Heart Disease Prediction

In [143…]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings("ignore")
from sklearn.model_selection import RandomizedSearchCV
from sklearn.metrics import accuracy_score,recall_score,precision_score,f1_score,classification_report
```

In [2]:
```
values = pd.read_csv("values.csv")
```

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

Out[3]:

	patient_id	slope_of_peak_exercise_st_segment	thal	resting_blood_pressure	chest_pain_type	num_major_vessels	fasting_blood_su
0	0z64un	1	normal	128	2	0	
1	ryoo3j	2	normal	110	3	0	
2	yt1s1x	1	normal	125	4	3	
3	l2xjde	1	reversible_defect	152	4	0	
4	oyt4ek	3	reversible_defect	178	1	0	

In [4]:
```
labels = pd.read_csv("labels.csv")
```

In [5]:
```
labels.head()
```

Out[5]:

	patient_id	heart_disease_present
0	0z64un	0
1	ryoo3j	0
2	yt1s1x	1
3	l2xjde	1
4	oyt4ek	0

In [6]:
```
## Performing outer join to merge the target variable present in different file on patient id
data = pd.merge(values,labels[['patient_id','heart_disease_present']],on='patient_id',how='outer',indicator=False)
```

In [7]:
```
data.head()
```

Out[7]:

	patient_id	slope_of_peak_exercise_st_segment	thal	resting_blood_pressure	chest_pain_type	num_major_vessels	fasting_blood_su
0	0z64un	1	normal	128	2	0	
1	ryoo3j	2	normal	110	3	0	
2	yt1s1x	1	normal	125	4	3	
3	l2xjde	1	reversible_defect	152	4	0	
4	oyt4ek	3	reversible_defect	178	1	0	

In [8]:
```
## Saving the data in my local repository
data.to_csv("Data.csv" , index=False)
```

In [9]:
```
## now a file name data.csv is saved in my repository where my present working directory
```

In [10]:
```
data
```

Out[10]:

	patient_id	slope_of_peak_exercise_st_segment	thal	resting_blood_pressure	chest_pain_type	num_major_vessels	fasting_blood_
0	0z64un	1	normal	128	2	0	
1	ryoo3j	2	normal	110	3	0	
2	yt1s1x	1	normal	125	4	3	
3	l2xjde	1	reversible_defect	152	4	0	
4	oyt4ek	3	reversible_defect	178	1	0	
...	...	...	...	...	...	...	
175	5qfar3	2	reversible_defect	125	4	2	
176	2s2b1f	2	normal	180	4	0	
177	nsd00i	2	reversible_defect	125	3	0	
178	0xw93k	1	normal	124	3	2	
179	2nx10r	1	normal	160	3	1	

180 rows × 15 columns

In [11]:
```
## Data Analysis
```

In [12]:
```
data.info() # to determine the
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 180 entries, 0 to 179
Data columns (total 15 columns):
 #   Column                                Non-Null Count  Dtype  
---  ------                                --------------  -----  
 0   patient_id                            180 non-null    object 
 1   slope_of_peak_exercise_st_segment     180 non-null    int64  
 2   thal                                  180 non-null    object 
 3   resting_blood_pressure                180 non-null    int64  
 4   chest_pain_type                       180 non-null    int64  
 5   num_major_vessels                     180 non-null    int64  
 6   fasting_blood_sugar_gt_120_mg_per_dl  180 non-null    int64  
 7   resting_ekg_results                   180 non-null    int64  
 8   serum_cholesterol_mg_per_dl           180 non-null    int64  
 9   oldpeak_eq_st_depression              180 non-null    float64
 10  sex                                   180 non-null    int64  
 11  age                                   180 non-null    int64  
 12  max_heart_rate_achieved               180 non-null    int64  
 13  exercise_induced_angina               180 non-null    int64  
 14  heart_disease_present                 180 non-null    int64  
dtypes: float64(1), int64(12), object(2)
memory usage: 22.5+ KB
```

We can observe from the data that there are no null values

1) We have patient ID and thal that are object type , as patient ID are unique , we will be dropping that column in the further and will have to encode thal for machine to undertand the importance of that column

2) There is one float value

3) There are 12 columns with integer data type

In [13]:
```
data.shape
```

Out[13]:
```
(180, 15)
```

In [14]:
```
# the data has 180 rows and 15 columns
```

In [15]:
```
data.describe()
```

Out[15]:

	slope_of_peak_exercise_st_segment	resting_blood_pressure	chest_pain_type	num_major_vessels	fasting_blood_sugar_gt_120_mg_per_dl	r
count	180.000000	180.000000	180.000000	180.000000	180.000000	
mean	1.550000	131.311111	3.155556	0.694444	0.161111	
std	0.618838	17.010443	0.938454	0.969347	0.368659	
min	1.000000	94.000000	1.000000	0.000000	0.000000	
25%	1.000000	120.000000	3.000000	0.000000	0.000000	
50%	1.000000	130.000000	3.000000	0.000000	0.000000	
75%	2.000000	140.000000	4.000000	1.000000	0.000000	
max	3.000000	180.000000	4.000000	3.000000	1.000000	

In [16]:
```
data.keys()
```

Out[16]:
```
Index(['patient_id', 'slope_of_peak_exercise_st_segment', 'thal',
       'resting_blood_pressure', 'chest_pain_type', 'num_major_vessels',
       'fasting_blood_sugar_gt_120_mg_per_dl', 'resting_ekg_results',
       'serum_cholesterol_mg_per_dl', 'oldpeak_eq_st_depression', 'sex', 'age',
       'max_heart_rate_achieved', 'exercise_induced_angina',
       'heart_disease_present'],
      dtype='object')
```

In [17]:
```
data.dtypes.value_counts()
```

Out[17]:
```
int64      12
object      2
float64     1
dtype: int64
```

In [18]:
```
# 12 integer data type 1 float and 2 object data type
```

In [19]:
```
## lets drop the patient id column as all values are unique
data.drop('patient_id' , axis=1, inplace=True)
```

Data Cleaning

In [20]:
```
## lets check the no of null values
data.isnull().sum()
```

Out[20]:
```
slope_of_peak_exercise_st_segment       0
thal                                    0
resting_blood_pressure                  0
chest_pain_type                         0
num_major_vessels                       0
fasting_blood_sugar_gt_120_mg_per_dl    0
resting_ekg_results                     0
serum_cholesterol_mg_per_dl             0
oldpeak_eq_st_depression                0
sex                                     0
age                                     0
max_heart_rate_achieved                 0
exercise_induced_angina                 0
heart_disease_present                   0
dtype: int64
```

In [21]:
```
## we have a perfect non-null data
```

Data Visualization

Univarient Analysis

In [140…
```
!pip install sweetviz
```

```
Requirement already satisfied: sweetviz in c:\users\hp\anaconda3\lib\site-packages (2.1.4)
Requirement already satisfied: importlib-resources>=1.2.0 in c:\users\hp\anaconda3\lib\site-packages (from sweetviz)
(5.12.0)
Requirement already satisfied: pandas!=1.0.0,!=1.0.1,!=1.0.2,>=0.25.3 in c:\users\hp\anaconda3\lib\site-packages (from
sweetviz) (1.4.4)
Requirement already satisfied: scipy>=1.3.2 in c:\users\hp\anaconda3\lib\site-packages (from sweetviz) (1.9.1)
Requirement already satisfied: matplotlib>=3.1.3 in c:\users\hp\anaconda3\lib\site-packages (from sweetviz) (3.5.2)
Requirement already satisfied: tqdm>=4.43.0 in c:\users\hp\anaconda3\lib\site-packages (from sweetviz) (4.64.1)
Requirement already satisfied: numpy>=1.16.0 in c:\users\hp\anaconda3\lib\site-packages (from sweetviz) (1.21.5)
Requirement already satisfied: jinja2>=2.11.1 in c:\users\hp\anaconda3\lib\site-packages (from sweetviz) (2.11.3)
Requirement already satisfied: zipp>=3.1.0 in c:\users\hp\anaconda3\lib\site-packages (from importlib-resources>=1.2.0-
>sweetviz) (3.8.0)
Requirement already satisfied: MarkupSafe>=0.23 in c:\users\hp\anaconda3\lib\site-packages (from jinja2>=2.11.1->sweetv
iz) (2.0.1)
Requirement already satisfied: pyparsing>=2.2.1 in c:\users\hp\anaconda3\lib\site-packages (from matplotlib>=3.1.3->swe
etviz) (3.0.9)
Requirement already satisfied: python-dateutil>=2.7 in c:\users\hp\anaconda3\lib\site-packages (from matplotlib>=3.1.3-
>sweetviz) (2.8.2)
Requirement already satisfied: cycler>=0.10 in c:\users\hp\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetvi
z) (0.11.0)
Requirement already satisfied: pillow>=6.2.0 in c:\users\hp\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sweetv
iz) (9.2.0)
Requirement already satisfied: packaging>=20.0 in c:\users\hp\anaconda3\lib\site-packages (from matplotlib>=3.1.3->swee
tviz) (21.3)
Requirement already satisfied: kiwisolver>=1.0.1 in c:\users\hp\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sw
eetviz) (1.4.2)
Requirement already satisfied: fonttools>=4.22.0 in c:\users\hp\anaconda3\lib\site-packages (from matplotlib>=3.1.3->sw
eetviz) (4.25.0)
Requirement already satisfied: pytz>=2020.1 in c:\users\hp\anaconda3\lib\site-packages (from pandas!=1.0.0,!=1.0.1,!=1.
0.2,>=0.25.3->sweetviz) (2022.1)
Requirement already satisfied: colorama in c:\users\hp\anaconda3\lib\site-packages (from tqdm>=4.43.0->sweetviz) (0.4.
5)
Requirement already satisfied: six>=1.5 in c:\users\hp\anaconda3\lib\site-packages (from python-dateutil>=2.7->matplotl
ib>=3.1.3->sweetviz) (1.16.0)
```

In [141…

```
import sweetviz as sv #  library for univariant analysis
my_report = sv.analyze(data)## pass the original dataframe
my_report.show_html() # Default arguments will generate to "SWEETVIZ_REPORT.html"
```

