In [1]:

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier as dtc
from sklearn.metrics  import confusion_matrix as cm
from sklearn.metrics import classification_report as cr
from sklearn.metrics import accuracy_score
from sklearn.linear_model import LogisticRegression as lr
from sklearn.preprocessing import StandardScaler
from sklearn.naive_bayes import GaussianNB as bs
from sklearn.svm import SVC
from sklearn.model_selection import cross_val_score as cvs
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\scipy\__init__.py:146: UserWarning: A NumPy version >=1.16.5 and <
1.23.0 is required for this version of SciPy (detected version 1.23.5
  warnings.warn(f"A NumPy version >={np_minversion} and <{np_maxversion}"
```

In [2]:

```
#loading the data set
df=pd.read_csv(r"heart.csv")
```

In [3]:

```
#seeing the top 5 values in the data set
df.head()
```

Out[3]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0

In [4]:

```
#seeing the top tail values in the data set
df.tail()
```

Out[4]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
913	45	M	TA	110	264	0	Normal	132	N	1.2	Flat	1
914	68	M	ASY	144	193	1	Normal	141	N	3.4	Flat	1
915	57	M	ASY	130	131	0	Normal	115	Y	1.2	Flat	1
916	57	F	ATA	130	236	0	LVH	174	N	0.0	Flat	1
917	38	M	NAP	138	175	0	Normal	173	N	0.0	Up	0

In [5]:

```
#seeing the shape of the data set
df.shape
```

Out[5]:

```
(918, 12)
```

In [6]:

```
#there are 918 rows and 12 columns are present in the data set
```

In [7]:

```
# seeing the size of the data set
df.size
```

Out[7]:

```
11016
```

In [8]:

```
#checking the data  types in the data set
df.dtypes.value_counts()
```

Out[8]:

```
int64      6
object     5
float64    1
dtype: int64
```

In [9]:

```
#in the above data set there are 6 integer columns ,5 object columns 1 float columns
```

In [10]:

```
#seeing the info of the data set
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   Age             918 non-null    int64  
 1   Sex             918 non-null    object 
 2   ChestPainType   918 non-null    object 
 3   RestingBP       918 non-null    int64  
 4   Cholesterol     918 non-null    int64  
 5   FastingBS       918 non-null    int64  
 6   RestingECG      918 non-null    object 
 7   MaxHR           918 non-null    int64  
 8   ExerciseAngina  918 non-null    object 
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    object 
 11  HeartDisease    918 non-null    int64  
dtypes: float64(1), int64(6), object(5)
memory usage: 86.2+ KB
```

In [11]:

```
#checking the  null values in the data set
df.isna().sum()
```

Out[11]:

```
Age               0
Sex               0
ChestPainType     0
RestingBP         0
Cholesterol       0
FastingBS         0
RestingECG        0
MaxHR             0
ExerciseAngina    0
Oldpeak           0
ST_Slope          0
HeartDisease      0
dtype: int64
```

In [12]:

```
#as you can see there are no null values in the data set
```

In [13]:

```
#describing the data
df.describe()
```

Out[13]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
count	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000
mean	53.510893	132.396514	198.799564	0.233115	136.809368	0.887364	0.553377
std	9.432617	18.514154	109.384145	0.423046	25.460334	1.066570	0.497414
min	28.000000	0.000000	0.000000	0.000000	60.000000	-2.600000	0.000000
25%	47.000000	120.000000	173.250000	0.000000	120.000000	0.000000	0.000000
50%	54.000000	130.000000	223.000000	0.000000	138.000000	0.600000	1.000000
75%	60.000000	140.000000	267.000000	0.000000	156.000000	1.500000	1.000000
max	77.000000	200.000000	603.000000	1.000000	202.000000	6.200000	1.000000

In [14]:

```
#seeing the column of the data set
df.columns
```

Out[14]:

```
Index(['Age', 'Sex', 'ChestPainType', 'RestingBP', 'Cholesterol', 'FastingBS',
       'RestingECG', 'MaxHR', 'ExerciseAngina', 'Oldpeak', 'ST_Slope',
       'HeartDisease'],
      dtype='object')
```

In [15]:

```
#performing eda on the data set
```

In [16]:

```
#now iam going to separate the categorical and numerical values
cat=df.select_dtypes(exclude=np.number)
```

In [17]:

```
num=df.select_dtypes(include=np.number)
```

In [18]:

```
#seeing the head values of the categorical and numerical data
cat.head()
```

Out[18]:

	Sex	ChestPainType	RestingECG	ExerciseAngina	ST_Slope
0	M	ATA	Normal	N	Up
1	F	NAP	Normal	N	Flat
2	M	ATA	ST	N	Up
3	F	ASY	Normal	Y	Flat
4	M	NAP	Normal	N	Up

In [19]:

```
num.head()
```

Out[19]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
0	40	140	289	0	172	0.0	0
1	49	160	180	0	156	1.0	1
2	37	130	283	0	98	0.0	0
3	48	138	214	0	108	1.5	1
4	54	150	195	0	122	0.0	0

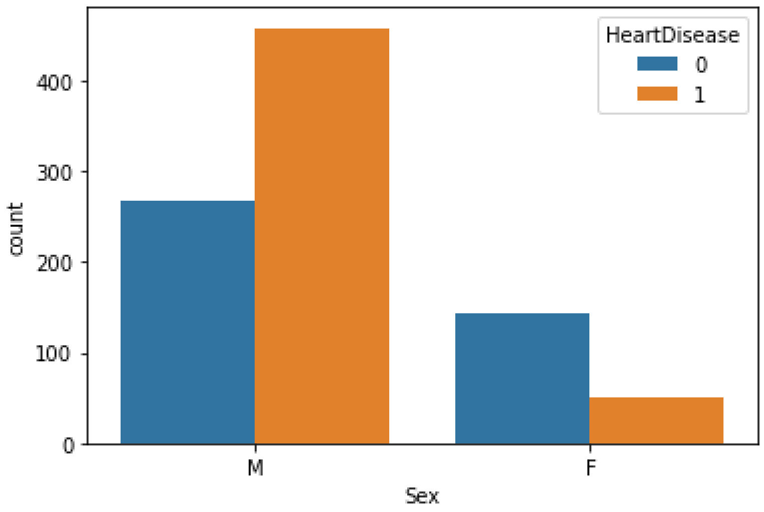
In [20]:

