In [2]:
```
#Import the libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
print('All library imported')
```

```
All library imported
```

1. Preliminary analysis:

Perform preliminary data inspection and report the findings as to the structure of the data, missing values, duplicates, etc.Based on the findings from the previous question remove duplicates (if any) , treat missing values using an appropriate strategy.

In [5]:
```
#Load the data
data=pd.read_excel('data_hd.xlsx')
```

In [6]:
```
#EDA

data.head()
```

Out[6]:

	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 [7]:
```
data.shape
```

Out[7]:
```
(303, 14)
```

In [8]:
```
data.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]:
```
#Check for null values

data.isnull().sum()
```

Out[11]:
```
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 [12]:
```
data.describe()
```

Out[12]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515	0.528053	149.646865
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.905161
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.500000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.000000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.000000

In [13]:
```
#check for unique values
data.nunique()
```

Out[13]:
```
age          41
sex           2
cp            4
trestbps     49
chol        152
fbs           2
restecg       3
thalach      91
exang         2
oldpeak      40
slope         3
ca            5
thal          4
target        2
dtype: int64
```

In [14]:
```
duplicated_data=data[data.duplicated(keep=False)]
duplicated_data
```

Out[14]:

	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

2. Prepare an informative report about the data explaining the distribution of the disease and the related factors. You could use the below approach to achieve the objective

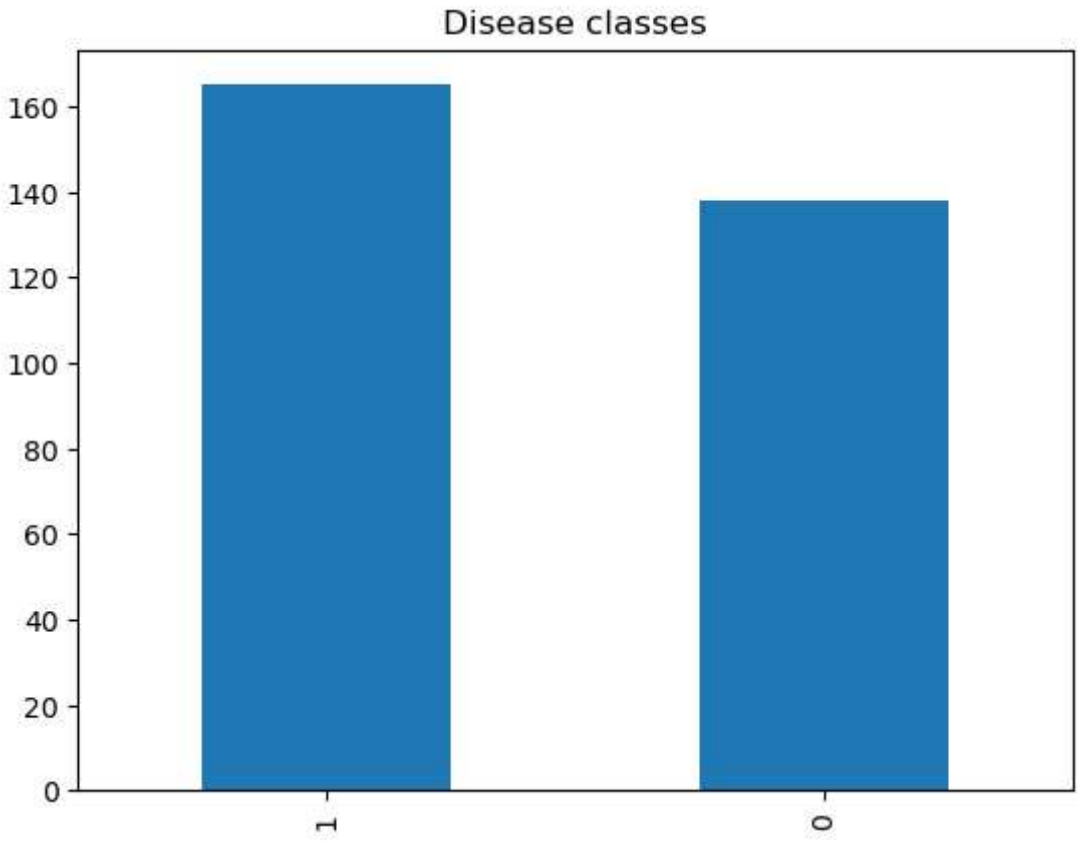
Get a preliminary statistical summary of the data. Explore the measures of central tendencies and the spread of the data overall.Identify the data variables which might be categorical in nature. Describe and explore these variables using appropriate tools e.g. count plot

Study the occurrence of CVD across Age. Study the composition of overall patients w.r.t. Gender. Can we detect a heart attack based on anomalies in the Resting Blood Pressure of the patient? Describe the relationship between Cholesterol levels and our target variable. What can be concluded about the relationship between peak exercising and the occurrence of a heart attack. Is thalassemia a major cause of CVD? How are the other factors determining the occurrence of CVD? Use a pair plot to understand the relationship between all the given variables.

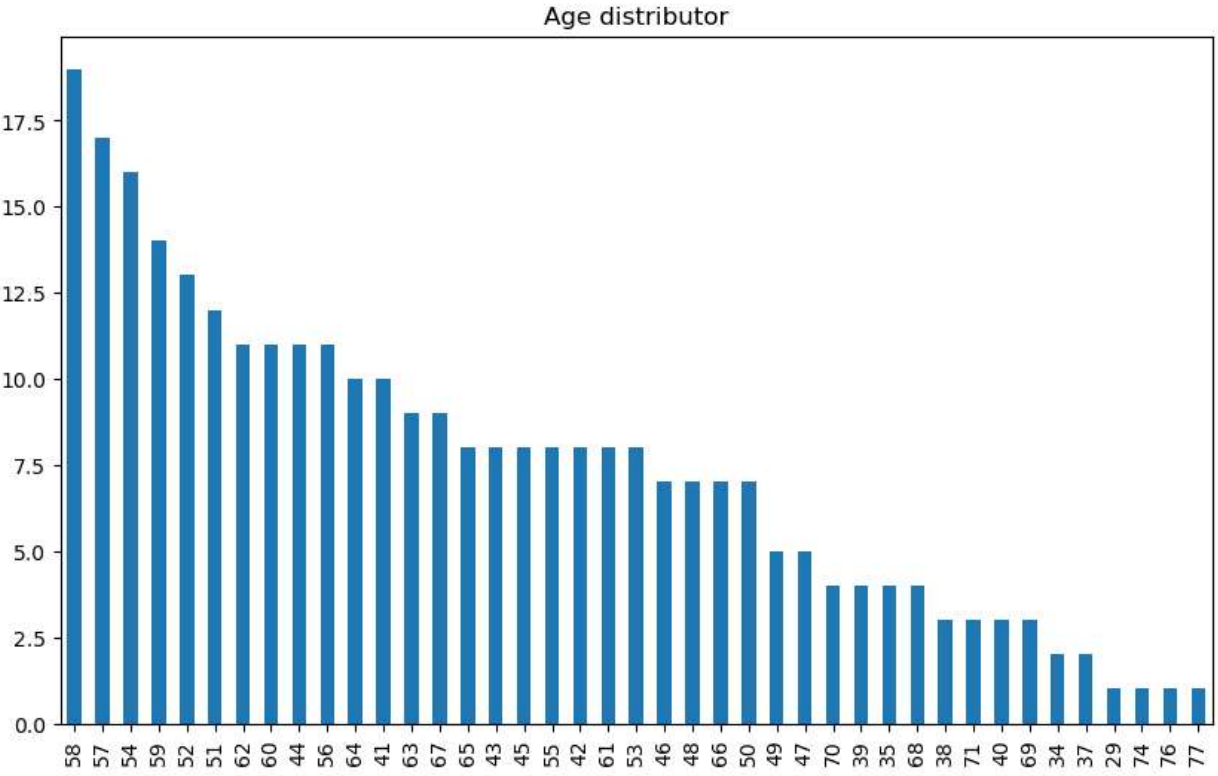
In [ ]:
```
# target column
data['target'].value_counts()
```