```
                                             |          | [  0%]   00:00 -> (? left)
Report SWEETVIZ_REPORT.html was generated! NOTEBOOK/COLAB USERS: the web browser MAY not pop up, regardless, the report
IS saved in your notebook/colab files.
```

1) We can observe that type 1 is the most common in slop_of_peak_exercise_st_segment and it has 3 segment values 1,2,3 and no missing values

2) We can observe that type 1 is the most common in thal and more than 50% people express the result as type 1 in thal

3) The majarity of resting_blood_pressure lies between 120-140

4) We can observe that chest_pain_type 4 is the most common chest_type recorded in sample data

5) Fasting blood sugar leel for 120mg/dl records 80 of the data as 0

6) Serum cholestrol mg/dl has an aveage values of 250mg/dl

7) We can observe that from the survey conducted , the heart disease not being present has an average percentage of 55% and heart disease present is 45%

Bivarient Analysis

In [22]:
```
# lets visualize the plots
#categorical columns are
cat_cols = data[['thal','sex','chest_pain_type','num_major_vessels','resting_ekg_results','slope_of_peak_exercise_st_se
num_cols = data[['resting_blood_pressure','fasting_blood_sugar_gt_120_mg_per_dl','serum_cholesterol_mg_per_dl','oldpeak
```

In [23]:
```
cat_cols
```

Out[23]:

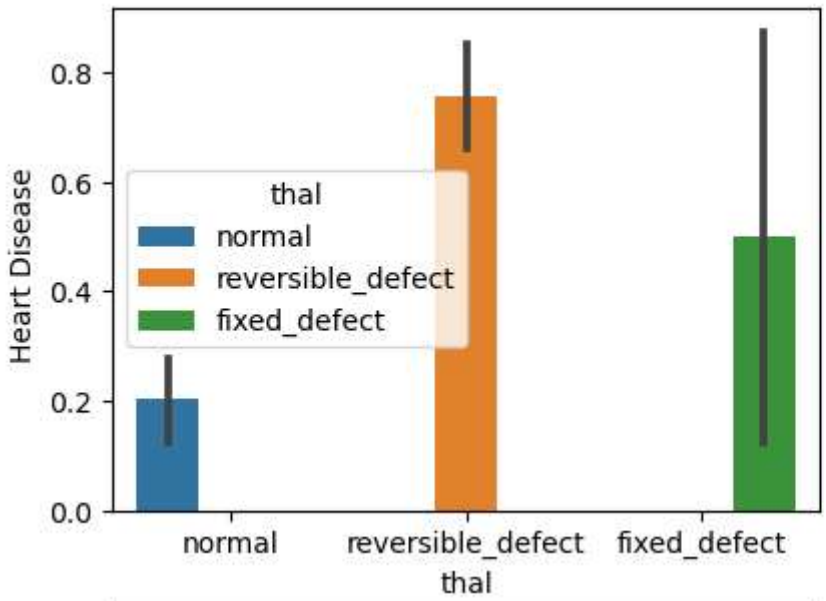
	thal	sex	chest_pain_type	num_major_vessels	resting_ekg_results	slope_of_peak_exercise_st_segment	exercise_induced_angina
0	normal	1	2	0	2	1	0
1	normal	0	3	0	0	2	0
2	normal	1	4	3	2	1	1
3	reversible_defect	1	4	0	0	1	0
4	reversible_defect	1	1	0	2	3	0
...	...	...	...	...	...	...	...
175	reversible_defect	1	4	2	0	2	0
176	normal	0	4	0	1	2	1
177	reversible_defect	1	3	0	0	2	1
178	normal	1	3	2	0	1	0
179	normal	0	3	1	0	1	0

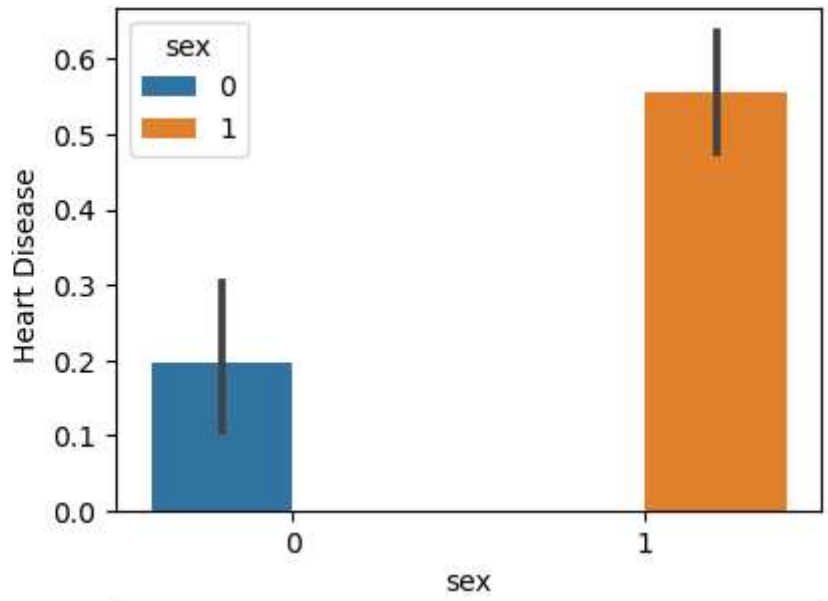
180 rows × 7 columns

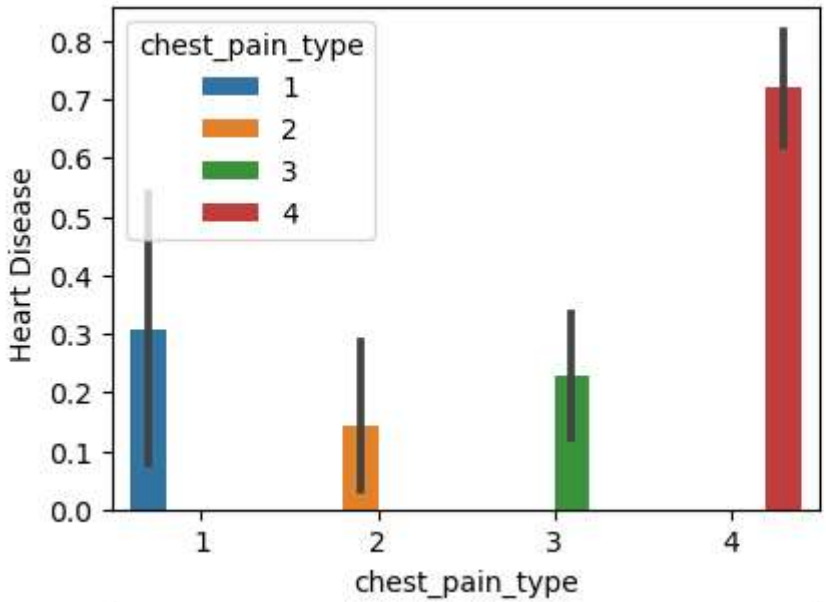
In [24]:
```
cat_cols['thal'].value_counts()
```

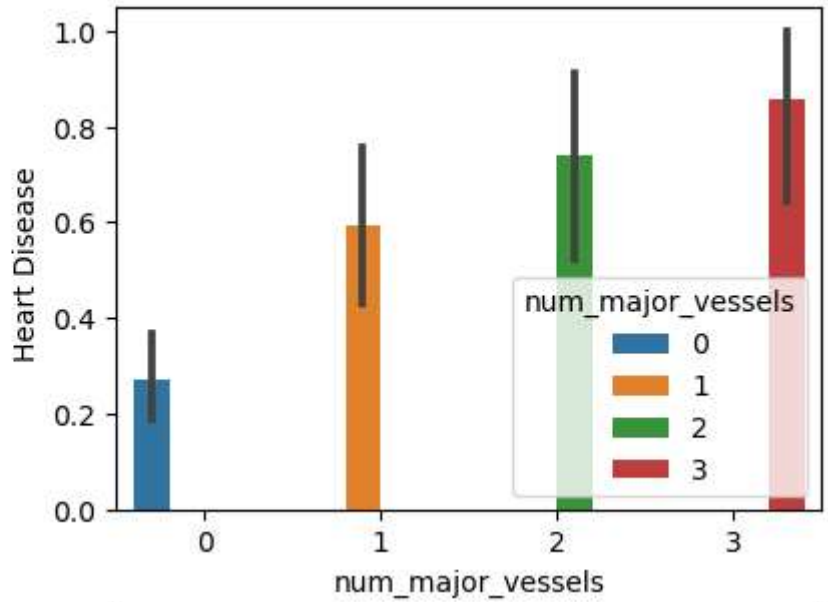
Out[24]:
```
normal               98
reversible_defect    74
fixed_defect          8
Name: thal, dtype: int64
```

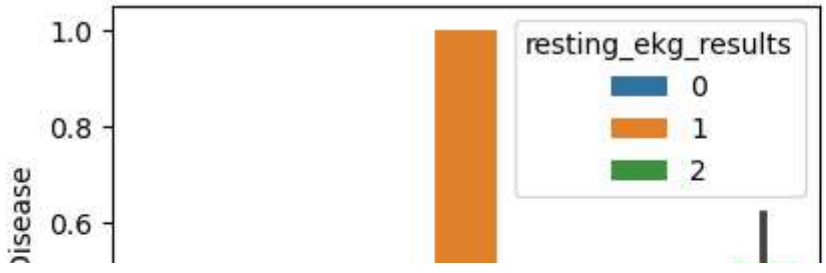
In [25]:
```
fig = plt.figure(figsize=(10,15))
plotnumber=1
for column in cat_cols:
    if plotnumber<=7:
        ax=plt.subplot(4,2,plotnumber)
        sns.barplot(x=column , y='heart_disease_present' , data=data[[column,'heart_disease_present']] , ax=ax , hue=co
        plt.xlabel(column)
        plt.ylabel('Heart Disease ')
    plotnumber+=1
plt.show()
```

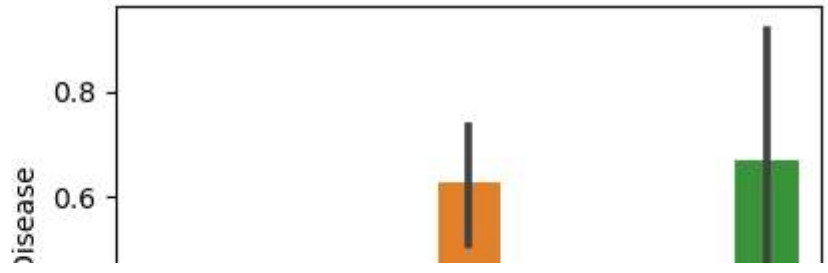

thal
normal
reversible_defect
fixed_defect
Heart Disease
0.0
0.2
0.4
0.6
0.8
normal
reversible_defect
fixed_defect
thal

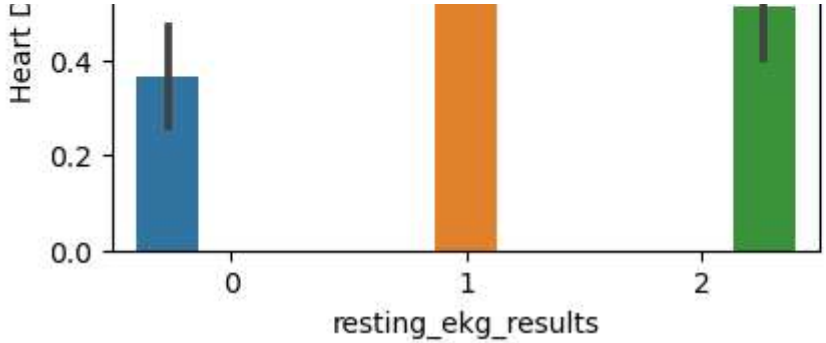

sex
0
1
Heart Disease
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0
1
sex

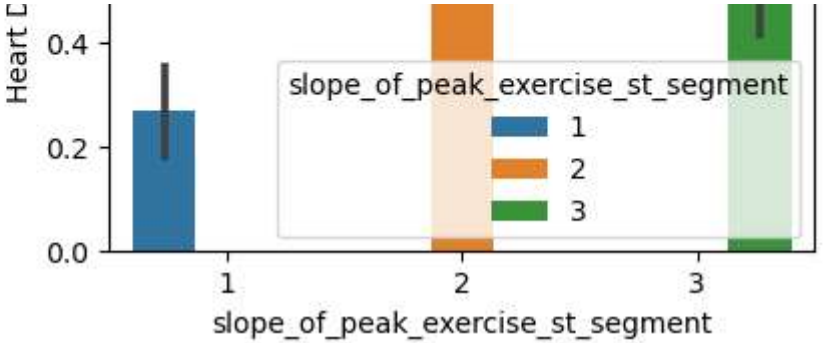

chest_pain_type
1
2
3
4
Heart Disease
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
1
2
3
4
chest_pain_type

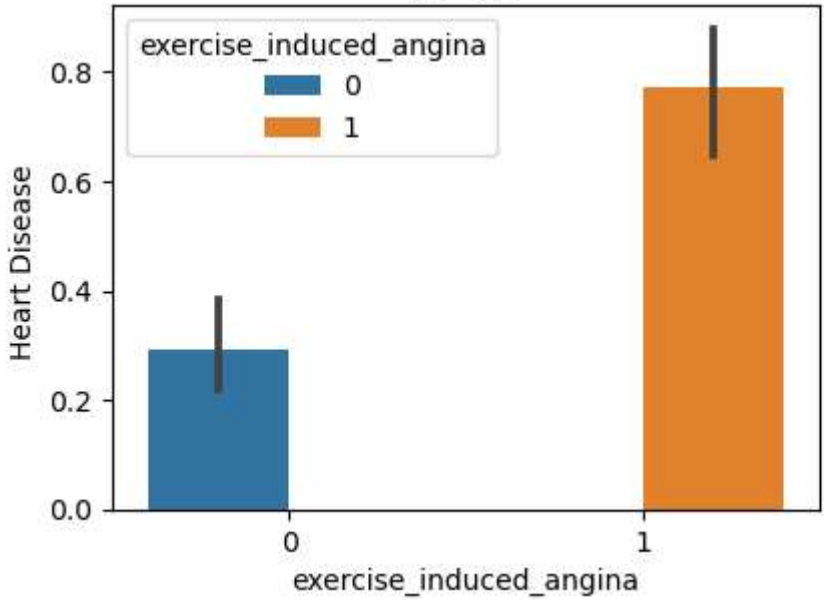

num_major_vessels
0
1
2
3
Heart Disease
0.0
0.2
0.4
0.6
0.8
1.0
0
1
2
3
num_major_vessels


resting_ekg_results
0
1
2
1.0
0.8
0.6


0.8
0.6







1) From data we can analyse that the results of thallium stress test(thal) , has the max result for reversible_defect

2) We can see that 1-Male are more prone to heart disease than 0_Female

3) The chest_pain_type 4 is the most common type of chest pain . We notice, that chest pain of '0', i.e. the ones with typical angina are much less likely to have heart problems

4) Most of the people has 3 major vessels

5) We realize that people with resting_ekg '1'are much more likely to have a heart disease than with resting_ekg '0' & '2'

6) People with slope of peak exercise = '2' & '3' are more likely to have heart problems

7) People with exercise_inducted_angina= 0 are much less likely to have heart problems

In [26]:
```
## Numerical columns plot
```

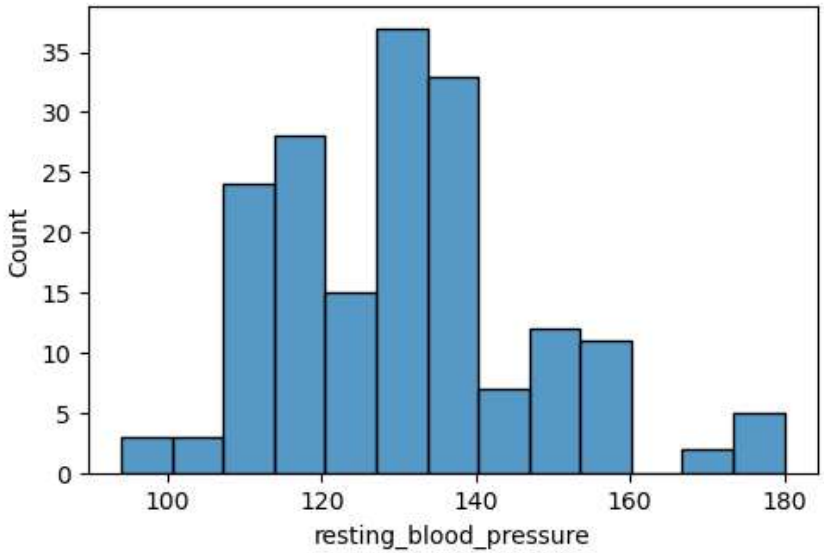
In [27]:
```
num_cols
```

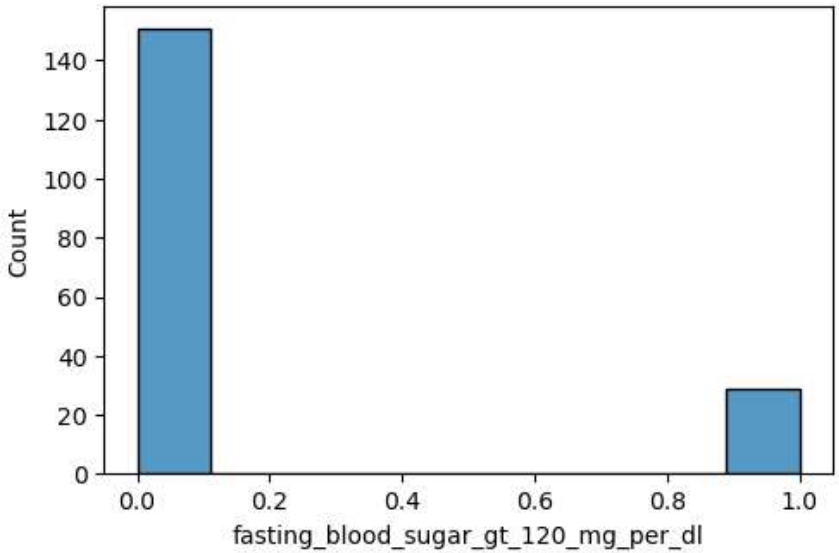
Out[27]:

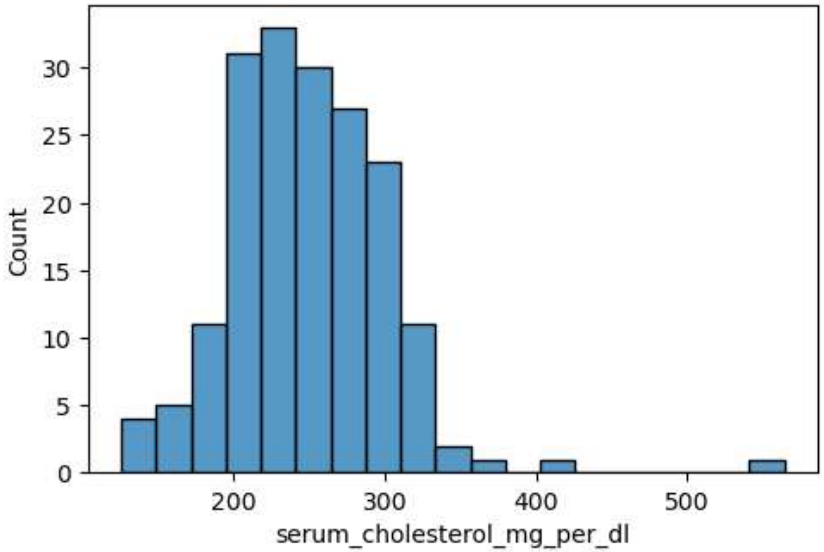
	resting_blood_pressure	fasting_blood_sugar_gt_120_mg_per_dl	serum_cholesterol_mg_per_dl	oldpeak_eq_st_depression	age	max_heart_rat
0	128	0	308	0.0	45	
1	110	0	214	1.6	54	
2	125	0	304	0.0	77	
3	152	0	223	0.0	40	
4	178	0	270	4.2	59	
...	...	...	...	...	...	
175	125	1	254	0.2	67	
176	180	0	327	3.4	55	
177	125	0	309	1.8	64	
178	124	1	255	0.0	48	
179	160	0	201	0.0	54	

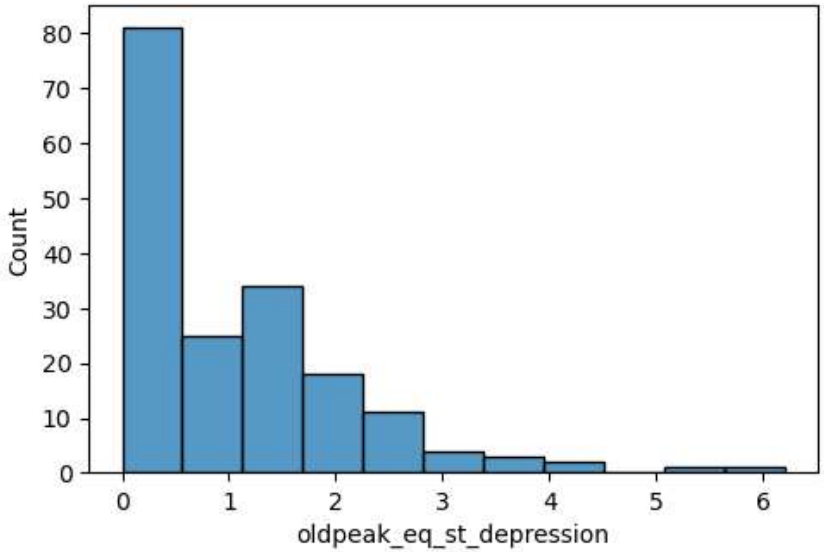
180 rows × 6 columns

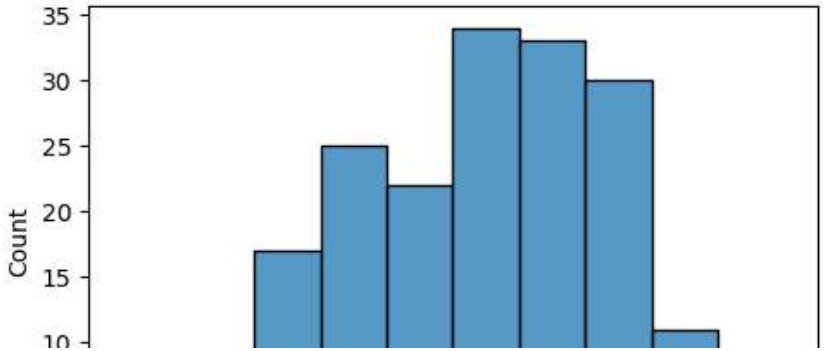
In [28]:
```
fig = plt.figure(figsize=(12,12))
plotnumber=1
for column in num_cols:
    if plotnumber<=6:
        ax=plt.subplot(3,2,plotnumber)
        sns.histplot(x=column , data=data[[column]])
        plt.xlabel(column)
    plotnumber+=1
plt.show()
```

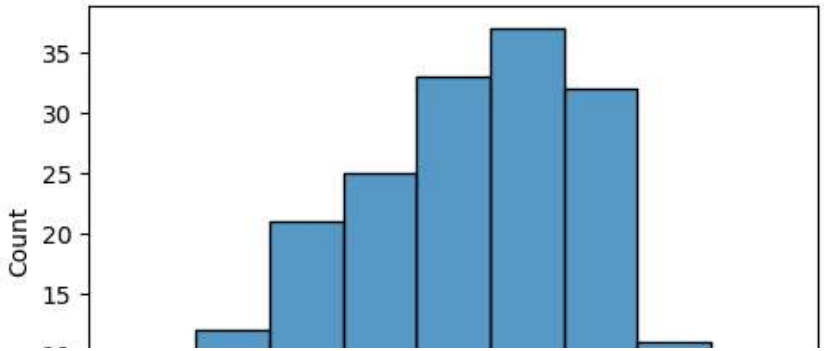

Count
resting_blood_pressure

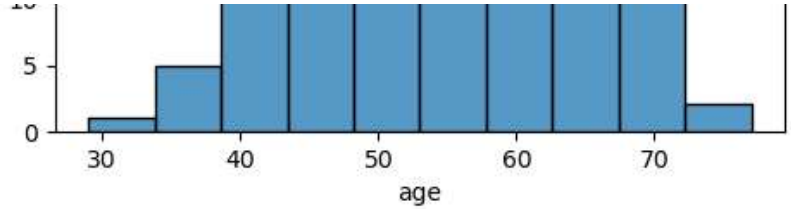

Count
fasting_blood_sugar_gt_120_mg_per_dl


Count
serum_cholesterol_mg_per_dl

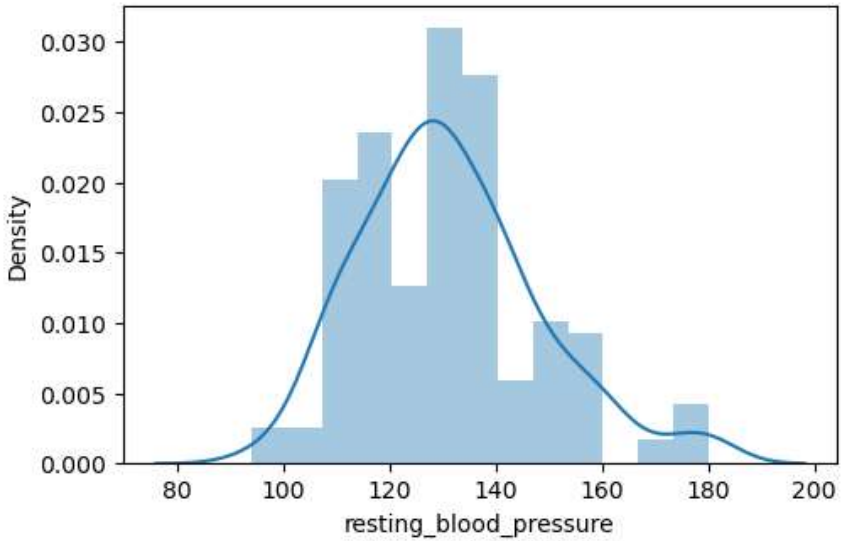

Count
oldpeak_eq_st_depression

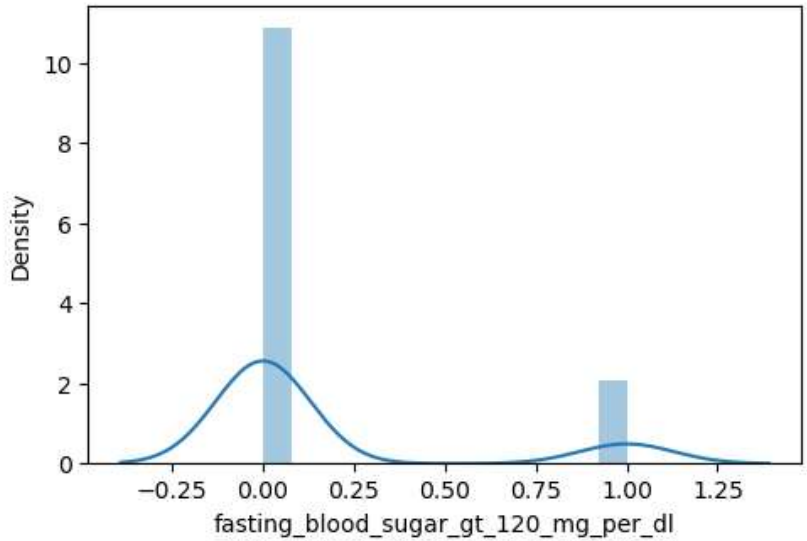

Count

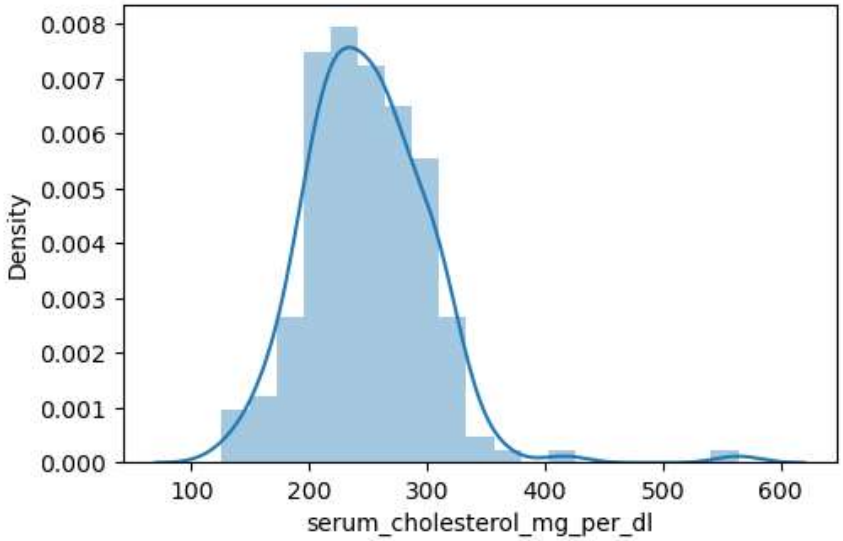

Count

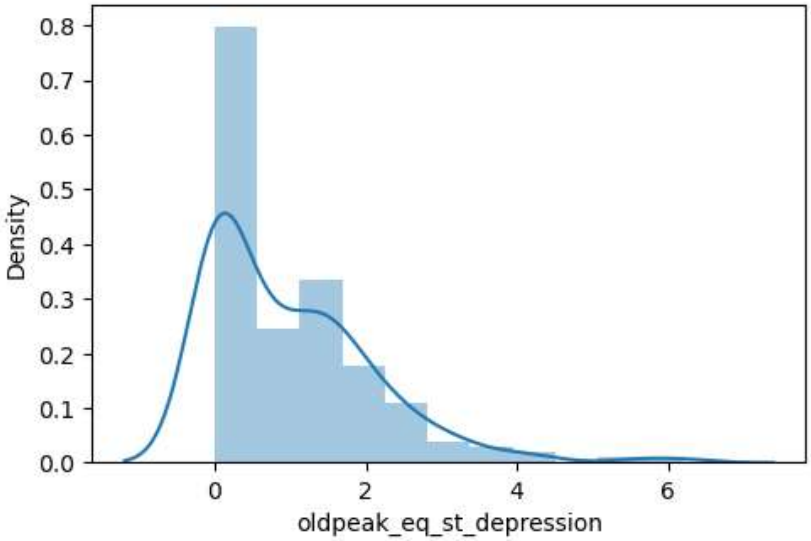


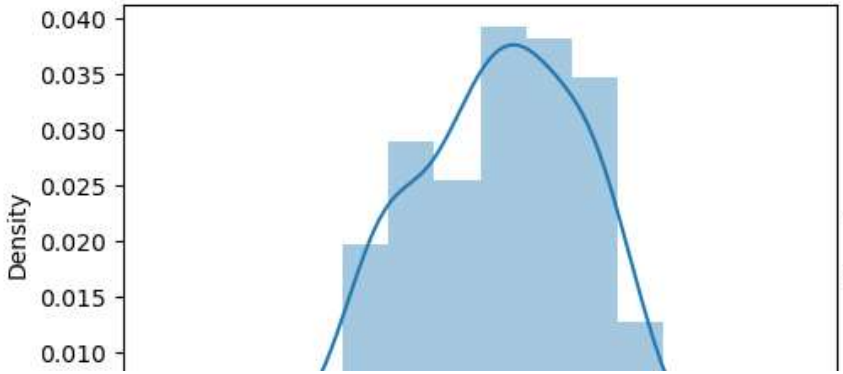
In [29]:
```
fig = plt.figure(figsize=(12,12))
plotnumber=1
for column in num_cols:
    if plotnumber<=6:
        ax=plt.subplot(3,2,plotnumber)
        sns.distplot(x=data[column])
        plt.xlabel(column)
    plotnumber+=1
plt.show()
```

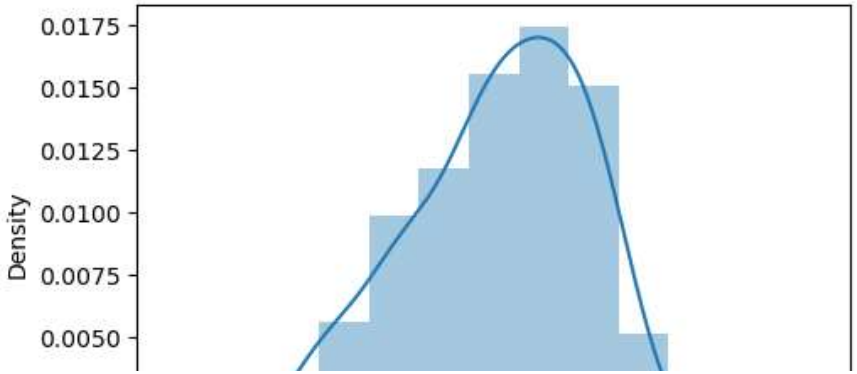

Density
0.030
0.025
0.020
0.015
0.010
0.005
0.000
80
100
120
140
160
180
200
resting_blood_pressure

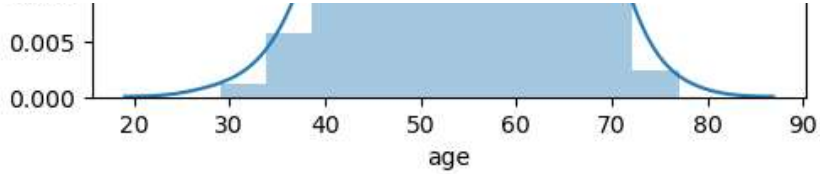

Density
10
8
6
4
2
0
−0.25
0.00
0.25
0.50
0.75
1.00
1.25
fasting_blood_sugar_gt_120_mg_per_dl

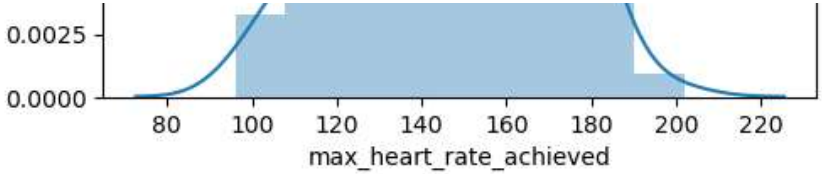

Density
0.008
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000
100
200
300
400
500
600
serum_cholesterol_mg_per_dl


Density
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
2
4
6
oldpeak_eq_st_depression


Density
0.040
0.035
0.030
0.025
0.020
0.015
0.010

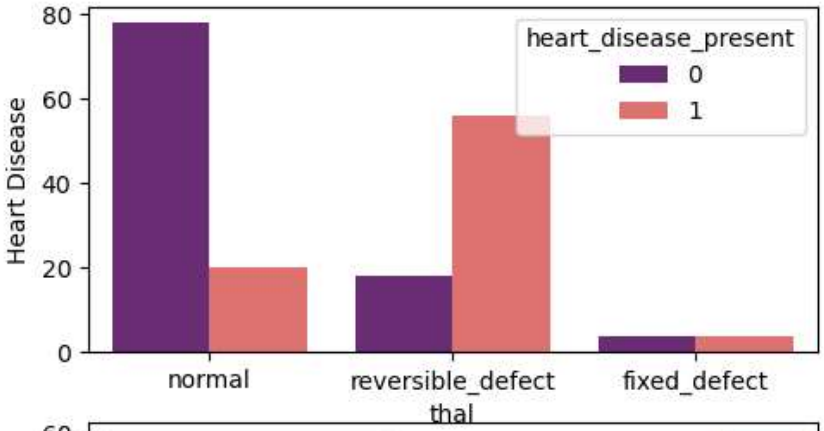

Density
0.0175
0.0150
0.0125
0.0100
0.0075
0.0050

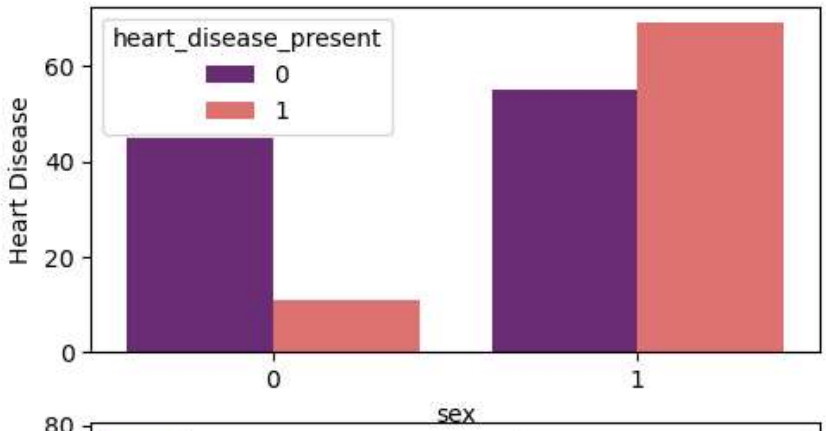


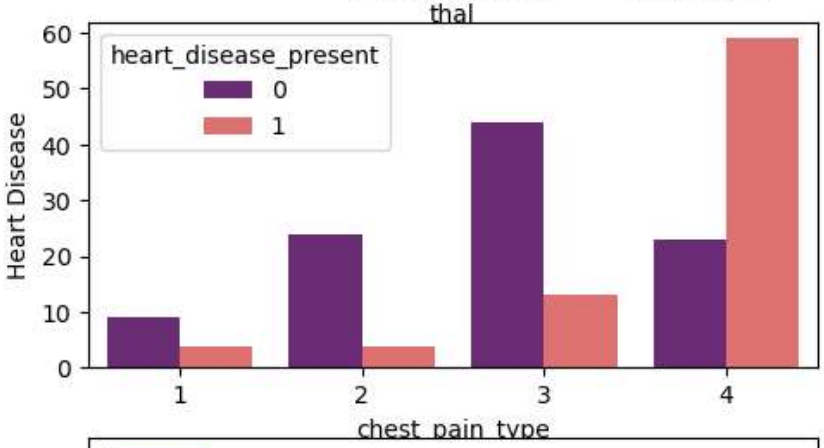


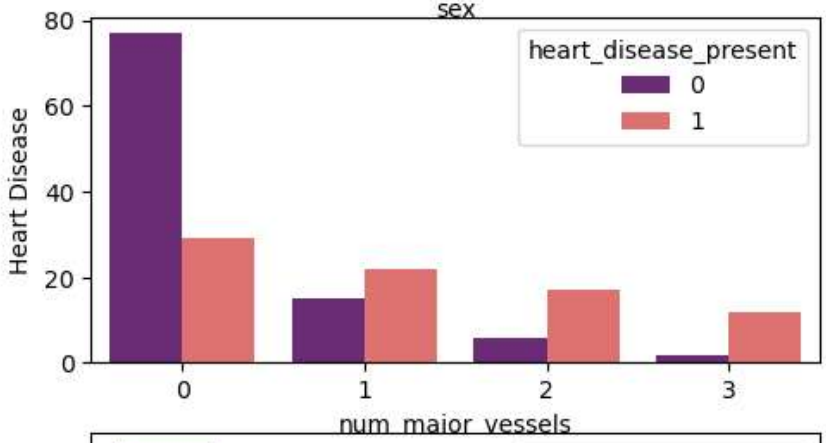
In [30]:
```
## Visualization using count plot
```

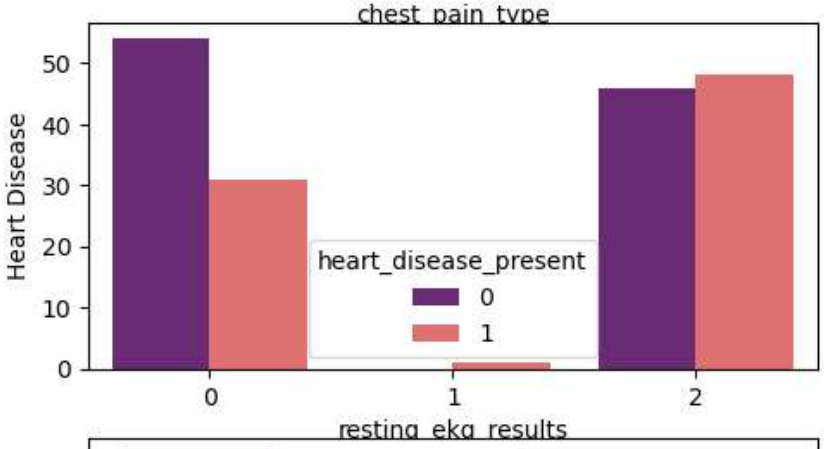
In [31]:
```
fig = plt.figure(figsize=(12,12))
plotnumber=1
for column in cat_cols:
    if plotnumber<=7:
        ax=plt.subplot(4,2,plotnumber)
        sns.countplot(x=column , data = data[[column,'heart_disease_present']] , ax=ax , hue= data['heart_disease_prese
        plt.xlabel(column , fontsize=10)
        plt.ylabel('Heart Disease',fontsize=10)
    plotnumber+=1
plt.show()
```

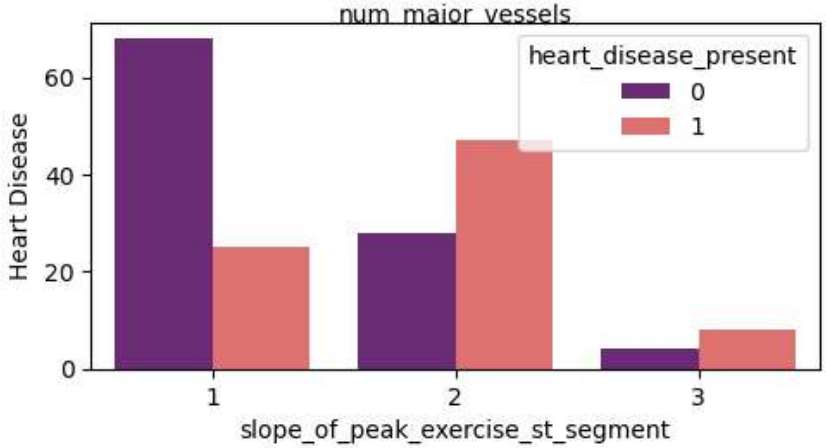

heart_disease_present
0
1
Heart Disease
normal
reversible_defect
fixed_defect
thal


heart_disease_present
0
1
Heart Disease
0
1
sex

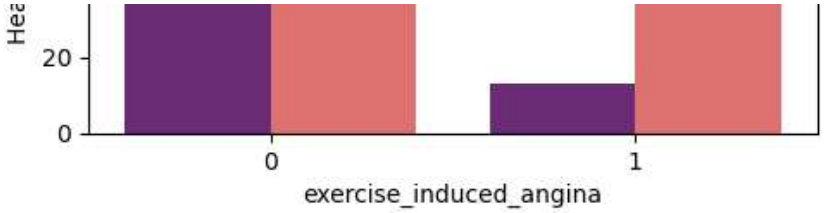

heart_disease_present
0
1
Heart Disease
chest_pain_type


heart_disease_present
0
1
Heart Disease
num_major_vessels


heart_disease_present
0
1
Heart Disease
resting_ekg_results


heart_disease_present
0
1
Heart Disease
slope_of_peak_exercise_st_segment


heart_disease_present
0
1



1) We notice that people whose thal is normal has very less chance of heart disease

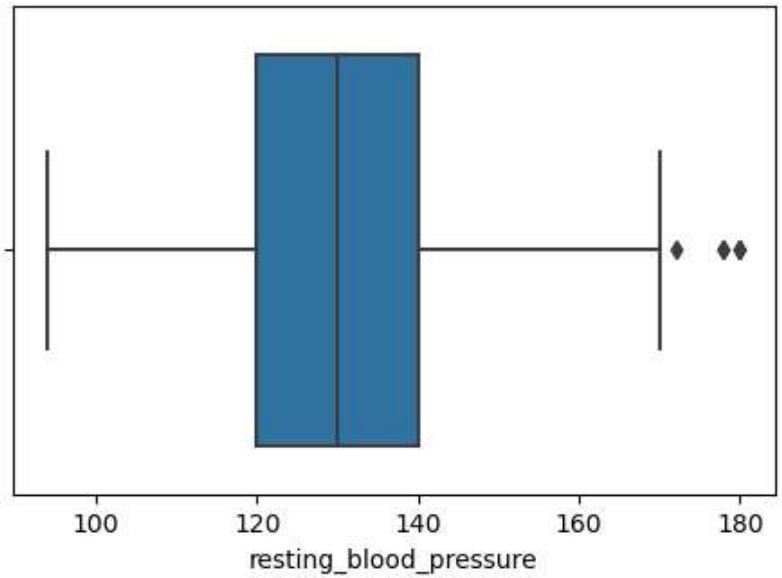
2) We notice that people with chest pain type 4 has the highest chances of heart diseases , and people with chest pain type 3 are less likely to have a heart attack

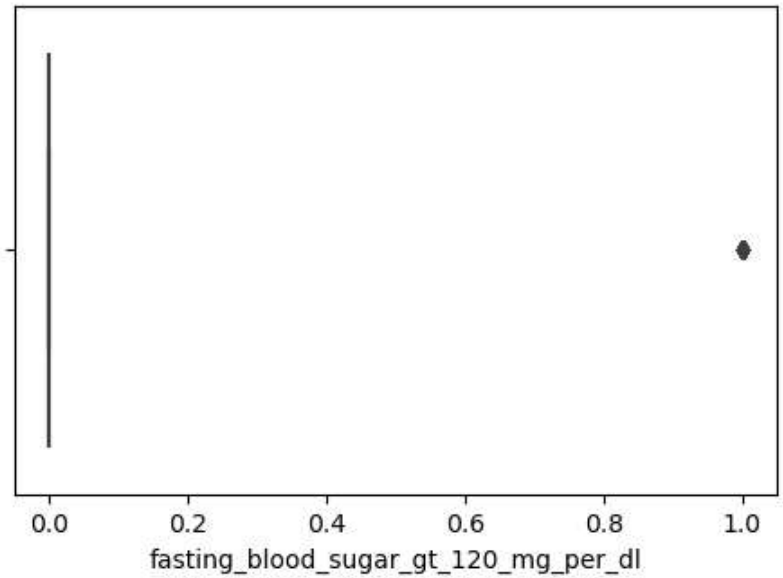
3) We observe that the patients who has the slope of 1 are less likely to have heart disease and those with slope='2' are more likely to have a heart disease

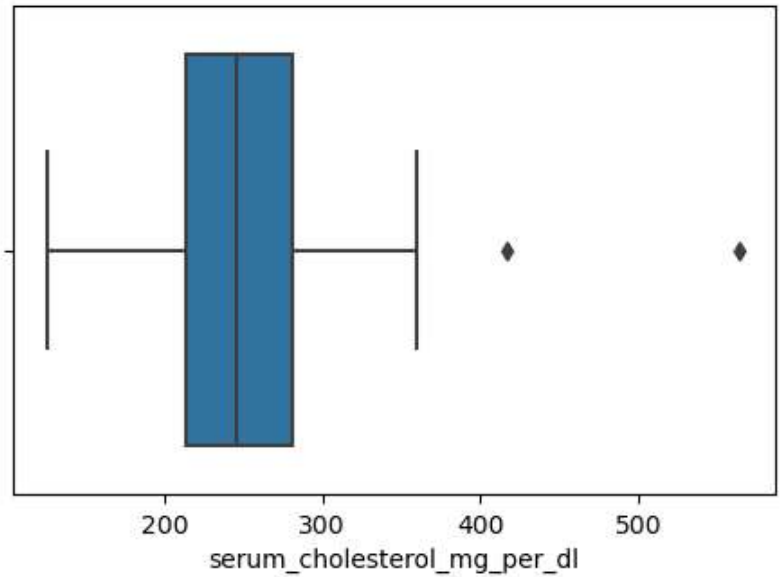
4) People who have 0 no of vessels are less likely to have a heart disease

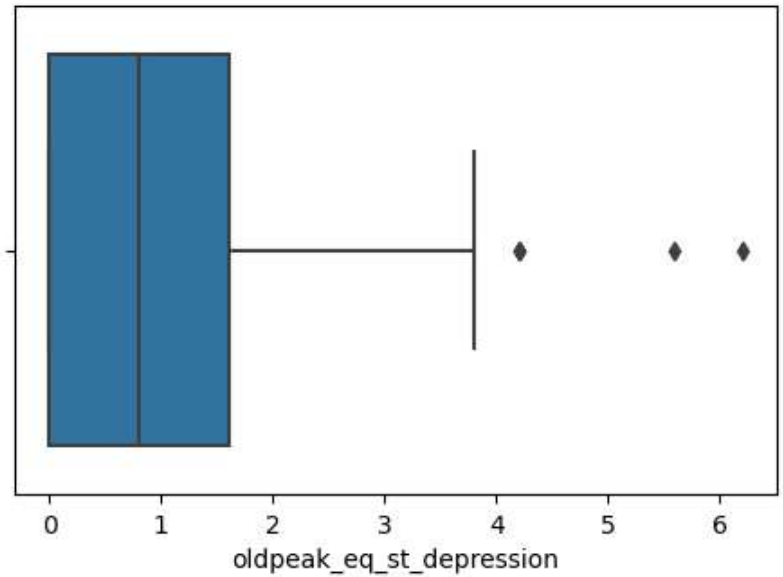
Checking for Outliers

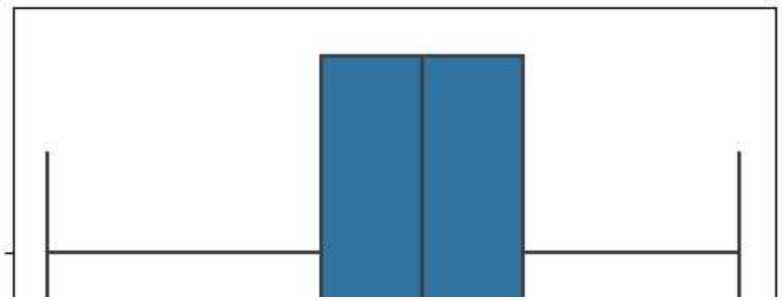
