# Healthcare

March 2, 2023

# 1 Healthcare

## 1.1 Problem statement:

Cardiovascular diseases are the leading cause of death globally. It is therefore necessary to identify the causes and develop a system to predict heart attacks in an effective manner. The data below has the information about the factors that might have an impact on cardiovascular health.

### 1.1.1 Preliminary analysis

[1]:
```
# Import our libraries
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pylab as plt
sns.set_style("whitegrid")
import warnings
warnings.filterwarnings('ignore')
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split, RandomizedSearchCV
from sklearn.metrics import accuracy_score, precision_score, recall_score,␣
 ↪f1_score
from sklearn.ensemble import RandomForestClassifier, AdaBoostClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion_matrix
from sklearn import metrics
from sklearn.metrics import classification_report
from sklearn.svm import SVC
from sklearn.preprocessing import MinMaxScaler
import statsmodels.api as sm

sns.set(style="ticks")

#import check_file as ch

%matplotlib inline
```

### 1.1.2 Understanding data

[2]:
```
# Read in our dataset
df = pd.read_csv('healthcare.csv')

# Take a look at the first few rows of the dataset
df.head()
```

[2]:
```
   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
```

[3]:
```
df.shape
```

[3]:
```
(303, 14)
```

[4]:
```
#data is clean
df.isnull().sum()
```

[4]:
```
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
```

[5]:
```
#Select the cell and click on run icon
df.duplicated().sum()
```

[5]: 1

[6]:
```
#1 duplicated row
df[df.duplicated(keep=False)]
```

[6]:

|     | 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 |

[7]:
```
#duplicate dropped
df2 = df.drop_duplicates(keep="first")
```

[8]:
```
df2.head()
```

[8]:

|   | 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 |

[9]:
```
#no more duplicates
df2.duplicated().sum()
```

[9]: 0

[10]:
```
#one less row because the duplicate row was removed from df2
df2.shape
```

[10]: (302, 14)

[11]:
```
df.describe()
```

[11]:

|   | age | sex | cp | trestbps | chol | fbs |
|---|---|---|---|---|---|---|
| count | 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 |

|  | | | | | | |
|---|---|---|---|---|---|---|
| std | 9.082101 | 0.466011 | 1.032052 | 17.538143 | 51.830751 | 0.356198 |
| min | 29.000000 | 0.000000 | 0.000000 | 94.000000 | 126.000000 | 0.000000 |
| 25% | 47.500000 | 0.000000 | 0.000000 | 120.000000 | 211.000000 | 0.000000 |
| 50% | 55.000000 | 1.000000 | 1.000000 | 130.000000 | 240.000000 | 0.000000 |
| 75% | 61.000000 | 1.000000 | 2.000000 | 140.000000 | 274.500000 | 0.000000 |
| max | 77.000000 | 1.000000 | 3.000000 | 200.000000 | 564.000000 | 1.000000 |

|  | restecg | thalach | exang | oldpeak | slope | ca \ |
|---|---|---|---|---|---|---|
| count | 303.000000 | 303.000000 | 303.000000 | 303.000000 | 303.000000 | 303.000000 |
| mean | 0.528053 | 149.646865 | 0.326733 | 1.039604 | 1.399340 | 0.729373 |
| std | 0.525860 | 22.905161 | 0.469794 | 1.161075 | 0.616226 | 1.022606 |
| min | 0.000000 | 71.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| 25% | 0.000000 | 133.500000 | 0.000000 | 0.000000 | 1.000000 | 0.000000 |
| 50% | 1.000000 | 153.000000 | 0.000000 | 0.800000 | 1.000000 | 0.000000 |
| 75% | 1.000000 | 166.000000 | 1.000000 | 1.600000 | 2.000000 | 1.000000 |
| max | 2.000000 | 202.000000 | 1.000000 | 6.200000 | 2.000000 | 4.000000 |

|  | thal | target |
|---|---|---|
| count | 303.000000 | 303.000000 |
| mean | 2.313531 | 0.544554 |
| std | 0.612277 | 0.498835 |
| min | 0.000000 | 0.000000 |
| 25% | 2.000000 | 0.000000 |
| 50% | 2.000000 | 1.000000 |
| 75% | 3.000000 | 1.000000 |
| max | 3.000000 | 1.000000 |

[12]:
```
#removing the duplicate row changed count, mean, std, 25%, and 50% by a little
df2.describe()
```

[12]:

|  | age | sex | cp | trestbps | chol | fbs \ |
|---|---|---|---|---|---|---|
| count | 302.00000 | 302.000000 | 302.000000 | 302.000000 | 302.000000 | 302.000000 |
| mean | 54.42053 | 0.682119 | 0.963576 | 131.602649 | 246.500000 | 0.149007 |
| std | 9.04797 | 0.466426 | 1.032044 | 17.563394 | 51.753489 | 0.356686 |
| min | 29.00000 | 0.000000 | 0.000000 | 94.000000 | 126.000000 | 0.000000 |
| 25% | 48.00000 | 0.000000 | 0.000000 | 120.000000 | 211.000000 | 0.000000 |
| 50% | 55.50000 | 1.000000 | 1.000000 | 130.000000 | 240.500000 | 0.000000 |
| 75% | 61.00000 | 1.000000 | 2.000000 | 140.000000 | 274.750000 | 0.000000 |
| max | 77.00000 | 1.000000 | 3.000000 | 200.000000 | 564.000000 | 1.000000 |

|  | restecg | thalach | exang | oldpeak | slope | ca \ |
|---|---|---|---|---|---|---|
| count | 302.000000 | 302.000000 | 302.000000 | 302.000000 | 302.000000 | 302.000000 |
| mean | 0.526490 | 149.569536 | 0.327815 | 1.043046 | 1.397351 | 0.718543 |
| std | 0.526027 | 22.903527 | 0.470196 | 1.161452 | 0.616274 | 1.006748 |
| min | 0.000000 | 71.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| 25% | 0.000000 | 133.250000 | 0.000000 | 0.000000 | 1.000000 | 0.000000 |
| 50% | 1.000000 | 152.500000 | 0.000000 | 0.800000 | 1.000000 | 0.000000 |

```
75%      1.000000  166.000000    1.000000    1.600000    2.000000    1.000000
max      2.000000  202.000000    1.000000    6.200000    2.000000    4.000000

             thal      target
count  302.000000  302.000000
mean     2.314570    0.543046
std      0.613026    0.498970
min      0.000000    0.000000
25%      2.000000    0.000000
50%      2.000000    1.000000
75%      3.000000    1.000000
max      3.000000    1.000000
```

[13]:

```
#Changing variable names
df2.rename({'cp' :'chest_pain_type',
             'trestbps':'resting_blood_pressure',
             'chol':'cholesterol',
             'fbs' :'fasting_blood_sugar',
             'restecg':'resting_ecg',
             'thalach' : 'max_heart_rate',
             'exang':'exercise_induced_angina',
             'oldpeak':'st_depression',
             'slope':'st_slope',
             'ca' : 'major_vessels',
             'thal' :'thalessimia' },axis = 1, inplace = True)
```

[14]:

```
df3 = df2.copy()
```

[15]:

```
df3.head()
```

[15]:

```
   age  sex  chest_pain_type  resting_blood_pressure  cholesterol  \
0   63    1                3                     145          233
1   37    1                2                     130          250
2   41    0                1                     130          204
3   56    1                1                     120          236
4   57    0                0                     120          354

   fasting_blood_sugar  resting_ecg  max_heart_rate  exercise_induced_angina  \
0                    1            0             150                        0
1                    0            1             187                        0
2                    0            0             172                        0
3                    0            1             178                        0
4                    0            1             163                        1

   st_depression  st_slope  major_vessels  thalessimia  target
0            2.3         0              0            1       1
1            3.5         0              0            2       1
```

```
2            1.4          2            0            2        1
3            0.8          2            0            2        1
4            0.6          2            0            2        1
```

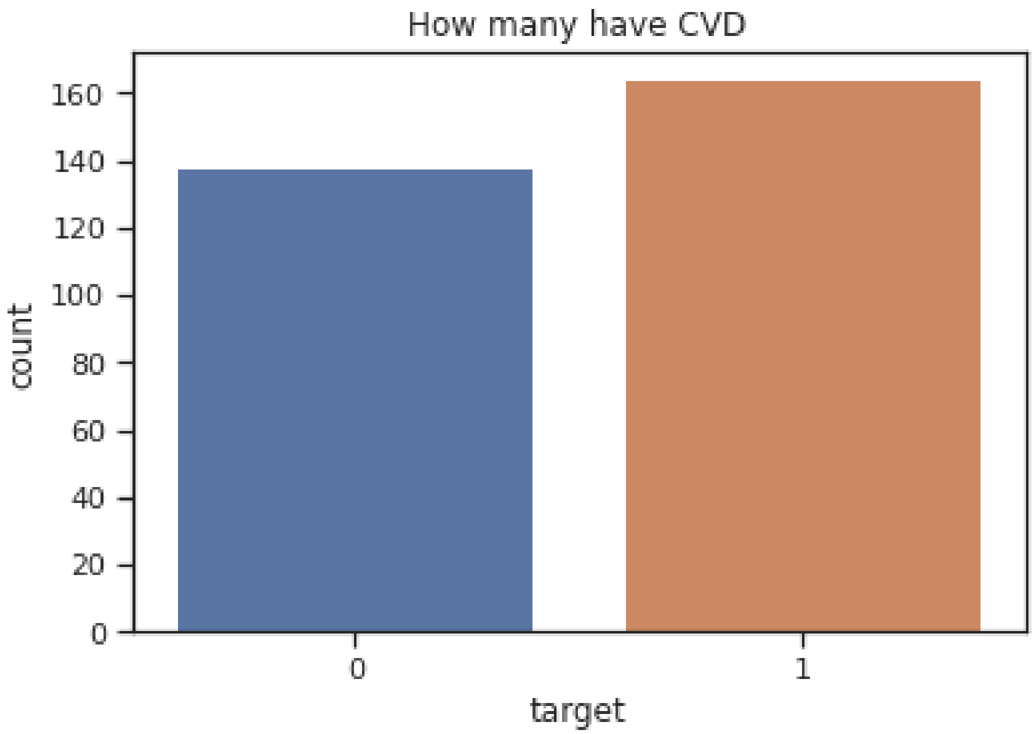
[16]:
```
#Converting the Numeric Categories to Relevent Descriptors
df2.loc[df2.sex == 0 , 'sex'] = 'female'
df2.loc[df2.sex == 1, 'sex'] = 'male'

df2.loc[df2.chest_pain_type == 0,'chest_pain_type'] = 'typical angina'
df2.loc[df2.chest_pain_type == 1,'chest_pain_type'] = 'atypical angina'
df2.loc[df2.chest_pain_type == 2,'chest_pain_type'] = 'non-anginal pain'
df2.loc[df2.chest_pain_type == 3,'chest_pain_type'] = 'asymptomatic'

df2.loc[df2.fasting_blood_sugar == 0,'fasting_blood_sugar'] = '< 120mg/ml'
df2.loc[df2.fasting_blood_sugar == 1,'fasting_blood_sugar'] = '> 120mg/ml'

df2.loc[df2.resting_ecg == 0, 'resting_ecg']  = 'normal'
df2.loc[df2.resting_ecg == 1 , 'resting_ecg'] = 'abnormal'
df2.loc[df2.resting_ecg == 2 , 'resting_ecg'] = 'hyper'

df2.loc[df2.exercise_induced_angina == 0, 'exercise_induced_angina'] = 'no'
df2.loc[df2.exercise_induced_angina == 1, 'exercise_induced_angina'] = 'yes'

df2.loc[df2.st_slope == 0, 'st_slope'] = 'upsloping'
df2.loc[df2.st_slope == 1, 'st_slope'] = 'flat'
df2.loc[df2.st_slope == 2, 'st_slope'] = 'downsloping'

df2.loc[df2.thalessimia == 1,'thalessimia'] = 'normal'
df2.loc[df2.thalessimia == 2,'thalessimia'] = 'fixed defect'
df2.loc[df2.thalessimia == 3,'thalessimia'] = 'reversable defect'
```

[17]:
```
# percentage of targets that have cvd
df2.target.value_counts(normalize=True)
```

[17]:
```
1    0.543046
0    0.456954
Name: target, dtype: float64
```

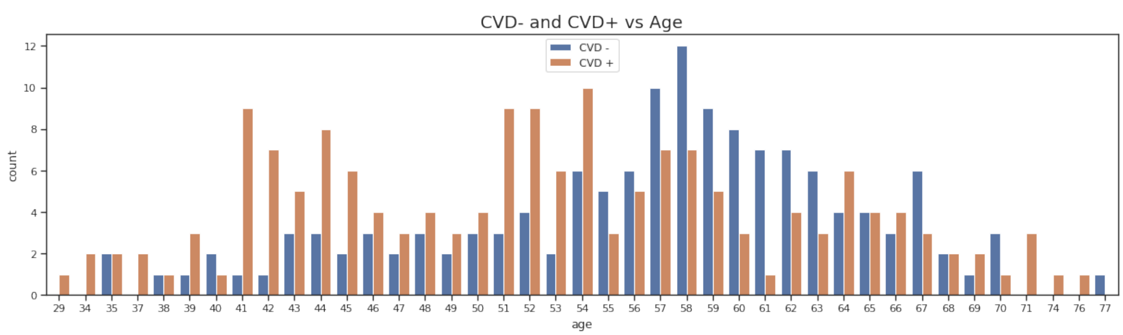
[18]:
```
# making dataframes where there is and isn't CVD
cvd1 = df2[df2.target == 1]
cvd0 = df2[df2.target == 0]
```

[19]:
```
# more people in the dataset have CVD than not
sns.countplot(x='target', data=df2).set(title='How many have CVD')
plt.show()
```

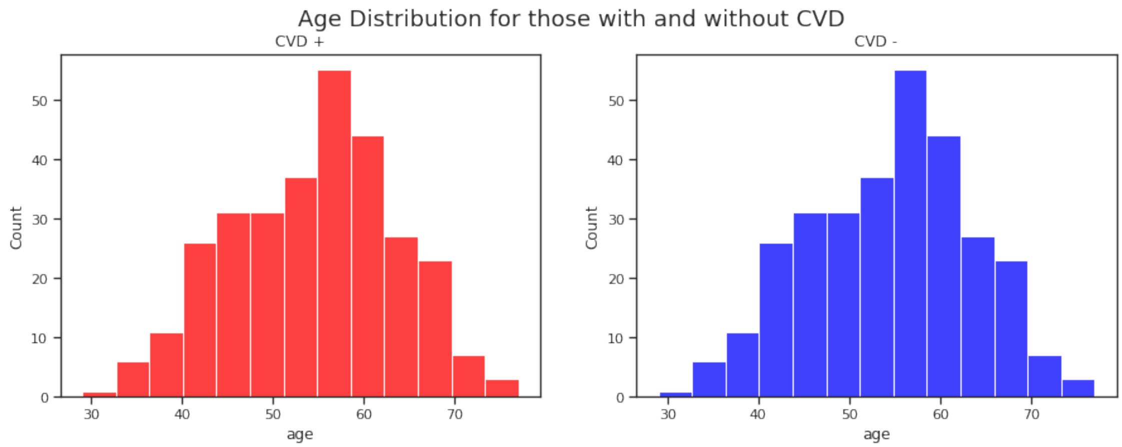



### 1.1.3 Relationships for target variable

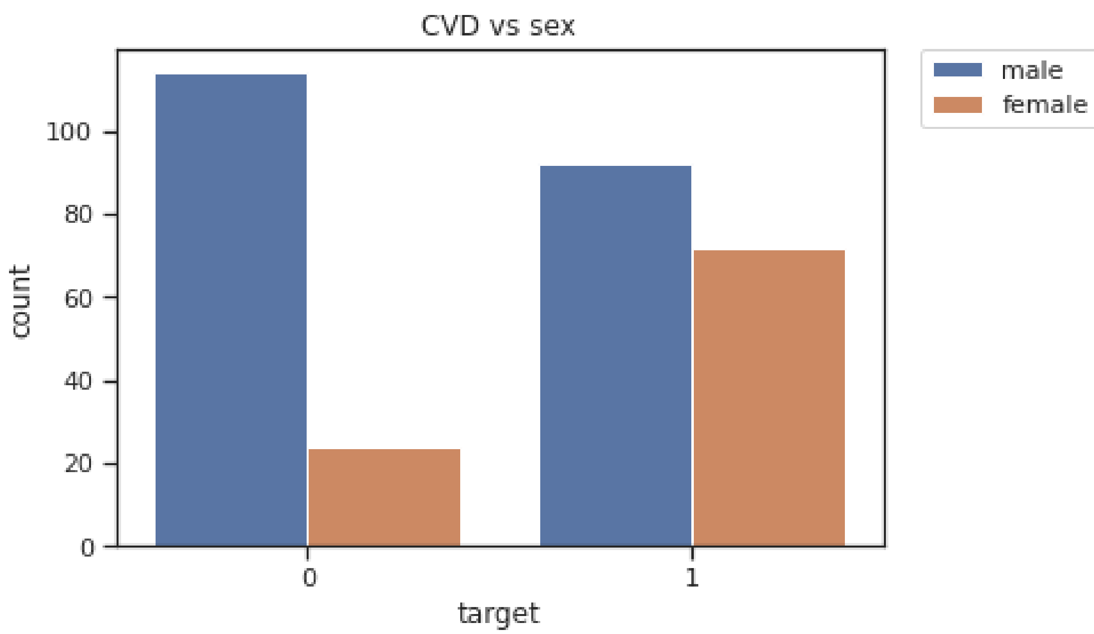
[20]:
```
# count of CVD according to age.
plt.figure(figsize = (20,5))
sns.countplot(df2.age, hue = df2.target)
plt.legend(['CVD -','CVD +'])
plt.title('CVD- and CVD+ vs Age', fontsize = 18)
plt.show()
```



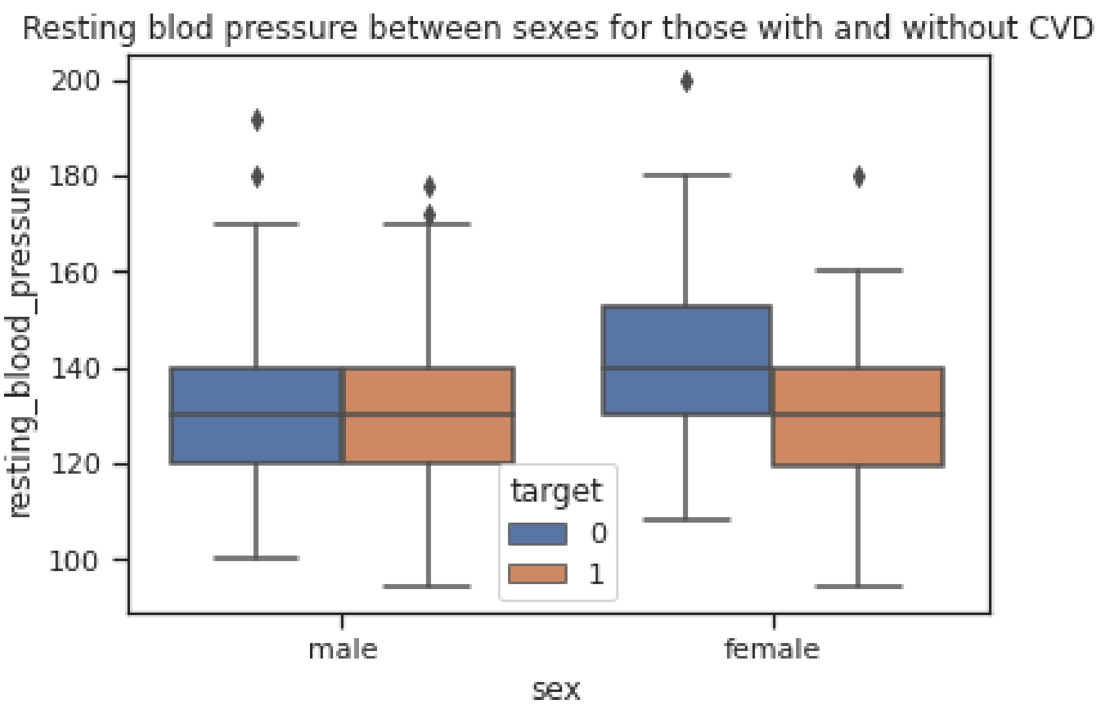
[21]:
```python
# age distribution for those with and without CVD
x,axes = plt.subplots(1,2, figsize = (15,5))
sns.histplot(df2.age, ax = axes[0], color='red')
sns.histplot(df2.age, ax = axes[1], color='blue')
axes[0].set_title('CVD +')
axes[1].set_title('CVD -')
plt.suptitle('Age Distribution for those with and without CVD',fontsize= 18)
plt.show()
```




[22]:
```python
# More of the subjects are male for both with and without CVD
sns.countplot(x='target', hue='sex', data=df2).set(title='CVD vs sex')
plt.legend(bbox_to_anchor=(1.05, 1), loc='upper left', borderaxespad=0)
plt.show()
```

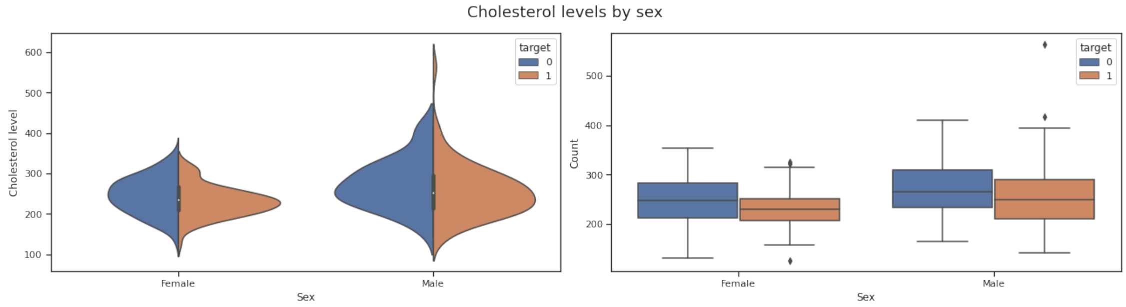


[23]:
```
# Blood pressures are pretty similar for those with and without CVD for both␣
↪genders
sns.boxplot(x = df2.sex,  y = df2.resting_blood_pressure, hue = df2.target).
↪set(title='Resting blod pressure between sexes for those with and without␣
↪CVD')
plt.show()
```

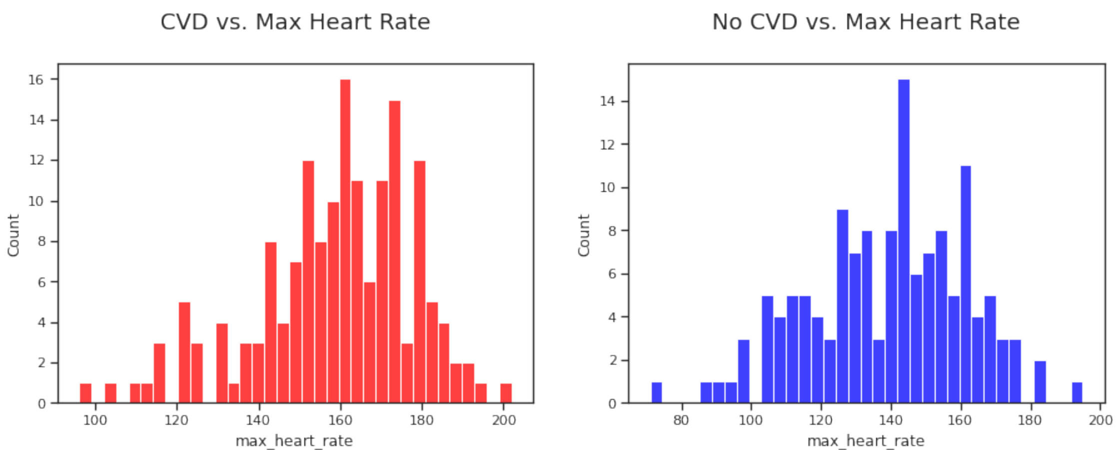



[24]:
```
# median blood pressures are about the same for male and female with and␣
↪without CVD besides some outliers
f,axes = plt.subplots(1,2,figsize = (18,5))
sns.violinplot(y = 'cholesterol', x = 'sex',hue = 'target',data = df2, split =␣
↪True, ax = axes[0])
axes[0].set_xlabel('Sex')
axes[0].set_ylabel('Cholesterol level')
axes[0].set_xticklabels(['Female','Male'])
sns.boxplot(x = df2.sex,  y = df2.cholesterol, hue = df2.target, ax = axes[1])
axes[1].set_xticklabels(['Female','Male'])
axes[1].set_xlabel('Sex')
axes[1].set_ylabel('Count')
plt.suptitle('Cholesterol levels by sex',fontsize= 18)
plt.tight_layout()
```

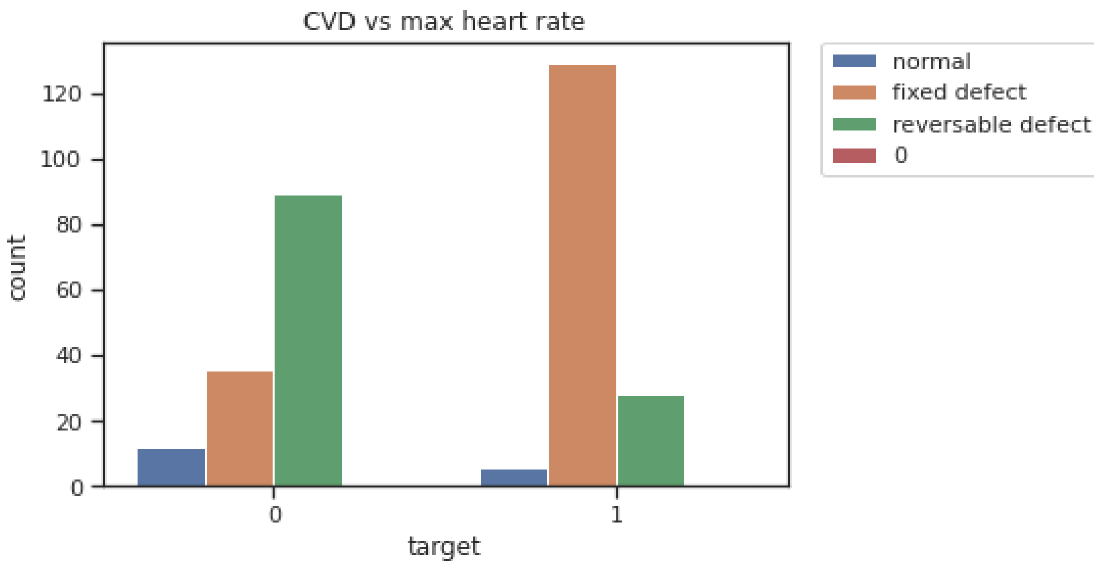
```
plt.show()
```



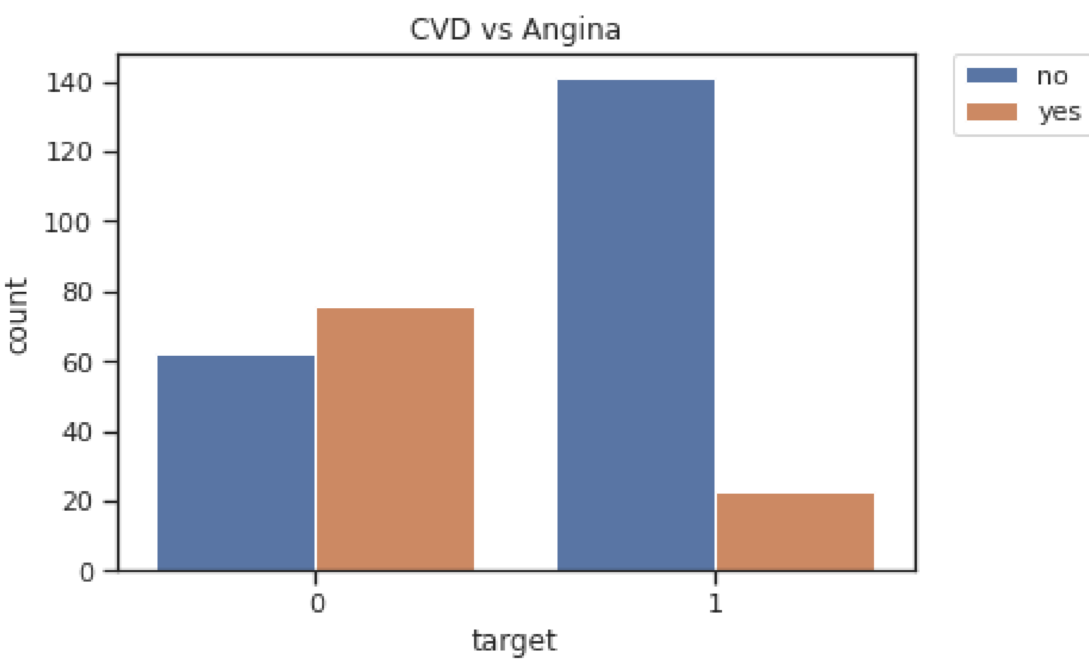

[25]:
```
# max heart rate distributions are pretty much the same
x,axes = plt.subplots(1,2, figsize = (15,5))
sns.histplot(cvd1.max_heart_rate, ax = axes[0], kde = False, bins = 35,␣
↪color='red')
sns.histplot(cvd0.max_heart_rate, ax = axes[1], kde = False, bins = 35,␣
↪color='blue')
axes[0].set_title('\nCVD vs. Max Heart Rate\n',fontsize= 18)
axes[1].set_title('\nNo CVD vs. Max Heart Rate\n',fontsize= 18)
plt.show()
```




[26]:
```
# a lot of fixed defect have CVD opposed to the others
sns.countplot(x='target', hue='thalessimia', data=df2).set(title='CVD vs max␣
↪heart rate')
plt.legend(bbox_to_anchor=(1.05, 1), loc='upper left', borderaxespad=0)
plt.show()
```




[27]:
```
# Angina is a type of chest pain caused by reduced blood flow to the heart.␣
↪Angina is a symptom of coronary artery disease.
# from this data, not too many of those with angina have CVD
sns.countplot(x='target', hue='exercise_induced_angina', data=df2).
↪set(title='CVD vs Angina')
plt.legend(bbox_to_anchor=(1.05, 1), loc='upper left', borderaxespad=0)
plt.show()
```

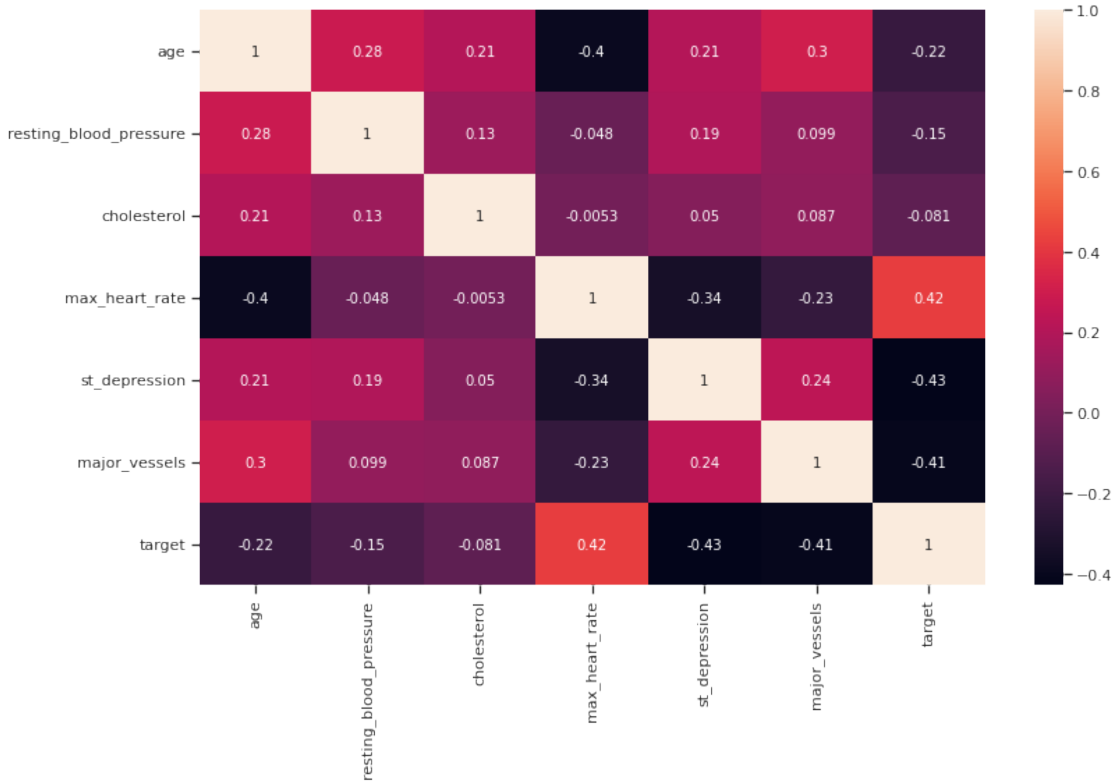


### 1.1.4 Correlation between CVD and other factors

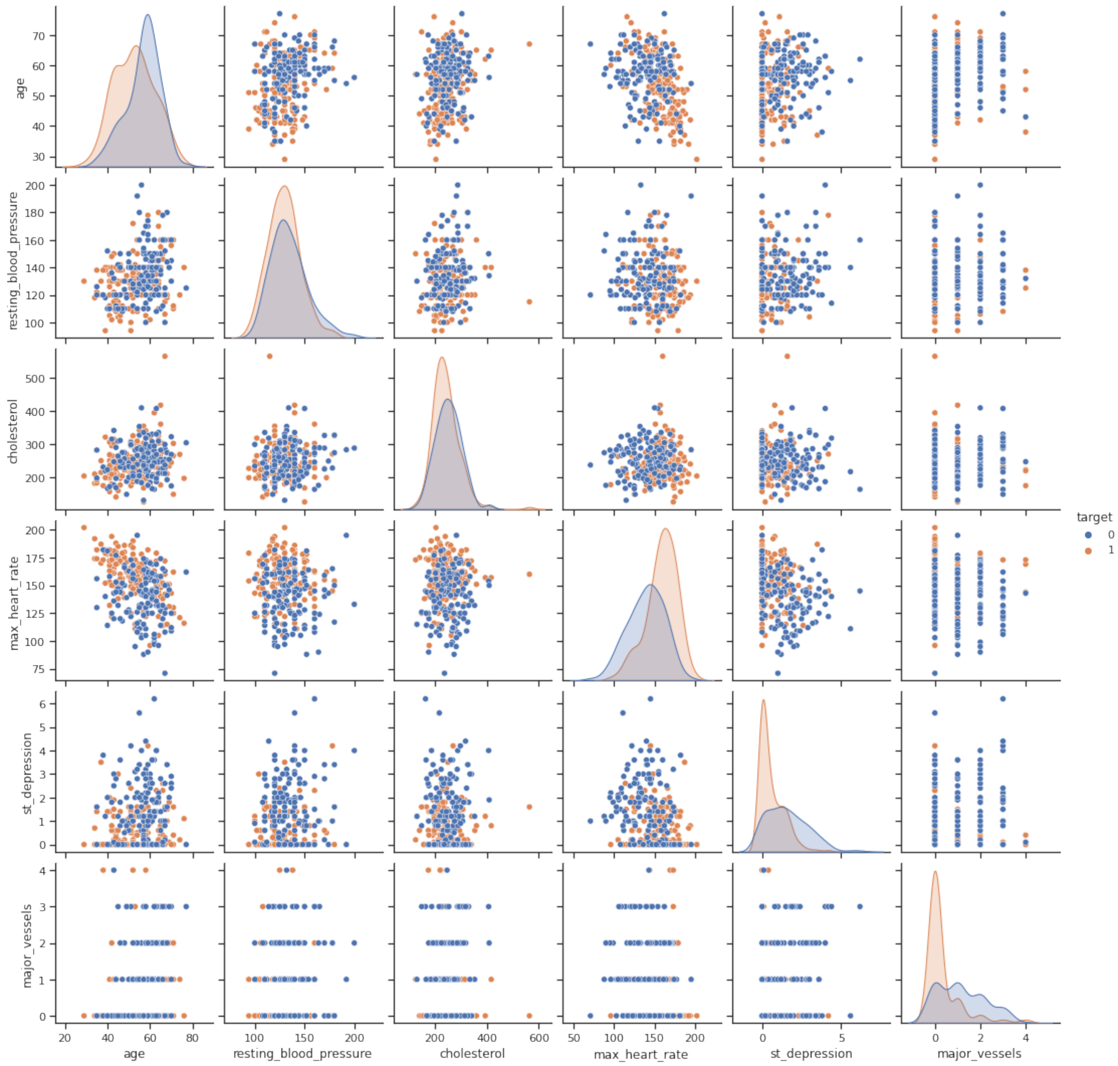
[28]:
```
#not much correlation (-0.146) between CVD and resting bps
df2.corr().sort_values(by='resting_blood_pressure')
```

[28]:
```
                             age  resting_blood_pressure  cholesterol  \
target                 -0.221476               -0.146269    -0.081437
max_heart_rate         -0.395235               -0.048023    -0.005308
major_vessels           0.302261                0.099248     0.086878
cholesterol             0.207216                0.125256     1.000000
st_depression           0.206040                0.194600     0.050086
age                     1.000000                0.283121     0.207216
resting_blood_pressure  0.283121                1.000000     0.125256

                        max_heart_rate  st_depression  major_vessels    target
target                        0.419955      -0.429146      -0.408992  1.000000
max_heart_rate                1.000000      -0.342201      -0.228311  0.419955
major_vessels                -0.228311       0.236560       1.000000 -0.408992
cholesterol                  -0.005308       0.050086       0.086878 -0.081437
st_depression                -0.342201       1.000000       0.236560 -0.429146
age                          -0.395235       0.206040       0.302261 -0.221476
resting_blood_pressure       -0.048023       0.194600       0.099248 -0.146269
```

[29]:
```
#not much correlation between resting blood pressure and cholesterol with the␣
↪target variable
#highest correlation is max heart rate
plt.figure(figsize=(12,8))
sns.heatmap(df2.corr(), annot=True)
plt.tight_layout()
```




[30]:
```python
#Pairplot to understand relationships between all given variables
sns.pairplot(df2, hue="target");
```




[31]:
```
#splitting data into train and test
y = df3['target']
X = df3.drop('target', axis=1)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.20,␣
 ↪random_state=42)
print(X_train.shape, X_test.shape)
print(y_train.shape, y_test.shape)
```

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

[32]:
```
scaler = MinMaxScaler()
scaled_train1 = scaler.fit_transform(X)
scaled_train2 = pd.DataFrame(scaled_train1, columns=X.columns, index=X.index)
```

### 1.1.5 Random forest model

[33]:
```
clf = RandomForestClassifier(n_estimators=100)
clf.fit(X_train, y_train)
```

[33]:
```
RandomForestClassifier()
```

[34]:
```
#Train the model using the training sets
y_pred=clf.predict(X_test)
```

[35]:
```
#Random forest has 88.5% accuracy in predicting someone has CVD
print("   Accuracy: {}".format(metrics.accuracy_score(y_test, y_pred)))

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

```
   Accuracy: 0.8852459016393442
              precision    recall  f1-score   support

           0       0.87      0.90      0.88        29
           1       0.90      0.88      0.89        32

    accuracy                           0.89        61
   macro avg       0.88      0.89      0.89        61
weighted avg       0.89      0.89      0.89        61
```

### 1.1.6 Random forest classifier

[36]:
```
# build a classifier this time using RandomForestClassifier class
clf_rf = RandomForestClassifier()

# Set up the hyperparameter search
param_dist = {"max_depth": [3, None],
              "n_estimators": list(range(10, 200)),
              "max_features": list(range(1, X_test.shape[1]+1)),
              "min_samples_split": list(range(2, 11)),
              "min_samples_leaf": list(range(1, 11)),
              "bootstrap": [True, False],
              "criterion": ["gini", "entropy"]}


# Run a randomized search over the hyperparameters
random_search = RandomizedSearchCV(clf_rf, param_distributions=param_dist)

# Fit the model on the training data
random_search.fit(X_train, y_train)
```

```python
# Make predictions on the test data
rf_preds = random_search.best_estimator_.predict(X_test)
```

[37]:
```python
#Random forest classifier has 84.2% accuracy in predicting someone has CVD
print("Results from Random Search:\n " )
print("-The best score across ALL searched params: ", random_search.best_score_)
print("-The best parameters across ALL searched params:\n ", random_search.
 ↪best_params_)

cm = confusion_matrix(y_test, rf_preds)
print("\nThe Confusion Matrix:\n", cm)
```

```
Results from Random Search:

-The best score across ALL searched params:  0.842517006802721
-The best parameters across ALL searched params:
  {'n_estimators': 84, 'min_samples_split': 7, 'min_samples_leaf': 1,
'max_features': 5, 'max_depth': None, 'criterion': 'gini', 'bootstrap': True}

The Confusion Matrix:
 [[26  3]
 [ 5 27]]
```

### 1.1.7 Logistic Regression

[38]:
```python
# Instantiate the classifier
LogReg = LogisticRegression()
```

[39]:
```python
# Train classifier. apply logistic reg to xtrain ytrain
LogReg.fit(X_train, y_train)
```

[39]:
```
LogisticRegression()
```

[40]:
```python
#storing pred by classifier
y_predlr = LogReg.predict(X_test)
```

[41]:
```python
#compute confusion matrix to find accuracy
metrics.confusion_matrix(y_test, y_pred)
```

[41]:
```
array([[26,  3],
       [ 4, 28]])
```

[42]:
```python
#Logistic regression is 88.5% correct if someone has CVD or not. Just as good␣
 ↪as random forest
metrics.accuracy_score(y_test, y_pred)
```

[42]: 0.8852459016393442

[43]:
```
print(classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.87      0.90      0.88        29
           1       0.90      0.88      0.89        32

    accuracy                           0.89        61
   macro avg       0.88      0.89      0.89        61
weighted avg       0.89      0.89      0.89        61
```

[44]:
```
#Apply logistic regression
model_LR = sm.Logit(y_train, X_train)
model_LR = model_LR.fit()
```

```
Optimization terminated successfully.
         Current function value: 0.351487
         Iterations 7
```

[45]:
```
# logistic regression summary
model_LR.summary()
```

[45]:
```
<class 'statsmodels.iolib.summary.Summary'>
"""
                           Logit Regression Results
==============================================================================
Dep. Variable:                 target   No. Observations:                  241
Model:                          Logit   Df Residuals:                      228
Method:                           MLE   Df Model:                           12
Date:                Thu, 02 Mar 2023   Pseudo R-squ.:                  0.4896
Time:                        02:20:35   Log-Likelihood:                -84.708
converged:                       True   LL-Null:                       -165.95
Covariance Type:            nonrobust   LLR p-value:                 1.639e-28
================================================================================
===========
                              coef    std err          z      P>|z|      [0.025
0.975]
--------------------------------------------------------------------------------
-----------
age                         0.0224      0.021      1.053      0.292      -0.019
0.064
sex                        -1.7130      0.511     -3.353      0.001      -2.714
-0.712
chest_pain_type             0.6956      0.202      3.452      0.001       0.301
```

```
1.091
resting_blood_pressure     -0.0233      0.011     -2.120      0.034      -0.045
-0.002
cholesterol                -0.0037      0.004     -0.879      0.380      -0.012
0.005
fasting_blood_sugar         0.4790      0.635      0.754      0.451      -0.766
1.724
resting_ecg                 0.6161      0.388      1.587      0.113      -0.145
1.377
max_heart_rate              0.0352      0.010      3.686      0.000       0.016
0.054
exercise_induced_angina    -0.9877      0.453     -2.182      0.029      -1.875
-0.100
st_depression              -0.4177      0.246     -1.700      0.089      -0.899
0.064
st_slope                    0.9236      0.387      2.388      0.017       0.166
1.682
major_vessels              -0.8784      0.243     -3.608      0.000      -1.356
-0.401
thalessimia                -1.0242      0.343     -2.983      0.003      -1.697
-0.351
================================================================================
===========
"""
```

### 1.1.8 Decision Tree

[46]:
```python
# build a classifier
clf_tree = DecisionTreeClassifier()

# Set up the hyperparameter search
param_dist = {"max_depth": [3, 5, 7, None],
              "max_features": list(range(1, X_test.shape[1]+1)),
              "min_samples_split": list(range(2, 11)),
              "min_samples_leaf": list(range(1, 11)),
              "criterion": ["gini", "entropy"]}


# Run a randomized search over the hyperparameters
dtree_search = RandomizedSearchCV(clf_tree, param_distributions=param_dist)

# Fit the model on the training data
dtree_search.fit(X_train, y_train)

# Make predictions on the test data
dt_preds = dtree_search.best_estimator_.predict(X_test)
```

[47]:
```
#Decision tree has 79.7% accuracy in predicting someone has CVD
print("Results from Decision Tree:\n " )
print("-The best score across ALL searched params: ", dtree_search.best_score_)
print("-The best parameters across ALL searched params:\n ", dtree_search.
↪best_params_)

cm = confusion_matrix(y_test, dt_preds)
print("\nThe Confusion Matrix:\n", cm)
```

```
Results from Decision Tree:

-The best score across ALL searched params:  0.797108843537415
-The best parameters across ALL searched params:
  {'min_samples_split': 7, 'min_samples_leaf': 5, 'max_features': 10,
'max_depth': None, 'criterion': 'entropy'}

The Confusion Matrix:
 [[26  3]
 [12 20]]
```

### 1.1.9 AdaBoostClassifier

[48]:
```
# build a classifier for AdaBoostClassifier()
clf_ada = AdaBoostClassifier()

# Set up the hyperparameter search
# look at  setting up your search for n_estimators, learning_rate

param_dist = {"n_estimators": [10, 100, 200, 400], #50 is default so try low␣
↪end and high ends
              "learning_rate": [0.001, 0.005, .01, 0.05, 0.1, 0.2, 0.3, 0.4, 0.
↪5, 1, 2, 10, 20]} #0.01 is a golden standard

#trial and error for the parameters. look at webpages or jupyter and see what␣
↪the parameters are in the help.


# Run a randomized search over the hyperparameters
ada_search =RandomizedSearchCV(clf_ada, param_distributions=param_dist)

# Fit the model on the training data
ada_search.fit(X_train, y_train)

# Make predictions on the test data
ada_preds = ada_search.best_estimator_.predict(X_test)
```

[49]:
```
#AdaBoost has 83.0% accuracy in predicting someone has CVD
print("Results from AdaBoost:\n " )
print("-The best score across ALL searched params: ", ada_search.best_score_)
print("-The best parameters across ALL searched params:\n ", ada_search.
↪best_params_)

cm = confusion_matrix(y_test, ada_preds)
print("\nThe Confusion Matrix:\n", cm)
```

```
Results from AdaBoost:

-The best score across ALL searched params:  0.8301020408163267
-The best parameters across ALL searched params:
  {'n_estimators': 10, 'learning_rate': 0.3}

The Confusion Matrix:
 [[24  5]
 [ 6 26]]
```

#### 1.1.10 Support vector

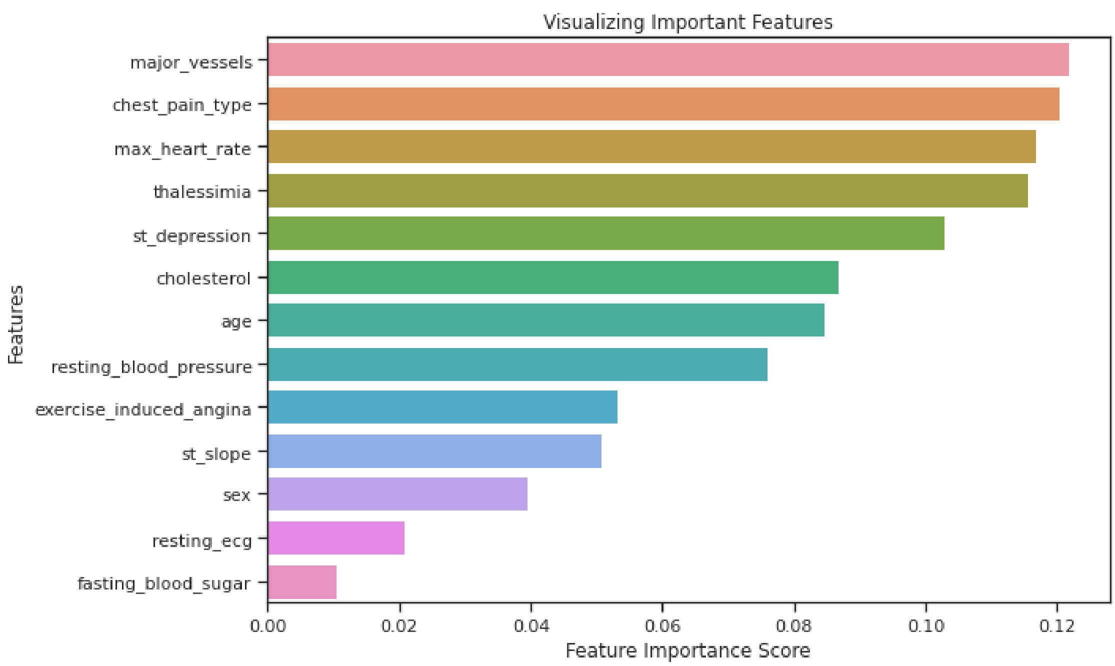
[50]:
```
# build a classifier for support vector machines
clf_svc = SVC()

# Set up the hyperparameter search
# look at setting up your search for C (recommend 0-10 range),
# kernel, and degree
# http://scikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html
param_dist = {"C": [0.1, 0.5, 1, 3, 5],
              "kernel": ['linear','rbf']
             }


# Run a randomized search over the hyperparameters
svc_search = RandomizedSearchCV(clf_svc, param_distributions=param_dist)

# Fit the model on the training data
svc_search.fit(X_train, y_train)

# Make predictions on the test data
svc_preds = svc_search.best_estimator_.predict(X_test)
```

[51]:
```
#Support vector has 84.2% accuracy in predicting someone has CVD
print("Results from Support Vector Machines (SVM):\n " )
print("-The best score across ALL searched params: ", svc_search.best_score_)
```

```
print("-The best parameters across ALL searched params:\n ", svc_search.
↪best_params_)

cm = confusion_matrix(y_test, svc_preds)
print("\nThe Confusion Matrix:\n", cm)
```

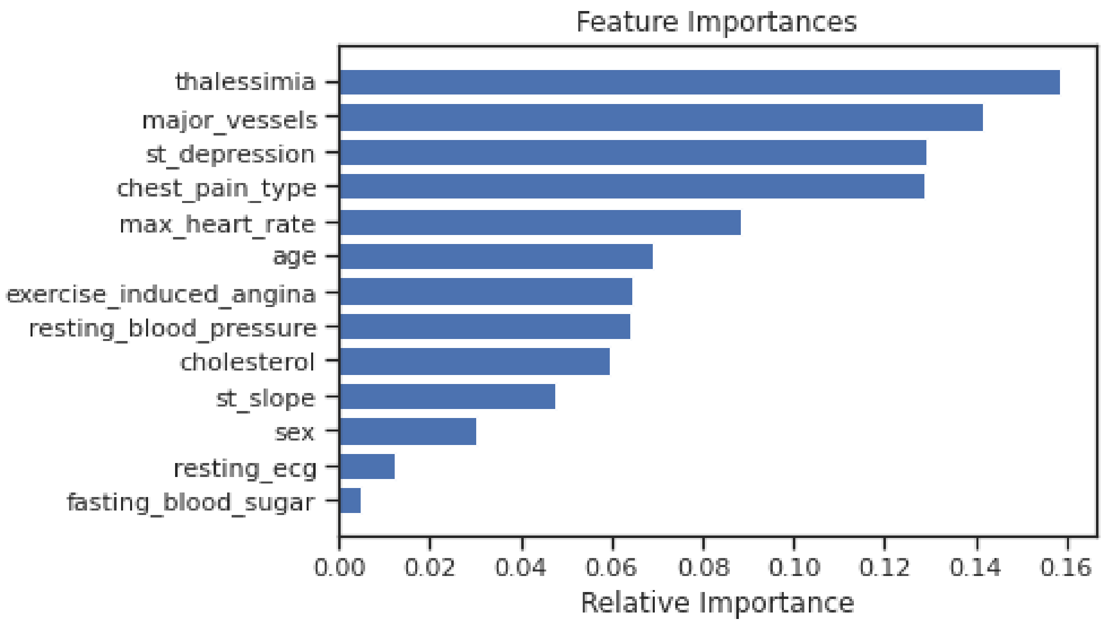
```
Results from Support Vector Machines (SVM):

-The best score across ALL searched params:  0.8424319727891157
-The best parameters across ALL searched params:
  {'kernel': 'linear', 'C': 0.1}

The Confusion Matrix:
 [[25  4]
 [ 4 28]]
```

[52]:
```
#checking most important features
feature_imp = pd.Series(clf.feature_importances_, index=scaled_train2.columns).
↪sort_values(ascending=False)

plt.figure(figsize=(10,6))
sns.barplot(x=feature_imp, y=feature_imp.index)
# Add labels to your graph
plt.xlabel('Feature Importance Score')
plt.ylabel('Features')
plt.title("Visualizing Important Features")
plt.tight_layout()
```



[53]:

```python
#most important relative features
features = df2.columns[:df2.shape[1]]
importances = random_search.best_estimator_.feature_importances_
indices = np.argsort(importances)

plt.title('Feature Importances')
plt.barh(range(len(indices)), importances[indices], color='b', align='center')
plt.yticks(range(len(indices)), features[indices])
plt.xlabel('Relative Importance');
```




[ ]:

```python

```