In [16]:
```
#EDA on heart diseases

data['target'].value_counts().plot(kind='bar')
plt.title('Disease classes')
```

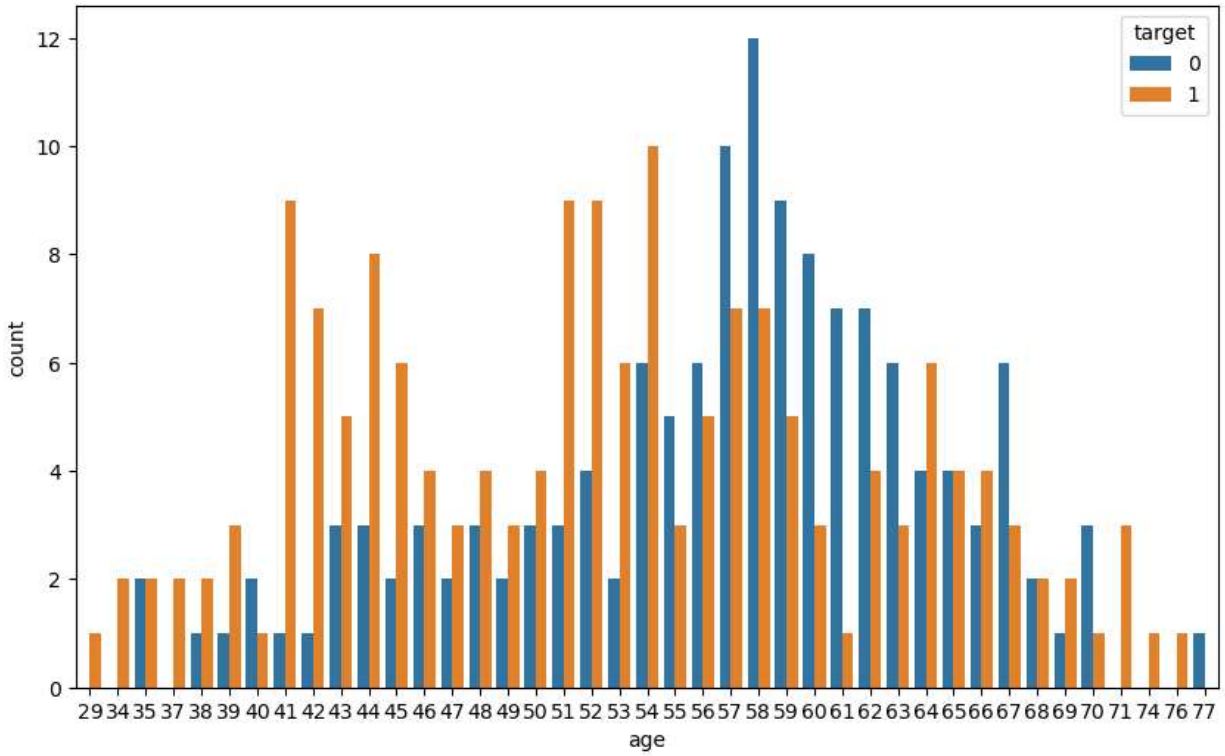
Out[16]:
```
Text(0.5, 1.0, 'Disease classes')
```



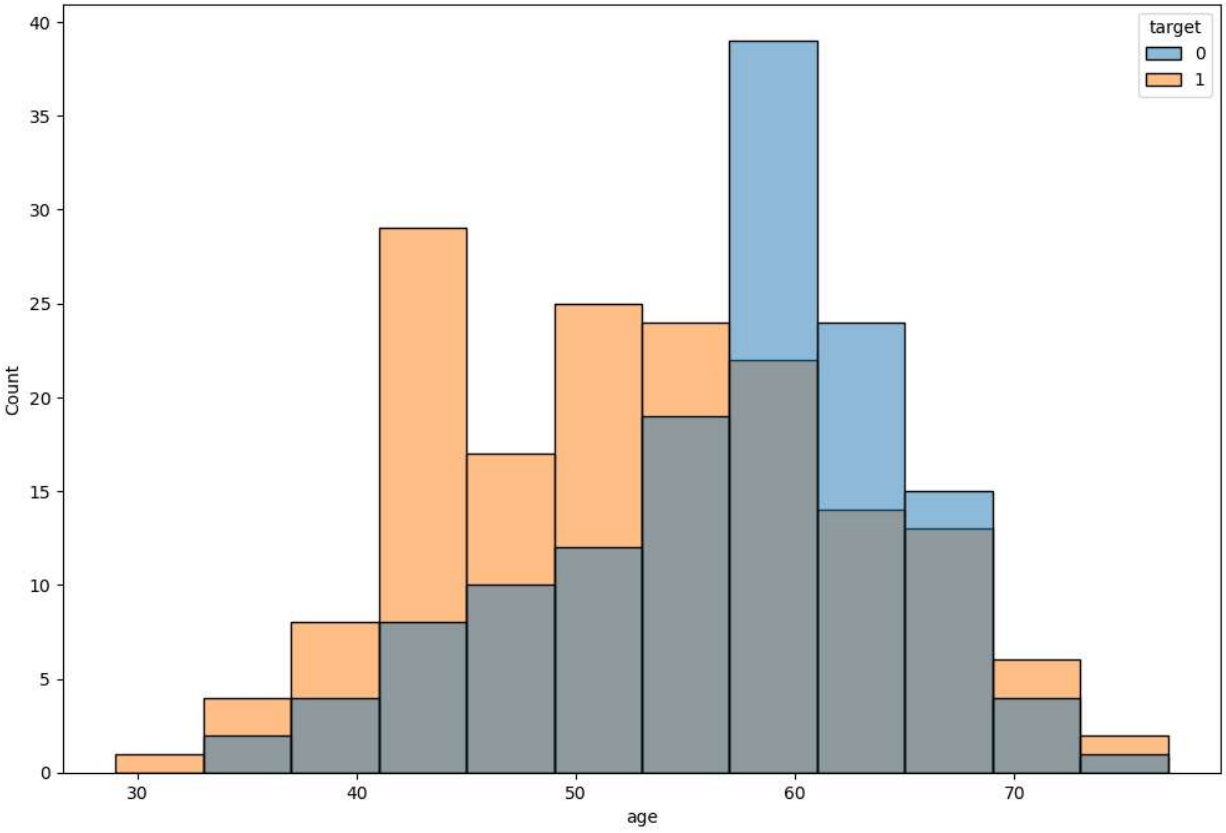
In [13]:
```
#distribution of age
plt.figure(figsize=(10,6))
data['age'].value_counts().plot(kind='bar')
plt.title('Age distributor')
plt.show()
```



