Health Care Project

Cardiovascular Disease Analysis EDA and Prediction

Importing Necessary Libraries

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


import warnings
warnings.filterwarnings('ignore')

#Read the dataset
data = pd.read_excel('Cardiovascular_dataset.xlsx')
df = pd.DataFrame(data)

df.head()
```

```
   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
```

```
df.tail()
```

```
     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
```

```
df.shape
```

```
(303, 14)
```

```
df.columns
```

```
Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

```
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
```

```
df.describe().round(3)
```

```
           age      sex       cp  trestbps     chol      fbs  restecg  \
count  303.000  303.000  303.000   303.000  303.000  303.000  303.000  
mean    54.366    0.683    0.967   131.624  246.264    0.149    0.528  
std      9.082    0.466    1.032    17.538   51.831    0.356    0.526  
min     29.000    0.000    0.000    94.000  126.000    0.000    0.000  
25%     47.500    0.000    0.000   120.000  211.000    0.000    0.000  
50%     55.000    1.000    1.000   130.000  240.000    0.000    1.000  
75%     61.000    1.000    2.000   140.000  274.500    0.000    1.000  
max     77.000    1.000    3.000   200.000  564.000    1.000    2.000  

       thalach    exang  oldpeak    slope       ca     thal   target  
count  303.000  303.000  303.000  303.000  303.000  303.000  303.000  
```

```
mean   149.647    0.327    1.040    1.399    0.729    2.314    0.545
std     22.905    0.470    1.161    0.616    1.023    0.612    0.499
min     71.000    0.000    0.000    0.000    0.000    0.000    0.000
25%    133.500    0.000    0.000    1.000    0.000    2.000    0.000
50%    153.000    0.000    0.800    1.000    0.000    2.000    1.000
75%    166.000    1.000    1.600    2.000    1.000    3.000    1.000
max    202.000    1.000    6.200    2.000    4.000    3.000    1.000
```

Data Cleaning

Check for Duplicate values

```
df[df.duplicated()]
```

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

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

```
df.drop_duplicates(inplace = True)
df.reset_index(drop=True,inplace =True)
df.head()
```

```
   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
```

Check for null values

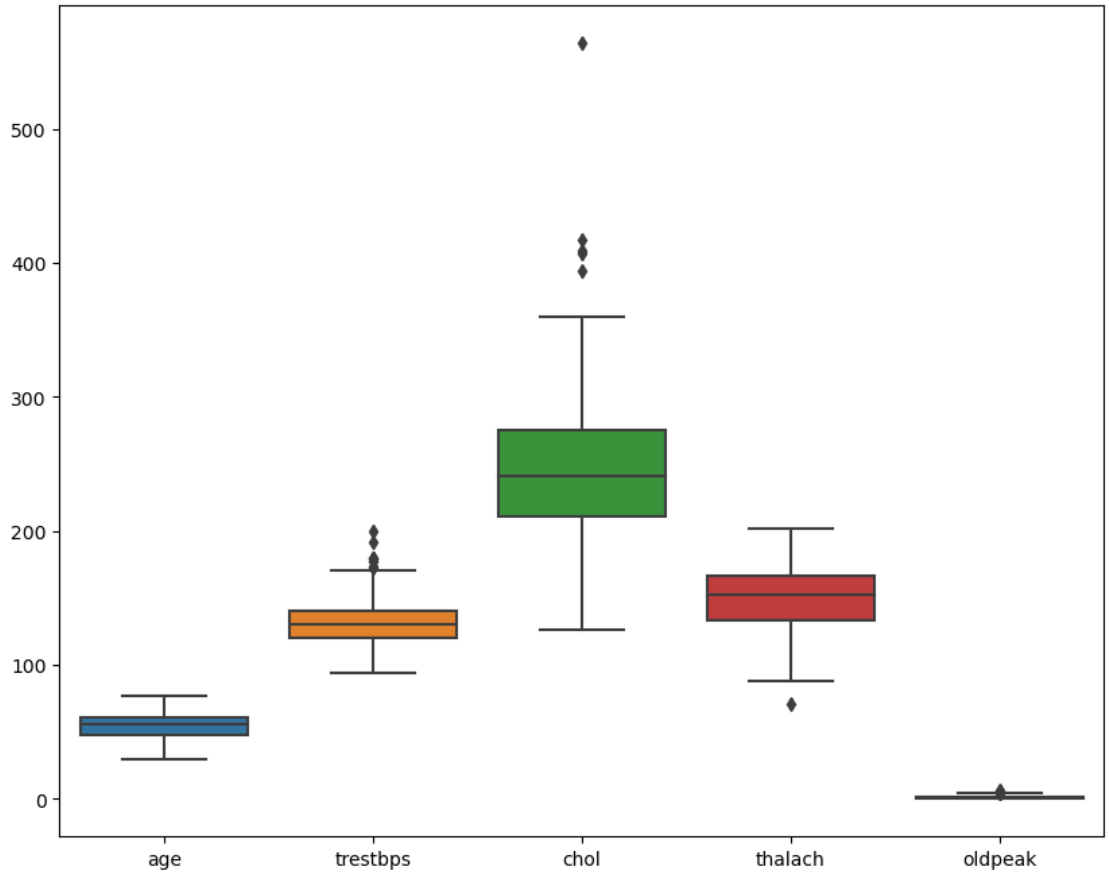
```
df.isna().sum()
```

```
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
```

Checking Outliers

```
# Checking for the presence of outliers in numeric columns
('age','trestbps','chol','thalach','oldpeak')

plt.figure(figsize=(10,8))
sns.boxplot(data = df[['age','trestbps','chol','thalach','oldpeak']])
plt.show()
```



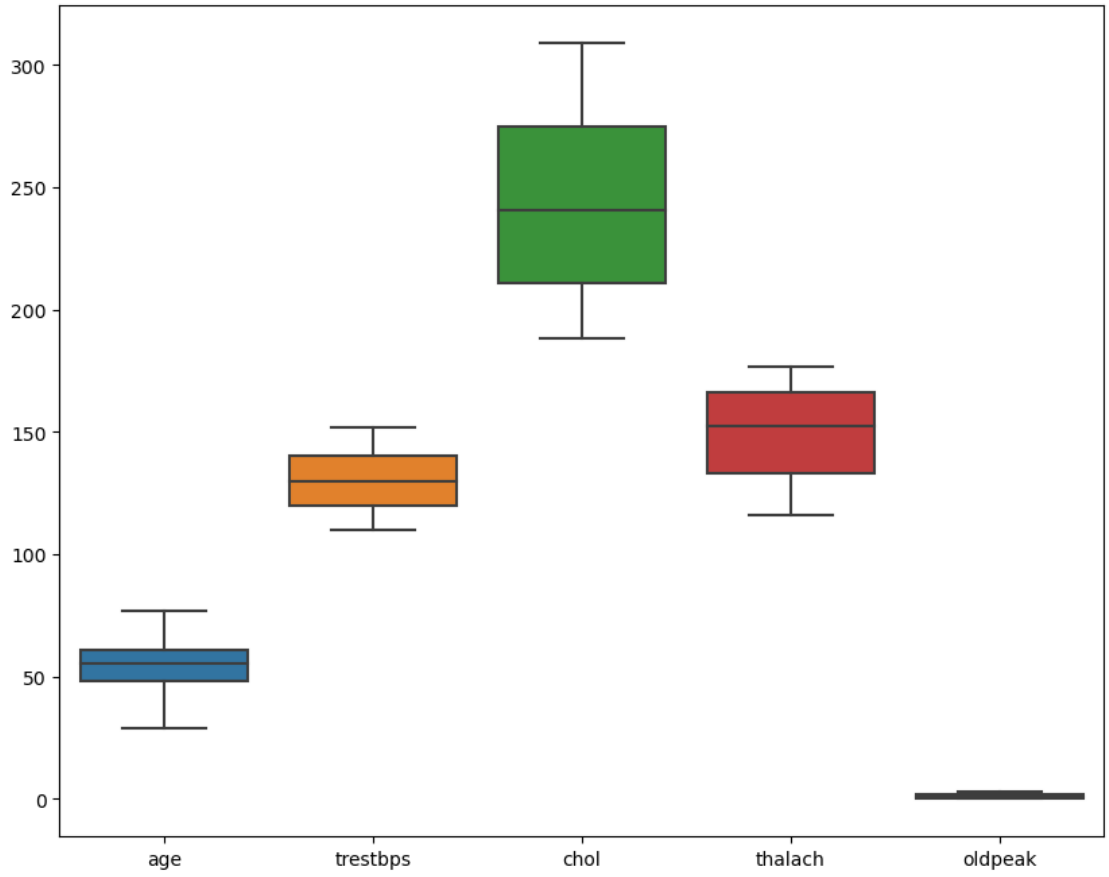

```
# Finding values of outliers(IQR method)

def detect_outliers_iqr(data):
    outlier_list = []
    data = sorted(data)
    Q1 = np.percentile(data, 25)
    Q3 = np.percentile(data, 75)
```

```
    print('the values of Q1 and Q3', Q1, Q3)
    IQR = Q3-Q1
    lower = Q1-(1.5*IQR)
    upper = Q3+(1.5*IQR)
    print('The lower and upper',lower,upper)
    for i in data:
        if (i<lower or i>upper):
            outlier_list.append(i)
    return outlier_list


for i in ['age','trestbps','chol','thalach','oldpeak']:
    outliers = detect_outliers_iqr(df[i])
    print('Outliers in',i,'attribute :',outliers)
```

```
the values of Q1 and Q3 48.0 61.0
The lower and upper 28.5 80.5
Outliers in age attribute : []
the values of Q1 and Q3 120.0 140.0
The lower and upper 90.0 170.0
Outliers in trestbps attribute : [172, 174, 178, 178, 180, 180, 180, 192,
200]
the values of Q1 and Q3 211.0 274.75
The lower and upper 115.375 370.375
Outliers in chol attribute : [394, 407, 409, 417, 564]
the values of Q1 and Q3 133.25 166.0
The lower and upper 84.125 215.125
Outliers in thalach attribute : [71]
the values of Q1 and Q3 0.0 1.6
The lower and upper -2.4000000000000004 4.0
Outliers in oldpeak attribute : [4.2, 4.2, 4.4, 5.6, 6.2]
```

```
# Handling outliers using Quantile based flooring and capping method.
# the outlier is capped at a certain value above the 90th percentile value or
floored at a factor below the 10th percentile value
# Computing 10th, 90th percentiles and replacing the outliers

def handle_outliers(data):

    tenth_percentile = np.percentile(data, 10)
    ninetieth_percentile = np.percentile(data, 90)

    b = np.where(data<tenth_percentile, tenth_percentile, data)

    b1 = np.where(b>ninetieth_percentile, ninetieth_percentile, b)
    return b1


for i in ['trestbps','chol','thalach','oldpeak']:
    df[i]=handle_outliers(df[i])
```

```
# verifying again with boxplot
plt.figure(figsize=(10,8))
sns.boxplot(data = df[['age','trestbps','chol','thalach','oldpeak']])
plt.show()
```




```
df.shape
```

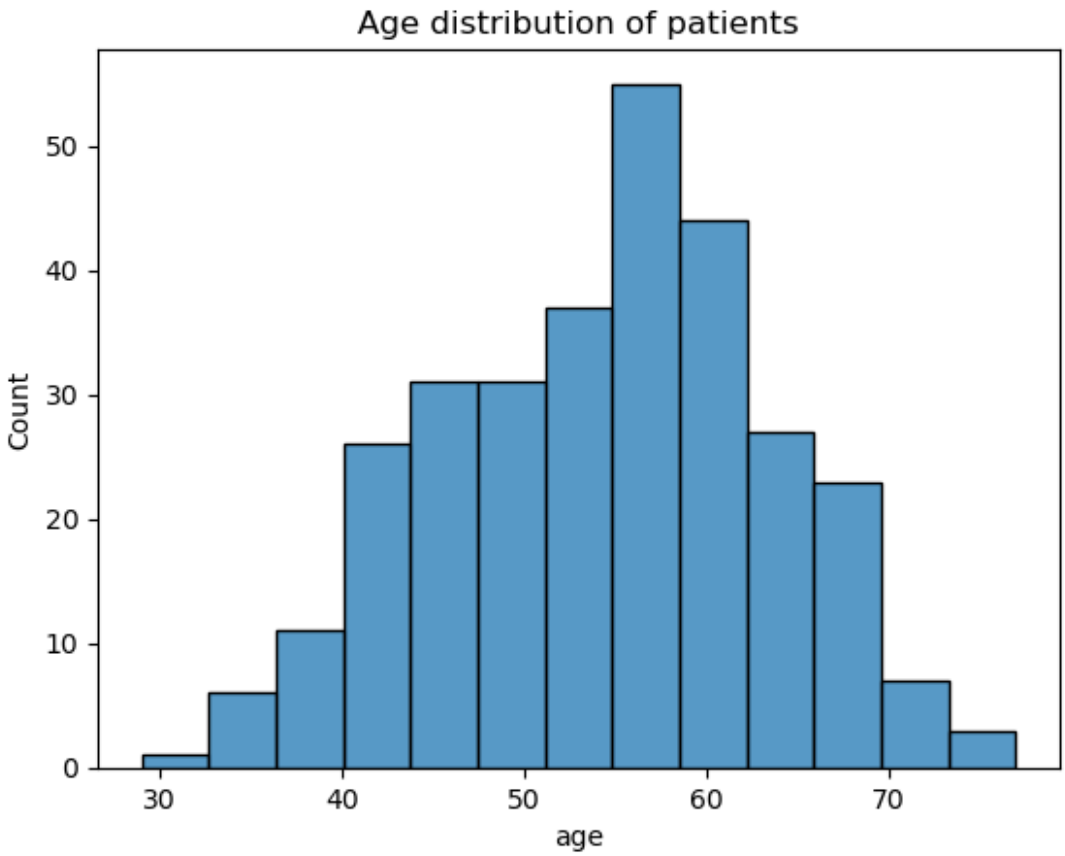
```
(302, 14)
```

Visualization

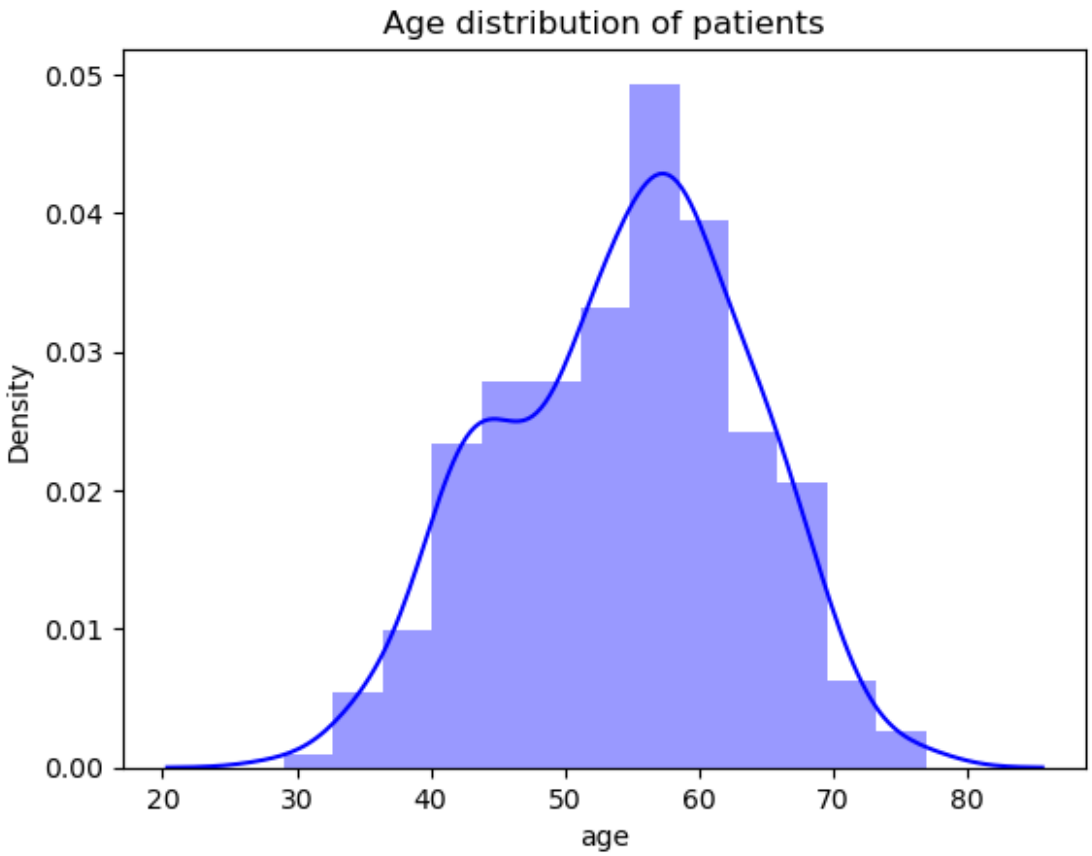
Univariate Analysis

In this section, we will get an idea about our patients by considering all the features separately.

```
sns.histplot(df.age)
plt.title('Age distribution of patients')
plt.show()
```

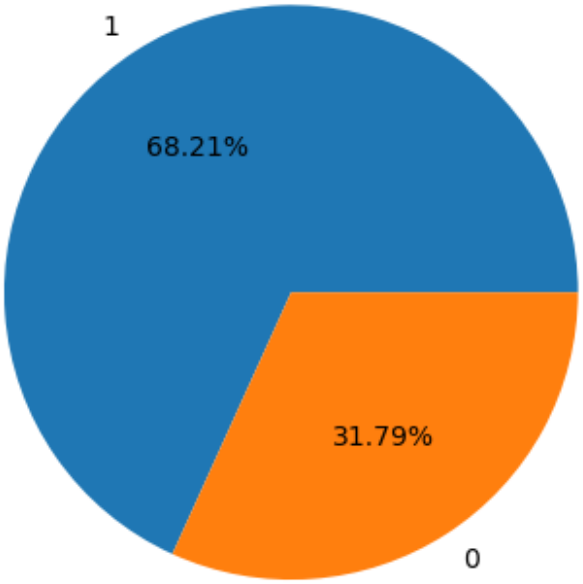



```
sns.distplot(df['age'],color='blue')
plt.title('Age distribution of patients')
plt.show()
```



The dataset contains information about older patients, which is to be expected. The majority of the patients are older than 40. The peak is at 57-60 years old.

```
#Gender
s_v = df.sex.value_counts().values
s_i = df.sex.value_counts().index

plt.pie(s_v,labels=s_i,autopct='%1.2f%%')
plt.show()
```

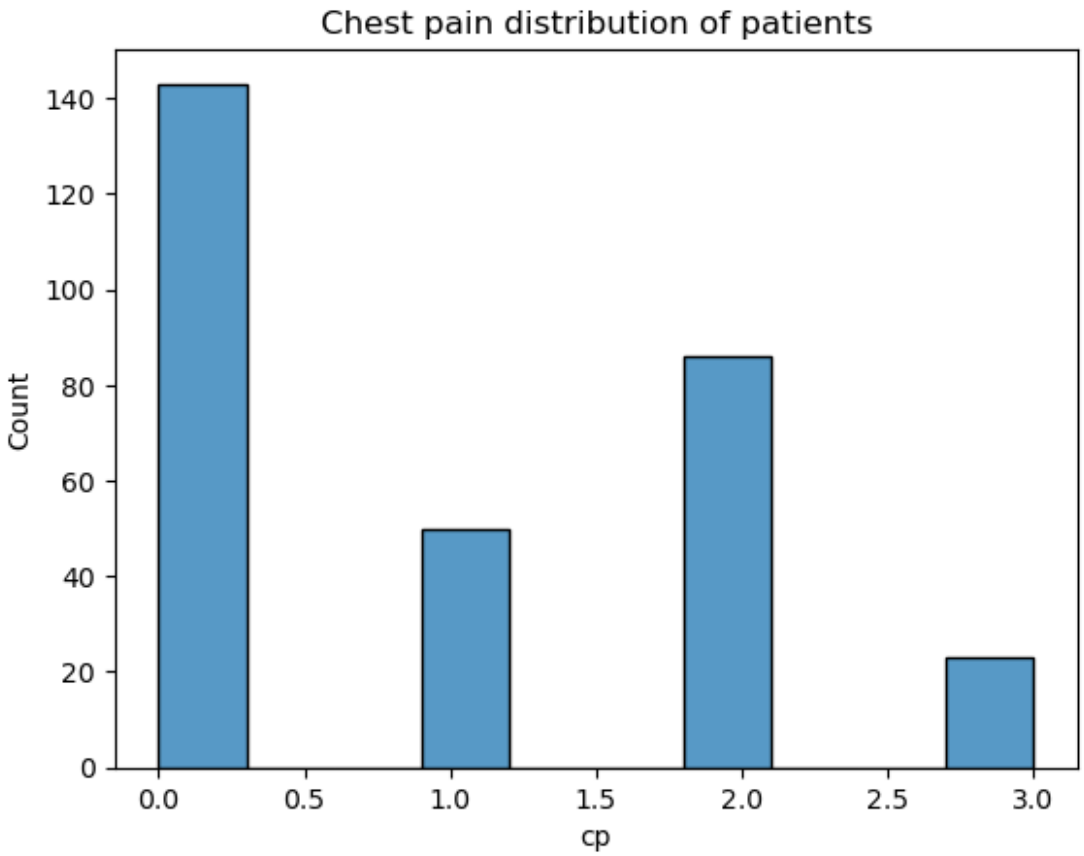


1 = Male

0 = Female

We have two times more Males than Females

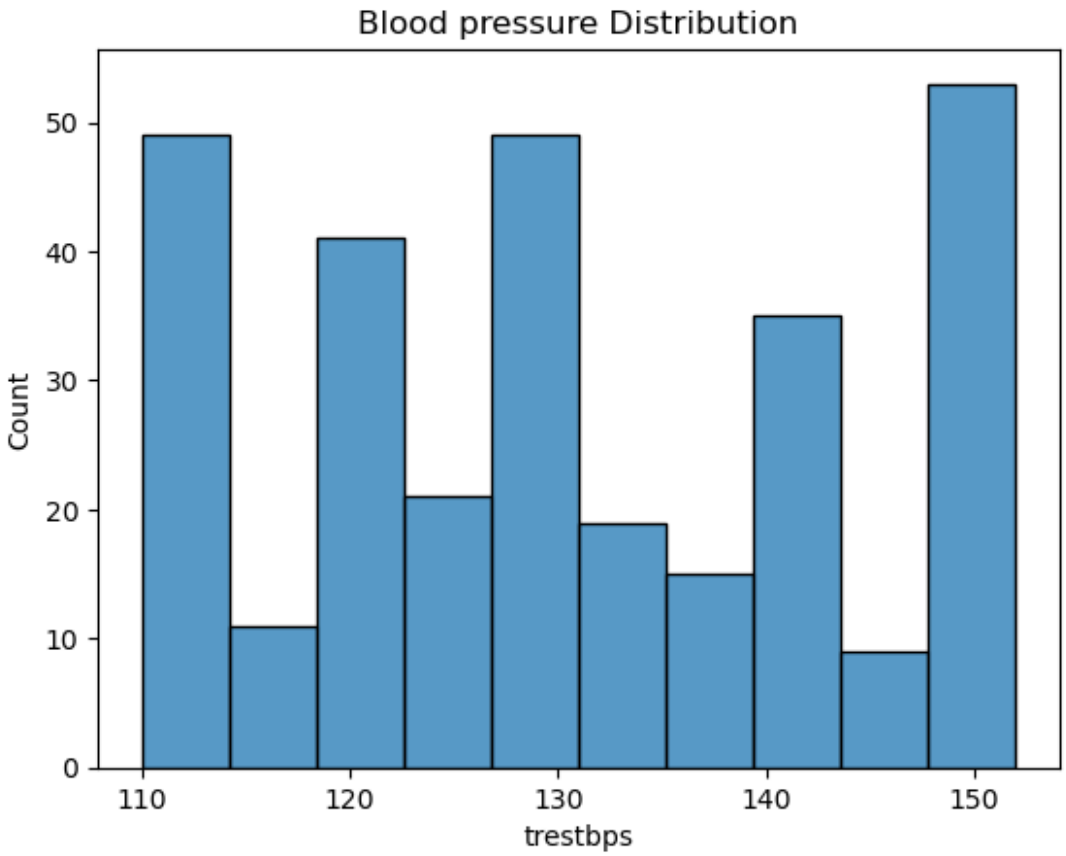
```
#Chest pain
sns.histplot(df.cp)
plt.title('Chest pain distribution of patients')
plt.show()
```



1 = typical angina; 2 = atypical angina; 3 = non-anginal pain; 0 = asymptomatic

Almost a half of the patients have no pain in the chest

```
#Blood pressure
sns.histplot(data = df.trestbps)
plt.title('Blood pressure Distribution')
plt.show()
```

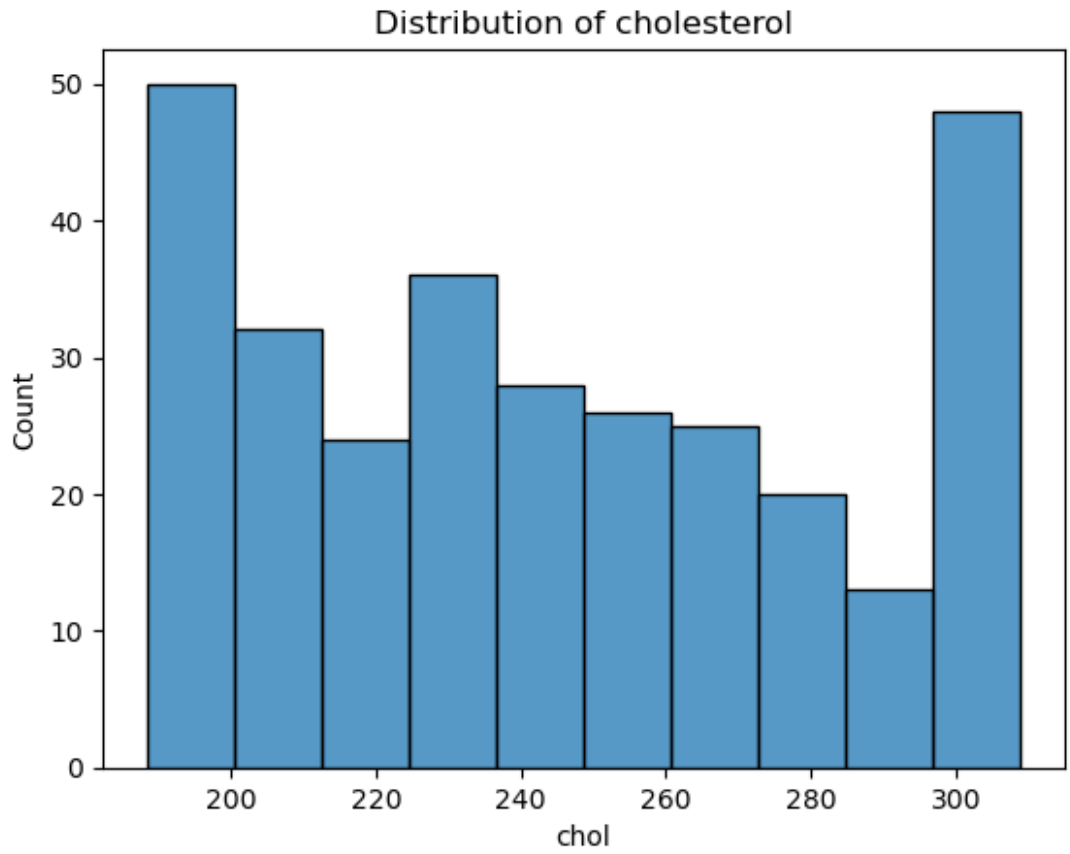


According to the European Society of Cardiology, the following classification for blood pressure is applied:

Category	Blood pressure
Optimal	< 120
Normal	120–129
High normal	130–139
Grade 1 hypertension	140–159
Grade 2 hypertension	160–179
Grade 3 hypertension	≥ 180

In our dataset, the resting blood pressure distribution has a peak at a value of approx. 150

```
#cholesterol
sns.histplot(data=df.chol)
plt.title('Distribution of cholesterol')
plt.show()
```



The following interpretation of cholesterol level is usually used:

Cholesterol	mg/dl	Interpretation
< 200		Desirable
200-239		Borderline
> 240		High

In our dataset some patients have an extremely high level of cholesterol.

```
#Fasting blood sugar
df.fbs.value_counts()
```

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

Reminder: 0 means less or equal to 120 mg/dl (which is good), 1 means higher than 120 mg/dl.

The majority of the patients don't have serious sugar problems.

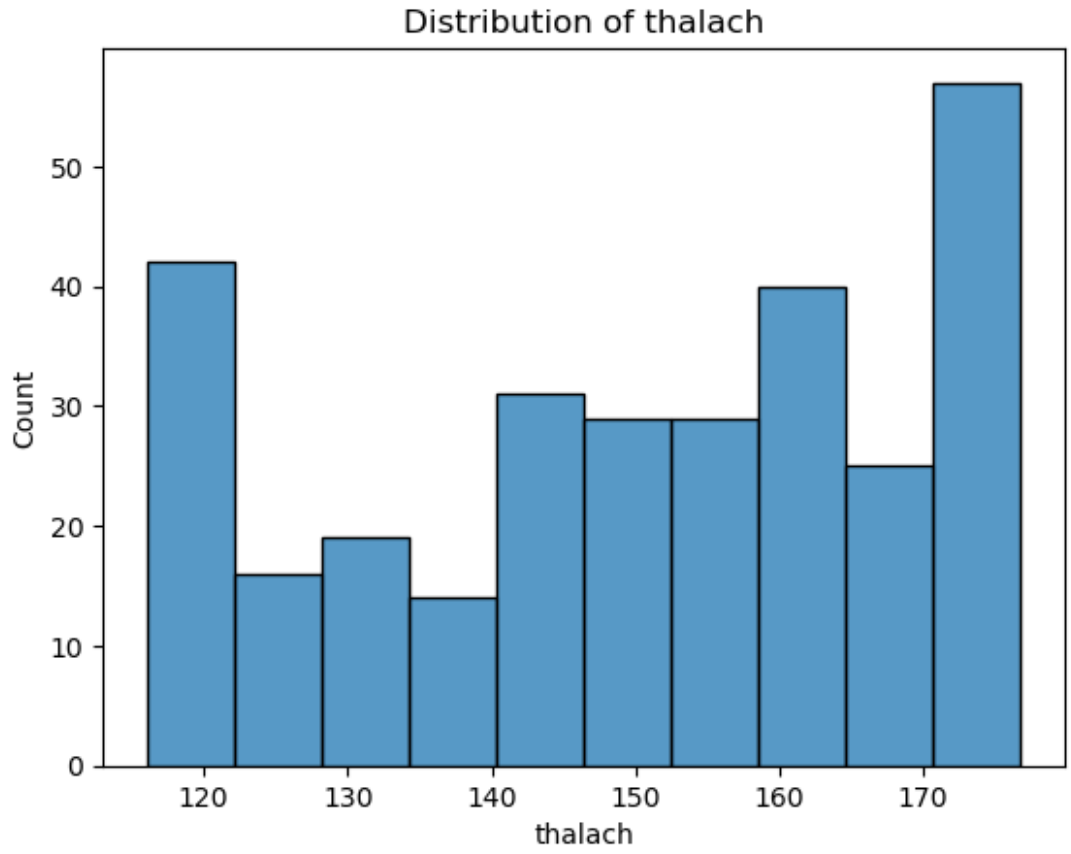
```
df.restecg.value_counts()
```

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

0 = normal; 1 = hypertrophy; 2 = having ST-T wave abnormality

About 50% of the patients have hypertrophy. Only a few of the patients have ST-T wave abnormality. The rest of them have normal results.

```
sns.histplot(df.thalach)
plt.title('Distribution of thalach')
plt.show()
```

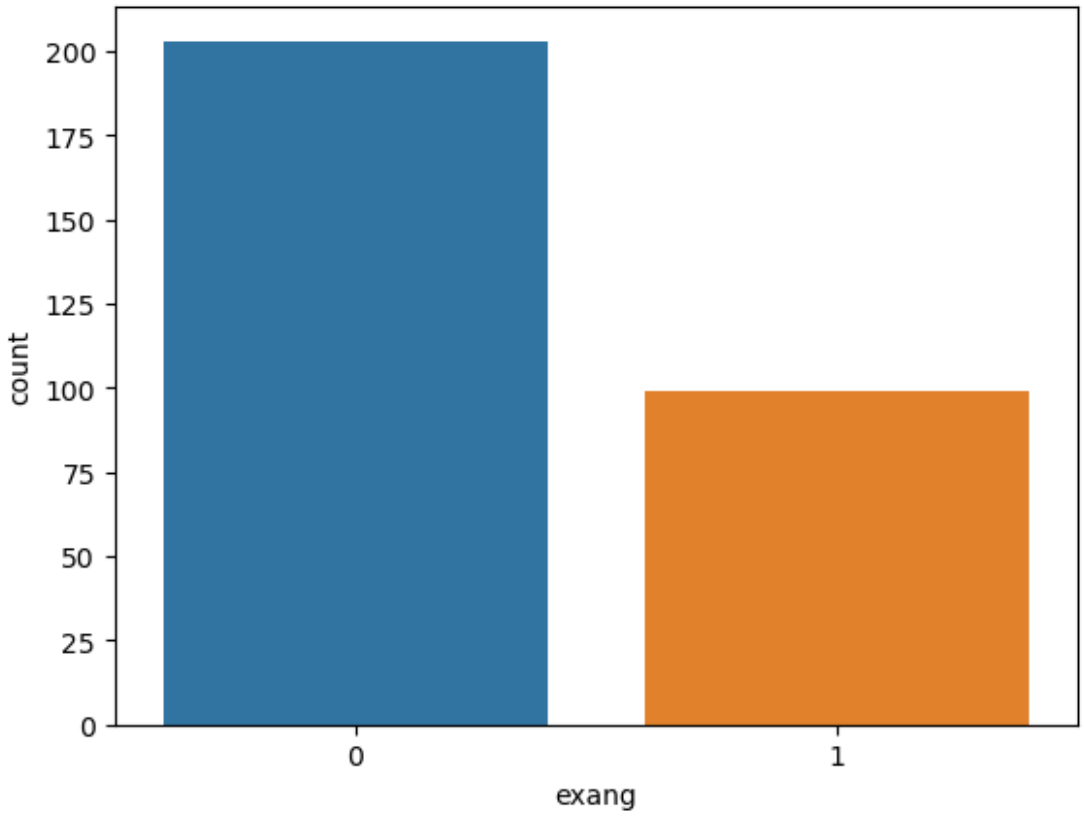


In our dataset ,the highest value of thalach is in between 170-175 (The person's maximum heart rate achieved)

```
df.exang.value_counts()
```

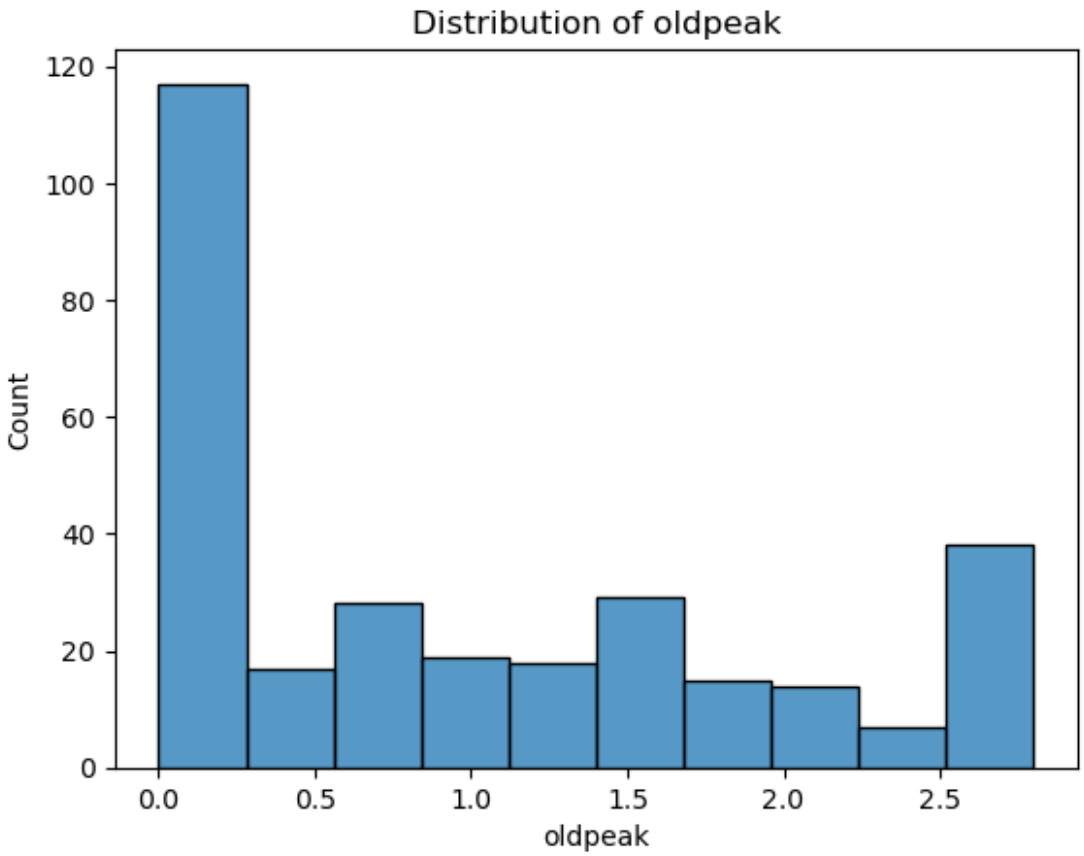
```
0    203
1     99
Name: exang, dtype: int64
```

```
sns.countplot(x='exang',data=df)
plt.show()
```



Exercise induced angina (1 = yes; 0 = no)

```
sns.histplot(df.oldpeak)
plt.title('Distribution of oldpeak')
plt.show()
```

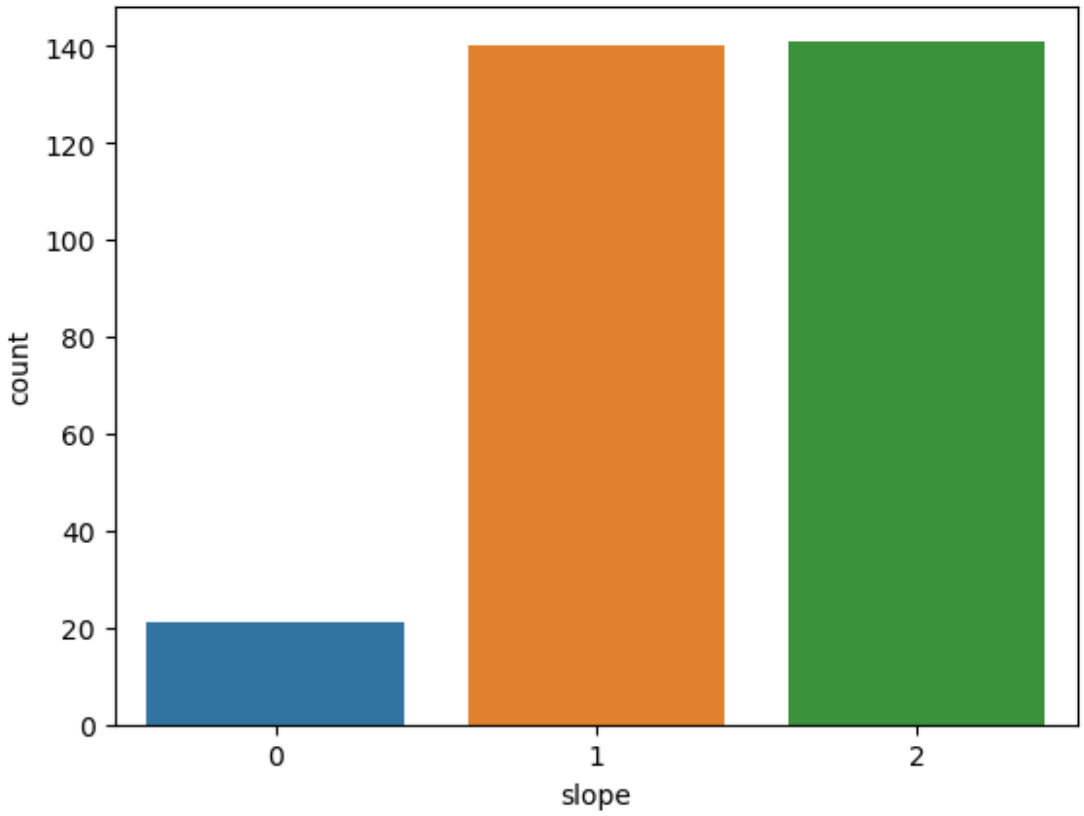


ST depression induced by exercise relative to rest ('ST' relates to positions on the ECG plot.)

```
df.slope.value_counts()
```

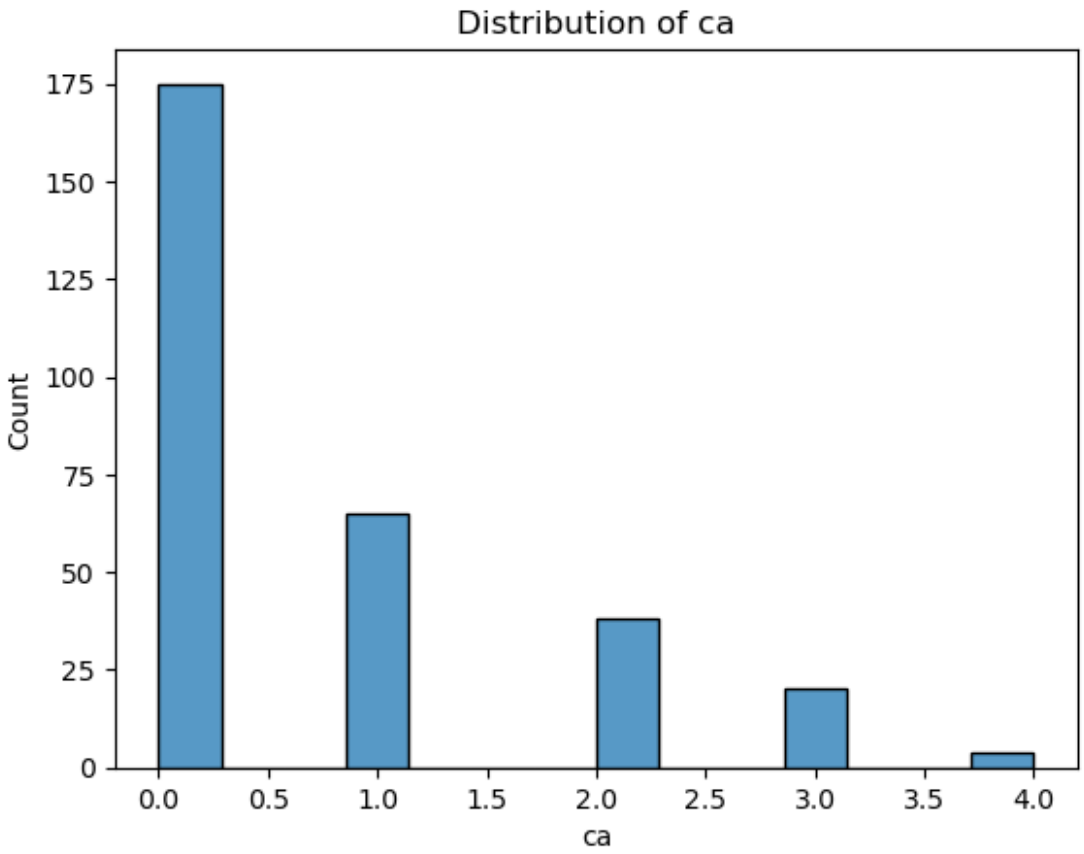
```
2    141
1    140
0     21
Name: slope, dtype: int64
```

```
sns.countplot(x='slope',data=df)
plt.show()
```



0: downsloping 1: flat 2: upsloping

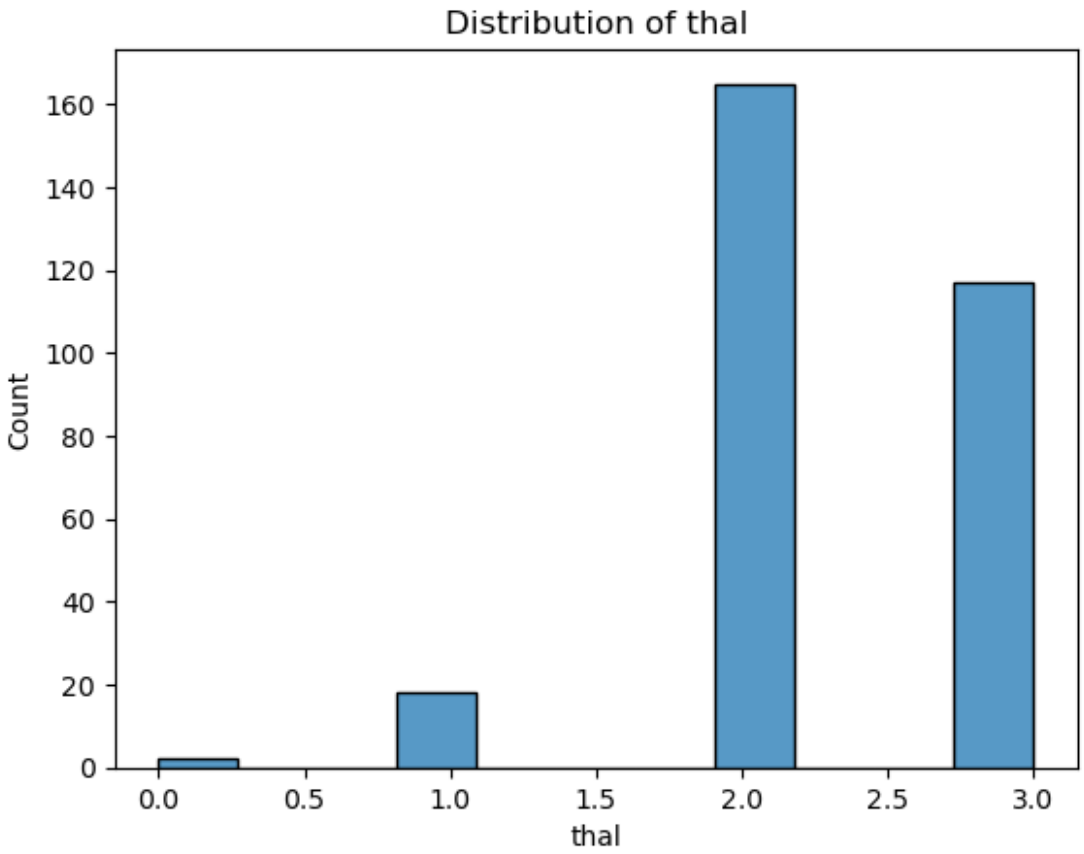
```
sns.histplot(df.ca)
plt.title('Distribution of ca')
plt.show()
```



Calcium test score,A normal calcium test score is zero.

In our dataset more than 50% of patients having zero score means there is no evidence of heart disease.

```
sns.histplot(df.thal)
plt.title('Distribution of thal')
plt.show()
```



A blood disorder called thalassemia

Value 0: Null

Value 1: fixed defect (no blood flow in some part of the heart)

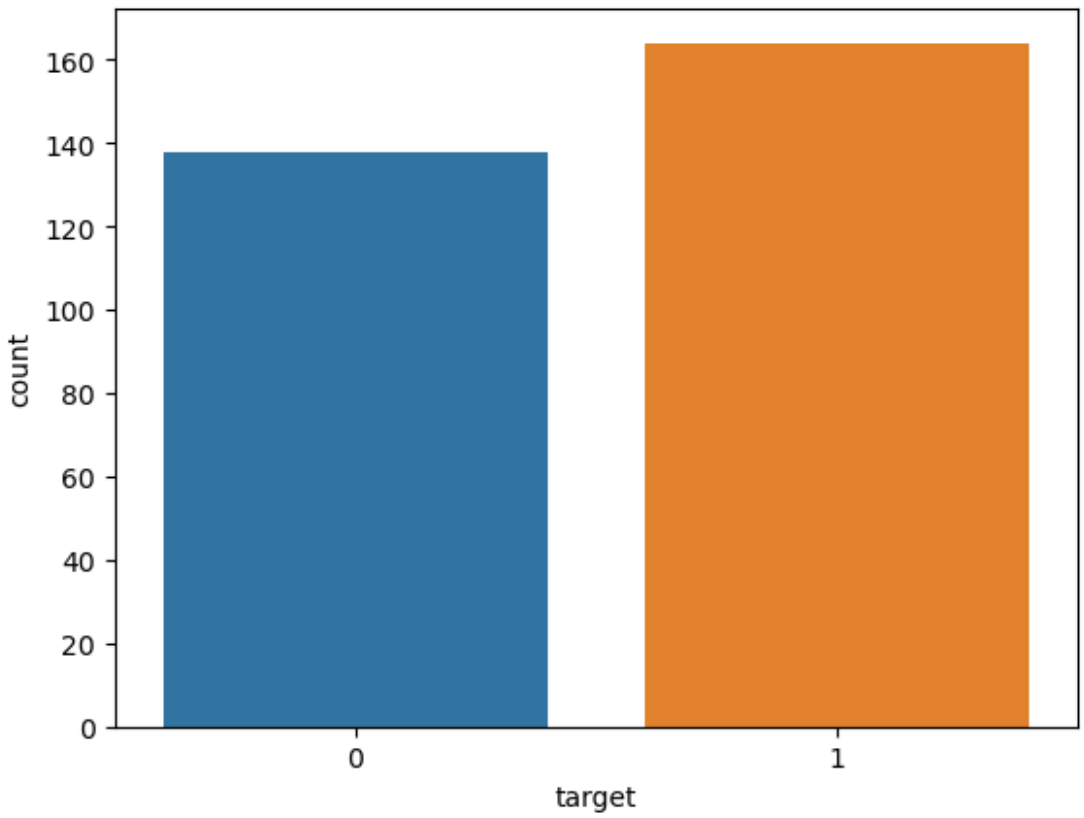
Value 2: normal blood flow

Value 3: reversible defect (a blood flow is observed but it is not normal)

```
df.target.value_counts()
```

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

```
sns.countplot(x='target',data=df)
plt.show()
```



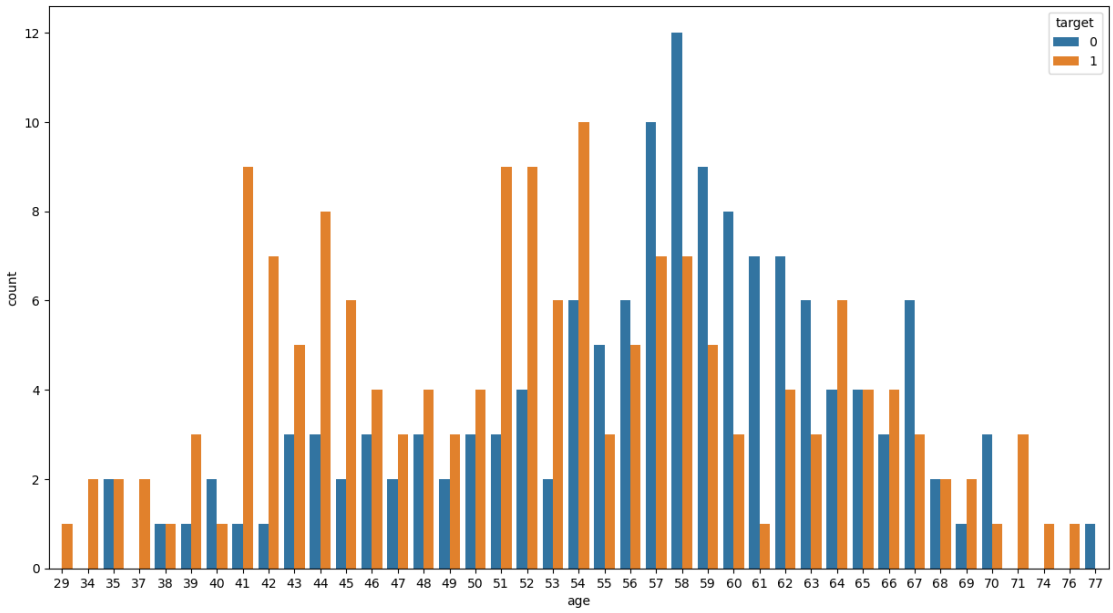
0 = less chance of heart attack; 1 = more chance of heart attack

56.67% of the patients have a high risk of heart attack, 43.33% - low risk of a heart attack.(target value is balanced)

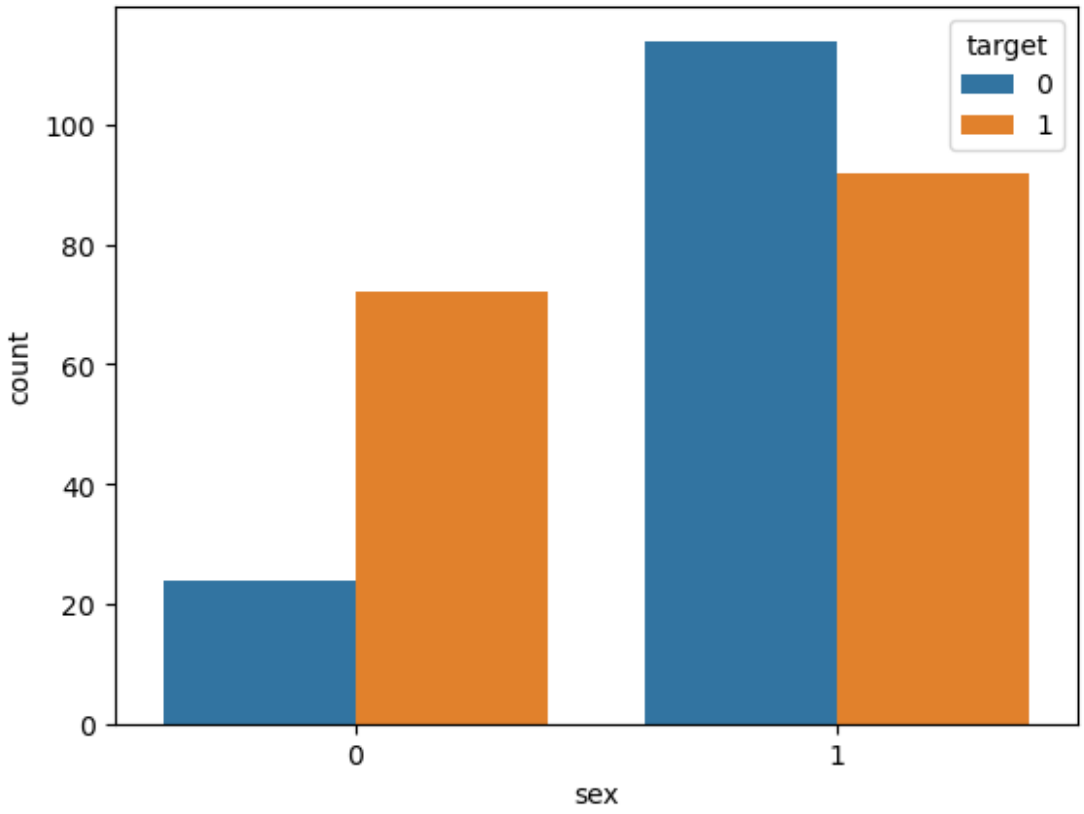
The conclusion is that people with good health condition has a lower chance to a heart attack.

Bivariate Analysis

```
plt.figure(figsize=(15,8))
sns.countplot(x='age',data=df,hue='target')
plt.show()
```

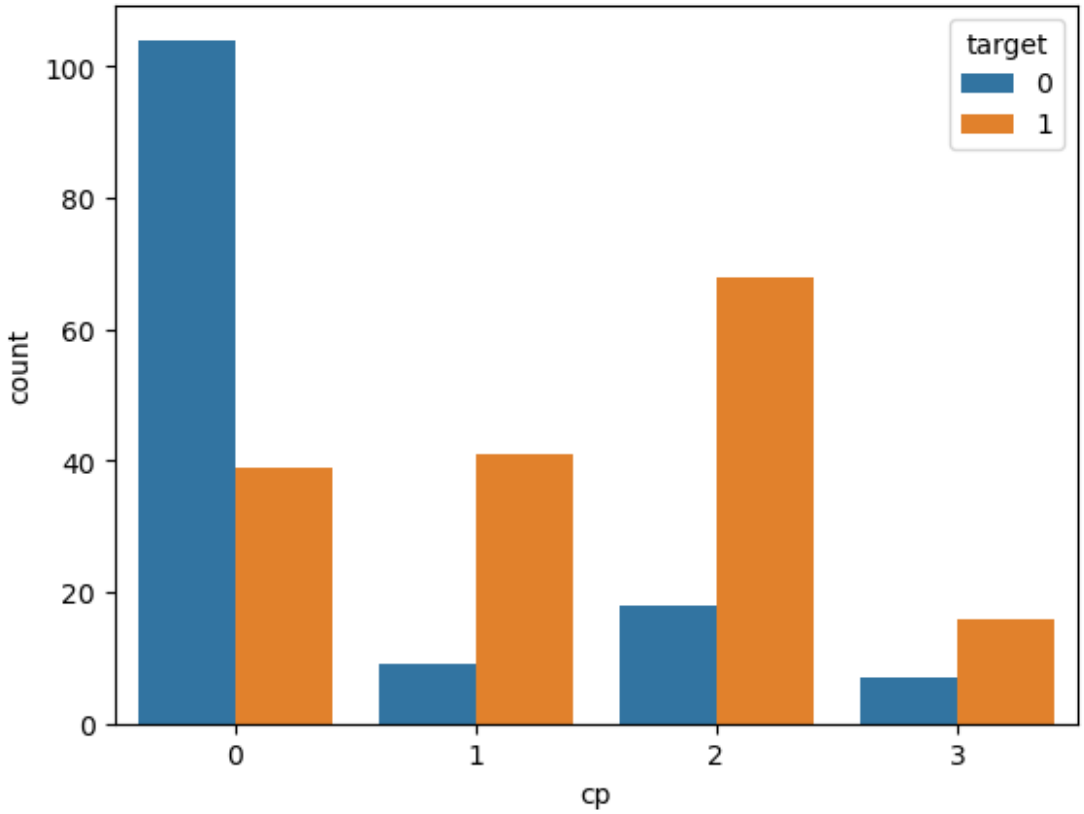



```
sns.countplot(x='sex',data=df,hue='target')
plt.show()
```



Females are more prone to heart attack compared to Males.

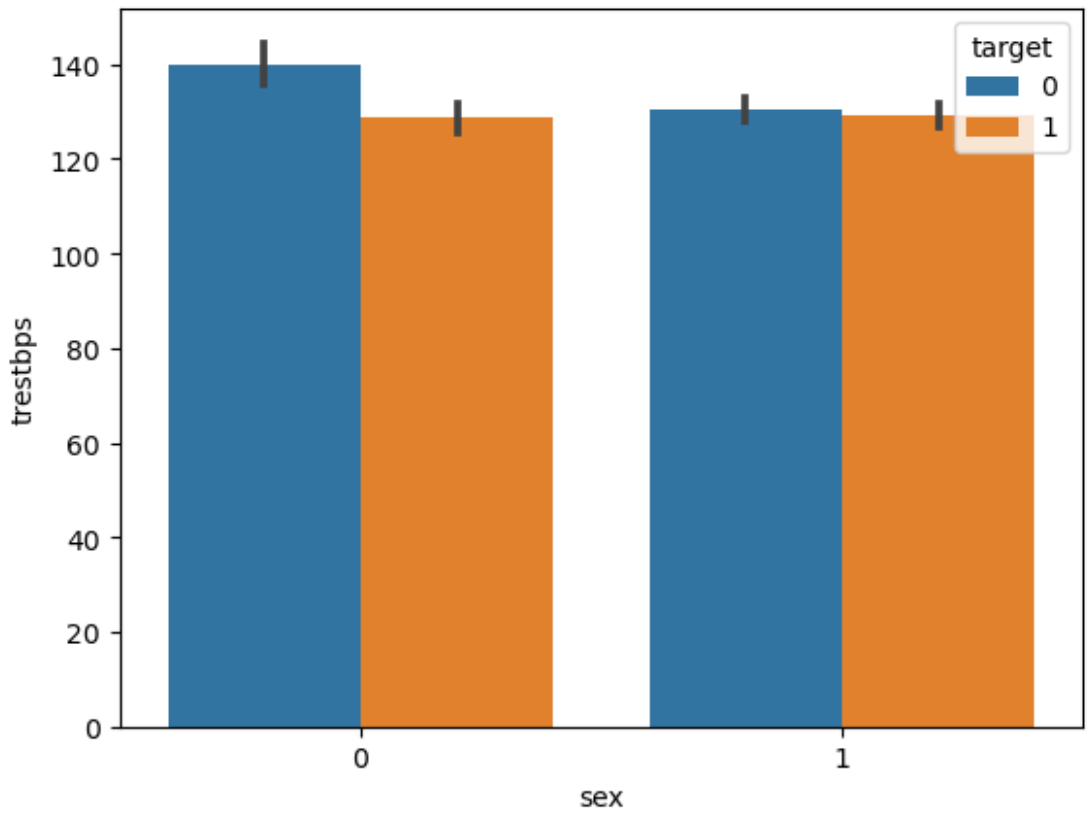
```
sns.countplot(x='cp',data=df,hue='target')
plt.show()
```



1 = typical angina; 2 = atypical angina; 3 = non-anginal pain; 0 = asymptomatic

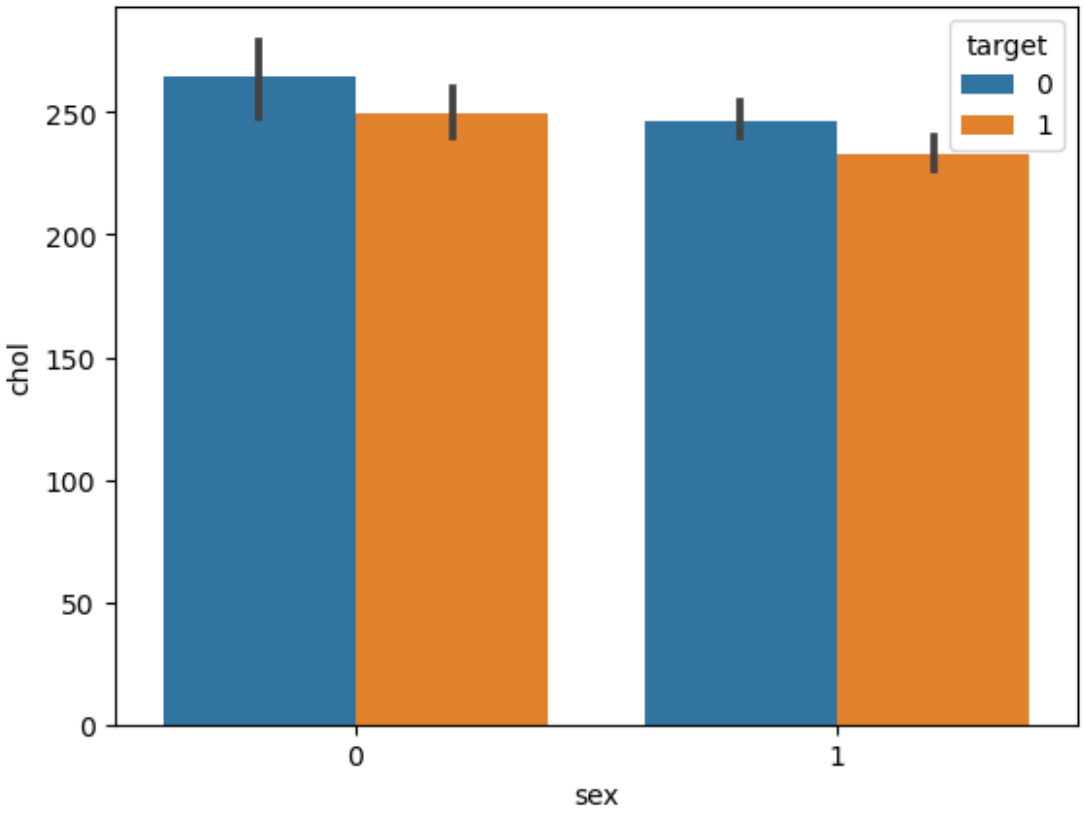
Most of the patients are having chest pain before getting heart attack,Especially people who having (atypical angina) are more prone to get heart attack. Almost all types of chest pains (1,2,3)except 0 type,are more prone to heart attack.

```
sns.barplot(x='sex',y='trestbps',hue='target',data=df)
plt.show()
```



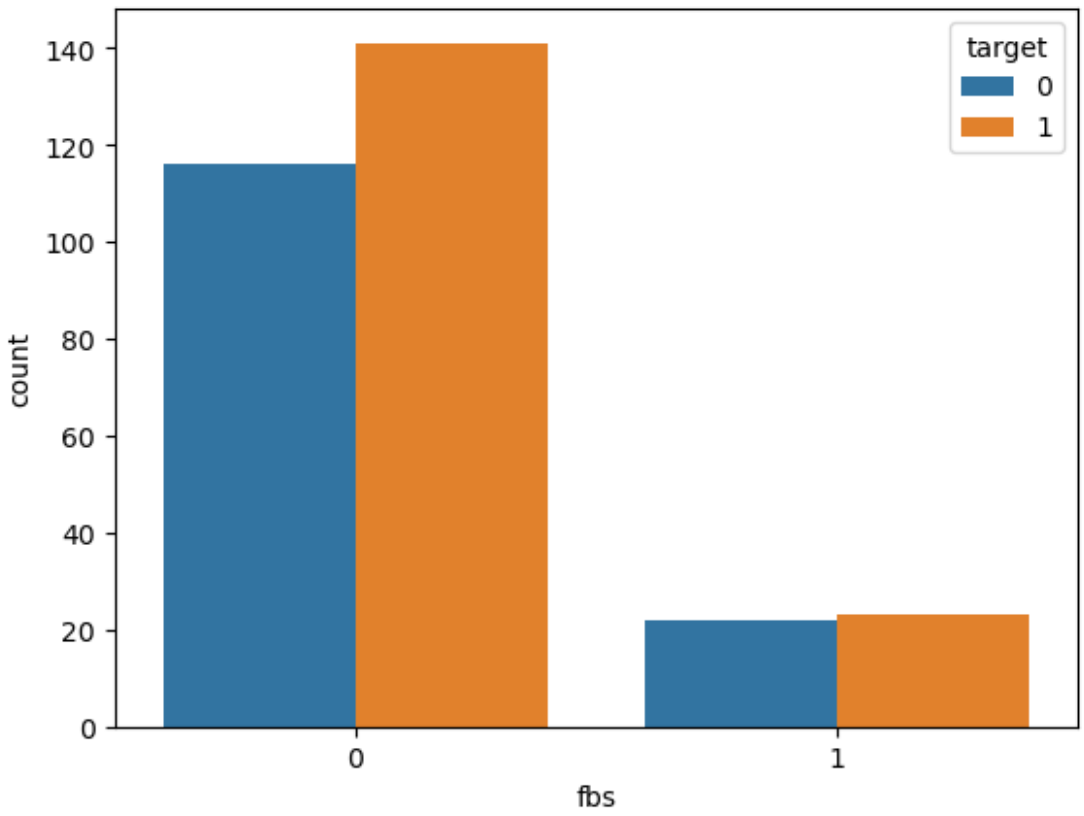
In both Females and Males at the time of heartattack Blood pressure almost same.

```
sns.barplot(x='sex',y='chol',hue='target',data=df)
plt.show()
```



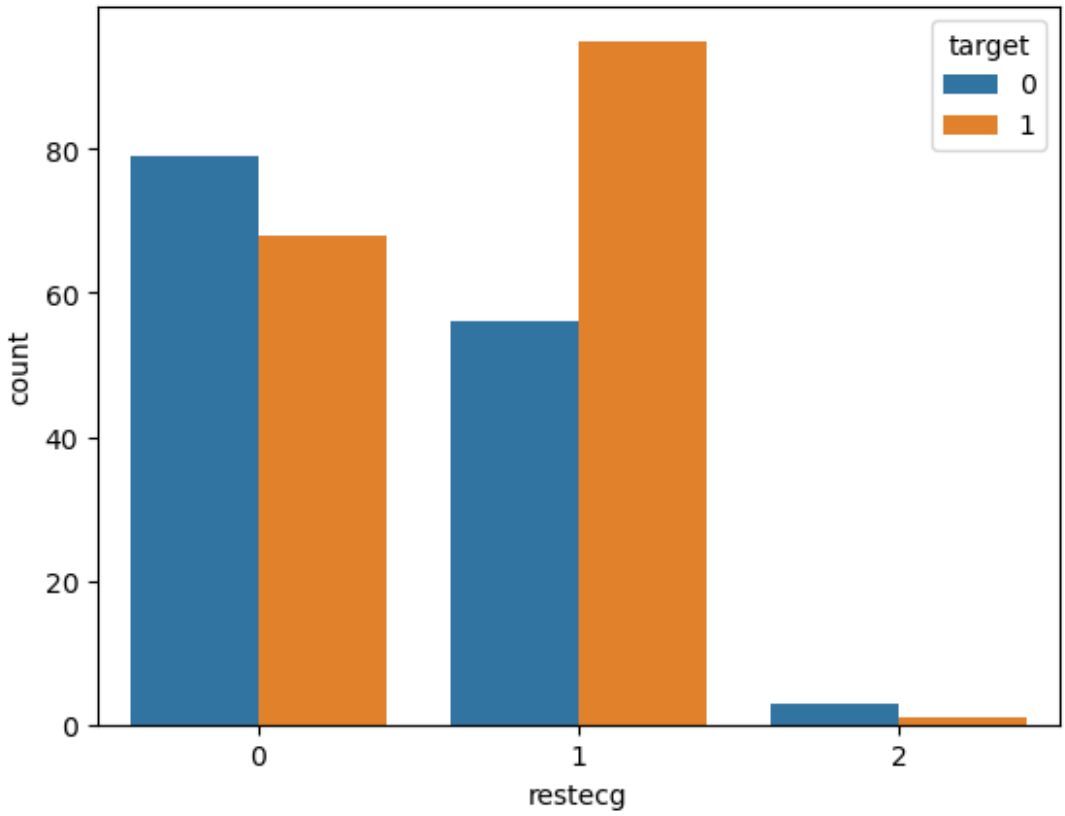
People who are prone to heartattack,Females are having more cholestrol compared to Males

```
sns.countplot(x='fbs',hue='target',data=df)
plt.show()
```



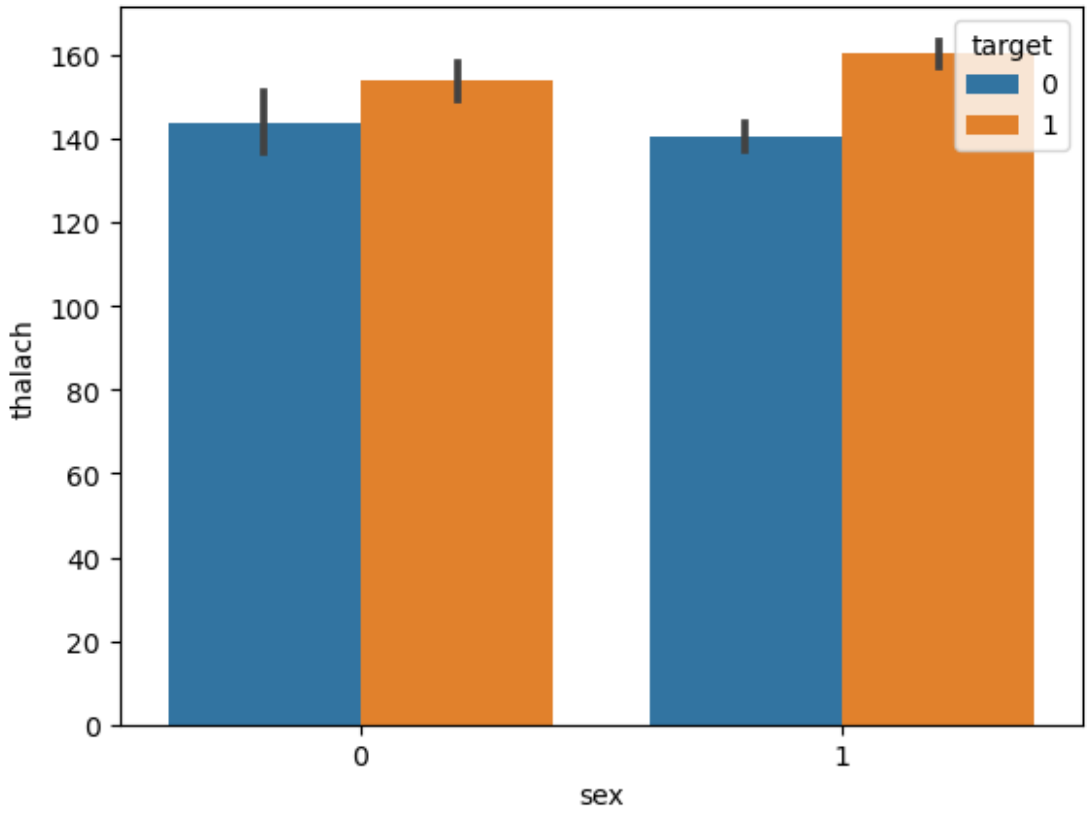
Majority of the patients don't have suger problems,Still people are prone to Heartattack.

```
sns.countplot(x='restecg',hue='target',data=df)
plt.show()
```



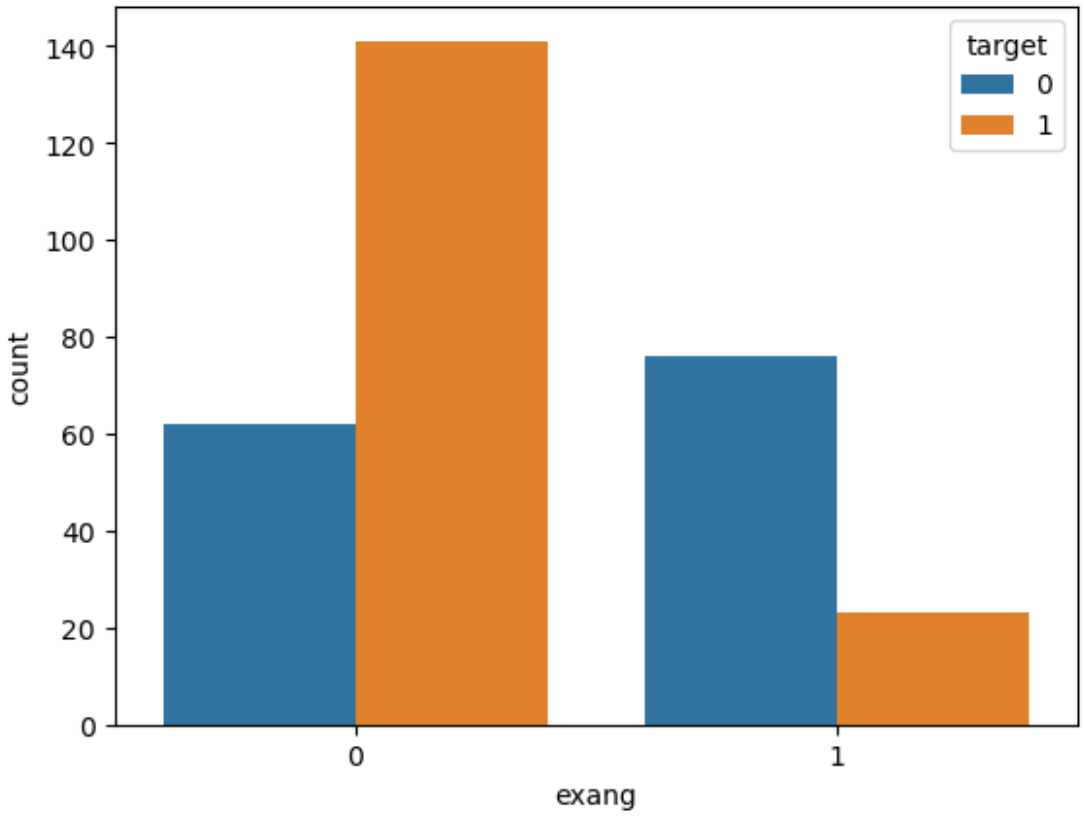
Patients who having Hypertropy are more prone to heartattack.

```
sns.barplot(x='sex',y='thalach',hue='target',data=df)
plt.show()
```



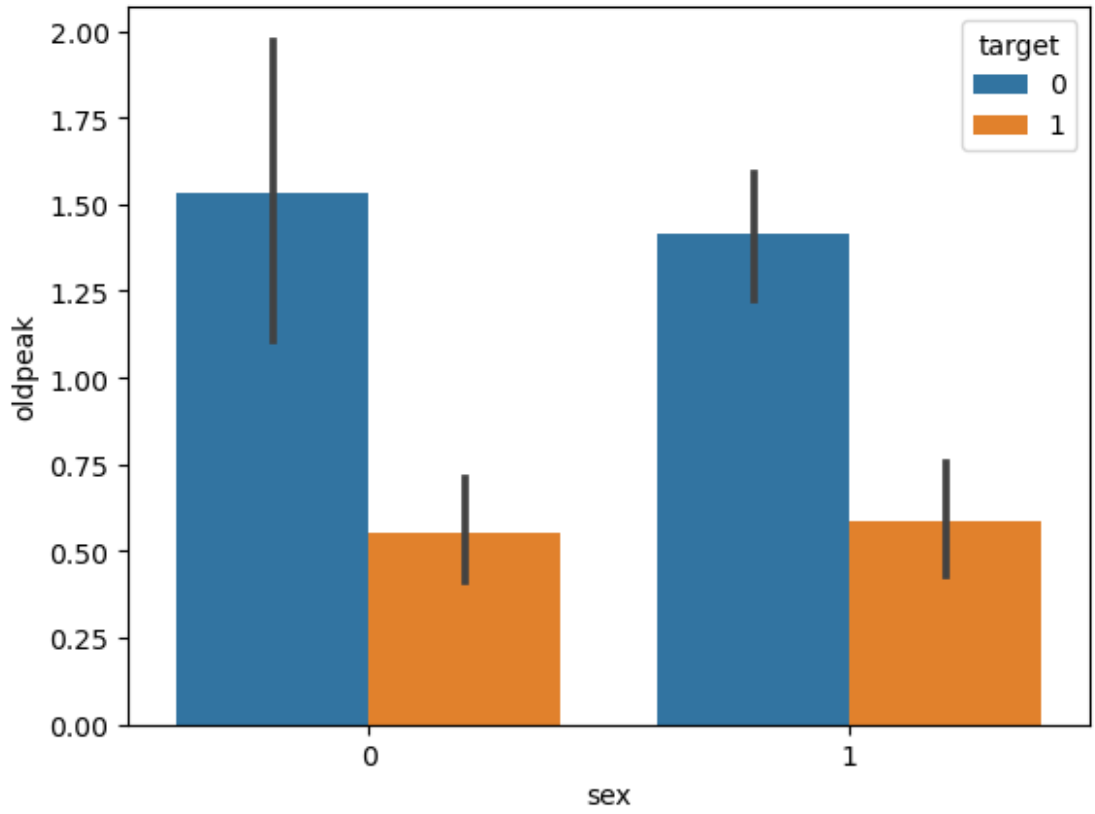
In both Females and Males heart rate is more at the time of heartattack.

```
sns.countplot(x='exang',hue='target',data=df)
plt.show()
```



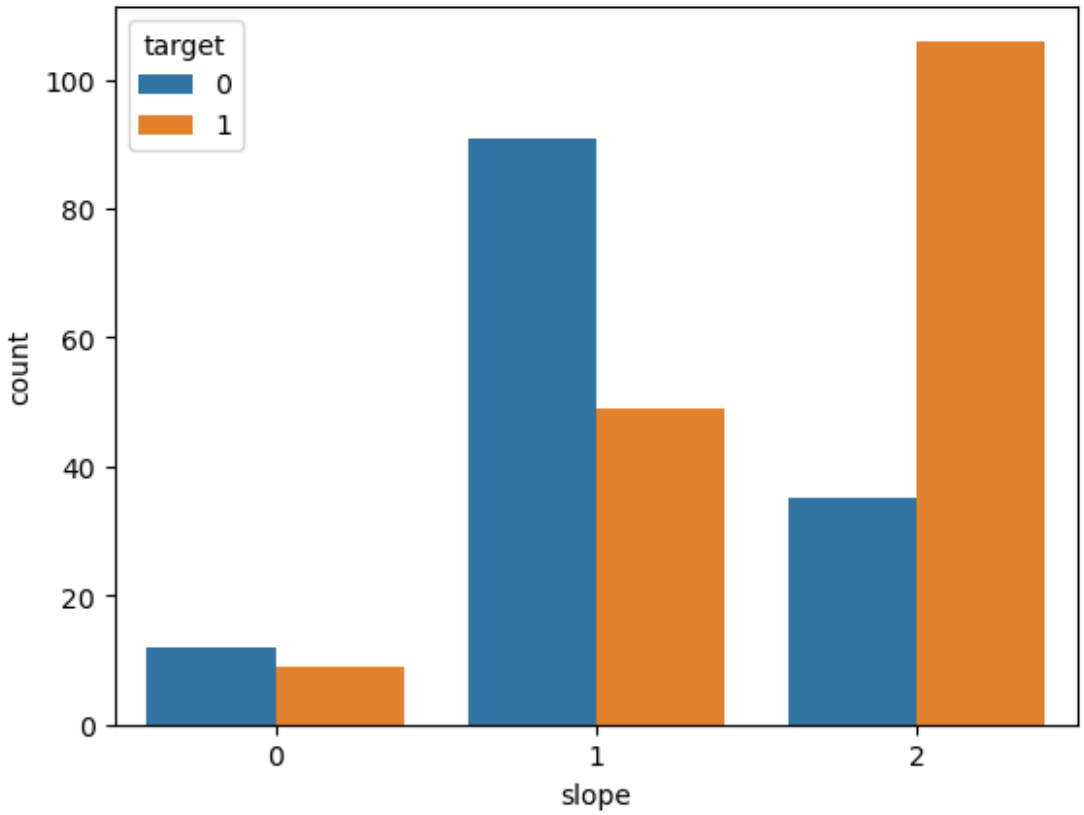
patients whose exercise induced angina no are more prone to heartattack.

```
sns.barplot(x='sex',y='oldpeak',hue='target',data=df)
plt.show()
```



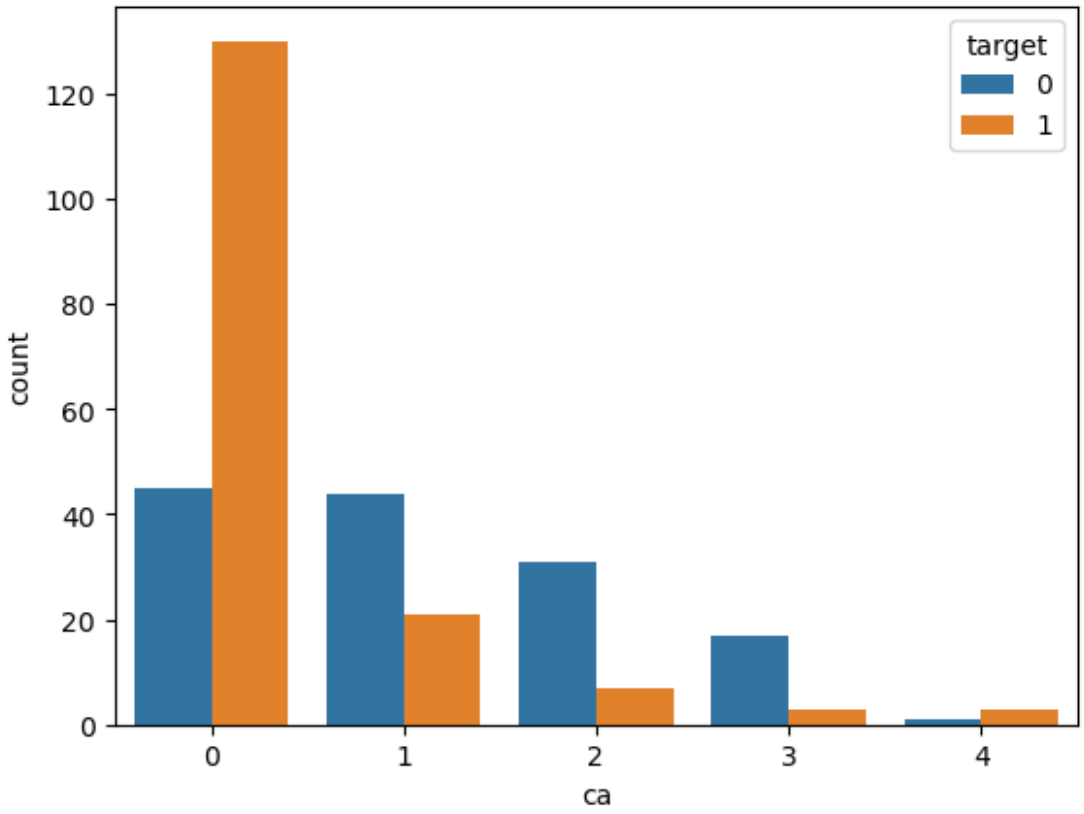
Patients who got heartattack Both Famales and Males are having same ECG plot.

```
sns.countplot(x='slope',hue='target',data=df)
plt.show()
```



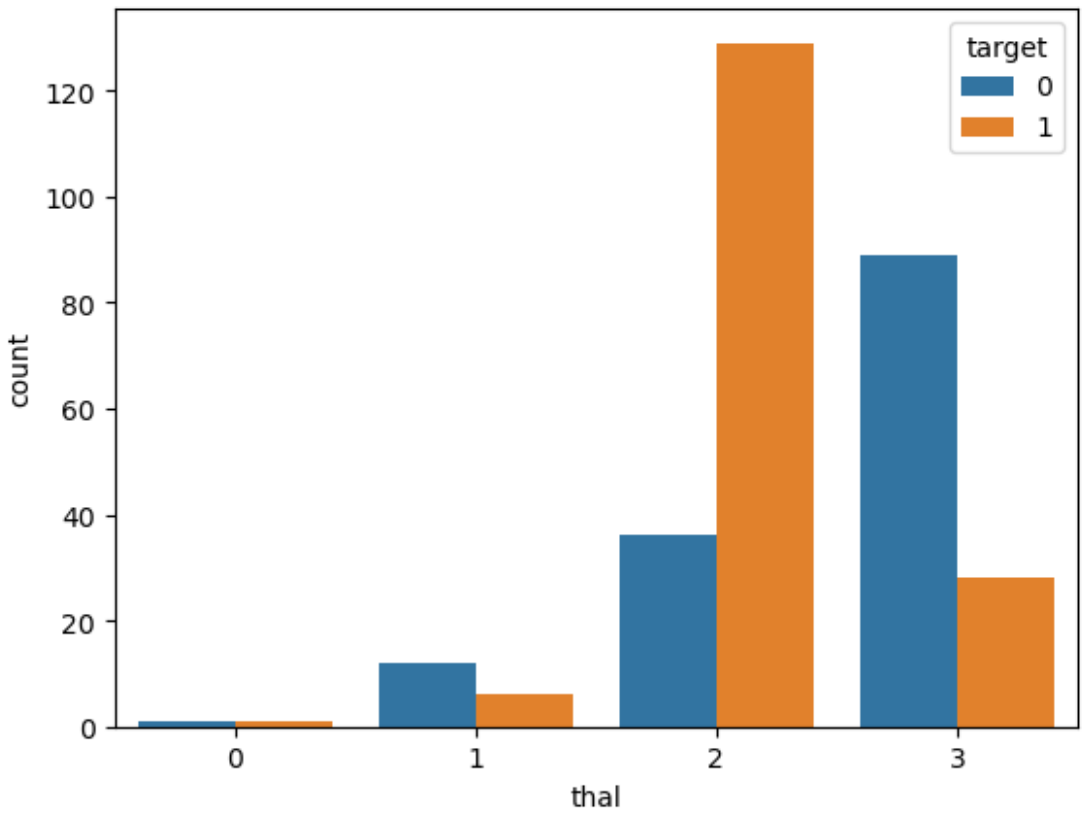
Patients who having upsloping(2) during test are more prone to heartattack.

```
sns.countplot(x='ca',hue='target',data=df)
plt.show()
```



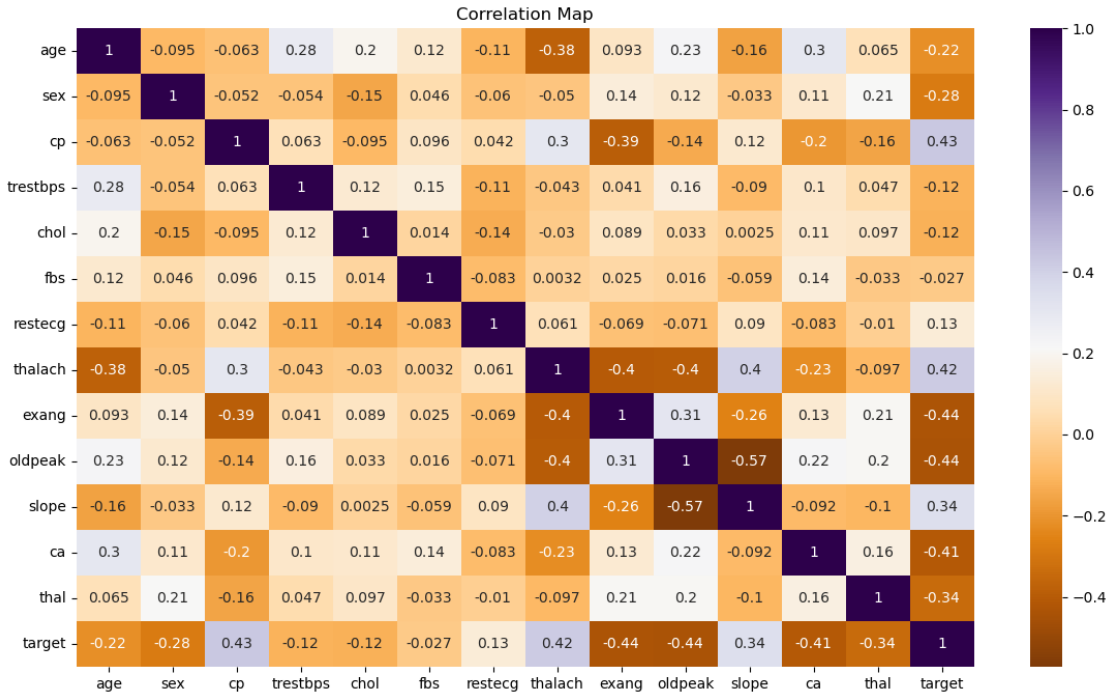
Patients who having Calcium test score zero(Means no evidence of heart disease before) are still got heartattack.

```
sns.countplot(x='thal',hue='target',data=df)
plt.show()
```



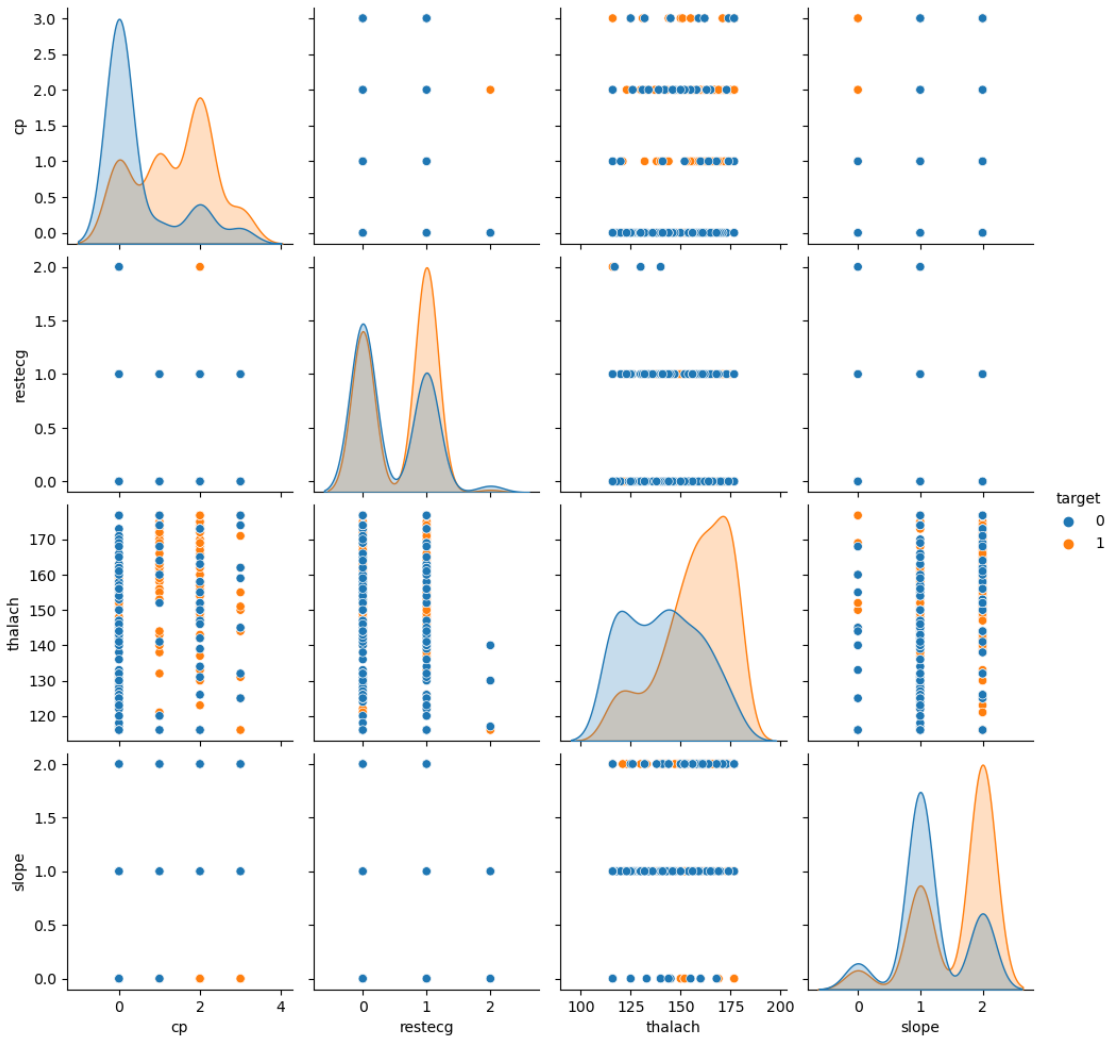
Patients having normal blood flow before they got heartattack.

```
plt.figure(figsize=(14,8))
sns.heatmap(df.corr(),annot=True,fmt='.2g',cmap='PuOr')
plt.title('Correlation Map')
plt.show()
```



From the above heatmap we can observe that the features 'cp', 'thalach', 'slope' are highly correlated to Target.

```
sns.pairplot(df[['cp','restecg','thalach','slope','target']],hue='target')
plt.show()
```



From the above pair plot we can conclude that our dataset is not linearly separable.

Conclusion

1.The majority of the patients are older than 40.

2.In the dataset there are 2 times more males than females.

3.56.67% of the patients have a high risk of heart attack, 43.33% - low risk of a heart attack.

4.Age distribution of patients from the high-risk group has a peak at 57-60 ages.

5.Patients that have normal analysis results (such as electrocardiography or thallium stress test) are less likely to have a heart attack.

6.The major factors influencing heart attacks are: Chest pain, Maximum heart rate achieved, Exercise induced angina, ST depression induced by exercise relative to rest and Number of major vessels

Feature Scaling

```
df.head()
```

```
   age  sex  cp  trestbps   chol  fbs  restecg  thalach  exang  oldpeak  \
0   63    1   3     145.0  233.0    1        0    150.0      0      2.3
1   37    1   2     130.0  250.0    0        1    176.8      0      2.8
2   41    0   1     130.0  204.0    0        0    172.0      0      1.4
3   56    1   1     120.0  236.0    0        1    176.8      0      0.8
4   57    0   0     120.0  308.9    0        1    163.0      1      0.6

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

```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()

df[['trestbps','chol','thalach','oldpeak']] =
scaler.fit_transform(df[['trestbps','chol','thalach','oldpeak']])

df.head()
```

```
   age  sex  cp  trestbps      chol  fbs  restecg   thalach  exang   oldpeak
\
0   63    1   3  0.833333  0.370124    1        0  0.559211      0  0.821429
1   37    1   2  0.476190  0.511203    0        1  1.000000      0  1.000000
2   41    0   1  0.476190  0.129461    0        0  0.921053      0  0.500000
3   56    1   1  0.238095  0.395021    0        1  1.000000      0  0.285714
4   57    0   0  0.238095  1.000000    0        1  0.773026      1  0.214286

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

Data Preparation

```
X = df.iloc[:,:-1]
y = df.iloc[:,-1]

X.shape
```

```
(302, 13)
```

```
y.shape
```

```
(302,)
```

```
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test =
train_test_split(X,y,test_size=0.25,random_state=42)
```

```
X_train.shape,X_test.shape,y_train.shape,y_test.shape
```

```
((226, 13), (76, 13), (226,), (76,))
```

Model Building

Logistic Regression

```
from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
```

```
lr.fit(X_train,y_train)
```

```
LogisticRegression()
```

```
y_pred = lr.predict(X_test)
```

```
y_pred
```

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

```
from sklearn import metrics
```

```
from sklearn.metrics import accuracy_score
```

```
a_s = accuracy_score(y_test,y_pred)
print('Accuracy_score: ',a_s)
```

```
Accuracy_score:  0.8421052631578947
```

```
metrics.confusion_matrix(y_test, y_pred)
```

```
array([[29,  6],
       [ 6, 35]], dtype=int64)
```

```
print(metrics.classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.83      0.83      0.83        35
           1       0.85      0.85      0.85        41

    accuracy                           0.84        76
   macro avg       0.84      0.84      0.84        76
```

```
weighted avg       0.84      0.84      0.84        76
```

Random Forest

```
from sklearn.ensemble import RandomForestClassifier
rf = RandomForestClassifier()

rf.fit(X_train,y_train)

RandomForestClassifier()

y_prediction = rf.predict(X_test)

acc_sco = accuracy_score(y_test,y_prediction)
print('R_F Accuracy_Score: ',acc_sco)

R_F Accuracy_Score:  0.8421052631578947

print(metrics.classification_report(y_test, y_prediction))

              precision    recall  f1-score   support

           0       0.83      0.83      0.83        35
           1       0.85      0.85      0.85        41

    accuracy                           0.84        76
   macro avg       0.84      0.84      0.84        76
weighted avg       0.84      0.84      0.84        76
```

Hyperparameter Tunning

```
rf_classifier =
RandomForestClassifier(n_estimators=200,max_features=5,criterion='gini')
rf_classifier.fit(X_train, y_train)
y_predic = rf_classifier.predict(X_test)
print(metrics.classification_report(y_test, y_predic))

              precision    recall  f1-score   support

           0       0.85      0.83      0.84        35
           1       0.86      0.88      0.87        41

    accuracy                           0.86        76
   macro avg       0.86      0.85      0.85        76
weighted avg       0.86      0.86      0.86        76
```

```
from sklearn.model_selection import GridSearchCV

params = {'criterion' : ['gini', 'entropy'],
          'n_estimators' : [150,200],
          'max_features' : [5,10]
         }

grid_search = GridSearchCV(rf_classifier, param_grid= params)

grid_search.fit(X_train,y_train)

GridSearchCV(estimator=RandomForestClassifier(max_features=5,
n_estimators=200),
             param_grid={'criterion': ['gini', 'entropy'],
                         'max_features': [5, 10], 'n_estimators': [150,
200]})

grid_search.best_params_

{'criterion': 'entropy', 'max_features': 5, 'n_estimators': 150}

best_prediction = grid_search.predict(X_test)

print(metrics.classification_report(y_test,best_prediction))

              precision    recall  f1-score   support

           0       0.83      0.83      0.83        35
           1       0.85      0.85      0.85        41

    accuracy                           0.84        76
   macro avg       0.84      0.84      0.84        76
weighted avg       0.84      0.84      0.84        76
```