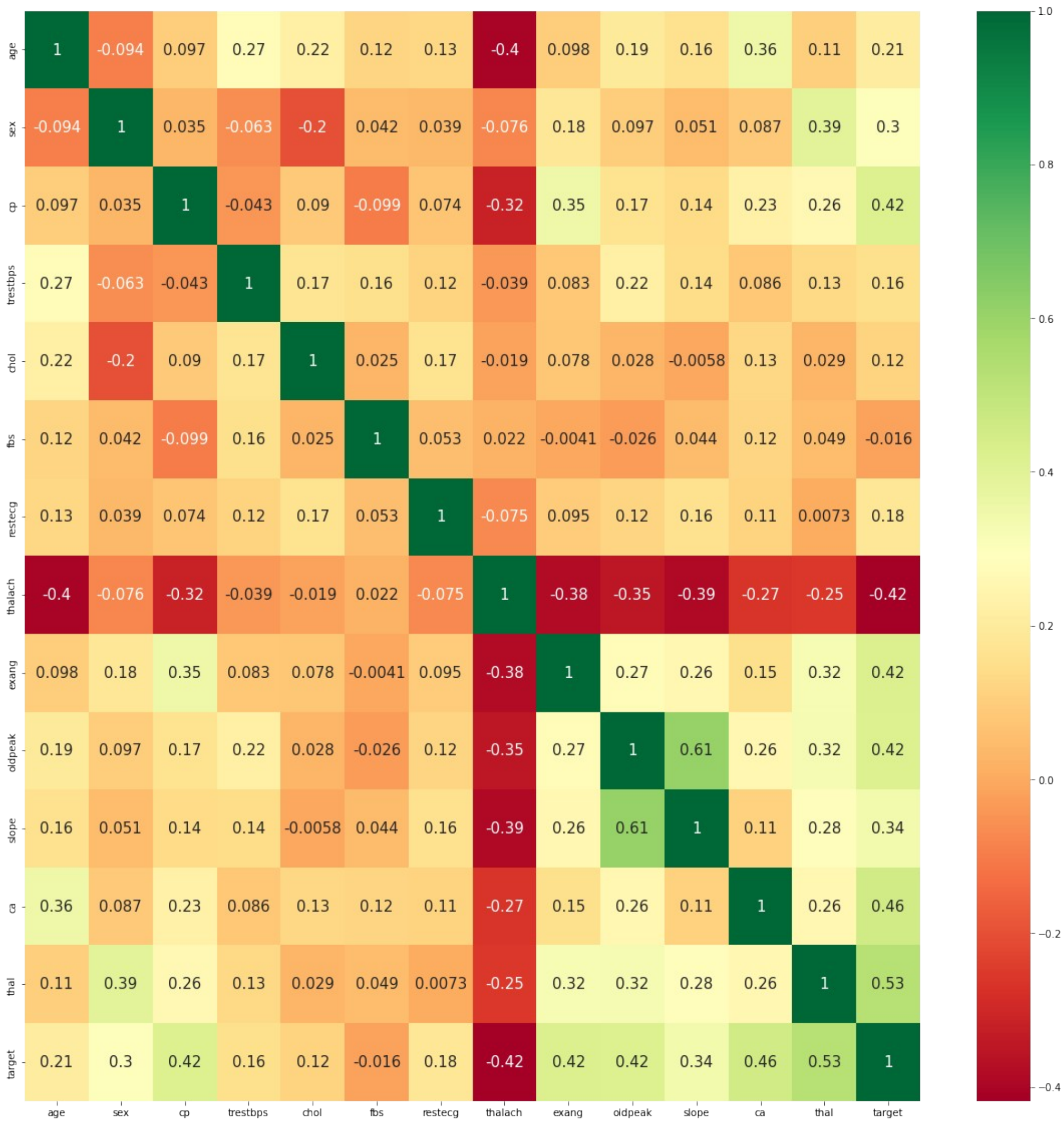


Correlation Matrix

The best way to compare relationship between various features is to look at the correlation matrix between those features.

```
corr_matrix = dataset.corr()
top_corr_feature = corr_matrix.index
plt.figure(figsize=(20, 20))
sns.heatmap(dataset[top_corr_feature].corr(), annot=True,
cmap="RdYlGn", annot_kws={"size":15})
```

```
<AxesSubplot:>
```



Taking a look at the correlation matrix above, it's easy to see that a few features have negative correlation with the target value while some have positive.

Data Processing

After exploring the dataset, we observed that we need to convert some categorical variables into dummy variables and scale all the values before training the Machine Learning models. First, we'll use the `get_dummies` method to create dummy columns for categorical variables.

```
dataset = pd.get_dummies(dataset, columns = ['sex', 'cp', 'fbs',
'restecg', 'exang', 'slope', 'ca', 'thal'])
```

Now, we will use the `StandardScaler` from `sklearn` to scale my dataset.

```
standardScaler = StandardScaler()
columns_to_scale = ['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
dataset[columns_to_scale] =
standardScaler.fit_transform(dataset[columns_to_scale])

dataset.head()

        age  trestbps      chol   thalach   oldpeak  target  sex_0
sex_1  \
0  1.712094 -0.075410  1.402212 -1.759208  1.181012       2      0
1
1  1.382140 -0.916759  6.093004  0.446409  0.481153       1      1
0
2  0.282294 -0.411950  0.219823 -0.375291 -0.656118       2      0
1
3  1.052186 -0.187590  0.258589 -1.932198 -0.743600       1      0
1
4  2.152032 -0.636310  0.374890 -1.240239 -0.743600       1      1
0

   cp_1  cp_2  ...  slope_1  slope_2  slope_3  ca_0  ca_1  ca_2  ca_3
thal_3  \
0     0     0  ...        0        1        0     0     0     0     1
1
1     0     0  ...        0        1        0     1     0     0     0
0
2     0     1  ...        1        0        0     1     0     0     0
0
3     0     0  ...        0        1        0     0     1     0     0
0
4     0     1  ...        1        0        0     0     1     0     0
1

   thal_6  thal_7
0       0       0
1       0       1
2       0       1
3       0       1
4       0       0

[5 rows x 29 columns]

dataset.describe()

                age      trestbps          chol       thalach
oldpeak  \
count  2.700000e+02  2.700000e+02  2.700000e+02  2.700000e+02
2.700000e+02
mean   3.667848e-16  5.723816e-16 -2.343804e-16 -1.266477e-16
4.111937e-17
std    1.001857e+00  1.001857e+00  1.001857e+00  1.001857e+00
```

```
1.001857e+00
min   -2.797275e+00 -2.094649e+00 -2.396942e+00 -3.402609e+00 -
9.185652e-01
25%   -7.075676e-01 -6.363095e-01 -7.105825e-01 -7.212705e-01 -
9.185652e-01
50%    6.232461e-02 -7.540984e-02 -9.031247e-02  1.653012e-01 -
2.187060e-01
75%    7.222322e-01  4.854898e-01  5.881079e-01  7.058937e-01
4.811532e-01
max    2.481986e+00  3.850888e+00  6.093004e+00  2.262800e+00
4.505343e+00

           target       sex_0       sex_1        cp_1        cp_2  ...
\
count  270.000000  270.000000  270.000000  270.000000  270.000000  ...

mean     1.444444    0.322222    0.677778    0.074074    0.155556  ...

std      0.497827    0.468195    0.468195    0.262378    0.363107  ...

min      1.000000    0.000000    0.000000    0.000000    0.000000  ...

25%      1.000000    0.000000    0.000000    0.000000    0.000000  ...

50%      1.000000    0.000000    1.000000    0.000000    0.000000  ...

75%      2.000000    1.000000    1.000000    0.000000    0.000000  ...

max      2.000000    1.000000    1.000000    1.000000    1.000000  ...


          slope_1     slope_2     slope_3        ca_0        ca_1
ca_2  \
count  270.000000  270.000000  270.000000  270.000000  270.000000
270.000000
mean     0.481481    0.451852    0.066667    0.592593    0.214815
0.122222
std      0.500585    0.498601    0.249907    0.492264    0.411456
0.328151
min      0.000000    0.000000    0.000000    0.000000    0.000000
0.000000
25%      0.000000    0.000000    0.000000    0.000000    0.000000
0.000000
50%      0.000000    0.000000    0.000000    1.000000    0.000000
0.000000
75%      1.000000    1.000000    0.000000    1.000000    0.000000
0.000000
max      1.000000    1.000000    1.000000    1.000000    1.000000
1.000000
```

```
          ca_3      thal_3      thal_6      thal_7
count  270.000000  270.000000  270.000000  270.000000
mean     0.070370    0.562963    0.051852    0.385185
std      0.256245    0.496941    0.222140    0.487543
min      0.000000    0.000000    0.000000    0.000000
25%      0.000000    0.000000    0.000000    0.000000
50%      0.000000    1.000000    0.000000    0.000000
75%      0.000000    1.000000    0.000000    1.000000
max      1.000000    1.000000    1.000000    1.000000

[8 rows x 29 columns]
```

Train Test Split

We'll now import train_test_split to split our dataset into training and testing datasets. Then, we'll import all Machine Learning models we'll be using to train and test the data.

```
Y = dataset['target'].values
X = dataset.drop('target',axis=1).values
```

```
X.shape
```

```
(270, 28)
```

```
Y.shape
```

```
(270,)
```

```
# Split the dataset into training and testing.
X_train, X_test, Y_train, Y_test = train_test_split(X, Y,
test_size=0.2, random_state=0)
print("Training features have {0} records and Testing features have
{1} records.".\
      format(X_train.shape[0], X_test.shape[0]))
```

```
Training features have 216 records and Testing features have 54
records.
```

Checking distribution of traget variable in train test split

```
print('--------------Training Set----------------')
print(X_train.shape)
print(Y_train.shape)
print('----------------Test Set------------------')
print(X_test.shape)
print(Y_test.shape)
```

```
--------------Training Set----------------
(216, 28)
(216,)
----------------Test Set------------------
```

```
(54, 28)
(54,)
```

Machine Learning Model

1. Random Forest Classifier

Now, we'll use the ensemble method, Random Forest Classifier, to create the model and vary the number of estimators to see their effect.

```
max_accuracy = 0

for x in range(500):
    rf_classifier = RandomForestClassifier(random_state=x)
    rf_classifier.fit(X_train,Y_train)
    Y_pred_rf = rf_classifier.predict(X_test)
    current_accuracy = round(accuracy_score(Y_pred_rf,Y_test)*100,2)
    if(current_accuracy>max_accuracy):
        max_accuracy = current_accuracy
        best_x = x

print(max_accuracy)
print(best_x)
```

```
85.19
192
```

```
rf_classifier = RandomForestClassifier(random_state=best_x)
rf_classifier.fit(X_train,Y_train)
Y_pred_rf = rf_classifier.predict(X_test)
Y_pred_rf.shape
```

```
(54,)
```

```
score_rf = round(accuracy_score(Y_pred_rf,Y_test)*100,2)
score_rf
```

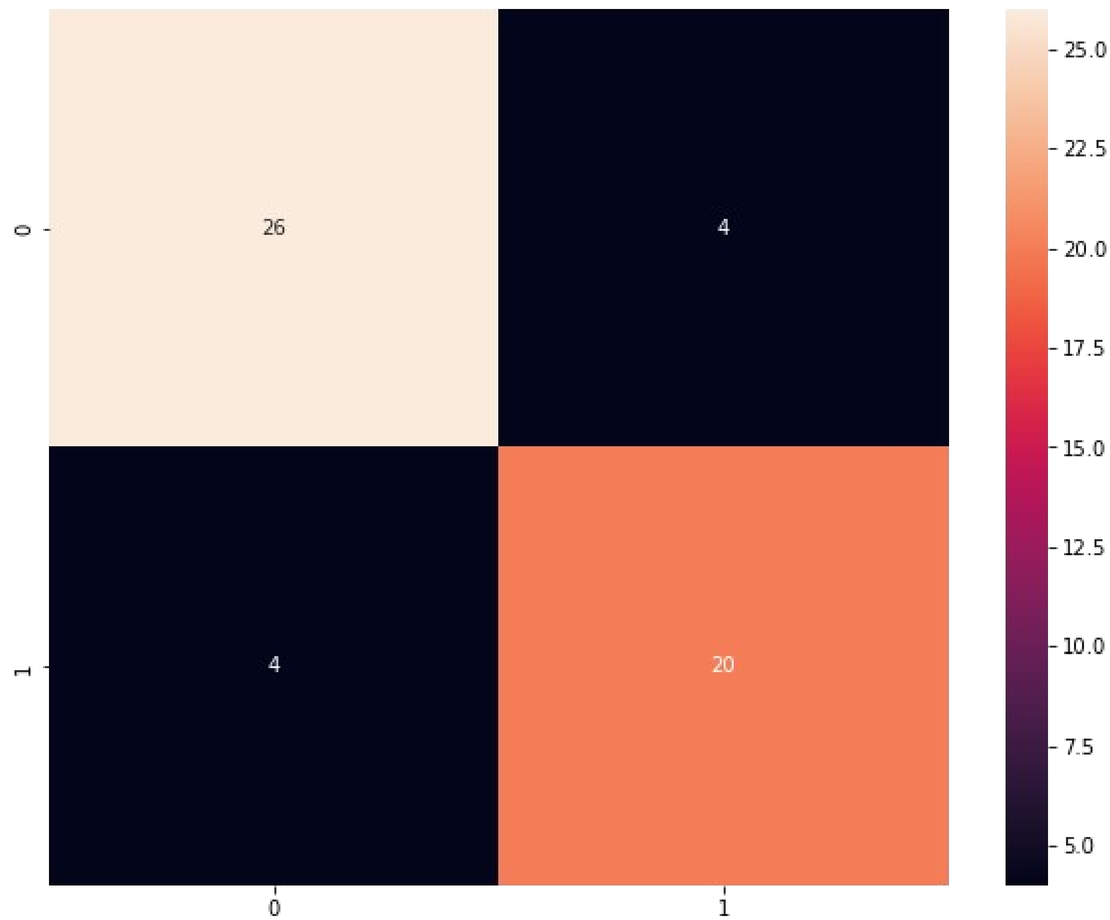
```
85.19
```

Model Evaluation:

```
y_pred_rfe = rf_classifier.predict(X_test)

plt.figure(figsize=(10, 8))
CM=confusion_matrix(Y_test,y_pred_rfe)
sns.heatmap(CM, annot=True)

TN = CM[0][0]
FN = CM[1][0]
TP = CM[1][1]
FP = CM[0][1]
```

```
specificity = TN/(TN+FP)
loss_log = log_loss(Y_test, y_pred_rfe)
acc= accuracy_score(Y_test, y_pred_rfe)
roc=roc_auc_score(Y_test, y_pred_rfe)
prec = precision_score(Y_test, y_pred_rfe)
rec = recall_score(Y_test, y_pred_rfe)
f1 = f1_score(Y_test, y_pred_rfe)

mathew = matthews_corrcoef(Y_test, y_pred_rfe)
model_results =pd.DataFrame([['Random Forest',acc,
prec,rec,specificity, f1,roc, loss_log,mathew]],
               columns = ['Model', 'Accuracy','Precision',
'Sensitivity','Specificity', 'F1
Score','ROC','Log_Loss','mathew_corrcoef'])

model_results
```

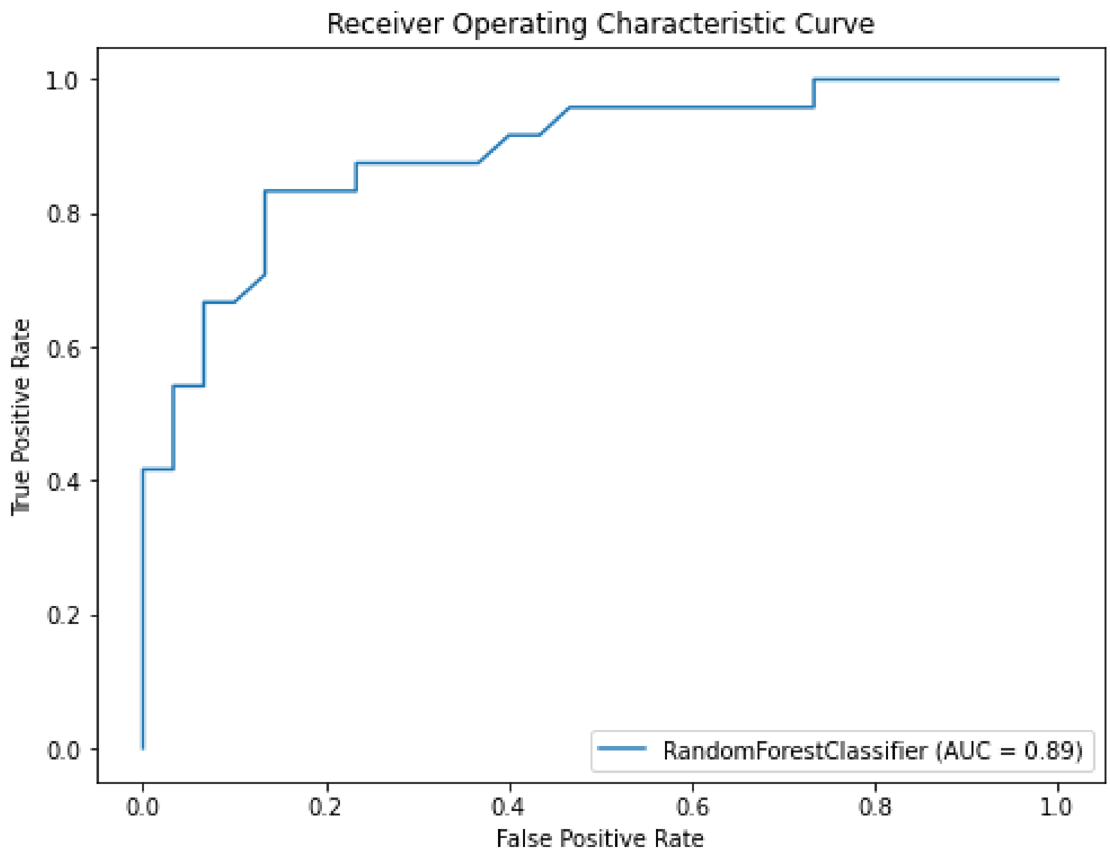
```
           Model  Accuracy  Precision  Sensitivity  Specificity  F1
Score  \
0  Random Forest  0.851852   0.866667     0.866667     0.866667
0.866667

    ROC   Log_Loss  mathew_corrcoef
0  0.85  19.188653              0.7
```




```
Y_pred_rf = np.around(Y_pred_rf)
print(metrics.classification_report(Y_test,Y_pred_rf))
```

```
              precision    recall  f1-score   support

           1       0.87      0.87      0.87        30
           2       0.83      0.83      0.83        24

    accuracy                           0.85        54
   macro avg       0.85      0.85      0.85        54
weighted avg       0.85      0.85      0.85        54
```

```
plot_roc_curve(rf_classifier,X_test,Y_test)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic Curve');
plt.savefig("RF.png")
```



2. K-Nearest Neighbors Classifier

The classification score varies based on different values of neighbors that we choose. Thus, we'll plot a score graph for different values of K (neighbors) and check when do we achieve the best score.

```
knn_classifier= KNeighborsClassifier(n_neighbors=31,leaf_size=30)
knn_classifier.fit(X_train,Y_train)
Y_pred_knn = knn_classifier.predict(X_test)
score_knn = round(accuracy_score(Y_pred_knn,Y_test)*100,2)
score_knn
```

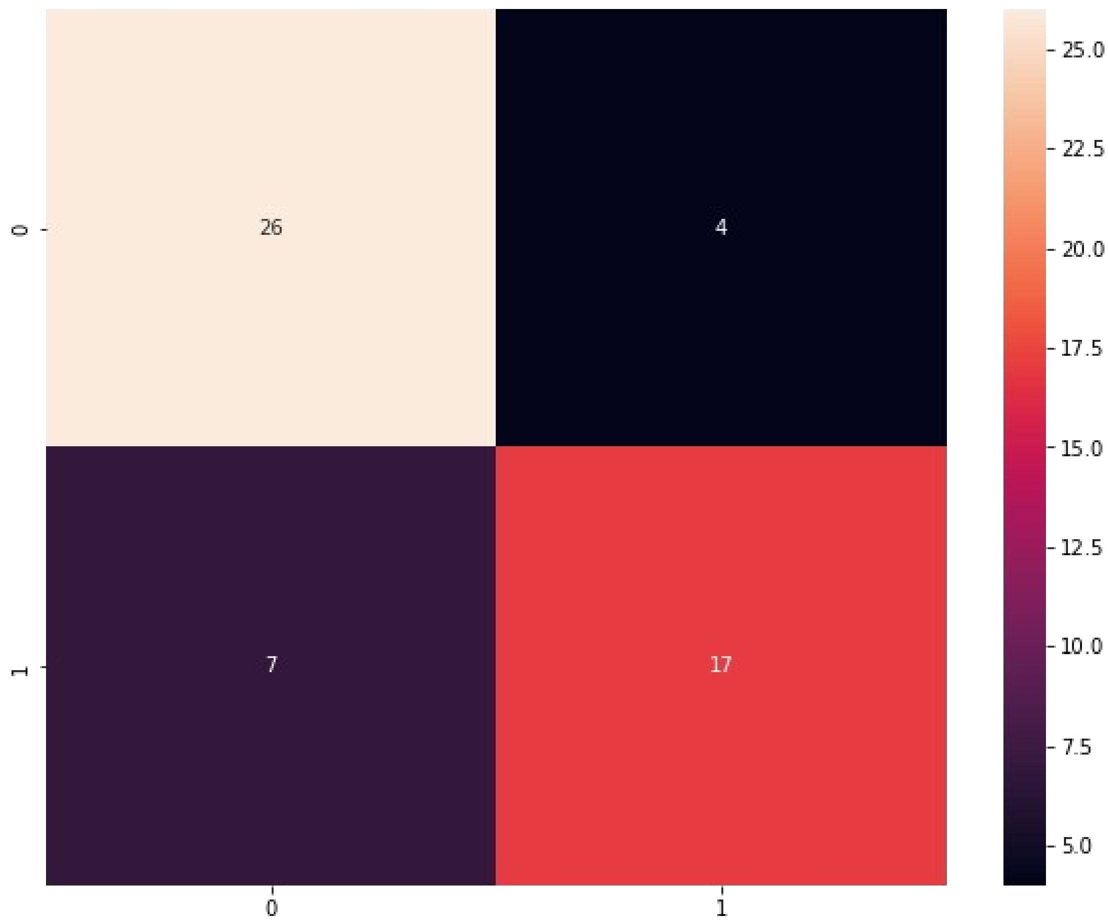
```
79.63
```

Model Evaluation:

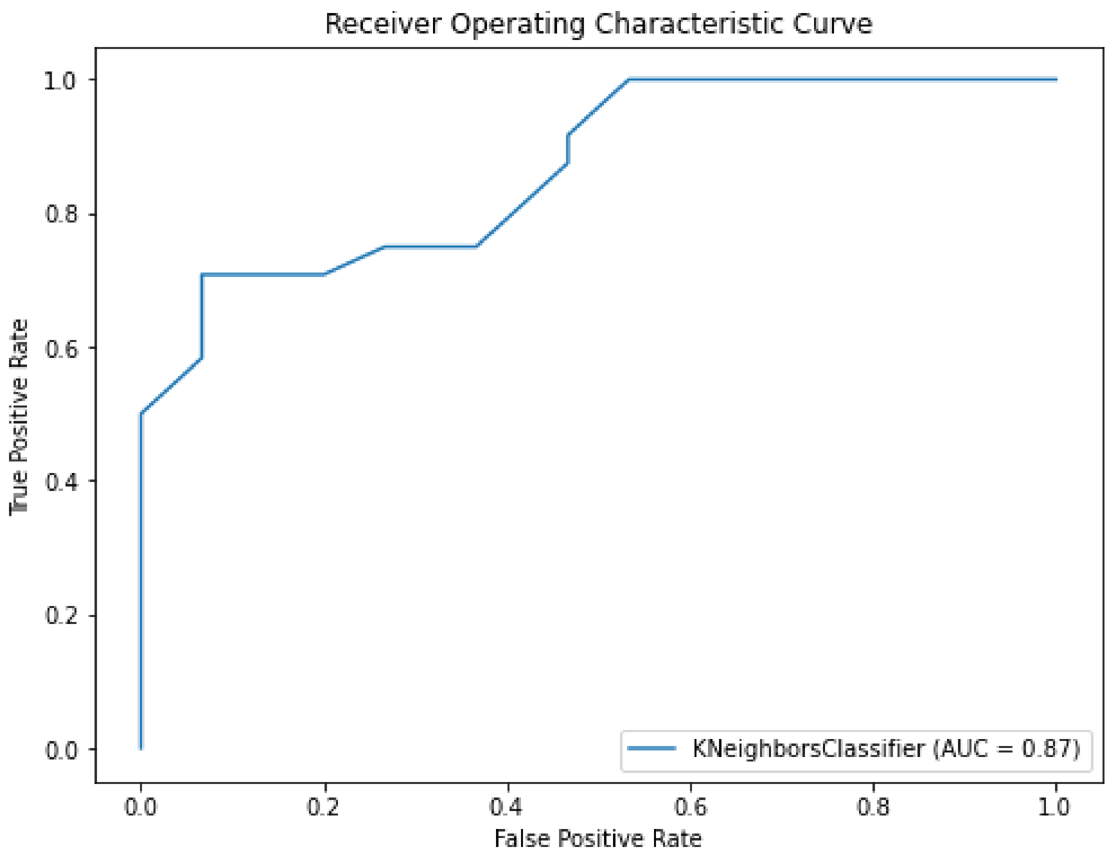
```
y_pred_knne = knn_classifier.predict(X_test)

plt.figure(figsize=(10, 8))
CM=confusion_matrix(Y_test,y_pred_knne)
sns.heatmap(CM, annot=True)

TN = CM[0][0]
FN = CM[1][0]
TP = CM[1][1]
```

```python
FP = CM[0][1]
specificity = TN/(TN+FP)
loss_log = log_loss(Y_test, y_pred_knne)
acc= accuracy_score(Y_test, y_pred_knne)
roc=roc_auc_score(Y_test, y_pred_knne)
prec = precision_score(Y_test, y_pred_knne)
rec = recall_score(Y_test, y_pred_knne)
f1 = f1_score(Y_test, y_pred_knne)

mathew = matthews_corrcoef(Y_test, y_pred_knne)
model_results =pd.DataFrame([['K-Nearest Neighbors ',acc,
prec,rec,specificity, f1,roc, loss_log,mathew]],
               columns = ['Model', 'Accuracy','Precision',
'Sensitivity','Specificity', 'F1
Score','ROC','Log_Loss','mathew_corrcoef'])

model_results
```

```
                  Model  Accuracy  Precision  Sensitivity  Specificity  \
0  K-Nearest Neighbors   0.796296   0.787879     0.866667     0.866667


   F1 Score     ROC   Log_Loss  mathew_corrcoef
0  0.825397  0.7875  19.188653         0.586094
```




```
Y_pred_knn = np.around(Y_pred_knn)
print(metrics.classification_report(Y_test,Y_pred_knn))

              precision    recall  f1-score   support

           1       0.79      0.87      0.83        30
           2       0.81      0.71      0.76        24

    accuracy                           0.80        54
   macro avg       0.80      0.79      0.79        54
weighted avg       0.80      0.80      0.79        54


plot_roc_curve(knn_classifier,X_test,Y_test)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic Curve');
plt.savefig("KNN.png")
```



3. Decision Tree Classifier

Here, we'll use the Decision Tree Classifier to model the problem at hand. We'll vary between a set of `max_features` and see which returns the best accuracy.

```
dt_classifier = DecisionTreeClassifier(
    max_depth=20,
    min_samples_split=2,
    min_samples_leaf=1,
    min_weight_fraction_leaf=0.00001,
    max_features='auto',
    random_state=46)
dt_classifier.fit(X_train, Y_train)
Y_pred_dt=dt_classifier.predict(X_test)
score_dt = round(accuracy_score(Y_pred_dt,Y_test)*100,2)
score_dt
```

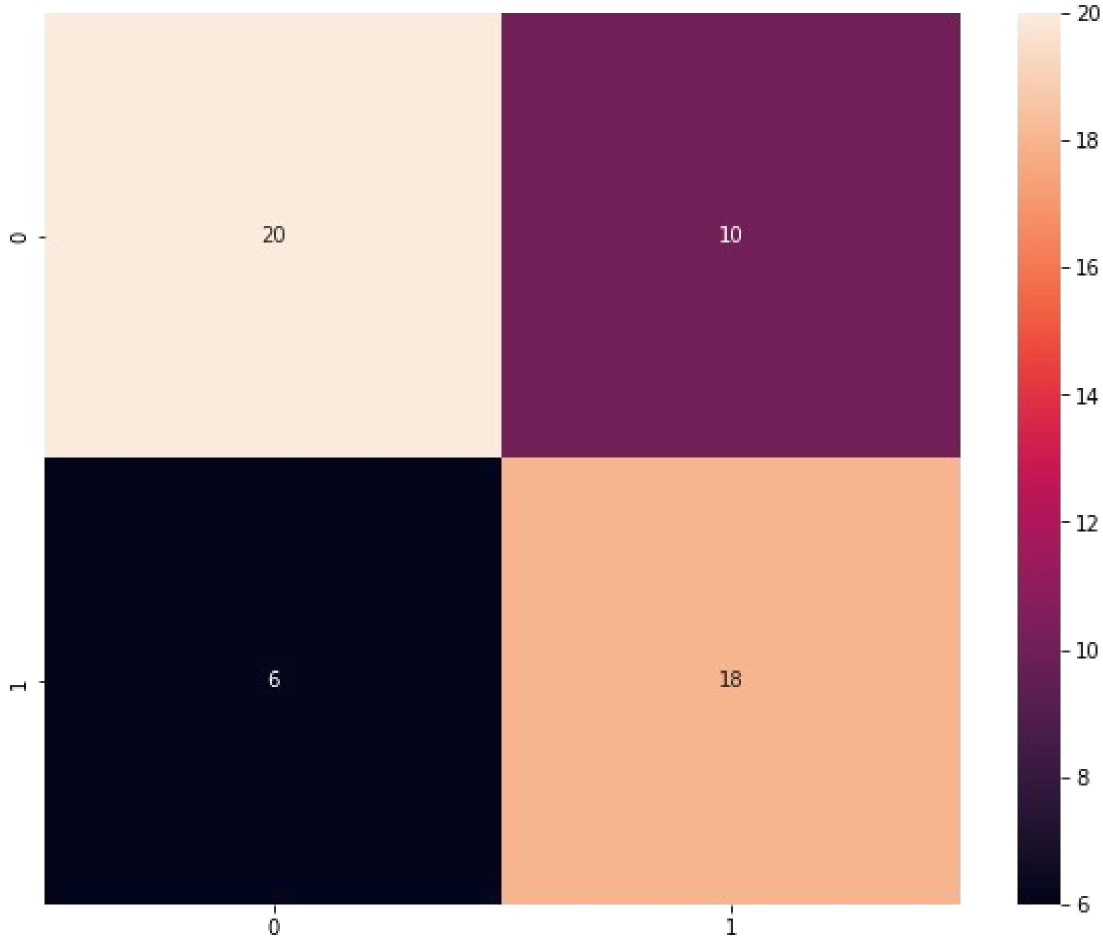
```
70.37
```

Model Evaluation:

```
y_pred_dte = dt_classifier.predict(X_test)

plt.figure(figsize=(10, 8))
CM=confusion_matrix(Y_test,y_pred_dte)
```

```
sns.heatmap(CM, annot=True)

TN = CM[0][0]
FN = CM[1][0]
TP = CM[1][1]
FP = CM[0][1]
specificity = TN/(TN+FP)
loss_log = log_loss(Y_test, y_pred_dte)
acc= accuracy_score(Y_test, y_pred_dte)
roc=roc_auc_score(Y_test, y_pred_dte)
prec = precision_score(Y_test, y_pred_dte)
rec = recall_score(Y_test, y_pred_dte)
f1 = f1_score(Y_test, y_pred_dte)

mathew = matthews_corrcoef(Y_test, y_pred_dte)
model_results =pd.DataFrame([['Decision Tree',acc,
prec,rec,specificity, f1,roc, loss_log,mathew]],
               columns = ['Model', 'Accuracy','Precision',
'Sensitivity','Specificity', 'F1
Score','ROC','Log_Loss','mathew_corrcoef'])

model_results
```

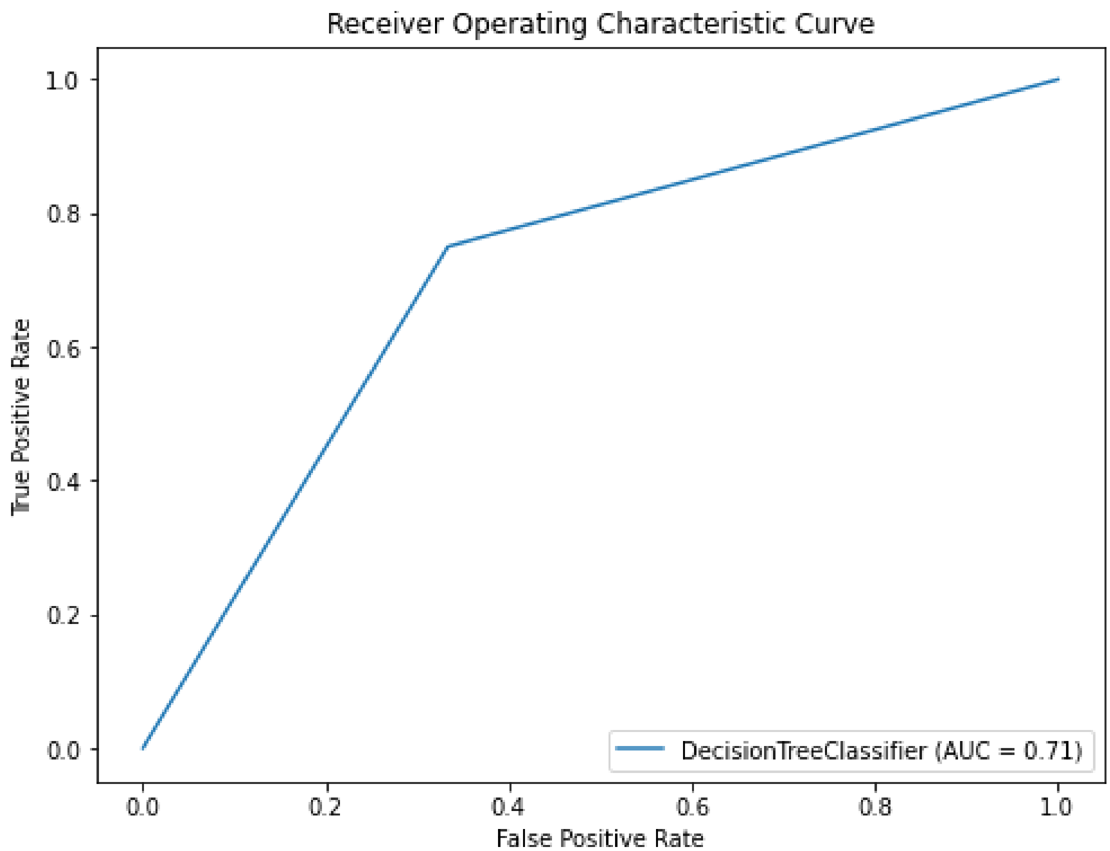
```
           Model  Accuracy  Precision  Sensitivity  Specificity  F1
Score  \
0  Decision Tree  0.703704   0.769231     0.666667     0.666667
0.714286

        ROC   Log_Loss  mathew_corrcoef
0  0.708333  19.188653         0.414371
```




```
Y_pred_dt = np.around(Y_pred_dt)
print(metrics.classification_report(Y_test,Y_pred_dt))
```

```
              precision    recall  f1-score   support

           1       0.77      0.67      0.71        30
           2       0.64      0.75      0.69        24

    accuracy                           0.70        54
   macro avg       0.71      0.71      0.70        54
weighted avg       0.71      0.70      0.70        54
```

```
plot_roc_curve(dt_classifier,X_test,Y_test)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic Curve');
```



4. Naive Bayes Classifier

Naïve Bayes algorithm is a supervised learning algorithm, which is based on Bayes theorem and used for solving classification problems.

```
nb_classifier = GaussianNB( var_smoothing=1e-50)
nb_classifier.fit(X_train,Y_train)
nb_classifier.predict(X_test)
Y_pred_nb = nb_classifier.predict(X_test)
score_nb = round(accuracy_score(Y_pred_nb,Y_test)*100,2)
score_nb
```

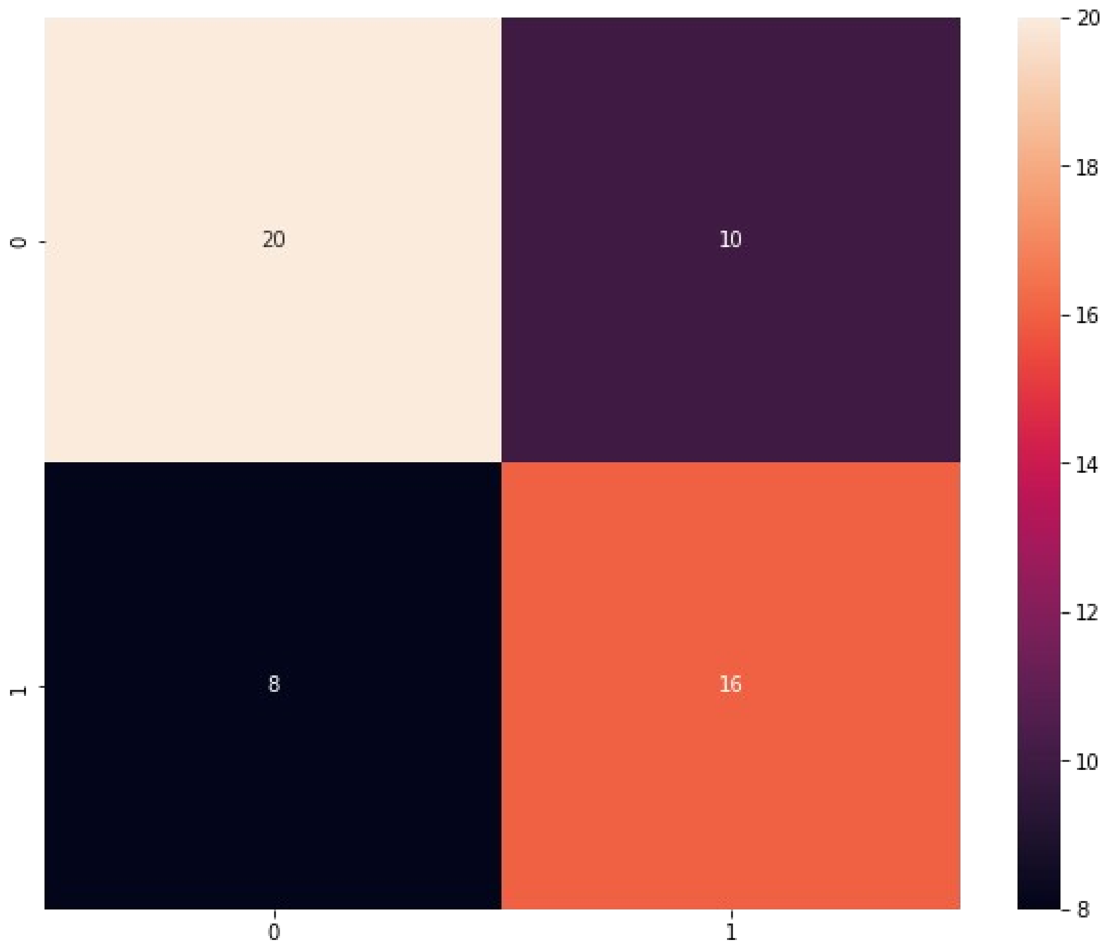
```
66.67
```

Model Evaluation:

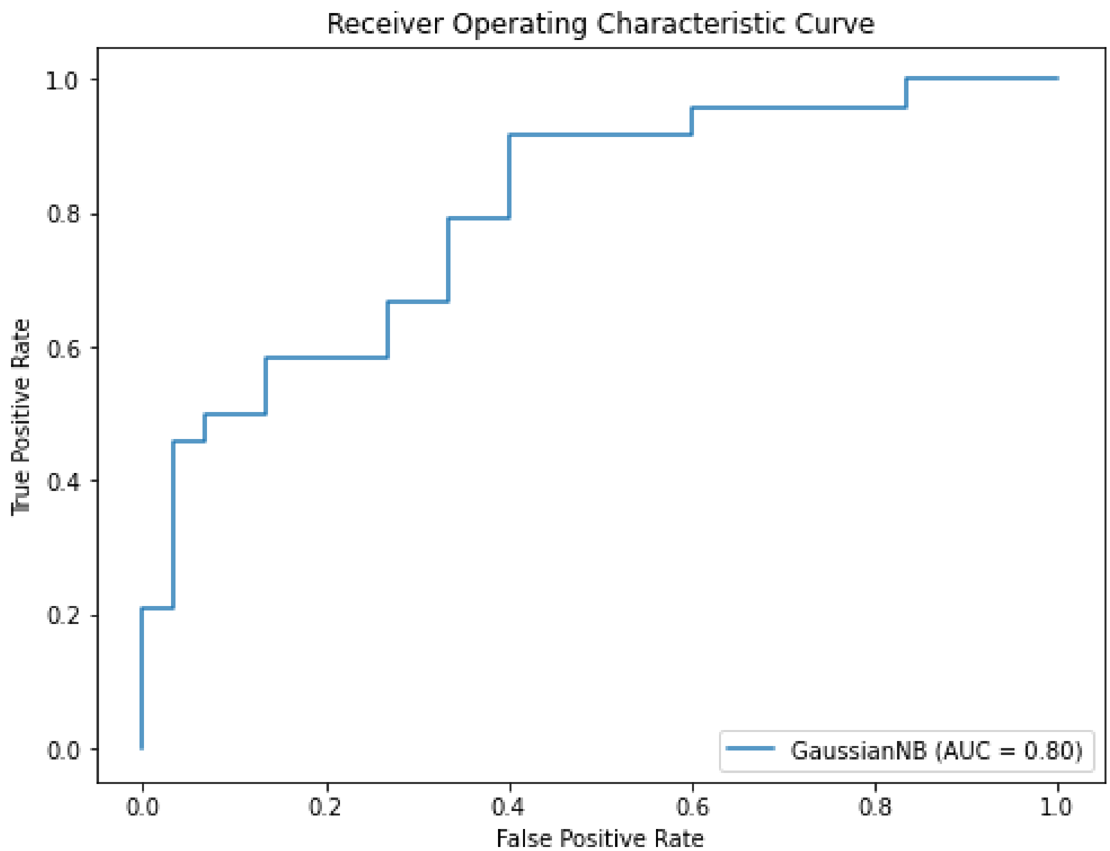
```
y_pred_nbe = nb_classifier.predict(X_test)

plt.figure(figsize=(10, 8))
CM=confusion_matrix(Y_test,y_pred_nbe)
sns.heatmap(CM, annot=True)

TN = CM[0][0]
FN = CM[1][0]
TP = CM[1][1]
```

```
FP = CM[0][1]
specificity = TN/(TN+FP)
loss_log = log_loss(Y_test, y_pred_nbe)
acc= accuracy_score(Y_test, y_pred_nbe)
roc=roc_auc_score(Y_test, y_pred_nbe)
prec = precision_score(Y_test, y_pred_nbe)
rec = recall_score(Y_test, y_pred_nbe)
f1 = f1_score(Y_test, y_pred_nbe)

mathew = matthews_corrcoef(Y_test, y_pred_nbe)
model_results =pd.DataFrame([['Naive Bayes ',acc,
prec,rec,specificity, f1,roc, loss_log,mathew]],
               columns = ['Model', 'Accuracy','Precision',
'Sensitivity','Specificity', 'F1
Score','ROC','Log_Loss','mathew_corrcoef'])

model_results
```

```
          Model  Accuracy  Precision  Sensitivity  Specificity  F1
Score  \
0  Naive Bayes   0.666667   0.714286     0.666667     0.666667
0.689655

        ROC   Log_Loss  mathew_corrcoef
0  0.666667  19.188653         0.331497
```

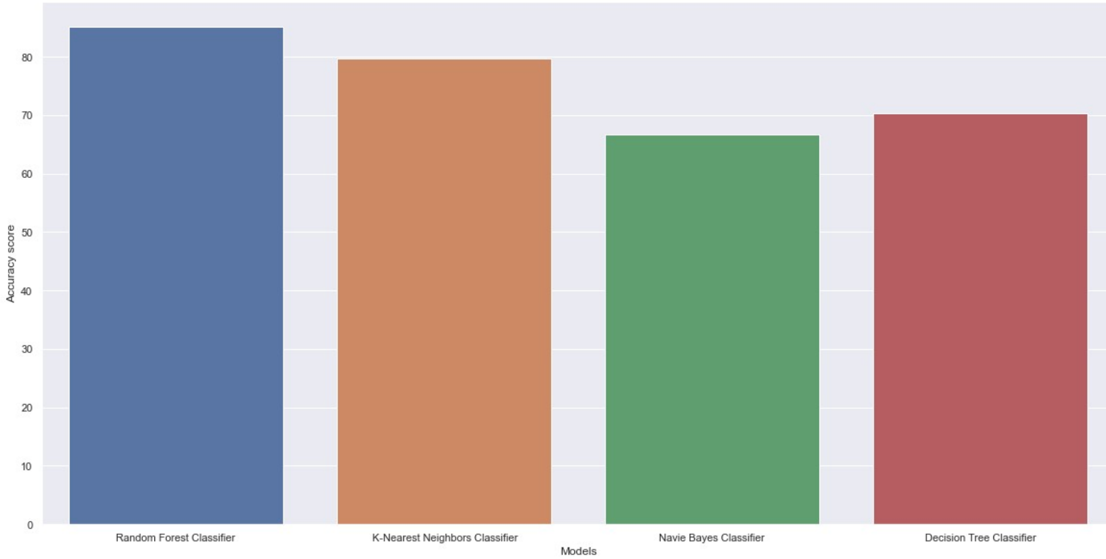



```
Y_pred_nb = np.around(Y_pred_nb)
print(metrics.classification_report(Y_test,Y_pred_nb))

              precision    recall  f1-score   support

           1       0.71      0.67      0.69        30
           2       0.62      0.67      0.64        24

    accuracy                           0.67        54
   macro avg       0.66      0.67      0.66        54
weighted avg       0.67      0.67      0.67        54


plot_roc_curve(nb_classifier,X_test,Y_test)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic Curve');
plt.savefig("GNB.png")
```



Final

```
scores = [score_rf,score_knn,score_nb,score_dt]
Models = ["Random Forest Classifier"," K-Nearest Neighbors
Classifier","Navie Bayes Classifier","Decision Tree Classifier"]

for i in range(len(Models)):
    print("The accuracy score achieved using "+Models[i]+" is:
"+str(scores[i])+" %")

The accuracy score achieved using Random Forest Classifier is: 85.19 %
The accuracy score achieved using  K-Nearest Neighbors Classifier is:
79.63 %
The accuracy score achieved using Navie Bayes Classifier is: 66.67 %
The accuracy score achieved using Decision Tree Classifier is: 70.37 %

sns.set(style="darkgrid",rc={'figure.figsize':(20,10)})
plt.xlabel("Models")
plt.ylabel("Accuracy score")

sns.barplot(Models,scores)
plt.savefig("AccuracyScores.png")
```



Save Model

Since The Random forest Classifier gets the best result, We will use it as our main model to connect it's API with the GUI

```
import pickle
with open('models.pkl', 'wb') as file:
  pickle.dump(rf_classifier, file)
```