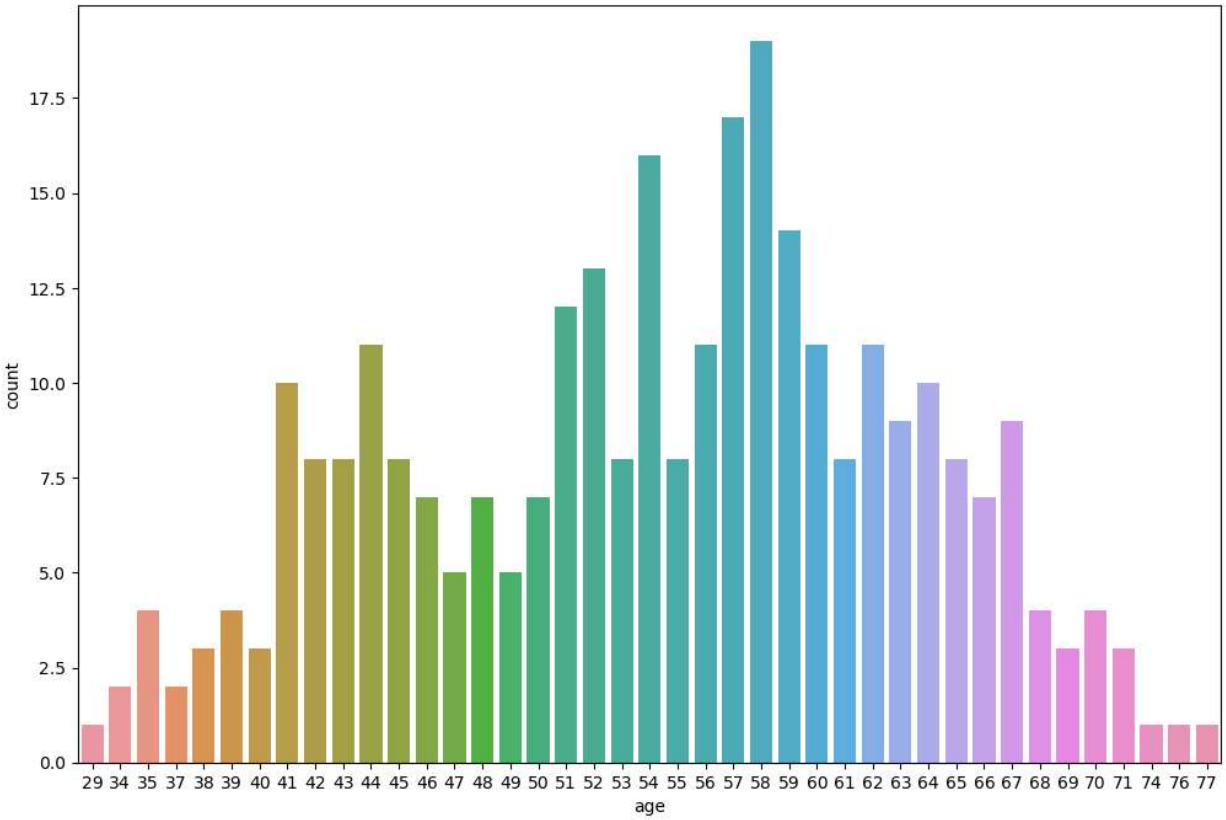
In [12]:
```
plt.figure(figsize=(10,6))
sns.countplot(x=data['age'], hue='target', data=data)
plt.show()
```



In [19]:
```
plt.figure(figsize=(12,8))
sns.histplot(x=data['age'], hue='target', data=data)
plt.show()
```



In [20]:
```
plt.figure(figsize=(12,8))
sns.countplot(x=data['age'], data=data)
plt.show()
```



In [14]:
```
#Identifying the categorical data
data.columns
```

Out[14]:
```
Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

In [15]:
```
print(data['sex'].value_counts())
```

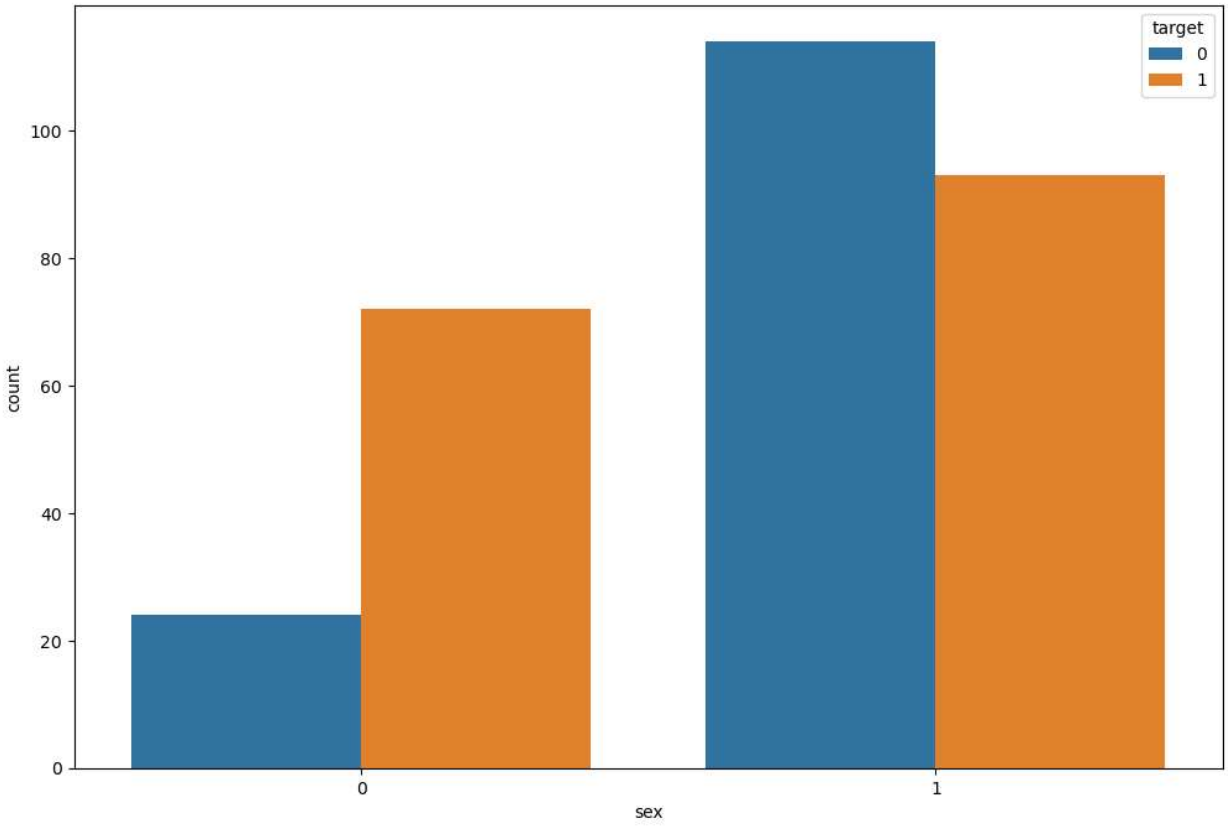
```
1    207
0     96
Name: sex, dtype: int64
```

In [23]:
```
data['sex'].value_counts
```

Out[23]:
```
<bound method IndexOpsMixin.value_counts of 0      1
1      1
2      0
3      1
4      0
      ..
298    0
299    1
300    1
301    1
302    0
Name: sex, Length: 303, dtype: int64>
```

In [24]:
```
plt.figure(figsize=(12,8))
sns.countplot(x=data['sex'], hue='target', data=data)
```

```
plt.show()
```



In [25]:
```
data.columns
```

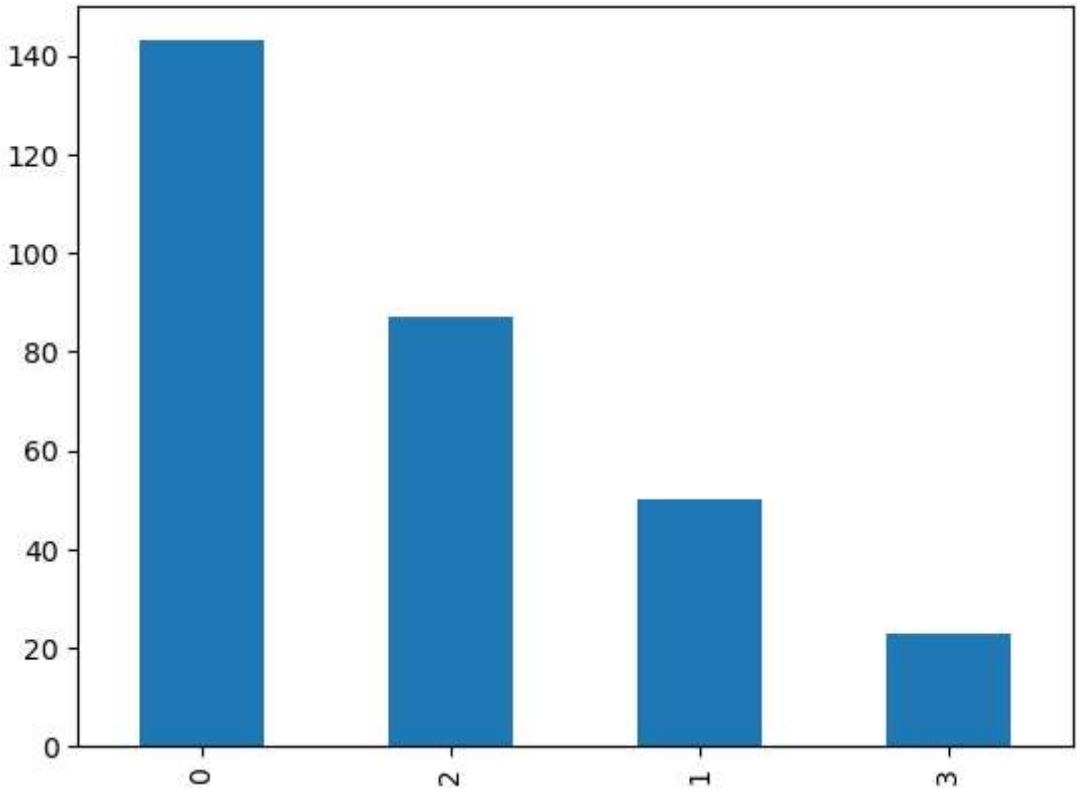
Out[25]:
```
Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

In [26]:
```
data['cp'].value_counts()
```

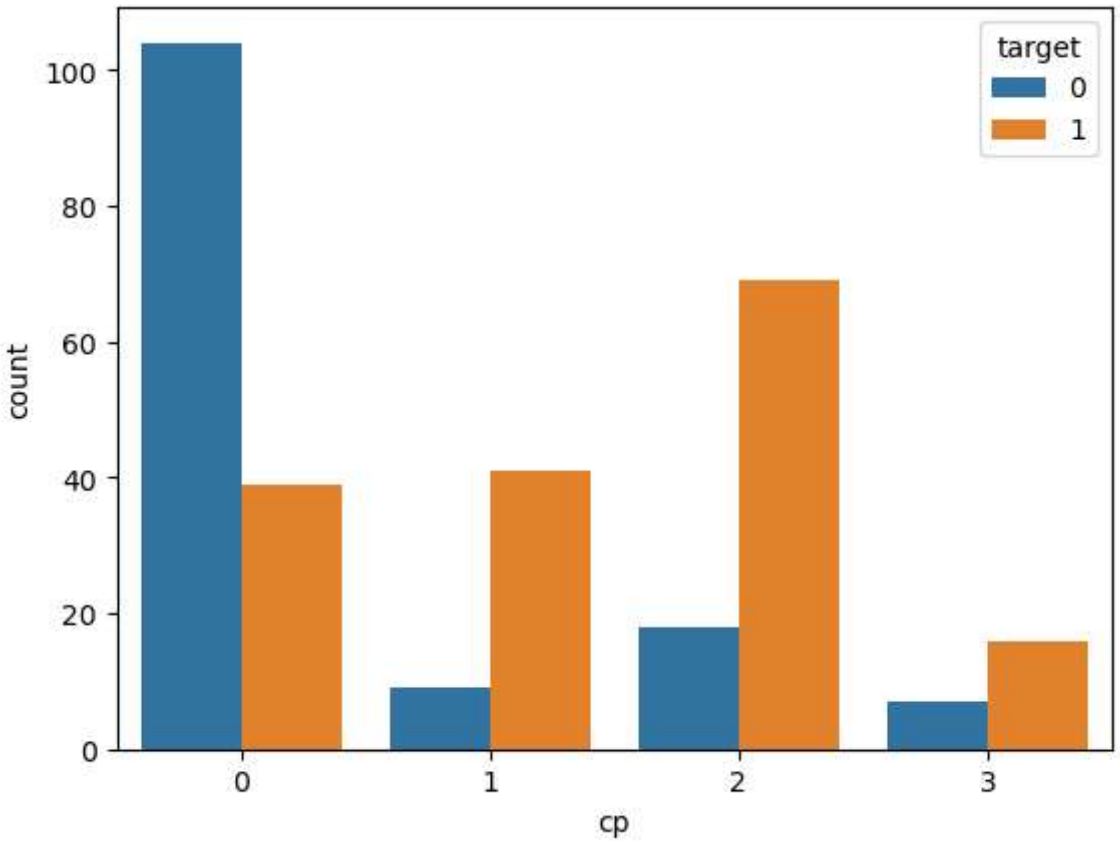
Out[26]:
```
0    143
2     87
1     50
3     23
Name: cp, dtype: int64
```

In [27]:
```
data['cp'].value_counts().plot(kind='bar')
```

Out[27]:
```
<Axes: >
```

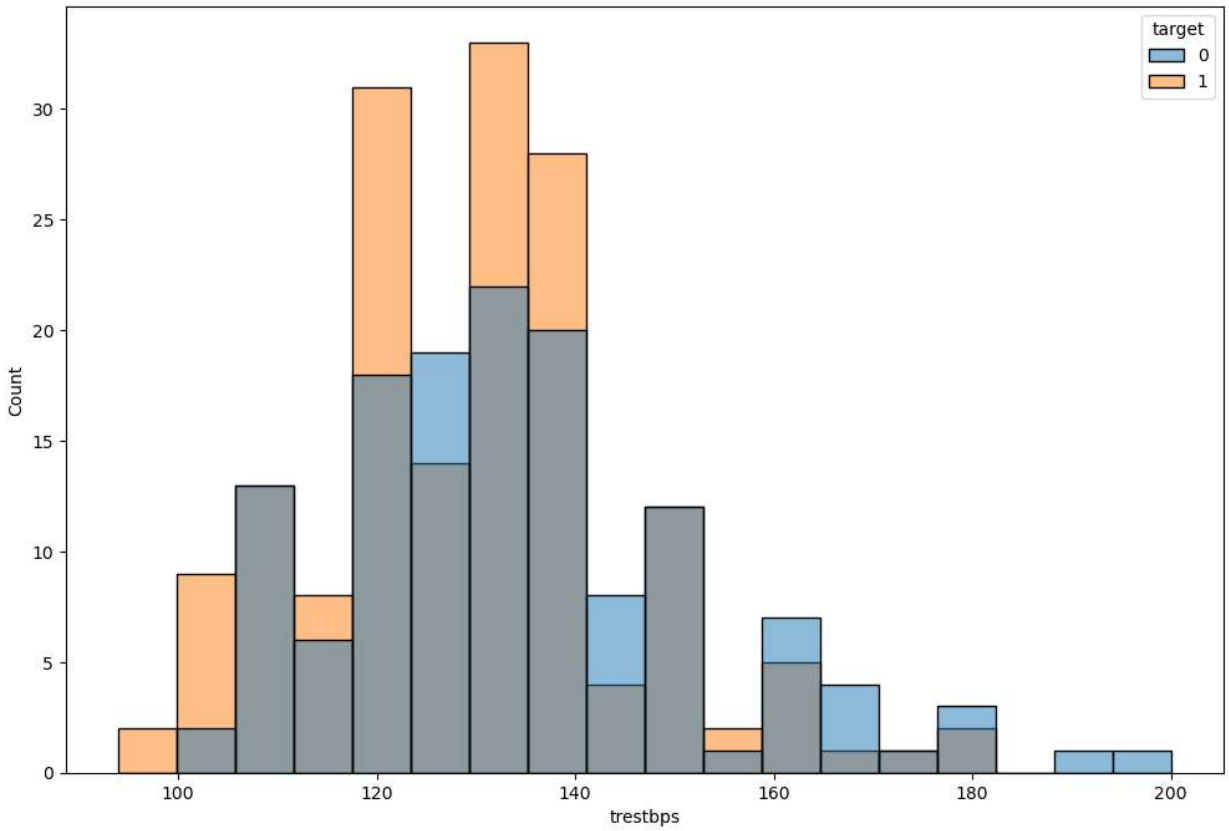


In [28]:
```
#type 2 has the highest patient of heart disease
sns.countplot(x=data['cp'], hue='target', data=data)
plt.show()
```

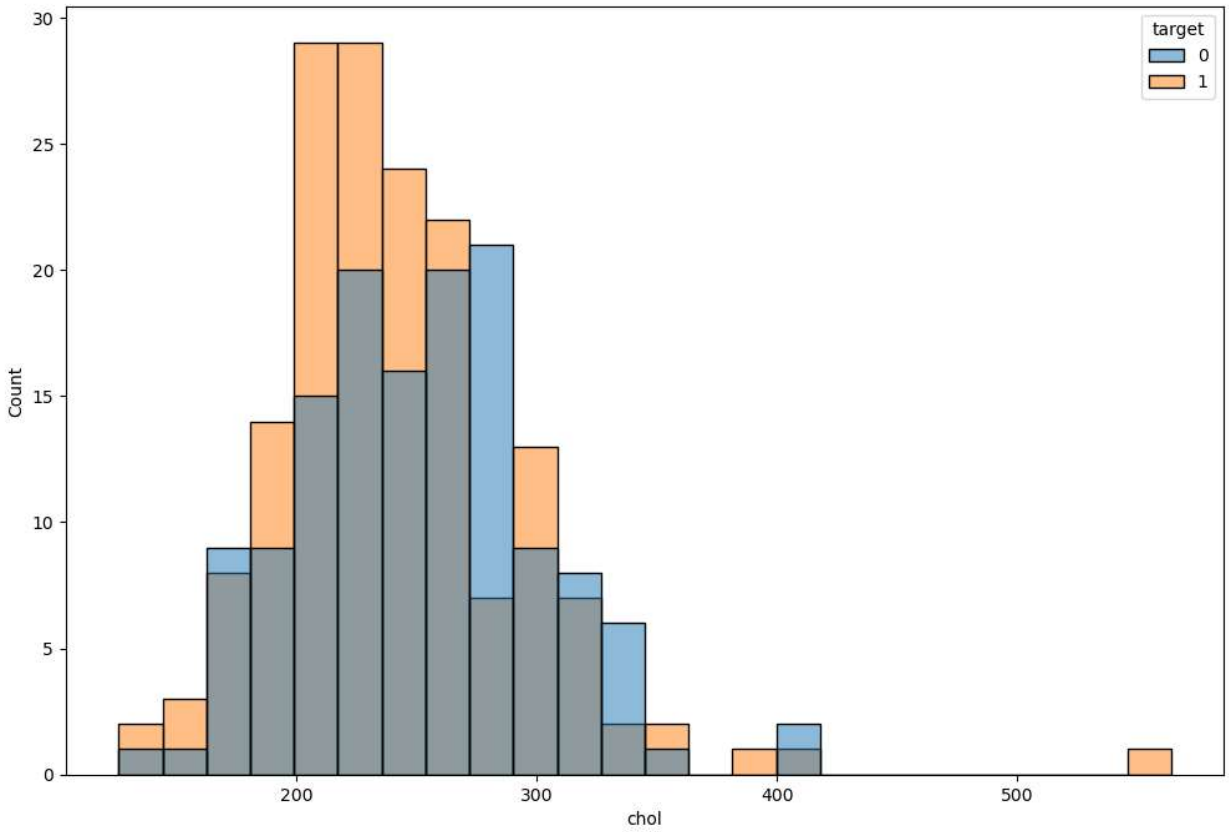


In [17]:
```
#We cannot detect heart attack based on anomalies in the Resting Blood Pressure
plt.figure(figsize=(12,8))
```

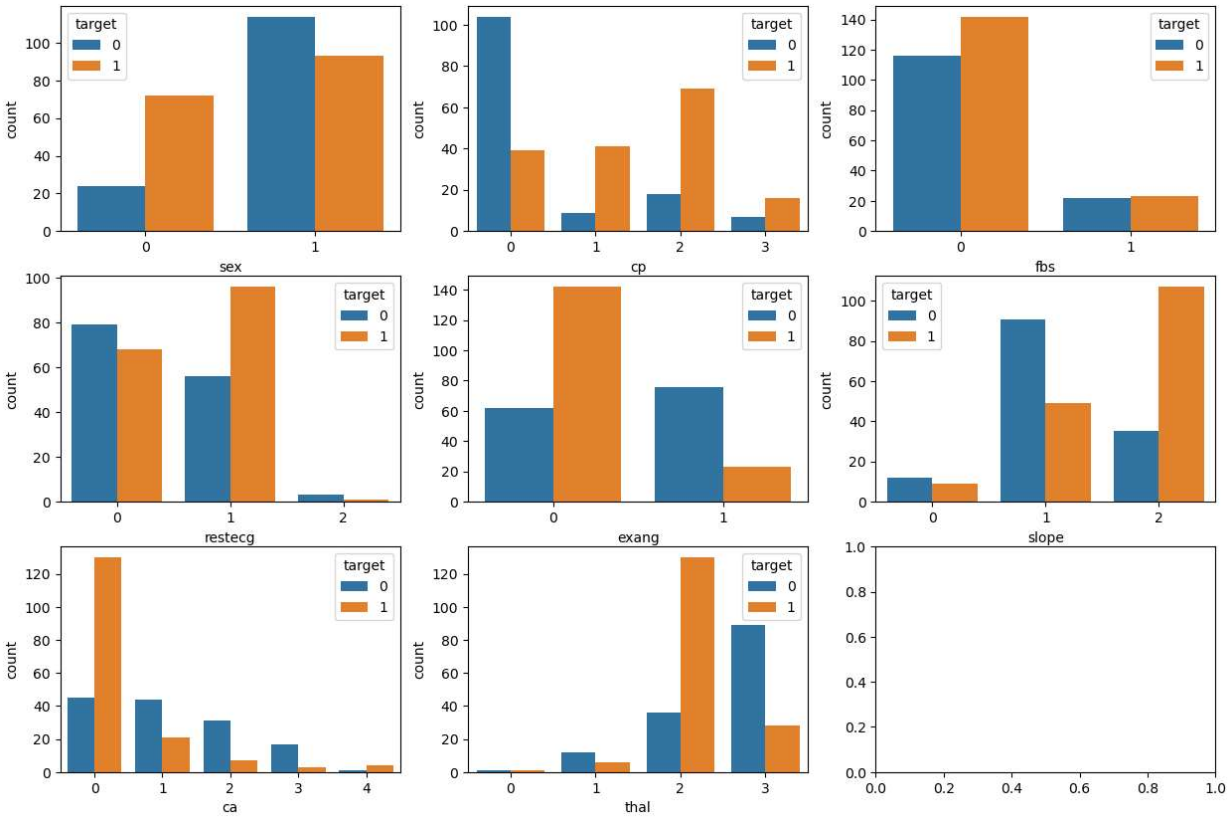
```
sns.histplot(x=data['trestbps'], hue='target', data=data)
plt.show()
```



In [18]:
```
#Relationship between Cholesterol levels and our target variable
plt.figure(figsize=(12,8))
sns.histplot(x=data['chol'], hue='target', data=data)
plt.show()

#Maximum people within 200 to 280 cholestrol level have heart disease
```

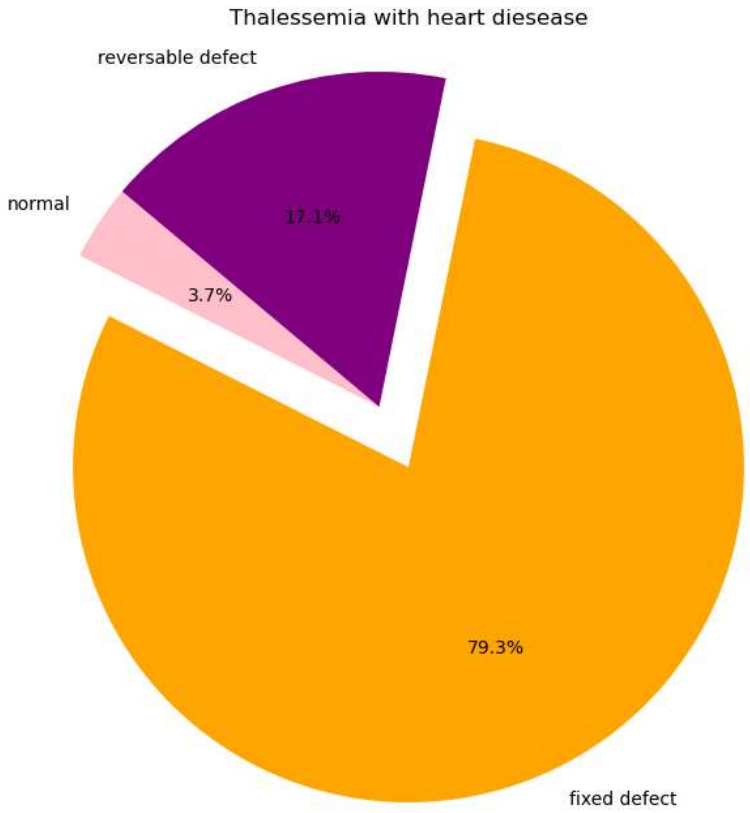


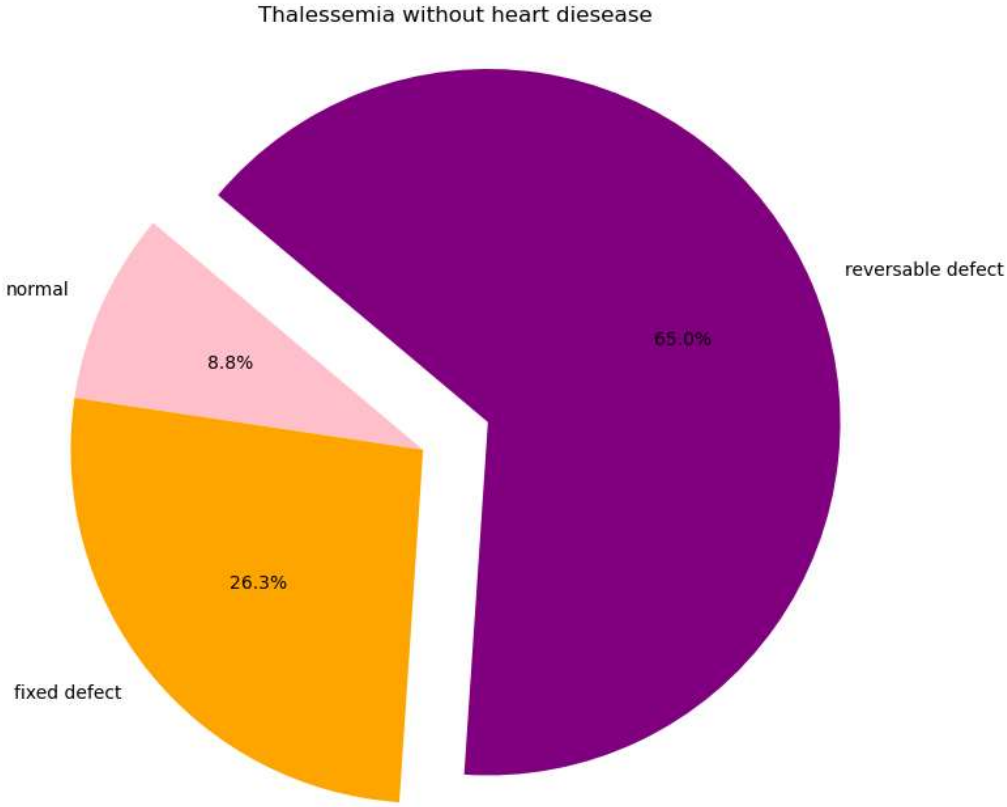
In [30]:
```
#Create a subplot
fig,axes=plt.subplots(nrows=3,ncols=3, figsize=(15,10))
cat_features=['sex','cp','fbs','restecg','exang','slope','ca','thal','target']
for idx, feature in enumerate (cat_features):
    if feature!='target':
        ax=axes[int(idx/3), idx%3]
        sns.countplot(x=feature, hue='target',ax=ax, data=data)
```



In [20]:

```
#Create a pie chart- have heart disease
plt.figure(figsize=(12,8))
labels= 'normal','fixed defect','reversable defect'
sizes=[6,130,28]
colors=['pink','orange','purple']
explode=[0,0.2,0]
plt.pie(sizes,labels=labels, autopct='%0.1f%%',colors=colors,startangle=140, explode=e
plt.axis('equal')
plt.title('Thalessemia with heart diesease')
plt.show()


#Create a pie chart- have no heart disease
plt.figure(figsize=(12,8))
labels= 'normal','fixed defect','reversable defect'
sizes=[12,36,89]
colors=['pink','orange','purple']
explode=[0,0,0.2]
plt.pie(sizes,labels=labels, autopct='%0.1f%%',colors=colors,startangle=140, explode=e
plt.axis('equal')
plt.title('Thalessemia without heart diesease')
plt.show()

#Thalessaemia can be one of cause of heart disease along with other factors but not th
```





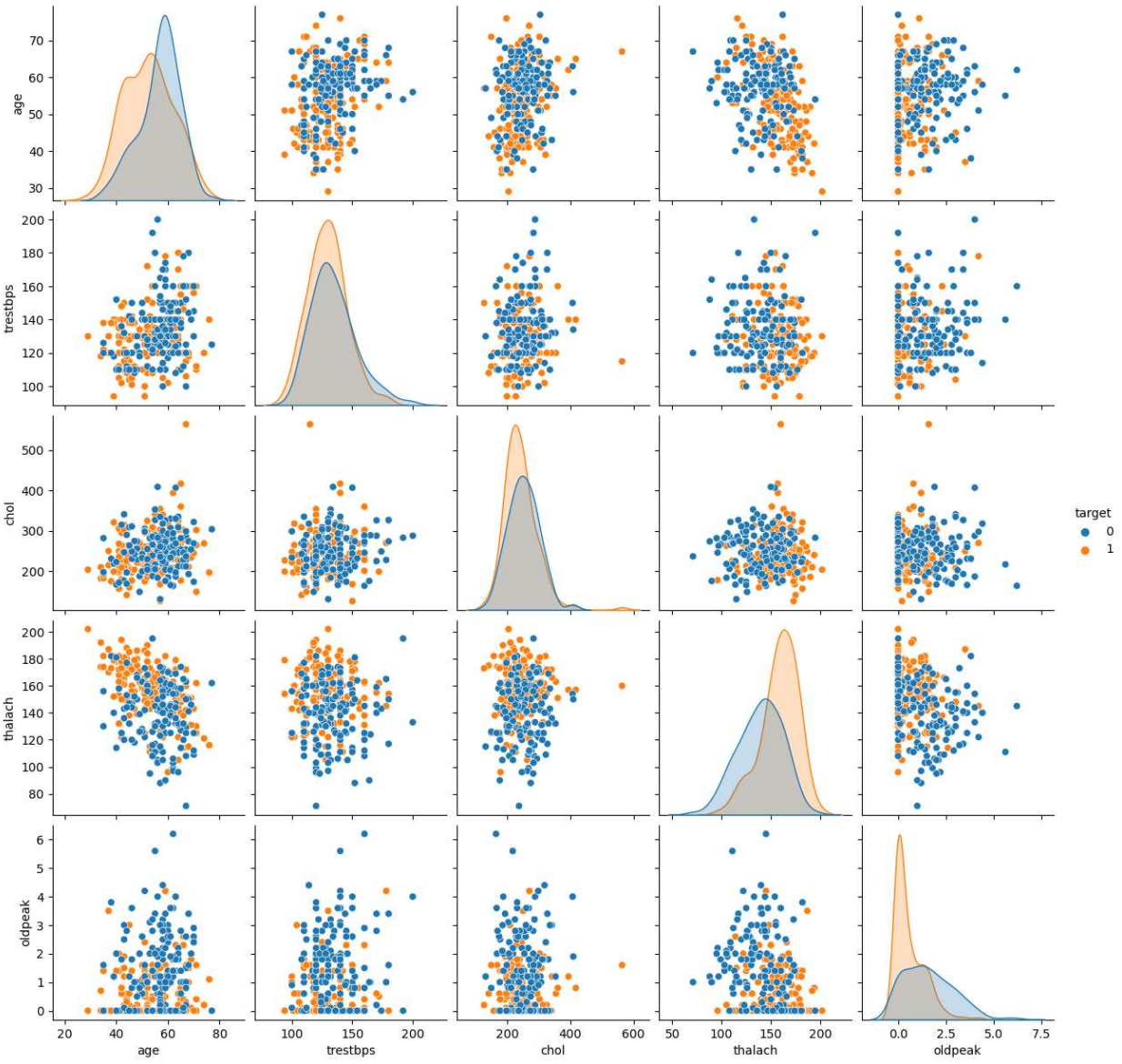
In [32]:
```
#distribution of continuous variables- Multivariate analysis
data.columns
```

Out[32]:
```
Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

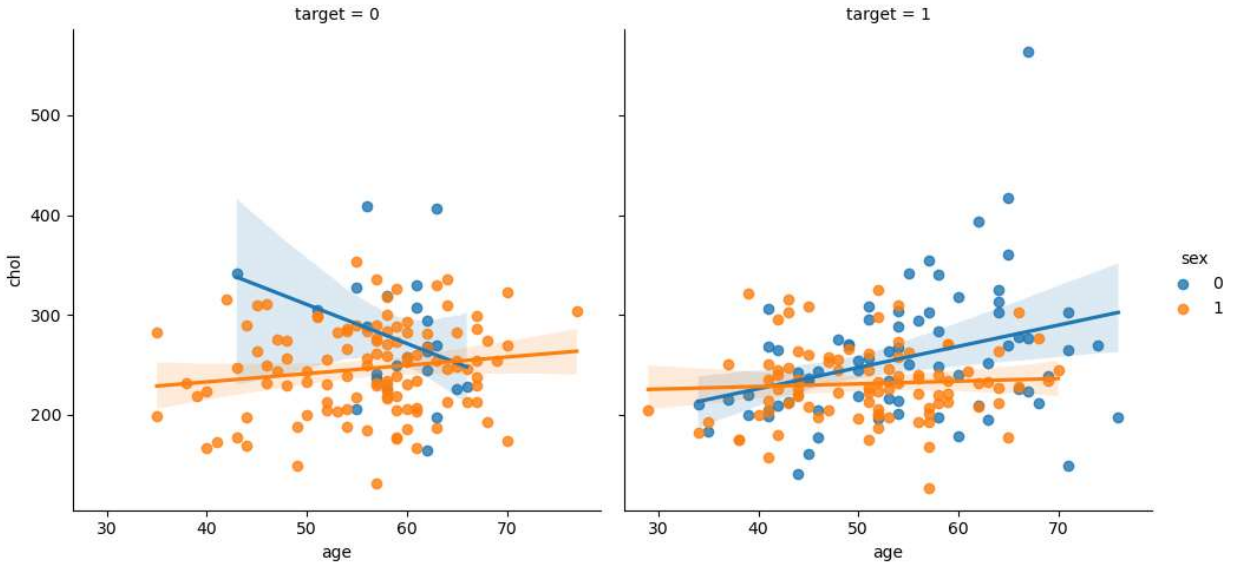
In [33]:
```
data.nunique()
```

Out[33]:
```
age          41
sex           2
cp            4
trestbps     49
chol        152
fbs           2
restecg       3
thalach      91
exang         2
oldpeak      40
slope         3
ca            5
thal          4
target        2
dtype: int64
```

In [34]:
```
num_var=['age', 'trestbps', 'chol', 'thalach','oldpeak']
sns.pairplot(data[num_var+['target']],hue='target')
plt.show()
```



In [35]:
```
#create a plot to understand relationship between age and cholestrol, acc to target  #
sns.lmplot(x='age',y='chol', hue='sex', col='target',data=data)
plt.show() #CHOLESTROL NOT A MAJOR FACTOR TO DECTECT HEART DIEASE
```



In [36]:
```
data.corr()
```

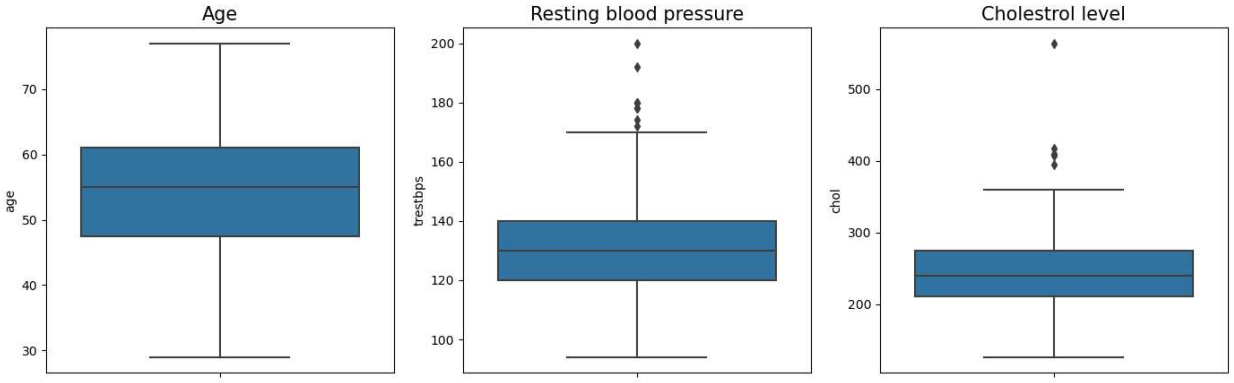
Out[36]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exa
age	1.000000	-0.098447	-0.068653	0.279351	0.213678	0.121308	-0.116211	-0.398522	0.0968
sex	-0.098447	1.000000	-0.049353	-0.056769	-0.197912	0.045032	-0.058196	-0.044020	0.1416
cp	-0.068653	-0.049353	1.000000	0.047608	-0.076904	0.094444	0.044421	0.295762	-0.3942
trestbps	0.279351	-0.056769	0.047608	1.000000	0.123174	0.177531	-0.114103	-0.046698	0.0676
chol	0.213678	-0.197912	-0.076904	0.123174	1.000000	0.013294	-0.151040	-0.009940	0.0670
fbs	0.121308	0.045032	0.094444	0.177531	0.013294	1.000000	-0.084189	-0.008567	0.0256
restecg	-0.116211	-0.058196	0.044421	-0.114103	-0.151040	-0.084189	1.000000	0.044123	-0.0707
thalach	-0.398522	-0.044020	0.295762	-0.046698	-0.009940	-0.008567	0.044123	1.000000	-0.3788
exang	0.096801	0.141664	-0.394280	0.067616	0.067023	0.025665	-0.070733	-0.378812	1.0000
oldpeak	0.210013	0.096093	-0.149230	0.193216	0.053952	0.005747	-0.058770	-0.344187	0.2882
slope	-0.168814	-0.030711	0.119717	-0.121475	-0.004038	-0.059894	0.093045	0.386784	-0.2577
ca	0.276326	0.118261	-0.181053	0.101389	0.070511	0.137979	-0.072042	-0.213177	0.1157
thal	0.068001	0.210041	-0.161736	0.062210	0.098803	-0.032019	-0.011981	-0.096439	0.2067
target	-0.225439	-0.280937	0.433798	-0.144931	-0.085239	-0.028046	0.137230	0.421741	-0.4367

In [37]:
```
plt.figure(figsize=(12,8))
sns.heatmap(data.corr(),annot=True)
```

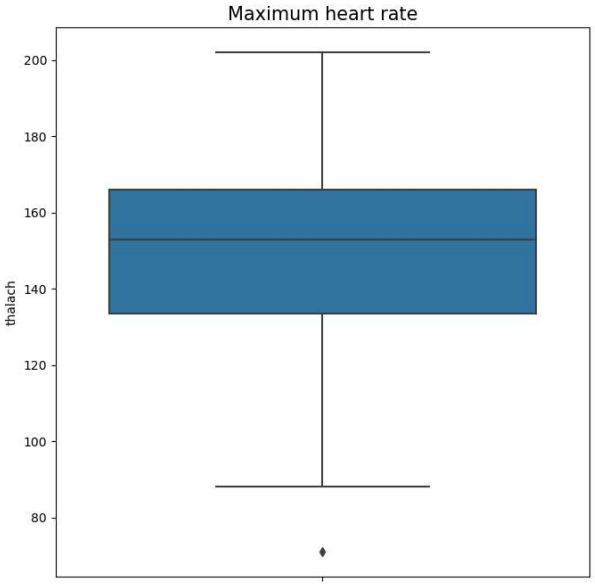
Out[37]:
```
<Axes: >
```

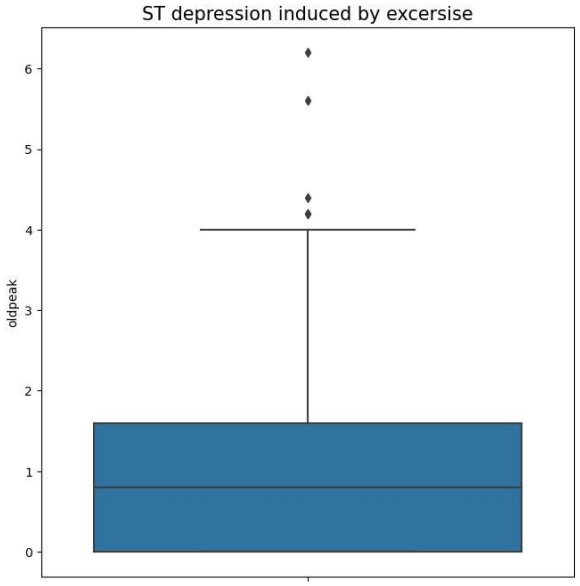
In [22]:
```
plt.figure(figsize=(17,5))
plt.subplot(1,3,1)
sns.boxplot(y= data['age'])
plt.title('Age', fontsize=15)

plt.subplot(1,3,2)
sns.boxplot(y= data['trestbps'])
plt.title('Resting blood pressure', fontsize=15)

plt.subplot(1,3,3)
sns.boxplot(y= data['chol'])
plt.title('Cholestrol level', fontsize=15)

plt.show()
```



In [23]:
```
plt.figure(figsize=(17,8))
plt.subplot(1,2,1)
sns.boxplot(y= data['thalach'])
plt.title('Maximum heart rate', fontsize=15)
```

```
plt.subplot(1,2,2)
sns.boxplot(y= data['oldpeak'])
plt.title('ST depression induced by excersise', fontsize=15)

plt.show()
```





In [37]:
```
#Separate the Independent & Dependent Variable
#Create train set & test set
#scaling
#applying classification algorithm
```

In [24]:
```
data.head()
```

Out[24]:

	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 [38]:
```
#Separate the Independent & Dependent Variable
X=data.drop(['target'], axis=1)
Y=data['target']
```

In [39]:
```
X
```

Out[39]:

	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
...	...	...	...	...	...	...	...	...	...	...	...	...	...
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2

303 rows × 13 columns

In [40]:
```
Y
```

Out[40]:
```
0      1
1      1
2      1
3      1
4      1
      ..
298    0
299    0
300    0
301    0
302    0
Name: target, Length: 303, dtype: int64
```

In [42]:
```
#Create train set & test set
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test=train_test_split(X,Y,test_size=0.3,random_state=42)
```

In [43]:
```
X_train.shape
```

Out[43]:
```
(212, 13)
```

In [44]:
```
X_test.shape
```

Out[44]:
```
(91, 13)
```

In [45]:
```
X_train
```

Out[45]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
124	39	0	2	94	199	0	1	179	0	0.0	2	0	2
72	29	1	1	130	204	0	0	202	0	0.0	2	0	2
15	50	0	2	120	219	0	1	158	0	1.6	1	0	2
10	54	1	0	140	239	0	1	160	0	1.2	2	0	2
163	38	1	2	138	175	0	1	173	0	0.0	2	4	2
...	...	...	...	...	...	...	...	...	...	...	...	...	...
188	50	1	2	140	233	0	1	163	0	0.6	1	1	3
71	51	1	2	94	227	0	1	154	1	0.0	2	1	3
106	69	1	3	160	234	1	0	131	0	0.1	1	1	2
270	46	1	0	120	249	0	0	144	0	0.8	2	0	3
102	63	0	1	140	195	0	1	179	0	0.0	2	2	2

212 rows × 13 columns

In [46]:
```
#normalise the data
from sklearn.preprocessing import StandardScaler
sc=StandardScaler()
```

In [47]:
```
X_train=sc.fit_transform(X_train)
X_test=sc.transform(X_test)
```

In [48]:
```
X_train
```

Out[48]:
```
array([[-1.67339636, -1.39443338,  0.95280942, ...,  0.955317  ,
        -0.67629057, -0.54888242],
       [-2.76362385,  0.71713717, -0.01367669, ...,  0.955317  ,
        -0.67629057, -0.54888242],
       [-0.47414611, -1.39443338,  0.95280942, ..., -0.67796691,
        -0.67629057, -0.54888242],
       ...,
       [ 1.59728613,  0.71713717,  1.91929553, ..., -0.67796691,
         0.37792709, -0.54888242],
       [-0.91023711,  0.71713717, -0.9801628 , ...,  0.955317  ,
        -0.67629057,  1.13753893],
       [ 0.94314964, -1.39443338, -0.01367669, ...,  0.955317  ,
         1.43214475, -0.54888242]])
```

In [49]:
```
#Create the model
from sklearn.linear_model import LogisticRegression
log_reg=LogisticRegression()
```

In [50]:
```
log_reg.fit(X_train,y_train)
```

Out[50]:
```
▾ LogisticRegression
LogisticRegression()
```

In [51]:
```
#Predicted Y

y_pred=log_reg.predict(X_test)
```

In [52]:
```
y_pred
```

Out[52]:
```
array([0, 1, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0,
       0, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 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, 0, 0, 1, 0, 1, 1, 0,
       1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 0, 0, 0, 1, 1, 1, 0, 0, 1,
       1, 0, 1], dtype=int64)
```

In [53]:
```
y_test #actual
```

Out[53]:
```
179    0
228    0
111    1
246    0
60     1
      ..
250    0
19     1
143    1
79     1
144    1
Name: target, Length: 91, dtype: int64
```

In [54]:
```
y_test.shape
```

Out[54]:
```
(91,)
```

In [55]:
```
y_pred.shape
```

Out[55]:
```
(91,)
```

In [56]:
```
# Evaluate Machine Learning Model
from sklearn.metrics import confusion_matrix
print(confusion_matrix(y_test,y_pred))
```

```
[[32  9]
 [ 8 42]]
```

In [57]:
```
#Accuracy by confusion matrix
(32+42)/(32+42+8+9)
```

Out[57]:
```
0.8131868131868132
```

In [58]:
```
# print accuracy & classification report
from sklearn.metrics import accuracy_score,classification_report
print(accuracy_score(y_test,y_pred))
```

```
0.8131868131868132
```

In [59]:
```
print(classification_report(y_test,y_pred))
```

	precision	recall	f1-score	support
0	0.80	0.78	0.79	41
1	0.82	0.84	0.83	50
accuracy			0.81	91
macro avg	0.81	0.81	0.81	91
weighted avg	0.81	0.81	0.81	91