In [1]:

```
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn import tree
from sklearn.metrics import accuracy_score,confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt
```

In [3]:

```
data = 'heart.csv'
df = pd.read_csv(data)
df.head()
```

Out[3]:

	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 [4]:

```
df[df['chol']>300].shape
```

Out[4]:

```
(43, 14)
```

In [5]:

```
f=df[df['thal']==2]
```

In [6]:

```
f[f['target']==1].shape
```

Out[6]:

```
(130, 14)
```

In [7]:

```
df.shape
```

Out[7]:

```
(303, 14)
```

In [9]:

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

Out[9]:

```
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 [10]:

```
df.dtypes
```

Out[10]:

```
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
```

In [ ]:

```

```

In [12]:

```
df.info()
```

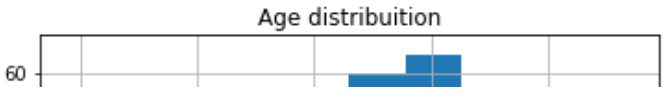
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       303 non-null    int64  
 1   sex       303 non-null    int64  
 2   cp        303 non-null    int64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

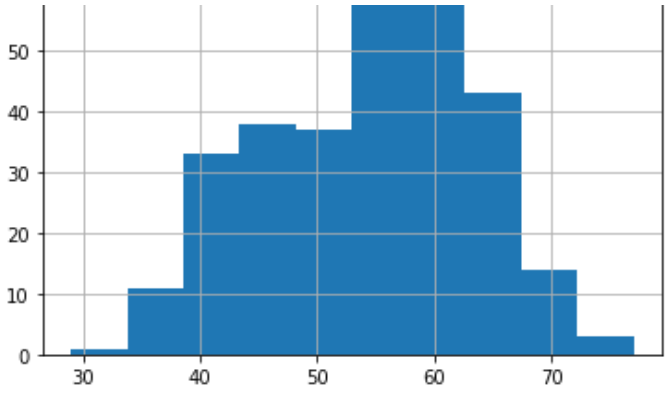
In [11]:

```
df['age'].hist(grid=True, bins=10);
plt.title('Age distribuition')
```

Out[11]:

```
Text(0.5, 1.0, 'Age distribuition')
```



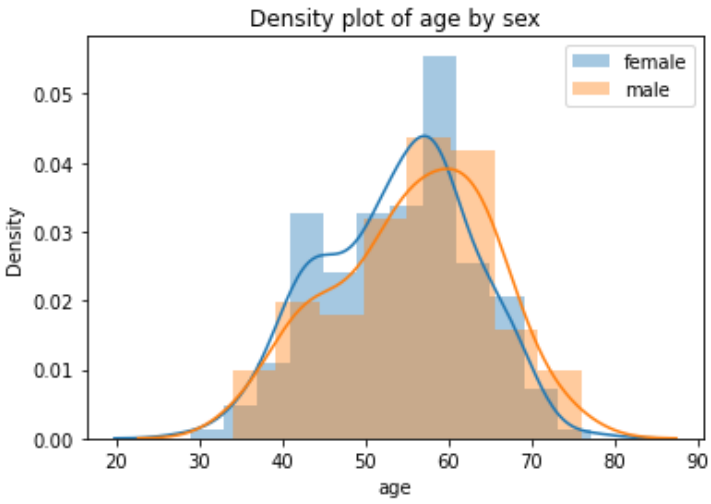


In the above graph, we can analyse the distribution of Age column, and we can say that there are 60+ people who are having age between 57 to 63.

In [16]:

```
sns.distplot(df[df['sex']==1]['age'],  label='female')
sns.distplot(df[df['sex']==0]['age'], label='male')
plt.legend()
plt.title('Density plot of age by sex')
plt.show()
```

```
C:\Users\lenovo\anaconda3\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
C:\Users\lenovo\anaconda3\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



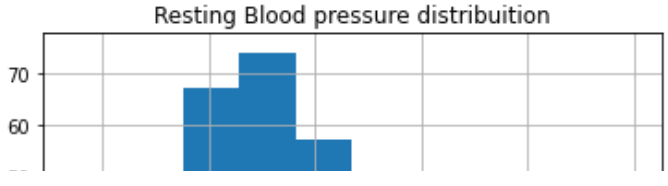
Density graph shows the smoothed distribution of points along the numerical axis. The density peaks where there is the highest concentration of points. In sum, density graphs can be considered smoothed histograms.

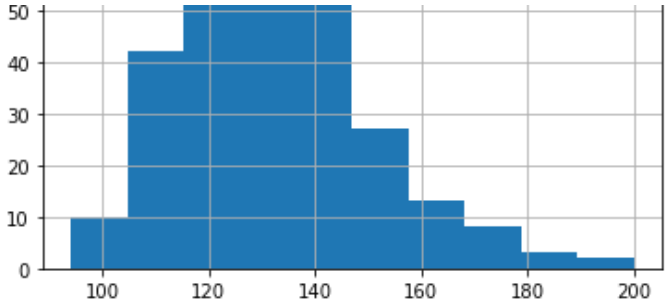
In [18]:

```
df['trestbps'].hist()
plt.title('Resting Blood pressure distribuition')
```

Out[18]:

```
Text(0.5, 1.0, 'Resting Blood pressure distribuition')
```

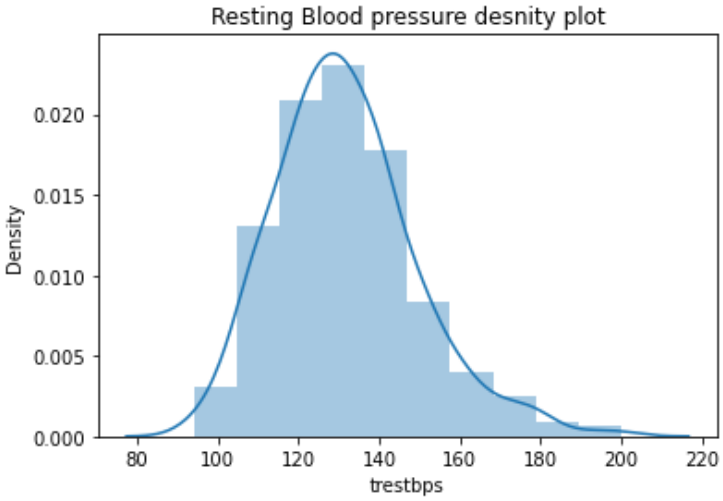




In [19]:

```
sns.distplot(df['trestbps'], bins=10)
plt.title('Resting Blood pressure desnity plot');
```

```
C:\Users\lenovo\anaconda3\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



In the above grapgh, we are having a normal distribution

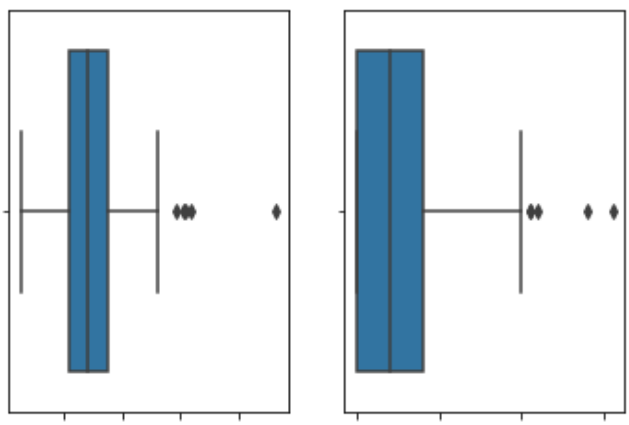
In [20]:

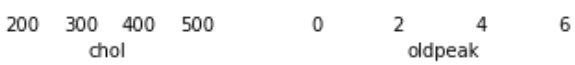
```
fig, axes = plt.subplots(nrows = 1, ncols=2)
sns.boxplot(x='chol', data=df, orient='v', ax=axes[0])
sns.boxplot(x='oldpeak', data=df,  orient='v', ax=axes[1])
```

```
C:\Users\lenovo\anaconda3\lib\site-packages\seaborn\_core.py:1319: UserWarning: Vertical orientation ignored with only `x` specified.
  warnings.warn(single_var_warning.format("Vertical", "x"))
C:\Users\lenovo\anaconda3\lib\site-packages\seaborn\_core.py:1319: UserWarning: Vertical orientation ignored with only `x` specified.
  warnings.warn(single_var_warning.format("Vertical", "x"))
```

Out[20]:

```
<AxesSubplot:xlabel='oldpeak'>
```

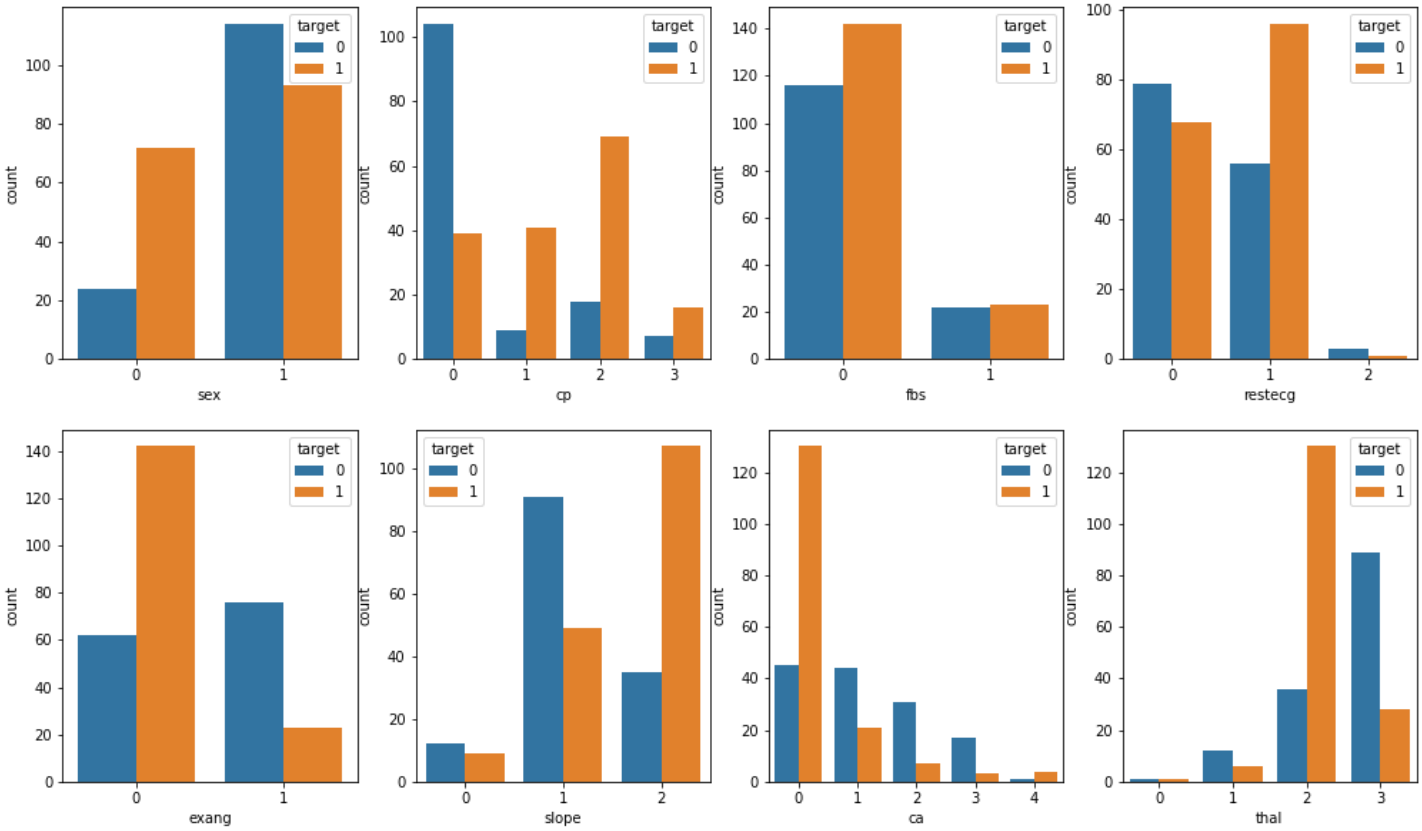




In [26]:

```
fig, axes = plt.subplots(nrows=2, ncols=4, figsize=(17,10))
cat_feat = ['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca', 'thal', 'target']

for idx, feature in enumerate(cat_feat):
    if feature != 'target':
        ax = axes[int(idx/4), idx%4]
        sns.countplot(x=feature, hue='target', data=df,ax=ax)
```



Let's get some insights frm this chart:

Chest pain: the heart desease diagnosis is greater among the patients that feel any chest pain.

Restegc - Eletrocardiagraph results: the rate of heart desease diagnoses higher for patients with a ST-T wabe abnormality .

Slope: The ratio of patients diagnosed with heart desease is higher for slope = 2

Ca: The diagonosed ratio decreases fo ca between 1 and 3.

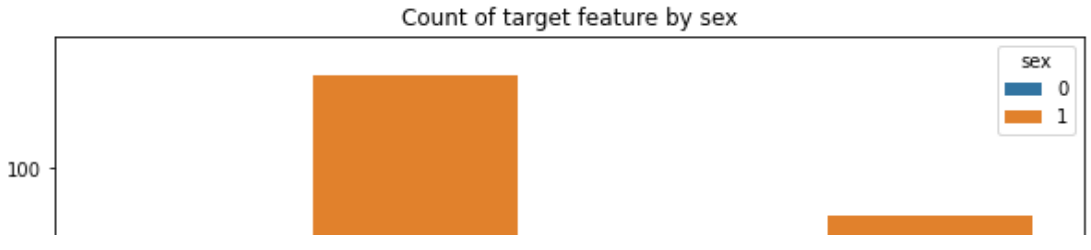
Thal: the diagnosed ratio is higher for thal = 2.

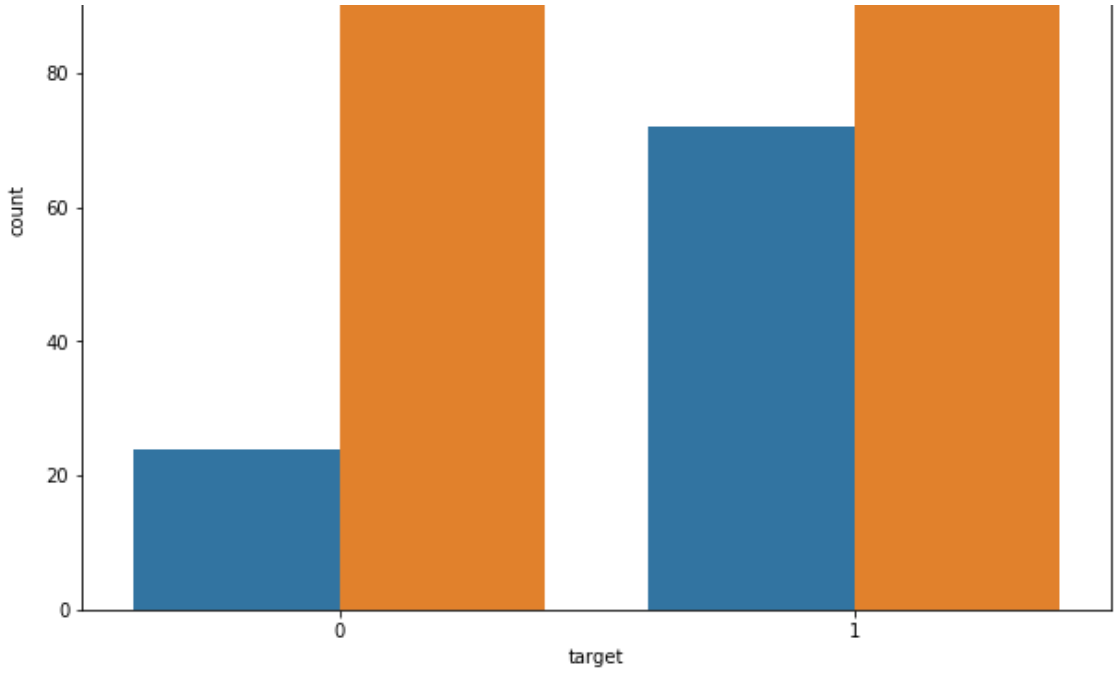
In [27]:

```
plt.rcParams['figure.figsize'] = (10,8)
sns.countplot(x='target', hue='sex', data=df);
plt.title('Count of target feature by sex')
```

Out[27]:

```
Text(0.5, 1.0, 'Count of target feature by sex')
```





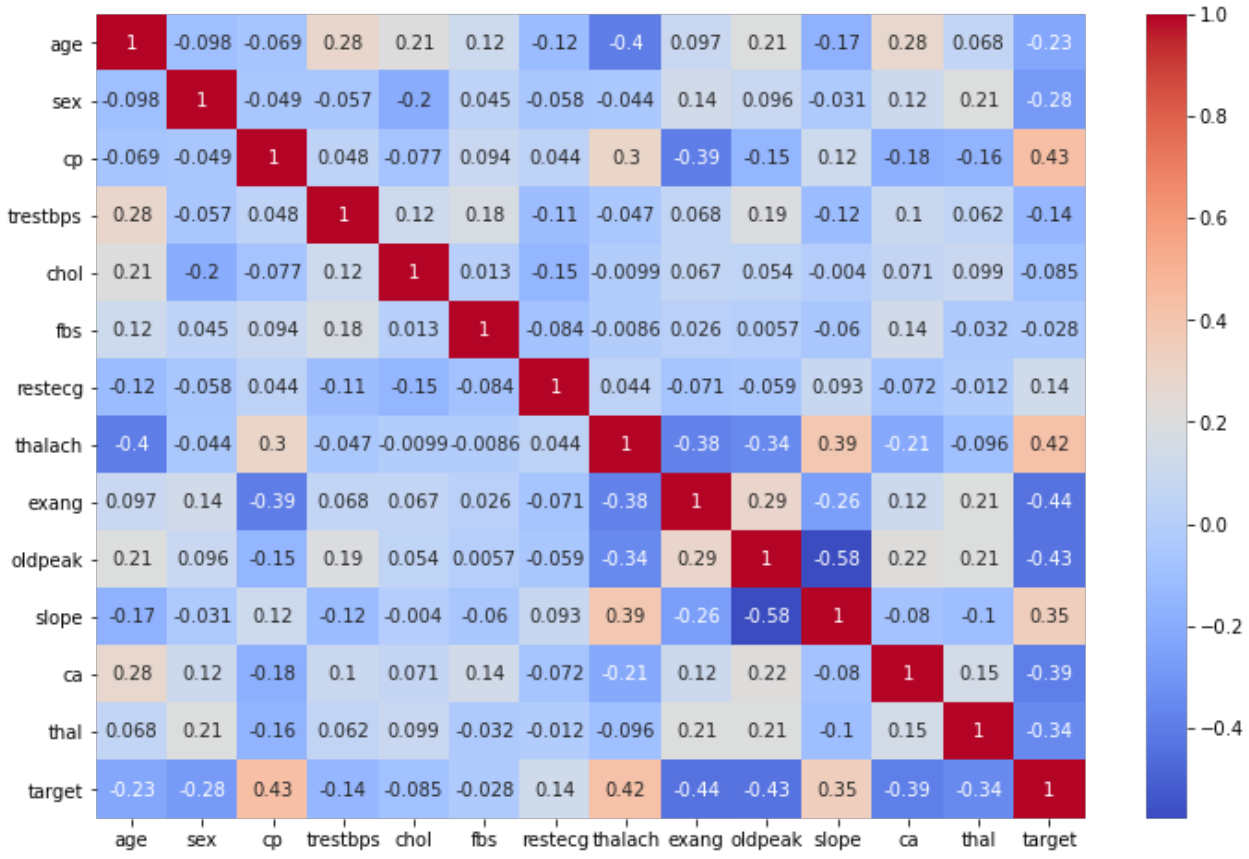
The amount of healthy male people is greater than the amount of unhealthy. For women, the number of unhealthy women is higher.

In [29]:

```
plt.figure(figsize=(12,8))
sns.heatmap(df.corr(), annot=True, cmap='coolwarm')
```

Out[29]:

<AxesSubplot:>



Apparently there are no features with a pretty strong correlation (above |0.7|)

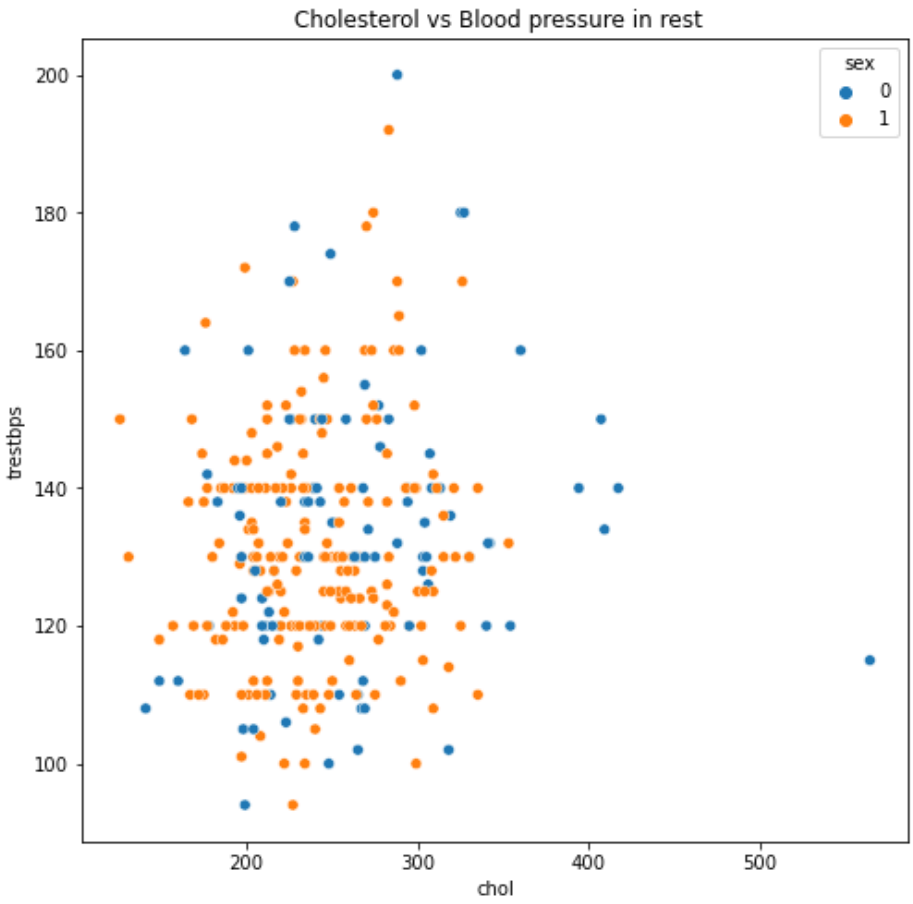
In [30]:

```
plt.rcParams['figure.figsize'] = (8,8)
sns.scatterplot(x='chol', y='trestbps', hue='sex', size=None, data=df)
```

```
plt.title(' Cholesterol vs Blood pressure in rest')
```

Out[30]:

```
Text(0.5, 1.0, ' Cholesterol vs Blood pressure in rest')
```



As can be seen there is a paitient with high cholesterol. But, there's not a specific division between those that feel pain during exercise practice and those of not feel pain. We can use hue to filter by sex. It's also possible to filter using size = 'label_to_filer'.

In [18]:

```
X = df.drop(columns=['target'])#independent variable
y = df['target']#dependnet or target value
print(X.shape)
print(y.shape)
```

```
(303, 13)
(303,)
```

In [20]:

```
x_train,x_test,y_train,y_test = train_test_split(X,y,random_state=0, test_size=0.3)
print(x_train.shape)
print(x_test.shape)
```

```
(212, 13)
(91, 13)
```

In [21]:

```
clf = tree.DecisionTreeClassifier()
clf.fit(x_train,y_train)
y_train_pred = clf.predict(x_train)
y_test_pred = clf.predict(x_test)
```

In [22]:

```
y_train_pred
```

Out[22]:

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

In [23]:

```
y_test_pred
```

Out[23]:

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

In [28]:

```
a=90
print('The value of a is', a)
```

```
The value of a is 90
```

In [29]:

```
print(f'The value of a is {a}')
```

```
The value of a is 90
```

In [1]:

```
# helper function
def plot_confusionmatrix(y_train_pred,y_train,dom):
    print(f'{dom} Confusion matrix')
    cf = confusion_matrix(y_train_pred,y_train)
    sns.heatmap(cf,annot=True,cmap='Blues', fmt='g')#For g and G , the maximum number of
significant digits
    plt.tight_layout()
    plt.show()
```

In [ ]:

```

```

In [31]:

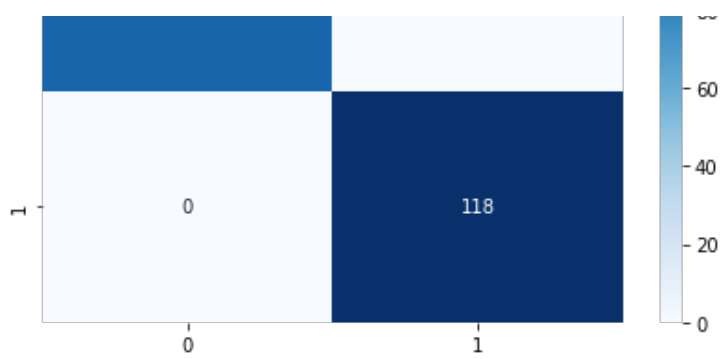
```
print(f'Train score {accuracy_score(y_train_pred,y_train)}')
print(f'Test score {accuracy_score(y_test_pred,y_test)}')
```

```
Train score 1.0
Test score 0.7252747252747253
```

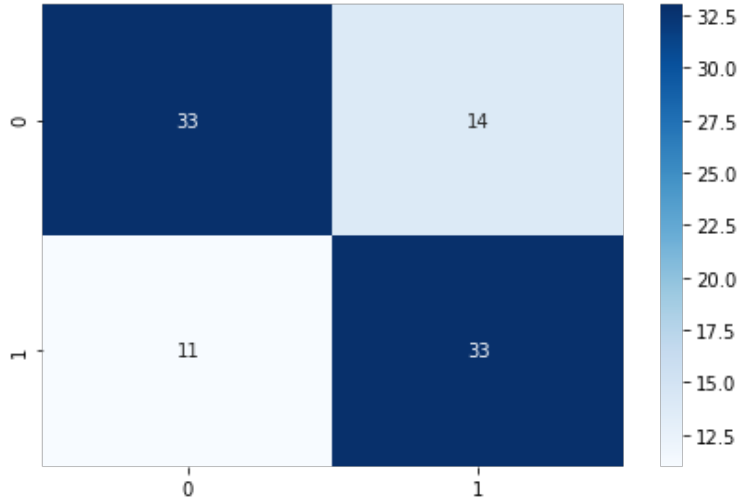
In [32]:

```
plot_confusionmatrix(y_train_pred,y_train,dom='Train')
plot_confusionmatrix(y_test_pred,y_test,dom='Test')
```

```
Train Confusion matrix
```



Test Confusion matrix



In [ ]:

```
#                Actual Values
#predicted        1    0
#              1  TP   FP
#              0  FN   TN
```

In [37]:

```
c_parameter_name = 'max_depth'
c_parameter_values = [1,2,3,4,5,6,7,8,9,10,11,12,13,14,15]
df = pd.DataFrame(columns=[c_parameter_name, 'accuracy'])

for input_parameter in c_parameter_values:
    model = tree.DecisionTreeClassifier(max_depth=input_parameter,splitter='best')
    model.fit(x_train, y_train)
    y_pred = model.predict(x_test)
    acc_score = accuracy_score(y_test,y_pred)*100
    df = df.append({c_parameter_name : input_parameter , 'accuracy' : acc_score}, ignore
_index=True)
print(df)
print("")
```

```
    max_depth   accuracy
0         1.0  76.923077
1         2.0  73.626374
2         3.0  81.318681
3         4.0  76.923077
4         5.0  73.626374
5         6.0  71.428571
6         7.0  74.725275
7         8.0  72.527473
8         9.0  74.725275
9        10.0  71.428571
10       11.0  71.428571
11       12.0  71.428571
12       13.0  74.725275
13       14.0  71.428571
14       15.0  72.527473
```

In [ ]:

```
for input_para in c_para_values:
    model = DecisionTreeClassifier(max_depth=input_para, splitter='best')
    model.fit(X_train, y_train)
    y_pred1 = model.predict(X_test)
    acc_score = accuracy_score(y_test, y_pred)*100
    df = df.append({c_para_name: input_para, 'accuracy':acc_score}, ignore_index=True)
```

In [34]:

```
from sklearn.metrics import classification_report
```

In [35]:

```
print(classification_report(y_test_pred,y_test))
```

```
              precision    recall  f1-score   support

           0       0.75      0.70      0.73        47
           1       0.70      0.75      0.73        44

    accuracy                           0.73        91
   macro avg       0.73      0.73      0.73        91
weighted avg       0.73      0.73      0.73        91
```

In [ ]:

```
#recall->tp / (tp + fn)
#The recall is the measure of our model correctly identifying True Positives.
#Thus, for all the customers who actually have heart disease, recall tells us how many we
correctly identified as a heart patient.

#precision of class 0 = TP of class 0/total number of object
#What is the Precision for our model? Yes, it is 0.843 or, when it predicts that a patien
t has heart disease, it is correct around 84% of the time.
#precision of class 1 = TP of class 1/total number of object

#macro average = (precision of class 0 + precision of class 1)/2

#weighted average is precision of all classes merge together
#weighted average = (TP of class 0 + TP of class 1)/(total number of class 0 + total numb
er of class 1)

#F1-score is a measure of a model's accuracy on a dataset
#a good F1 score means that you have low false positives and low false negatives,
#Accuracy is used when the True Positives and True negatives are more important while
#F1-score is used when the False Negatives and False Positives are crucial.
#Support is the number of actual occurrences of the class in the specified dataset.
```

In [ ]:

```

```