Project_Health Care

December 3, 2022

[1]:
```
import warnings
warnings.filterwarnings('ignore')
```

[2]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
from scipy.stats import chi2_contingency
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import␣
↪accuracy_score,confusion_matrix,classification_report
from sklearn.model_selection import GridSearchCV
import numpy as np
```

[3]:
```
data = pd.read_excel('1645792390_cep1_dataset.xlsx')
data.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
```

1 1. Preliminary analysis:

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

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

[4]:
```python
print('Shape of the data :',data.shape)
```

```
Shape of the data : (303, 14)
```

[5]:
```python
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
```

[6]:
```python
# Find out missing values

data.isna().sum().any()
```

[6]: False

[7]:
```python
# Find out duplicates

data.duplicated().sum()
```

[7]: 1

[8]:
```python
data = data[data.duplicated() == False]
print('Shape of the dataset after removing duplicates :',data.shape)
```

```
Shape of the dataset after removing duplicates : (302, 14)
```

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

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

2.0.1 a. Get a preliminary statistical summary of the data and explore the measures of central tendencies and spread of the data

[9]:
```python
data.mean()
```

[9]:
```
age          54.420530
sex           0.682119
cp            0.963576
trestbps    131.602649
chol        246.500000
fbs           0.149007
restecg       0.526490
thalach     149.569536
exang         0.327815
oldpeak       1.043046
slope         1.397351
ca            0.718543
thal          2.314570
target        0.543046
dtype: float64
```

[10]:
```
data.median()
```

[10]:
```
age          55.5
sex           1.0
cp            1.0
trestbps    130.0
chol        240.5
fbs           0.0
restecg       1.0
thalach     152.5
exang         0.0
oldpeak       0.8
slope         1.0
ca            0.0
thal          2.0
target        1.0
dtype: float64
```

[11]:
```
data.mode()
```

[11]:
```
    age  sex   cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  \
0  58.0  1.0  0.0     120.0   197  0.0      1.0    162.0    0.0      0.0
1   NaN  NaN  NaN       NaN   204  NaN      NaN      NaN    NaN      NaN
2   NaN  NaN  NaN       NaN   234  NaN      NaN      NaN    NaN      NaN

   slope   ca  thal  target
0    2.0  0.0   2.0     1.0
1    NaN  NaN   NaN     NaN
2    NaN  NaN   NaN     NaN
```

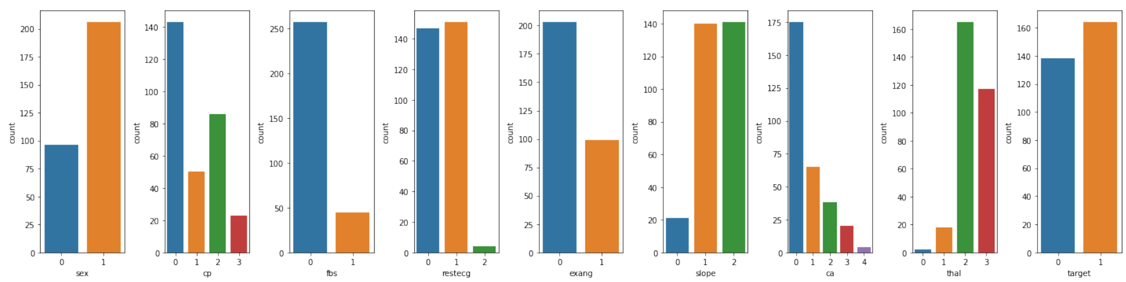
2.0.2 b. Identify the data variables which are categorical and describe and explore these variables using the appropriate tools, such as count plot

[12]:
```
data.describe().T
```

[12]:
```
          count        mean        std    min     25%    50%     75%    max
age       302.0   54.420530   9.047970   29.0   48.00   55.5   61.00   77.0
sex       302.0    0.682119   0.466426    0.0    0.00    1.0    1.00    1.0
cp        302.0    0.963576   1.032044    0.0    0.00    1.0    2.00    3.0
trestbps  302.0  131.602649  17.563394   94.0  120.00  130.0  140.00  200.0
chol      302.0  246.500000  51.753489  126.0  211.00  240.5  274.75  564.0
fbs       302.0    0.149007   0.356686    0.0    0.00    0.0    0.00    1.0
restecg   302.0    0.526490   0.526027    0.0    0.00    1.0    1.00    2.0
thalach   302.0  149.569536  22.903527   71.0  133.25  152.5  166.00  202.0
exang     302.0    0.327815   0.470196    0.0    0.00    0.0    1.00    1.0
oldpeak   302.0    1.043046   1.161452    0.0    0.00    0.8    1.60    6.2
slope     302.0    1.397351   0.616274    0.0    1.00    1.0    2.00    2.0
```