```
#now its time to plot sum graphs to analyze data
sns.countplot(cat["Sex"],hue=num["HeartDisease"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

Out[20]:

```
<AxesSubplot:xlabel='Sex', ylabel='count'>
```



In [21]:

```
# from the above data we can say that most of the males are affected the heart diseases
```

In [22]:

```
#now we will analyze male data and female data separately
df.groupby(df["Sex"]).mean()
```

Out[22]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
Sex							
F	52.492228	132.212435	241.196891	0.134715	146.139896	0.668912	0.259067
M	53.782069	132.445517	187.513103	0.259310	134.325517	0.945517	0.631724

In [23]:

```
#from the above we can say that average age for getting heart disease for both male and female are similar
#fasting blood sugar was high when compared to female
```

In [24]:

```
df.groupby(df["Sex"]).median()
```

Out[24]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
Sex							
F	53.0	130.0	243.0	0.0	150.0	0.0	0.0
M	55.0	130.0	219.0	0.0	134.0	0.8	1.0

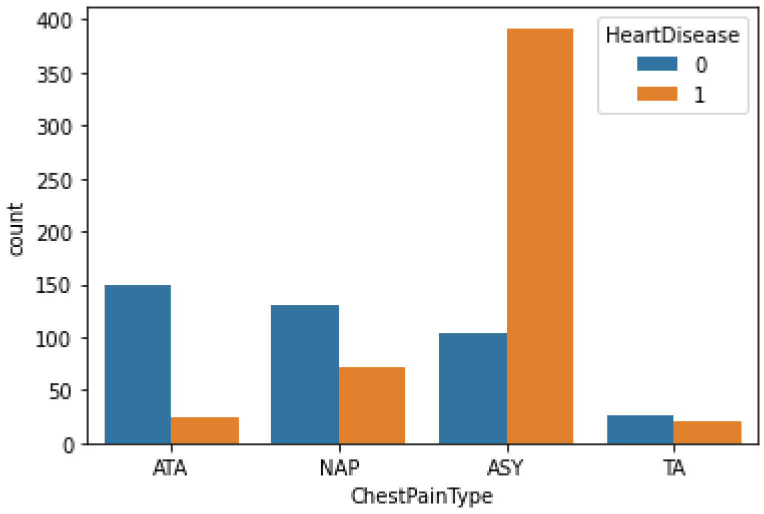
In [25]:

```
#now comparing the Heart Disease with other features
sns.countplot(df["ChestPainType"],hue=df["HeartDisease"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

Out[25]:

```
<AxesSubplot:xlabel='ChestPainType', ylabel='count'>
```



In [26]:

```
#from the above graph we acn say that asy chest pain type are affecting more for heart diseases
```

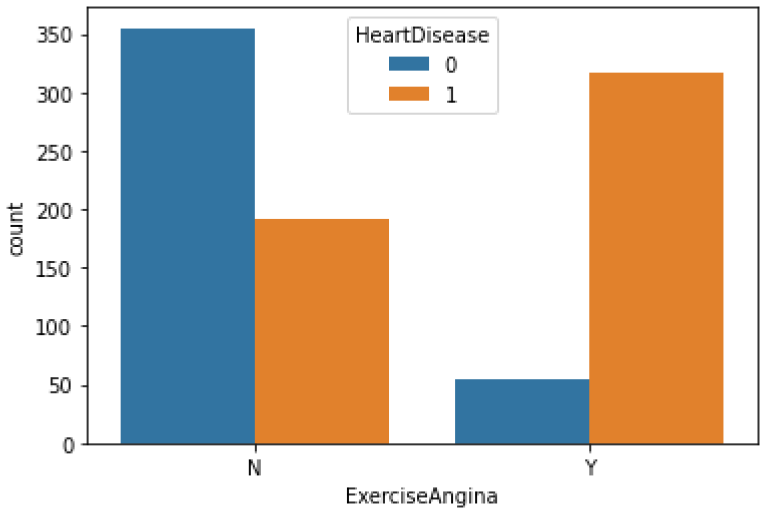
In [27]:

```
sns.countplot(df["ExerciseAngina"],hue=df["HeartDisease"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

Out[27]:

```
<AxesSubplot:xlabel='ExerciseAngina', ylabel='count'>
```



In [28]:

```
#the above feature exerciseagina means the heart strokes that happend because of the exercises for female it was high
```

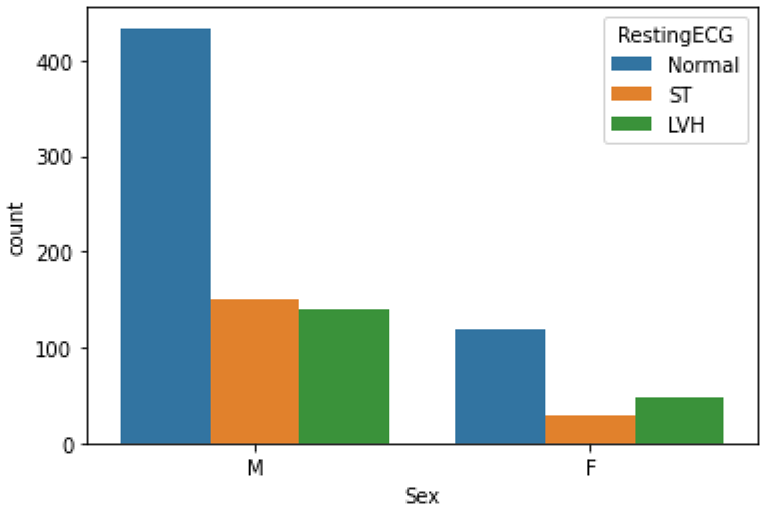
In [29]:

```
#now we will see the restingecg it is used to predict the electrical activity of heart
#whether the person have heart strock or not and it finds rhythm of the heart
sns.countplot(df["Sex"],hue=df["RestingECG"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

Out[29]:

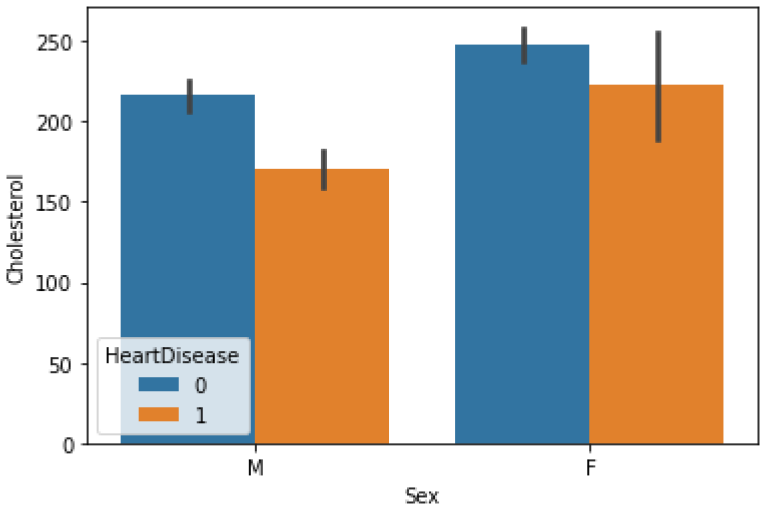
```
<AxesSubplot:xlabel='Sex', ylabel='count'>
```



In [30]:
```
#in the above graph we can see the resting ecg values in the data set for both males and females
```

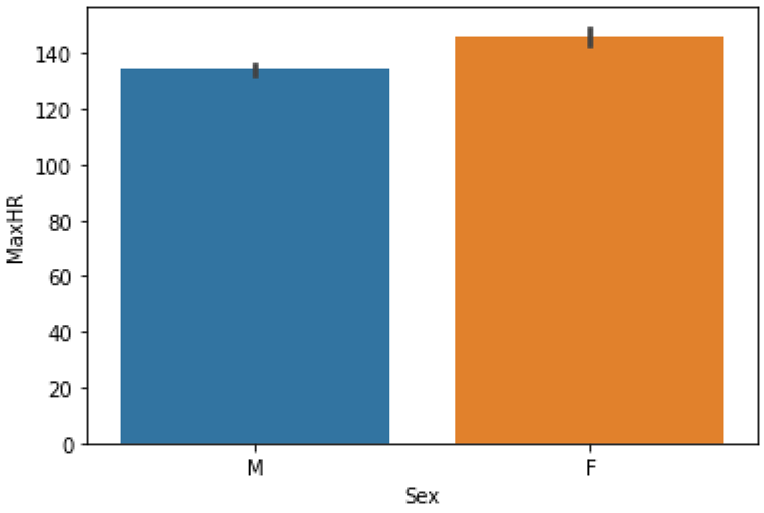
In [31]:
```
#now we will see some barplots for more understanding of data
sns.barplot(x='Sex',y="Cholesterol",hue="HeartDisease",data=df)
```

Out[31]:
```
<AxesSubplot:xlabel='Sex', ylabel='Cholesterol'>
```



In [32]:
```
sns.barplot(x="Sex",y="MaxHR",data=df)
```

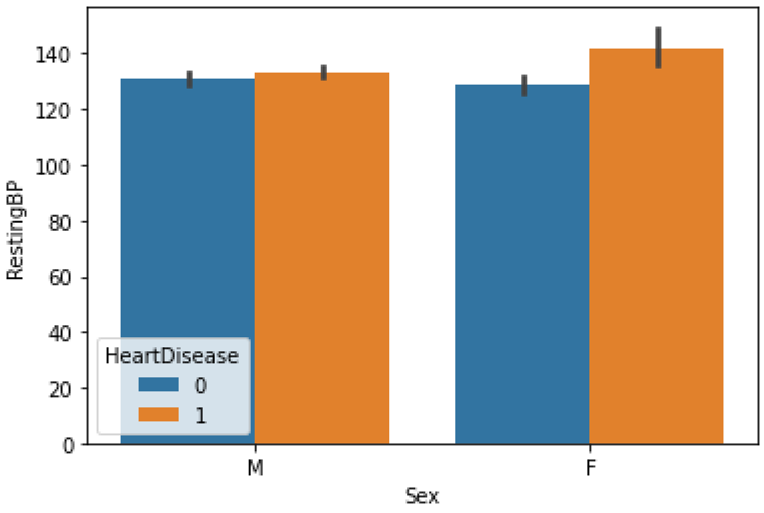
Out[32]:
```
<AxesSubplot:xlabel='Sex', ylabel='MaxHR'>
```



In [33]:
```
#maximum heart rate is more for females when compared to males
```

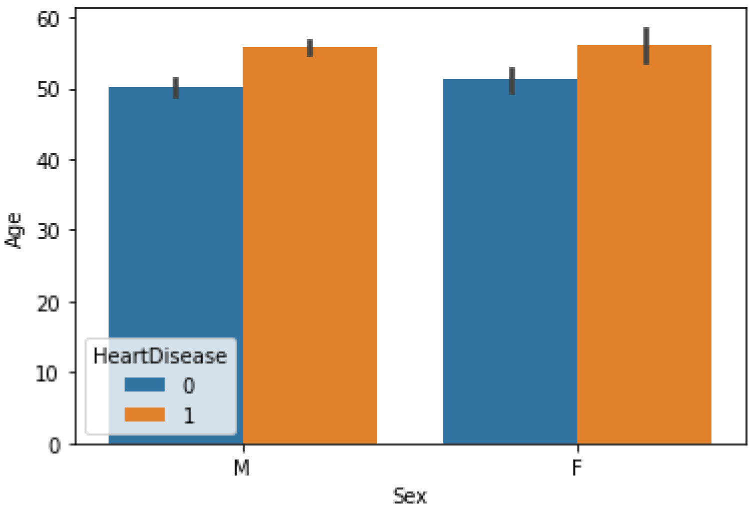
In [34]:
```
sns.barplot(x="Sex",y="RestingBP",data=df,hue="HeartDisease")
```

Out[34]:
```
<AxesSubplot:xlabel='Sex', ylabel='RestingBP'>
```



In [35]:
```
sns.barplot(x="Sex",y="Age",data=df,hue="HeartDisease")
```

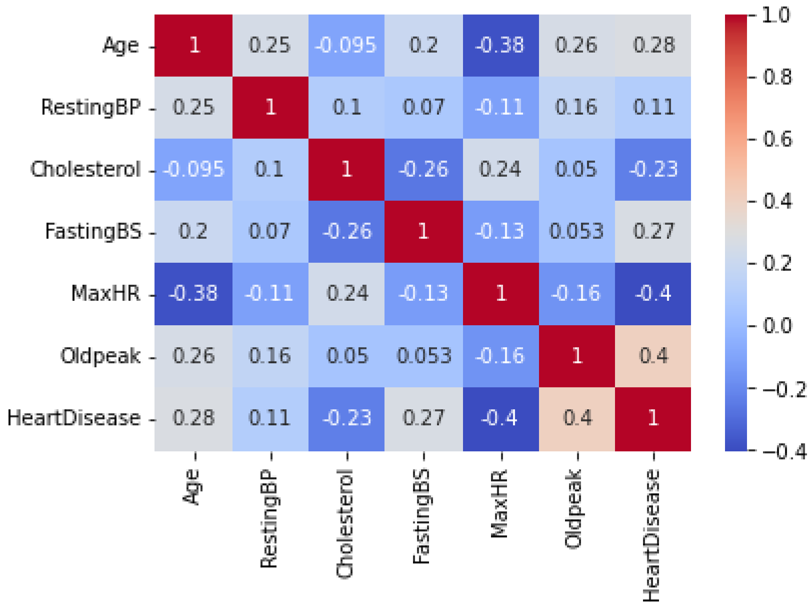
Out[35]:
```
<AxesSubplot:xlabel='Sex', ylabel='Age'>
```



In [36]:
```
#people affected by the heart disease are above the 50 age
```

In [37]:
```
#now we will the correlation matrix in order to get the relation
sns.heatmap(df.corr(),annot=True,cmap="coolwarm")
```

Out[37]:
```
<AxesSubplot:>
```

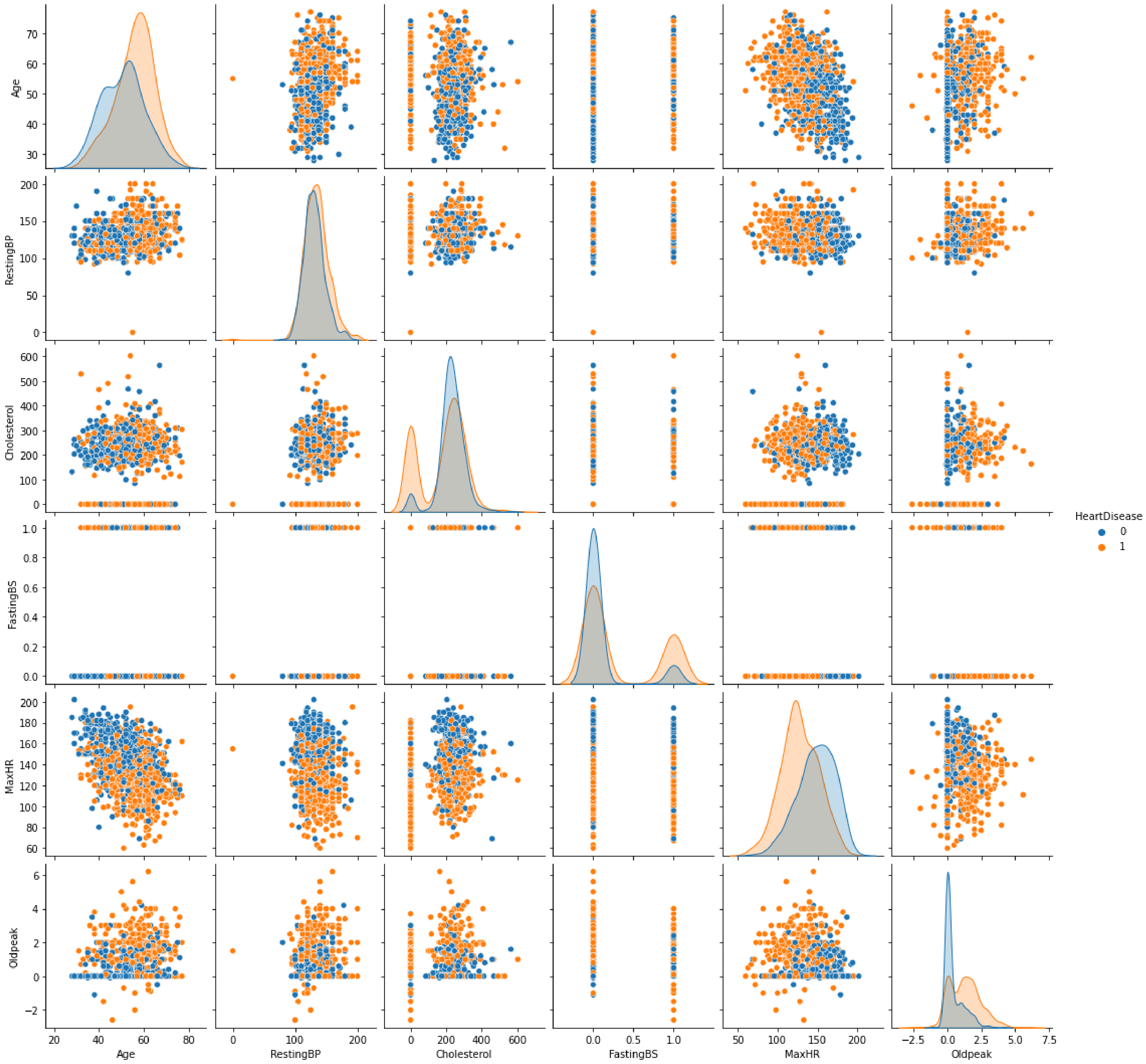


In [38]:

```
#from the above we can say that mostly
sns.pairplot(df,hue="HeartDisease")
```

Out[38]:

```
<seaborn.axisgrid.PairGrid at 0x243f054f910>
```



In [39]:

```
#from the above we can see the distribution of the both heartdisease having and not having people
```

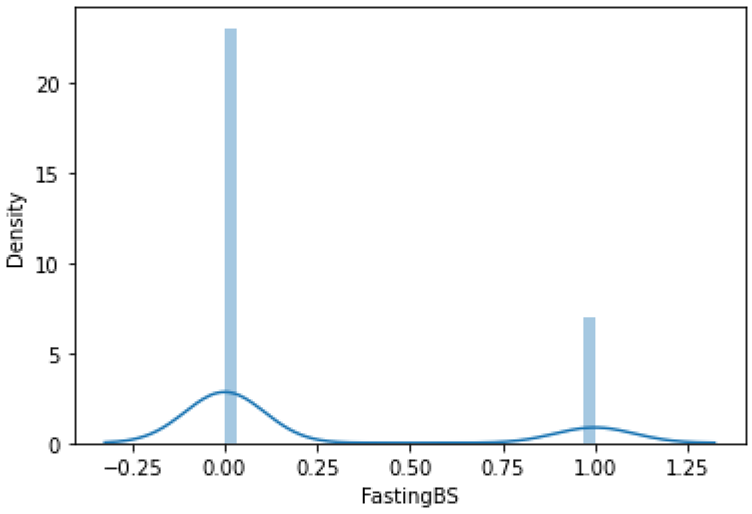
In [40]:

```
sns.distplot(df["FastingBS"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a depr
ecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-lev
el function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[40]:

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



In [41]:
```
num.head()
```

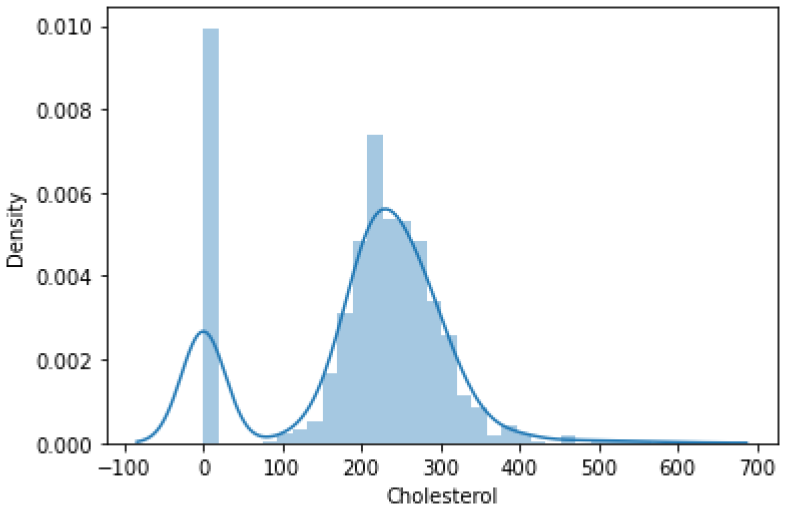
Out[41]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
0	40	140	289	0	172	0.0	0
1	49	160	180	0	156	1.0	1
2	37	130	283	0	98	0.0	0
3	48	138	214	0	108	1.5	1
4	54	150	195	0	122	0.0	0

In [42]:
```
sns.distplot(df["Cholesterol"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a depr
ecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-lev
el function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

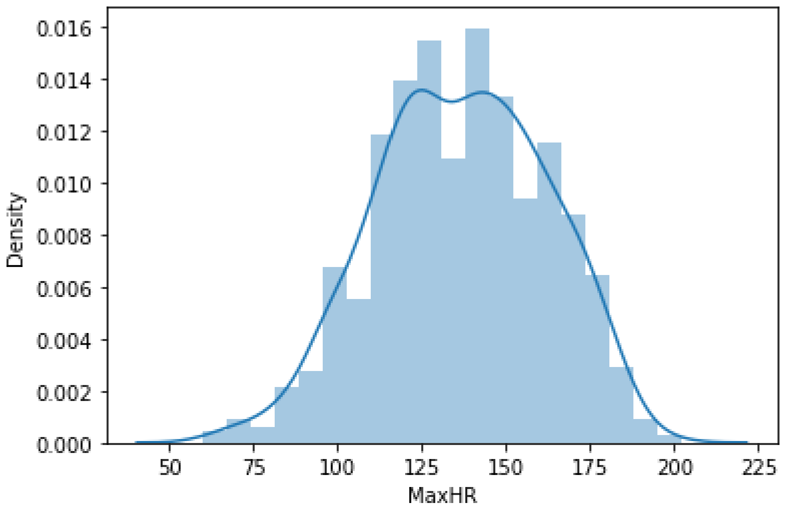
Out[42]:
```
<AxesSubplot:xlabel='Cholesterol', ylabel='Density'>
```



In [43]:
```
sns.distplot(df["MaxHR"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a depr
ecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-lev
el function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

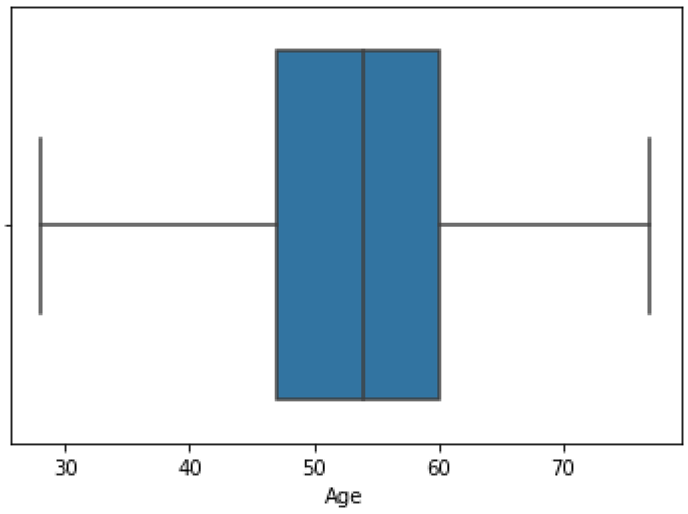
Out[43]:
```
<AxesSubplot:xlabel='MaxHR', ylabel='Density'>
```



In [44]:
```
#now it time to detect outliers in the data set
sns.boxplot(df["Age"],hue=df["HeartDisease"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

Out[44]:
```
<AxesSubplot:xlabel='Age'>
```

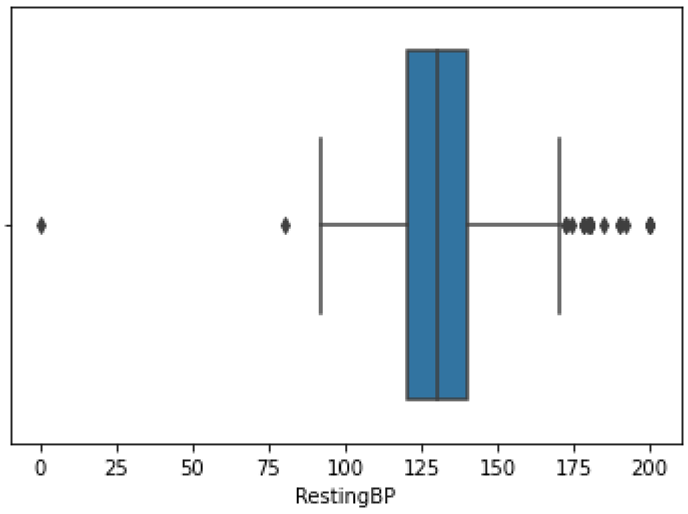


In [45]:
```
#there are no outliers in the age
```

In [46]:
```
sns.boxplot(df["RestingBP"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

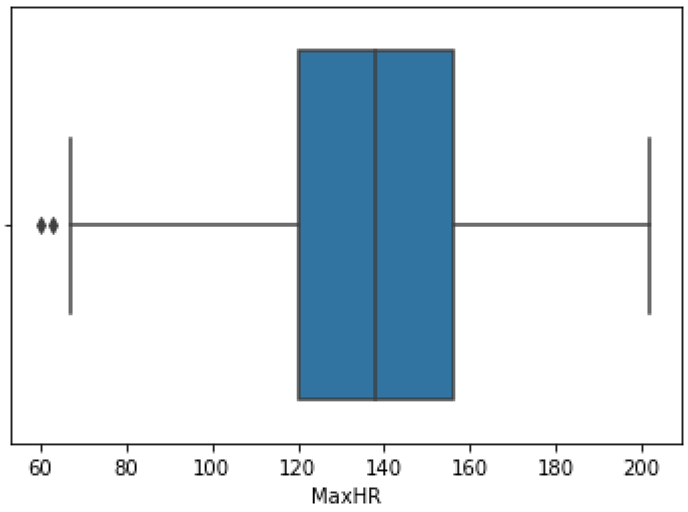
Out[46]:
```
<AxesSubplot:xlabel='RestingBP'>
```



In [47]:
```
sns.boxplot(df["MaxHR"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

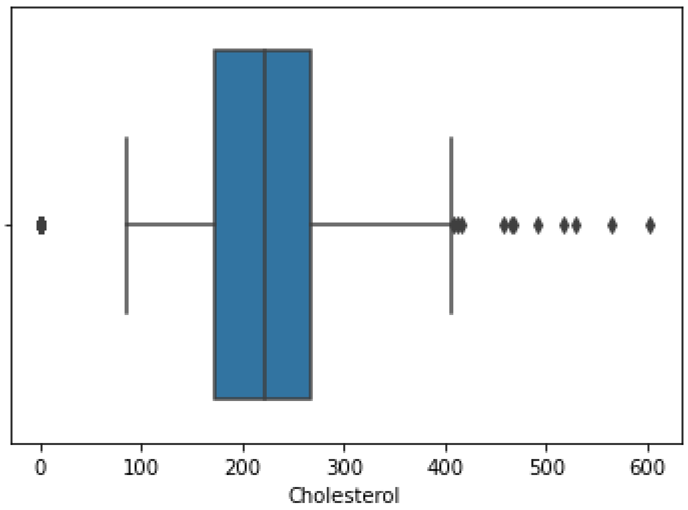
Out[47]:
```
<AxesSubplot:xlabel='MaxHR'>
```



In [48]:
```
sns.boxplot(df["Cholesterol"])
```

```
c:\Users\VIVEKANANDA D\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following varia
ble as a keyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other argu
ments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

Out[48]:
```
<AxesSubplot:xlabel='Cholesterol'>
```



In [49]:
```
#now we will remove the outliers in the data set using the zscore method
from scipy import stats
data=df[(np.abs(stats.zscore(num))<3).all(axis=1)]
```

In [50]:
```
data
```

Out[50]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0
...	...	...	...	...	...	...	...	...	...	...	...	...
913	45	M	TA	110	264	0	Normal	132	N	1.2	Flat	1
914	68	M	ASY	144	193	1	Normal	141	N	3.4	Flat	1
915	57	M	ASY	130	131	0	Normal	115	Y	1.2	Flat	1
916	57	F	ATA	130	236	0	LVH	174	N	0.0	Flat	1
917	38	M	NAP	138	175	0	Normal	173	N	0.0	Up	0

899 rows × 12 columns

In [51]:
```
#we removed outliers from the data set
data.shape
```

Out[51]:
```
(899, 12)
```

In [52]:
```
#now its time to transform catogorical data into numerical data
sub=pd.get_dummies(cat,drop_first=True)
```

In [53]:
```
sub.head()
```

Out[53]:

	Sex_M	ChestPainType_ATA	ChestPainType_NAP	ChestPainType_TA	RestingECG_Normal	RestingECG_ST	ExerciseAngina_Y	ST_Slope_Flat	S
0	1	1	0	0	1	0	0	0	
1	0	0	1	0	1	0	0	1	
2	1	1	0	0	0	1	0	0	
3	0	0	0	0	1	0	1	1	
4	1	0	1	0	1	0	0	0	

In [54]:
```
data.drop(cat,axis=1,inplace=True)
```

```
C:\Users\VIVEKANANDA D\AppData\Local\Temp\ipykernel_15056\486506185.py:1: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning
-a-view-versus-a-copy (https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-
a-copy)
  data.drop(cat,axis=1,inplace=True)
```

In [55]:

```
#now we will concatenate our transformed data with the numerical data
df1=pd.concat([sub,data],axis=1)
```

In [56]:

```
#now we need to remove the null values
df1.head()
```

Out[56]:

	Sex_M	ChestPainType_ATA	ChestPainType_NAP	ChestPainType_TA	RestingECG_Normal	RestingECG_ST	ExerciseAngina_Y	ST_Slope_Flat	S
0	1	1	0	0	1	0	0	0	
1	0	0	1	0	1	0	0	1	
2	1	1	0	0	0	1	0	0	
3	0	0	0	0	1	0	1	1	
4	1	0	1	0	1	0	0	0	

In [57]:

```
df1.isna().sum()
```

Out[57]:

```
Sex_M                 0
ChestPainType_ATA     0
ChestPainType_NAP     0
ChestPainType_TA      0
RestingECG_Normal     0
RestingECG_ST         0
ExerciseAngina_Y      0
ST_Slope_Flat         0
ST_Slope_Up           0
Age                  19
RestingBP            19
Cholesterol          19
FastingBS            19
MaxHR                19
Oldpeak              19
HeartDisease         19
dtype: int64
```

In [58]:

```
df1=df1.dropna()
```

In [59]:

```
df1.shape
```

Out[59]:

```
(899, 16)
```

In [60]:

```
#scaling down features
```

In [61]:

```
#dividing of independent and dependent variables
x=StandardScaler().fit_transform(df1.drop("HeartDisease",axis=1))
y=df1["HeartDisease"]
```

In [62]:

```
d=pd.DataFrame(x)
```

In [63]:

```
#these are scale down features
d.head()
```

Out[63]:

	0	1	2	3	4	5	6	7	8	9	10	11	12	
0	0.515943	2.063325	-0.534905	-0.22955	0.809702	-0.489898	-0.822945	-0.998888	1.134695	-1.428154	0.465900	0.849636	-0.550362	1.384
1	-1.938199	-0.484655	1.869492	-0.22955	0.809702	-0.489898	-0.822945	1.001113	-0.881294	-0.475855	1.634714	-0.168122	-0.550362	0.752
2	0.515943	2.063325	-0.534905	-0.22955	-1.235023	2.041241	-0.822945	-0.998888	1.134695	-1.745588	-0.118507	0.793612	-0.550362	-1.535
3	-1.938199	-0.484655	-0.534905	-0.22955	0.809702	-0.489898	1.215148	1.001113	-0.881294	-0.581666	0.349019	0.149344	-0.550362	-1.141
4	0.515943	-0.484655	1.869492	-0.22955	0.809702	-0.489898	-0.822945	-0.998888	1.134695	0.053200	1.050307	-0.028064	-0.550362	-0.588

In [64]:

```
#modelling
```

In [65]:

```
#now its time for spliting of data
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.3,random_state=1)
```

In [66]:

```
#now viewing the shapes of trainning and testing data
x_train.shape,y_train.shape,x_test.shape,y_test.shape
```

Out[66]:

```
((629, 15), (629,), (270, 15), (270,))
```

In [67]:
```
#there are 629 values for training and 270 values for testing
```

In [68]:
```
model=dtc()
```

In [69]:
```
#fitting the model
model.fit(x_train,y_train)
```

Out[69]:
```
DecisionTreeClassifier()
```

In [70]:
```
pre=model.predict(x_test)
```

In [71]:
```
pre
```

Out[71]:
```
array([1., 0., 0., 1., 1., 0., 0., 0., 1., 0., 1., 1., 1., 0., 1., 1., 0.,
       0., 0., 1., 0., 1., 1., 1., 1., 0., 1., 1., 0., 0., 1., 0., 0., 0.,
       1., 0., 0., 0., 0., 1., 1., 0., 0., 0., 1., 0., 0., 0., 1., 0., 0.,
       1., 1., 1., 1., 1., 1., 0., 0., 0., 1., 0., 0., 1., 1., 1., 1., 0.,
       0., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 0., 1., 1., 0., 1., 1.,
       1., 1., 0., 0., 1., 0., 1., 0., 1., 0., 0., 1., 1., 1., 1., 0., 1.,
       1., 0., 1., 1., 1., 1., 1., 0., 0., 0., 1., 0., 1., 0., 0., 0., 0.,
       1., 1., 1., 0., 0., 1., 1., 0., 0., 1., 0., 1., 1., 0., 0., 0., 1.,
       1., 1., 0., 0., 0., 1., 1., 0., 0., 1., 1., 0., 1., 0., 0., 1., 0.,
       1., 1., 0., 0., 1., 0., 1., 1., 0., 0., 0., 0., 1., 0., 0., 0., 1.,
       1., 0., 1., 0., 1., 0., 0., 1., 0., 1., 1., 0., 1., 1., 1., 1., 0.,
       0., 1., 1., 1., 0., 1., 0., 0., 0., 1., 1., 0., 0., 1., 1., 0., 0.,
       0., 0., 0., 1., 0., 1., 0., 1., 1., 0., 1., 1., 0., 0., 1., 0., 0.,
       0., 0., 1., 0., 0., 1., 1., 0., 1., 1., 1., 0., 0., 0., 0., 1., 0.,
       1., 0., 1., 1., 1., 1., 0., 1., 1., 1., 1., 0., 0., 0., 1., 1., 0.,
       0., 0., 1., 1., 0., 0., 1., 0., 1., 1., 1., 0., 1., 1., 1.])
```

In [72]:
```
accuracy_score(pre,y_test)
```

Out[72]:
```
0.7666666666666667
```

In [74]:
```
print(cr(pre,y_test))
```

```
              precision    recall  f1-score   support

         0.0       0.78      0.72      0.75       131
         1.0       0.75      0.81      0.78       139

    accuracy                           0.77       270
   macro avg       0.77      0.77      0.77       270
weighted avg       0.77      0.77      0.77       270
```

In [75]:
```
#accuracy of our model is 77 percent
```

In [76]:
```
#now logistic regression
m=lr()
```

In [77]:
```
m.fit(x_train,y_train)
```

Out[77]:
```
LogisticRegression()
```

In [78]:
```
predict=m.predict(x_test)
```

In [79]:
```
accuracy_score(predict,y_test)
```

Out[79]:
```
0.8629629629629629
```

In [81]:
```
print(cr(predict,y_test))
```

```
              precision    recall  f1-score   support

         0.0       0.85      0.84      0.85       121
         1.0       0.87      0.88      0.88       149

    accuracy                           0.86       270
   macro avg       0.86      0.86      0.86       270
weighted avg       0.86      0.86      0.86       270
```

In [82]:
```
bayes=bs()
```

```
In [83]: bayes.fit(x_train,y_train)

Out[83]: GaussianNB()

In [84]: p=bayes.predict(x_test)

In [85]: p

Out[85]: array([1., 0., 0., 0., 1., 0., 1., 1., 1., 0., 0., 0., 0., 1., 1., 1., 0.,
                0., 1., 0., 0., 1., 0., 1., 1., 1., 1., 1., 0., 0., 1., 0., 0., 0.,
                1., 0., 0., 0., 0., 1., 1., 0., 0., 0., 1., 1., 0., 0., 1., 0., 0.,
                0., 1., 1., 1., 1., 1., 0., 1., 1., 1., 1., 1., 1., 1., 1., 0., 1.,
                0., 1., 0., 1., 1., 1., 1., 1., 1., 0., 1., 0., 0., 0., 0., 1., 0.,
                1., 1., 1., 0., 1., 0., 1., 0., 1., 1., 0., 1., 1., 1., 1., 1., 1.,
                1., 0., 1., 1., 1., 0., 1., 0., 0., 0., 1., 0., 1., 0., 0., 0., 0.,
                0., 1., 1., 0., 0., 1., 1., 0., 0., 1., 1., 1., 1., 1., 1., 0., 1.,
                1., 1., 0., 0., 0., 1., 1., 1., 0., 1., 1., 0., 1., 1., 1., 1., 0.,
                0., 0., 0., 1., 1., 0., 0., 0., 0., 1., 0., 1., 1., 0., 0., 0., 1.,
                1., 0., 0., 0., 1., 1., 0., 1., 0., 1., 1., 0., 1., 0., 1., 1., 0.,
                1., 1., 0., 0., 1., 0., 1., 0., 0., 1., 0., 0., 1., 1., 1., 0., 0.,
                0., 0., 0., 1., 1., 1., 1., 1., 0., 0., 1., 1., 1., 0., 1., 0., 0.,
                0., 1., 1., 0., 0., 1., 1., 0., 1., 1., 1., 1., 0., 0., 1., 1., 0.,
                1., 0., 1., 0., 0., 0., 0., 1., 1., 1., 1., 0., 1., 0., 1., 1., 0.,
                0., 0., 1., 0., 0., 0., 1., 0., 1., 1., 1., 0., 0., 1., 1.])

In [86]: accuracy_score(p,y_test)

Out[86]: 0.8629629629629629

In [88]: print(cr(p,y_test))

                       precision    recall  f1-score   support

                 0.0       0.87      0.83      0.85       125
                 1.0       0.86      0.89      0.87       145

            accuracy                           0.86       270
           macro avg       0.86      0.86      0.86       270
        weighted avg       0.86      0.86      0.86       270


In [89]: mod=SVC()

In [90]: mod.fit(x_train,y_train)

Out[90]: SVC()

In [91]: pred=mod.predict(x_test)

In [92]: accuracy_score(pred,y_test)

Out[92]: 0.8925925925925926

In [94]: print(cr(pred,y_test))

                       precision    recall  f1-score   support

                 0.0       0.85      0.90      0.88       113
                 1.0       0.93      0.89      0.91       157

            accuracy                           0.89       270
           macro avg       0.89      0.89      0.89       270
        weighted avg       0.89      0.89      0.89       270


In [95]: #svc got more accuracy when compared to other models

In [96]: #############################END###########################################
```