Health Care

Problem statement:

Cardiovascular diseases are the leading cause of death globally. It is therefore necessary to identify the causes and develop a system to predict heart attacks in an effective manner. The data below has the information about the factors that might have an impact on cardiovascular health.

Task to be performed:

1. Preliminary analysis:

- a. Perform preliminary data inspection and report the findings on the structure of the data, missing values, duplicates, etc.
- b. Based on these findings, remove duplicates (if any) and treat missing values using an appropriate strategy.

1. Prepare a report about the data explaining the distribution of the disease and the related factors using the steps listed below:

- a. Get a preliminary statistical summary of the data and explore the measures of central tendencies and spread of the data.
- b. Identify the data variables which are categorical and describe and explore these variables using the appropriate tools, such as count plot.
- c. Study the occurrence of CVD across the Age category.
- d. Study the composition of all patients with respect to the Sex category.
- e. Study if one can detect heart attacks based on anomalies in the resting blood pressure (trestbps) of a patient.
- f. Describe the relationship between cholesterol levels and a target variable.
- g. State what relationship exists between peak exercising and the occurrence of a heart attack.
- h. Check if thalassemia is a major cause of CVD.
- i. List how the other factors determine the occurrence of CVD.
- j. Use a pair plot to understand the relationship between all the given variables.

1. Build a baseline model to predict the risk of a heart attack using a logistic regression and random forest and explore the results while using correlation analysis and logistic regression (leveraging standard error and p-values from statsmodels) for feature selection.

Dataset description:

- Age: Age in years
- Sex: 1 = male; 0 = female
- cp: Chest pain type

- trestbps: Resting blood pressure (in mm Hg on admission to the hospital)
- chol: Serum cholesterol in mg/dl
- fbs: Fasting blood sugar > 120 mg/dl (1 = true; 0 = false)
- restecg: Resting electrocardiographic results
- thalach: Maximum heart rate achieved
- exang: Exercise induced angina (1 = yes; 0 = no)
- oldpeak: ST depression induced by exercise relative to rest
- slope: Slope of the peak exercise ST segment
- ca: Number of major vessels (0-3) colored by fluoroscopy
- thal: 3 = normal; 6 = fixed defect; 7 = reversible defect
- Target: 0 for no presence of heart disease, 1 for presence of heart disease

In [ ]:

```

```

In [156…

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

from sklearn.preprocessing import StandardScaler

from statsmodels.api import GLM

from sklearn.model_selection import train_test_split, GridSearchCV

from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import AdaBoostClassifier, GradientBoostingClassifier, RandomForest(
from xgboost import XGBClassifier

from sklearn.metrics import confusion_matrix, classification_report
from sklearn.metrics import plot_confusion_matrix

import warnings
warnings.filterwarnings("ignore")
```

In [ ]:

```

```

In [3]:

```
df = pd.read_excel("Health Care.xlsx")
```

In [4]:

```
df.head()
```

Out[4]:

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

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

In [13]:

```
df.tail()
```

Out[13]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	0
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	0
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	0

In [ ]:

```

```

1) Preliminary analysis:

1.a) Perform preliminary data inspection and report the findings on the structure of the data, missing values, duplicates, etc:

In [9]:

```
df.head()
```

Out[9]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

In [10]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   age       303 non-null    int64
 1   sex       303 non-null    int64
 2   cp        303 non-null    int64
 3   trestbps  303 non-null    int64
 4   chol      303 non-null    int64
 5   fbs       303 non-null    int64
 6   restecg   303 non-null    int64
```

```
 7   thalach   303 non-null    int64
 8   exang     303 non-null    int64
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64
 11  ca        303 non-null    int64
 12  thal      303 non-null    int64
 13  target    303 non-null    int64
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

In [11]:
```
df.shape
```

Out[11]:
```
(303, 14)
```

In [12]:
```
df.describe().T
```

Out[12]:

	count	mean	std	min	25%	50%	75%	max
age	303.0	54.366337	9.082101	29.0	47.5	55.0	61.0	77.0
sex	303.0	0.683168	0.466011	0.0	0.0	1.0	1.0	1.0
cp	303.0	0.966997	1.032052	0.0	0.0	1.0	2.0	3.0
trestbps	303.0	131.623762	17.538143	94.0	120.0	130.0	140.0	200.0
chol	303.0	246.264026	51.830751	126.0	211.0	240.0	274.5	564.0
fbs	303.0	0.148515	0.356198	0.0	0.0	0.0	0.0	1.0
restecg	303.0	0.528053	0.525860	0.0	0.0	1.0	1.0	2.0
thalach	303.0	149.646865	22.905161	71.0	133.5	153.0	166.0	202.0
exang	303.0	0.326733	0.469794	0.0	0.0	0.0	1.0	1.0
oldpeak	303.0	1.039604	1.161075	0.0	0.0	0.8	1.6	6.2
slope	303.0	1.399340	0.616226	0.0	1.0	1.0	2.0	2.0
ca	303.0	0.729373	1.022606	0.0	0.0	0.0	1.0	4.0
thal	303.0	2.313531	0.612277	0.0	2.0	2.0	3.0	3.0
target	303.0	0.544554	0.498835	0.0	0.0	1.0	1.0	1.0

In [14]:
```
df.isna().sum()
```

Out[14]:
```
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
```

In [19]:

```
df[df.duplicated(keep= False)]
```

Out[19]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
163	38	1	2	138	175	0	1	173	0	0.0	2	4	2	1
164	38	1	2	138	175	0	1	173	0	0.0	2	4	2	1

In [ ]:

- 1) Data has 303 Observations (Rows), 13 Features (Columns) and a Target Variable.
- 2) Data has No Missing Values.
- 3) Data has a duplicate observation (Row 163 and Row 164 are Same). We can Remove One of These Rows.

In [ ]:

1.b) Based on these findings, remove duplicates (if any) and treat missing values using an appropriate strategy:

In [20]:

```
df[df.duplicated(keep= "first")]
```

Out[20]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
164	38	1	2	138	175	0	1	173	0	0.0	2	4	2	1

In [ ]:

```
# We can Remove this Row From Data.
```

In [21]:

```
df[df.duplicated(keep= "first")].index
```

Out[21]:

```
Int64Index([164], dtype='int64')
```

In [22]:

```
list(df[df.duplicated(keep= "first")].index)
```

Out[22]:

```
[164]
```

In [24]:

```
df= df.drop(list(df[df.duplicated(keep= "first")].index), axis= 0)
```

In [25]:

```
df.shape
```

Out[25]:

```
(302, 14)
```

In [26]:

```
df[df.duplicated(keep= "first")]
```

Out[26]:

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

In [ ]:

- Duplicate Row is removed from Data.
- As seen earlier, we have no missing values in Data.

In [ ]:

2) Prepare a report about the data explaining the distribution of the disease and the related factors using the steps listed below:

2.a) Get a preliminary statistical summary of the data and explore the measures of central tendencies and spread of the data:

In [28]:

```
df.describe().T
```

Out[28]:

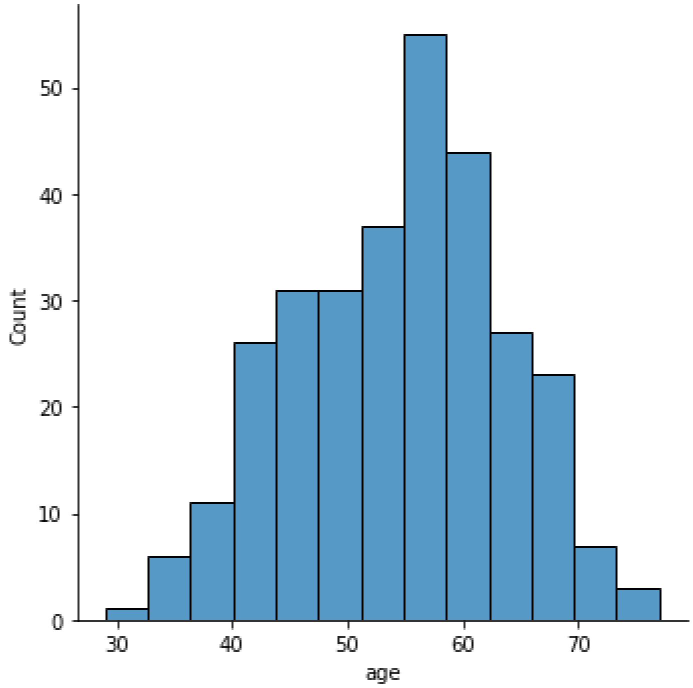
	count	mean	std	min	25%	50%	75%	max
age	302.0	54.420530	9.047970	29.0	48.00	55.5	61.00	77.0
sex	302.0	0.682119	0.466426	0.0	0.00	1.0	1.00	1.0
cp	302.0	0.963576	1.032044	0.0	0.00	1.0	2.00	3.0
trestbps	302.0	131.602649	17.563394	94.0	120.00	130.0	140.00	200.0
chol	302.0	246.500000	51.753489	126.0	211.00	240.5	274.75	564.0
fbs	302.0	0.149007	0.356686	0.0	0.00	0.0	0.00	1.0
restecg	302.0	0.526490	0.526027	0.0	0.00	1.0	1.00	2.0
thalach	302.0	149.569536	22.903527	71.0	133.25	152.5	166.00	202.0
exang	302.0	0.327815	0.470196	0.0	0.00	0.0	1.00	1.0
oldpeak	302.0	1.043046	1.161452	0.0	0.00	0.8	1.60	6.2
slope	302.0	1.397351	0.616274	0.0	1.00	1.0	2.00	2.0
ca	302.0	0.718543	1.006748	0.0	0.00	0.0	1.00	4.0
thal	302.0	2.314570	0.613026	0.0	2.00	2.0	3.00	3.0
target	302.0	0.543046	0.498970	0.0	0.00	1.0	1.00	1.0

In [ ]:

In [29]:

```
plt.figure(figsize= (8,6))

sns.displot(data= df, x= "age")

plt.show()
```

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



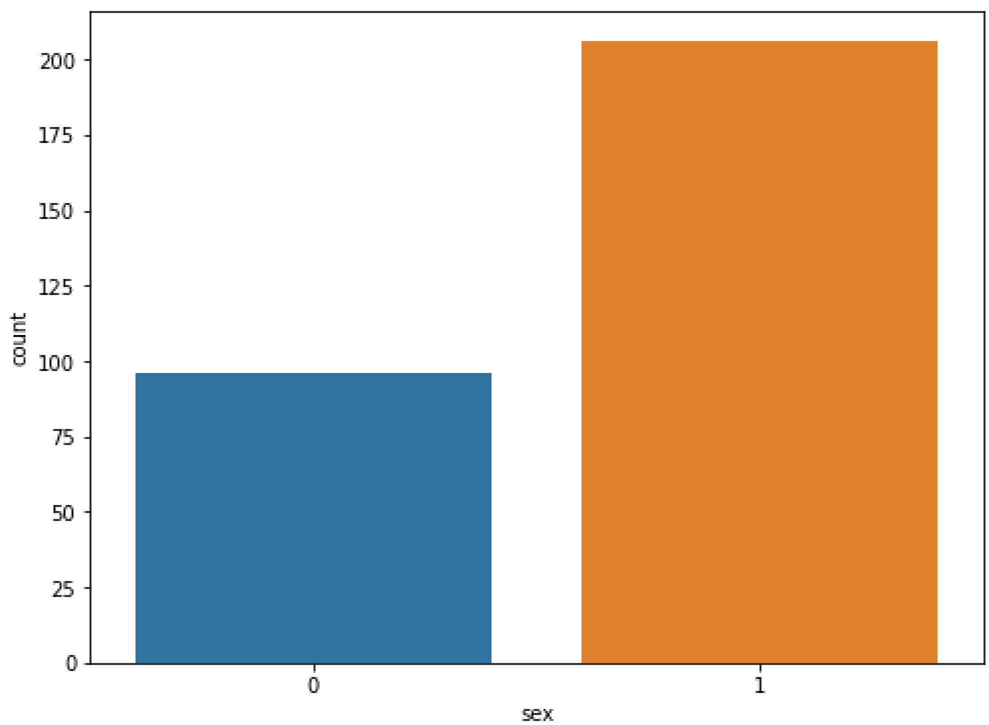
- Age is Continuous Feature and Seems to be Normally Distributed.

In [ ]:

```

```

In [30]:

```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "sex")

plt.show()
```



In [31]:

```
df["sex"].value_counts()
```

Out[31]:

```
1    206
0     96
```

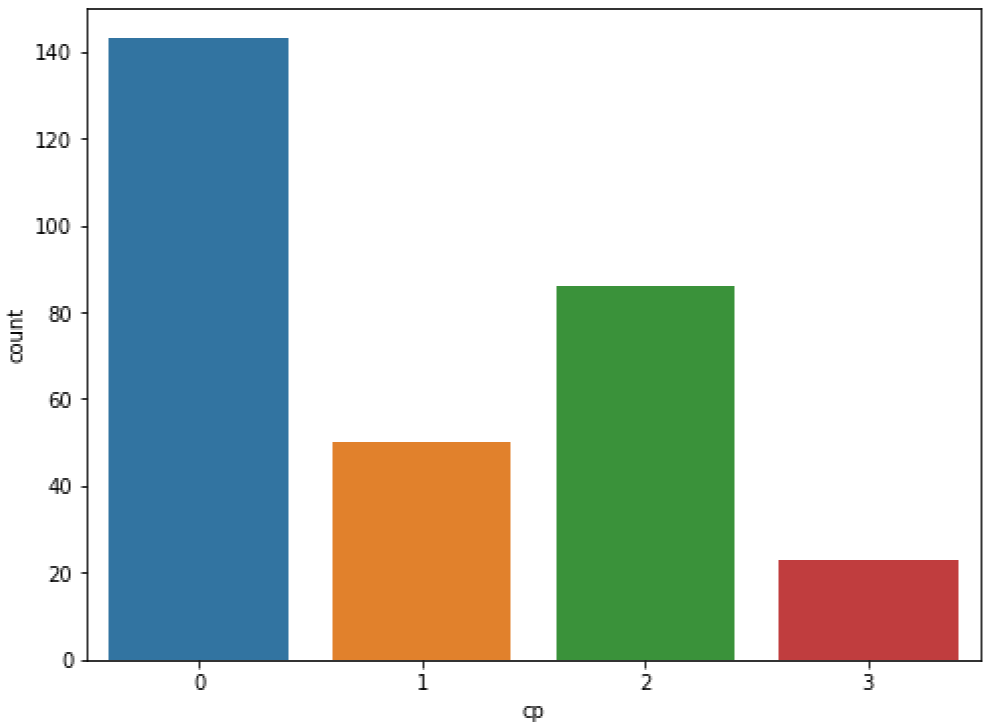
```
Name: sex, dtype: int64
```

- 0: Female, 1: Male
- We Have Twice as many Observations for Male than Female in our Data.

In [ ]:

In [32]:

```python
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "cp")

plt.show()
```



In [33]:

```python
df["cp"].value_counts()
```

Out[33]:

```
0    143
2     86
1     50
3     23
Name: cp, dtype: int64
```

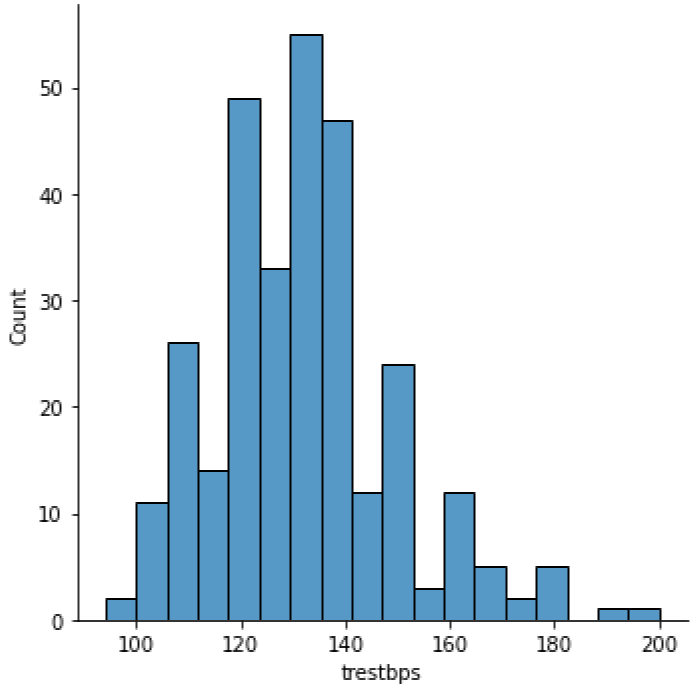
- Chest Pain (cp): seems to be ordinal Categorical Variable.
- We Won't have to get Dummy Variables for "cp" as it's ordinal in nature.

In [ ]:

In [34]:

```python
plt.figure(figsize= (8,6))

sns.displot(data= df, x= "trestbps")

plt.show()
```

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



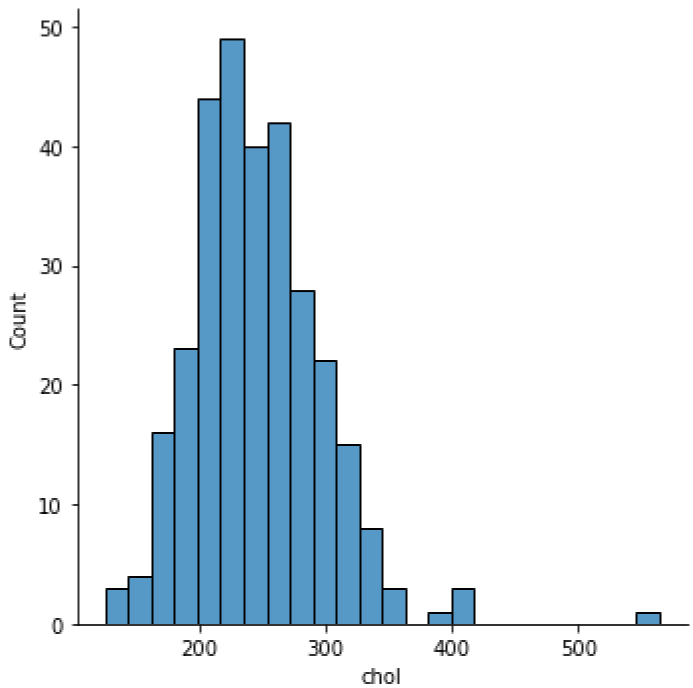
- Resting Blood Pressure "trestbps" is Continuous and seems to be Normally Distributed with Some Outliers at Right Tail.

In [ ]:

In [35]:

```
plt.figure(figsize= (8,6))

sns.displot(data= df, x= "chol")

plt.show()
```

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

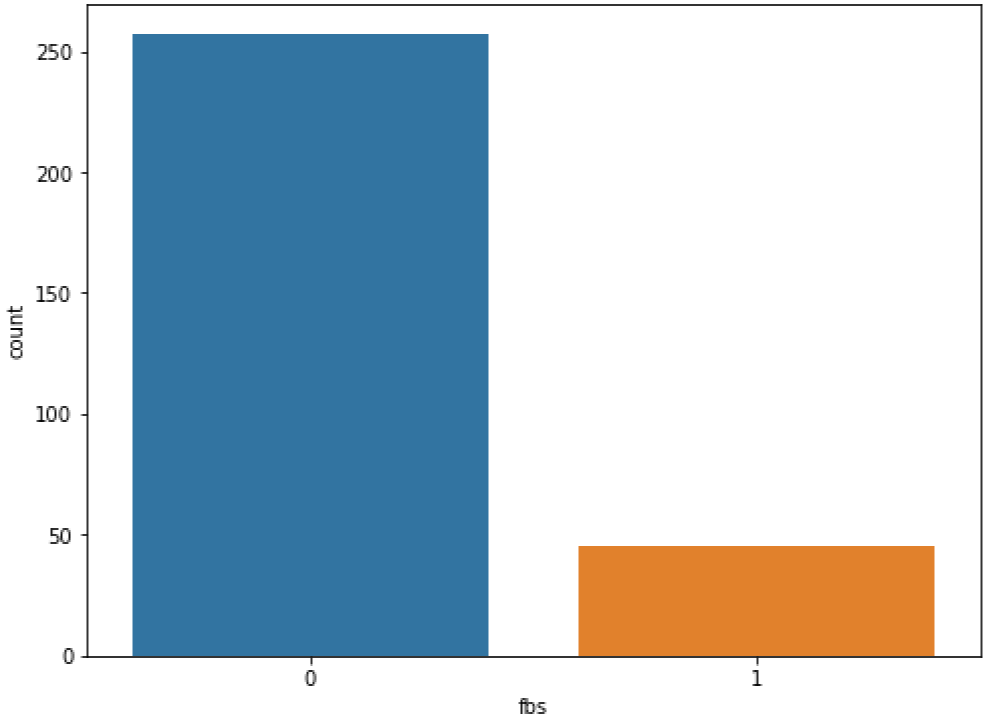


- Cholesterol "chol" is Continuous and seems to be Normally Distributed with Some Outliers at Right Tail.

In [ ]:

In [36]:

```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "fbs")

plt.show()
```



In [37]:

```
df["fbs"].value_counts()
```

Out[37]:

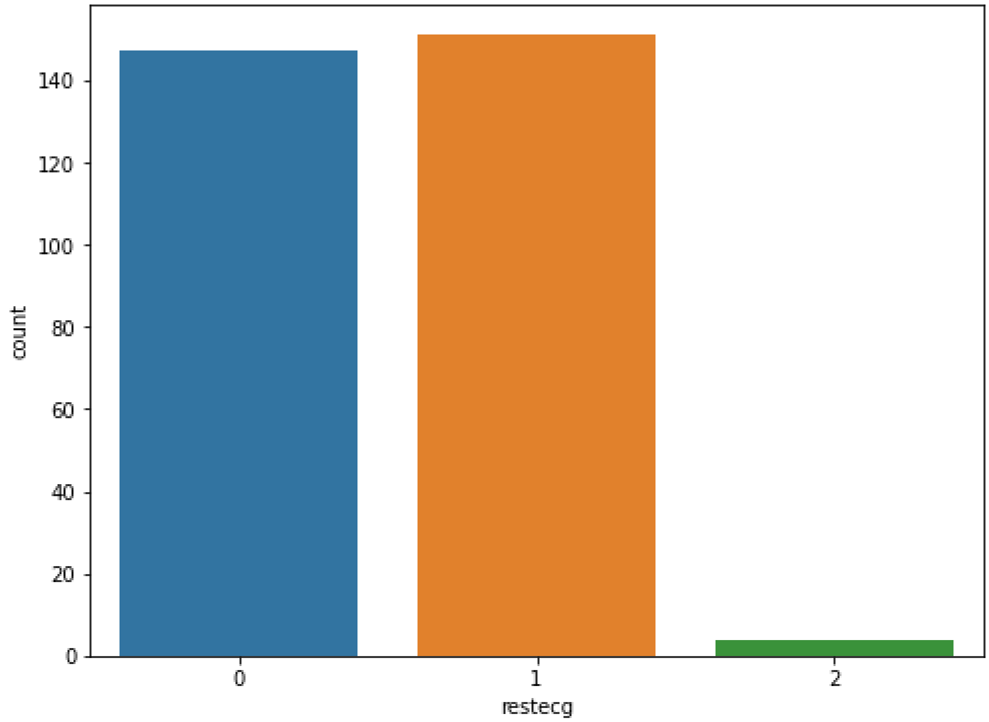
```
0    257
1     45
Name: fbs, dtype: int64
```

- Fasting Blood Sugar "fbs" is Ordinal Categorical Feature.

In [ ]:

In [38]:

```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "restecg")

plt.show()
```



In [39]:

```
df["restecg"].value_counts()
```

Out[39]:

```
1    151
0    147
2      4
Name: restecg, dtype: int64
```

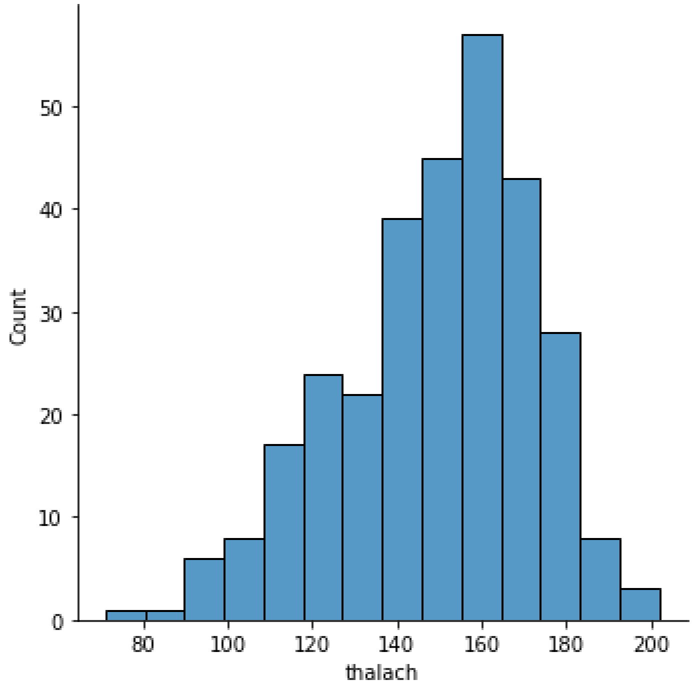
- Resting electrocardiographic results "restecg" is Ordinal Categorical Feature.

In [ ]:

In [40]:

```
plt.figure(figsize= (8,6))

sns.displot(data= df, x= "thalach")

plt.show()
```

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



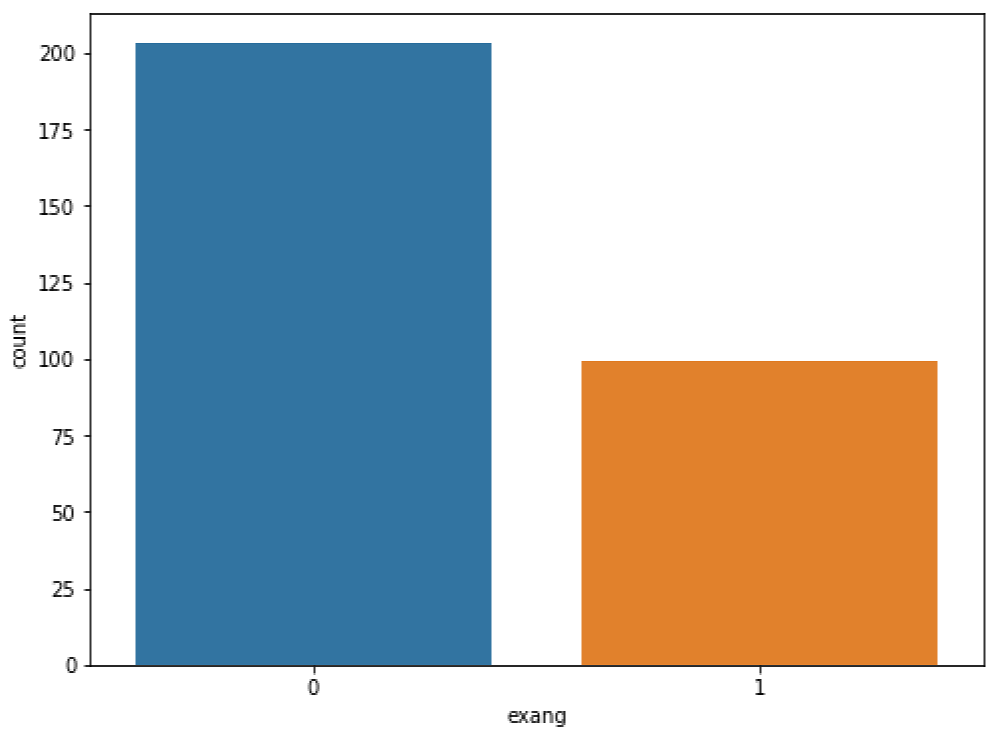
- Maximum Heart Rate Achieved "thalach" is Continuous Feature and it is Left Skewed.

In [ ]:

```

```

In [41]:

```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "exang")

plt.show()
```



In [42]:

```
df["exang"].value_counts()
```

Out[42]:

```
0    203
1     99
```

```
Name: exang, dtype: int64
```

- Exercise Induced Enigma "exang" is Categorical Feature.

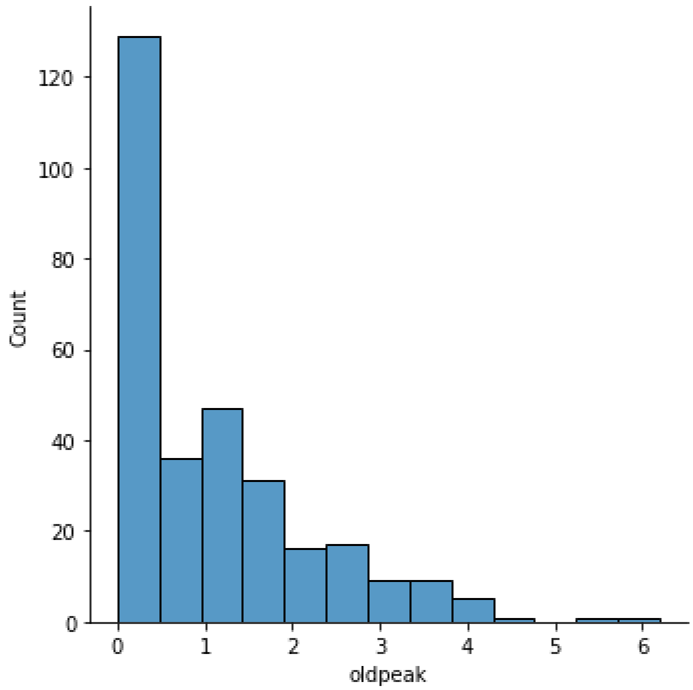
In [ ]:

```

```

In [43]:

```
plt.figure(figsize= (8,6))

sns.displot(data= df, x= "oldpeak")

plt.show()
```

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



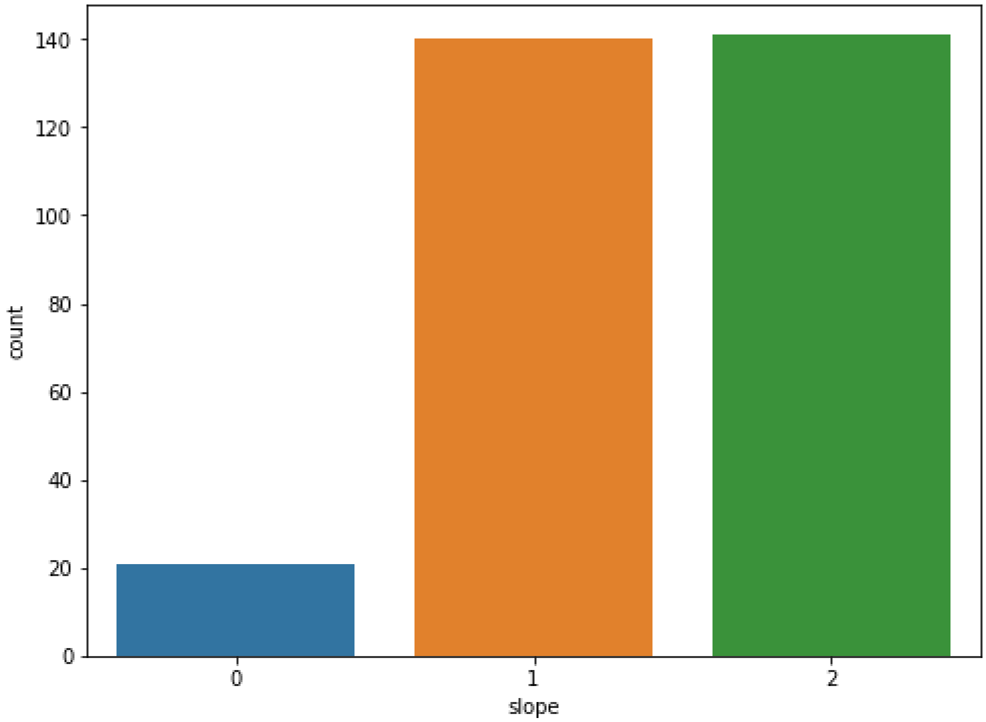
- ST depression induced by exercise relative to rest "oldpeak" is Continuous feature and is Highly Right Skewed.

In [ ]:

```

```

In [44]:

```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "slope")

plt.show()
```



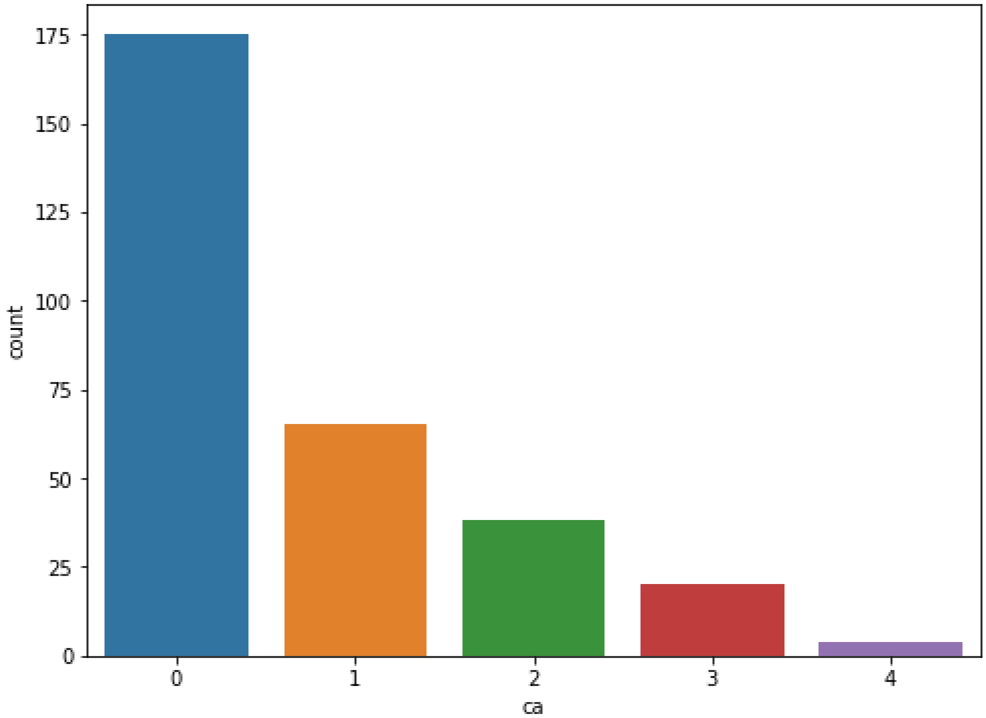
In [45]:
```
df["slope"].value_counts()
```

Out[45]:
```
2    141
1    140
0     21
Name: slope, dtype: int64
```

- Slope of the peak exercise ST segment "slope" is Ordinal Categorical Feature.

In [ ]:
```

```

In [46]:
```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "ca")

plt.show()
```



In [47]:

```
df["ca"].value_counts()
```

Out[47]:

```
0    175
1     65
2     38
3     20
4      4
Name: ca, dtype: int64
```

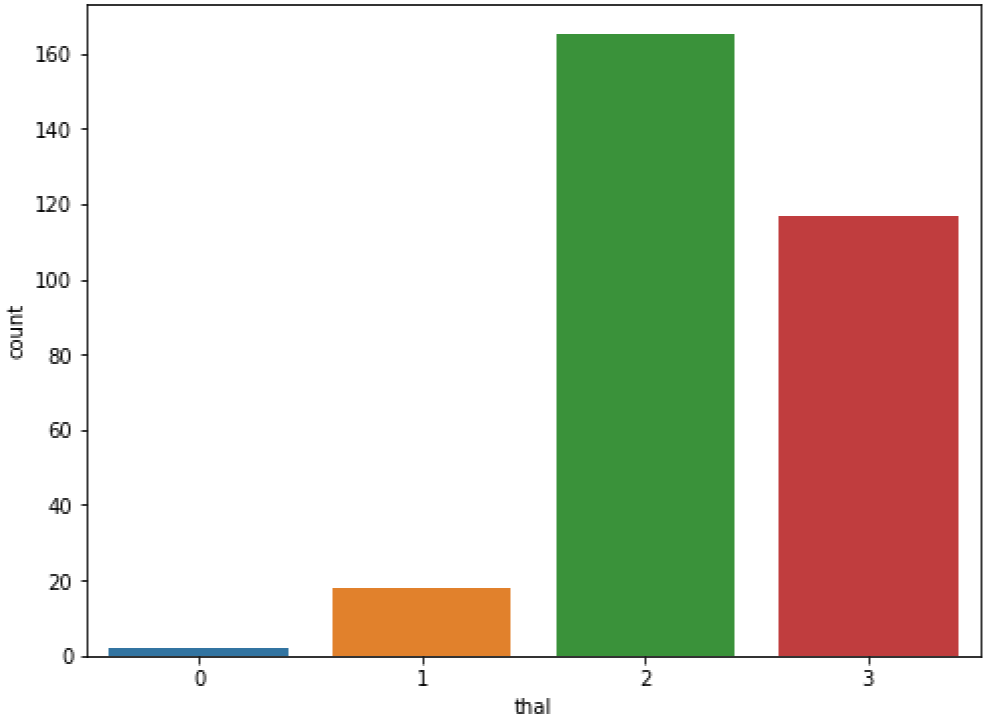
- Number of major vessels (0-3) colored by fluoroscopy "ca" is Ordinal Categorical Feature.

In [ ]:

```

```

In [48]:

```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "thal")

plt.show()
```



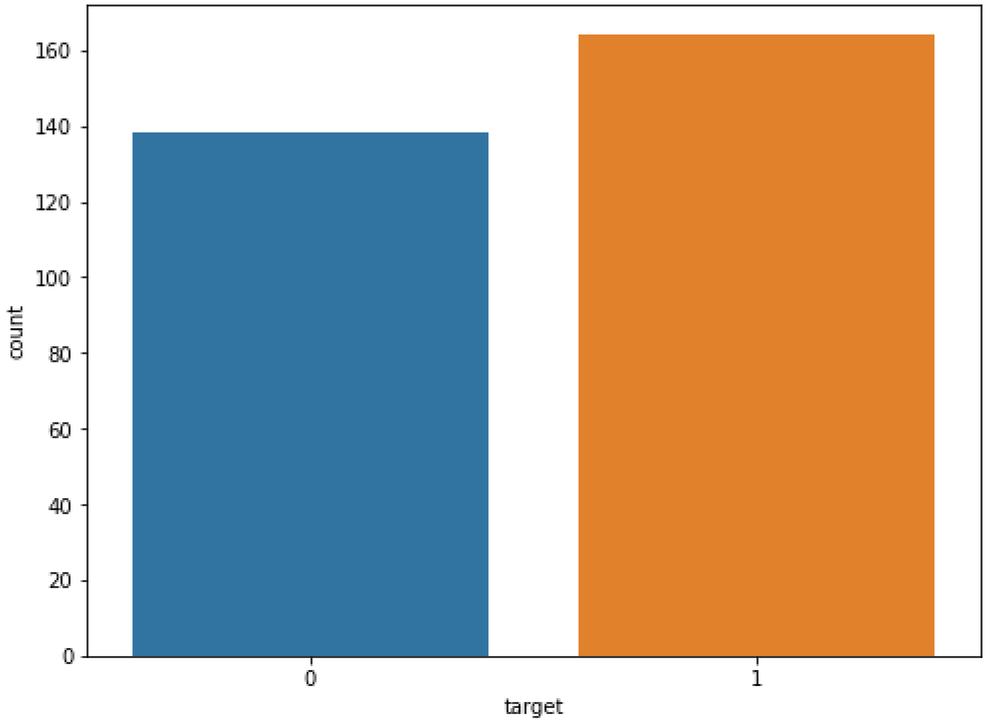
In [49]:
```
df["thal"].value_counts()
```

Out[49]:
```
2    165
3    117
1     18
0      2
Name: thal, dtype: int64
```

- Thalassaemia "thal" is Nominal Categorical Variable.

In [ ]:
```

```

In [50]:
```
plt.figure(figsize= (8,6))

sns.countplot(data= df, x= "target")

plt.show()
```



In [51]:

```
df["target"].value_counts()
```

Out[51]:

```
1    164
0    138
Name: target, dtype: int64
```

- "Target" is our Target Variable and we have No Class Imbalance here.

In [ ]:

```

```

2.b) Identify the data variables which are categorical and describe and explore these variables using the appropriate tools, such as count plot:

In [52]:

```
df.dtypes
```

Out[52]:

```
age           int64
sex           int64
cp            int64
trestbps      int64
chol          int64
fbs           int64
restecg       int64
thalach       int64
exang         int64
oldpeak     float64
slope         int64
ca            int64
thal          int64
target        int64
dtype: object
```

- All the Features have Numeric Data Type in Data.
- We won't be able to tell apart Numeric and Categorical Variables Using Data Types.

- We will have to use How Many Unique Values are there in Each Feature to tell apart Numeric and Categorical Features.

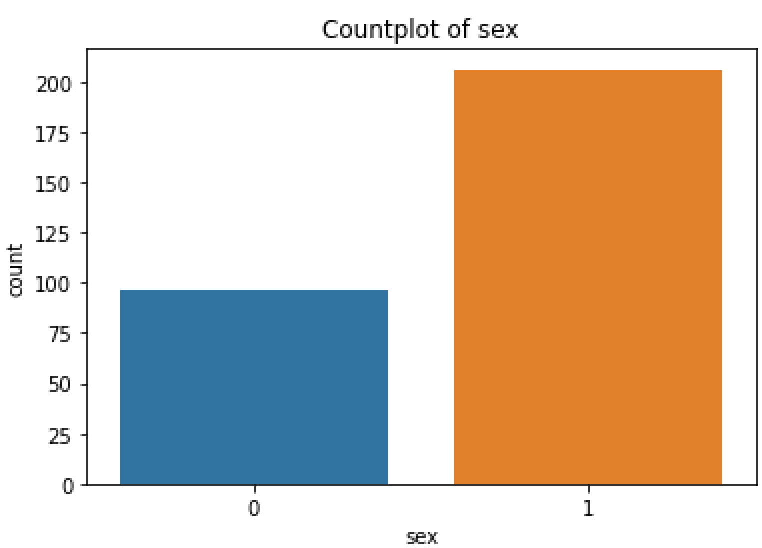
In [53]:
```
for col in df.columns:
    print(f"Number of Unique Values in {col} : {df[col].nunique()}")
```

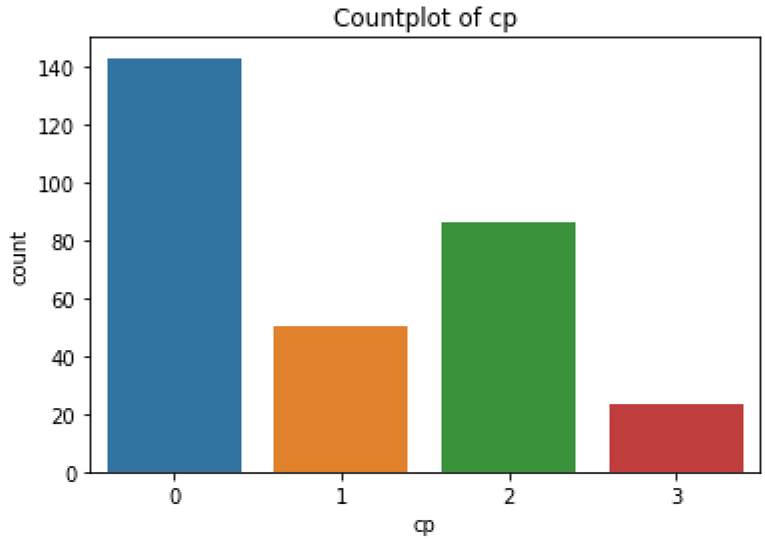
```
Number of Unique Values in age : 41
Number of Unique Values in sex : 2
Number of Unique Values in cp : 4
Number of Unique Values in trestbps : 49
Number of Unique Values in chol : 152
Number of Unique Values in fbs : 2
Number of Unique Values in restecg : 3
Number of Unique Values in thalach : 91
Number of Unique Values in exang : 2
Number of Unique Values in oldpeak : 40
Number of Unique Values in slope : 3
Number of Unique Values in ca : 5
Number of Unique Values in thal : 4
Number of Unique Values in target : 2
```

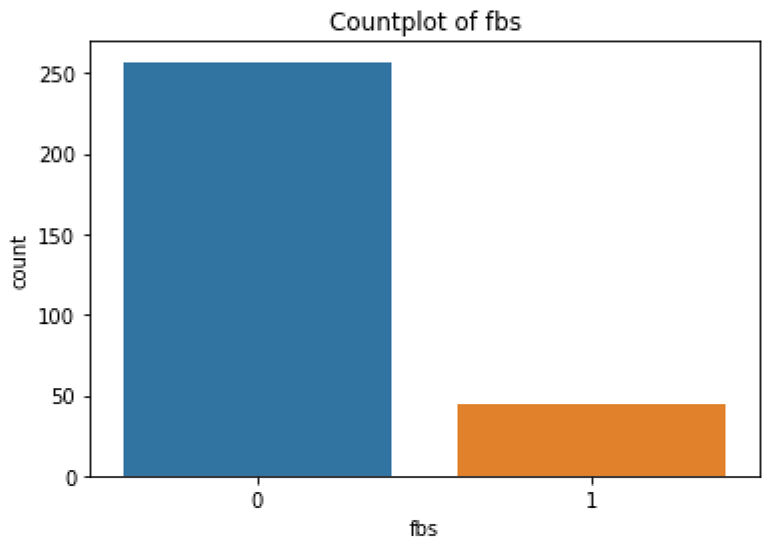
- "age", "trestbps", "chol", "thalach", "oldpeak" are continuous Feature.
- All Other Features are Categorical.

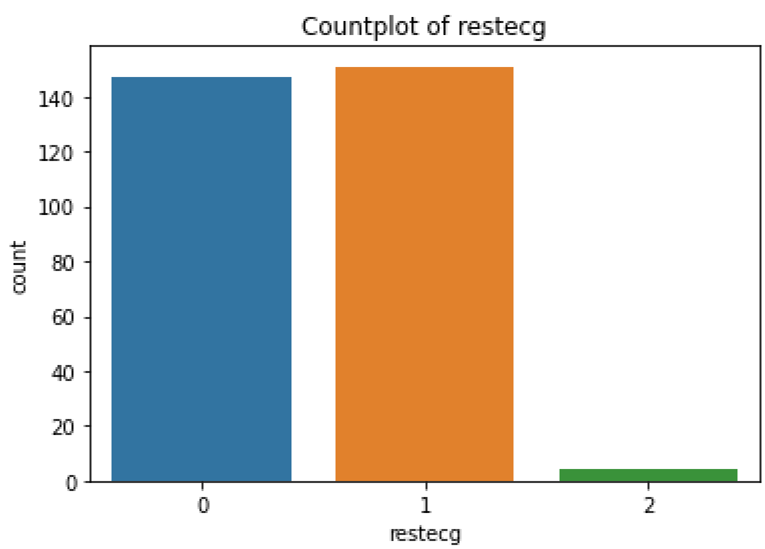
In [ ]:

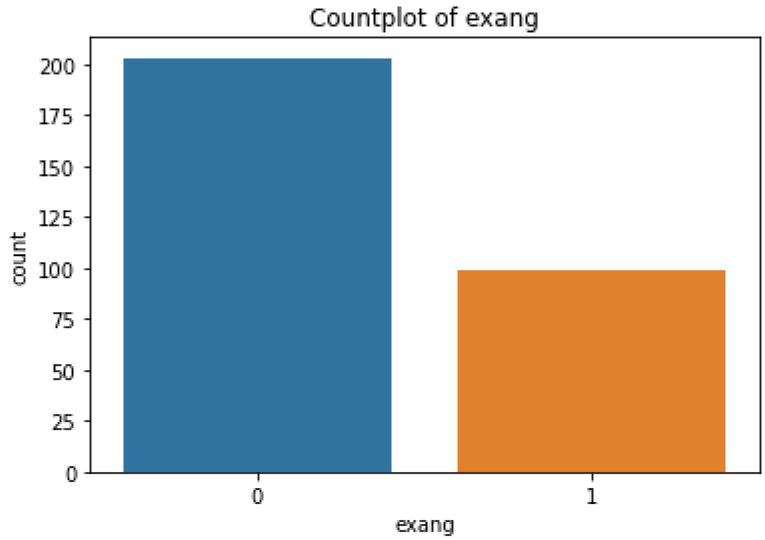
In [56]:
```
for col in df.columns:

    if df[col].nunique() <= 5:

        plt.figure(figsize= (6,4))

        sns.countplot(data= df, x= col)

        plt.title(f"Countplot of {col}")

        plt.show()
```

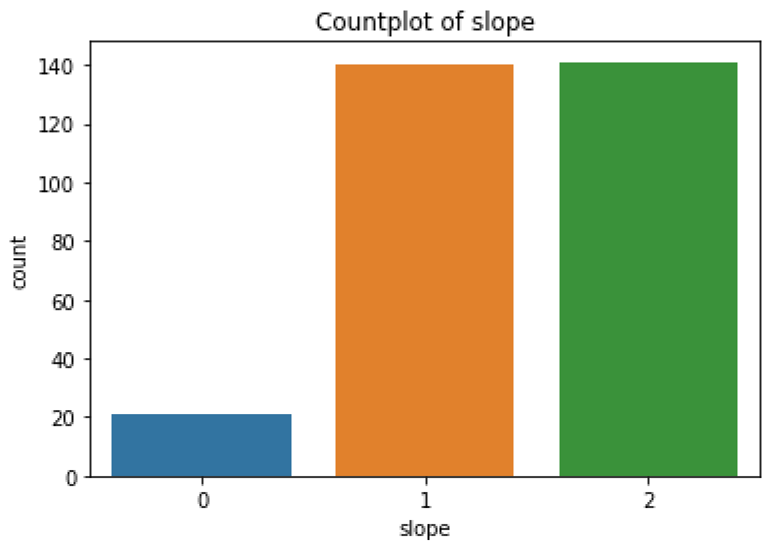


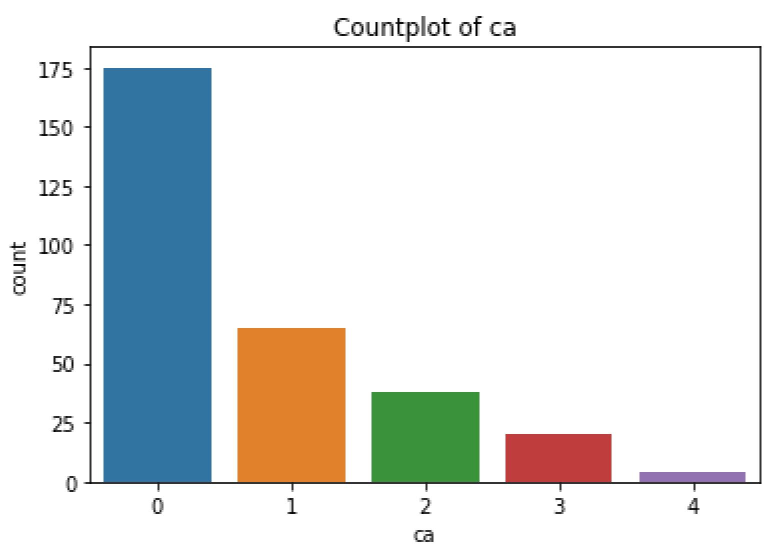

Countplot of cp
count
140
120
100
80
60
40
20
0
0
1
2
3
cp

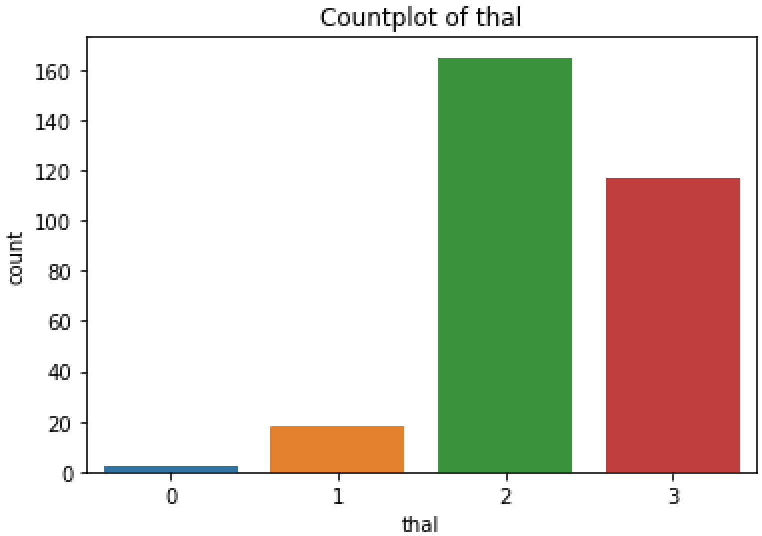

Countplot of fbs
count
250
200
150
100
50
0
0
1
fbs

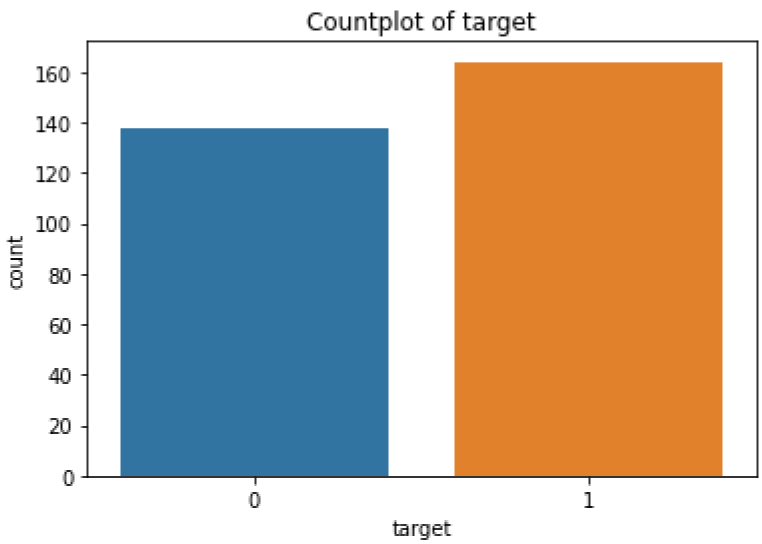

Countplot of restecg
count
140
120
100
80
60
40
20
0
0
1
2
restecg


Countplot of exang
count
200
175
150
125
100
75
50
25
0
0
1
exang


Countplot of slope
count
140
120
100
80
60
40
20
0
0
1
2
slope


Countplot of ca
count
175
150
125
100
75
50
25
0
0
1
2
3
4
ca





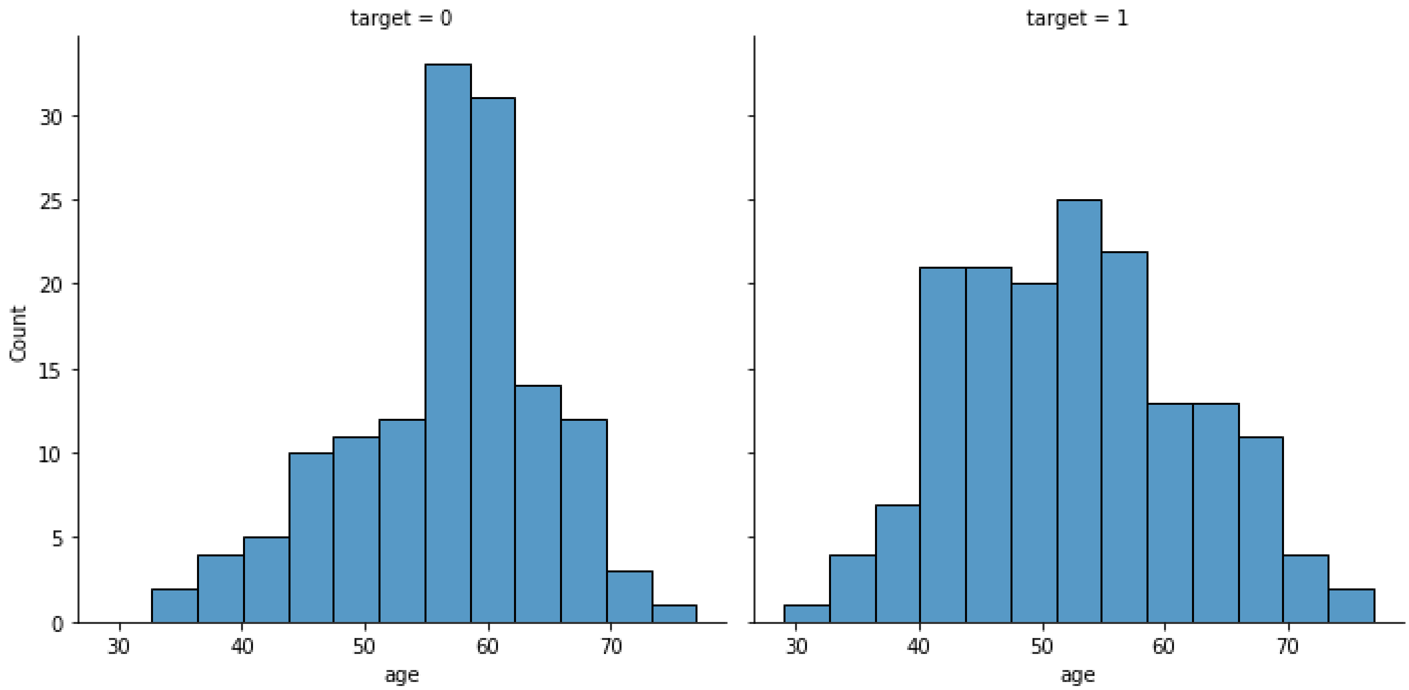
In [ ]:

2.c) Study the occurrence of CVD across the Age category:

In [57]:

```
plt.figure(figsize= (8,6))

sns.displot(data= df, x= "age", col= "target")

plt.show()
```

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



- 40-70 seems to be the Age range Where there are more chances of Cardiovascular Diseases.
- Although, looking at target= 0 graph, 55-62 seems to be the Age Range in which Amny Observations from Our Data have no CVD.
- Also, CVD seems to be present in all Age Ranges in our Data, which can be a Cause of Concern.

In [ ]:

```

```

2.d) Study the composition of all patients with respect to the Sex category:

In [58]:

```
# We will Compare Features of all Observations with respect to Gender.
```

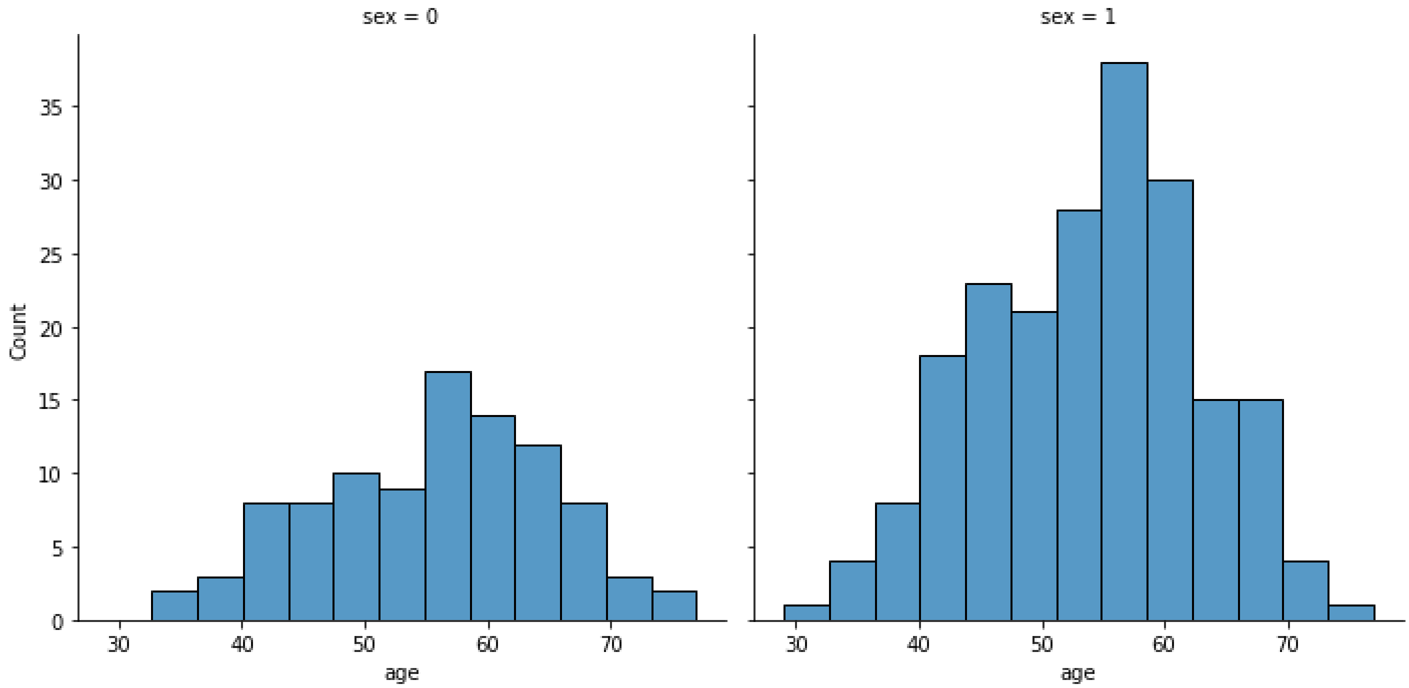
In [ ]:

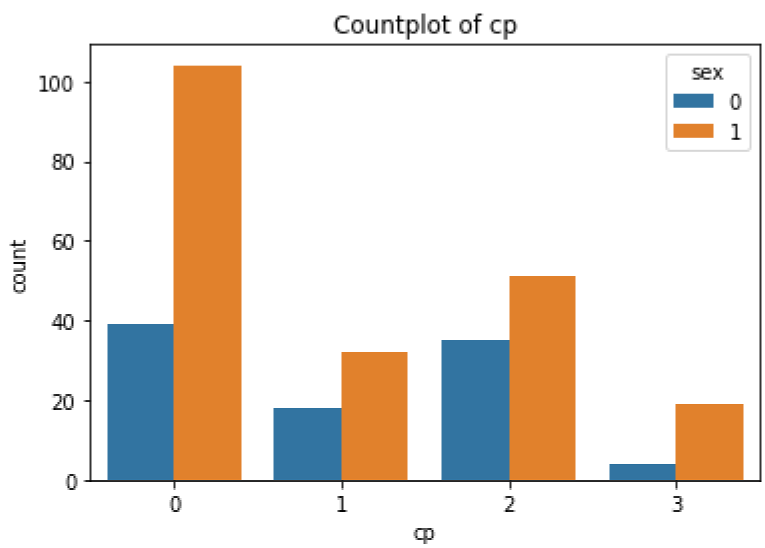
```

```

In [62]:

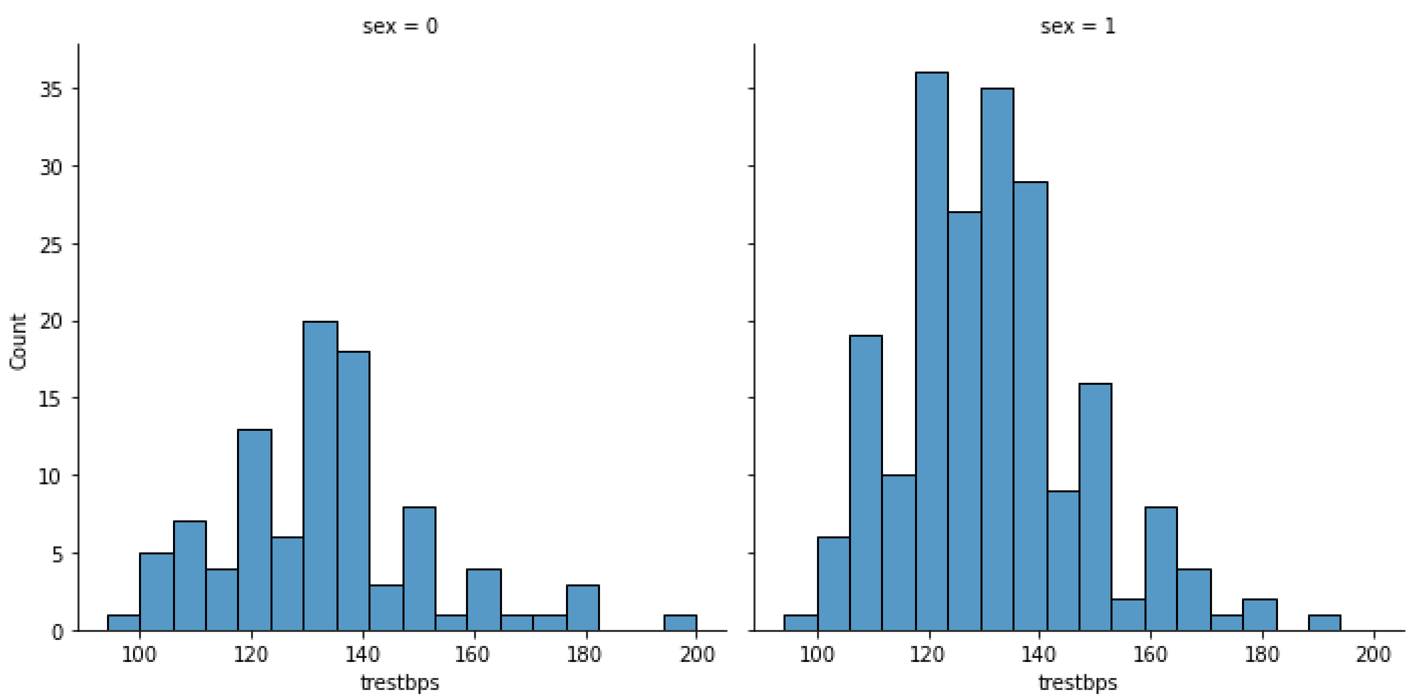
```
for cols in df.drop("sex",axis= 1).columns:

    if df[cols].nunique() <= 5:

        plt.figure(figsize= (6,4))

        sns.countplot(data= df, x= cols, hue= "sex")

        plt.title(f"Countplot of {cols}")

        plt.show()

    else:

        plt.figure(figsize= (6,4))

        sns.displot(data= df, x= cols, col= "sex")

        #plt.title(f"Distribution of {cols} by Gender:")

        plt.show()
```

<Figure size 432x288 with 0 Axes>

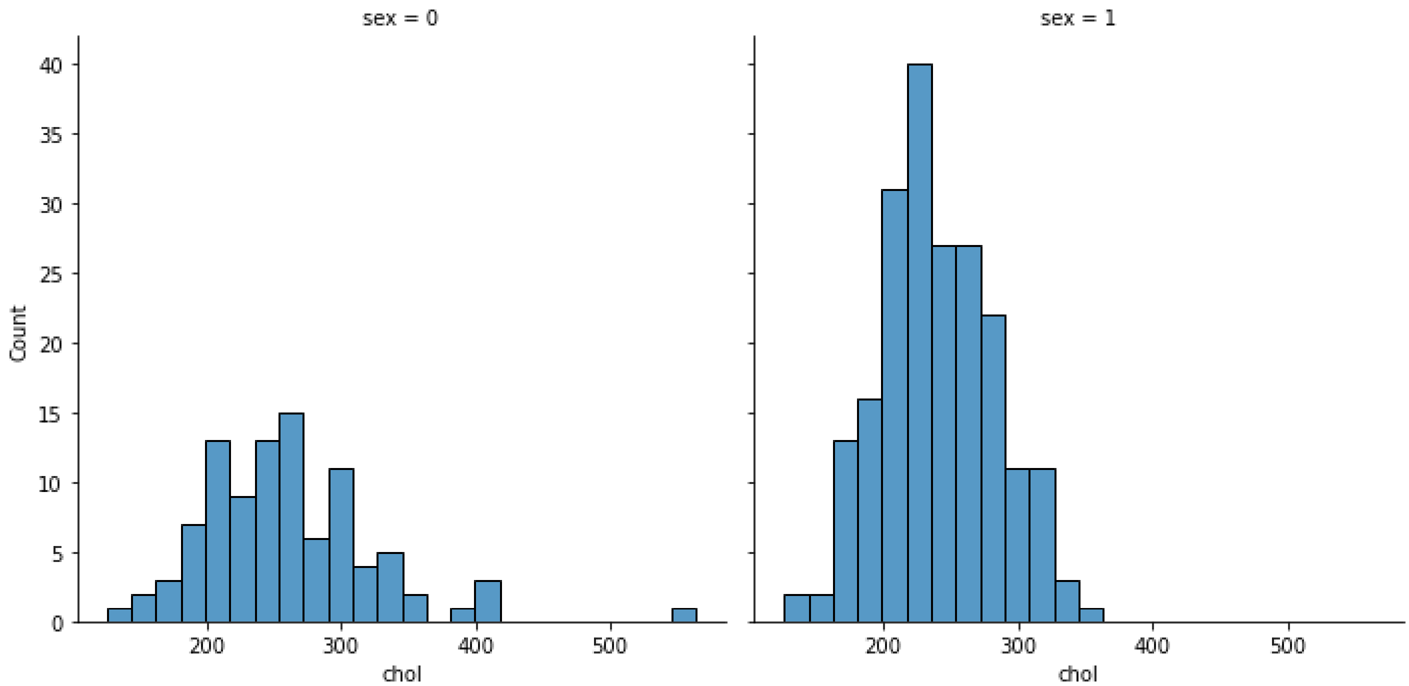


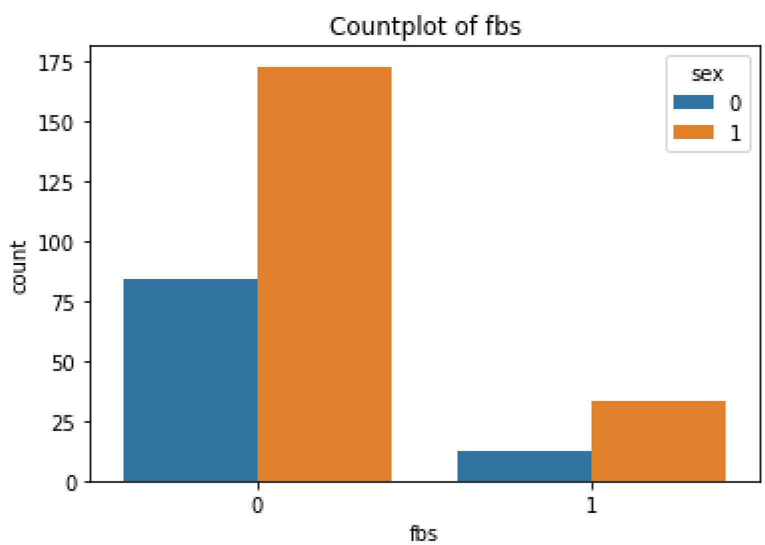


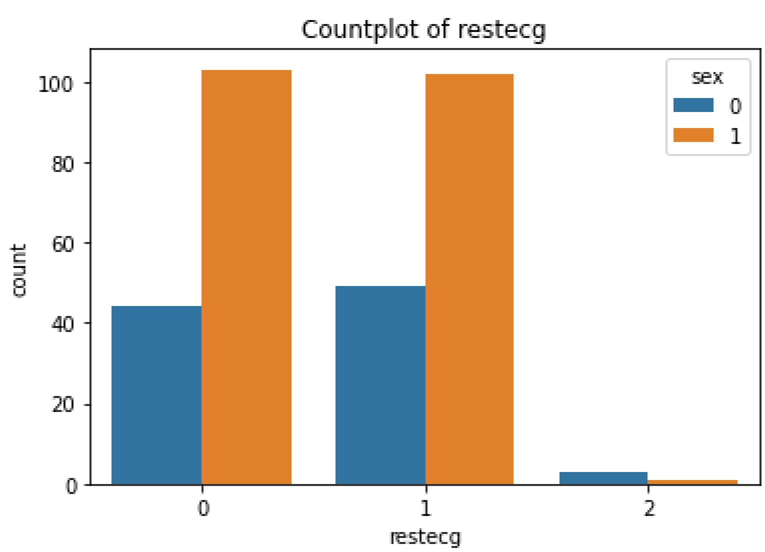
<Figure size 432x288 with 0 Axes>



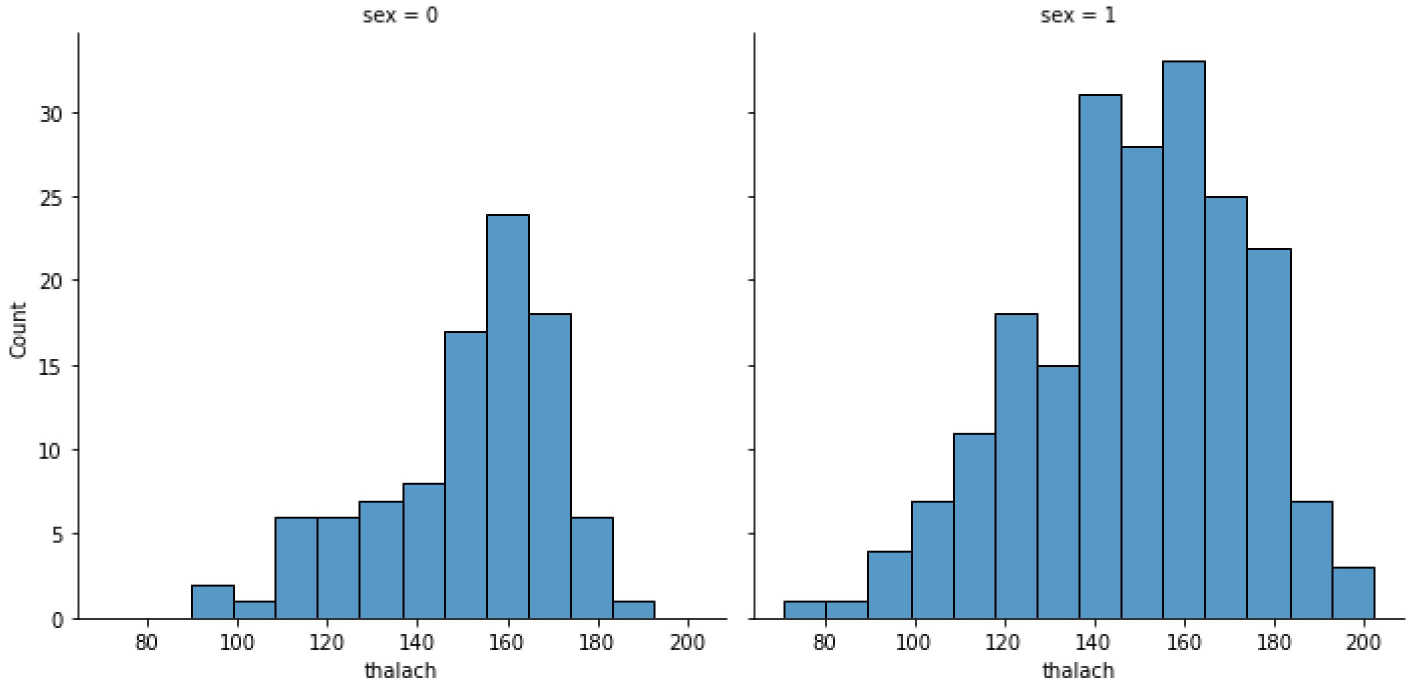
<Figure size 432x288 with 0 Axes>

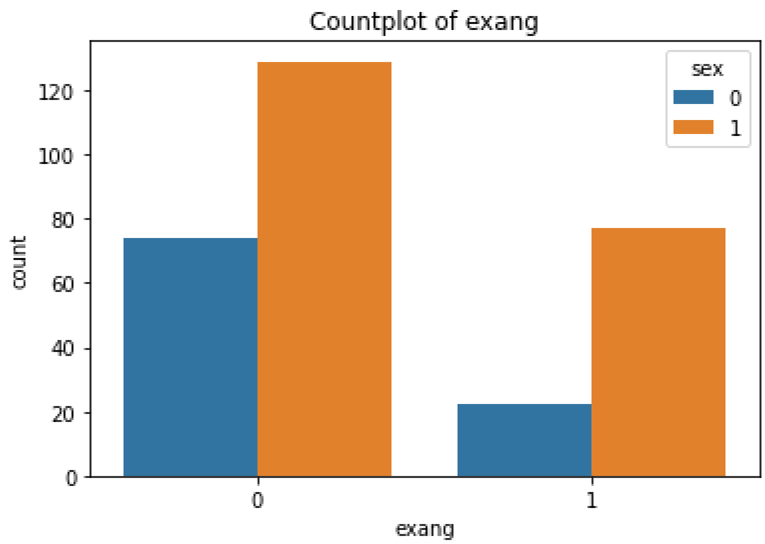




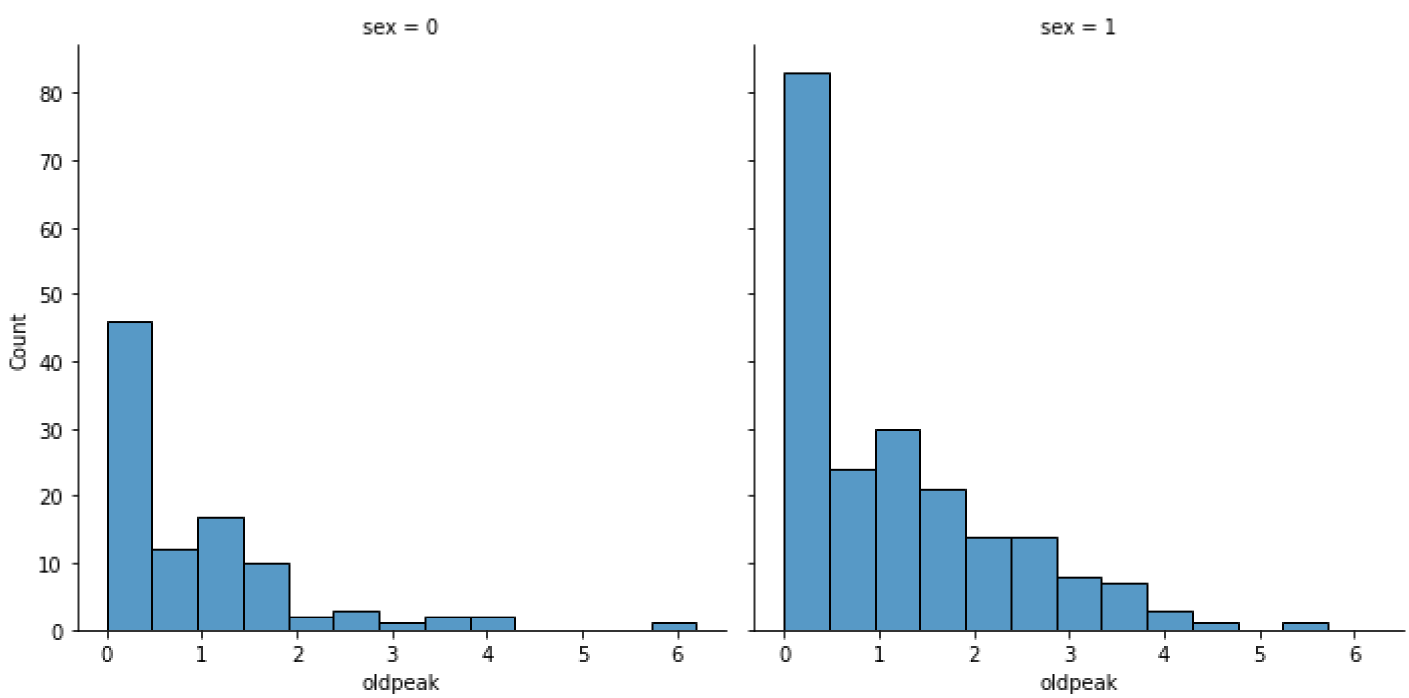


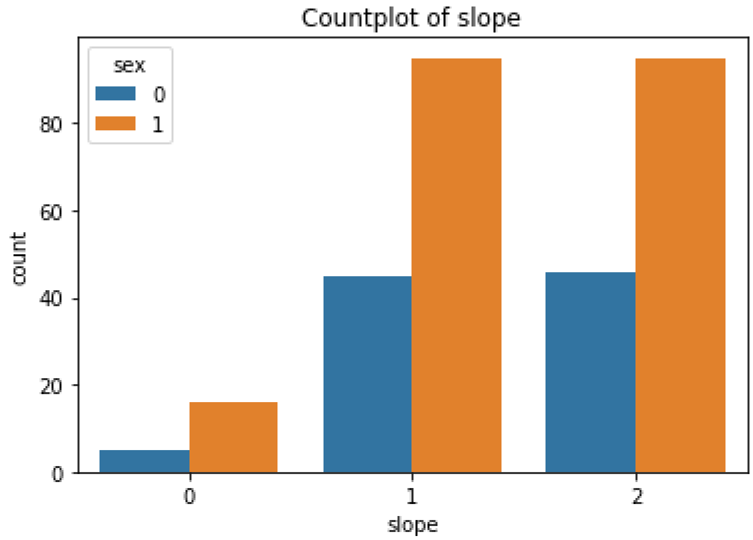
<Figure size 432x288 with 0 Axes>

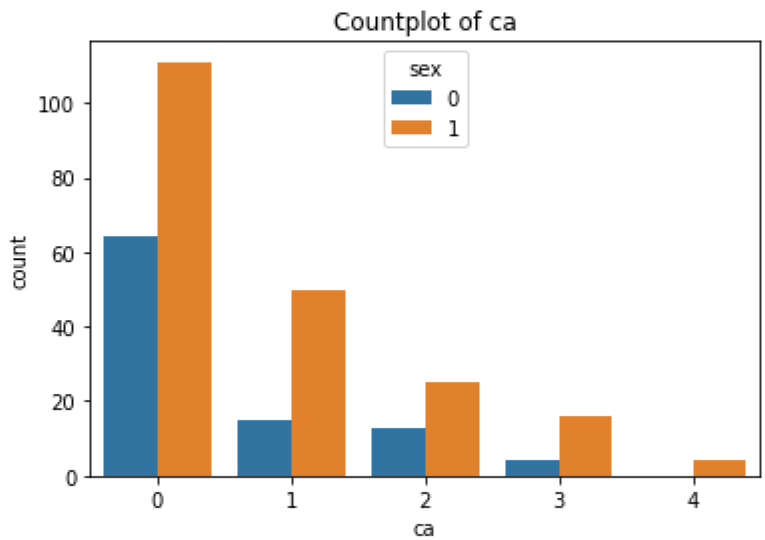


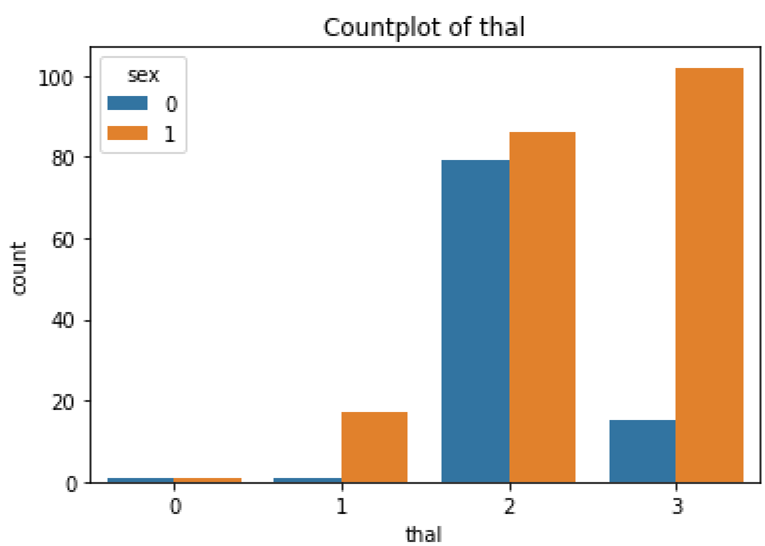


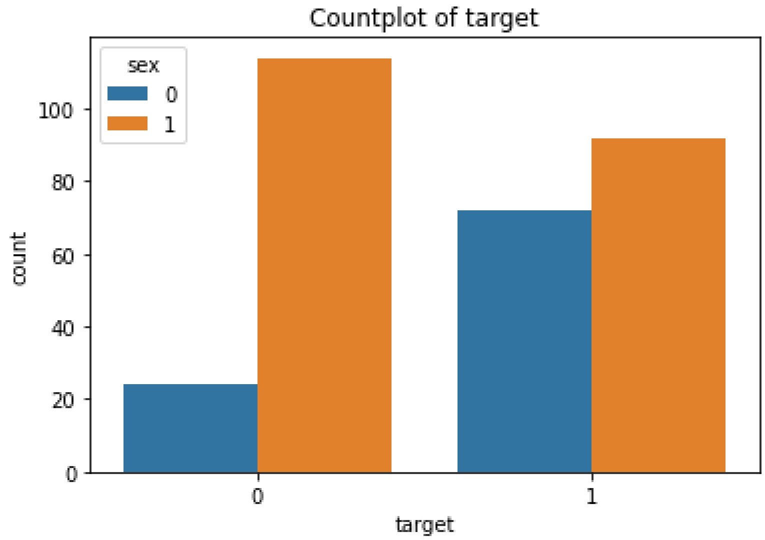
<Figure size 432x288 with 0 Axes>




Countplot of slope
sex
0
1
count
slope
0
20
40
60
80
0
1
2


Countplot of ca
sex
0
1
count
ca
0
20
40
60
80
100
0
1
2
3
4


Countplot of thal
sex
0
1
count
thal
0
20
40
60
80
100
0
1
2
3



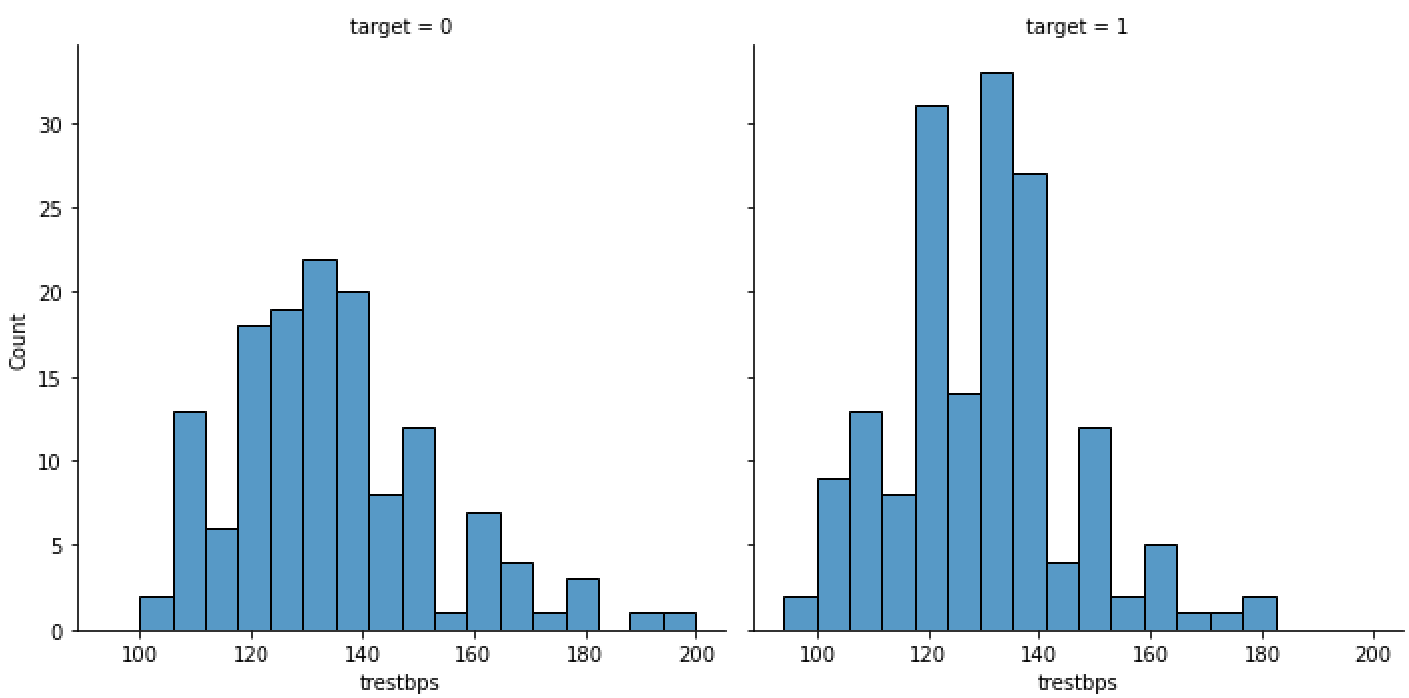
In [ ]:

2.e) Study if one can detect heart attacks based on anomalies in the resting blood pressure (trestbps) of a patient:

In [68]:

```
plt.figure(figsize= (6,4))

sns.displot(data= df, x= "trestbps", col= "target")

plt.show()
```

```
<Figure size 432x288 with 0 Axes>
```



- We have some observations with very High Resting Blood Pressure values without occurence of CVD.
- In general, we can see that Resting Blood Pressure values from 120-160 has more chances of CVD.
- Still, This feature alone can not be said to be conclusive of CVD.

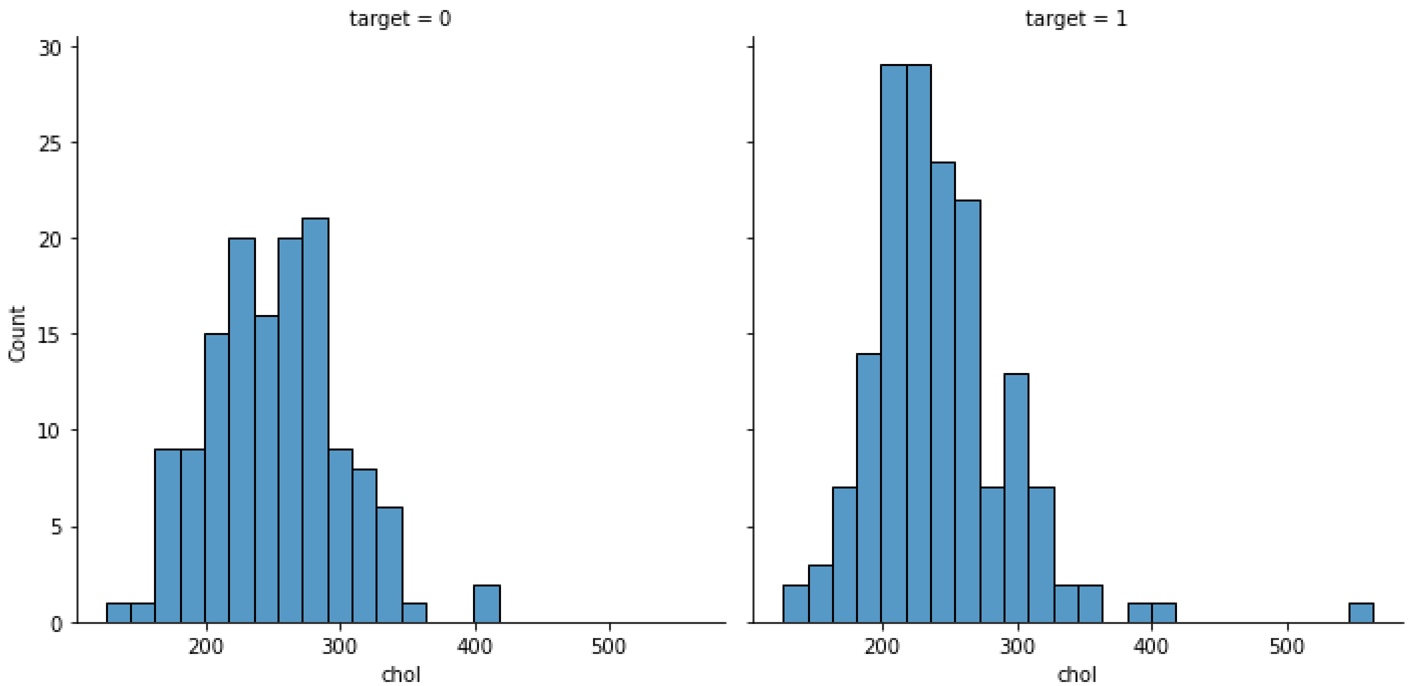
In [ ]:

2.f) Describe the relationship between cholesterol levels and a target variable:

In [72]:

```
plt.figure(figsize= (6,4))

sns.displot(data= df, x= "chol", col= "target")

plt.show()
```

```
<Figure size 432x288 with 0 Axes>
```



- Here too, No considerable conclusion can be made about CVD by Cholesterol Levels alone.

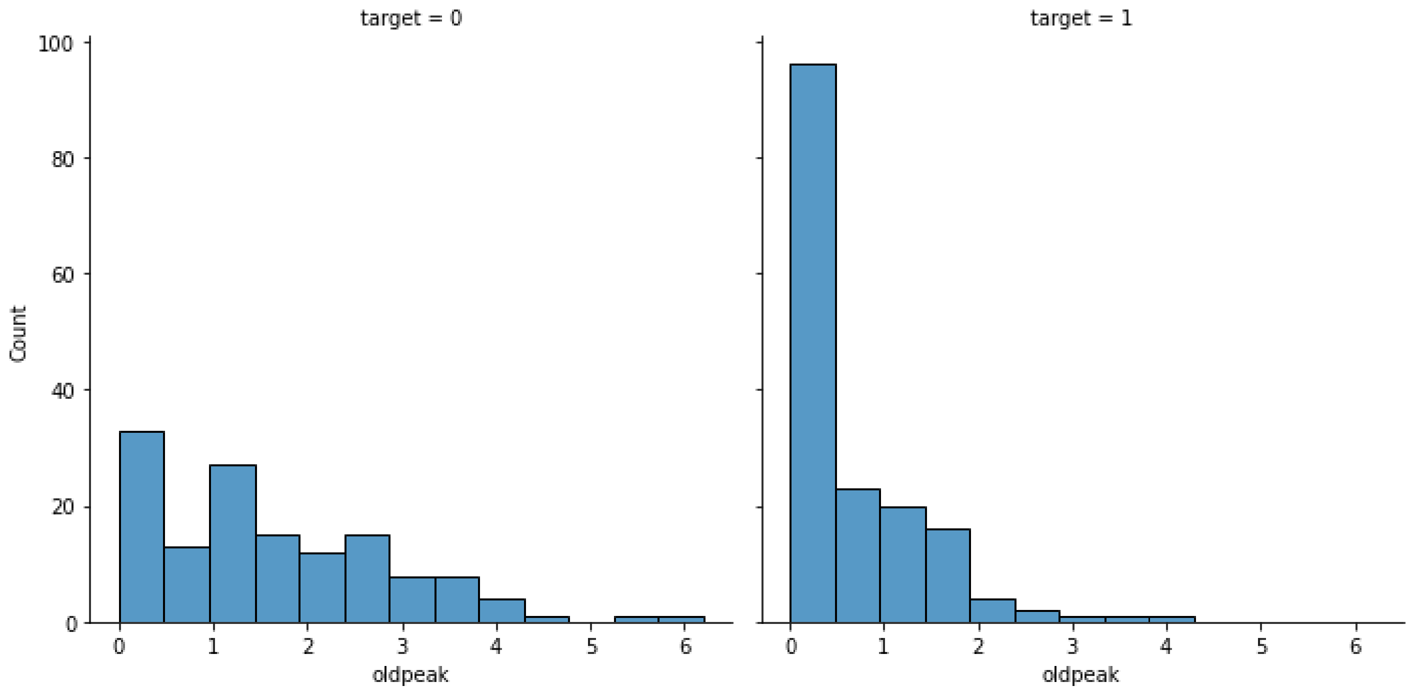
In [ ]:

2.g) State what relationship exists between peak exercising and the occurrence of a heart attack:

In [73]:

```
plt.figure(figsize= (6,4))

sns.displot(data= df, x= "oldpeak", col= "target")

plt.show()
```

```
<Figure size 432x288 with 0 Axes>
```

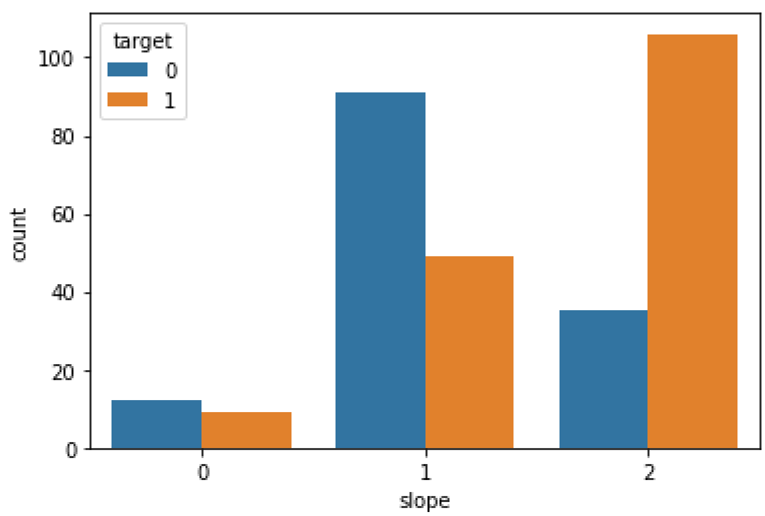


- As can be seen above, Lower Values of ST Depression Induced by Exercise relative to Rest clearly has more chanced of CVD Occurence.

In [ ]:

In [76]:

```
plt.figure(figsize= (6,4))

sns.countplot(data= df, x= "slope", hue= "target")

plt.show()
```



- Clear Relationship Between Slope of the Peak Exercise ST Segment and Occurence of CVD, having more value of "slope" clearly has more chances of CVD Occurence.

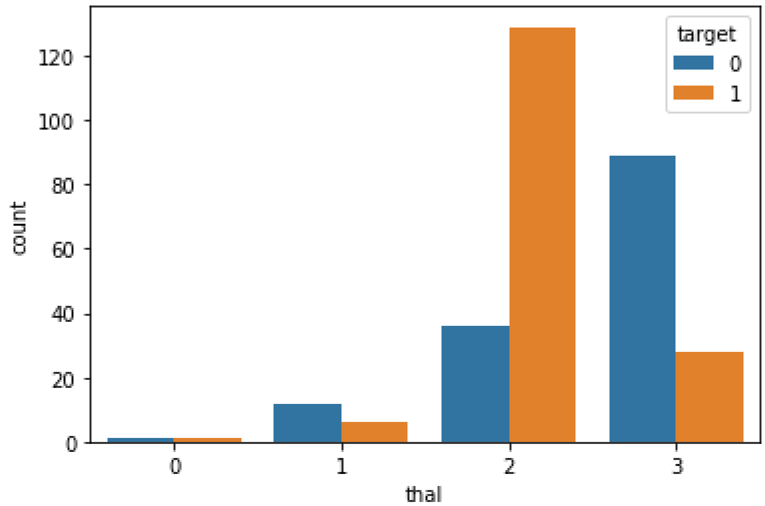
In [ ]:

2.h) Check if thalassemia is a major cause of CVD:

In [79]:

```
plt.figure(figsize= (6,4))
```

```python
sns.countplot(data= df, x= "thal", hue= "target")

plt.show()
```



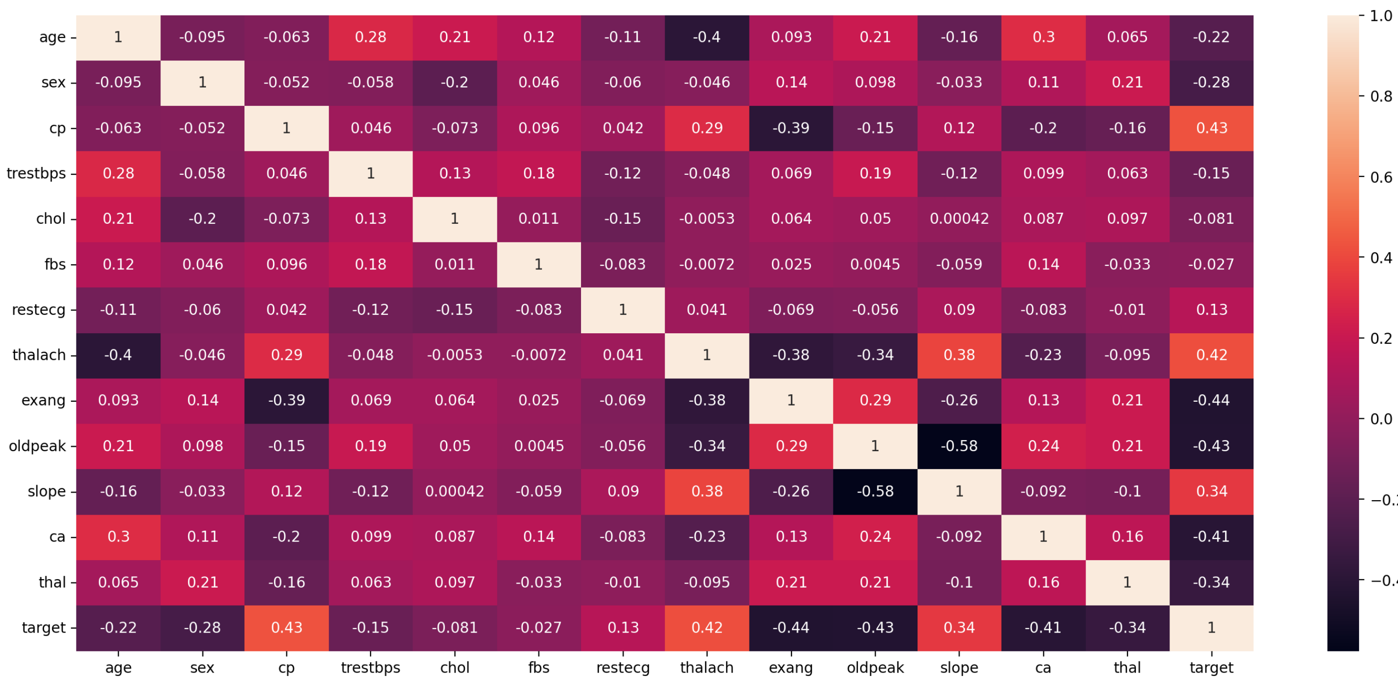
- As can be seen clearly, Thalassemia seems to be major Factor in Occurence of CVD.

In [ ]:

2.i) List how the other factors determine the occurrence of CVD:

In [80]:
```python
# Checking Correlation of Features with Target:
```

In [86]:
```python
plt.figure(figsize= (18,8), dpi= 200)

sns.heatmap(df.corr(), annot= True)

plt.show()
```



- Chest Pain (cp), Maximum Heart Rate Achieved (thalach), Slope of the peak exercise ST segment (slope) have Decently High Positive Correlation with Occurence of CVD.

- Exercise Induced Enigma (exang), ST depression induced by exercise relative to rest (oldpeak), Number of major vessels (0-3) colored by fluoroscopy (ca) and Thalassemia (thal) have Decently High Negative Correlation with Occurence of CVD.
- Cholesterol (chol) and Fasting Blood Sugar (fbs) have Very Low Correlation to Heart Disease.

In [ ]:

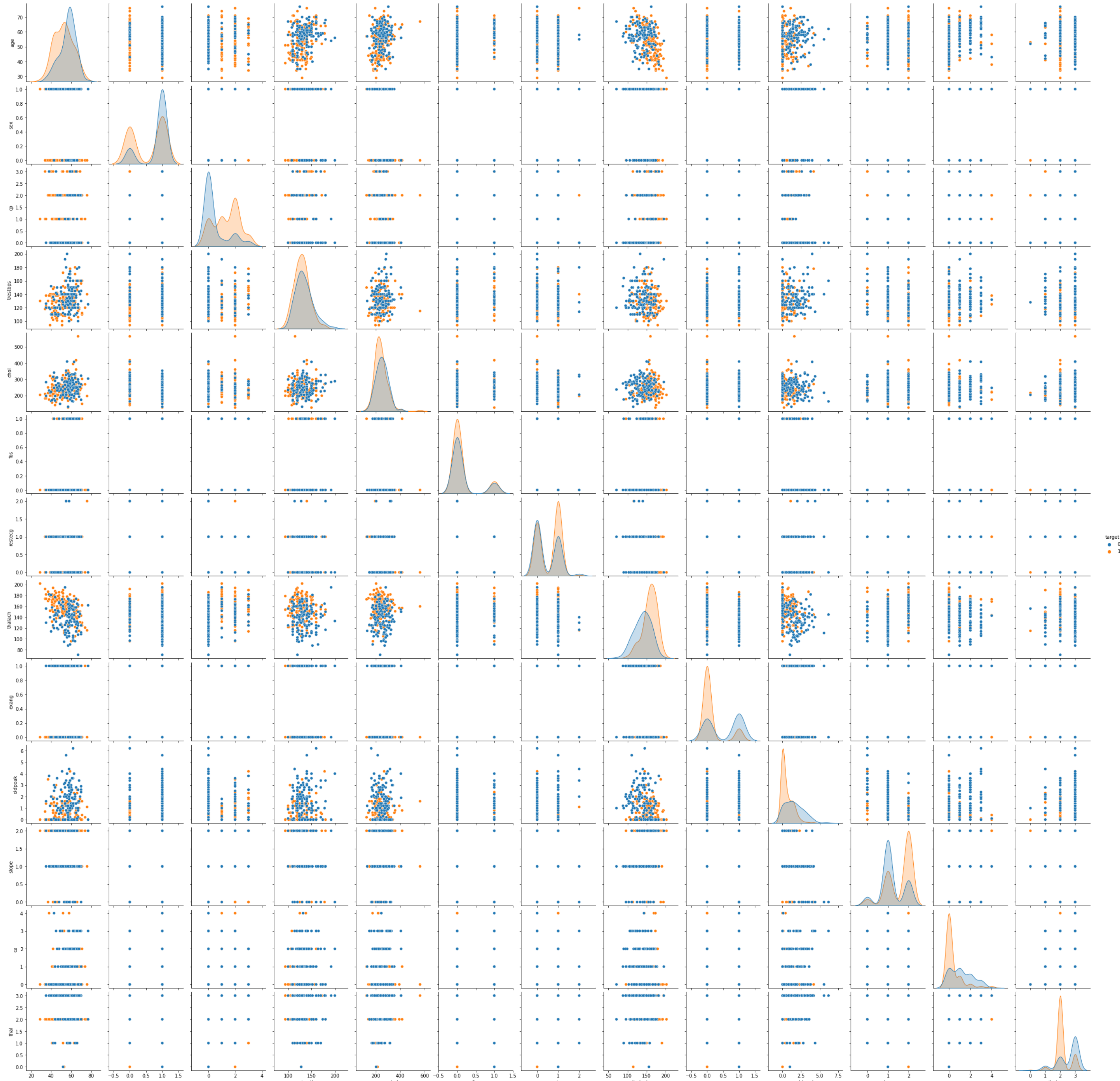
```

```

2.j) Use a pair plot to understand the relationship between all the given variables:

In [91]:

```
plt.figure(dpi= 200)

sns.pairplot(df, hue= "target")

plt.show()
```

```
<Figure size 1200x800 with 0 Axes>
```



- There aren't any Clearly Discernible Relationship Between any of the Features.

In [ ]:

3) Build a baseline model to predict the risk of a heart attack using a logistic regression and random forest and explore the results while using correlation analysis and logistic regression (leveraging standard error and p-values from statsmodels) for feature selection:

In [ ]:

Seperating Features and Target in Different Data Frames:

In [93]:

```
# Features:

x = df.drop("target", axis= 1)
```

In [94]:
```
x.head()
```

Out[94]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2

In [95]:
```
x.shape
```

Out[95]:
```
(302, 13)
```

In [ ]:

In [96]:
```
# Target:

y = df["target"]
```

In [97]:
```
y.head()
```

Out[97]:
```
0    1
1    1
2    1
3    1
4    1
Name: target, dtype: int64
```

In [98]:
```
y.shape
```

Out[98]:
```
(302,)
```

In [ ]:

Using Generalized Linear Model from statsmodel library to determine which Features are Significant in Decidind Target Variable.

In [99]:
```
glm_model = GLM(y, x)
```

In [100…
```
glm_results = glm_model.fit()
```

In [102…
```
glm_results.summary()
```

Out[102…

Generalized Linear Model Regression Results

Dep. Variable:	target	**No. Observations:**	302

Model:	GLM	**Df Residuals:**	289
Model Family:	Gaussian	**Df Model:**	12
Link Function:	identity	**Scale:**	0.12814
Method:	IRLS	**Log-Likelihood:**	-111.63
Date:	Sat, 26 Nov 2022	**Deviance:**	37.034
Time:	22:24:26	**Pearson chi2:**	37.0
No. Iterations:	3	**Pseudo R-squ. (CS):**	0.6249
Covariance Type:	nonrobust		

	coef	std err	z	P>|z|	[0.025	0.975]
age	0.0035	0.002	1.503	0.133	-0.001	0.008
sex	-0.1706	0.047	-3.652	0.000	-0.262	-0.079
cp	0.1091	0.023	4.812	0.000	0.065	0.154
trestbps	-0.0008	0.001	-0.708	0.479	-0.003	0.001
chol	-0.0001	0.000	-0.254	0.799	-0.001	0.001
fbs	0.0084	0.060	0.139	0.889	-0.110	0.126
restecg	0.0686	0.040	1.728	0.084	-0.009	0.146
thalach	0.0050	0.001	5.605	0.000	0.003	0.007
exang	-0.1202	0.051	-2.350	0.019	-0.221	-0.020
oldpeak	-0.0526	0.023	-2.274	0.023	-0.098	-0.007
slope	0.0887	0.043	2.078	0.038	0.005	0.172
ca	-0.1120	0.023	-4.924	0.000	-0.157	-0.067
thal	-0.1021	0.036	-2.866	0.004	-0.172	-0.032

In [ ]:

- There are Some Features which Have p-Value > 0.05.
- Those Features are not Significant in Predicting Target Variable.
- We will Build our Model Twice, once Using all The Features and Once Using Only Those Features deemed Significant by GLM.

In [ ]:

Creating new Data Frame with Feature deemed Significan by GLM.

In [104…

```
glm_results.pvalues
```

Out[104…

```
age         1.329240e-01
sex         2.602821e-04
cp          1.491747e-06
trestbps    4.789596e-01
chol        7.991127e-01
```

```
fbs           8.894247e-01
restecg       8.391343e-02
thalach       2.086209e-08
exang         1.879360e-02
oldpeak       2.297834e-02
slope         3.773797e-02
ca            8.465524e-07
thal          4.157151e-03
dtype: float64
```

In [105…

```
glm_results.pvalues[glm_results.pvalues < 0.05]
```

Out[105…

```
sex          2.602821e-04
cp           1.491747e-06
thalach      2.086209e-08
exang        1.879360e-02
oldpeak      2.297834e-02
slope        3.773797e-02
ca           8.465524e-07
thal         4.157151e-03
dtype: float64
```

In [106…

```
significant_cols = list(glm_results.pvalues[glm_results.pvalues < 0.05].index)
```

In [107…

```
significant_cols
```

Out[107…

```
['sex', 'cp', 'thalach', 'exang', 'oldpeak', 'slope', 'ca', 'thal']
```

In [ ]:

In [112…

```
x_glm = x[significant_cols].copy()
```

In [113…

```
x_glm.head()
```

Out[113…

	sex	cp	thalach	exang	oldpeak	slope	ca	thal
0	1	3	150	0	2.3	0	0	1
1	1	2	187	0	3.5	0	0	2
2	0	1	172	0	1.4	2	0	2
3	1	1	178	0	0.8	2	0	2
4	0	0	163	1	0.6	2	0	2

In [ ]:

4) Train Test Split:

Train Test Split of Datafrmae with All Features:

In [114…

```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size= 0.2, random_state= 42
```

In [115…

```
print(x_train.shape)
```

```
print(x_test.shape)
print(y_train.shape)
print(y_test.shape)
```

```
(241, 13)
(61, 13)
(241,)
(61,)
```

In [ ]:

Train Test Split of Datafrmae with GLM Features:

In [116…

```
x_glm_train, x_glm_test, y_train, y_test = train_test_split(x_glm, y, test_size= 0.2, ranc
```

In [117…

```
print(x_glm_train.shape)
print(x_glm_test.shape)
print(y_train.shape)
print(y_test.shape)
```

```
(241, 8)
(61, 8)
(241,)
(61,)
```

In [ ]:

5) Scalling:

Scalling of Datafrmae with All Features:

In [118…

```
sc_all = StandardScaler()
```

In [119…

```
temp = sc_all.fit_transform(x_train)
x_train = pd.DataFrame(temp, columns= x_train.columns)
x_train.head()
```

Out[119…

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slop
0	-1.350641	0.731459	0.000000	-0.630711	0.927138	-0.391293	0.890028	0.549139	-0.659184	-0.895837	0.96543
1	1.487426	0.731459	0.966493	2.753363	0.526980	2.555631	-0.991522	0.012071	1.517027	0.543474	-0.68470
2	1.378270	0.731459	-0.966493	-0.348705	0.145878	2.555631	0.890028	0.593894	-0.659184	-0.715923	-0.68470
3	0.068393	-1.367131	0.000000	0.215308	0.069658	-0.391293	-0.991522	0.504383	-0.659184	0.363560	-0.68470
4	1.050801	0.731459	0.966493	0.497314	1.689342	-0.391293	0.890028	0.370116	-0.659184	-0.895837	0.96543

In [120…

```
temp = sc_all.transform(x_test)
x_test = pd.DataFrame(temp, columns= x_test.columns)
x_test.head()
```

Out[120…

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slo
0	0.068393	0.731459	-0.966493	0.046104	2.032334	-0.391293	0.890028	-0.793531	1.517027	0.183647	-0.6847

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slo
1	1.050801	0.731459	0.966493	-0.348705	1.193909	-0.391293	0.890028	-0.838286	1.517027	0.723388	-0.6847
2	0.286705	0.731459	0.966493	1.061326	-2.293175	2.555631	0.890028	1.041451	-0.659184	-0.715923	0.9654
3	1.269113	0.731459	0.000000	1.625339	-0.006563	-0.391293	0.890028	-1.330598	1.517027	-0.895837	-0.6847
4	1.814896	-1.367131	0.966493	-1.194723	0.355484	2.555631	-0.991522	-0.883042	-0.659184	-0.895837	0.9654

In [ ]:

Scalling of Datafrmae with GLM Features:

In [121…

```
sc_glm = StandardScaler()
```

In [122…

```
temp = sc_glm.fit_transform(x_glm_train)
x_glm_train = pd.DataFrame(temp, columns= x_glm_train.columns)
x_glm_train.head()
```

Out[122…

	sex	cp	thalach	exang	oldpeak	slope	ca	thal
0	0.731459	0.000000	0.549139	-0.659184	-0.895837	0.965436	-0.683490	-0.545762
1	0.731459	0.966493	0.012071	1.517027	0.543474	-0.684707	-0.683490	1.140502
2	0.731459	-0.966493	0.593894	-0.659184	-0.715923	-0.684707	1.350103	1.140502
3	-1.367131	0.000000	0.504383	-0.659184	0.363560	-0.684707	-0.683490	-0.545762
4	0.731459	0.966493	0.370116	-0.659184	-0.895837	0.965436	-0.683490	-0.545762

In [123…

```
temp = sc_glm.transform(x_glm_test)
x_glm_test = pd.DataFrame(temp, columns= x_glm_test.columns)
x_glm_test.head()
```

Out[123…

	sex	cp	thalach	exang	oldpeak	slope	ca	thal
0	0.731459	-0.966493	-0.793531	1.517027	0.183647	-0.684707	0.333307	1.140502
1	0.731459	0.966493	-0.838286	1.517027	0.723388	-0.684707	-0.683490	1.140502
2	0.731459	0.966493	1.041451	-0.659184	-0.715923	0.965436	0.333307	1.140502
3	0.731459	0.000000	-1.330598	1.517027	-0.895837	-0.684707	2.366899	-2.232025
4	-1.367131	0.966493	-0.883042	-0.659184	-0.895837	0.965436	0.333307	-0.545762

In [ ]:

6) Building Logistic Regression Model and Random Forest Model:

6.1) Logistic Regression:

Logistic Regression Model Using All Features:

In [124…

```
log_model_all = LogisticRegression()
```

In [125…

```
log_model_all.fit(x_train, y_train)
```

Out[125…

```
LogisticRegression()
```

In [126…

```
preds = log_model_all.predict(x_test)
```

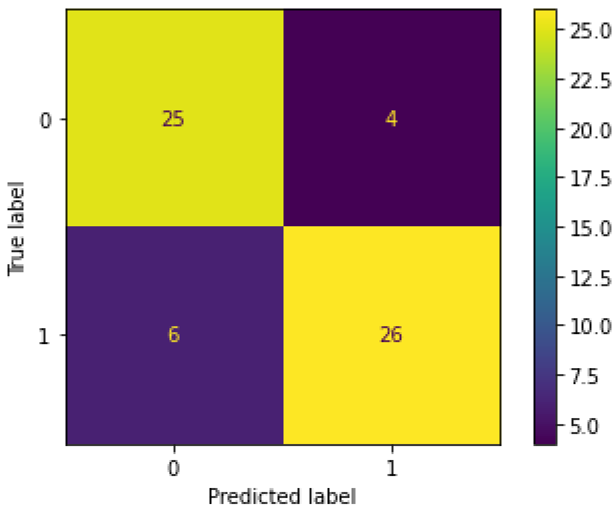
In [129…

```
print(classification_report(y_test, preds))
```

```
              precision    recall  f1-score   support

           0       0.81      0.86      0.83        29
           1       0.87      0.81      0.84        32

    accuracy                           0.84        61
   macro avg       0.84      0.84      0.84        61
weighted avg       0.84      0.84      0.84        61
```

In [138…

```
plot_confusion_matrix(log_model_all, x_test, y_test)
plt.show()
```



In [ ]:

```

```

Logistic Regression Model Using GLM Features:

In [130…

```
log_model_glm = LogisticRegression()
```

In [131…

```
log_model_glm.fit(x_glm_train, y_train)
```

Out[131…

```
LogisticRegression()
```

In [133…

```
preds = log_model_glm.predict(x_glm_test)
```

In [134…

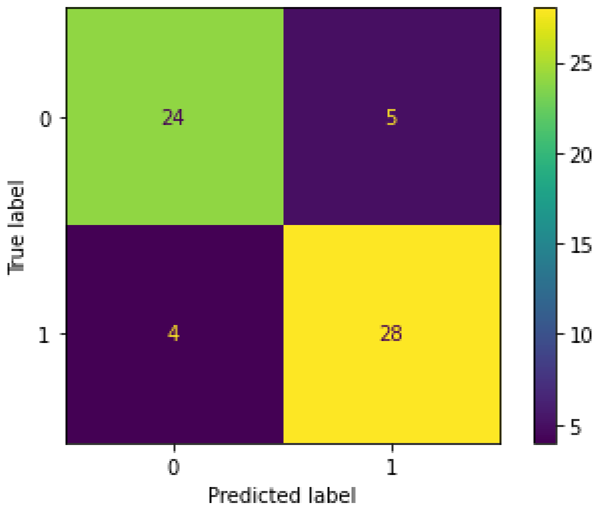
```
print(classification_report(y_test, preds))
```

```
              precision    recall  f1-score   support

           0       0.86      0.83      0.84        29
```

```
           1       0.85      0.88      0.86        32

    accuracy                           0.85        61
   macro avg       0.85      0.85      0.85        61
weighted avg       0.85      0.85      0.85        61
```

In [139…

```
plot_confusion_matrix(log_model_glm, x_glm_test, y_test)
plt.show()
```



- There's not a Significant Improvement in Overall Accuracy of Model with using Only Significant Features.

In [ ]:

6.2) Random Forest Classifier:

Random Forest Classifier Using All Features:

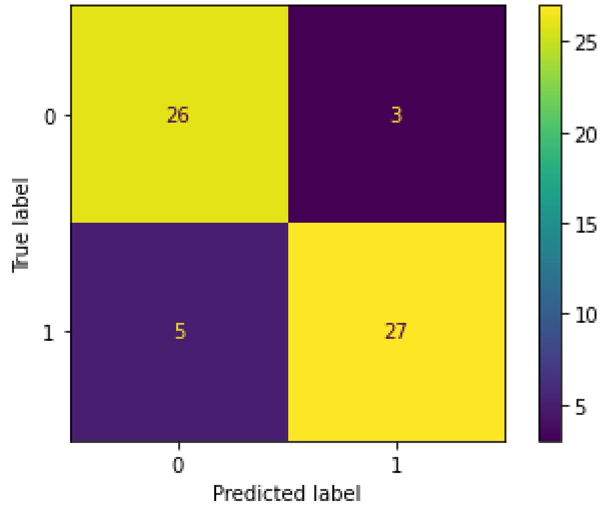
In [136…

```
rf_model_all = RandomForestClassifier()

rf_model_all.fit(x_train, y_train)

preds = rf_model_all.predict(x_test)

print(classification_report(y_test, preds))
```

```
              precision    recall  f1-score   support

           0       0.84      0.90      0.87        29
           1       0.90      0.84      0.87        32

    accuracy                           0.87        61
   macro avg       0.87      0.87      0.87        61
weighted avg       0.87      0.87      0.87        61
```

In [140…

```
plot_confusion_matrix(rf_model_all, x_test, y_test)
plt.show()
```



Random Forest Classifier Using GLM Features:

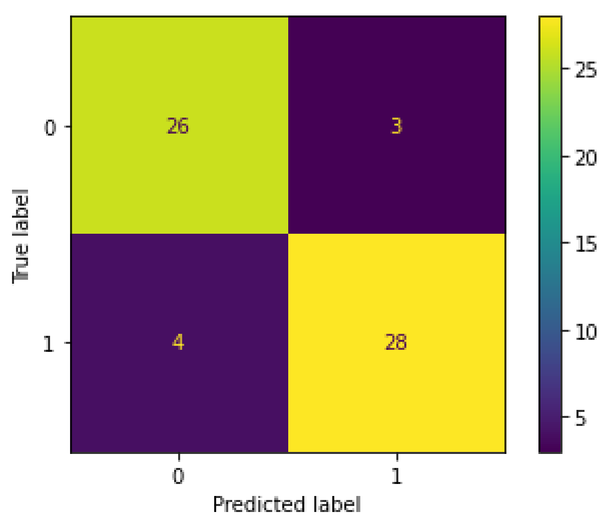
In [137…

```
rf_model_glm = RandomForestClassifier()

rf_model_glm.fit(x_glm_train, y_train)

preds = rf_model_glm.predict(x_glm_test)

print(classification_report(y_test, preds))
```

```
              precision    recall  f1-score   support

           0       0.87      0.90      0.88        29
           1       0.90      0.88      0.89        32

    accuracy                           0.89        61
   macro avg       0.88      0.89      0.89        61
weighted avg       0.89      0.89      0.89        61
```

In [141…

```
plot_confusion_matrix(rf_model_glm, x_glm_test, y_test)
plt.show()
```



- Same as in Logistic Regression, Not a Significant Improvement in Accuracy of Model Using only Significant Features.

In [ ]:

We should use Significant Features Found using GLM to Train and Build Model to Predict CVD as it uses less features to Provide same Rate of Accuracy.

In [ ]:

Extra:

Running Grid Search for All Models and Comparing Accuracies

Model Fitting and Evaluation Function:

In [142…

```
def model_fit_eval(model, param_dict):
    '''
    This Function will Take in Model and Parameter Dictionary as Input Parameters.
    Prints Concise Report about Model Performance.

    Grid Search Will Run on Significant Features Selected Using GLM.
    '''

    grid_model = GridSearchCV(estimator= model, param_grid= param_dict, cv=5)

    grid_model.fit(x_glm_train, y_train)

    print("Best Parameters:\n")

    print(grid_model.best_params_)

    print("\n")

    pred = grid_model.predict(x_glm_test)

    print(classification_report(y_test, pred))

    plot_confusion_matrix(grid_model.best_estimator_, x_glm_test, y_test)
```

In [ ]:

1) Grid Search on Logistic Regression:

In [143…

```
log_model = LogisticRegression()
```

In [144…

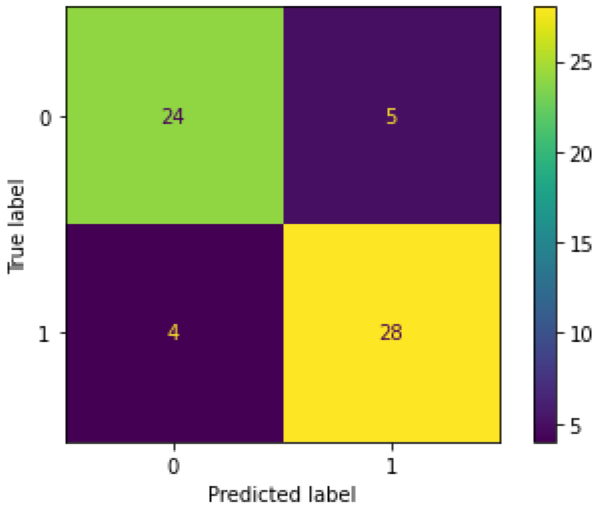
```
param_dict = {"penalty" : ["l1", "l2", "elasticnet"], "C" : np.logspace(0, 5, 10),
                                          "l1_ratio" : [0, 0.01, 0.1, 0.25, 0.5, 0.75, 0.9, 0.9
```

In [151…

```
model_fit_eval(log_model, param_dict)
```

```
Best Parameters:

{'C': 1.0, 'l1_ratio': 0, 'penalty': 'l2'}


              precision    recall  f1-score   support

           0       0.86      0.83      0.84        29
           1       0.85      0.88      0.86        32
```

```
    accuracy                           0.85        61
   macro avg       0.85      0.85      0.85        61
weighted avg       0.85      0.85      0.85        61
```



In [ ]:

Grid Search on Support Vector Classifier:

In [152…

```
svc = SVC()
```

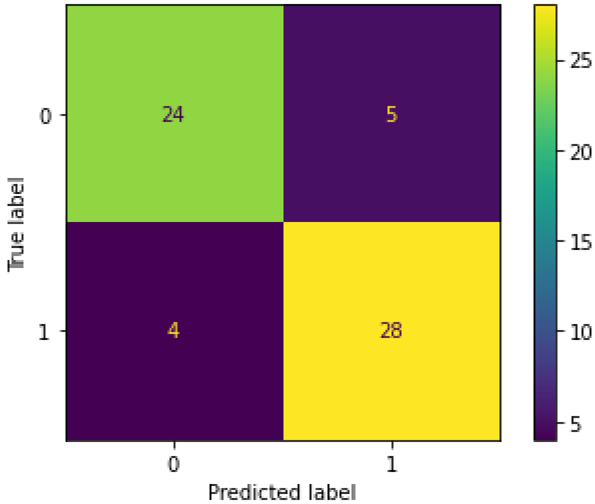
In [153…

```
param_dict = {"kernel" : ["linear", "rbf", "poly", "sigmoid"],
             "C" : [0.01, 0,1, 1, 10, 100],
             "degree" : [1,2,3], "gamma" : ["scale", "auto"]}
```

In [154…

```
model_fit_eval(svc, param_dict)
```

```
Best Parameters:

{'C': 1, 'degree': 1, 'gamma': 'scale', 'kernel': 'poly'}


              precision    recall  f1-score   support

           0       0.86      0.83      0.84        29
           1       0.85      0.88      0.86        32

    accuracy                           0.85        61
   macro avg       0.85      0.85      0.85        61
weighted avg       0.85      0.85      0.85        61
```



In [ ]:

Grid Search on KNN Classifier:

In [157…

```
knn = KNeighborsClassifier()
```

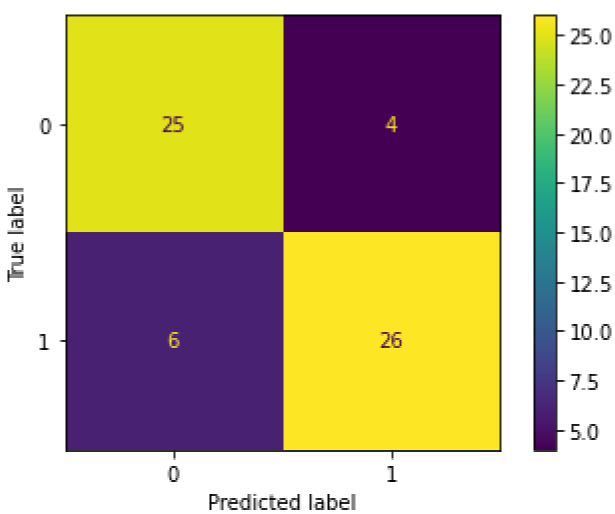
In [158…

```
param_dict = {"n_neighbors" : list(range(1,15)),
             "metric" : ["euclidean", "cosine", "manhattan","minkowski"]}
```

In [159…

```
model_fit_eval(knn, param_dict)
```

```
Best Parameters:

{'metric': 'manhattan', 'n_neighbors': 8}


              precision    recall  f1-score   support

           0       0.81      0.86      0.83        29
           1       0.87      0.81      0.84        32

    accuracy                           0.84        61
   macro avg       0.84      0.84      0.84        61
weighted avg       0.84      0.84      0.84        61
```



In [ ]:

Grid Search on Decision Tree Classifier:

In [160…

```
dt = DecisionTreeClassifier()
```

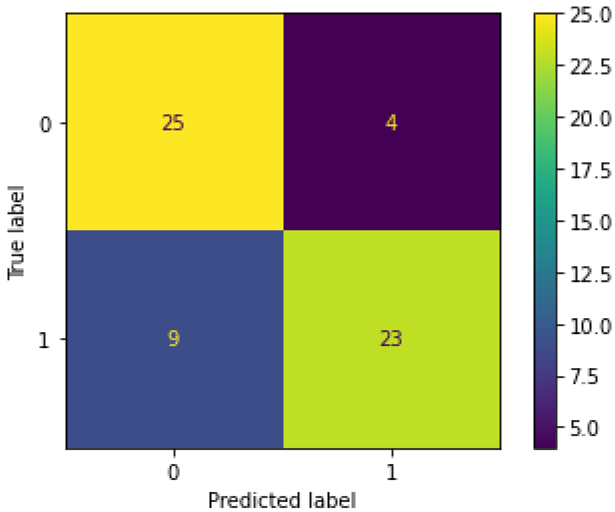
In [161…

```
param_dict = {"criterion" : ["gini", "entropy"],
             "splitter" : ["best","random"]}
```

In [162…

```
model_fit_eval(dt, param_dict)
```

```
Best Parameters:

{'criterion': 'gini', 'splitter': 'best'}


              precision    recall  f1-score   support

           0       0.74      0.86      0.79        29
           1       0.85      0.72      0.78        32

    accuracy                           0.79        61
   macro avg       0.79      0.79      0.79        61
weighted avg       0.80      0.79      0.79        61
```



In [ ]:

Grid Search on Random Forest Classifier:

In [163…

```
rf = RandomForestClassifier()
```

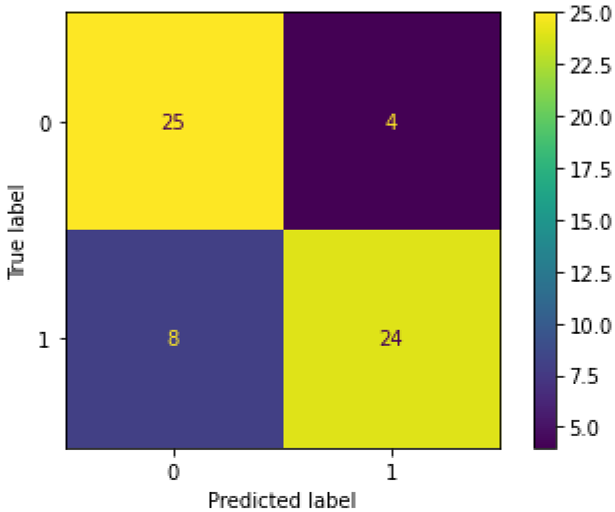
In [164…

```
param_dict = {"n_estimators" : range(1,25),
             "criterion" : ["gini", "entropy"],
             "max_features" : [2,3,4],
             "bootstrap" : [True, False],
             "oob_score" : [True,False]}
```

In [165…

```
model_fit_eval(rf, param_dict)
```

```
Best Parameters:

{'bootstrap': True, 'criterion': 'entropy', 'max_features': 4, 'n_estimators': 9, 'oob_sco
re': False}


              precision    recall  f1-score   support

           0       0.76      0.86      0.81        29
           1       0.86      0.75      0.80        32

    accuracy                           0.80        61
   macro avg       0.81      0.81      0.80        61
weighted avg       0.81      0.80      0.80        61
```



In [ ]:

Grid Search on AdaBoost Classifier:

In [166…

```
adc = AdaBoostClassifier()
```

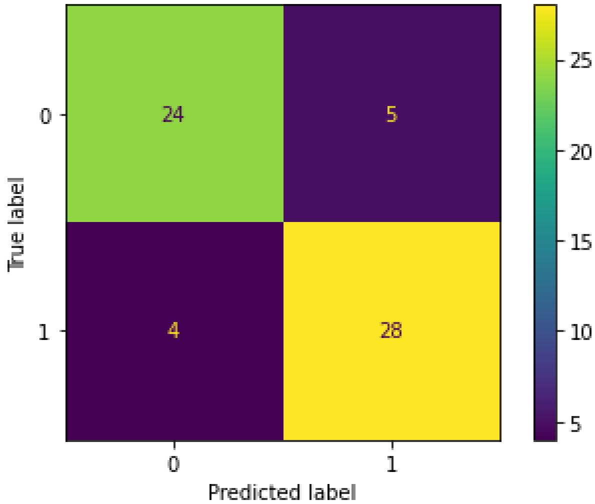
In [167…

```
param_dict = {"n_estimators" : range(1,25),
             "learning_rate" : [0.01, 0.1, 1, 10],
             "algorithm" : ["SAMME","SAMME.R"]}
```

In [168…

```
model_fit_eval(adc, param_dict)
```

```
Best Parameters:

{'algorithm': 'SAMME', 'learning_rate': 1, 'n_estimators': 6}


              precision    recall  f1-score   support

           0       0.86      0.83      0.84        29
           1       0.85      0.88      0.86        32

    accuracy                           0.85        61
   macro avg       0.85      0.85      0.85        61
weighted avg       0.85      0.85      0.85        61
```



In [ ]:

Grid Search on Gradient Boost Classifier:

In [169…

```
gbc = GradientBoostingClassifier()
```

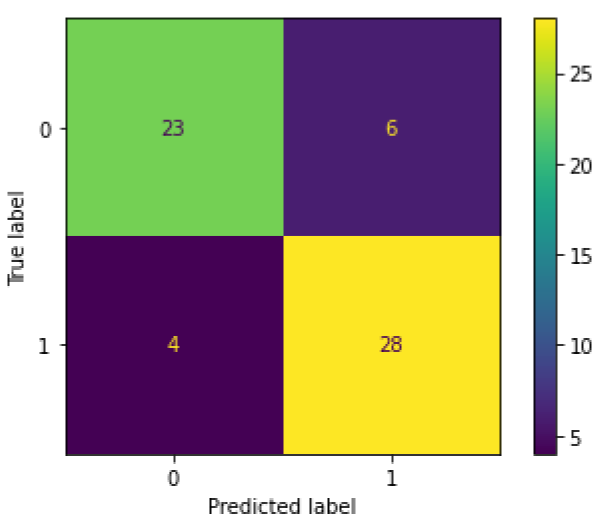
In [170…

```
param_dict = {"n_estimators": range(1,25),
              "max_depth": [3,4,5,6],
             "max_features": ["auto", "sqrt", "log2"]}
```

In [171…

```
model_fit_eval(gbc, param_dict)
```

```
Best Parameters:

{'max_depth': 3, 'max_features': 'sqrt', 'n_estimators': 8}


              precision    recall  f1-score   support

           0       0.85      0.79      0.82        29
           1       0.82      0.88      0.85        32

    accuracy                           0.84        61
   macro avg       0.84      0.83      0.83        61
weighted avg       0.84      0.84      0.84        61
```



In [ ]:

Grid Search on XGB Classifier:

In [172…

```
xgbc = XGBClassifier()
```

In [177…

```
param_dict = {
    'n_estimators': range(1,10),
    'max_depth': range(1, 10),
    'learning_rate': [.4, .45, .5, .55, .6],
    'colsample_bytree': [.6, .7, .8, .9, 1]}
```

In [ ]:

```
model_fit_eval(xgbc, param_dict)
```

```
Best Parameters:

{'colsample_bytree': 0.6, 'learning_rate': 0.4, 'max_depth': 1, 'n_estimators': 8}


              precision    recall  f1-score   support

           0       0.88      0.79      0.84        29
           1       0.83      0.91      0.87        32

    accuracy                           0.85        61
   macro avg       0.86      0.85      0.85        61
weighted avg       0.86      0.85      0.85        61
```