```
ca        302.0    0.718543   1.006748    0.0    0.00    0.0    1.00    4.0
thal      302.0    2.314570   0.613026    0.0    2.00    2.0    3.00    3.0
target    302.0    0.543046   0.498970    0.0    0.00    1.0    1.00    1.0
```

[13]:
```python
cols = data[['sex','cp','fbs','restecg','exang','slope','ca','thal','target']]

n=len(cols.columns)
fig,ax = plt.subplots(1,n, figsize=(20,5))
for i in range(n):
    plt.sca(ax[i])
    col = cols.columns[i]
    sns.countplot(cols[col].values)
    plt.xlabel(col)
    plt.tight_layout()
plt.show()
```



2.1 c. Study the occurrence of CVD across the Age category

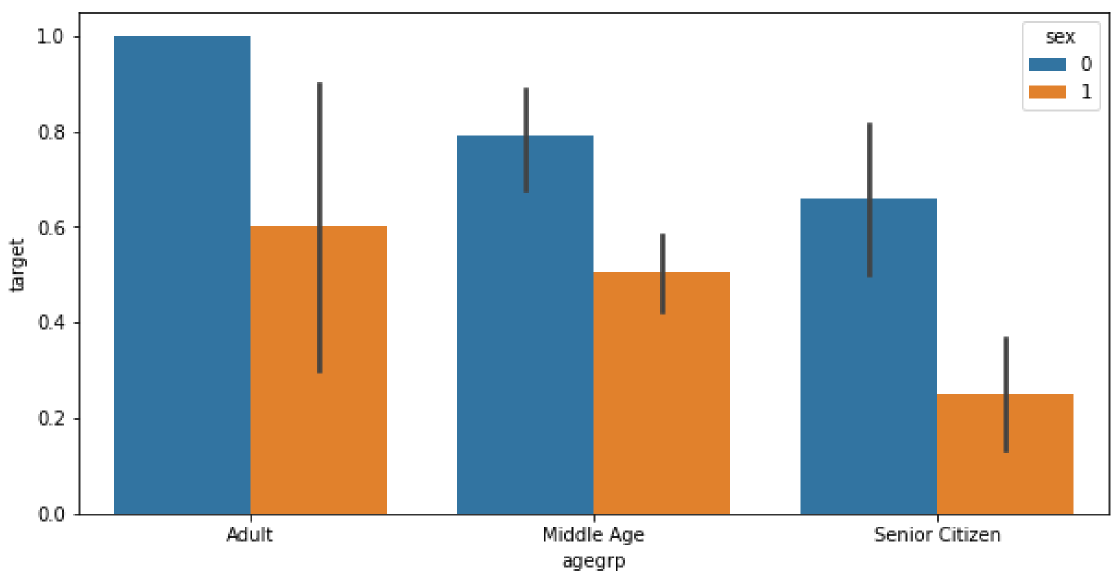
[14]:
```python
bins = [20,40,60,80]
agegroup = ['Adult','Middle Age','Senior Citizen']
data['agegrp'] = pd.cut(data['age'],bins=bins,labels=agegroup,right=False)
data
```

[14]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	\
0	63	1	3	145	233	1	0	150	0	2.3	
1	37	1	2	130	250	0	1	187	0	3.5	
2	41	0	1	130	204	0	0	172	0	1.4	
3	56	1	1	120	236	0	1	178	0	0.8	
4	57	0	0	120	354	0	1	163	1	0.6	
..	…	…	..	…	…	…	…	…	…	…	
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          agegrp
0        0   0     1       1  Senior Citizen
1        0   0     2       1           Adult
2        2   0     2       1      Middle Age
3        2   0     2       1      Middle Age
4        2   0     2       1      Middle Age
..     ...  ..   ...     ...             ...
298      1   0     3       0      Middle Age
299      1   0     3       0      Middle Age
300      1   2     3       0  Senior Citizen
301      1   1     3       0      Middle Age
302      1   1     2       0      Middle Age

[302 rows x 15 columns]
```

[15]:
```python
plt.figure(figsize=(10,5))
sns.barplot(x='agegrp',y='target',data=data,hue='sex')
plt.show()
```



2.1.1 d. Study the composition of all patients with respect to the Sex category

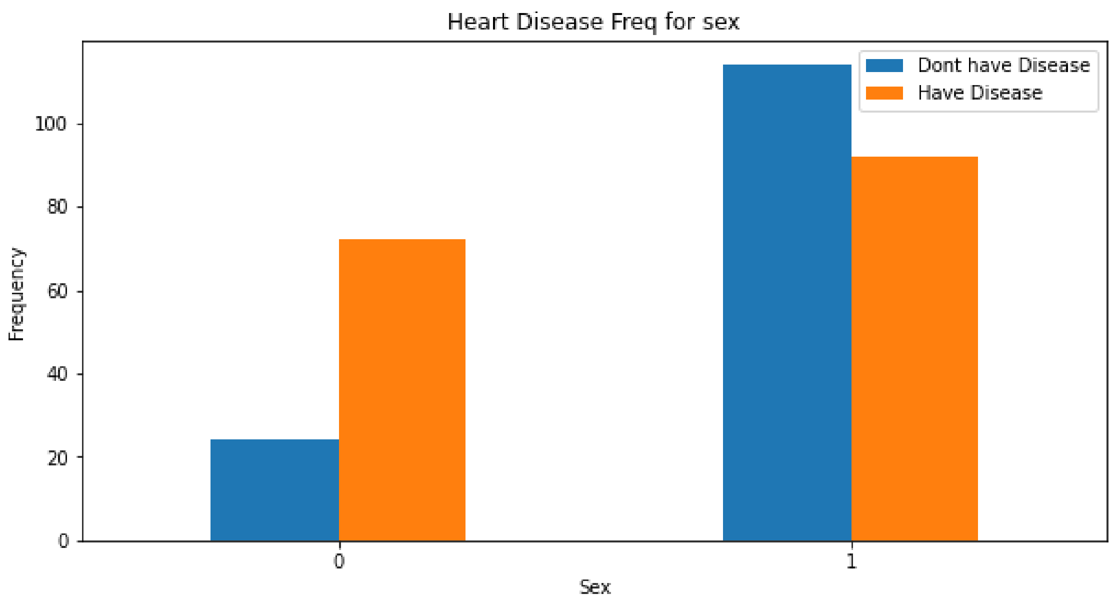
[16]:
```python
data['sex'].value_counts()
```

[16]:
```
1    206
0     96
Name: sex, dtype: int64
```

[17]:
```
data.groupby(by='sex').mean()
```

[17]:
```
              age        cp    trestbps        chol       fbs   restecg  \
sex
0       55.677083  1.041667  133.083333  261.302083  0.125000  0.572917
1       53.834951  0.927184  130.912621  239.601942  0.160194  0.504854

          thalach     exang   oldpeak     slope        ca      thal    target
sex
0       151.12500  0.229167  0.876042  1.427083  0.552083  2.125000  0.750000
1       148.84466  0.373786  1.120874  1.383495  0.796117  2.402913  0.446602
```

[18]:
```
pd.crosstab(data['sex'],data['target']).plot(kind='bar',figsize=(10,5))
plt.title('Heart Disease Freq for sex')
plt.xlabel('Sex')
plt.xticks(rotation=0)
plt.ylabel('Frequency')
plt.legend(['Dont have Disease','Have Disease'])
plt.show()
```

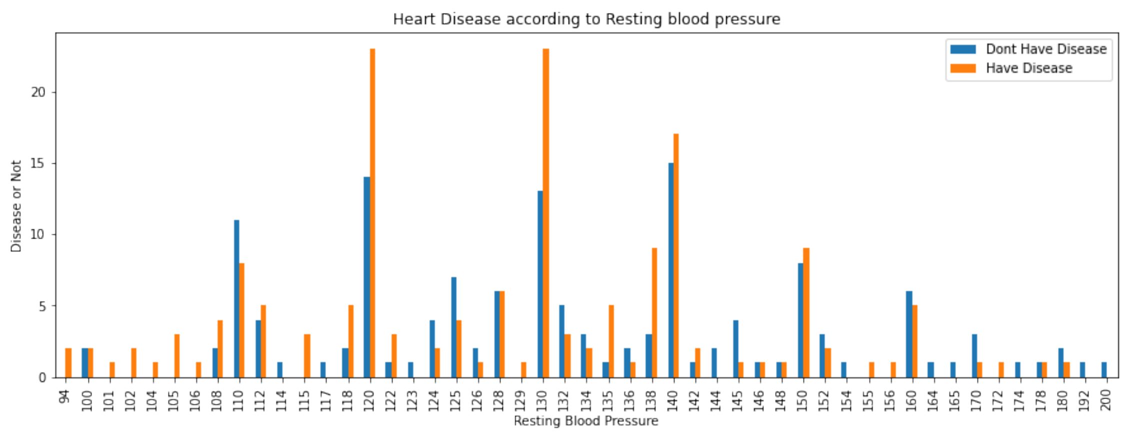


2.1.2 e. Study if one can detect heart attacks based on anomalies in the resting blood pressure (trestbps) of a patient

[19]:
```
data['trestbps'].unique()
```

[19]:
```
array([145, 130, 120, 140, 172, 150, 110, 135, 160, 105, 125, 142, 155,
       104, 138, 128, 108, 134, 122, 115, 118, 100, 124,  94, 112, 102,
       152, 101, 132, 148, 178, 129, 180, 136, 126, 106, 156, 170, 146,
       117, 200, 165, 174, 192, 144, 123, 154, 114, 164], dtype=int64)
```

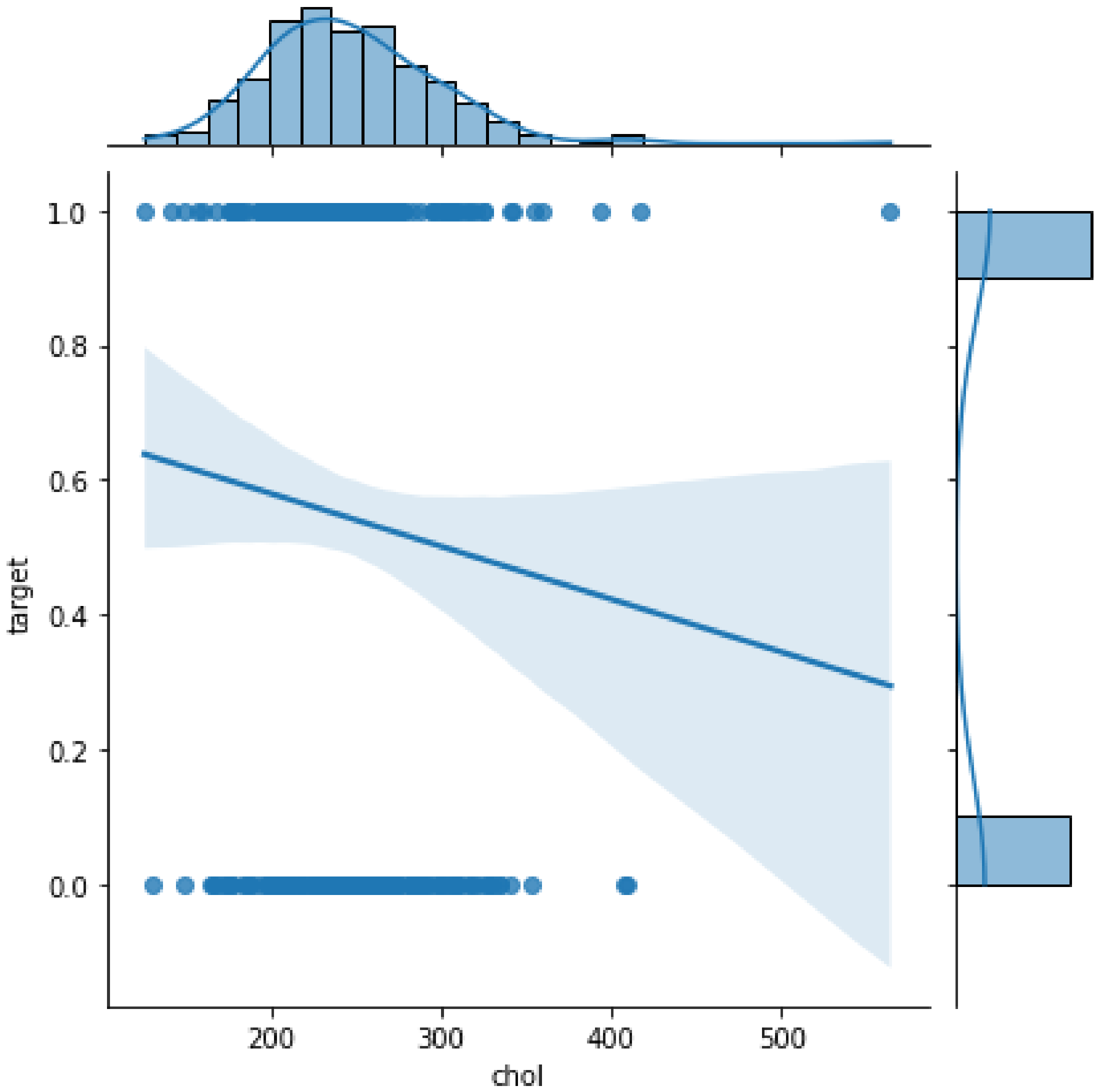
[20]:
```python
pd.crosstab(data['trestbps'],data['target']).plot(kind='bar',figsize=(15,5))
plt.title('Heart Disease according to Resting blood pressure')
plt.xlabel('Resting Blood Pressure')
plt.ylabel('Disease or Not')
plt.legend(['Dont Have Disease','Have Disease'])
plt.show()
```



2.1.3 f. Describe the relationship between cholesterol levels and a target variable

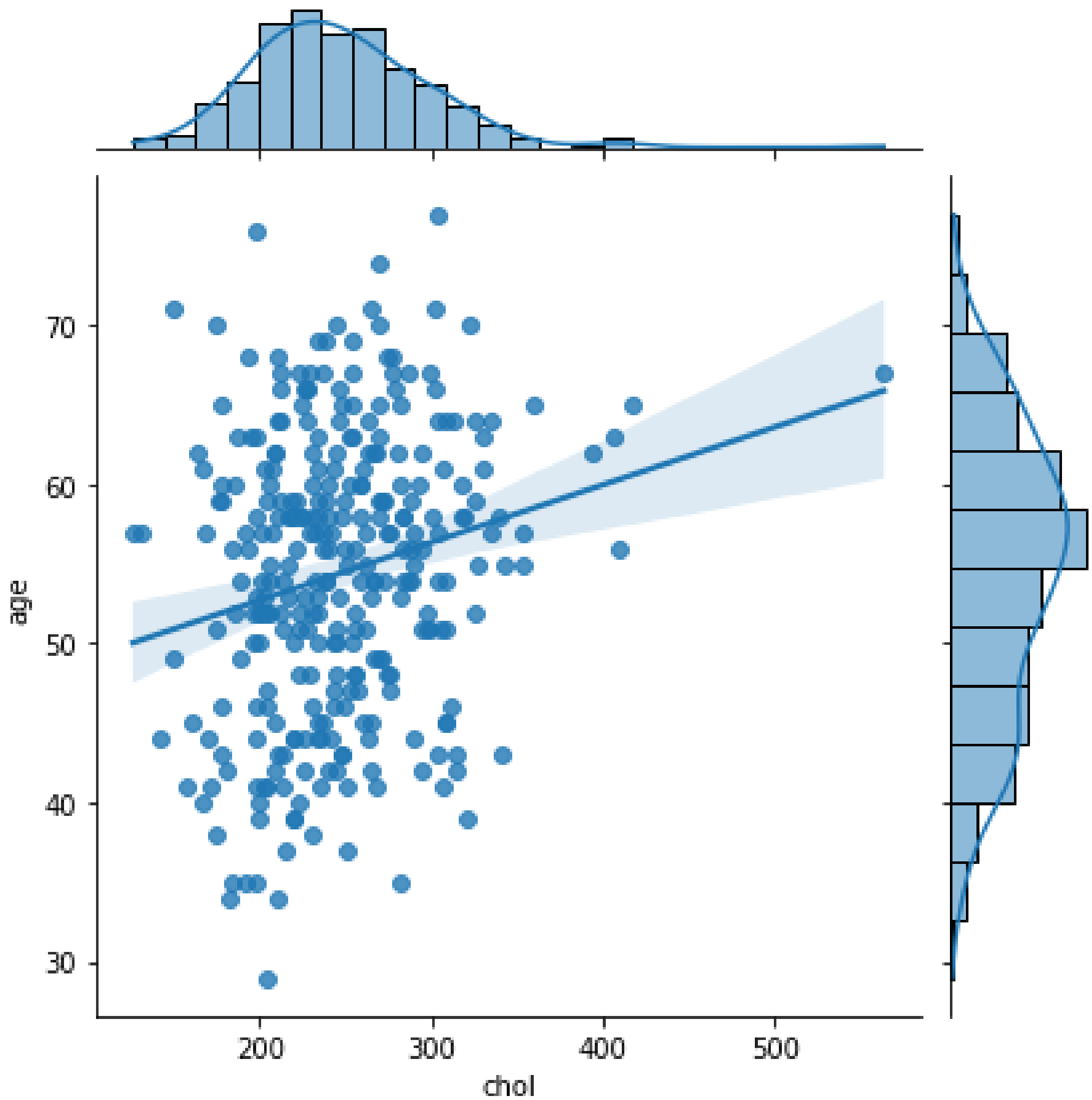
[21]:
```python
sns.jointplot(x='chol',y='target',data=data,height=6,kind='reg')
```

[21]:
```
<seaborn.axisgrid.JointGrid at 0x202a61b7430>
```



[22]:
```
sns.jointplot(x='chol',y='age',data=data,height=6,kind='reg')
```

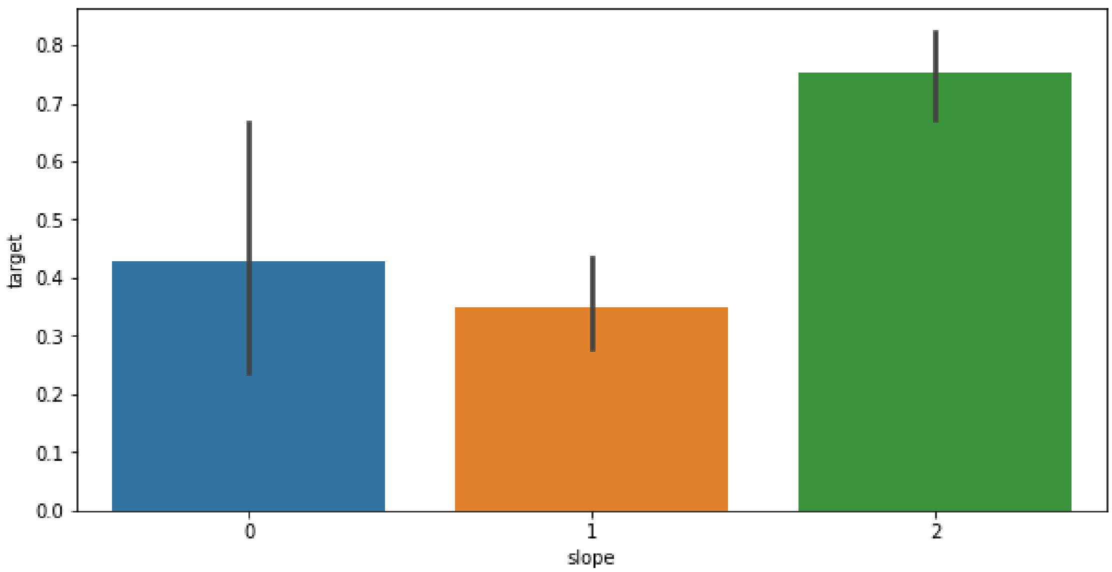
[22]: <seaborn.axisgrid.JointGrid at 0x202a7332e80>



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

[23]:
```
plt.figure(figsize=(10,5))
sns.barplot(data['slope'],data['target'])
```

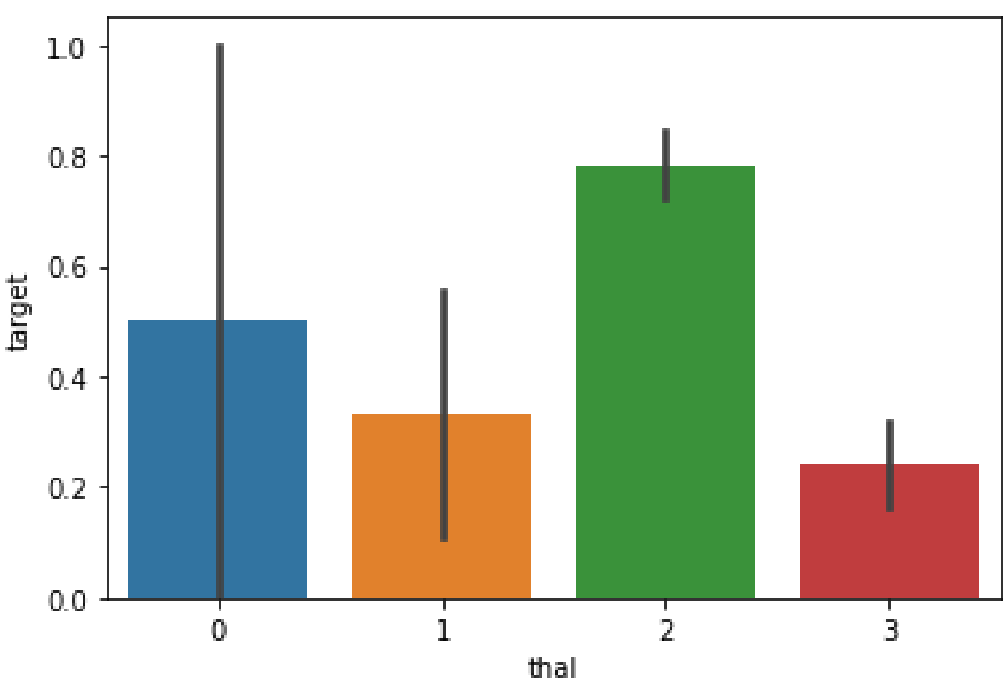
[23]: <AxesSubplot:xlabel='slope', ylabel='target'>



2.1.5 h. Check if thalassemia is a major cause of CVD

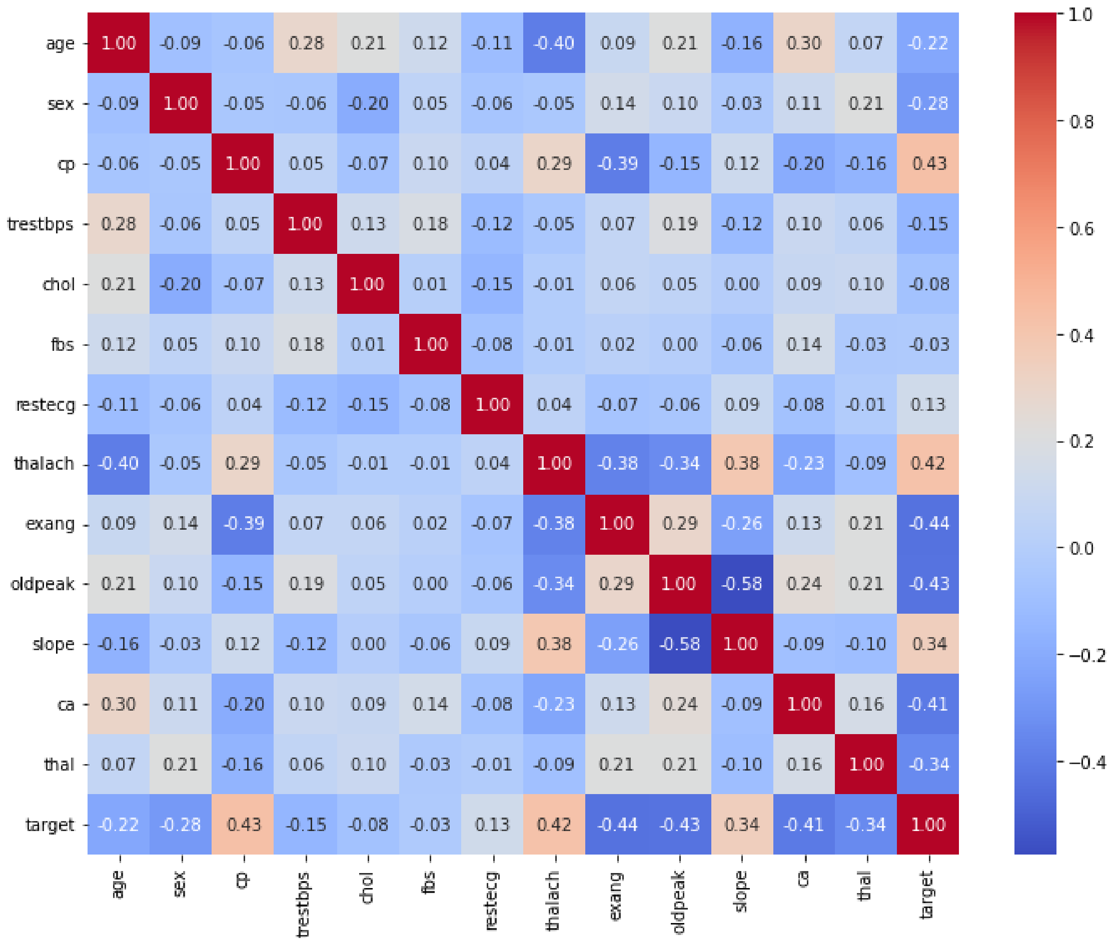
[24]:
```
sns.barplot(data['thal'],data['target'])
```

[24]: <AxesSubplot:xlabel='thal', ylabel='target'>

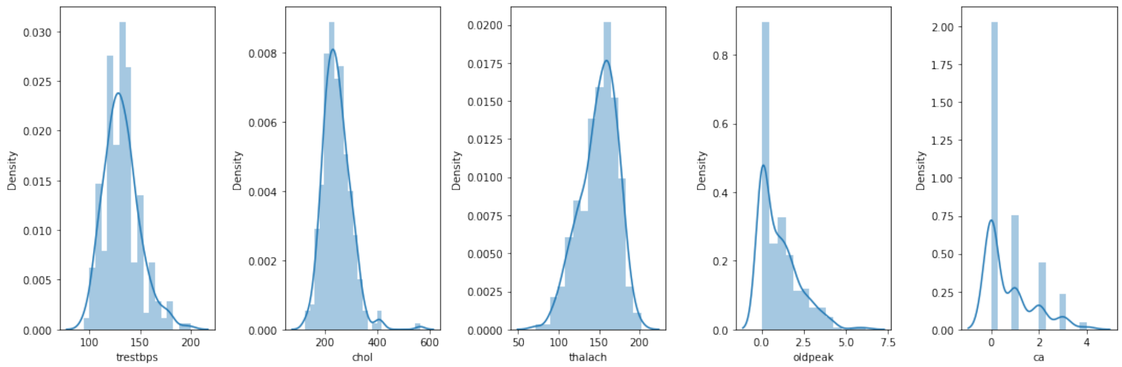


2.1.6 i. List how the other factors determine the occurrence of CVD

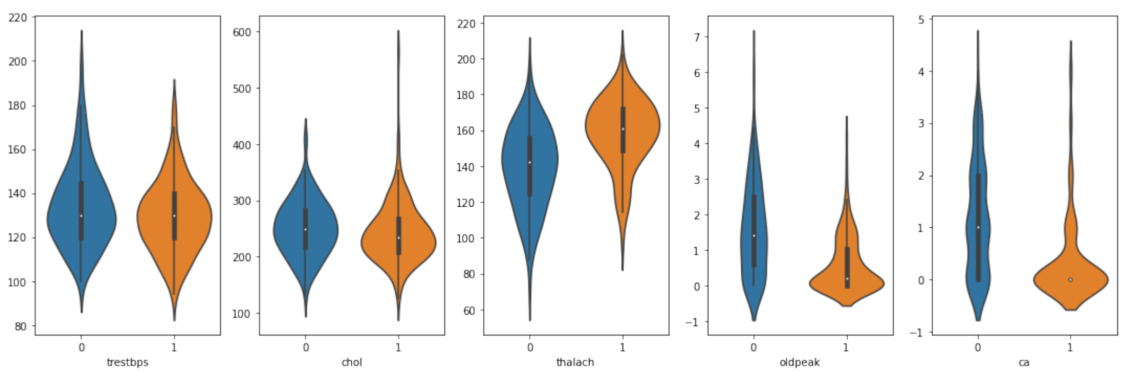
[25]:
```
plt.figure(figsize=(10,8))
sns.heatmap(data.corr(),annot=True,cmap='coolwarm',fmt='.2f')
plt.tight_layout()
plt.show()
```



[26]:
```
cols = data[['trestbps','chol','thalach','oldpeak','ca']]

n_samples = len(cols.columns)
plt.figure(figsize=(15,5))
for i in range(n_samples):
    col = cols.columns[i]
    plt.subplot(1,n_samples,1 + i)
    sns.distplot(cols[col].values)
    plt.xlabel(col)
    plt.tight_layout()
plt.show()
```



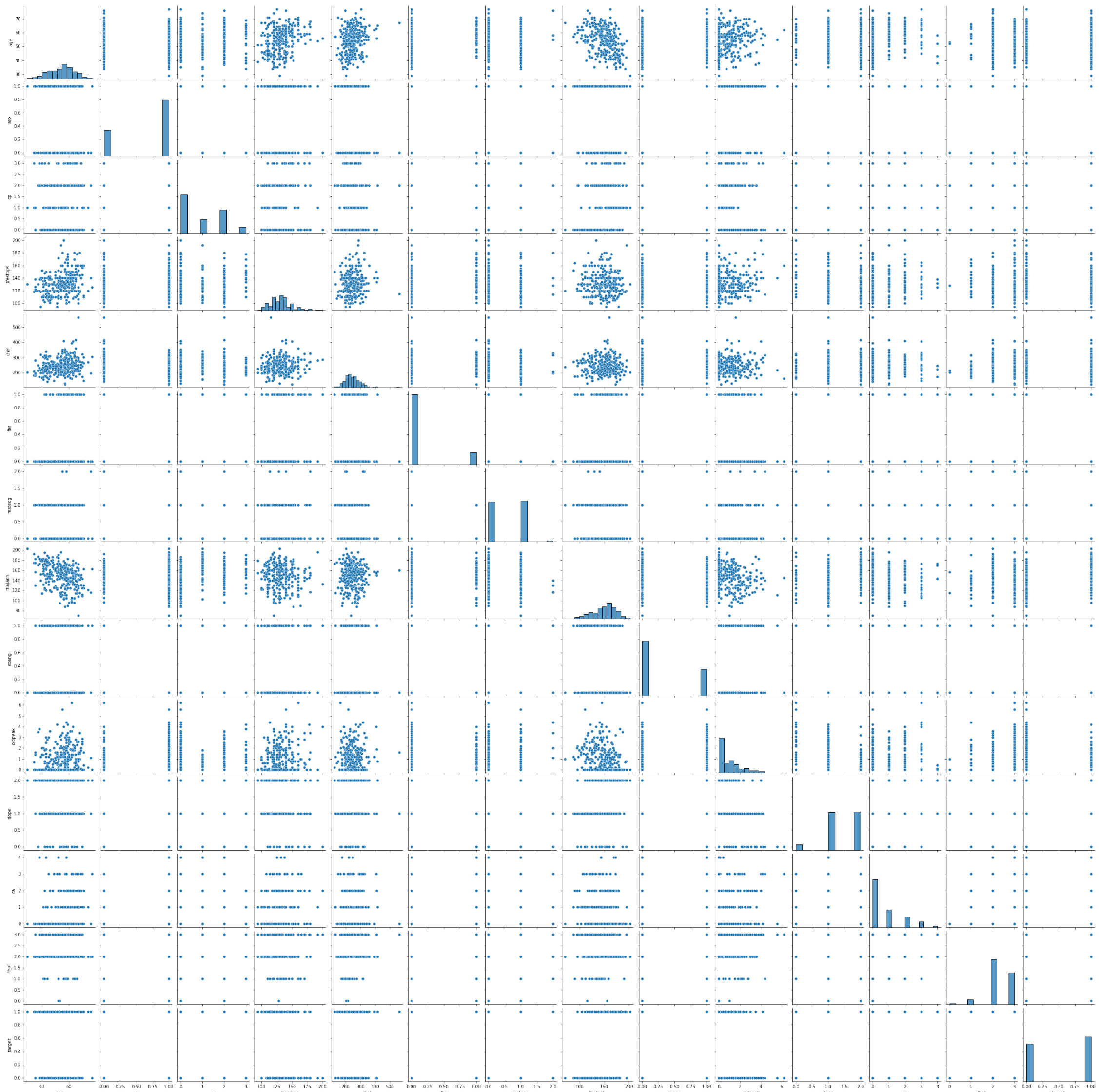

```
[27]: cols = data[['trestbps','chol','thalach','oldpeak','ca','target']]

      plt.figure(figsize=(15,5))
      for i in range(n_samples):
          col = cols.columns[i]
          plt.subplot(1,n_samples,1 + i)
          sns.violinplot(x='target',y=cols[col].values,data=cols)
          plt.xlabel(col)
          plt.tight_layout()
      plt.show()
```



2.1.7 j. Use a pair plot to understand the relationship between all the given variables

```
[28]: sns.pairplot(data)
```

```
[28]: <seaborn.axisgrid.PairGrid at 0x202a5d78160>
```



3 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

[29]:
```
data = data.drop('agegrp',axis=1)
```

[30]:
```
x = data.drop('target',axis=1)
y = data['target']
```

```
[31]: # Scale the data in 0-1.
scaler = StandardScaler()
data_scale = pd.DataFrame(scaler.fit_transform(x))
data_scale.columns = x.columns
```

```
[32]: xtrain,xtest,ytrain,ytest = train_test_split(data_scale,y,test_size=0.
 ↪2,random_state=41)
(xtrain.shape,xtest.shape,ytrain.shape,ytest.shape)
```

```
[32]: ((241, 13), (61, 13), (241,), (61,))
```

3.1 Logistic Regression

```
[33]: lr_model = LogisticRegression()
lr_model.fit(xtrain,ytrain)
```

```
[33]: LogisticRegression()
```

```
[34]: def evalution(test,pred):
    print('Accuracy Score :',accuracy_score(test,pred))
    print('\nConfusion Maxtrix :\n',confusion_matrix(test,pred))
    print('\n Classification Report :\n',classification_report(test,pred))
```

```
[35]: preds =lr_model.predict(xtest)
evalution(ytest,preds)
```

```
Accuracy Score : 0.7868852459016393

Confusion Maxtrix :
 [[31  8]
 [ 5 17]]

 Classification Report :
               precision    recall  f1-score   support

           0       0.86      0.79      0.83        39
           1       0.68      0.77      0.72        22

    accuracy                           0.79        61
   macro avg       0.77      0.78      0.78        61
weighted avg       0.80      0.79      0.79        61
```

3.2 Random Forest Classifier

[36]:
```
rfc_model = RandomForestClassifier(n_estimators=100,criterion='gini')
rfc_model.fit(xtrain,ytrain)
```

[36]:
```
RandomForestClassifier()
```

[37]:
```
rfc_pred = rfc_model.predict(xtest)
evalution(ytest,rfc_pred)
```

```
Accuracy Score : 0.819672131147541

Confusion Maxtrix :
 [[32  7]
 [ 4 18]]

 Classification Report :
               precision    recall  f1-score   support

           0       0.89      0.82      0.85        39
           1       0.72      0.82      0.77        22

    accuracy                           0.82        61
   macro avg       0.80      0.82      0.81        61
weighted avg       0.83      0.82      0.82        61
```

[38]:
```
param_grid = {
    'n_estimators': [100, 150, 200, 250],
    'max_features': ['auto', 'sqrt', 'log2'],
    'max_depth' : [4,5,6,7,8,9],
    'criterion' :['gini', 'entropy']
}

rfc_model = RandomForestClassifier()
CV_rfc = GridSearchCV(estimator=rfc_model, param_grid=param_grid, cv= 5)
CV_rfc.fit(xtrain, ytrain)
```

[38]:
```
GridSearchCV(cv=5, estimator=RandomForestClassifier(),
             param_grid={'criterion': ['gini', 'entropy'],
                         'max_depth': [4, 5, 6, 7, 8, 9],
                         'max_features': ['auto', 'sqrt', 'log2'],
                         'n_estimators': [100, 150, 200, 250]})
```

[39]:
```
CV_rfc.best_params_
```

[39]:
```
{'criterion': 'entropy',
 'max_depth': 5,
```

```
 'max_features': 'log2',
 'n_estimators': 100}
```

[40]:
```
rfc_model_tune =␣
↪RandomForestClassifier(n_estimators=500,criterion='entropy',max_depth=4,max_features='sqrt'
rfc_model_tune.fit(xtrain,ytrain)
```

[40]:
```
RandomForestClassifier(criterion='entropy', max_depth=4, n_estimators=500)
```

[41]:
```
rfc_pred_tune = rfc_model_tune.predict(xtest)
evalution(ytest,rfc_pred_tune)
```

```
Accuracy Score : 0.8360655737704918

Confusion Maxtrix :
 [[32  7]
 [ 3 19]]

 Classification Report :
               precision    recall  f1-score   support

           0       0.91      0.82      0.86        39
           1       0.73      0.86      0.79        22

    accuracy                           0.84        61
   macro avg       0.82      0.84      0.83        61
weighted avg       0.85      0.84      0.84        61
```

[42]:
```
csq1=chi2_contingency(pd.crosstab(data['thalach'], data['target']))
print("P-value: ",csq1[1])
```

```
P-value:  0.07918631828372703
```

[ ]: