----------Project----------

.....Heart Disease Prediction.....

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import libraries

In [1]:
```
import pandas as pd
import numpy as np

# data visualization
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns

from sklearn.model_selection import train_test_split

#model validation
from sklearn.metrics import log_loss,precision_score,f1_score,recall_score,roc_auc_scor
from sklearn.metrics import confusion_matrix,accuracy_score,matthews_corrcoef
from sklearn import metrics

# machine learning algorithms
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier,GradientBoostingClassifier,ExtraTre
from sklearn.tree import DecisionTreeClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
import xgboost as xgb

from scipy import stats
```

In [2]:
```
dt = pd.read_csv("heart.csv")
dt.head()
```

Out[2]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1.0	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0.0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0

here i can check the quick information of our data

In [3]:
```
dt.info()
```

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

Checking the null values

In [4]:
```
dt.isnull().sum()
```

Out[4]:
```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

Check the Shape of the data

In [5]:
```
dt.shape
```

Out[5]:
```
(1025, 14)
```

In [6]:
```
rows, columns = dt.shape
print("The total rows/instances in our data is: ", rows)
print("The total columns/labels in our data is: ", columns)
```

```
The total rows/instances in our data is:  1025
The total columns/labels in our data is:  14
```

Here's the summary statistics of our data

In [7]:
```
dt.describe()
```

Out[7]:

	age	sex	cp	trestbps	chol	fbs	restecg	t
count	1025.000000	1025.000000	1025.000000	1025.000000	1025.00000	1025.000000	1025.000000	1025.
mean	54.434146	0.695610	0.942439	131.611707	246.00000	0.149268	0.529756	149.
std	9.072290	0.460373	1.029641	17.516718	51.59251	0.356527	0.527878	23.
min	29.000000	0.000000	0.000000	94.000000	126.00000	0.000000	0.000000	71.
25%	48.000000	0.000000	0.000000	120.000000	211.00000	0.000000	0.000000	132.
50%	56.000000	1.000000	1.000000	130.000000	240.00000	0.000000	1.000000	152.
75%	61.000000	1.000000	2.000000	140.000000	275.00000	0.000000	1.000000	166.
max	77.000000	1.000000	3.000000	200.000000	564.00000	1.000000	2.000000	202.

In [ ]:
```
```

Now i can separte the numerical columns and categorical columns

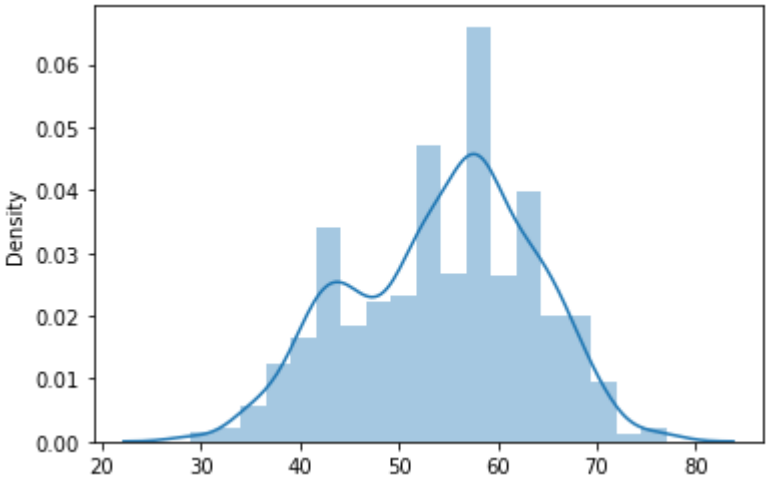
In [8]:
```
df_num = ["age","trestbps","chol","thalach","oldpeak"]
df_cat = ["sex","cp","fbs","restecg","exang","slope","ca","thal","target"]
```

here i see the age distribution

In [9]:
```
sns.distplot(x= dt["age"])
```

```
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `di
stplot` is a deprecated function and will be removed in a future version. Please adapt y
our code to use either `displot` (a figure-level function with similar flexibility) or `
histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[9]:
```
<AxesSubplot:ylabel='Density'>
```

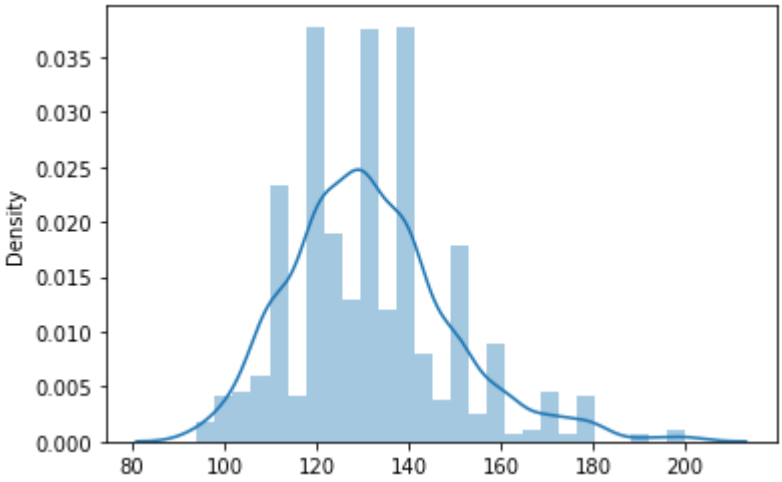


here i can see the distribution of resting bp

In [10]:
```
sns.distplot(x= dt["trestbps"])
```

```
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `di
stplot` is a deprecated function and will be removed in a future version. Please adapt y
our code to use either `displot` (a figure-level function with similar flexibility) or `
histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[10]:
```
<AxesSubplot:ylabel='Density'>
```

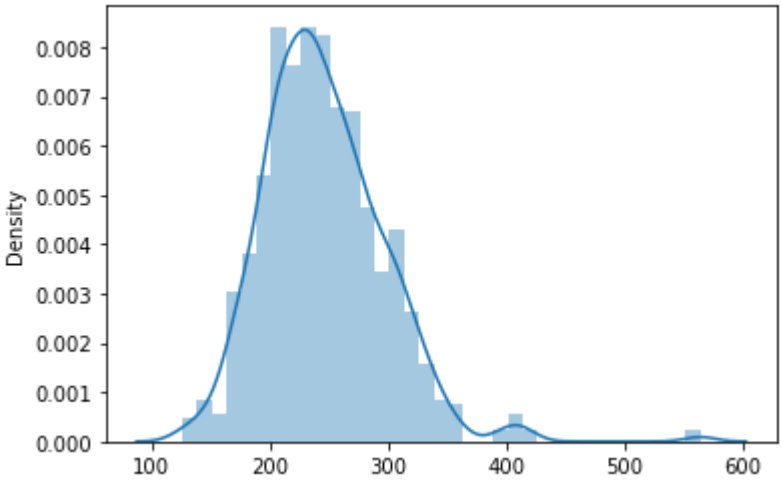


here i can see the distribution of cholestrol

In [11]:
```
sns.distplot(x= dt["chol"])
```

```
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `di
stplot` is a deprecated function and will be removed in a future version. Please adapt y
our code to use either `displot` (a figure-level function with similar flexibility) or `
histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[11]:
```
<AxesSubplot:ylabel='Density'>
```



Checking the uniquness and counts in multiple columns

In [12]:
```
# checking the unique values of the columns
dt["sex"].unique()
```

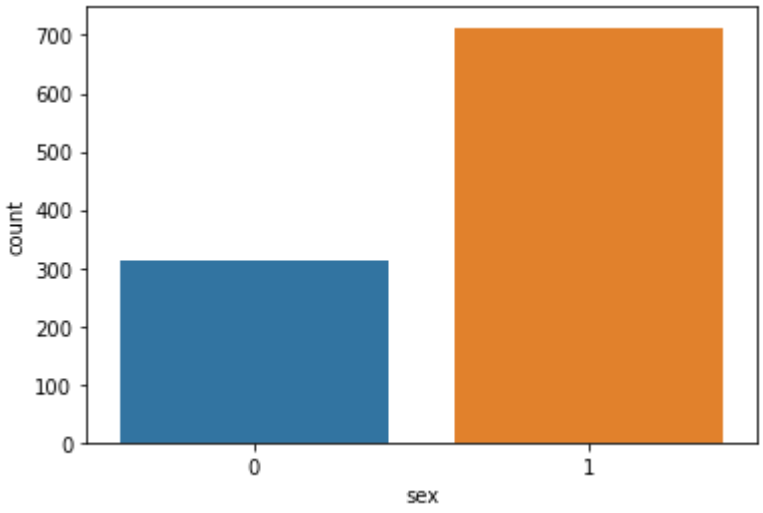
Out[12]:
```
array([1, 0], dtype=int64)
```

In [13]:
```
dt["sex"].value_counts()
```

Out[13]:
```
1    713
0    312
Name: sex, dtype: int64
```

In [14]:
```
sns.countplot(dt["sex"],data = dt)
```

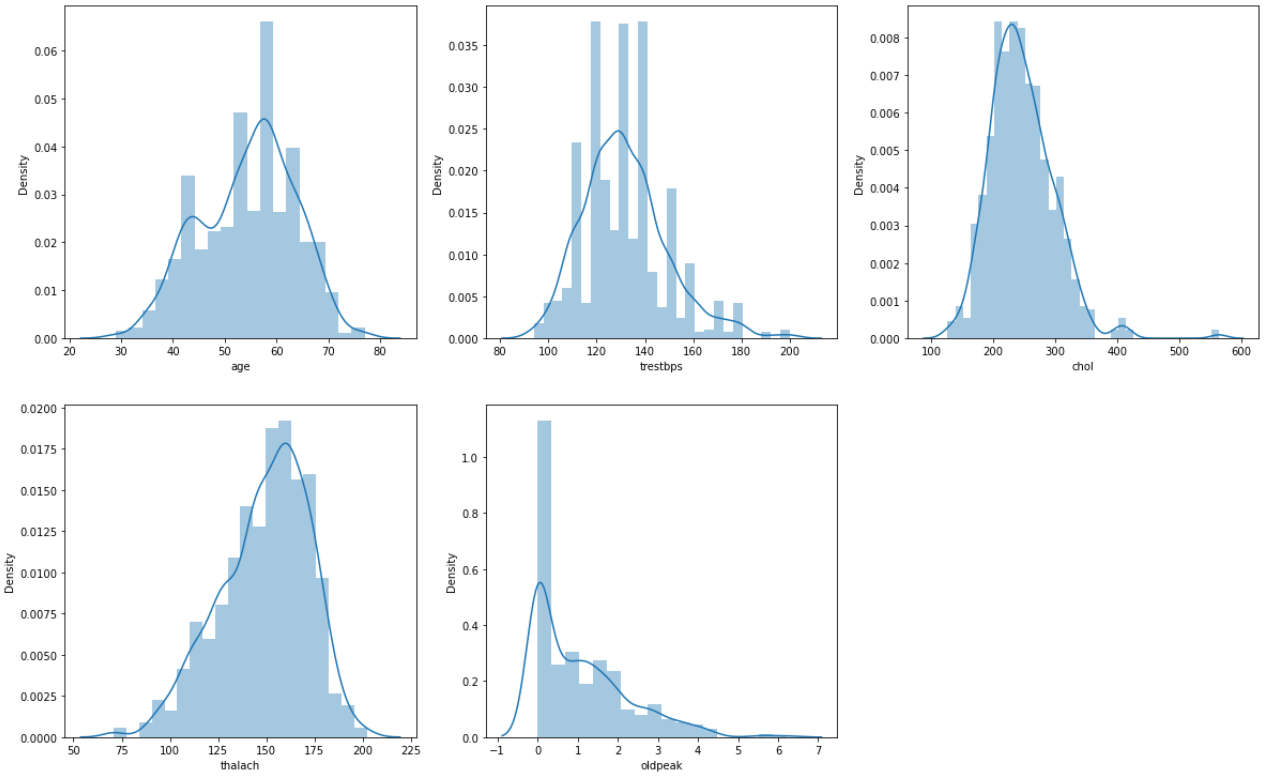
Out[14]:
```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
<AxesSubplot:xlabel='sex', ylabel='count'>
```



In [15]:

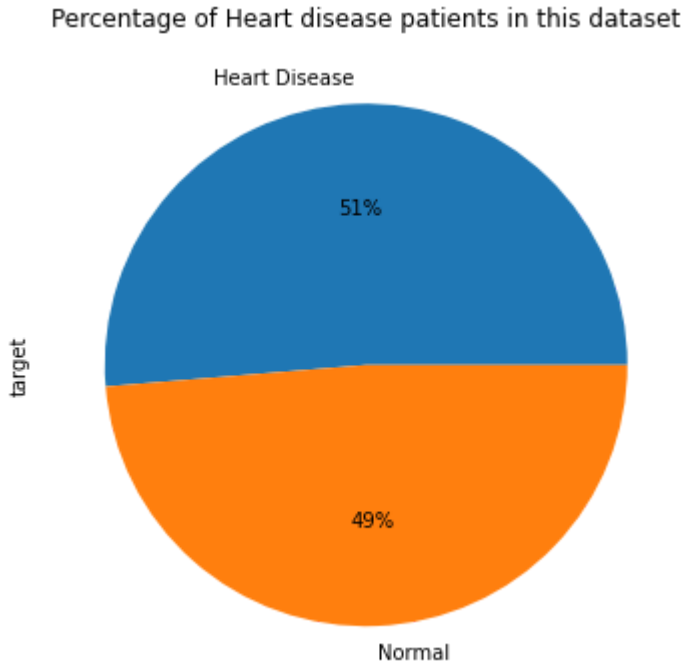
```
# Plotting Continous/Numerical columns

c = 1
plt.figure(figsize=(20,40))

for j in df_num:
    plt.subplot(6,3,c)
    sns.distplot(dt[j])
    c = c+1
plt.show()
```

```
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



Distribution of Heart disease (target variable)

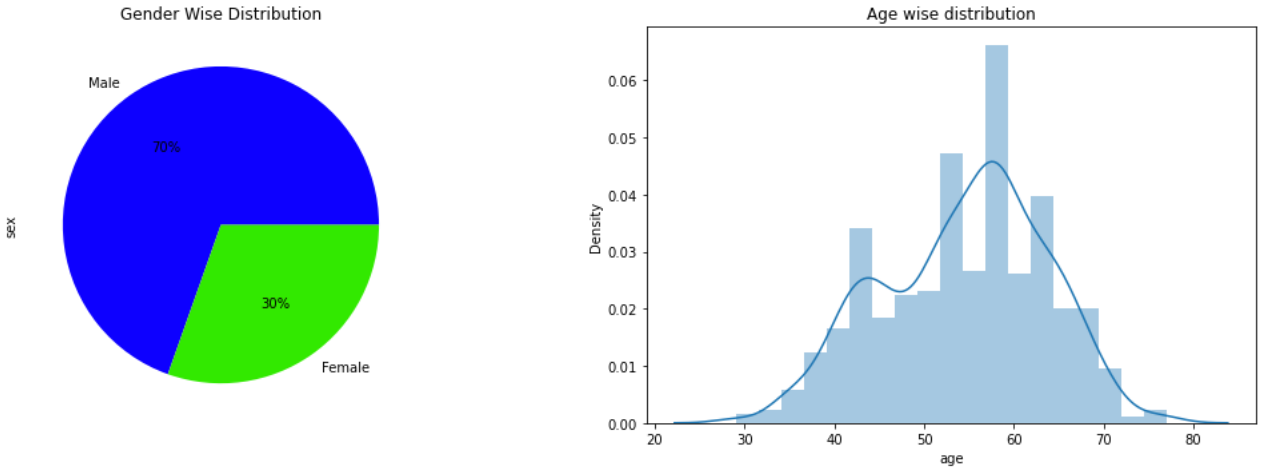
In [16]:
```
fig = plt.figure(figsize=(14,6))
ax1 = dt['target'].value_counts().plot.pie( x="Heart disease" ,y ='no.of patients',
                    autopct = "%1.0f%%",labels=["Heart Disease","Normal"]);
ax1.set(title = 'Percentage of Heart disease patients in this dataset')
plt.show()
```



Gender & Agewise Distribution

In [17]:
```
plt.figure(figsize=(18,12))
plt.subplot(221)
dt["sex"].value_counts().plot.pie(autopct = "%1.0f%%",colors = sns.color_palette("prism
plt.title("Gender Wise Distribution")

#here i can check the distribution of age

plt.subplot(222)
ax= sns.distplot(dt['age'])
plt.title("Age wise distribution")
plt.show()
```

```
H:\download\Anaconda\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `di
stplot` is a deprecated function and will be removed in a future version. Please adapt y
our code to use either `displot` (a figure-level function with similar flexibility) or `
histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

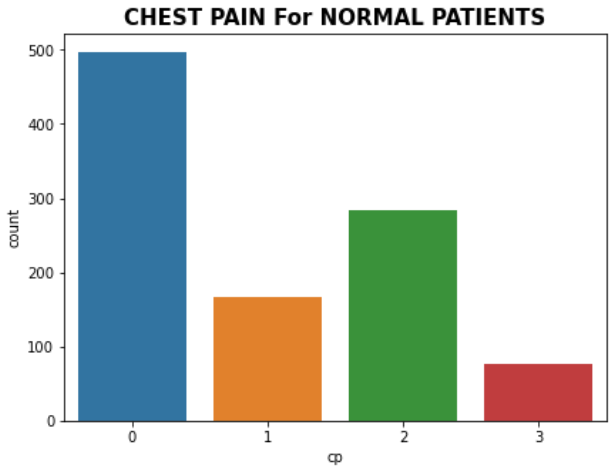


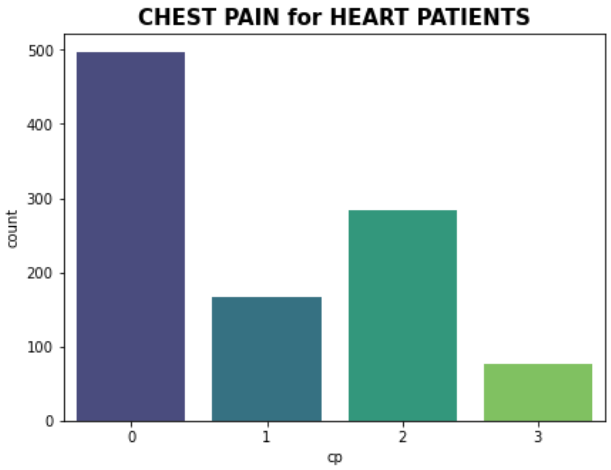
Distribution of Chest Pain Type

In [18]:
```
# plotting normal patients
fig = plt.figure(figsize=(15,5))
ax1 = plt.subplot2grid((1,2),(0,0))
sns.countplot(dt['cp'])
plt.title('CHEST PAIN For NORMAL PATIENTS', fontsize=15, weight='bold')

#plotting heart patients
ax1 = plt.subplot2grid((1,2),(0,1))
sns.countplot(dt['cp'], palette='viridis')
plt.title('CHEST PAIN for HEART PATIENTS', fontsize=15, weight='bold' )
plt.show()
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
```

```
ult in an error or misinterpretation.
  warnings.warn(
```



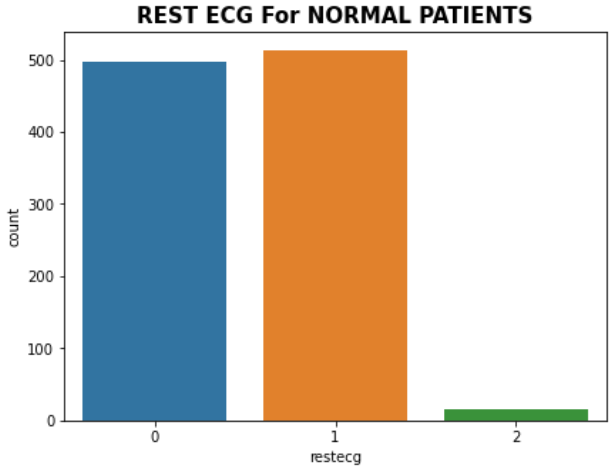


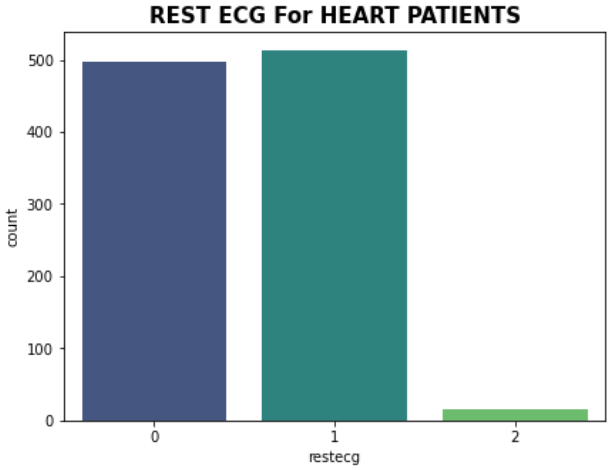
Distribution of Rest ECG

In [19]:

```
# plotting normal patients
fig = plt.figure(figsize=(15,5))
ax1 = plt.subplot2grid((1,2),(0,0))
sns.countplot(dt['restecg'])
plt.title('REST ECG For NORMAL PATIENTS', fontsize=15, weight='bold')

#plotting heart patients
ax1 = plt.subplot2grid((1,2),(0,1))
sns.countplot(dt['restecg'], palette='viridis')
plt.title('REST ECG For HEART PATIENTS', fontsize=15, weight='bold' )
plt.show()
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
```

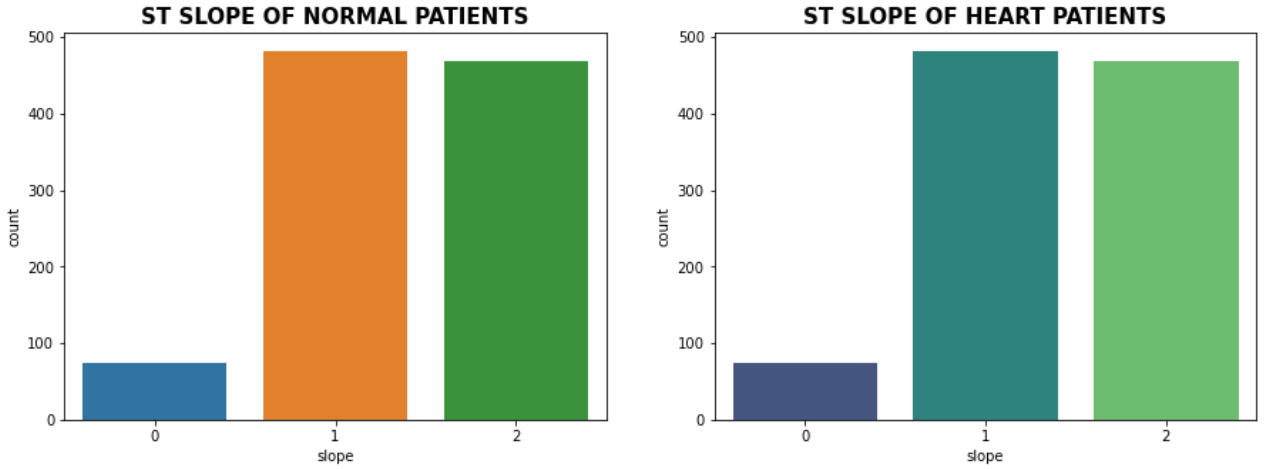




Distribution of slope

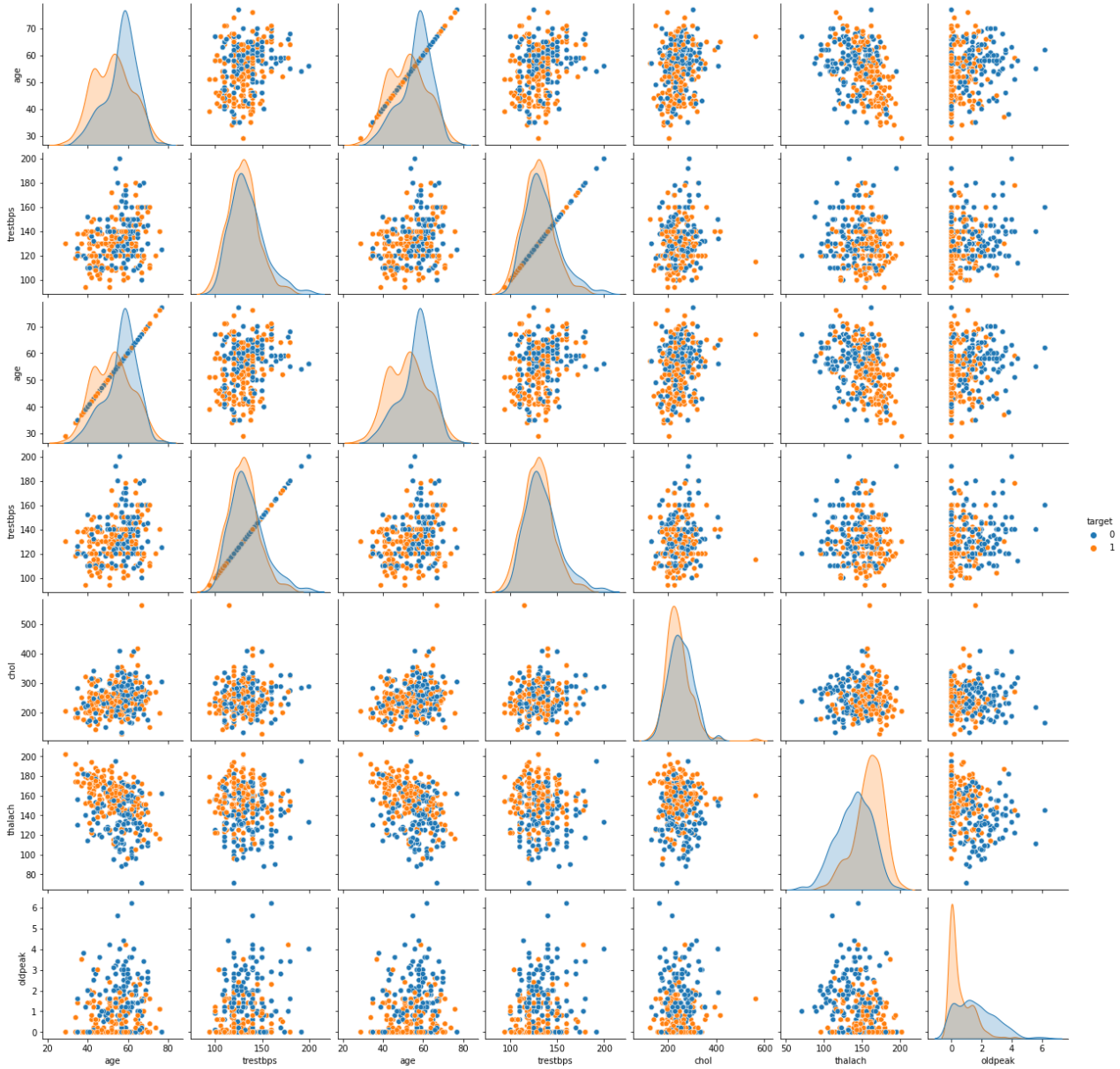
In [20]:
```
# plotting normal patients
fig = plt.figure(figsize=(15,5))
ax1 = plt.subplot2grid((1,2),(0,0))
sns.countplot(dt['slope'])
plt.title('ST SLOPE OF NORMAL PATIENTS', fontsize=15, weight='bold')

#plotting heart patients
ax1 = plt.subplot2grid((1,2),(0,1))
sns.countplot(dt['slope'], palette='viridis')
plt.title('ST SLOPE OF HEART PATIENTS', fontsize=15, weight='bold' )
plt.show()
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
```



In [21]:
```
sns.pairplot(dt, hue = 'target', vars = ['age',"trestbps","age","trestbps","chol","thal
```

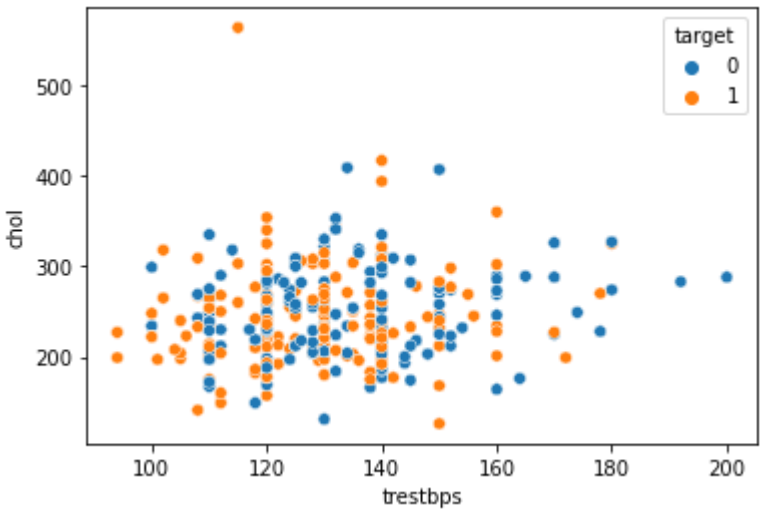
Out[21]:
```
<seaborn.axisgrid.PairGrid at 0x1bea1d83880>
```



Here i can draw a scatter plot

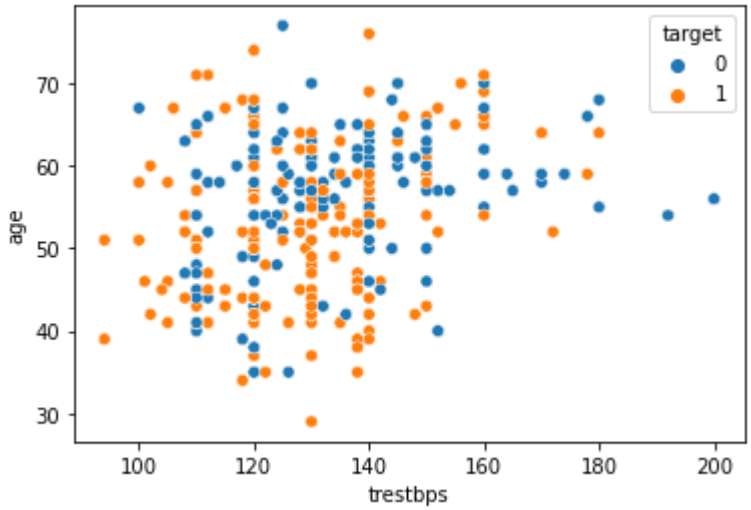
In [22]:
```
sns.scatterplot(x = 'trestbps', y = 'chol', hue = 'target', data = dt)
```

Out[22]:
```
<AxesSubplot:xlabel='trestbps', ylabel='chol'>
```



In [23]:
```
sns.scatterplot( x = 'trestbps', y = 'age', hue = 'target', data = dt)
```

Out[23]:
```
<AxesSubplot:xlabel='trestbps', ylabel='age'>
```



Here i can remove the outlier using

In [24]:
```
df_num = dt[["age","trestbps","chol","thalach","oldpeak"]]
```

In [25]:
```
df_num.head()
```

Out[25]:

	age	trestbps	chol	thalach	oldpeak
0	52	125	212	168	1.0
1	53	140	203	155	3.1
2	70	145	174	125	2.6
3	61	148	203	161	0.0
4	62	138	294	106	1.9

here i can import z score from scipy stas

In [26]:
```
# calculating zscore of numeric columns in the dataset

from scipy import stats
z = np.abs(stats.zscore(df_num))
print(z)
```

```
          age  trestbps      chol   thalach   oldpeak
0    0.268437  0.377636  0.659332  0.821321  0.060888
1    0.158157  0.479107  0.833861  0.255968  1.727137
2    1.716595  0.764688  1.396233  1.048692  1.301417
3    0.724079  0.936037  0.833861  0.516900  0.912329
4    0.834359  0.364875  0.930822  1.874977  0.705408
...       ...       ...       ...       ...       ...
1020 0.503520  0.479107  0.484803  0.647366  0.912329
1021 0.613800  0.377636  0.232705  0.352873  1.471705
1022 0.819834  1.234378  0.562371  1.353113  0.060888
1023 0.488996  1.234378  0.155137  0.429923  0.912329
1024 0.047877  0.663216  1.124743  1.570556  0.279688

[1025 rows x 5 columns]
```

In [27]:
```
# Defining threshold for filtering outliers
threshold = 3
print(np.where(z > 3))
```

```
(array([ 54,  55,  69, 123, 151, 158, 175, 179, 192, 246, 267, 294, 296,
       326, 378, 393, 450, 464, 481, 508, 526, 559, 613, 641, 665, 685,
       688, 833, 889, 958, 996], dtype=int64), array([4, 4, 4, 2, 1, 2, 1, 2, 2, 1, 3,
1, 3, 1, 3, 4, 2, 2, 2, 1, 4, 3,
       4, 2, 2, 2, 1, 4, 2, 2, 2], dtype=int64))
```

In [28]:
```
#filtered where threshold is less than 3
dt = dt[(z < 3).all(axis=1)]
```

In [29]:
```
dt.shape
```

Out[29]:
```
(994, 14)
```

Correlation

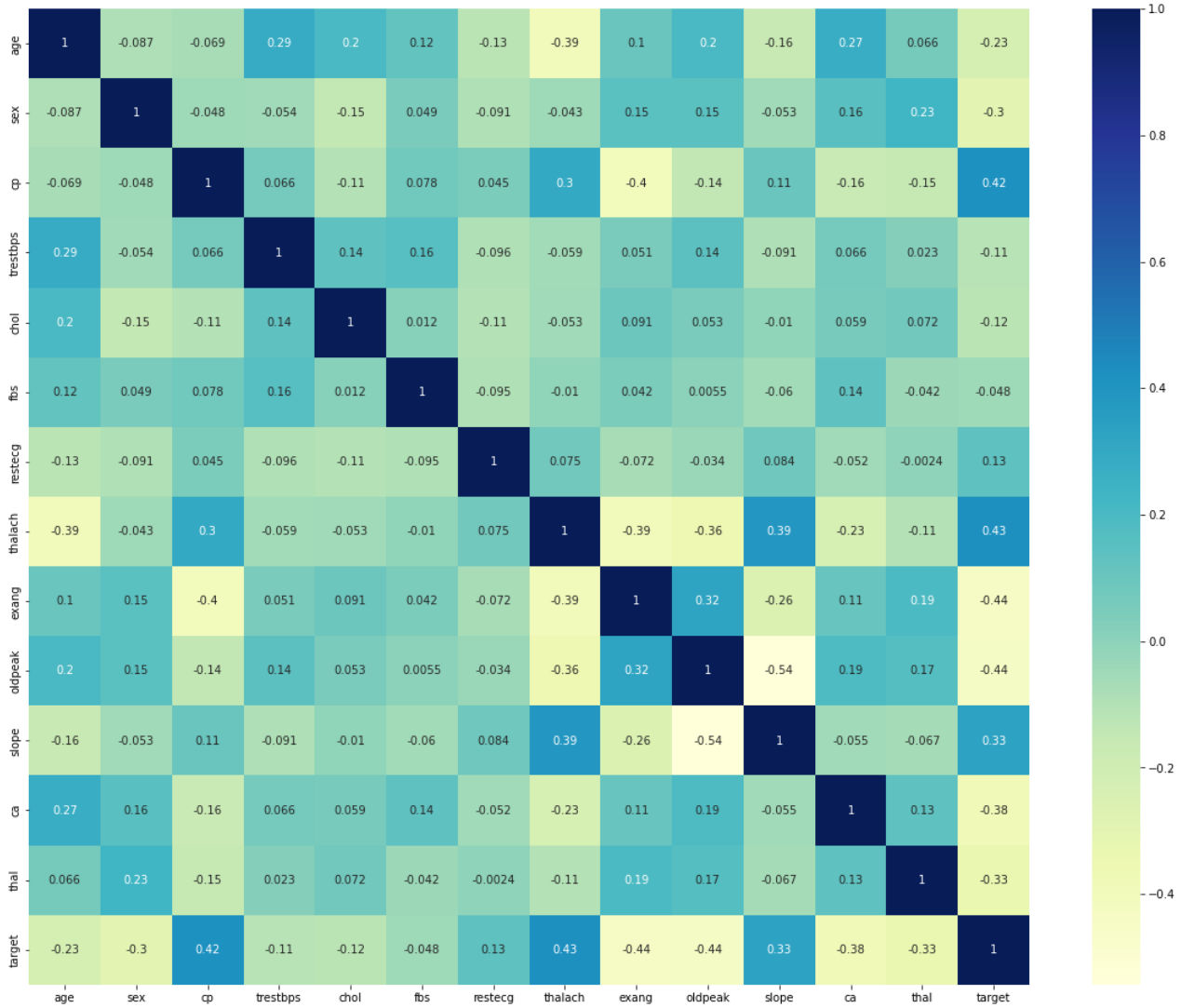
In [30]:
```
corr = dt.corr()
corr
```

Out[30]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
age	1.000000	-0.087280	-0.069128	0.285929	0.200024	0.122203	-0.126012	-0.392439	0.10235
sex	-0.087280	1.000000	-0.048426	-0.053918	-0.145201	0.049226	-0.091359	-0.042984	0.14550
cp	-0.069128	-0.048426	1.000000	0.065850	-0.108144	0.077960	0.044571	0.297943	-0.40142
trestbps	0.285929	-0.053918	0.065850	1.000000	0.136774	0.161166	-0.096239	-0.058570	0.05096

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
chol	0.200024	-0.145201	-0.108144	0.136774	1.000000	0.011746	-0.108515	-0.052669	0.091332
fbs	0.122203	0.049226	0.077960	0.161166	0.011746	1.000000	-0.094645	-0.010288	0.041767
restecg	-0.126012	-0.091359	0.044571	-0.096239	-0.108515	-0.094645	1.000000	0.075493	-0.071684
thalach	-0.392439	-0.042984	0.297943	-0.058570	-0.052669	-0.010288	0.075493	1.000000	-0.390851
exang	0.102357	0.145504	-0.401426	0.050968	0.091332	0.041767	-0.071684	-0.390851	1.000000
oldpeak	0.203698	0.146967	-0.143971	0.139878	0.053062	0.005451	-0.033572	-0.356368	0.320477
slope	-0.163046	-0.052830	0.106634	-0.090646	-0.010255	-0.059806	0.083985	0.385838	-0.257997
ca	0.272587	0.155924	-0.164602	0.065880	0.058614	0.135036	-0.052260	-0.234226	0.112791
thal	0.065701	0.229561	-0.153447	0.022886	0.072217	-0.042327	-0.002379	-0.107926	0.193999
target	-0.229328	-0.297362	0.420497	-0.110103	-0.122853	-0.047673	0.133995	0.425543	-0.442332

In [31]:
```
plt.figure(figsize=(20,16))
sns.heatmap(corr,annot=True,cmap="YlGnBu")
plt.show()
```

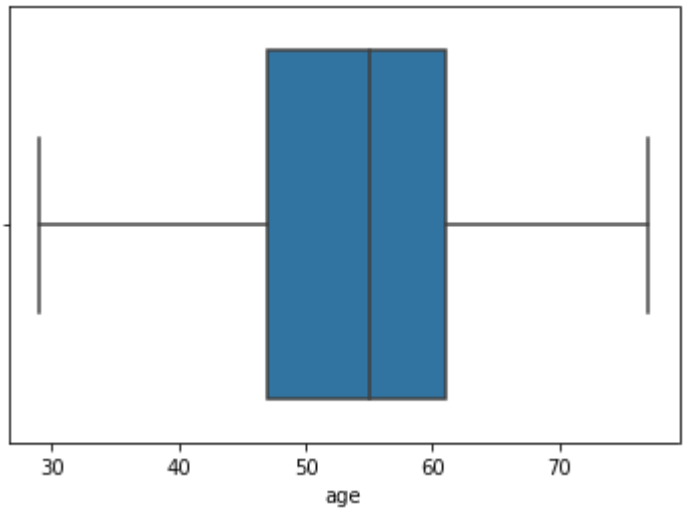


Draw a boxplot

In [32]:
```
sns.boxplot(dt.age)
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
```

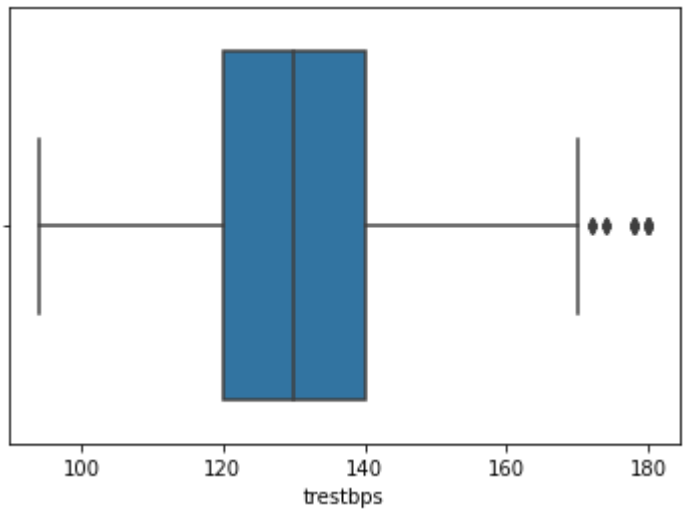
Out[32]:
```
<AxesSubplot:xlabel='age'>
```



In [33]:
```
sns.boxplot(dt["trestbps"])
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
```

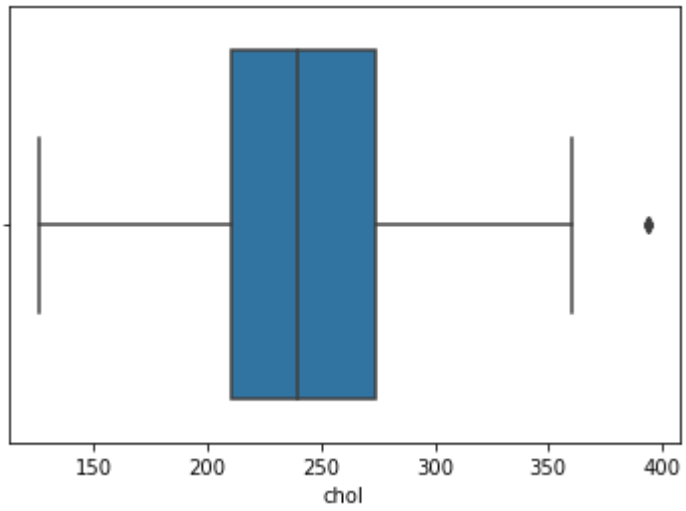
Out[33]:
```
<AxesSubplot:xlabel='trestbps'>
```



In [34]:
```
sns.boxplot(dt["chol"])
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
```

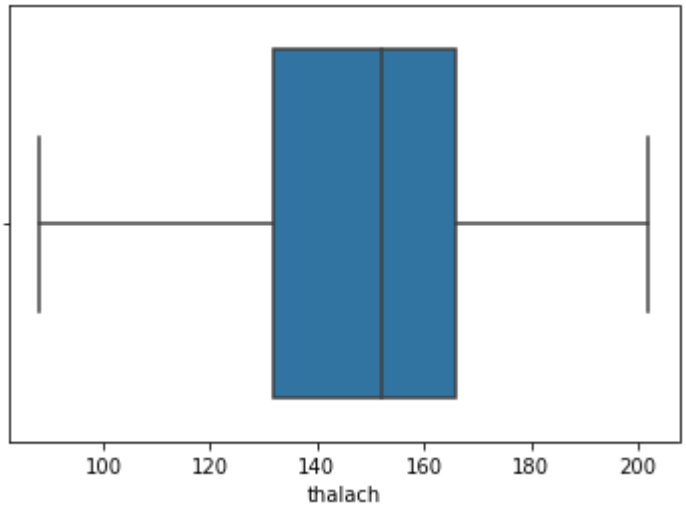
Out[34]:
```
<AxesSubplot:xlabel='chol'>
```



In [35]:
```
sns.boxplot(dt["thalach"])
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
```

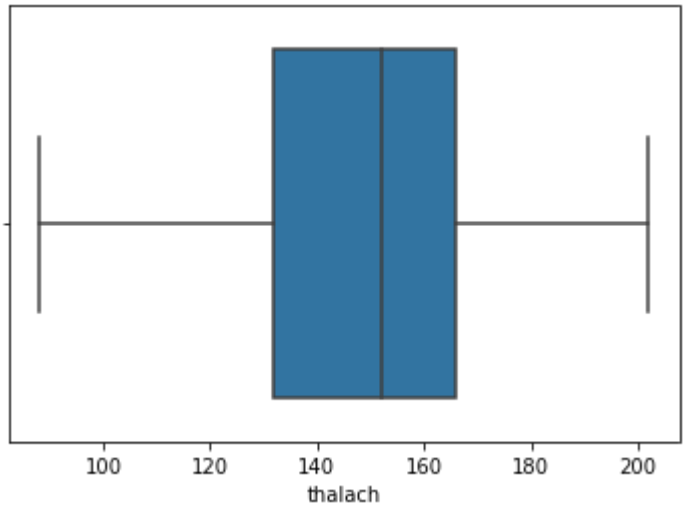
Out[35]:
```
<AxesSubplot:xlabel='thalach'>
```



In [36]:
```
sns.boxplot(dt["thalach"])
```

```
H:\download\Anaconda\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass th
e following variable as a keyword arg: x. From version 0.12, the only valid positional a
rgument will be `data`, and passing other arguments without an explicit keyword will res
ult in an error or misinterpretation.
  warnings.warn(
```

Out[36]: <AxesSubplot:xlabel='thalach'>



In [37]:
```
dt.groupby(by= "sex").sum()
```

Out[37]:

sex	age	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	16199	302	38668	74132	35	179	44075	67	223.9	424	143	610	220
1	37720	649	91571	167911	111	356	104470	267	784.5	970	589	1686	300

In [38]:
```
dt.groupby(by= ["sex","cp"]).count()
```

Out[38]:

sex	cp	age	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	**0**	119	119	119	119	119	119	119	119	119	119	119	119
	1	57	57	57	57	57	57	57	57	57	57	57	57
	2	103	103	103	103	103	103	103	103	103	103	103	103
	3	13	13	13	13	13	13	13	13	13	13	13	13
1	**0**	356	356	356	356	356	356	356	356	356	356	356	356
	1	107	107	107	107	107	107	107	107	107	107	107	107
	2	175	175	175	175	175	175	175	175	175	175	175	175
	3	64	64	64	64	64	64	64	64	64	64	64	64

In [39]:
```
grp = dt.groupby(by= ['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca', 'thal', 't
grp.head(20)
```

Out[39]:

									age	trestbps	chol	thalach	oldpeak
sex	**cp**	**fbs**	**restecg**	**exang**	**slope**	**ca**	**thal**	**target**					

sex	cp	fbs	restecg	exang	slope	ca	thal	target	age	trestbps	chol	thalach	oldpeak
0	0	0	0	0	0	2	2	0	4	4	4	4	4
					1	0	2	1	12	12	12	12	12
						2	3	0	3	3	3	3	3
						3	3	0	4	4	4	4	4
					2	0	2	0	4	4	4	4	4
								1	6	6	6	6	6
						1	2	1	3	3	3	3	3
				1	1	0	2	1	6	6	6	6	6
							3	0	4	4	4	4	4
			1	0	1	0	2	1	8	8	8	8	8
						2	2	1	3	3	3	3	3
					2	0	2	1	11	11	11	11	11
						2	2	1	3	3	3	3	3
				1	1	0	2	0	9	9	9	9	9
							3	0	6	6	6	6	6
						2	2	0	4	4	4	4	4
					2	0	2	1	6	6	6	6	6
			2	1	1	0	2	0	4	4	4	4	4
						1	3	0	4	4	4	4	4
		1	0	1	1	0	3	0	4	4	4	4	4

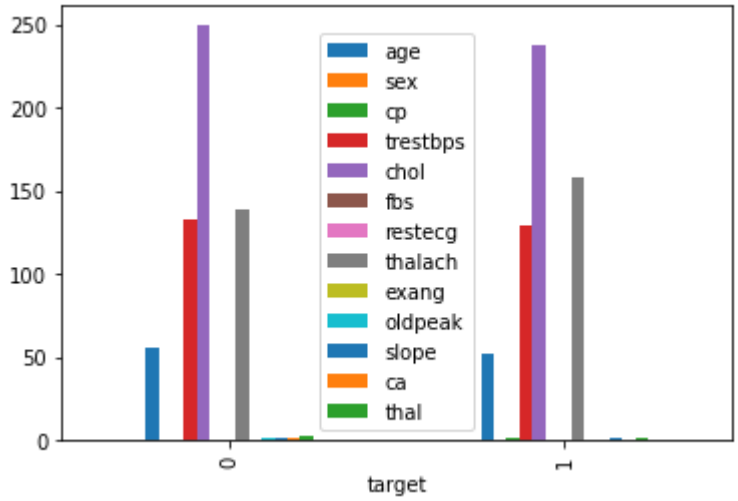
In [40]:
```
dt.groupby(by= "target").mean()
```

Out[40]:

target	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
0	56.430380	0.848101	0.502110	132.955696	249.432489	0.164557	0.464135	139.409283	0.554852
1	52.251923	0.576923	1.371154	129.265385	238.100000	0.130769	0.605769	158.586538	0.136538

In [41]:
```
dt.groupby(by= "target").mean().plot(kind= 'bar')
```

Out[41]:
```
<AxesSubplot:xlabel='target'>
```



checking the unique values of each column

In [42]:
```
dt["cp"].unique()
```

Out[42]:
```
array([0, 1, 2, 3], dtype=int64)
```

In [43]:
```
dt["cp"].value_counts()
```

Out[43]:
```
0    475
2    278
1    164
3     77
Name: cp, dtype: int64
```

In [44]:
```
dt["fbs"].value_counts()
```

Out[44]:
```
0    848
1    146
Name: fbs, dtype: int64
```

In [45]:
```
dt["restecg"].value_counts()
```

Out[45]:
```
1    505
0    474
2     15
Name: restecg, dtype: int64
```

In [46]:
```
dt["exang"].value_counts()
```

Out[46]:
```
0    660
1    334
Name: exang, dtype: int64
```

In [47]:
```
dt["slope"].value_counts()
```

Out[47]:
```
1    468
2    463
```

```
0     63
Name: slope, dtype: int64
```

In [48]:
```
dt["ca"].value_counts()
```

Out[48]:
```
0    567
1    220
2    127
3     62
4     18
Name: ca, dtype: int64
```

In [49]:
```
dt["thal"].value_counts()
```

Out[49]:
```
2    537
3    386
1     64
0      7
Name: thal, dtype: int64
```

In [50]:
```
dt["target"].value_counts()
```

Out[50]:
```
1    520
0    474
Name: target, dtype: int64
```

In [51]:
```
X = dt.drop(columns="target")
y = dt["target"]
```

In [52]:
```
X.head()
```

Out[52]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
0	52	1	0	125	212	0	1	168	0	1.0	2	2	3
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3
3	61	1	0	148	203	0	1	161	0	0.0	2	1	3
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2

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

Out[53]:
```
0    0
1    0
2    0
3    0
4    0
Name: target, dtype: int64
```

In [54]:
```
print(f"Feature Matrix X shape {X.shape}")
print(f"Target Vector y shape {y.shape}")
```

```
Feature Matrix X shape (994, 13)
Target Vector y shape (994,)
```

Model training and evaluation

In [55]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=4
```

In [56]:
```
## checking distribution of traget variable in train test split
print('Distribution of traget variable in training set')
print(y_train.value_counts())

print('Distribution of traget variable in test set')
print(y_test.value_counts())
```

```
Distribution of traget variable in training set
1    412
0    383
Name: target, dtype: int64
Distribution of traget variable in test set
1    108
0     91
Name: target, dtype: int64
```

In [57]:
```
print('------------Training Set------------------')
print(X_train.shape)
print(y_train.shape)

print('------------Test Set------------------')
print(X_test.shape)
print(y_test.shape)
```

```
------------Training Set------------------
(795, 13)
(795,)
------------Test Set------------------
(199, 13)
(199,)
```

In [58]:
```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
X_train[["age","trestbps","chol","thalach","oldpeak"]] = scaler.fit_transform(X_train[[
X_train.head()
```

```
H:\download\Anaconda\lib\site-packages\pandas\core\frame.py:3678: SettingWithCopyWarnin
g:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_
guide/indexing.html#returning-a-view-versus-a-copy
  self[col] = igetitem(value, i)
```

Out[58]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
937	0.729167	1	2	0.534884	0.779851	0	1	0.614035	0	0.000000	2	0	2

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
953	0.333333	0	0	0.511628	0.410448	0	0	0.561404	1	0.045455	1	0	2
686	0.479167	1	0	0.395349	0.291045	1	1	0.596491	1	0.227273	1	0	0
791	0.520833	1	0	0.186047	0.421642	0	1	0.333333	1	0.636364	1	1	3
939	0.416667	0	1	0.465116	0.541045	0	1	0.649123	0	0.000000	1	0	2

In [59]:
```
X_test[["age","trestbps","chol","thalach","oldpeak"]] = scaler.transform(X_test[["age",
X_test.head()
```

```
H:\download\Anaconda\lib\site-packages\pandas\core\frame.py:3678: SettingWithCopyWarnin
g:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_
guide/indexing.html#returning-a-view-versus-a-copy
  self[col] = igetitem(value, i)
```

Out[59]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
948	0.854167	1	0	0.593023	0.179104	0	1	0.324561	1	0.590909	0	0	3
546	0.854167	1	0	0.418605	0.731343	0	0	0.184211	0	0.545455	1	3	2
589	0.520833	1	0	0.325581	0.597015	0	0	0.245614	1	0.727273	1	2	2
681	0.625000	1	0	0.883721	0.746269	0	0	0.456140	1	0.772727	0	0	3
955	0.687500	1	2	0.418605	0.391791	0	1	0.508772	0	0.409091	1	3	3

In [ ]:
```
```

In [60]:
```
from sklearn import model_selection
from sklearn.model_selection import cross_val_score
import xgboost as xgb
# function initializing baseline machine learning models
def GetBasedModel():
    basedModels = []
    basedModels.append(('LR_L2'   , LogisticRegression(penalty='l2')))
    basedModels.append(('KNN7'  , KNeighborsClassifier(7)))
    basedModels.append(('KNN9'  , KNeighborsClassifier(9)))
    basedModels.append(('CART' , DecisionTreeClassifier()))
    basedModels.append(('NB'   , GaussianNB()))
    basedModels.append(('SVM Linear'  , SVC(kernel='linear',gamma='auto',probability=Tr
    basedModels.append(('SVM RBF'  , SVC(kernel='rbf',gamma='auto',probability=True)))
    basedModels.append(('RF_Ent100'   , RandomForestClassifier(criterion='entropy',n_es
    basedModels.append(('RF_Gini100'   , RandomForestClassifier(criterion='gini',n_esti
    basedModels.append(('ET100'   , ExtraTreesClassifier(n_estimators= 100)))
    basedModels.append(('XGB_100', xgb.XGBClassifier(n_estimators= 100)))

    return basedModels

# function for performing 10-fold cross validation of all the baseline models
```

```
def BasedLine2(X_train, y_train,models):
    # Test options and evaluation metric
    num_folds = 10
    scoring = 'accuracy'
    seed = 7
    results = []
    names = []
    for name, model in models:
        kfold = model_selection.KFold(n_splits=10)
        cv_results = model_selection.cross_val_score(model, X_train, y_train, cv=kfold,
        results.append(cv_results)
        names.append(name)
        msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
        print(msg)


    return results,msg
```

In [61]:

```
models = GetBasedModel()
names,results = BasedLine2(X_train, y_train,models)
```

```
LR_L2: 0.847848 (0.033783)
KNN7: 0.854114 (0.031305)
KNN9: 0.870491 (0.044680)
CART: 0.987405 (0.015962)
NB: 0.816377 (0.015779)
SVM Linear: 0.836519 (0.037641)
SVM RBF: 0.884320 (0.040066)
RF_Ent100: 0.983623 (0.018749)
RF_Gini100: 0.982358 (0.016137)
ET100: 0.984889 (0.016710)
XGB_100: 0.986155 (0.015355)
```

Random Forest Classifier (criterion = 'entropy')

In [62]:

```
rf_ent = RandomForestClassifier(criterion='entropy',n_estimators=100)
rf_ent.fit(X_train, y_train)
y_pred_rfe = rf_ent.predict(X_test)
```

Draw the Confusion matrix

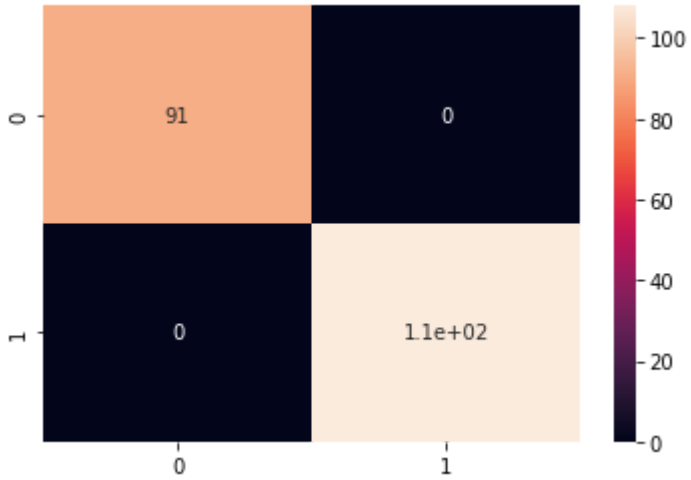
In [63]:

```
cm=confusion_matrix(y_test,y_pred_rfe)
sns.heatmap(cm, annot=True)

TN = cm[0][0]
FN = cm[1][0]
TP = cm[1][1]
FP = cm[0][1]
acc= accuracy_score(y_test, y_pred_rfe)
roc=roc_auc_score(y_test, y_pred_rfe)
loss_log = log_loss(y_test, y_pred_rfe)
prec = precision_score(y_test, y_pred_rfe)
rec = recall_score(y_test, y_pred_rfe)
f1 = f1_score(y_test, y_pred_rfe)

mathew = matthews_corrcoef(y_test, y_pred_rfe)
```

```
model_results =pd.DataFrame([['Random Forest',acc, prec,rec, f1,roc,mathew,loss_log]],
               columns = ['Model', 'Accuracy','Precision', 'Recall_Score', 'F1 Score','

model_results
```

Out[63]:

	Model	Accuracy	Precision	Recall_Score	F1 Score	ROC	mathew_corrcoef	Log Loss
0	Random Forest	1.0	1.0	1.0	1.0	1.0	1.0	9.992007e-16



Soft voting

In [64]:

```
import xgboost as xgb
clf1=RandomForestClassifier(criterion='entropy',n_estimators=100)

clf2=DecisionTreeClassifier()
clf3=xgb.XGBClassifier(n_estimators= 1000)
clf4=ExtraTreesClassifier(n_estimators= 500)

clf5=GradientBoostingClassifier(n_estimators=100,max_features='sqrt')


eclf1 = VotingClassifier(estimators=[('rfe', clf1), ('decc', clf2), ('xgb', clf3),('ET'
                         voting='soft', weights=[4,1,2,3,1])
eclf1.fit(X_train,y_train)
y_pred_sv =eclf1.predict(X_test)
```

In [ ]:

```
```

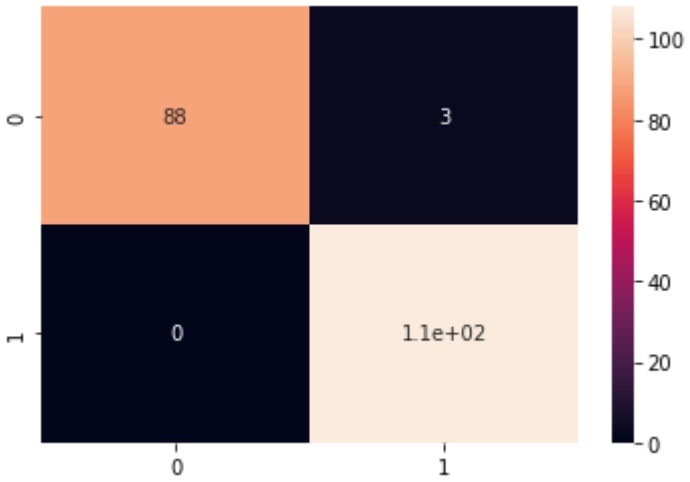
In [65]:

```
CM=confusion_matrix(y_test,y_pred_sv)
sns.heatmap(CM, annot=True)

TN = CM[0][0]
FN = CM[1][0]
TP = CM[1][1]
FP = CM[0][1]
loss_log = log_loss(y_test, y_pred_sv)
acc= accuracy_score(y_test, y_pred_sv)
roc=roc_auc_score(y_test, y_pred_sv)
prec = precision_score(y_test, y_pred_sv)
```

```
rec = recall_score(y_test, y_pred_sv)
f1 = f1_score(y_test, y_pred_sv)

mathew = matthews_corrcoef(y_test, y_pred_sv)
model_results =pd.DataFrame([['Soft Voting',acc, prec,rec, f1,roc, loss_log,mathew]],
               columns = ['Model', 'Accuracy','Precision', 'Recall Score', 'F1 Score','

model_results
```

Out[65]:

	Model	Accuracy	Precision	Recall Score	F1 Score	ROC	Log_Loss	mathew_corrcoef
0	Soft Voting	0.984925	0.972973	1.0	0.986301	0.983516	0.520697	0.969998



In [66]:
```
rf_ent = RandomForestClassifier(criterion='entropy',n_estimators=100)
rf_ent.fit(X_train, y_train)
y_pred_rfe = rf_ent.predict(X_test)
```

In [67]:
```
knn = KNeighborsClassifier(9)
knn.fit(X_train,y_train)
y_pred_knn = knn.predict(X_test)
```

In [68]:
```
et_100 = ExtraTreesClassifier(n_estimators= 100)
et_100.fit(X_train,y_train)
y_pred_et100 = et_100.predict(X_test)
```

In [69]:
```
import xgboost as xgb
xgb = xgb.XGBClassifier(n_estimators= 1000)
xgb.fit(X_train,y_train)
y_pred_xgb = xgb.predict(X_test)
```

In [70]:
```
svc = SVC(kernel='linear',gamma='auto',probability=True)
svc.fit(X_train,y_train)
y_pred_svc = svc.predict(X_test)
```

In [71]:
```
decc = DecisionTreeClassifier()
decc.fit(X_train,y_train)
```

```
y_pred_decc = decc.predict(X_test)
```

In [72]:

```
data = {
             'Random Forest Entropy': y_pred_rfe,
                'KNN2': y_pred_knn,
                'EXtra tree classifier': y_pred_et100,
                'XGB2': y_pred_xgb,
                'SVC2': y_pred_svc,
                'CART': y_pred_decc
}

models = pd.DataFrame(data)

for column in models:
    CM=confusion_matrix(y_test,models[column])

    TN = CM[0][0]
    FN = CM[1][0]
    TP = CM[1][1]
    FP = CM[0][1]
    loss_log = log_loss(y_test, models[column])
    acc= accuracy_score(y_test, models[column])
    roc=roc_auc_score(y_test, models[column])
    prec = precision_score(y_test, models[column])
    rec = recall_score(y_test, models[column])
    f1 = f1_score(y_test, models[column])

    mathew = matthews_corrcoef(y_test, models[column])
    results =pd.DataFrame([[column,acc, prec,rec, f1,roc, loss_log,mathew]],
              columns = ['Model', 'Accuracy','Precision', 'Recall Score', 'F1 Score','
    model_results = model_results.append(results, ignore_index = True)

model_results
```

Out[72]:

	Model	Accuracy	Precision	Recall Score	F1 Score	ROC	Log_Loss	mathew_corrcoef
0	Soft Voting	0.984925	0.972973	1.000000	0.986301	0.983516	5.206971e-01	0.969998
1	Random Forest Entropy	1.000000	1.000000	1.000000	1.000000	1.000000	9.992007e-16	1.000000
2	KNN2	0.889447	0.898148	0.898148	0.898148	0.888635	3.818401e+00	0.777269
3	EXtra tree classifier	1.000000	1.000000	1.000000	1.000000	1.000000	9.992007e-16	1.000000
4	XGB2	0.984925	0.972973	1.000000	0.986301	0.983516	5.206971e-01	0.969998
5	SVC2	0.819095	0.846154	0.814815	0.830189	0.819495	6.248285e+00	0.637307
6	CART	0.969849	0.972222	0.972222	0.972222	0.969628	1.041382e+00	0.939255

In [ ]: