HealthCare-ML-Project

December 5, 2022

[1]:
```python
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')
```

[2]:
```python
health = pd.read_excel('healthcare.xlsx')
```

[3]:
```python
health.head()
```

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

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

[4]:
```python
health.tail()
```

[4]:
```
     age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  \
298   57    0   0       140   241    0        1      123      1      0.2
299   45    1   3       110   264    0        1      132      0      1.2
300   68    1   0       144   193    1        1      141      0      3.4
301   57    1   0       130   131    0        1      115      1      1.2
302   57    0   1       130   236    0        0      174      0      0.0

     slope  ca  thal  target
298      1   0     3       0
299      1   0     3       0
```

```
300        1   2      3        0
301        1   1      3        0
302        1   1      2        0
```

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

[5]:
```python
health.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
```

[6]:
```python
health.shape
```

[6]: (303, 14)

[7]:
```python
health.describe().T
```

[7]:

	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
```

[8]:
```
health.isna().sum()
```

[8]:
```
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
```

[9]:
```
health[health.duplicated(keep= False)]
```

[9]:
```
     age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  \
163   38    1   2       138   175    0        1      173      0      0.0
164   38    1   2       138   175    0        1      173      0      0.0

     slope  ca  thal  target
163      2   4     2       1
164      2   4     2       1
```

Our Data has no Missing Values, but it has a Duplicate ROW.

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

[10]:
```
#Drop the Duplicate Row.
health = health.drop(164)
```

[11]:
```
#Check size after dropping the duplicate row.
health.shape
```

[11]:
```
(302, 14)
```

[12]:
```
health[health.duplicated(keep= False)]
```

[12]:
```
Empty DataFrame
Columns: [age, sex, cp, trestbps, chol, fbs, restecg, thalach, exang, oldpeak,
slope, ca, thal, target]
Index: []
```

NOW no Duplicate Values.

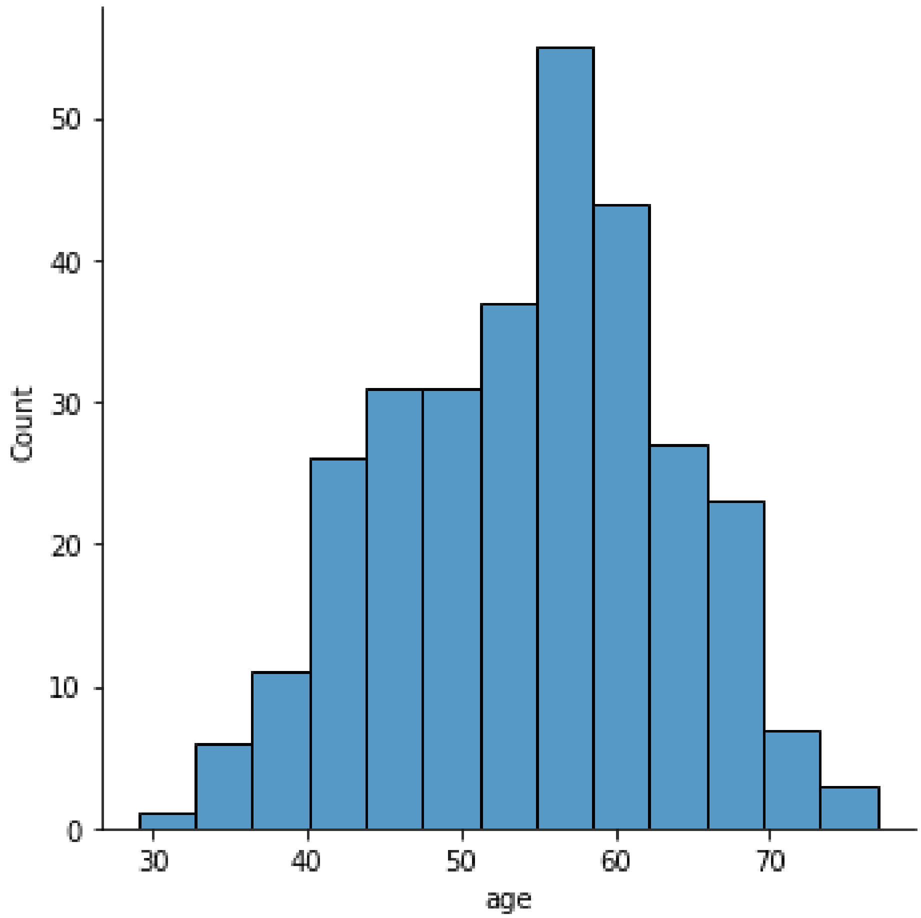
CONCLUSION- 1. There are no missing values in our DataFrame. 2. Thare are no Duplicates in our DataFrame. 3. Our data has 302 ROWS and 14 COLUMNS.

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.

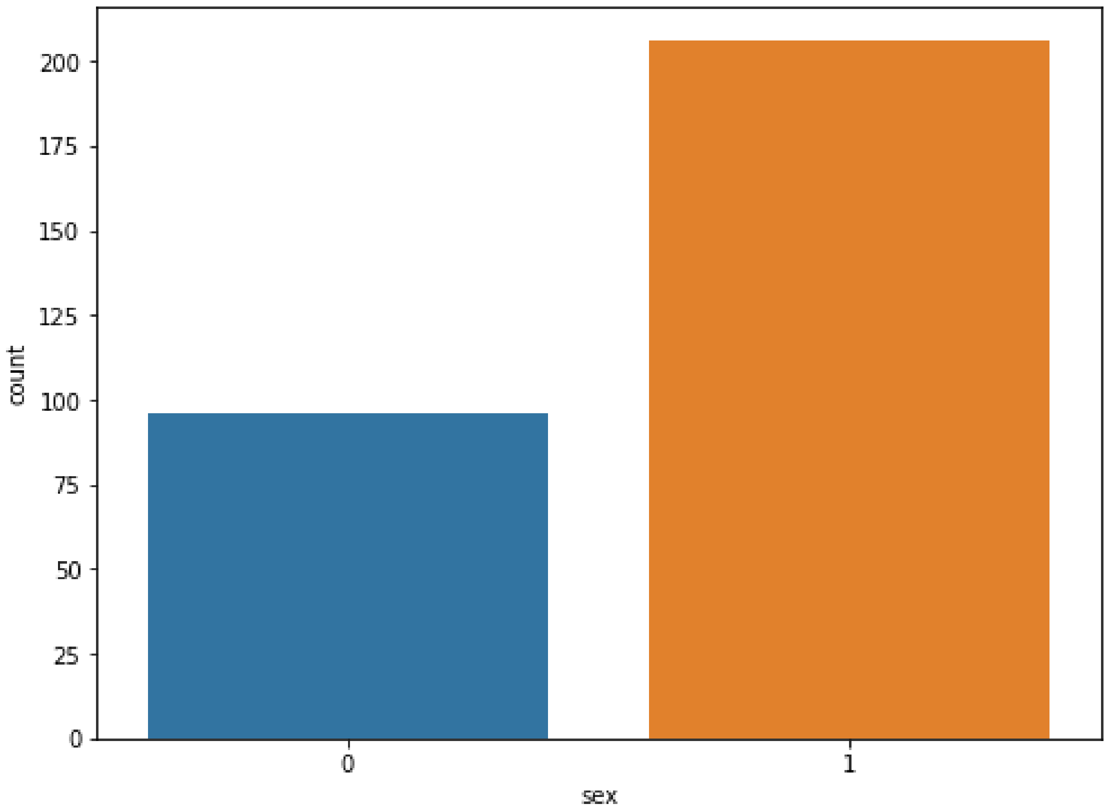
[13]:
```
#Check the Distribution of Age in our Data.

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

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

plt.show()
```

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



- Age is Continuous Feature and Normally Distributed.

[14]:
```
#Check Sex column usng Count Plot.

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

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

plt.show()
```

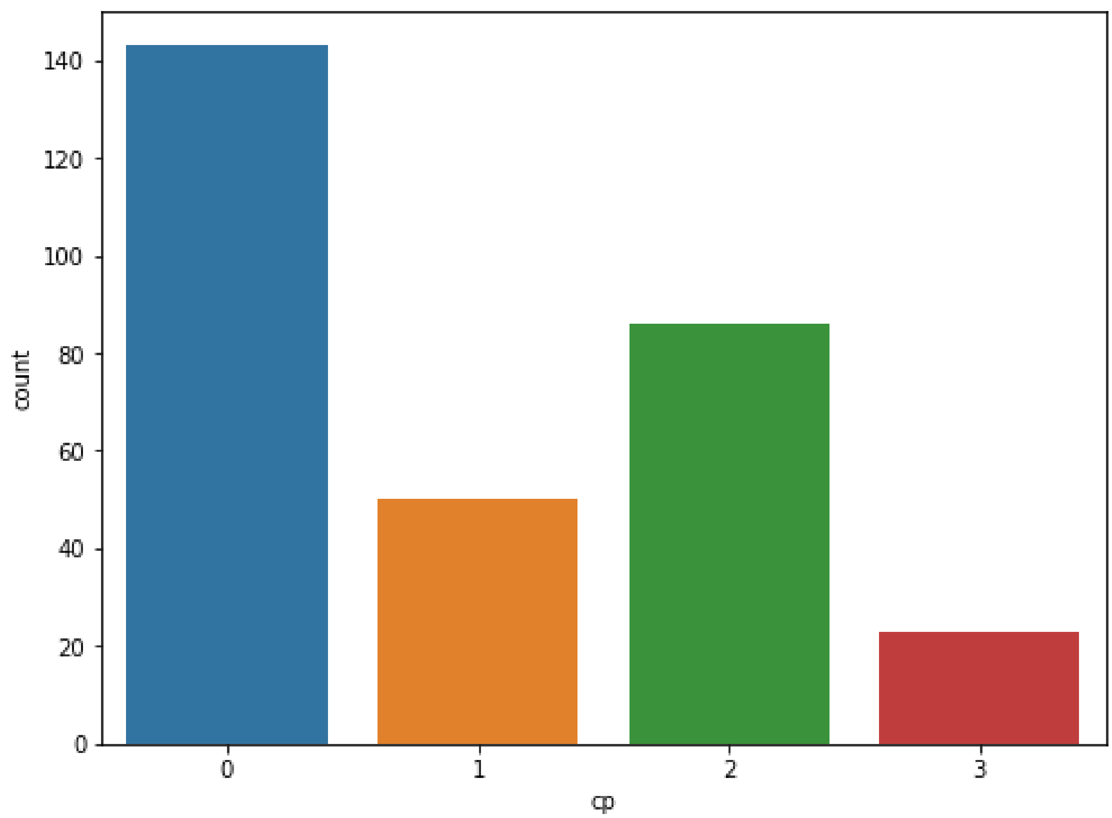


[15]:
```
health["sex"].value_counts()
```

[15]:
```
1    206
0     96
Name: sex, dtype: int64
```

- 0 is for FEMALE and 1 is for MALE
- Here we can see that we have twice the number of observations for MALE than FEMALE.

[16]:
```
#Check CP column (Chest Pain) using Count Plot.

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

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

plt.show()
```



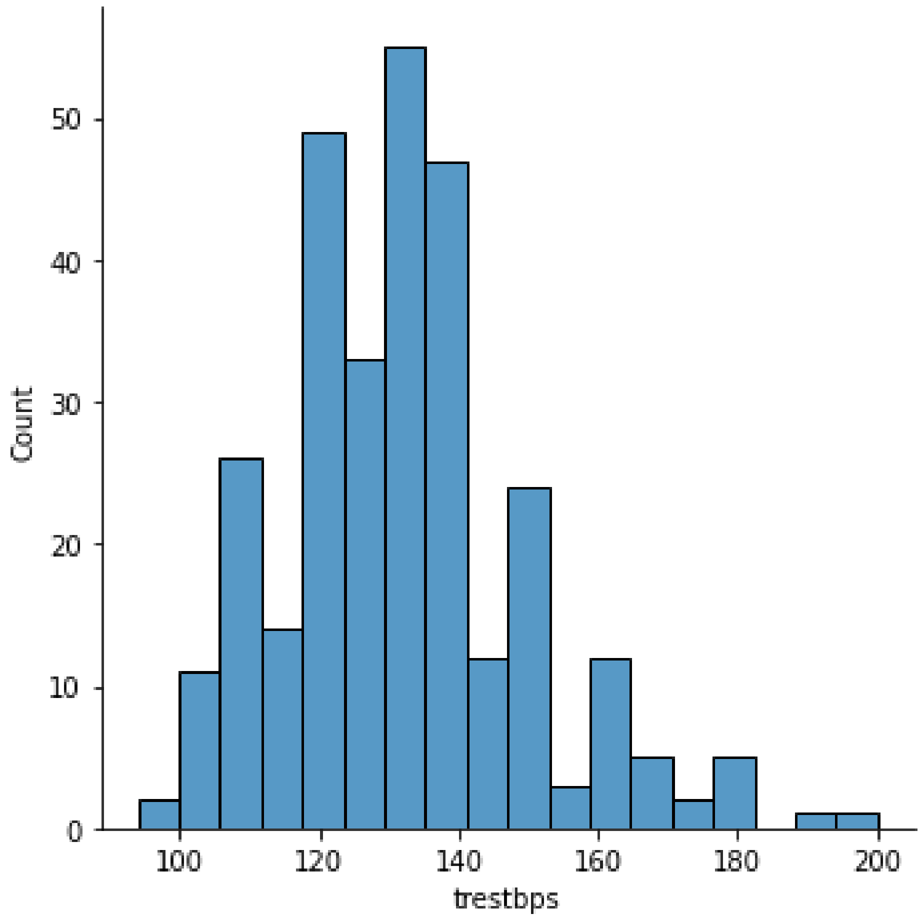
[17]:
```
health["cp"].value_counts()
```

[17]:
```
0    143
2     86
1     50
3     23
Name: cp, dtype: int64
```

- Chest Pain (cp): seems to be ordinal Categorical Variable.

[18]:
```
#Check trestbps column using Distribution Plot.

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

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

plt.show()
```

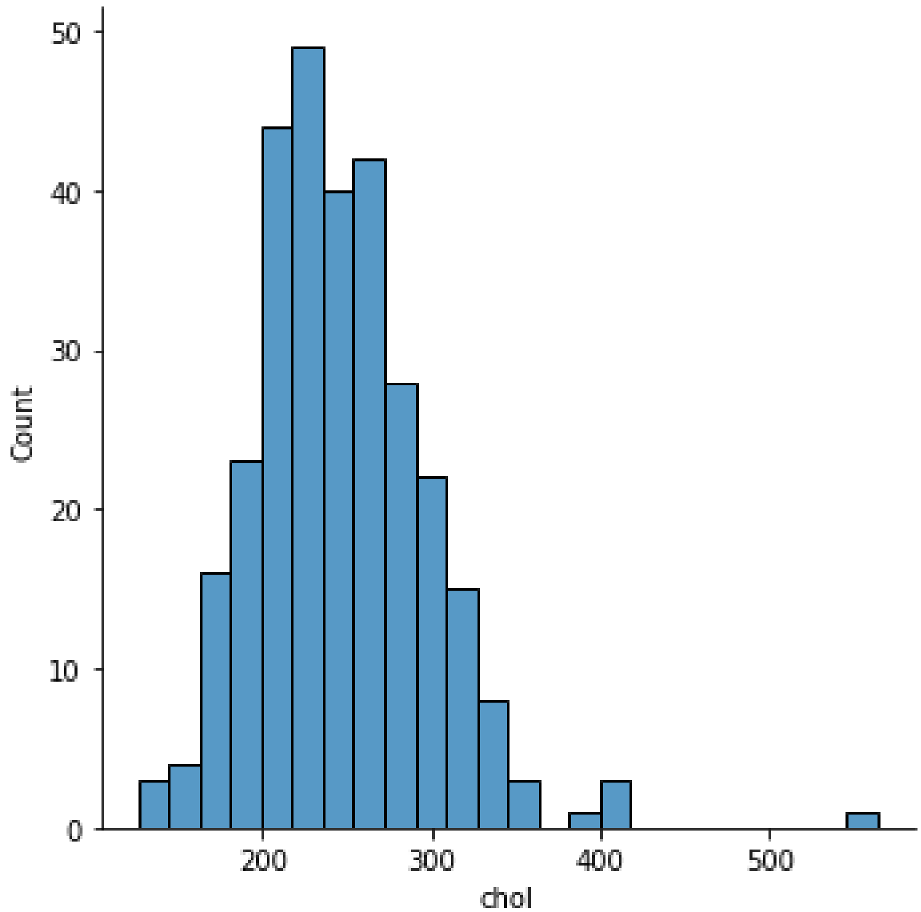
```
<Figure size 576x432 with 0 Axes>
```



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

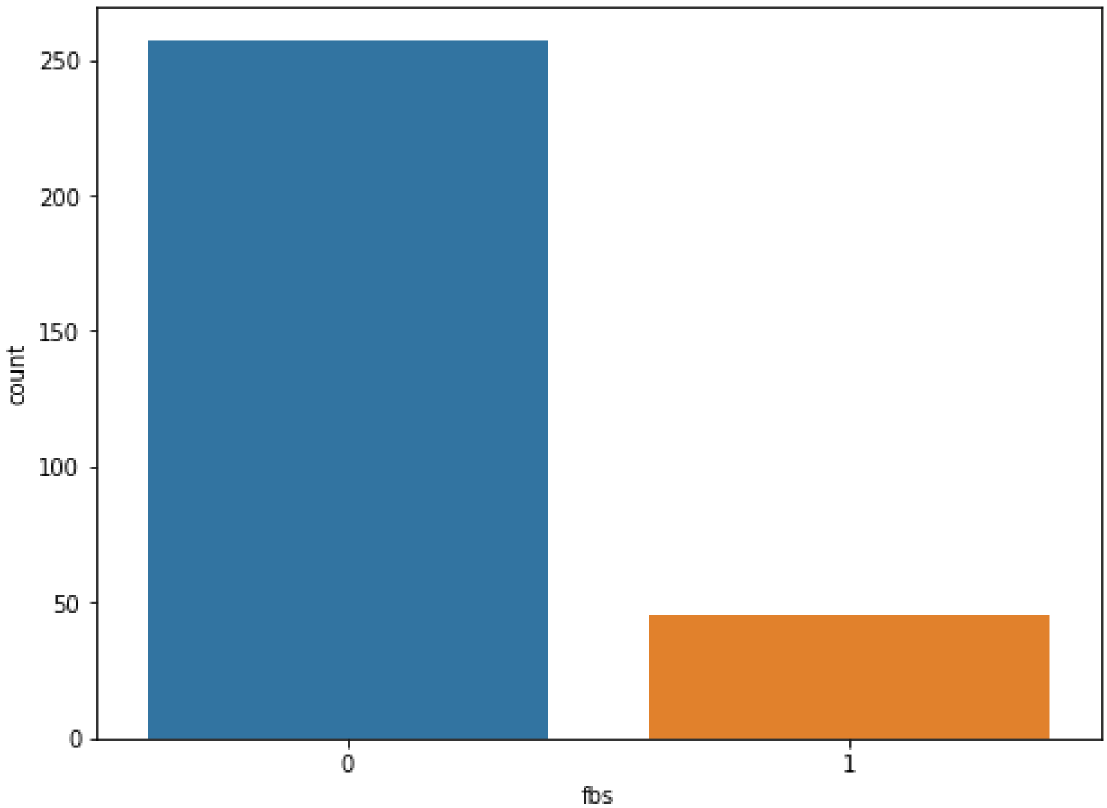
[19]:
```
#Check chol column using Distribution Plot.

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

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

plt.show()
```

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



- Here we can see that Cholestrol(chol) is Continuous and Normally Distributed with some Outliers on the Right.

[20]:
```
#Check fbs column using Count Plot.

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

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

plt.show()
```

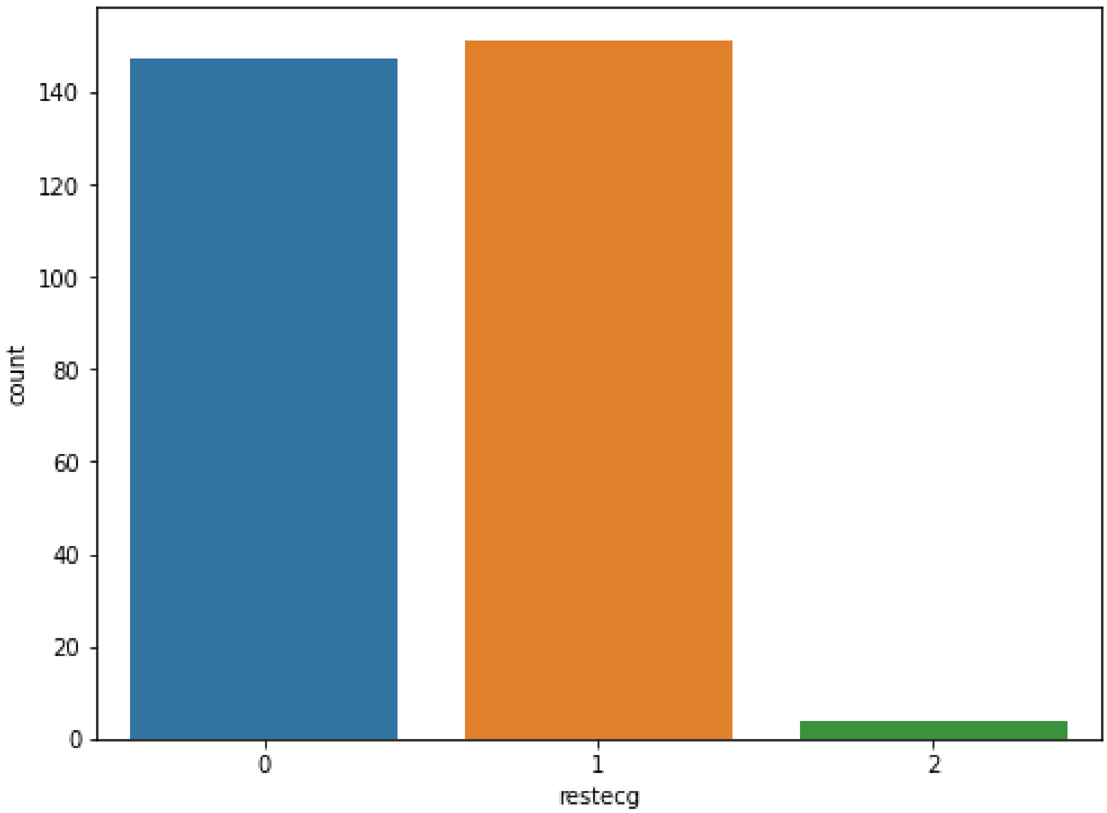


[21]:
```
health["fbs"].value_counts()
```

[21]:
```
0    257
1     45
Name: fbs, dtype: int64
```

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

[22]:
```
#Check column restecg using Count Plot.

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

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

plt.show()
```



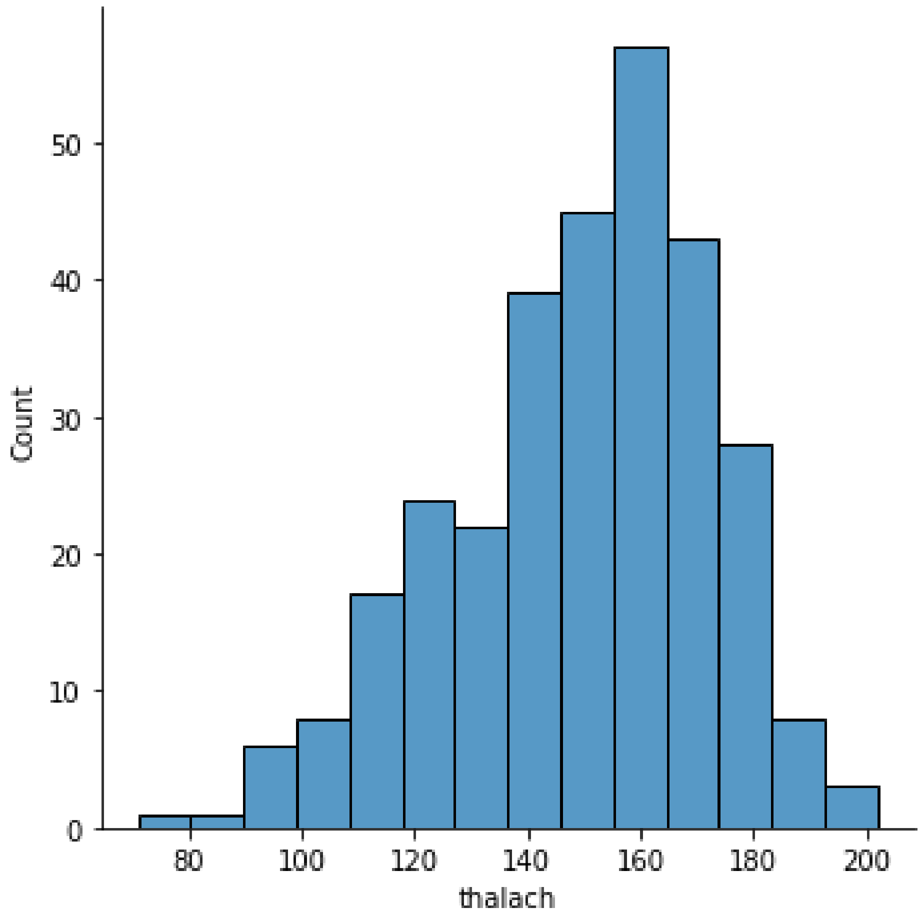
[23]:
```
health["restecg"].value_counts()
```

[23]:
```
1    151
0    147
2      4
Name: restecg, dtype: int64
```

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

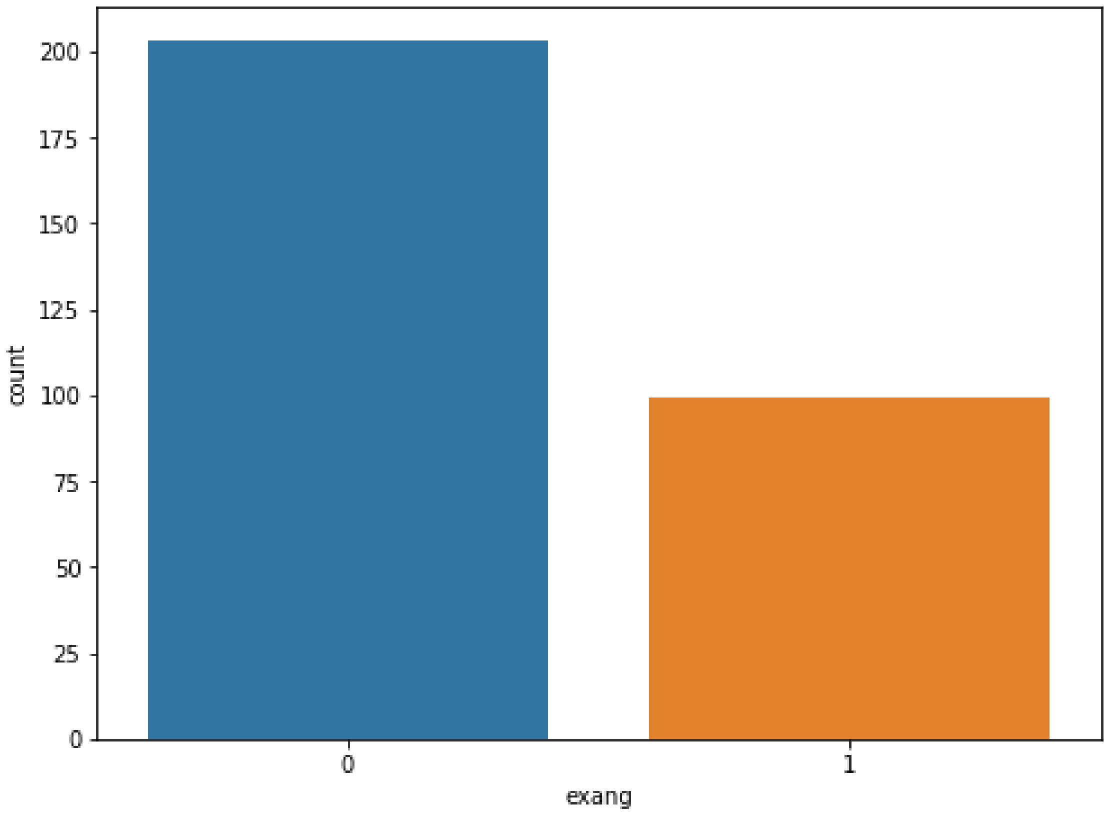
[24]:
```
#Check thalac column using Distribution Plot.

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

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

plt.show()
```

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



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

[25]:
```
#Check for column exang using Count Plot.

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

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

plt.show()
```



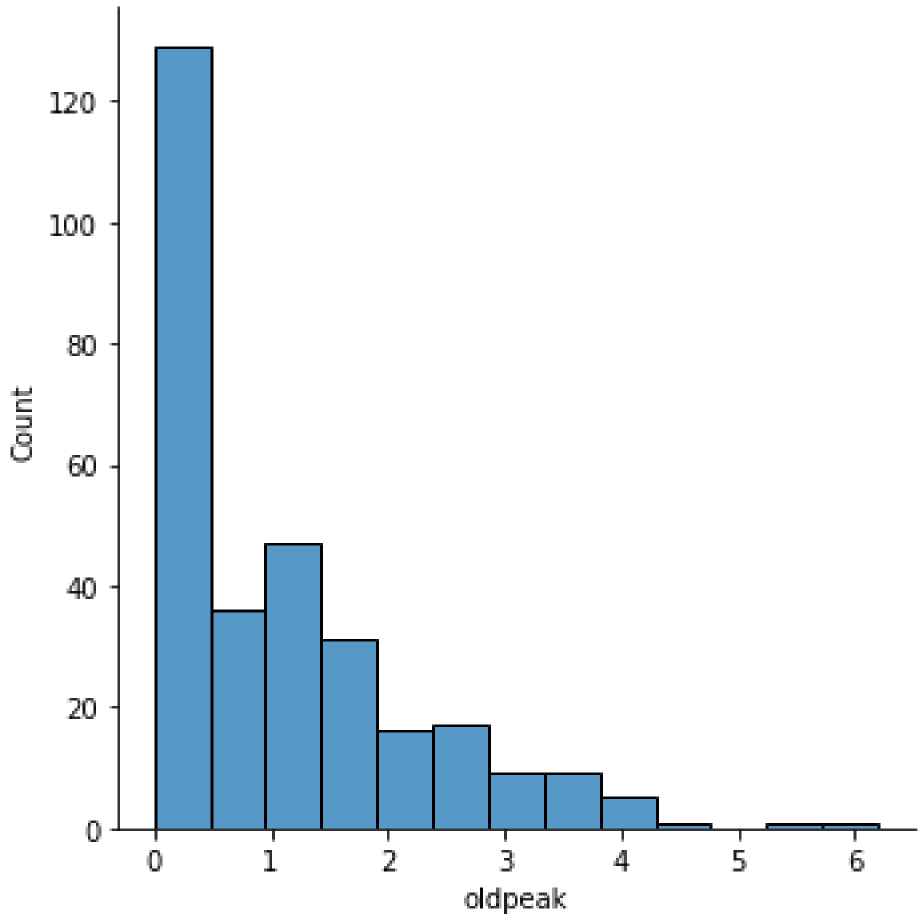
[26]:
```
health["exang"].value_counts()
```

[26]:
```
0    203
1     99
Name: exang, dtype: int64
```

- Exercise Induced Enigma(exang) is Categorical Feature.

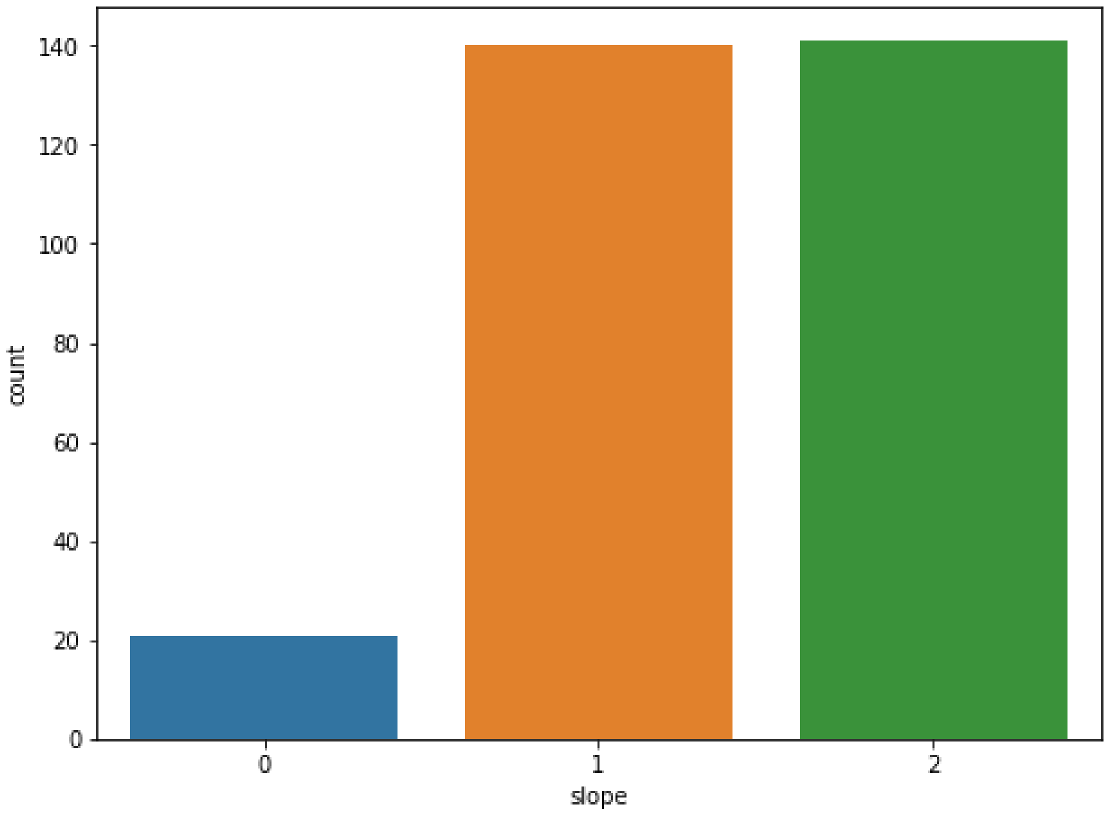
[27]:
```
#Check for column oldpeak using Distribution Plot.

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

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

plt.show()
```

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



- ST depression induced by exercise relative to rest ”oldpeak” is Continuous Feature and it is Highly Right Skewed.

[28]:
```
#Check for column slope using Count Plot.

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

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

plt.show()
```

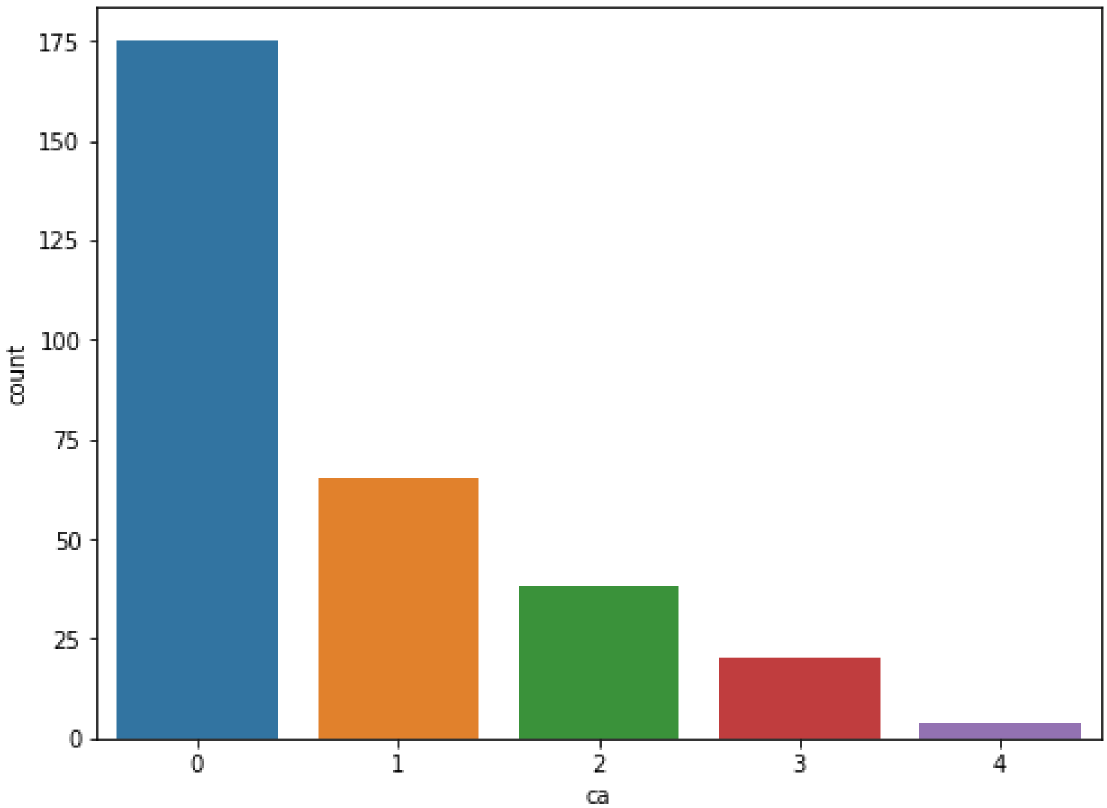


[29]:
```
health["slope"].value_counts()
```

[29]:
```
2    141
1    140
0     21
Name: slope, dtype: int64
```

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

[30]:
```
#Check for column 'ca' using Count Plot.

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

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

plt.show()
```

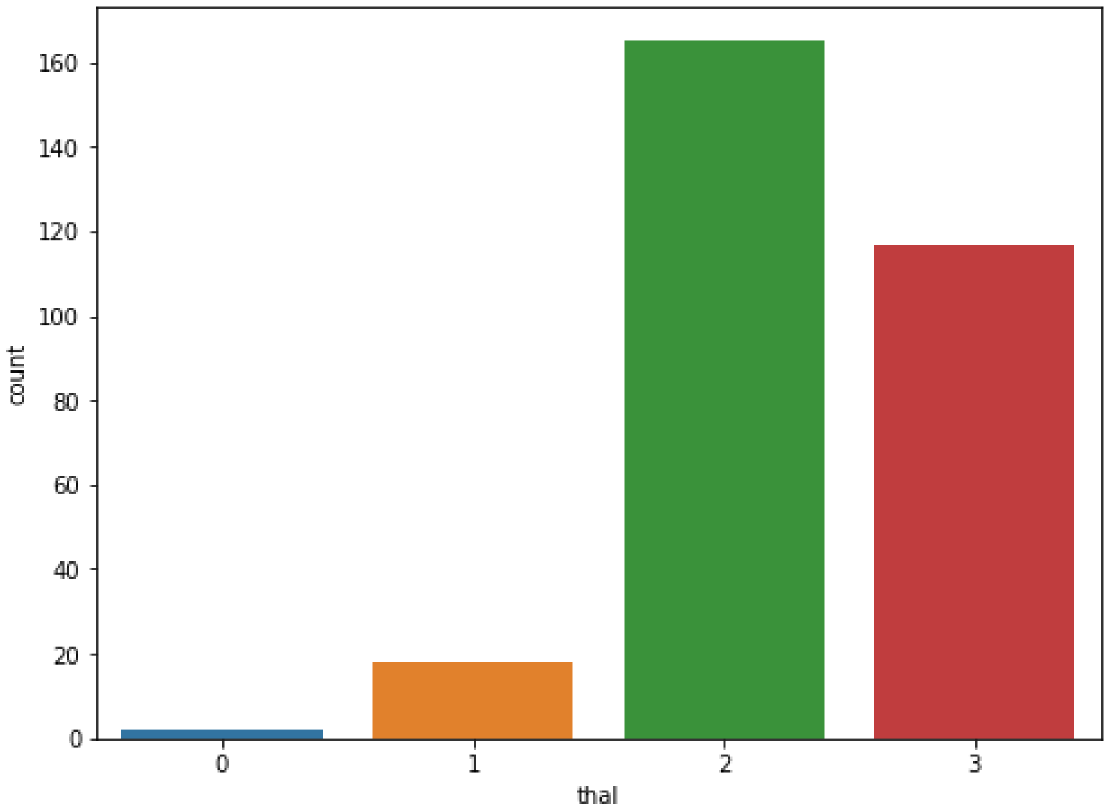


[31]:
```
health["ca"].value_counts()
```

[31]:
```
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.

[32]:
```
#Check for column 'thal' using Count Plot.

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

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

plt.show()
```

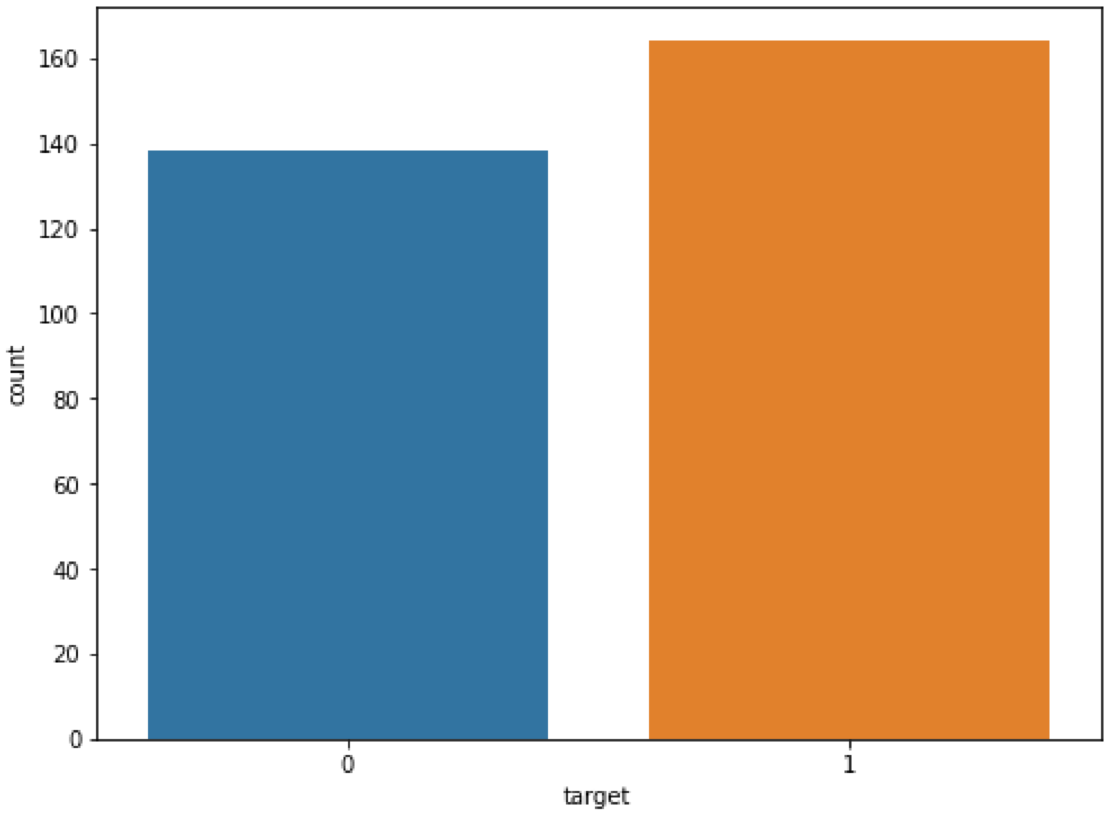


[33]:
```
health["thal"].value_counts()
```

[33]:
```
2    165
3    117
1     18
0      2
Name: thal, dtype: int64
```

- Thalassaemia "thal" is Nominal Categorical Variable.

[34]:
```
#Check for column 'target' using Count Plot.

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

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

plt.show()
```



[35]:
```
health["target"].value_counts()
```

[35]:
```
1    164
0    138
Name: target, dtype: int64
```

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

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

[36]:
```
health.dtypes
```

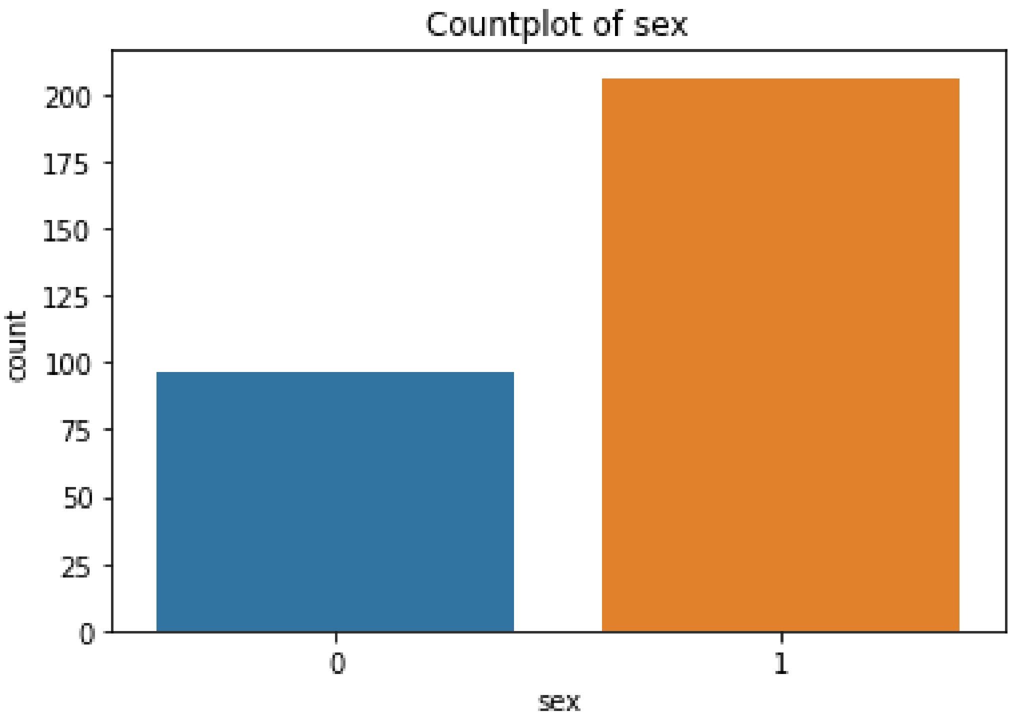
[36]:
```
age            int64
sex            int64
cp             int64
trestbps       int64
chol           int64
fbs            int64
restecg        int64
thalach        int64
exang          int64
```

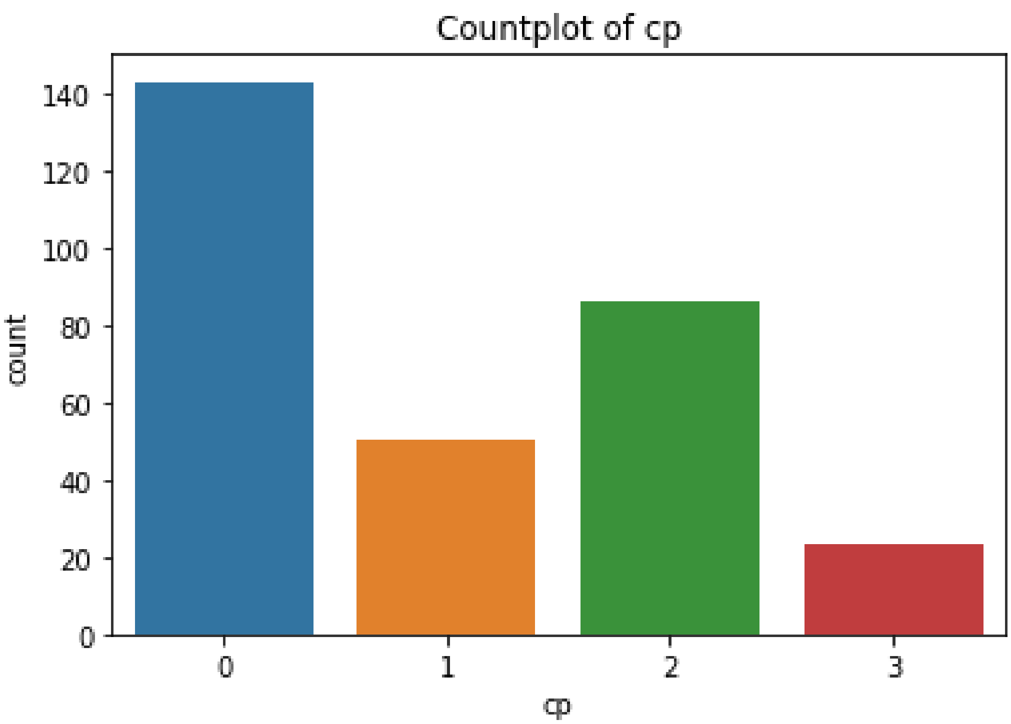
```
oldpeak     float64
slope         int64
ca            int64
thal          int64
target        int64
dtype: object
```

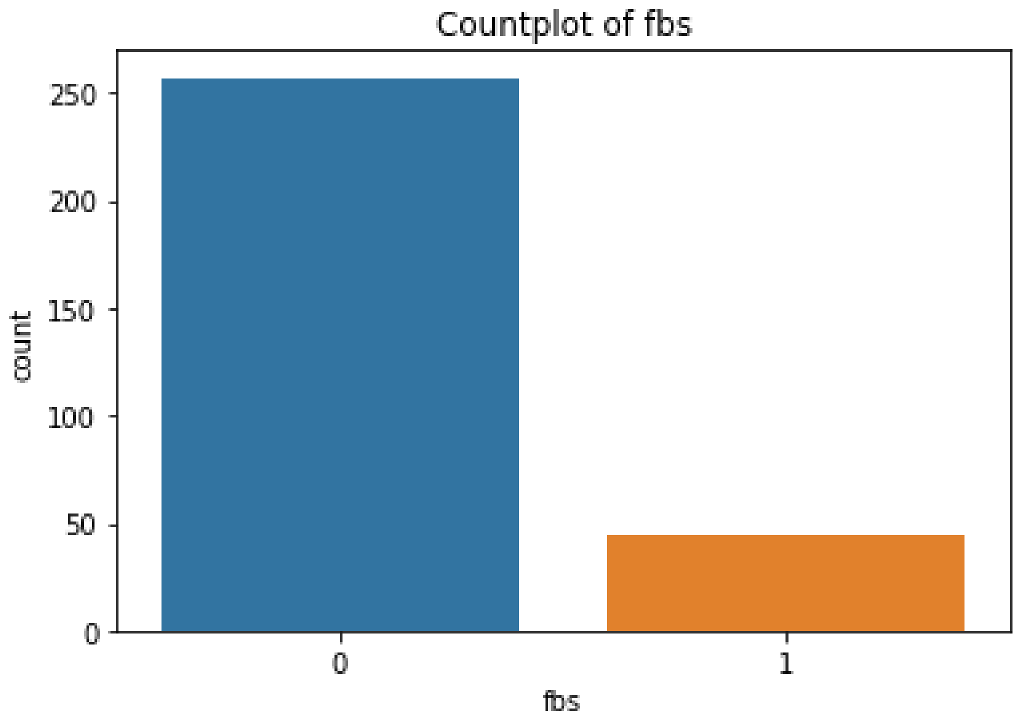
[37]:
```
for col in health.columns:
    print(f"Number of Unique Values in {col} : {health[col].nunique()}")
```

```
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
```

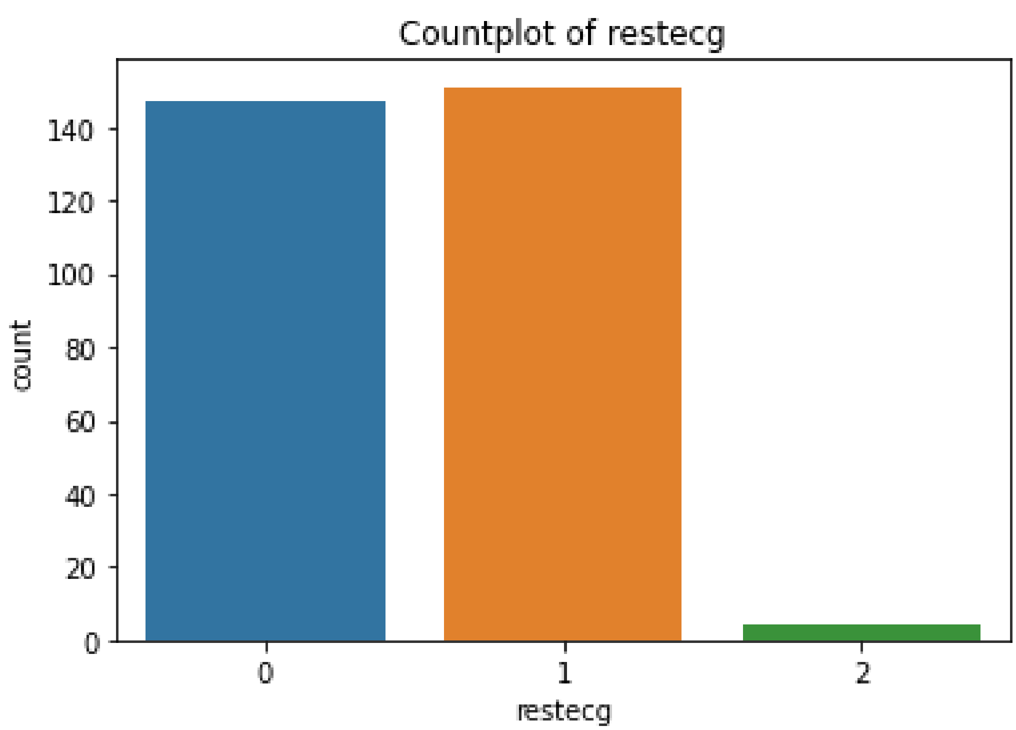
[38]:
```
for col in health.columns:

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

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

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

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

        plt.show()
```


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

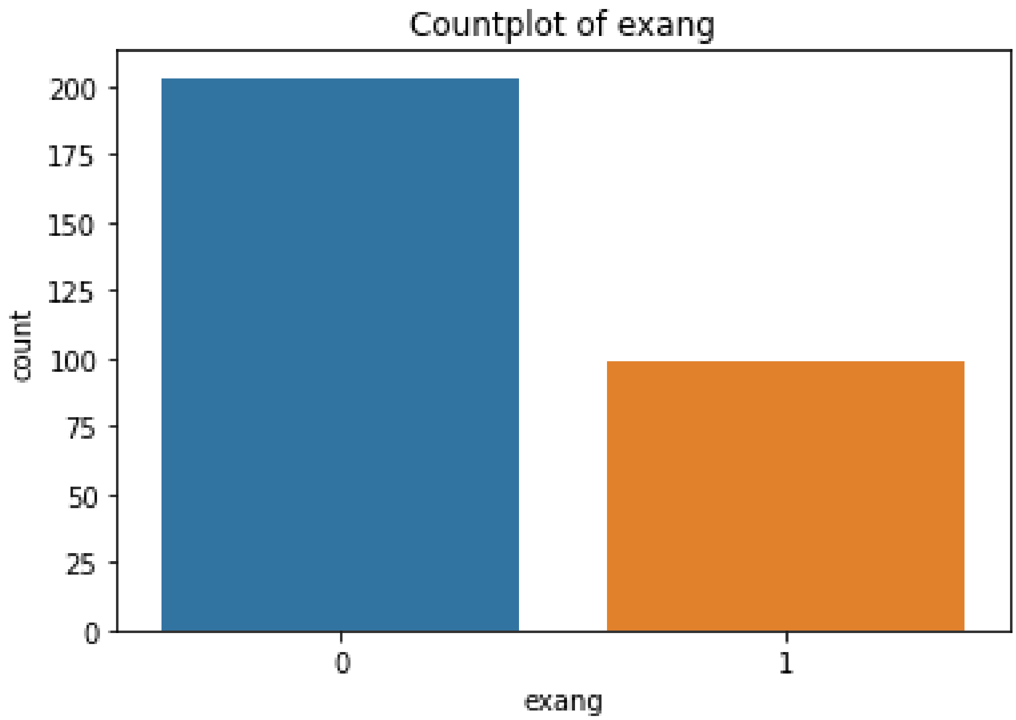

Countplot of cp
count
cp
0
1
2
3
0
20
40
60
80
100
120
140

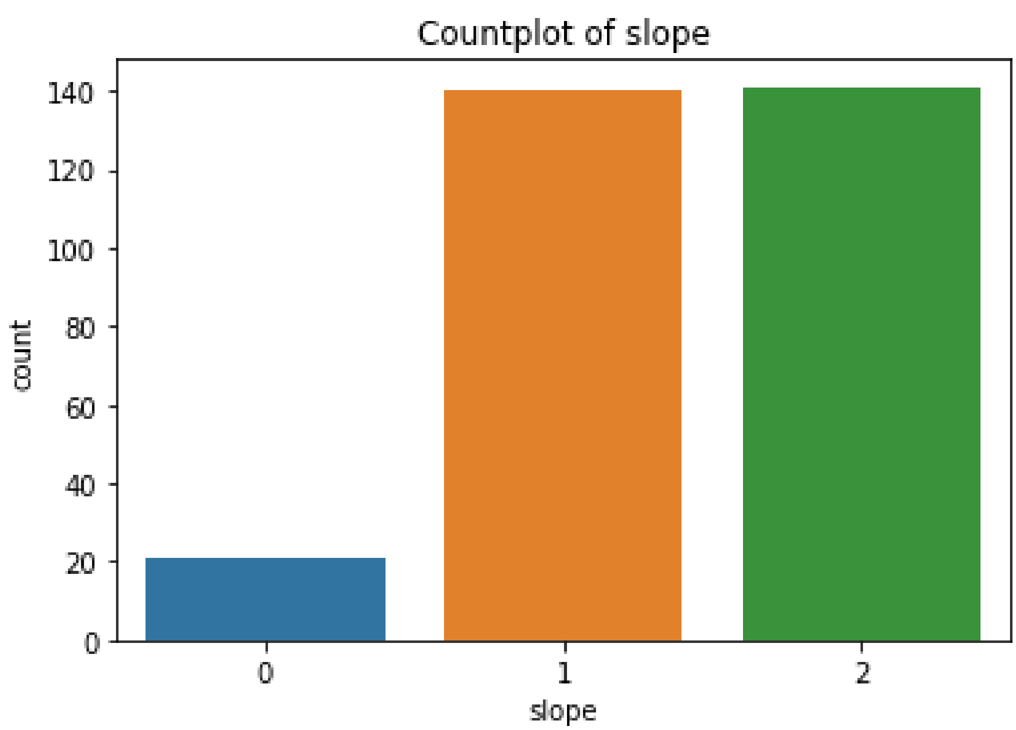


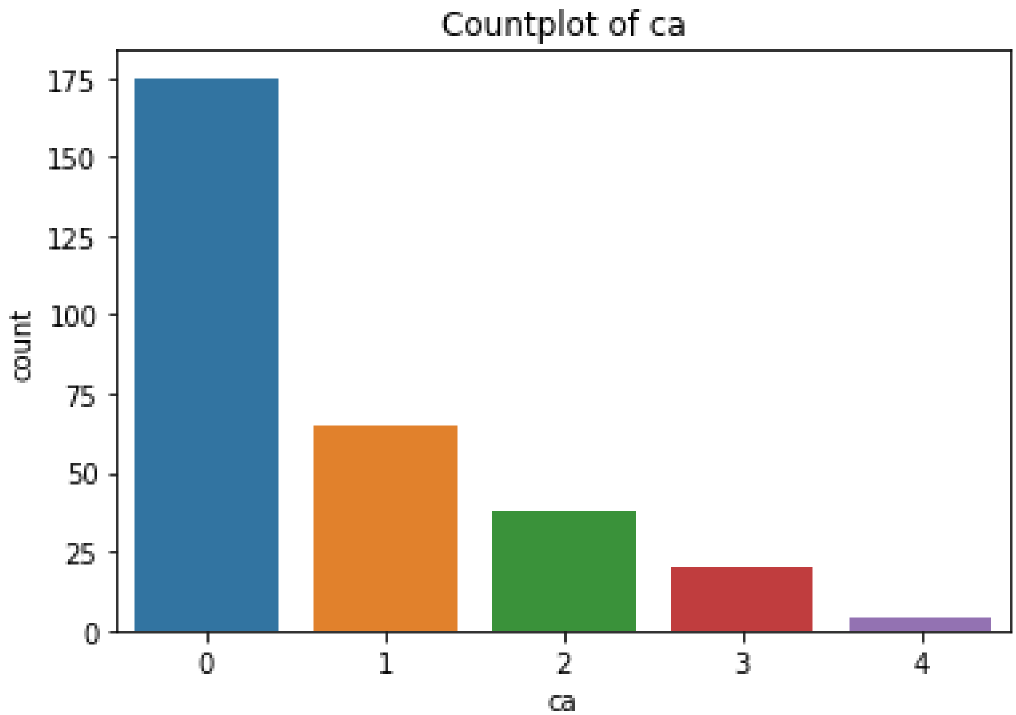
Countplot of fbs
250
200
150
100
50
0
count
0
1
fbs



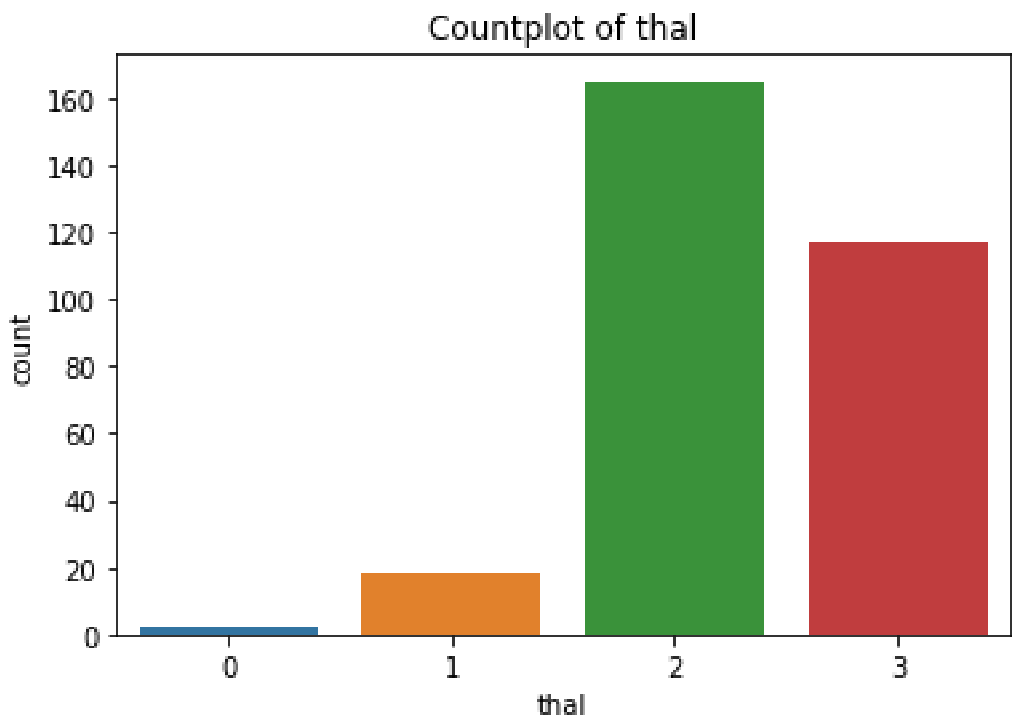
Countplot of restecg
140
120
100
80
60
40
20
0
count
0
1
2
restecg


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

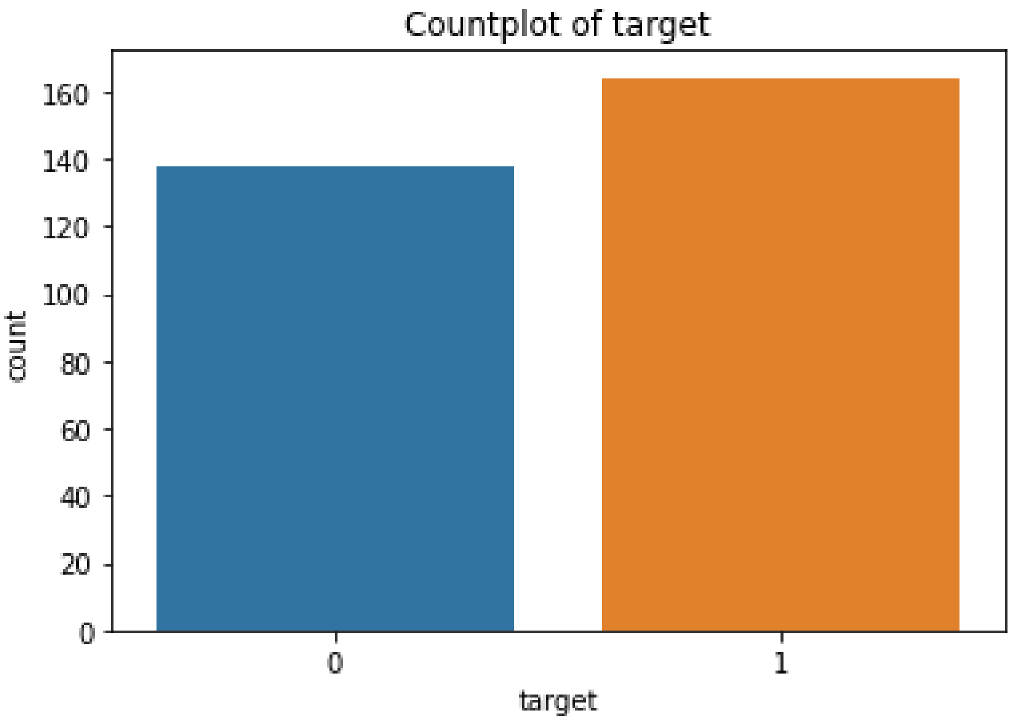

Countplot of slope
count
140
120
100
80
60
40
20
0
0
1
2
slope



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



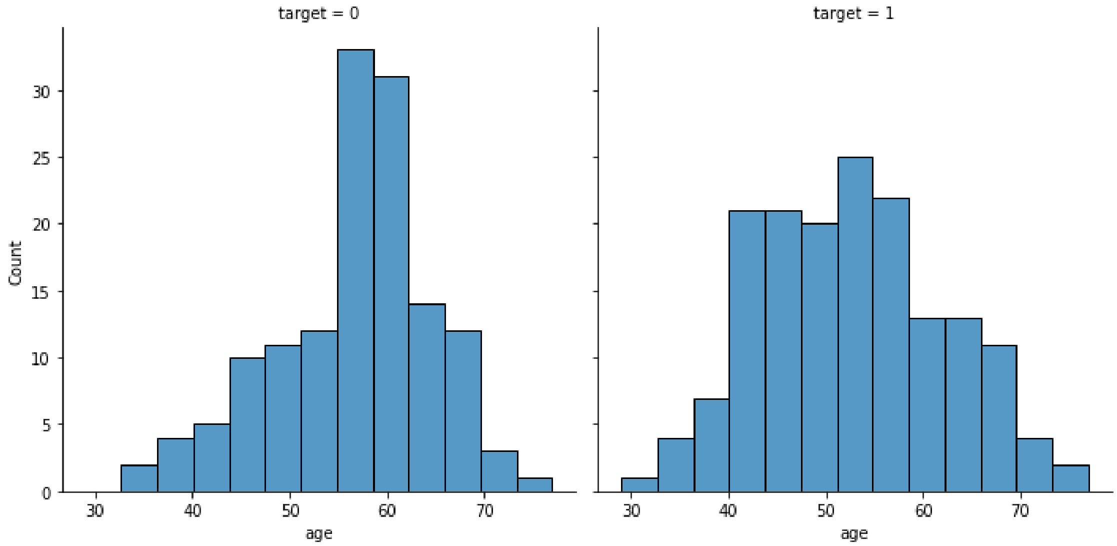
Countplot of thal
count
160
140
120
100
80
60
40
20
0
0
1
2
3
thal



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

[39]:
```
plt.figure(figsize= (8,6))

sns.displot(data= health, 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.

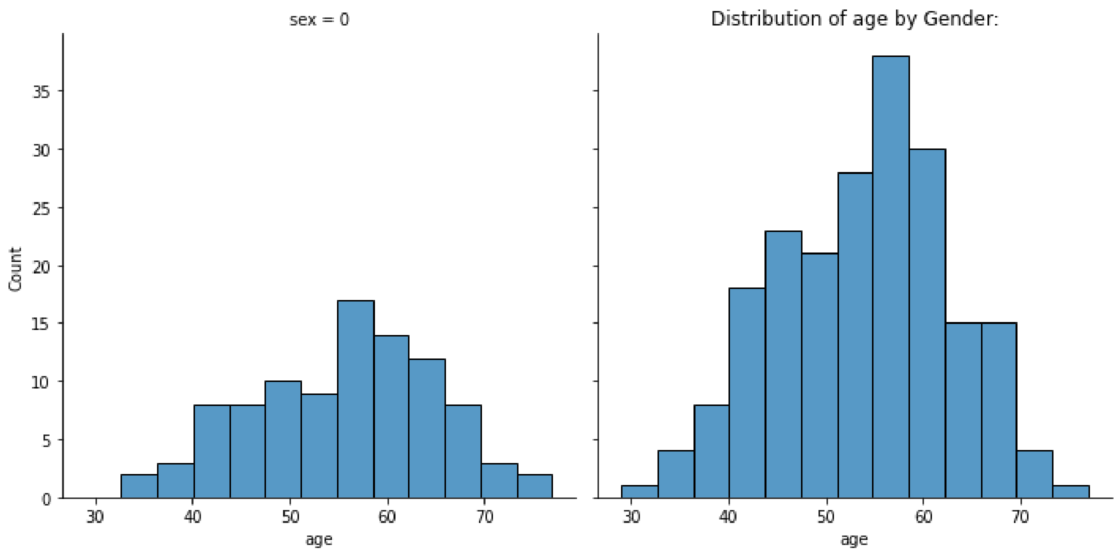
2.(d). Study the composition of all patients with respect to the Sex category.

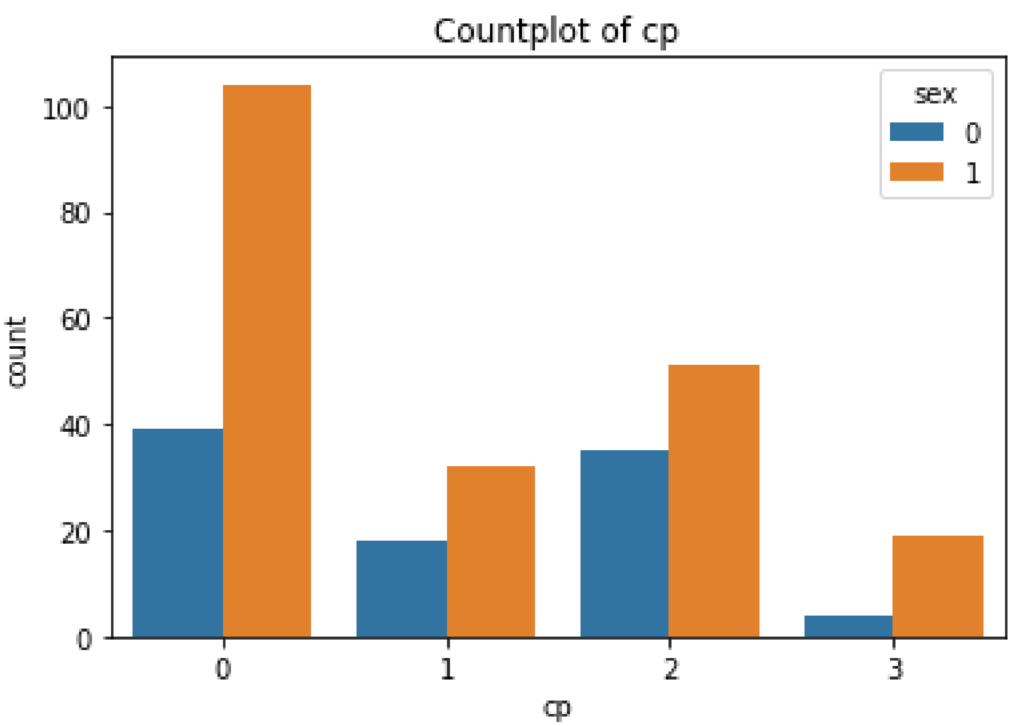
[40]:
```
# We will Compare Features of all Observations with respect to Gender.
```

[41]:
```
for cols in health.drop("sex",axis= 1).columns:

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

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

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

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

        plt.show()

    else:

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

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

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

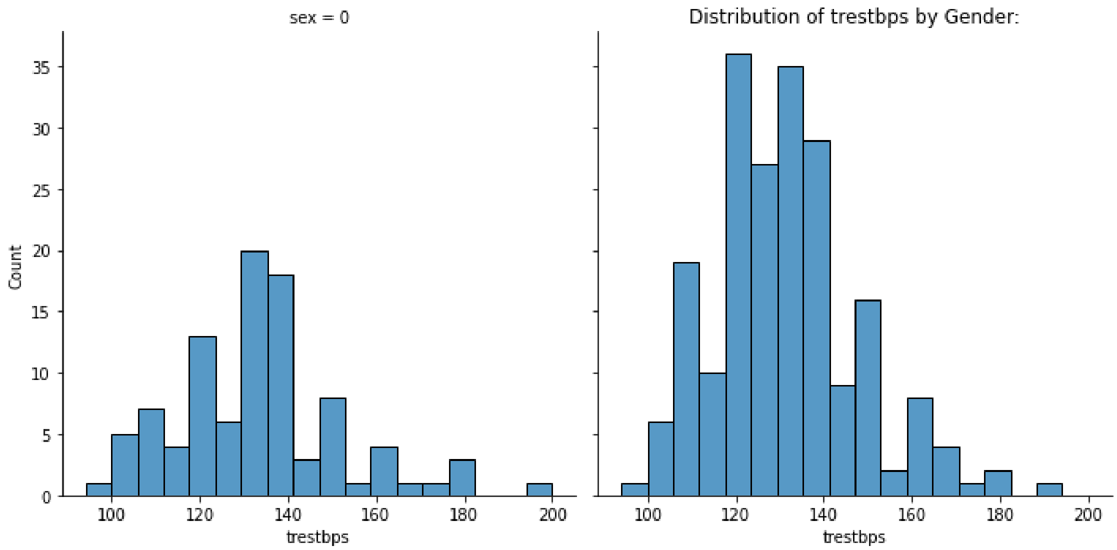
```
plt.show()
```

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

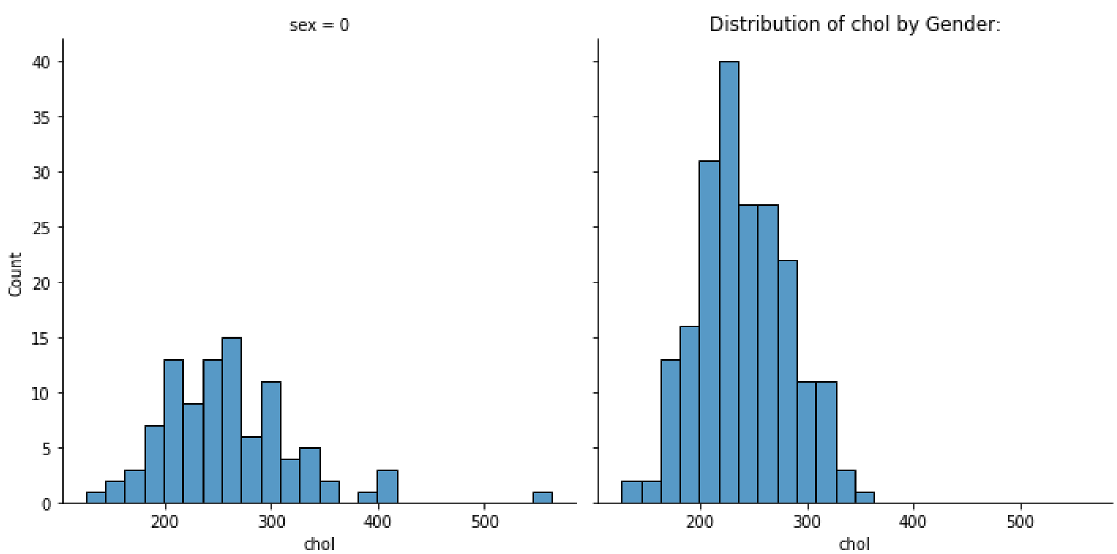


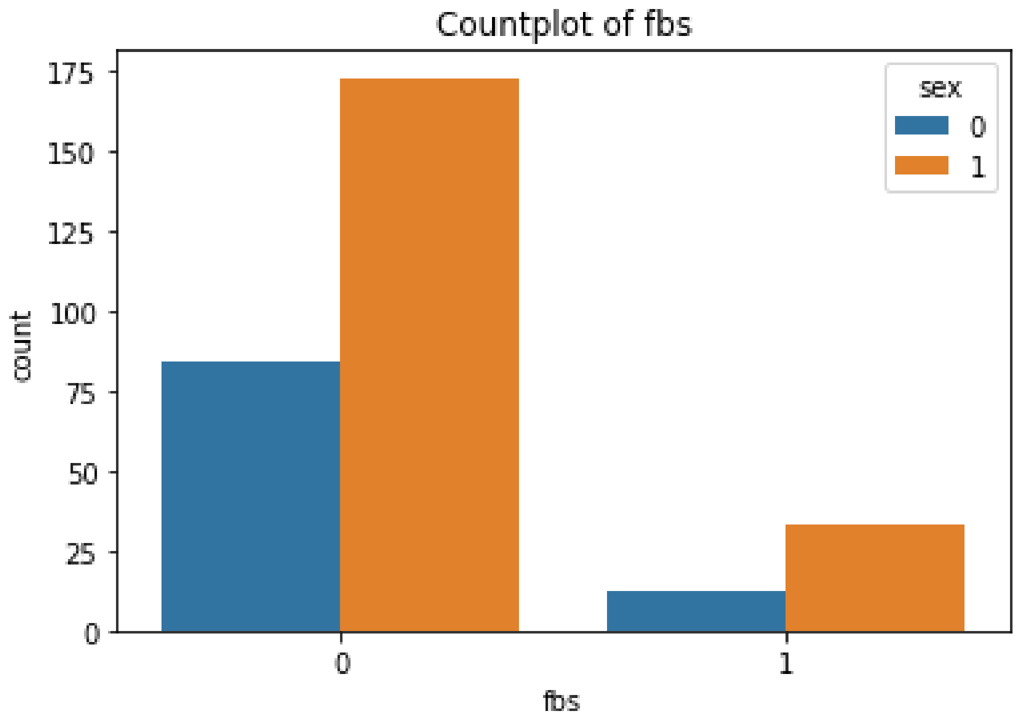


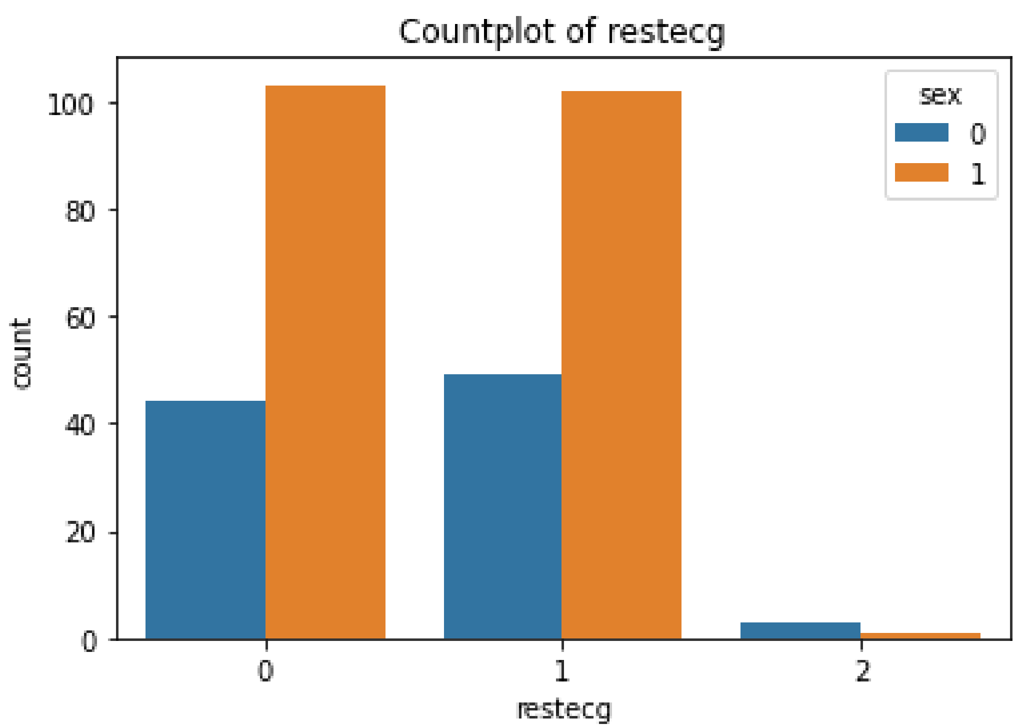
<Figure size 432x288 with 0 Axes>



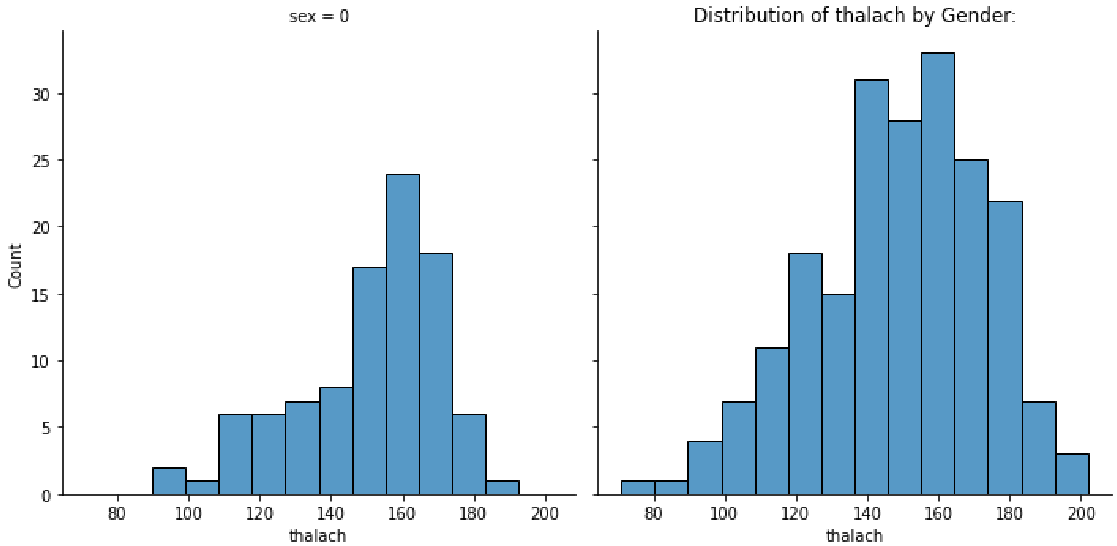
<Figure size 432x288 with 0 Axes>

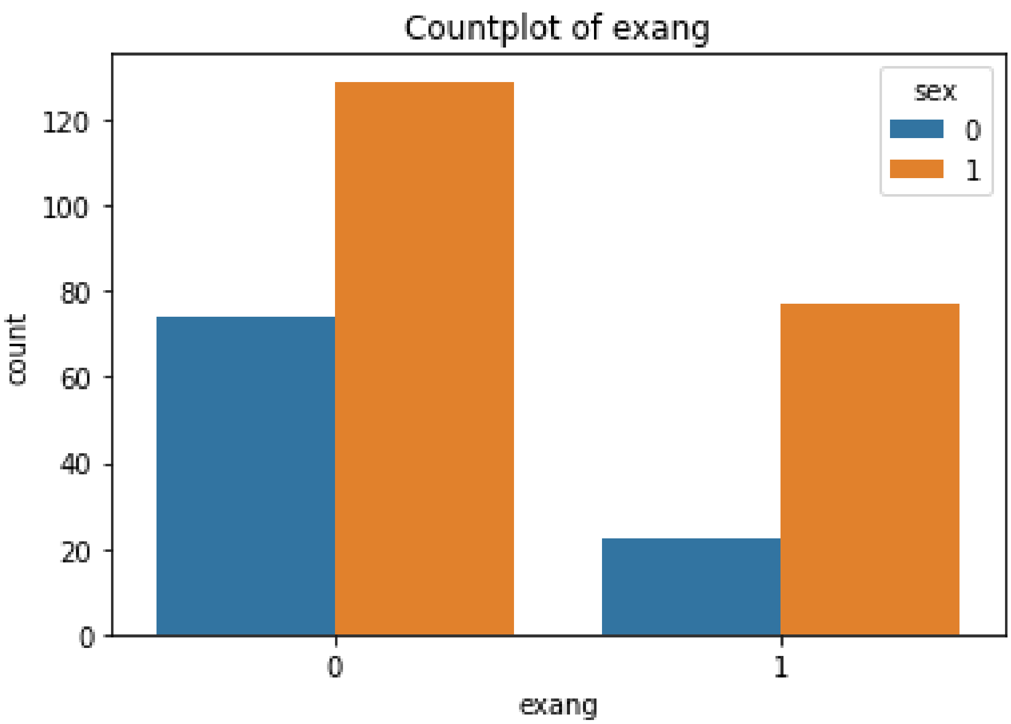



Countplot of fbs
sex
0
1
175
150
125
100
75
50
25
0
count
0
1
fbs

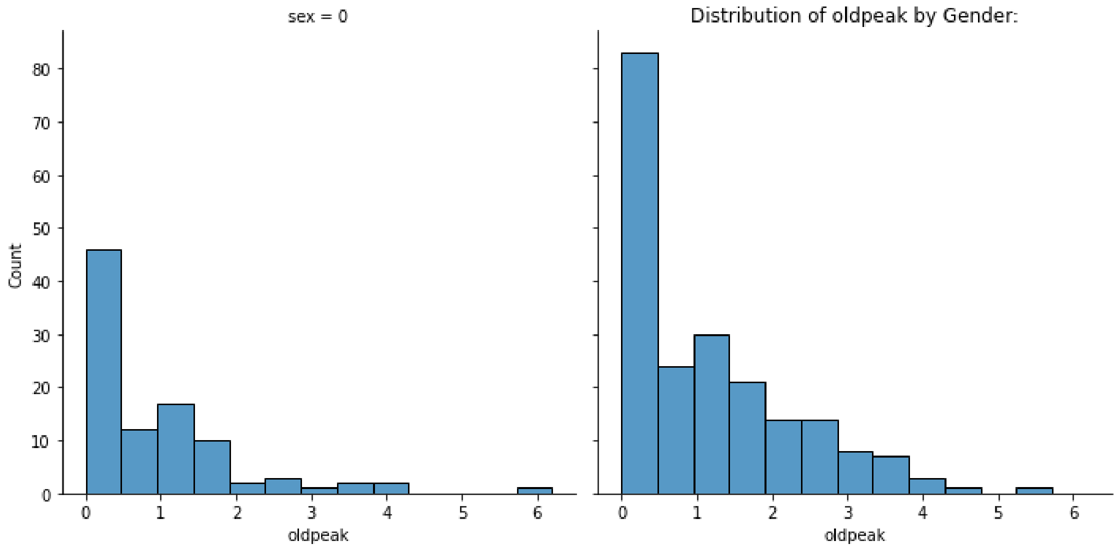

Countplot of restecg
sex
0
1
100
80
60
40
20
0
count
0
1
2
restecg

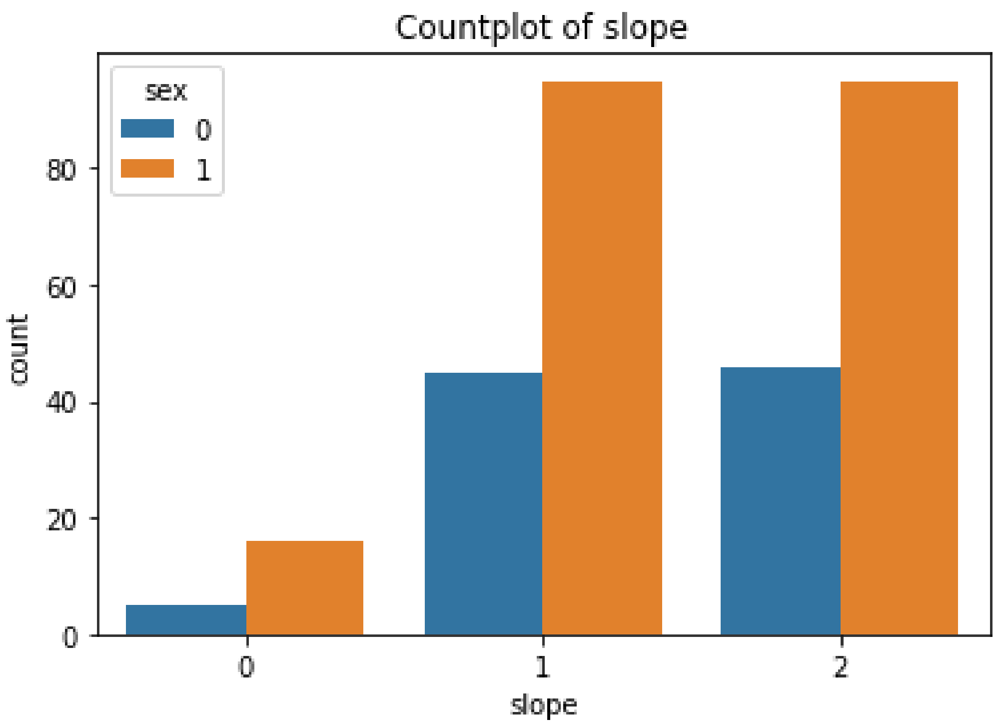
<Figure size 432x288 with 0 Axes>

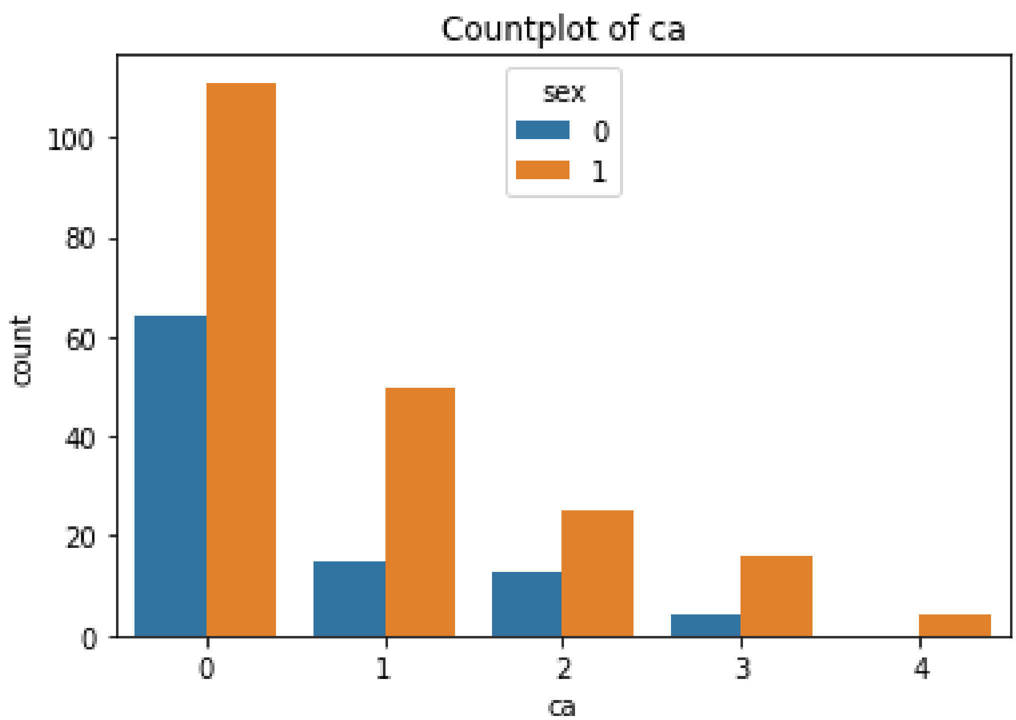


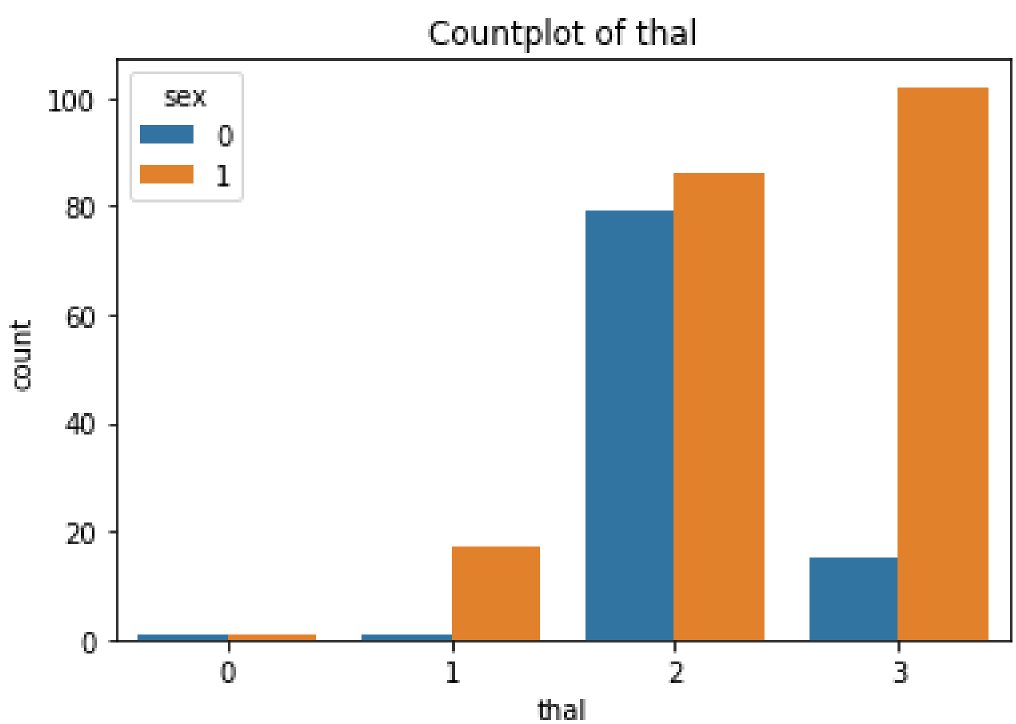


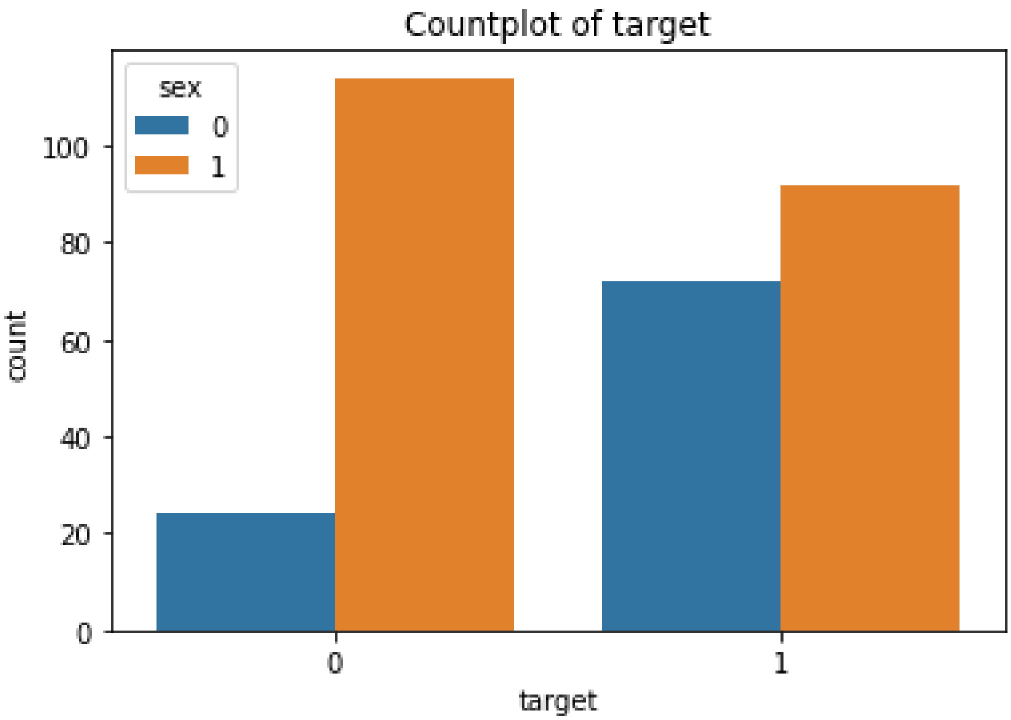
<Figure size 432x288 with 0 Axes>


sex = 0
Distribution of oldpeak by Gender:
Count
oldpeak
oldpeak


Countplot of slope
sex
0
1
count
slope


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

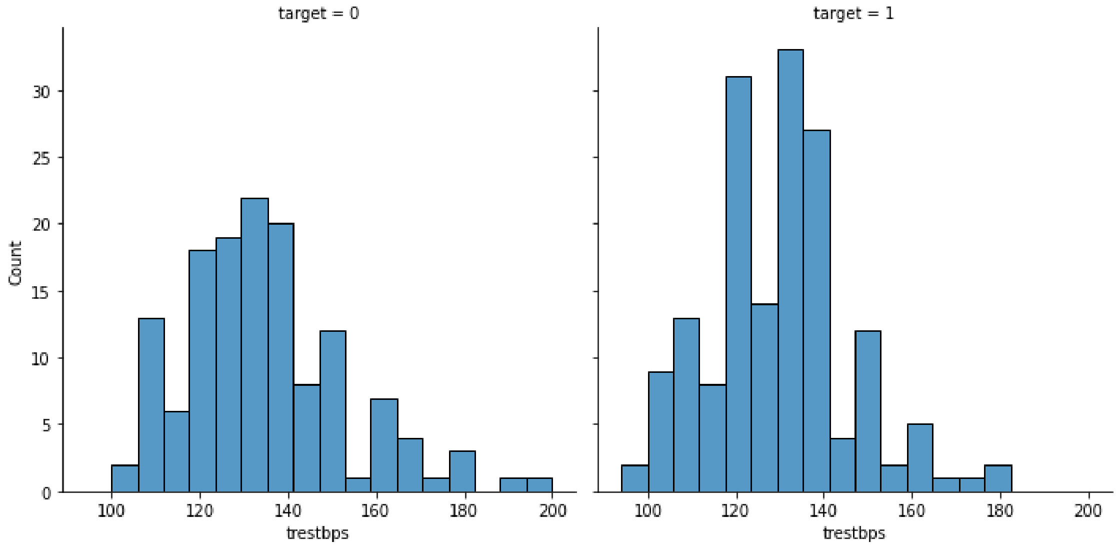

Countplot of thal
sex
0
1
count
100
80
60
40
20
0
0
1
2
3
thal



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

[42]:
```
plt.figure(figsize= (6,4))

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

plt.show()
```

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

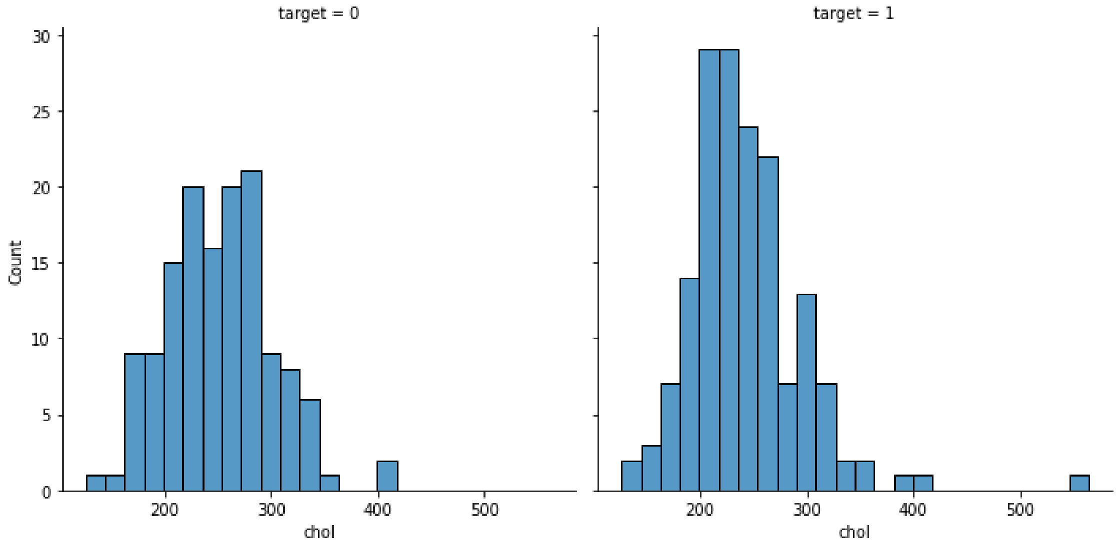


- We have some observations with very High Resting Blood Pressure values without occurence of CVD.
- In general, we can see that Resting Blood Pressure values from 120-160 has more chances of CVD.
- Still, This feature alone can not be said to be conclusive of CVD.

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

[43]:
```
plt.figure(figsize= (6,4))

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

plt.show()
```

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

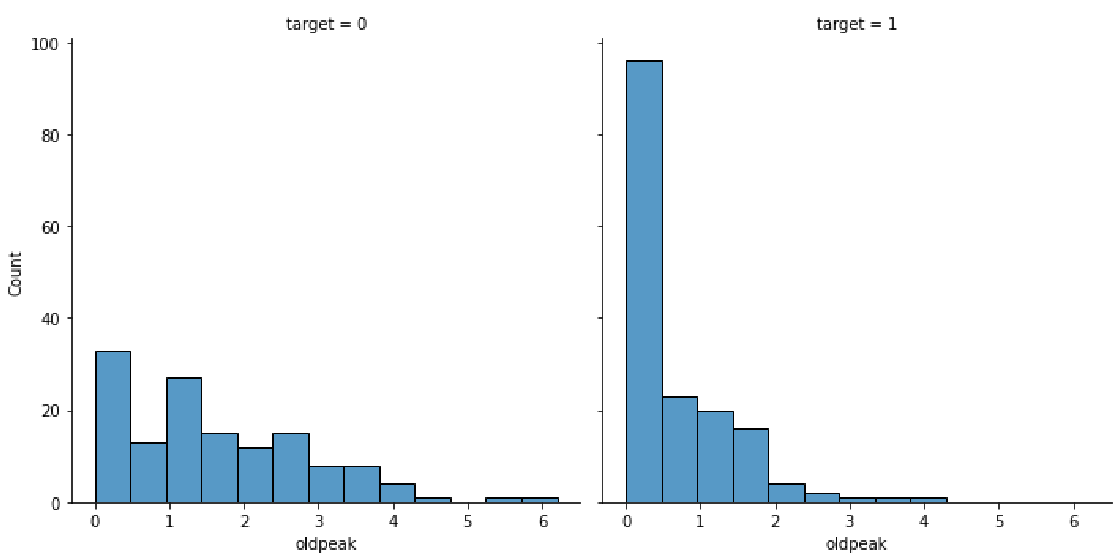


- Here too, No considerable conclusion can be made about CVD by Cholesterol Levels alone.

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

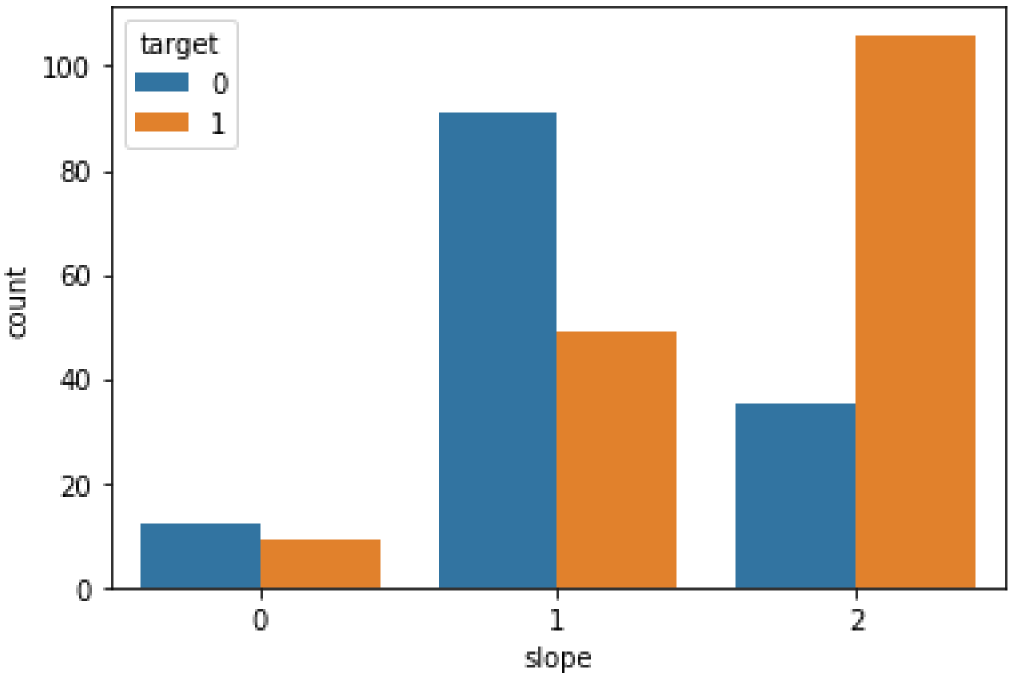
[44]:
```
plt.figure(figsize= (6,4))

sns.displot(data= health, 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 chances of CVD Occurence.

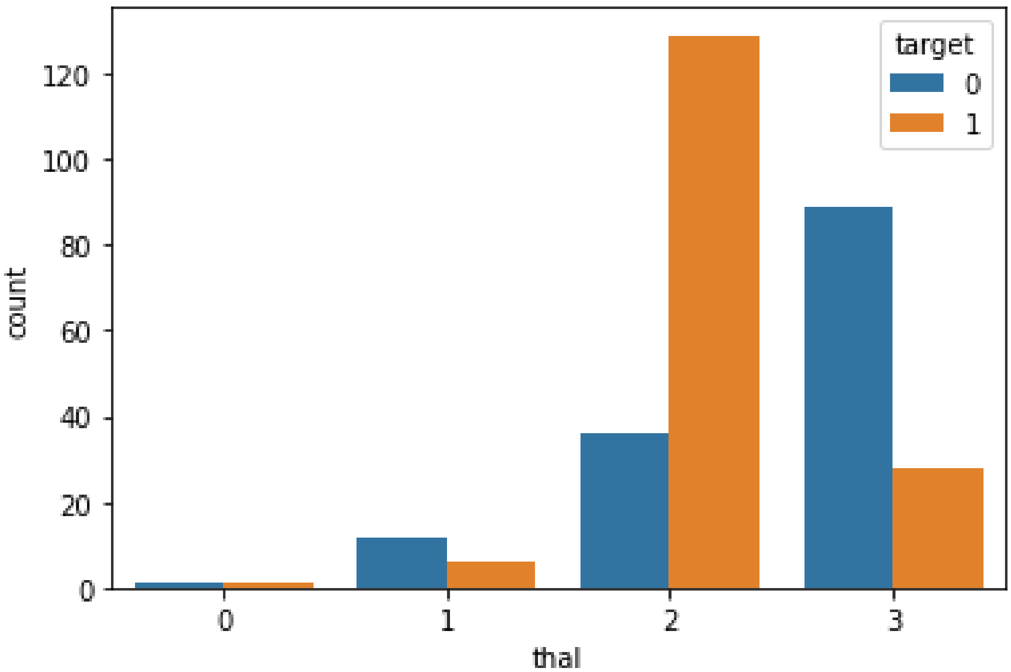
[45]:
```
plt.figure(figsize= (6,4))

sns.countplot(data= health, 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.

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

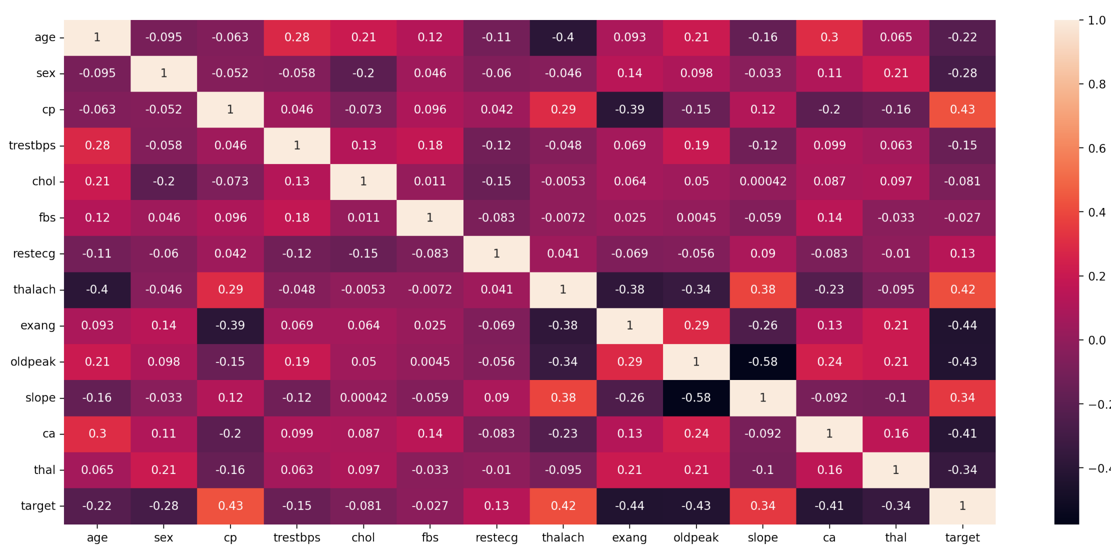
[46]:
```
plt.figure(figsize= (6,4))

sns.countplot(data= health, x= "thal", hue= "target")

plt.show()
```



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

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

[47]:
```
plt.figure(figsize= (18,8), dpi= 200)

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

plt.show()
```

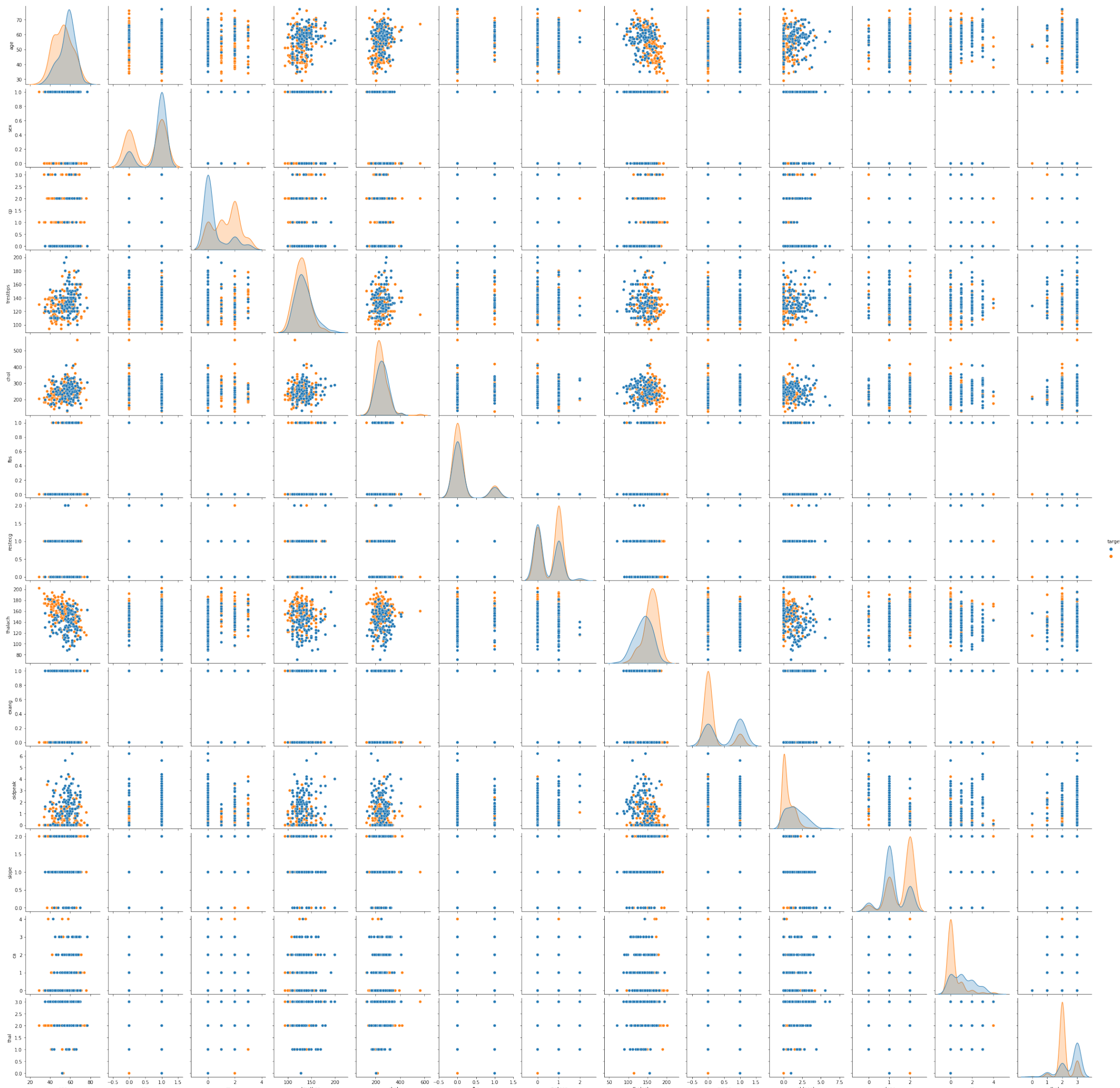


- Chest Pain (cp), Maximum Heart Rate Achieved (thalach), Slope of the peak exercise ST segment (slope) have Decently High Positive Correlation with Occurence of CVD.
- Exercise Induced Enigma (exang), ST depression induced by exercise relative to rest (oldpeak), Number of major vessels (0-3) colored 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.

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

[48]:
```
plt.figure(dpi= 200)

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

plt.show()
```

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



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

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.

[49]:
```
#Separate Features and Target into diffrent DataFrame.
x = health.drop("target", axis= 1)
```

[50]:
```
x.head()
```

[50]:
```
   age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  slope  \
0   63    1   3       145   233    1        0      150      0      2.3      0
1   37    1   2       130   250    0        1      187      0      3.5      0
```

```
2   41   0   1      130   204   0        0      172      0      1.4      2
3   56   1   1      120   236   0        1      178      0      0.8      2
4   57   0   0      120   354   0        1      163      1      0.6      2

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

[51]:
```python
x.shape
```

[51]:
```
(302, 13)
```

[52]:
```python
y = health["target"]
```

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

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

[54]:
```python
y.shape
```

[54]:
```
(302,)
```

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

[55]:
```python
from statsmodels.api import GLM
glm_model = GLM(y, x)
```

[56]:
```python
glm_results = glm_model.fit()
```

[57]:
```python
glm_results.summary()
```

[57]:
```
<class 'statsmodels.iolib.summary.Summary'>
"""
                 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:                 Mon, 05 Dec 2022   Deviance:                       37.034
Time:                         14:21:57   Pearson chi2:                     37.0
No. Iterations:                      3
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
==============================================================================
"""
```

- 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.

Creating new Data Frame with Feature deemed Significan by GLM.

[58]:
```
glm_results.pvalues
```

[58]:
```
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
```

[59]:
```
glm_results.pvalues[glm_results.pvalues < 0.05]
```

[59]:
```
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
```

[60]:
```
significant_cols = list(glm_results.pvalues[glm_results.pvalues < 0.05].index)
```

[61]:
```
significant_cols
```

[61]:
```
['sex', 'cp', 'thalach', 'exang', 'oldpeak', 'slope', 'ca', 'thal']
```

[62]:
```
x_glm = x[significant_cols].copy()
```

[63]:
```
x_glm.head()
```

[63]:

	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

Train Test Split of Datafrmae with All Features:

[64]:
```
from sklearn.model_selection import train_test_split, GridSearchCV
```

[65]:
```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size= 0.2,␣
↪random_state= 42)
```

[66]:
```
print(x_train.shape)
print(x_test.shape)
print(y_train.shape)
print(y_test.shape)
```

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

Train Test Split of Datafrmae with GLM Features:

[67]:
```
x_glm_train, x_glm_test, y_train, y_test = train_test_split(x_glm, y,␣
↪test_size= 0.2, random_state= 42)
```

[68]:
```
print(x_glm_train.shape)
print(x_glm_test.shape)
print(y_train.shape)
print(y_test.shape)
```

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

Scalling of Datafrmae with All Features:

[69]:
```
from sklearn.preprocessing import StandardScaler
```

[70]:
```
sc_all = StandardScaler()
```

[71]:
```
temp = sc_all.fit_transform(x_train)
x_train = pd.DataFrame(temp, columns= x_train.columns)
x_train.head()
```

[71]:
```
        age       sex        cp  trestbps      chol       fbs   restecg  \
0 -1.350641  0.731459  0.000000 -0.630711  0.927138 -0.391293  0.890028
1  1.487426  0.731459  0.966493  2.753363  0.526980  2.555631 -0.991522
2  1.378270  0.731459 -0.966493 -0.348705  0.145878  2.555631  0.890028
3  0.068393 -1.367131  0.000000  0.215308  0.069658 -0.391293 -0.991522
4  1.050801  0.731459  0.966493  0.497314  1.689342 -0.391293  0.890028

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

[72]:
```
temp = sc_all.transform(x_test)
x_test = pd.DataFrame(temp, columns= x_test.columns)
x_test.head()
```

[72]:
```
        age       sex        cp  trestbps      chol       fbs   restecg  \
0  0.068393  0.731459 -0.966493  0.046104  2.032334 -0.391293  0.890028
1  1.050801  0.731459  0.966493 -0.348705  1.193909 -0.391293  0.890028
2  0.286705  0.731459  0.966493  1.061326 -2.293175  2.555631  0.890028
3  1.269113  0.731459  0.000000  1.625339 -0.006563 -0.391293  0.890028
```

```
4  1.814896 -1.367131  0.966493 -1.194723  0.355484  2.555631 -0.991522

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

Scalling of Datafrmae with GLM Features:

[73]:
```
sc_glm = StandardScaler()
```

[74]:
```
temp = sc_glm.fit_transform(x_glm_train)
x_glm_train = pd.DataFrame(temp, columns= x_glm_train.columns)
x_glm_train.head()
```

[74]:
```
        sex        cp   thalach     exang   oldpeak     slope        ca  \
0  0.731459  0.000000  0.549139 -0.659184 -0.895837  0.965436 -0.683490
1  0.731459  0.966493  0.012071  1.517027  0.543474 -0.684707 -0.683490
2  0.731459 -0.966493  0.593894 -0.659184 -0.715923 -0.684707  1.350103
3 -1.367131  0.000000  0.504383 -0.659184  0.363560 -0.684707 -0.683490
4  0.731459  0.966493  0.370116 -0.659184 -0.895837  0.965436 -0.683490

       thal
0 -0.545762
1  1.140502
2  1.140502
3 -0.545762
4 -0.545762
```

[75]:
```
temp = sc_glm.transform(x_glm_test)
x_glm_test = pd.DataFrame(temp, columns= x_glm_test.columns)
x_glm_test.head()
```

[75]:
```
        sex        cp   thalach     exang   oldpeak     slope        ca  \
0  0.731459 -0.966493 -0.793531  1.517027  0.183647 -0.684707  0.333307
1  0.731459  0.966493 -0.838286  1.517027  0.723388 -0.684707 -0.683490
2  0.731459  0.966493  1.041451 -0.659184 -0.715923  0.965436  0.333307
3  0.731459  0.000000 -1.330598  1.517027 -0.895837 -0.684707  2.366899
4 -1.367131  0.966493 -0.883042 -0.659184 -0.895837  0.965436  0.333307

       thal
0  1.140502
1  1.140502
2  1.140502
3 -2.232025
```

```
4 -0.545762
```

** Building Logistic Regression Model and Random Forest Model:

- Logistic Regression Model Using All Features:

[76]:
```python
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, classification_report
from sklearn.metrics import plot_confusion_matrix
```

[77]:
```python
log_model_all = LogisticRegression()
```

[78]:
```python
log_model_all.fit(x_train, y_train)
```

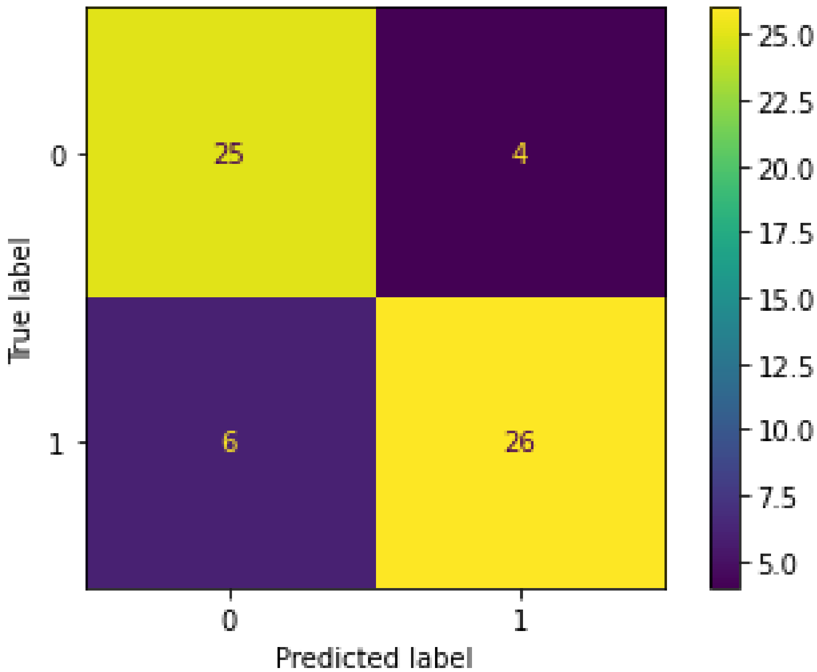
[78]:
```
LogisticRegression()
```

[79]:
```python
preds = log_model_all.predict(x_test)
```

[80]:
```python
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
```

[81]:
```python
plot_confusion_matrix(log_model_all, x_test, y_test)
plt.show()
```



- Logistic Regression Model Using GLM Features:

[82]:
```
log_model_glm = LogisticRegression()
```

[83]:
```
log_model_glm.fit(x_glm_train, y_train)
```

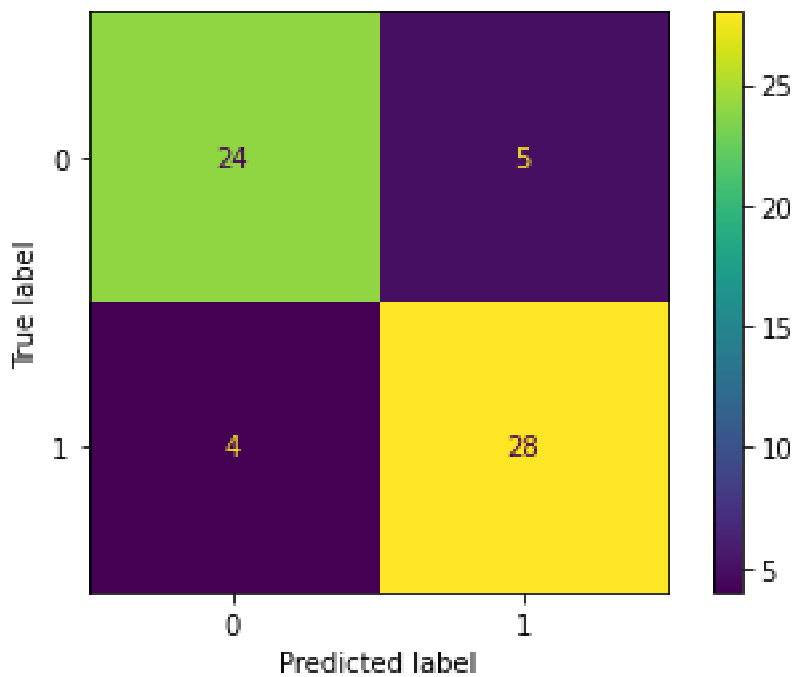
[83]:
```
LogisticRegression()
```

[84]:
```
preds = log_model_glm.predict(x_glm_test)
```

[85]:
```
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
```

[86]:
```
plot_confusion_matrix(log_model_glm, x_glm_test, y_test)
plt.show()
```



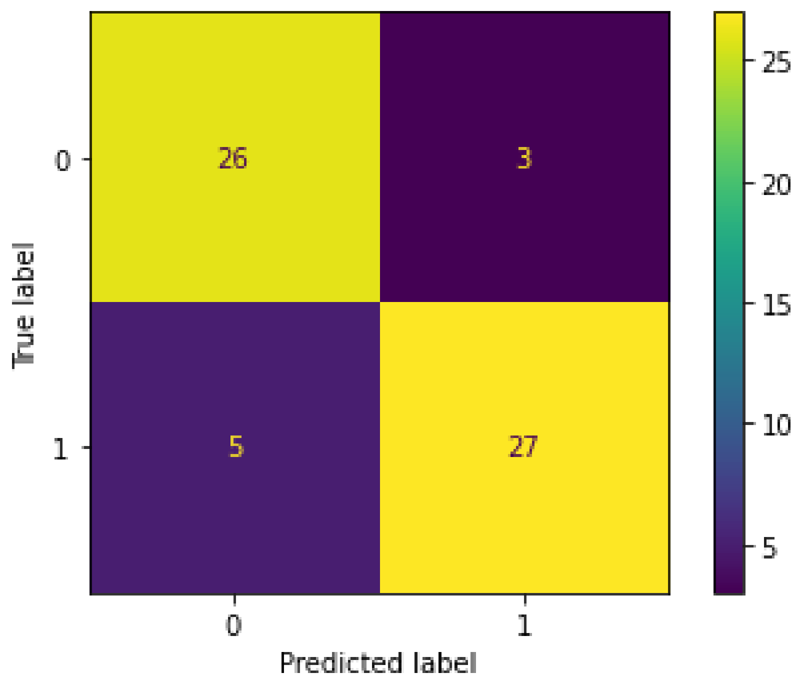
- Random Forest Classifier Using All Features:

[87]:
```
from sklearn.ensemble import RandomForestClassifier
```

[88]:
```
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
```

[89]:
```
plot_confusion_matrix(rf_model_all, x_test, y_test)
plt.show()
```

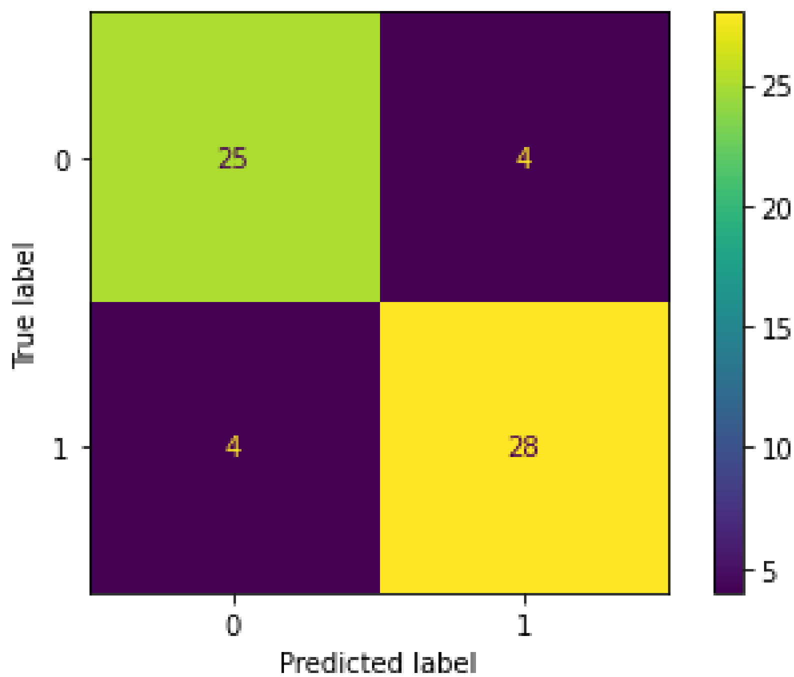


- Random Forest Classifier Using GLM Features:

[90]:
```
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       0.86      0.86      0.86        29
           1       0.88      0.88      0.88        32

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

[91]:
```
plot_confusion_matrix(rf_model_glm, x_glm_test, y_test)
plt.show()
```



- 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.