In [32]:
```
fig = plt.figure(figsize=(12,12))
plotnumber=1
for column in num_cols:
    if plotnumber<=6:
        ax=plt.subplot(3,2,plotnumber)
        sns.boxplot(x=data[column])
        plt.xlabel(column)
    plotnumber+=1
plt.show()
```

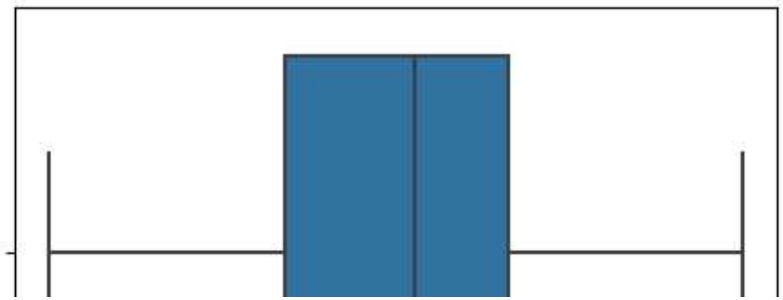

100
120
140
160
180
resting_blood_pressure

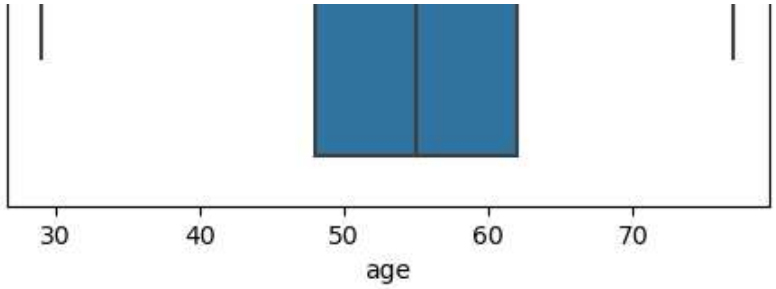

0.0
0.2
0.4
0.6
0.8
1.0
fasting_blood_sugar_gt_120_mg_per_dl

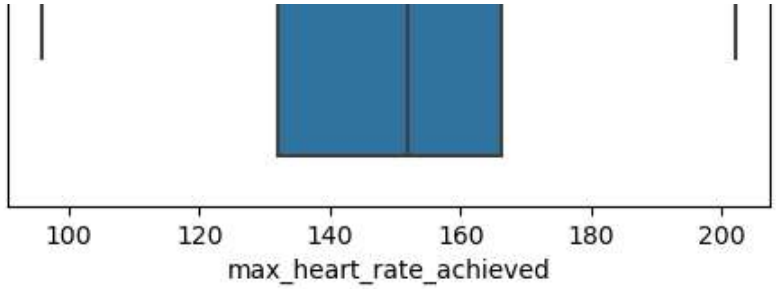

200
300
400
500
serum_cholesterol_mg_per_dl


0
1
2
3
4
5
6
oldpeak_eq_st_depression







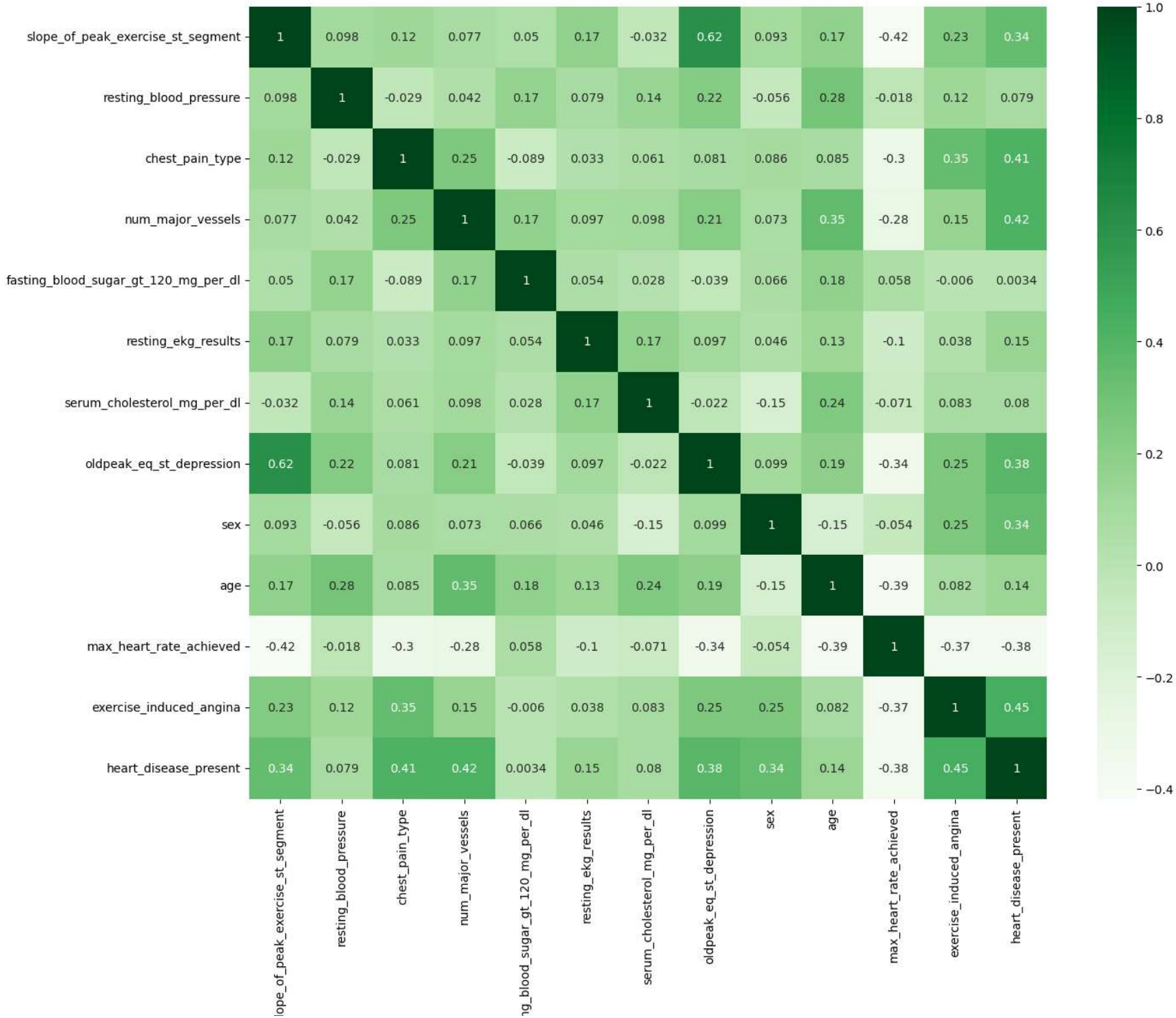


In [33]:
```
## there are very few outliers and we need not handle them as there might be few extreme cases whose bp might be high a
```

Correlation Matrix / HeatMap

In [34]:
```
plt.figure(figsize=(15,12))
sns.heatmap(data.corr(),annot=True , cmap='Greens')
```

Out[34]:
```
<AxesSubplot:>
```


slope_of_peak_exercise_st_segment 1 0.098 0.12 0.077 0.05 0.17 -0.032 0.62 0.093 0.17 -0.42 0.23 0.34
resting_blood_pressure 0.098 1 -0.029 0.042 0.17 0.079 0.14 0.22 -0.056 0.28 -0.018 0.12 0.079
chest_pain_type 0.12 -0.029 1 0.25 -0.089 0.033 0.061 0.081 0.086 0.085 -0.3 0.35 0.41
num_major_vessels 0.077 0.042 0.25 1 0.17 0.097 0.098 0.21 0.073 0.35 -0.28 0.15 0.42
fasting_blood_sugar_gt_120_mg_per_dl 0.05 0.17 -0.089 0.17 1 0.054 0.028 -0.039 0.066 0.18 0.058 -0.006 0.0034
resting_ekg_results 0.17 0.079 0.033 0.097 0.054 1 0.17 0.097 0.046 0.13 -0.1 0.038 0.15
serum_cholesterol_mg_per_dl -0.032 0.14 0.061 0.098 0.028 0.17 1 -0.022 -0.15 0.24 -0.071 0.083 0.08
oldpeak_eq_st_depression 0.62 0.22 0.081 0.21 -0.039 0.097 -0.022 1 0.099 0.19 -0.34 0.25 0.38
sex 0.093 -0.056 0.086 0.073 0.066 0.046 -0.15 0.099 1 -0.15 -0.054 0.25 0.34
age 0.17 0.28 0.085 0.35 0.18 0.13 0.24 0.19 -0.15 1 -0.39 0.082 0.14
max_heart_rate_achieved -0.42 -0.018 -0.3 -0.28 0.058 -0.1 -0.071 -0.34 -0.054 -0.39 1 -0.37 -0.38
exercise_induced_angina 0.23 0.12 0.35 0.15 -0.006 0.038 0.083 0.25 0.25 0.082 -0.37 1 0.45
heart_disease_present 0.34 0.079 0.41 0.42 0.0034 0.15 0.08 0.38 0.34 0.14 -0.38 0.45 1
lope_of_peak_exercise_st_segment
resting_blood_pressure
chest_pain_type
num_major_vessels
ng_blood_sugar_gt_120_mg_per_dl
resting_ekg_results
serum_cholesterol_mg_per_dl
oldpeak_eq_st_depression
sex
age
max_heart_rate_achieved
exercise_induced_angina
heart_disease_present
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4

Scaling data

In [35]:
```
## Encoding of Categorical columns are required for machine to understand and intepret
```

In [36]:
```
#label Encoding for Thal
```

In [37]:
```
from sklearn.preprocessing import LabelEncoder
```

In [38]:
```
labelencoder = LabelEncoder()
```

In [39]:
```
data['thal'] = labelencoder.fit_transform(data['thal'])
```

In [40]:
```
data
```

Out[40]:

	slope_of_peak_exercise_st_segment	thal	resting_blood_pressure	chest_pain_type	num_major_vessels	fasting_blood_sugar_gt_120_mg_per_d
0	1	1	128	2	0	
1	2	1	110	3	0	
2	1	1	125	4	3	
3	1	2	152	4	0	
4	3	2	178	1	0	
...	...	...	...	...	...	
175	2	2	125	4	2	
176	2	1	180	4	0	
177	2	2	125	3	0	
178	1	1	124	3	2	
179	1	1	160	3	1	

180 rows × 14 columns

In [41]:
```
## Standard Scaling for the machine to view all the columns as equally as other columns
```

In [42]:
```
from sklearn.preprocessing import StandardScaler
```

In [43]:
```
scaler = StandardScaler()
```

In [44]:
```
scaler
```

Out[44]:
```
StandardScaler()
```

In [45]:
```
from sklearn.model_selection import train_test_split
```

In [46]:
```
X = data.drop(columns='heart_disease_present')
```

In [47]:
```
y = data['heart_disease_present']
```

In [48]:
```
X
```

Out[48]:

	slope_of_peak_exercise_st_segment	thal	resting_blood_pressure	chest_pain_type	num_major_vessels	fasting_blood_sugar_gt_120_mg_per_d
0	1	1	128	2	0	
1	2	1	110	3	0	
2	1	1	125	4	3	
3	1	2	152	4	0	
4	3	2	178	1	0	
...	...	...	...	...	...	
175	2	2	125	4	2	
176	2	1	180	4	0	
177	2	2	125	3	0	
178	1	1	124	3	2	
179	1	1	160	3	1	

180 rows × 13 columns

In [49]:
```
y
```

Out[49]:
```
0      0
1      0
2      1
3      1
4      0
      ..
175    1
176    1
177    1
178    0
179    0
Name: heart_disease_present, Length: 180, dtype: int64
```

In [50]:
```
X_scaled = scaler.fit_transform(X.astype('float'))
```

In [51]:
```
X_train,X_test,y_train,y_test = train_test_split(X_scaled,y,test_size=0.20,random_state=4)
```

In [52]:
```
X_train
```

Out[52]:
```
array([[ 0.72919727, -2.41176471, -0.31309742, ...,  0.44999378,
        -0.70371942, -0.68074565],
       [ 0.72919727, -0.64705882, -0.07729183, ..., -1.05396422,
         1.15973567, -0.68074565],
       [-0.89124111, -0.64705882,  0.27641655, ...,  0.34256821,
         0.11438281, -0.68074565],
       ...,
       [ 2.34963566, -0.64705882, -0.66680581, ...,  0.98712164,
        -2.43082415,  1.46897745],
       [-0.89124111, -0.64705882,  0.51222214, ..., -0.08713407,
         0.47798381, -0.68074565],
       [ 0.72919727, -2.41176471,  0.51222214, ...,  0.23514264,
        -0.06741768, -0.68074565]])
```

In [53]:
```
X_test
```

Out[53]:
```
array([[-0.89124111, -0.64705882, -0.66680581, -0.16621968, -0.71840267,
        -0.4382385 , -1.05425489, -0.44151656, -0.90320689,  0.67202151,
        -1.16138979,  0.88703493, -0.68074565],
       [ 0.72919727,  1.11764706, -0.19519463,  0.90233541,  0.31609717,
        -0.4382385 , -1.05425489,  0.26228916, -0.72435404,  0.67202151,
         0.98712164, -2.02177303,  1.46897745],
       [ 0.72919727, -0.64705882, -1.84583375,  0.90233541,  1.35059702,
        -0.4382385 ,  0.95384966,  0.9470731 , -0.09836907,  0.67202151,
         1.30939835, -1.11277054,  1.46897745],
       [ 0.72919727, -0.64705882,  0.51222214, -1.23477477, -0.71840267,
        -0.4382385 ,  0.95384966,  0.85196422,  0.25933663, -1.48804762,
         0.12771707,  0.15983294, -0.68074565],
       [ 0.72919727,  1.11764706, -0.07729183,  0.90233541, -0.71840267,
        -0.4382385 , -1.05425489,  1.06120376,  0.16991021, -1.48804762,
        -0.40941079, -0.34011843,  1.46897745],
       [-0.89124111, -0.64705882,  1.10173612, -2.30332986, -0.71840267,
         2.28186252,  0.95384966,  0.64272468, -0.00894264, -1.48804762,
         0.34256821,  0.56888406, -0.68074565],
       [-0.89124111,  1.11764706, -0.66680581, -1.23477477, -0.71840267,
        -0.4382385 , -1.05425489,  0.26228916, -0.90320689,  0.67202151,
        -1.16138979,  1.06883542, -0.68074565],
       [-0.89124111,  1.11764706, -0.43100022, -1.23477477, -0.71840267,
        -0.4382385 , -1.05425489,  0.22424561, -0.63492762,  0.67202151,
         0.23514264, -0.38556855, -0.68074565],
       [ 0.72919727,  1.11764706, -0.66680581, -2.30332986, -0.71840267,
        -0.4382385 , -1.05425489, -0.34640768,  2.49499726,  0.67202151,
        -1.80594322,  1.47788654,  1.46897745],
       [ 0.72919727, -0.64705882, -1.25631978, -0.16621968, -0.71840267,
        -0.4382385 , -1.05425489, -0.66977788,  0.52761591, -1.48804762,
        -0.08713407,  0.38708356, -0.68074565],
       [ 0.72919727, -0.64705882,  0.27641655, -0.16621968, -0.71840267,
        -0.4382385 ,  0.95384966, -1.01216985, -0.81378047, -1.48804762,
        -0.30198522,  0.88703493, -0.68074565],
       [-0.89124111, -0.64705882,  1.21963891, -0.16621968,  0.31609717,
        -0.4382385 , -1.05425489,  0.52859403, -0.90320689, -1.48804762,
         1.30939835,  1.0233853 , -0.68074565],
       [-0.89124111, -0.64705882, -0.07729183, -1.23477477, -0.71840267,
        -0.4382385 ,  0.95384966, -0.85999564, -0.90320689,  0.67202151,
        -2.77277336,  2.38688903, -0.68074565],
       [ 0.72919727, -0.64705882, -1.13841698,  0.90233541, -0.71840267,
        -0.4382385 , -1.05425489, -1.90619333,  0.52761591, -1.48804762,
         1.73910064, -1.11277054, -0.68074565],
       [-0.89124111, -0.64705882, -1.13841698,  0.90233541,  0.31609717,
        -0.4382385 ,  0.95384966,  0.77587712, -0.90320689,  0.67202151,
        -1.16138979,  0.15983294, -0.68074565],
```

```
[-0.89124111,  1.11764706, -0.66680581,  0.90233541, -0.71840267,
 -0.4382385 ,  0.95384966, -0.00401571, -0.18779549,  0.67202151,
 -0.94653865, -0.24921818, -0.68074565],
[-0.89124111, -0.64705882, -0.07729183, -0.16621968, -0.71840267,
 -0.4382385 ,  0.95384966,  0.12913673, -0.45607477, -1.48804762,
 -0.40941079, -0.02196756, -0.68074565],
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 -0.4382385 ,  0.95384966,  1.02316021, -0.90320689, -1.48804762,
  0.23514264,  0.43253368, -0.68074565],
[ 0.72919727,  1.11764706, -0.66680581, -0.16621968, -0.71840267,
 -0.4382385 ,  0.95384966,  0.16718028, -0.54550119,  0.67202151,
 -0.08713407, -0.11286781, -0.68074565],
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 -0.4382385 ,  0.95384966, -0.72684321,  0.70646876,  0.67202151,
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 -0.4382385 , -1.05425489, -0.87901741, -0.90320689,  0.67202151,
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  0.55741935,  0.34163343, -0.68074565],
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 -0.4382385 , -1.05425489, -1.03119162, -0.90320689, -1.48804762,
  0.87969607,  1.34153617, -0.68074565],
[-0.89124111,  1.11764706, -0.66680581,  0.90233541, -0.71840267,
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  1.09454721, -0.43101868, -0.68074565],
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  0.55741935,  0.93248505, -0.68074565],
[ 0.72919727,  1.11764706, -0.66680581, -2.30332986, -0.71840267,
 -0.4382385 ,  0.95384966, -1.06923518,  0.79589518,  0.67202151,
  0.12771707,  0.56888406, -0.68074565],
```

```
[-0.89124111, -0.64705882,  2.87027804,  0.90233541, -0.71840267,
 -0.4382385 , -1.05425489,  1.44163929, -0.90320689, -1.48804762,
  0.98712164,  0.20528306,  1.46897745],
[ 2.34963566,  1.11764706, -1.25631978, -1.23477477, -0.71840267,
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 -0.7316875 ,  0.8415848 , -0.68074565],
[ 0.72919727,  1.11764706, -0.66680581, -1.23477477,  0.31609717,
 -0.4382385 ,  0.95384966,  0.60468113,  0.34876306,  0.67202151,
  0.7722705 , -2.11267328, -0.68074565],
[-0.89124111, -0.64705882,  0.51222214, -0.16621968, -0.71840267,
 -0.4382385 , -1.05425489,  1.63185705, -0.90320689,  0.67202151,
  0.98712164,  0.38708356, -0.68074565],
[ 2.34963566, -2.41176471,  0.80697913, -2.30332986, -0.71840267,
  2.28186252,  0.95384966, -0.30836413,  1.15360088,  0.67202151,
  0.87969607,  0.02348256, -0.68074565],
[ 0.72919727,  1.11764706, -1.25631978,  0.90233541, -0.71840267,
 -0.4382385 ,  0.95384966, -1.56380136,  0.88532161,  0.67202151,
 -1.59109207, -1.61272191,  1.46897745]])
```

In [54]:
```
y_train
```

Out[54]:
```
74     1
16     0
19     1
2      1
132    0
      ..
87     1
104    0
129    1
174    0
122    0
Name: heart_disease_present, Length: 144, dtype: int64
```

In [55]:
```
y_test
```

Out[55]:
```
158    0
110    0
91     1
101    0
61     1
99     0
142    0
45     1
14     1
1      0
76     0
165    0
18     0
47     0
153    1
167    1
84     0
26     0
127    0
169    0
88     0
92     0
172    1
116    0
125    0
6      1
145    0
135    0
93     1
141    0
33     0
82     1
48     1
12     1
168    0
143    1
Name: heart_disease_present, dtype: int64
```

In [56]:
```
print(X_train.shape)
print(y_train.shape)
print(X_test.shape)
print(y_test.shape)
```

```
(144, 13)
(144,)
(36, 13)
(36,)
```

In [57]:
```
## We can analyze that the target has just 2 values [0,1] , hence we can say that this is a classification algorithm
```

Model Preperation

KNN

In [58]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, confusion_matrix,classification_report
```

In [59]:
```
knn=KNeighborsClassifier(n_neighbors=9, weights='uniform')
```

In [60]:
```
knn
```

Out[60]:
```
KNeighborsClassifier(n_neighbors=9)
```

In [61]:
```
help(knn)
```

```
Help on KNeighborsClassifier in module sklearn.neighbors._classification object:

class KNeighborsClassifier(sklearn.neighbors._base.KNeighborsMixin, sklearn.base.ClassifierMixin, sklearn.neighbors._ba
se.NeighborsBase)
 |  KNeighborsClassifier(n_neighbors=5, *, weights='uniform', algorithm='auto', leaf_size=30, p=2, metric='minkowski',
metric_params=None, n_jobs=None)
 |
 |  Classifier implementing the k-nearest neighbors vote.
 |
 |  Read more in the :ref:`User Guide <classification>`.
 |
 |  Parameters
 |  ----------
 |  n_neighbors : int, default=5
 |      Number of neighbors to use by default for :meth:`kneighbors` queries.
 |
 |  weights : {'uniform', 'distance'} or callable, default='uniform'
 |      Weight function used in prediction.  Possible values:
 |
 |      - 'uniform' : uniform weights.  All points in each neighborhood
 |        are weighted equally.
 |      - 'distance' : weight points by the inverse of their distance.
 |        in this case, closer neighbors of a query point will have a
 |        greater influence than neighbors which are further away.
 |      - [callable] : a user-defined function which accepts an
 |        array of distances, and returns an array of the same shape
 |        containing the weights.
 |
 |  algorithm : {'auto', 'ball_tree', 'kd_tree', 'brute'}, default='auto'
 |      Algorithm used to compute the nearest neighbors:
 |
 |      - 'ball_tree' will use :class:`BallTree`
 |      - 'kd_tree' will use :class:`KDTree`
 |      - 'brute' will use a brute-force search.
 |      - 'auto' will attempt to decide the most appropriate algorithm
 |        based on the values passed to :meth:`fit` method.
 |
 |      Note: fitting on sparse input will override the setting of
 |      this parameter, using brute force.
 |
 |  leaf_size : int, default=30
 |      Leaf size passed to BallTree or KDTree.  This can affect the
 |      speed of the construction and query, as well as the memory
 |      required to store the tree.  The optimal value depends on the
 |      nature of the problem.
```

```
|
|  p : int, default=2
|      Power parameter for the Minkowski metric. When p = 1, this is
|      equivalent to using manhattan_distance (l1), and euclidean_distance
|      (l2) for p = 2. For arbitrary p, minkowski_distance (l_p) is used.
|
|  metric : str or callable, default='minkowski'
|      The distance metric to use for the tree.  The default metric is
|      minkowski, and with p=2 is equivalent to the standard Euclidean
|      metric. For a list of available metrics, see the documentation of
|      :class:`~sklearn.metrics.DistanceMetric`.
|      If metric is "precomputed", X is assumed to be a distance matrix and
|      must be square during fit. X may be a :term:`sparse graph`,
|      in which case only "nonzero" elements may be considered neighbors.
|
|  metric_params : dict, default=None
|      Additional keyword arguments for the metric function.
|
|  n_jobs : int, default=None
|      The number of parallel jobs to run for neighbors search.
|      ``None`` means 1 unless in a :obj:`joblib.parallel_backend` context.
|      ``-1`` means using all processors. See :term:`Glossary <n_jobs>`
|      for more details.
|      Doesn't affect :meth:`fit` method.
|
|  Attributes
|  ----------
|  classes_ : array of shape (n_classes,)
|      Class labels known to the classifier
|
|  effective_metric_ : str or callble
|      The distance metric used. It will be same as the `metric` parameter
|      or a synonym of it, e.g. 'euclidean' if the `metric` parameter set to
|      'minkowski' and `p` parameter set to 2.
|
|  effective_metric_params_ : dict
|      Additional keyword arguments for the metric function. For most metrics
|      will be same with `metric_params` parameter, but may also contain the
|      `p` parameter value if the `effective_metric_` attribute is set to
|      'minkowski'.
|
|  n_features_in_ : int
|      Number of features seen during :term:`fit`.
|
|      .. versionadded:: 0.24
```

```
|
|  feature_names_in_ : ndarray of shape (`n_features_in_`,)
|      Names of features seen during :term:`fit`. Defined only when `X`
|      has feature names that are all strings.
|
|      .. versionadded:: 1.0
|
|  n_samples_fit_ : int
|      Number of samples in the fitted data.
|
|  outputs_2d_ : bool
|      False when `y`'s shape is (n_samples, ) or (n_samples, 1) during fit
|      otherwise True.
|
|  See Also
|  --------
|  RadiusNeighborsClassifier: Classifier based on neighbors within a fixed radius.
|  KNeighborsRegressor: Regression based on k-nearest neighbors.
|  RadiusNeighborsRegressor: Regression based on neighbors within a fixed radius.
|  NearestNeighbors: Unsupervised learner for implementing neighbor searches.
|
|  Notes
|  -----
|  See :ref:`Nearest Neighbors <neighbors>` in the online documentation
|  for a discussion of the choice of ``algorithm`` and ``leaf_size``.
|
|  .. warning::
|
|     Regarding the Nearest Neighbors algorithms, if it is found that two
|     neighbors, neighbor `k+1` and `k`, have identical distances
|     but different labels, the results will depend on the ordering of the
|     training data.
|
|  https://en.wikipedia.org/wiki/K-nearest_neighbor_algorithm
|
|  Examples
|  --------
|  >>> X = [[0], [1], [2], [3]]
|  >>> y = [0, 0, 1, 1]
|  >>> from sklearn.neighbors import KNeighborsClassifier
|  >>> neigh = KNeighborsClassifier(n_neighbors=3)
|  >>> neigh.fit(X, y)
|  KNeighborsClassifier(...)
|  >>> print(neigh.predict([[1.1]]))
|  [0]
```

```
 |  >>> print(neigh.predict_proba([[0.9]]))
 |  [[0.666... 0.333...]]
 |
 |  Method resolution order:
 |      KNeighborsClassifier
 |      sklearn.neighbors._base.KNeighborsMixin
 |      sklearn.base.ClassifierMixin
 |      sklearn.neighbors._base.NeighborsBase
 |      sklearn.base.MultiOutputMixin
 |      sklearn.base.BaseEstimator
 |      builtins.object
 |
 |  Methods defined here:
 |
 |  __init__(self, n_neighbors=5, *, weights='uniform', algorithm='auto', leaf_size=30, p=2, metric='minkowski', metric
_params=None, n_jobs=None)
 |      Initialize self.  See help(type(self)) for accurate signature.
 |
 |  fit(self, X, y)
 |      Fit the k-nearest neighbors classifier from the training dataset.
 |
 |      Parameters
 |      ----------
 |      X : {array-like, sparse matrix} of shape (n_samples, n_features) or                (n_samples, n_samples) if m
etric='precomputed'
 |          Training data.
 |
 |      y : {array-like, sparse matrix} of shape (n_samples,) or                (n_samples, n_outputs)
 |          Target values.
 |
 |      Returns
 |      -------
 |      self : KNeighborsClassifier
 |          The fitted k-nearest neighbors classifier.
 |
 |  predict(self, X)
 |      Predict the class labels for the provided data.
 |
 |      Parameters
 |      ----------
 |      X : array-like of shape (n_queries, n_features),                or (n_queries, n_indexed) if metric == 'precom
puted'
 |          Test samples.
 |
 |      Returns
```

```
 |      -------
 |      y : ndarray of shape (n_queries,) or (n_queries, n_outputs)
 |          Class labels for each data sample.
 |
 |  predict_proba(self, X)
 |      Return probability estimates for the test data X.
 |
 |      Parameters
 |      ----------
 |      X : array-like of shape (n_queries, n_features),                or (n_queries, n_indexed) if metric == 'precom
puted'
 |          Test samples.
 |
 |      Returns
 |      -------
 |      p : ndarray of shape (n_queries, n_classes), or a list of n_outputs                of such arrays if n_outputs
> 1.
 |          The class probabilities of the input samples. Classes are ordered
 |          by lexicographic order.
 |
 |  ----------------------------------------------------------------------
 |  Data and other attributes defined here:
 |
 |  __abstractmethods__ = frozenset()
 |
 |  ----------------------------------------------------------------------
 |  Methods inherited from sklearn.neighbors._base.KNeighborsMixin:
 |
 |  kneighbors(self, X=None, n_neighbors=None, return_distance=True)
 |      Find the K-neighbors of a point.
 |
 |      Returns indices of and distances to the neighbors of each point.
 |
 |      Parameters
 |      ----------
 |      X : array-like, shape (n_queries, n_features),             or (n_queries, n_indexed) if metric == 'precompute
d',                default=None
 |          The query point or points.
 |          If not provided, neighbors of each indexed point are returned.
 |          In this case, the query point is not considered its own neighbor.
 |
 |      n_neighbors : int, default=None
 |          Number of neighbors required for each sample. The default is the
 |          value passed to the constructor.
 |
```

```
 |      return_distance : bool, default=True
 |          Whether or not to return the distances.
 |
 |      Returns
 |      -------
 |      neigh_dist : ndarray of shape (n_queries, n_neighbors)
 |          Array representing the lengths to points, only present if
 |          return_distance=True.
 |
 |      neigh_ind : ndarray of shape (n_queries, n_neighbors)
 |          Indices of the nearest points in the population matrix.
 |
 |      Examples
 |      --------
 |      In the following example, we construct a NearestNeighbors
 |      class from an array representing our data set and ask who's
 |      the closest point to [1,1,1]
 |
 |      >>> samples = [[0., 0., 0.], [0., .5, 0.], [1., 1., .5]]
 |      >>> from sklearn.neighbors import NearestNeighbors
 |      >>> neigh = NearestNeighbors(n_neighbors=1)
 |      >>> neigh.fit(samples)
 |      NearestNeighbors(n_neighbors=1)
 |      >>> print(neigh.kneighbors([[1., 1., 1.]]))
 |      (array([[0.5]]), array([[2]]))
 |
 |      As you can see, it returns [[0.5]], and [[2]], which means that the
 |      element is at distance 0.5 and is the third element of samples
 |      (indexes start at 0). You can also query for multiple points:
 |
 |      >>> X = [[0., 1., 0.], [1., 0., 1.]]
 |      >>> neigh.kneighbors(X, return_distance=False)
 |      array([[1],
 |             [2]]...)
 |
 |  kneighbors_graph(self, X=None, n_neighbors=None, mode='connectivity')
 |      Compute the (weighted) graph of k-Neighbors for points in X.
 |
 |      Parameters
 |      ----------
 |      X : array-like of shape (n_queries, n_features),                 or (n_queries, n_indexed) if metric == 'precom
puted',                 default=None
 |          The query point or points.
 |          If not provided, neighbors of each indexed point are returned.
 |          In this case, the query point is not considered its own neighbor.
```

```
|          For ``metric='precomputed'`` the shape should be
|          (n_queries, n_indexed). Otherwise the shape should be
|          (n_queries, n_features).
|
|      n_neighbors : int, default=None
|          Number of neighbors for each sample. The default is the value
|          passed to the constructor.
|
|      mode : {'connectivity', 'distance'}, default='connectivity'
|          Type of returned matrix: 'connectivity' will return the
|          connectivity matrix with ones and zeros, in 'distance' the
|          edges are distances between points, type of distance
|          depends on the selected metric parameter in
|          NearestNeighbors class.
|
|      Returns
|      -------
|      A : sparse-matrix of shape (n_queries, n_samples_fit)
|          `n_samples_fit` is the number of samples in the fitted data.
|          `A[i, j]` gives the weight of the edge connecting `i` to `j`.
|          The matrix is of CSR format.
|
|      See Also
|      --------
|      NearestNeighbors.radius_neighbors_graph : Compute the (weighted) graph
|          of Neighbors for points in X.
|
|      Examples
|      --------
|      >>> X = [[0], [3], [1]]
|      >>> from sklearn.neighbors import NearestNeighbors
|      >>> neigh = NearestNeighbors(n_neighbors=2)
|      >>> neigh.fit(X)
|      NearestNeighbors(n_neighbors=2)
|      >>> A = neigh.kneighbors_graph(X)
|      >>> A.toarray()
|      array([[1., 0., 1.],
|             [0., 1., 1.],
|             [1., 0., 1.]])
|
|  ----------------------------------------------------------------------
|  Data descriptors inherited from sklearn.neighbors._base.KNeighborsMixin:
|
|  __dict__
|      dictionary for instance variables (if defined)
```

```
|
|  __weakref__
|      list of weak references to the object (if defined)
|
|  ----------------------------------------------------------------------
|  Methods inherited from sklearn.base.ClassifierMixin:
|
|  score(self, X, y, sample_weight=None)
|      Return the mean accuracy on the given test data and labels.
|
|      In multi-label classification, this is the subset accuracy
|      which is a harsh metric since you require for each sample that
|      each label set be correctly predicted.
|
|      Parameters
|      ----------
|      X : array-like of shape (n_samples, n_features)
|          Test samples.
|
|      y : array-like of shape (n_samples,) or (n_samples, n_outputs)
|          True labels for `X`.
|
|      sample_weight : array-like of shape (n_samples,), default=None
|          Sample weights.
|
|      Returns
|      -------
|      score : float
|          Mean accuracy of ``self.predict(X)`` wrt. `y`.
|
|  ----------------------------------------------------------------------
|  Methods inherited from sklearn.base.BaseEstimator:
|
|  __getstate__(self)
|
|  __repr__(self, N_CHAR_MAX=700)
|      Return repr(self).
|
|  __setstate__(self, state)
|
|  get_params(self, deep=True)
|      Get parameters for this estimator.
|
|      Parameters
|      ----------
```

```
|      deep : bool, default=True
|          If True, will return the parameters for this estimator and
|          contained subobjects that are estimators.
|
|      Returns
|      -------
|      params : dict
|          Parameter names mapped to their values.
|
|  set_params(self, **params)
|      Set the parameters of this estimator.
|
|      The method works on simple estimators as well as on nested objects
|      (such as :class:`~sklearn.pipeline.Pipeline`). The latter have
|      parameters of the form ``<component>__<parameter>`` so that it's
|      possible to update each component of a nested object.
|
|      Parameters
|      ----------
|      **params : dict
|          Estimator parameters.
|
|      Returns
|      -------
|      self : estimator instance
|          Estimator instance.
```

In [62]:
```
knn.fit(X_train,y_train)
```

Out[62]:
```
KNeighborsClassifier(n_neighbors=9)
```

In [63]:
```
y_pred_knn = knn.predict(X_test)
```

In [64]:
```
y_pred_knn
```

Out[64]:
```
array([0, 1, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0,
       1, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1], dtype=int64)
```

In [65]:
```
y_test
```

Out[65]:
```
158    0
110    0
91     1
101    0
61     1
99     0
142    0
45     1
14     1
1      0
76     0
165    0
18     0
47     0
153    1
167    1
84     0
26     0
127    0
169    0
88     0
92     0
172    1
116    0
125    0
6      1
145    0
135    0
93     1
141    0
33     0
82     1
48     1
12     1
168    0
143    1
Name: heart_disease_present, dtype: int64
```

In [66]:
```
# Checking Accuracy score
print("The accuracy score is : ", accuracy_score(y_test,y_pred_knn))
```

```
The accuracy score is :  0.8055555555555556
```

In [67]:
```
print(classification_report(y_test,y_pred_knn))
```

	precision	recall	f1-score	support
0	0.83	0.87	0.85	23
1	0.75	0.69	0.72	13
accuracy			0.81	36
macro avg	0.79	0.78	0.79	36
weighted avg	0.80	0.81	0.80	36

In [68]:
```
## The accuracy score achieved is 77% , we can try to increase the accuracy , by equallying the number of samples . i.e
```

SMOTE

In [69]:
```
# Apply SMOTE to balance the data
from imblearn.over_sampling import SMOTE
smote = SMOTE() ## object creation
```

In [70]:
```
## Not using SMOTE for testing data.Because the data may or may not be balanced one.
```

In [71]:
```
X_train_smote,y_train_smote = smote.fit_resample(X_train,y_train)
```

In [72]:
```
from collections import Counter
print("Actual Classes",Counter(y_train))
print("SMOTE Classes",Counter(y_train_smote))
```

```
Actual Classes Counter({0: 77, 1: 67})
SMOTE Classes Counter({1: 77, 0: 77})
```

In [73]:
```
knn2 = KNeighborsClassifier(n_neighbors=9)
knn2.fit(X_train_smote, y_train_smote)
```

Out[73]:
```
KNeighborsClassifier(n_neighbors=9)
```

In [74]:
```
y_pred_knn = knn2.predict(X_test)
```

In [75]:
```
# Checking Accuracy score
print("The accuracy score is : ", accuracy_score(y_test,y_pred_knn))
```

```
The accuracy score is :  0.8055555555555556
```

In [76]:
```
## SMOTE works fairly on large data set , here the accuracy score made no difference . Due to overfitting
```

In [77]:
```
results=[]
for k in range(1,11):
    knn=KNeighborsClassifier(n_neighbors=k)
    knn.fit(X_train,y_train)
    y_pred=knn.predict(X_test)
    accuracy=accuracy_score(y_test,y_pred)
    results.append((k,accuracy))

result_df = pd.DataFrame(results,columns=['k','accuracy'])
print(result_df)
```

```
    k  accuracy
0   1  0.722222
1   2  0.777778
2   3  0.777778
3   4  0.777778
4   5  0.777778
5   6  0.777778
6   7  0.777778
7   8  0.805556
8   9  0.805556
9  10  0.750000
```

In [78]:
```
# We can observe that , when the value of k is 8,9 then the accuracy is the highest
```

Logistic Regression

In [79]:
```
##Model creation
from sklearn.linear_model import LogisticRegression
log_reg = LogisticRegression()#object creation of logistic regression

log_reg.fit(X_train,y_train)#training model with training data
```

Out[79]:
```
LogisticRegression()
```

In [80]:
```
y_predLR = log_reg.predict(X_test)
```

In [81]:
```
y_predLR
```

Out[81]:
```
array([0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1], dtype=int64)
```

In [82]:
```
# Checking Accuracy score
print("The accuracy score is : ", accuracy_score(y_test,y_predLR))
```

```
The accuracy score is :  0.8055555555555556
```

In [83]:
```
print(classification_report(y_test,y_predLR))
```

```
              precision    recall  f1-score   support

           0       0.79      0.96      0.86        23
           1       0.88      0.54      0.67        13

    accuracy                           0.81        36
   macro avg       0.83      0.75      0.76        36
weighted avg       0.82      0.81      0.79        36
```

Support Vector Machine (SVM)

In [84]:
```
from sklearn.svm import SVC
svclassifier = SVC()
```

In [85]:
```
svclassifier
```

Out[85]:
```
SVC()
```

In [86]:
```
svclassifier.fit(X_train,y_train)
```

Out[86]:
```
SVC()
```

In [87]:
```
y_predSVM=svclassifier.predict(X_test)
```

In [88]:
```
y_predSVM
```

Out[88]:
```
array([0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0,
       1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 0, 0, 1], dtype=int64)
```

In [89]:
```
print("The accuracy score is of SVM : ", accuracy_score(y_test,y_predSVM))
```

```
The accuracy score is of SVM :  0.7777777777777778
```

In [94]:
```
print(classification_report(y_test,y_predSVM))
```

```
              precision    recall  f1-score   support

           0       0.80      0.87      0.83        23
           1       0.73      0.62      0.67        13

    accuracy                           0.78        36
   macro avg       0.76      0.74      0.75        36
weighted avg       0.77      0.78      0.77        36
```

Hyperparameter Tuning for SVM

In [147…

```
# Logistic Regression
parameters =   {
        'C': np.logspace(-4, 4, 20),
        'kernel': ['linear', 'poly', 'rbf'],
        'degree': [2, 3, 4, 5],
        'gamma': ['scale', 'auto'] + list(np.logspace(-4, 4, 9))
    }
print("The parameters are :" , parameters)
clf = RandomizedSearchCV(svclassifier,parameters,random_state=0)
search=clf.fit(X_train,y_train)
print("The best parameters are - ", search.best_params_)
svclassifier2 = SVC(kernel= 'linear', gamma= 'scale', degree = 5, C = 10000.0)
svclassifier2.fit(X_train,y_train)
y_pred_svc2 = svclassifier2.predict(X_test)
accuracy=accuracy_score(y_test,y_pred_svc2)
print("Accuracy = ",accuracy)
```

```
The parameters are : {'C': array([1.00000000e-04, 2.63665090e-04, 6.95192796e-04, 1.83298071e-03,
       4.83293024e-03, 1.27427499e-02, 3.35981829e-02, 8.85866790e-02,
       2.33572147e-01, 6.15848211e-01, 1.62377674e+00, 4.28133240e+00,
       1.12883789e+01, 2.97635144e+01, 7.84759970e+01, 2.06913808e+02,
       5.45559478e+02, 1.43844989e+03, 3.79269019e+03, 1.00000000e+04]), 'kernel': ['linear', 'poly', 'rbf'], 'degree':
[2, 3, 4, 5], 'gamma': ['scale', 'auto', 0.0001, 0.001, 0.01, 0.1, 1.0, 10.0, 100.0, 1000.0, 10000.0]}
The best parameters are -  {'kernel': 'linear', 'gamma': 'scale', 'degree': 5, 'C': 10000.0}
Accuracy =  0.8055555555555556
```

Bagging

In [96]:

```
from sklearn.ensemble import BaggingClassifier
```

In [97]:
```
estimator_range=[2,4,6,8,10,12,14,16,18,20]
```

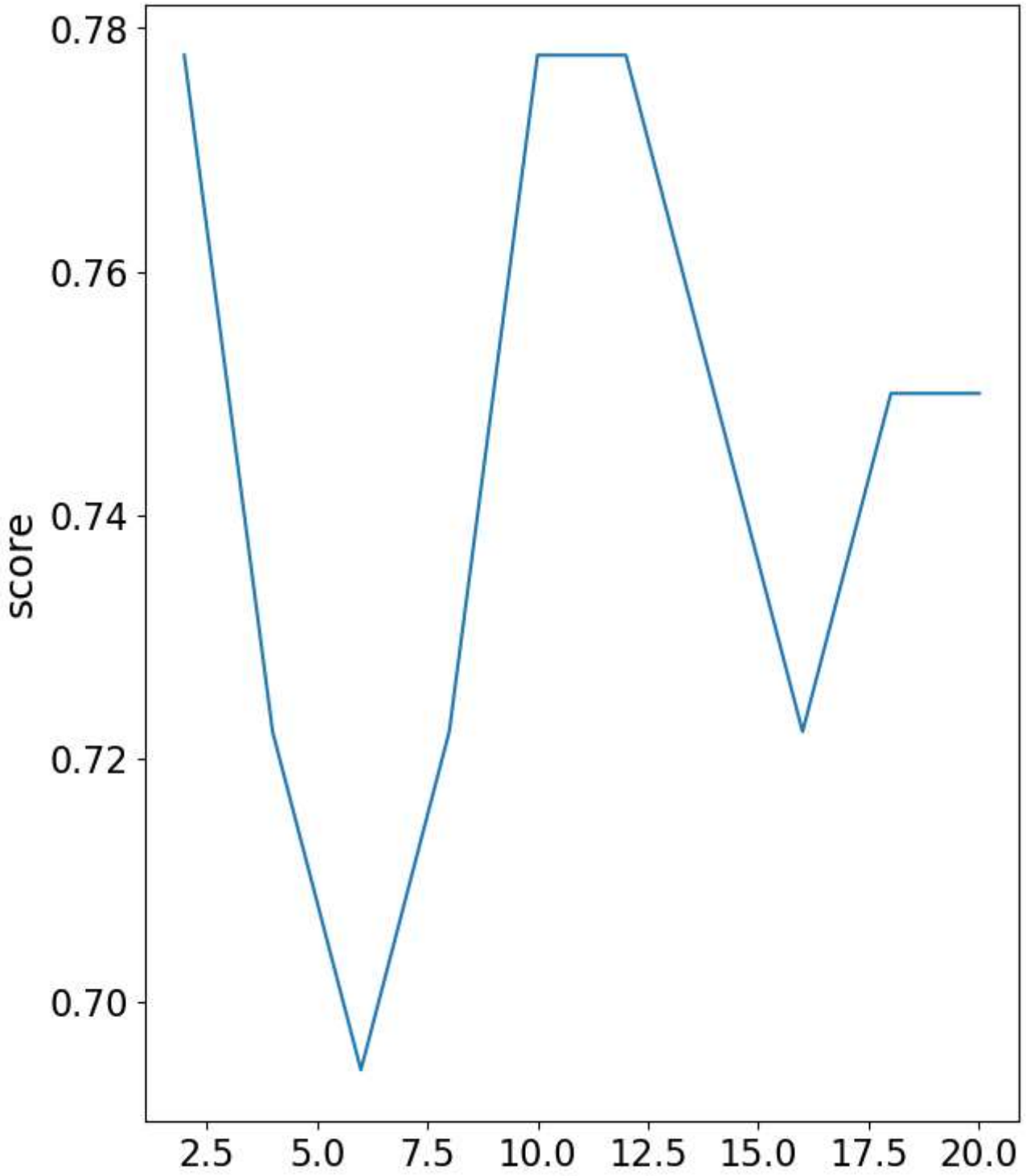
In [98]:
```
models = []
scores = []
for n_estimator in estimator_range:
    bagging = BaggingClassifier(n_estimators=n_estimator , random_state=22)
    bagging.fit(X_train , y_train)
    y_pred = bagging.predict(X_test)
    models.append(bagging)
    scores.append(accuracy_score(y_test,y_pred))
print("Models : ", models)
print("Scores : ",scores)
```

```
Models :  [BaggingClassifier(n_estimators=2, random_state=22), BaggingClassifier(n_estimators=4, random_state=22), Bagg
ingClassifier(n_estimators=6, random_state=22), BaggingClassifier(n_estimators=8, random_state=22), BaggingClassifier(r
andom_state=22), BaggingClassifier(n_estimators=12, random_state=22), BaggingClassifier(n_estimators=14, random_state=2
2), BaggingClassifier(n_estimators=16, random_state=22), BaggingClassifier(n_estimators=18, random_state=22), BaggingCl
assifier(n_estimators=20, random_state=22)]
Scores :  [0.7777777777777778, 0.7222222222222222, 0.6944444444444444, 0.7222222222222222, 0.7777777777777778, 0.777777
7777777778, 0.75, 0.7222222222222222, 0.75, 0.75]
```

In [99]:
```
plt.figure(figsize=(7,9))
plt.plot(estimator_range,scores)

plt.xlabel("n_estimator", fontsize = 18)
plt.ylabel("score", fontsize = 18)
plt.tick_params(labelsize = 16)

plt.show()
```


0.78
0.76
0.74
0.72
0.70
score
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0

n_estimator

Bagging using base estimator as Linear Regression Model

In [100…
```
bgclassifier = BaggingClassifier(base_estimator=log_reg, n_estimators=100,max_features=10,max_samples=100,random_state=
bgclassifier.fit(X_train, y_train)
```

Out[100]:
```
BaggingClassifier(base_estimator=LogisticRegression(), max_features=10,
                  max_samples=100, n_estimators=100, n_jobs=5, random_state=1)
```

In [101…
```
y_pred_bag = bgclassifier.predict(X_test)
```

In [102…
```
accuracy=accuracy_score(y_test,y_pred_bag)
accuracy
```

Out[102]:
```
0.8333333333333334
```

Boosting

In [103…
```
from sklearn.ensemble import GradientBoostingClassifier
```

In [104…
```
gbc = GradientBoostingClassifier()
```

In [105…
```
gbc.fit(X_train,y_train)
```

Out[105]:
```
GradientBoostingClassifier()
```

In [106…
```
y_pred_gbc = gbc.predict(X_test)
```

In [107…
```
y_pred_gbc
```

Out[107]:
```
array([0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0,
       1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 0, 0, 1], dtype=int64)
```

In [108…
```
accuracy = accuracy_score(y_test,y_pred_gbc)
```

In [109…
```
accuracy
```

Out[109]:
```
0.7777777777777778
```

In [110…
```
## xg boost
```

In [111…
```
import xgboost
```

In [112…
```
from xgboost import XGBClassifier
xgb_r=XGBClassifier()
xgb_r.fit(X_train,y_train)
y_pred_xgb=xgb_r.predict(X_test)
```

In [113…
```
y_pred_xgb
```

Out[113]:
```
array([0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0,
       1, 0, 0, 1, 0, 0, 1, 1, 1, 0, 1, 0, 0, 1])
```

In [114…
```
accuracy = accuracy_score(y_pred_xgb,y_test)
```

In [115…
```
accuracy
```

Out[115]:
```
0.7777777777777778
```

In [116…
```
print(classification_report(y_pred_xgb,y_test))
```

```
              precision    recall  f1-score   support

           0       0.83      0.83      0.83        23
           1       0.69      0.69      0.69        13

    accuracy                           0.78        36
   macro avg       0.76      0.76      0.76        36
weighted avg       0.78      0.78      0.78        36
```

Hyperparameter Tuning using XGBoost

In [117…
```
param_grid = {'gamma': [0,0.1,0.2,0.4,0.8,1.6,3.2,6.4,12.8,25.6,51.2,102.4, 200],
              'learning_rate': [0.01, 0.03, 0.06, 0.1, 0.15, 0.2, 0.25, 0.300000012, 0.4, 0.5, 0.6, 0.7],
              'max_depth': [5,6,7,8,9,10,11,12,13,14],
              'n_estimators': [50,65,80,100,115,130,150],
              'reg_alpha': [0,0.1,0.2,0.4,0.8,1.6,3.2,6.4,12.8,25.6,51.2,102.4,200],
              'reg_lambda': [0,0.1,0.2,0.4,0.8,1.6,3.2,6.4,12.8,25.6,51.2,102.4,200]}
```

```
XGB=XGBClassifier(random_state=42,verbosity=0,silent=0)
rcv= RandomizedSearchCV(estimator=XGB, scoring='f1',param_distributions=param_grid, n_iter=100, cv=3,
                                verbose=2, random_state=42, n_jobs=-1)

#estimator--number of decision tree
#scoring--->performance matrix to check performance
#param_distribution-->hyperparametes(dictionary we created)
#n_iter--->Number of parameter settings that are sampled. n_iter trades off runtime vs quality of the solution.default=
##cv------> number of flods
#verbose=Controls the verbosity: the higher, the more messages.
#n_jobs---->Number of jobs to run in parallel,-1 means using all processors.

rcv.fit(X_train, y_train)##training data on randomsearch cv
cv_best_params = rcv.best_params_##it will give you best parameters
print(f"Best paramters: {cv_best_params})")##printing  best parameters
```

```
Fitting 3 folds for each of 100 candidates, totalling 300 fits
Best paramters: {'reg_lambda': 0.2, 'reg_alpha': 0.4, 'n_estimators': 115, 'max_depth': 12, 'learning_rate': 0.2, 'gamm
a': 0})
```

In [118…

```
XGB2=XGBClassifier(reg_lambda= 0.2, reg_alpha= 0.4, n_estimators=115, max_depth=12, learning_rate=0.2, gamma=0)
XGB2.fit(X_train, y_train)#training
```

Out[118]:

```
XGBClassifier(base_score=None, booster=None, callbacks=None,
              colsample_bylevel=None, colsample_bynode=None,
              colsample_bytree=None, early_stopping_rounds=None,
              enable_categorical=False, eval_metric=None, feature_types=None,
              gamma=0, gpu_id=None, grow_policy=None, importance_type=None,
              interaction_constraints=None, learning_rate=0.2, max_bin=None,
              max_cat_threshold=None, max_cat_to_onehot=None,
              max_delta_step=None, max_depth=12, max_leaves=None,
              min_child_weight=None, missing=nan, monotone_constraints=None,
              n_estimators=115, n_jobs=None, num_parallel_tree=None,
              predictor=None, random_state=None, ...)
```

In [119…

```
y_pred_xgb2=XGB2.predict(X_test)
```

In [120…

```
f1_score=f1_score(y_pred_xgb2,y_test)
```

In [121…

```
f1_score
```

Out[121]:

```
0.6923076923076923
```

In [122…
```
print(classification_report(y_pred_xgb2,y_test))
```

```
              precision    recall  f1-score   support

           0       0.83      0.83      0.83        23
           1       0.69      0.69      0.69        13

    accuracy                           0.78        36
   macro avg       0.76      0.76      0.76        36
weighted avg       0.78      0.78      0.78        36
```

In [123…
```
accuracy = accuracy_score(y_pred_xgb2,y_test)
```

In [124…
```
accuracy
```

Out[124]:
```
0.7777777777777778
```

In [125…
```
## The accuracy has not improved after hyper-parameter tuning as well
```

Random Forest

In [126…
```
from sklearn.ensemble import RandomForestClassifier#importing randomforest

rf_clf = RandomForestClassifier(n_estimators=100)#object creation ,taking 100 decision tree in random forest
rf_clf.fit(X_train,y_train)#training the data
```

Out[126]:
```
RandomForestClassifier()
```

In [127…
```
y_pred_rf=rf_clf.predict(X_test)#testing
```

In [128…
```
print(classification_report(y_test,y_pred_rf))
```

```
              precision    recall  f1-score   support

           0       0.81      0.91      0.86        23
           1       0.80      0.62      0.70        13

    accuracy                           0.81        36
   macro avg       0.80      0.76      0.78        36
weighted avg       0.80      0.81      0.80        36
```

In [129…
```python
from sklearn.ensemble import RandomForestClassifier

max_accuracy = 0


for x in range(100):
    rf = RandomForestClassifier(random_state=x)
    rf.fit(X_train,y_train)
    Y_pred_rf = rf.predict(X_test)
    current_accuracy = accuracy_score(y_test,Y_pred_rf)
    if(current_accuracy>max_accuracy):
        max_accuracy = current_accuracy
        best_x = x

print(max_accuracy)
print(best_x)

rf = RandomForestClassifier(random_state=best_x)
rf.fit(X_train,y_train)
Y_pred_rf = rf.predict(X_test)
```

```
0.8611111111111112
19
```

In [130…
```python
accuracy = accuracy_score(y_test,Y_pred_rf)
```

In [131…
```python
accuracy
```

Out[131]:
```
0.8611111111111112
```

Naive Bayes

In [132…
```
from sklearn.naive_bayes import GaussianNB
```

In [133…
```
nb = GaussianNB()
```

In [134…
```
nb.fit(X_train,y_train)
```

Out[134]:
```
GaussianNB()
```

In [135…
```
y_pred_nb = nb.predict(X_test)
```

In [136…
```
accuracy = accuracy_score(y_test,y_pred_nb)
accuracy
```

Out[136]:
```
0.8055555555555556
```

Analysing the best fit moel

In [137…
```
print("KNN score : ")
print("-------------------------------------")
print("The accuracy score is : ", accuracy_score(y_test,y_pred_knn))
print('Classification report of KNN :')
print(classification_report(y_test,y_pred_knn))
print('\n')
print("Naive Bayes score : ")
print("-------------------------------------")
print("The accuracy score is : ", accuracy_score(y_test,y_pred_nb))
print('Classification report of KNN :')
print(classification_report(y_test,y_pred_nb))
print('\n')
print("Random Forest score : ")
print("-------------------------------------")
print("The accuracy score is : ", accuracy_score(y_test,y_pred_knn))
print('Classification report of Random Forest :')
print(classification_report(y_test,Y_pred_rf))
print('\n')
print("Boosting  score : ")
print("-------------------------------------")
print("The accuracy score of XGBoosting : ", accuracy_score(y_test,y_pred_xgb2))
print('Classification report of Random Forest :')
print(classification_report(y_test,y_pred_xgb2))
print('\n')
```

```
print("Bagging  score : ")
print("-------------------------------------")
print("The accuracy score of Bagging : ", accuracy_score(y_test,y_pred_bag))
print('Classification report of Bagging :')
print(classification_report(y_test,y_pred_bag))
print('\n')
print("Support Vector Machine score : ")
print("-------------------------------------")
print("The accuracy score of SVM : ", accuracy_score(y_test,y_predSVM))
print('Classification report of SVM :')
print(classification_report(y_test,y_predSVM))
print('\n')
print("LogisticRegression  score : ")
print("-------------------------------------")
print("The accuracy score of LogisticRegression : ", accuracy_score(y_test,y_predLR))
print('Classification report of LogisticRegression :')
print(classification_report(y_test,y_predLR))
print('\n')
```

```
KNN score :
-----------------------------------
The accuracy score is :  0.8055555555555556
Classification report of KNN :
              precision    recall  f1-score   support

           0       0.83      0.87      0.85        23
           1       0.75      0.69      0.72        13

    accuracy                           0.81        36
   macro avg       0.79      0.78      0.79        36
weighted avg       0.80      0.81      0.80        36



Naive Bayes score :
-----------------------------------
The accuracy score is :  0.8055555555555556
Classification report of KNN :
              precision    recall  f1-score   support

           0       0.79      0.96      0.86        23
           1       0.88      0.54      0.67        13

    accuracy                           0.81        36
   macro avg       0.83      0.75      0.76        36
weighted avg       0.82      0.81      0.79        36



Random Forest score :
-----------------------------------
The accuracy score is :  0.8055555555555556
Classification report of Random Forest :
              precision    recall  f1-score   support

           0       0.88      0.91      0.89        23
           1       0.83      0.77      0.80        13

    accuracy                           0.86        36
   macro avg       0.85      0.84      0.85        36
weighted avg       0.86      0.86      0.86        36
```

```
Boosting  score :
-----------------------------------
The accuracy score of XGBoosting :  0.7777777777777778
Classification report of Random Forest :
              precision    recall  f1-score   support

           0       0.83      0.83      0.83        23
           1       0.69      0.69      0.69        13

    accuracy                           0.78        36
   macro avg       0.76      0.76      0.76        36
weighted avg       0.78      0.78      0.78        36


Bagging  score :
-----------------------------------
The accuracy score of Bagging :  0.8333333333333334
Classification report of Bagging :
              precision    recall  f1-score   support

           0       0.81      0.96      0.88        23
           1       0.89      0.62      0.73        13

    accuracy                           0.83        36
   macro avg       0.85      0.79      0.80        36
weighted avg       0.84      0.83      0.82        36


Support Vector Machine score :
-----------------------------------
The accuracy score of SVM :  0.7777777777777778
Classification report of SVM :
              precision    recall  f1-score   support

           0       0.80      0.87      0.83        23
           1       0.73      0.62      0.67        13

    accuracy                           0.78        36
   macro avg       0.76      0.74      0.75        36
weighted avg       0.77      0.78      0.77        36
```

```
LogisticRegression  score :
-------------------------------------
The accuracy score of LogisticRegression :  0.8055555555555556
Classification report of LogisticRegression :
              precision    recall  f1-score   support

           0       0.79      0.96      0.86        23
           1       0.88      0.54      0.67        13

    accuracy                           0.81        36
   macro avg       0.83      0.75      0.76        36
weighted avg       0.82      0.81      0.79        36
```

Conclusion

When we compare the accuracy score all the models, the Bagging model has the highest accuracy of 83% followed by Logistic Regression has the decond highest accuracy of 80.05% . Bagging is achieving good accuracy using Logistic Regression as its base model . So, finally baggingt model is the best model for classifying and predicting the heart disease in a patient.

In [ ]: