Kaggle Heart Attack Data Analysis Prediction/Classification using Logistic Regression, Random Forest

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July 26, 2021

```
In [1]: # By : Rohit Gupta, Date : Date : 12 July 2021
        # Reading and Analyzing covid data from the following kaggle dataset :
        # https://www.kaggle.com/rashikrahmanpritom/heart-attack-analysis-prediction-dataset

        import os
```

```
In [32]: os.getcwd()
         os.chdir("C:\\Users\\....\\Desktop\\Self_Learning\heart_dataset")
```

```
In [33]:  import os
          path = "C:\\Users\\....\\Desktop\\Self_Learning\heart_dataset"
          arr = os.listdir(path)
          print(arr)

['heart.csv', 'o2Saturation.csv']
```

```
In [34]: import pandas as pd
         data_heart = pd.read_csv('heart.csv')
         data_heart.head()

Out[34]:    age  sex  cp  trtbps  chol  fbs  restecg  thalachh  exng  oldpeak  slp  \
         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

            caa  thall  output
         0    0      1       1
         1    0      2       1
         2    0      2       1
         3    0      2       1
         4    0      2       1
```

```
In [5]: data_heart.columns
```

```
Out[5]: Index([u'age', u'sex', u'cp', u'trtbps', u'chol', u'fbs', u'restecg',
               u'thalachh', u'exng', u'oldpeak', u'slp', u'caa', u'thall', u'output'],
              dtype='object')
```

```
In [6]: # What does the 1 and 0 stand in the sex column ? Assume 1 stands for male and 0 stands

        data_heart.shape
```

```
Out[6]: (303, 14)
```

```
In [7]: # what kind of exploratory data analysis can we perform here ? Let us see
        # the correlation between Age, Sex, exang: exercise induced angina and trtbps : resting
        # Possibility that with age, and increased stress levels of life, resting blood pressure
        import seaborn as sns
        import matplotlib.pyplot as plt

        # allow plots to occur inline
        %matplotlib inline
```

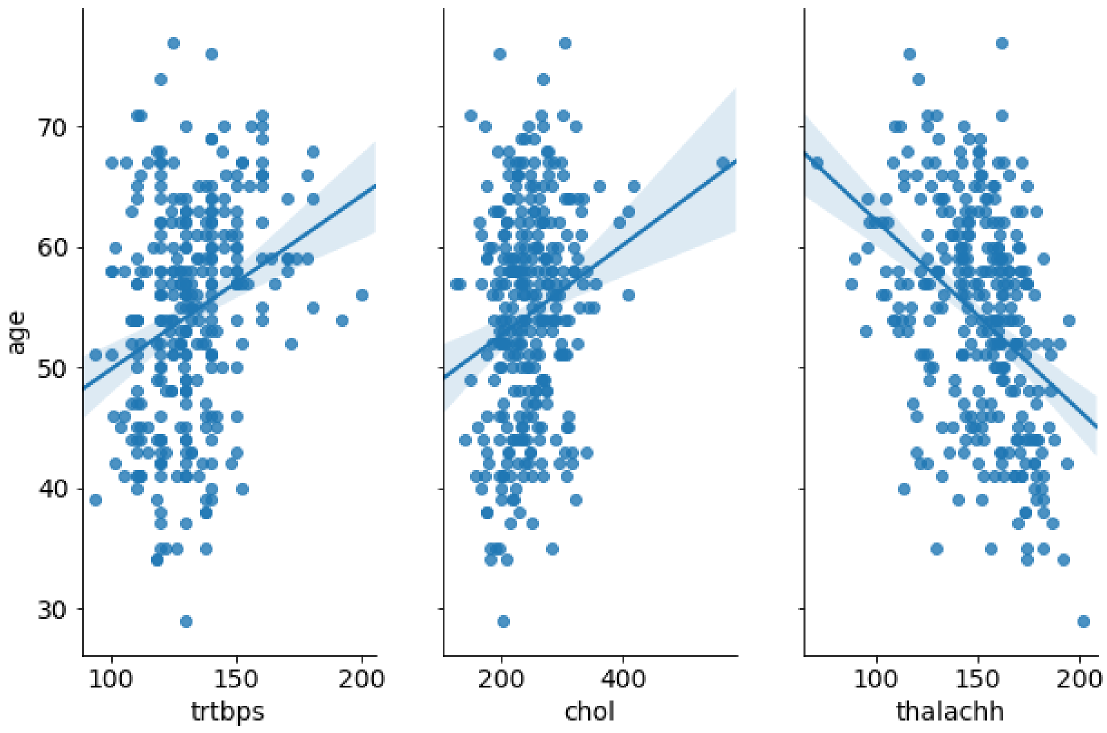
```
In [8]: data_heart.sort_values(by=['age'],axis=0,ascending=True).head()
```

```
Out[8]:      age  sex  cp  trtbps  chol  fbs  restecg  thalachh  exng  oldpeak  slp  \
        72    29    1   1     130   204    0        0       202     0      0.0    2
        58    34    1   3     118   182    0        0       174     0      0.0    2
        125   34    0   1     118   210    0        1       192     0      0.7    2
        239   35    1   0     126   282    0        0       156     1      0.0    2
        65    35    0   0     138   183    0        1       182     0      1.4    2

             caa  thall  output
        72     0      2       1
        58     0      2       1
        125    0      2       1
        239    0      3       0
        65     0      2       1
```

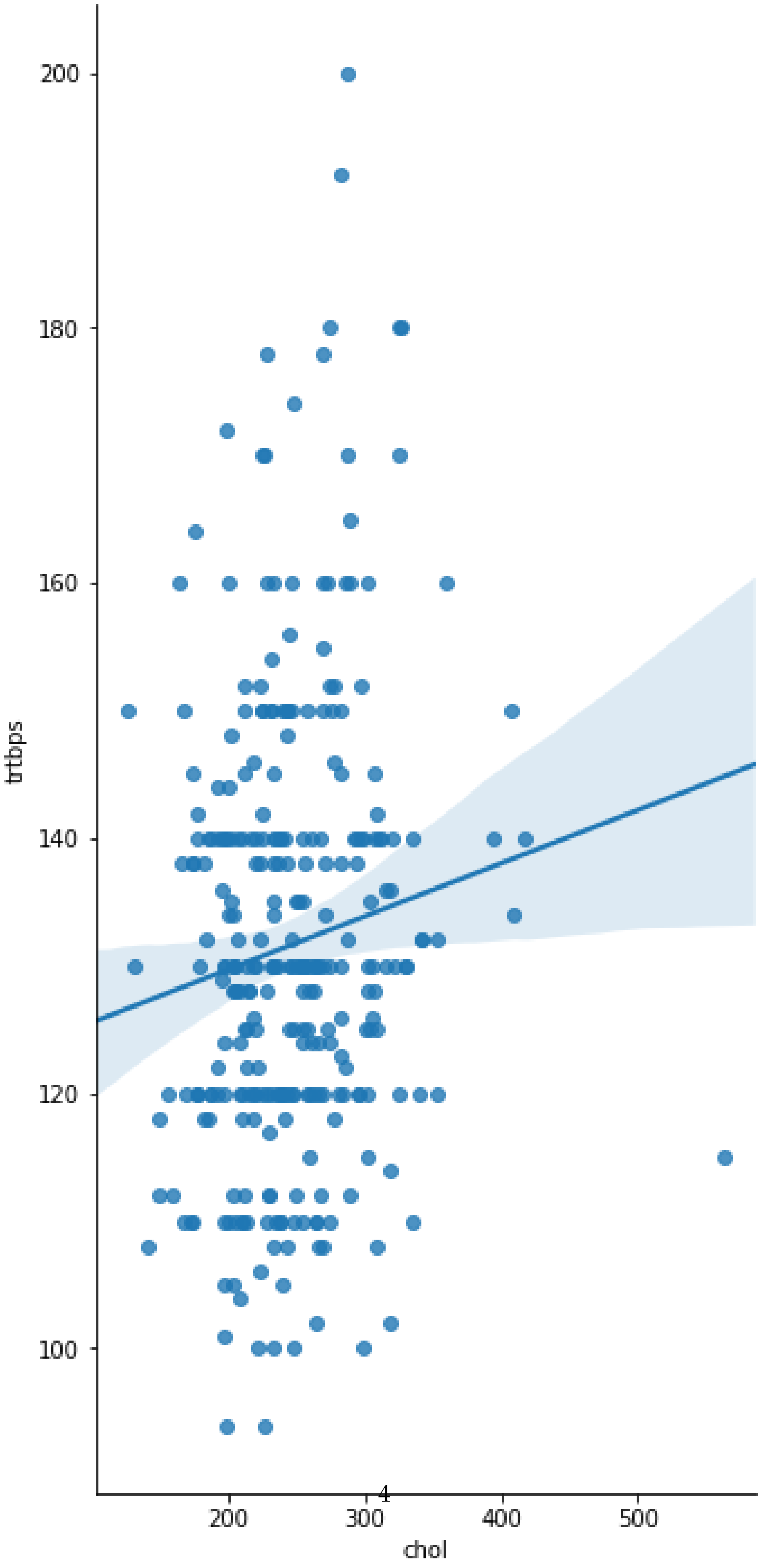
```
In [65]: # Using just scatter plots we do not get much insight. However we can use kind = 'reg'
         # are somewhat correlated.
         # sns.pairplot(data_heart, x_vars=['trtbps', 'chol', 'cp'], y_vars=['age'], aspect = 0.
```

```
In [228]: # What other plots can be drawn that provide other descriptive insights into the datas
          sns.pairplot(data_heart, x_vars=['trtbps', 'chol', 'thalachh'], y_vars=['age'], aspect
```

```
Out[228]: <seaborn.axisgrid.PairGrid at 0x16738518>
```

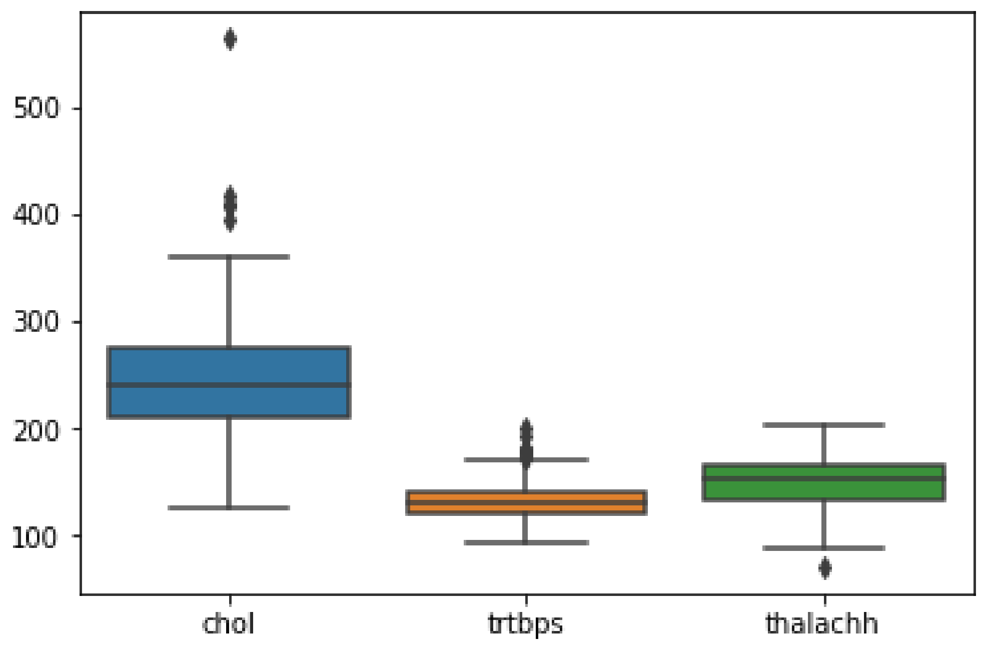


```
In [64]: # It will be interesting to see how the variables age and rest_ecg are related.
         # sns.pairplot(data_heart, x_vars = ['restecg'], y_vars = ['age'], height = 6 ,aspect =

In [24]: # Further see how other variables are related to each other
         # how is resting blodd pressure associated with cholestrol levels ?
         # In the process determine which features will predict heart attack.

         sns.pairplot(data_heart, x_vars = ['chol'], y_vars = ['trtbps'], height = 10 ,aspect =

Out[24]: <seaborn.axisgrid.PairGrid at 0xe987898>
```


trtbps
chol
200
180
160
140
120
100
200
300
400
500

```
In [25]: # Draw boxplots to see the measures of the features - since there are several continous
         # using boxplot we can get the distribution of the data.
         #help(sns.boxplot)

         feature_cols = ['chol','trtbps','thalachh']
         sns.boxplot(data=data_heart[feature_cols])

         ## Grouped boxplots for Male and Female :

         # select all rows with Sex = 0 ---> Male ----> df1
         # select all rows with Sex = 1 ---> Female ---> df 2

         # then compare boxplots across the chol, trtbps and thalachh
```

```
Out[25]: <matplotlib.axes._subplots.AxesSubplot at 0xf1c6d30>
```



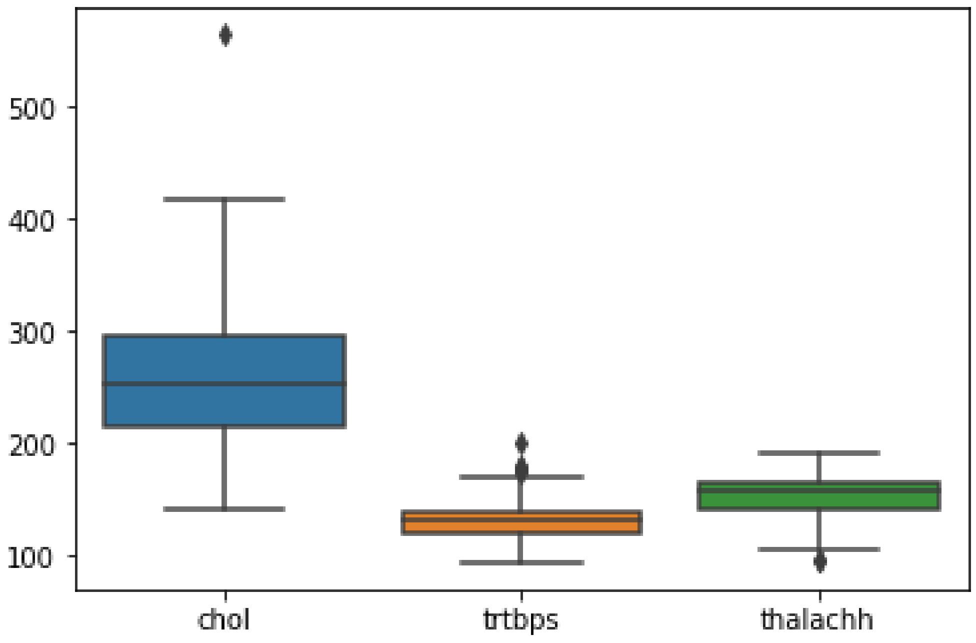
```
In [26]: data_heart_male = data_heart.loc[data_heart['sex']==0]
         data_heart_female = data_heart.loc[data_heart['sex']==1]
```

```
In [27]: data_heart_male.shape
```

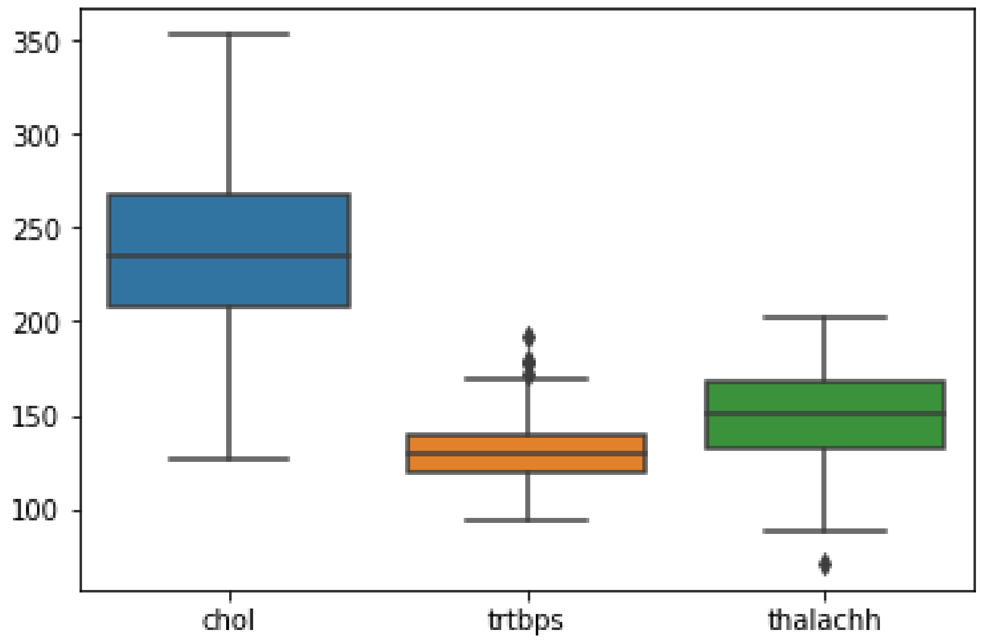
```
Out[27]: (96, 14)
```

```
In [28]: data_heart_female.shape
```

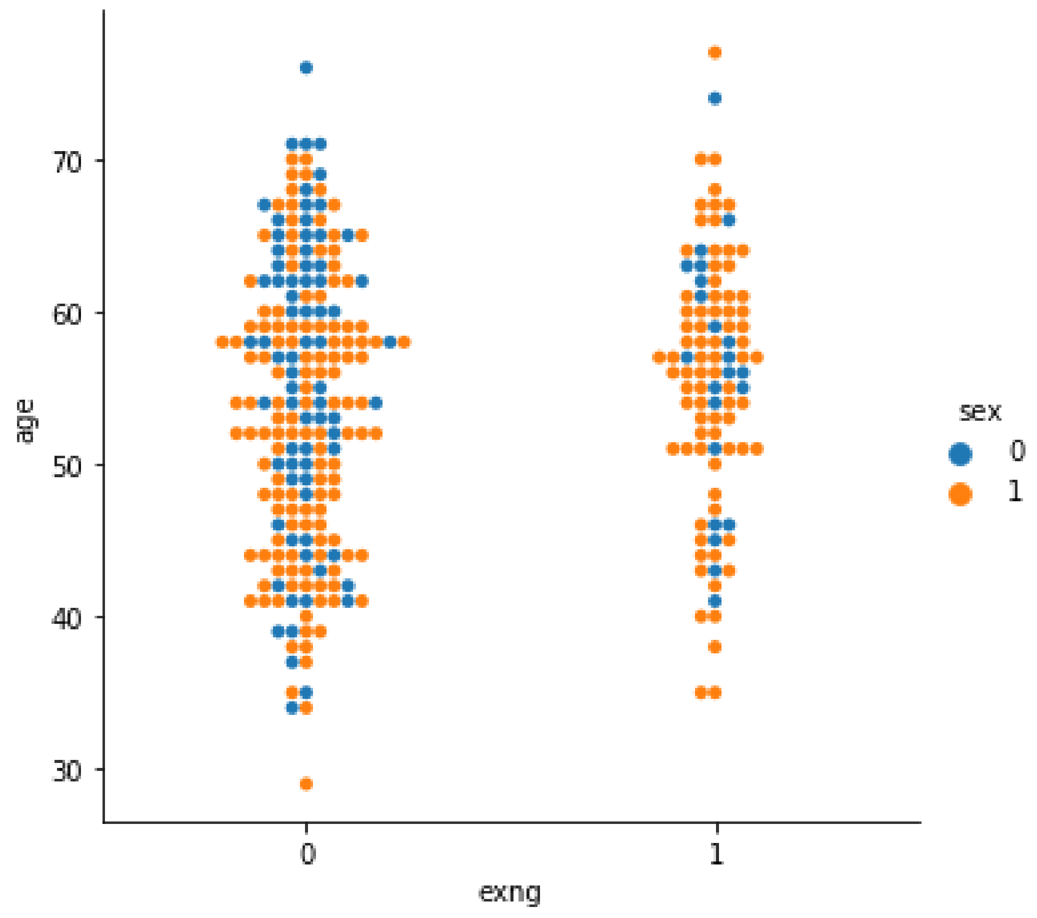
```
Out[28]: (207, 14)

In [17]: # Category Male boxplot

         feature_cols = ['chol','trtbps','thalachh']
         sns.boxplot(data=data_heart_male[feature_cols])

Out[17]: <matplotlib.axes._subplots.AxesSubplot at 0xe1337f0>
```



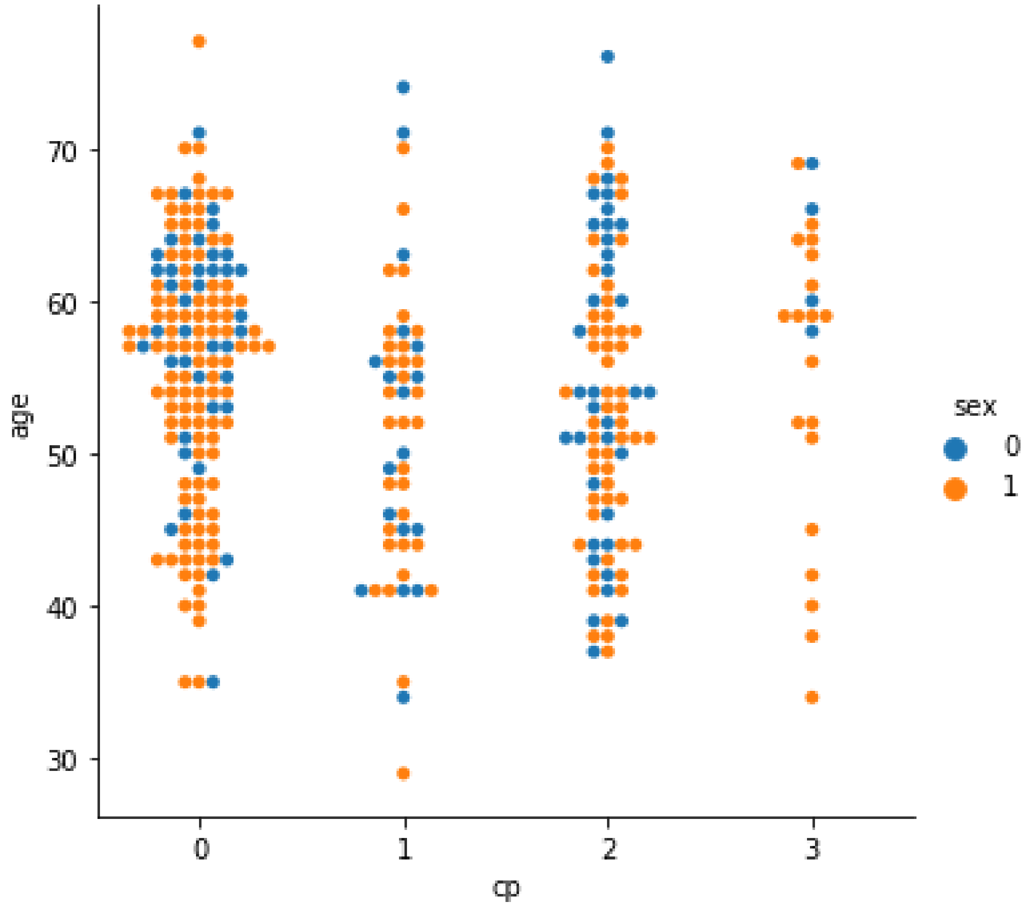
```
In [18]: # Category Female boxplots

         feature_cols = ['chol','trtbps','thalachh']
         sns.boxplot(data=data_heart_female[feature_cols])

Out[18]: <matplotlib.axes._subplots.AxesSubplot at 0xe3a3470>
```



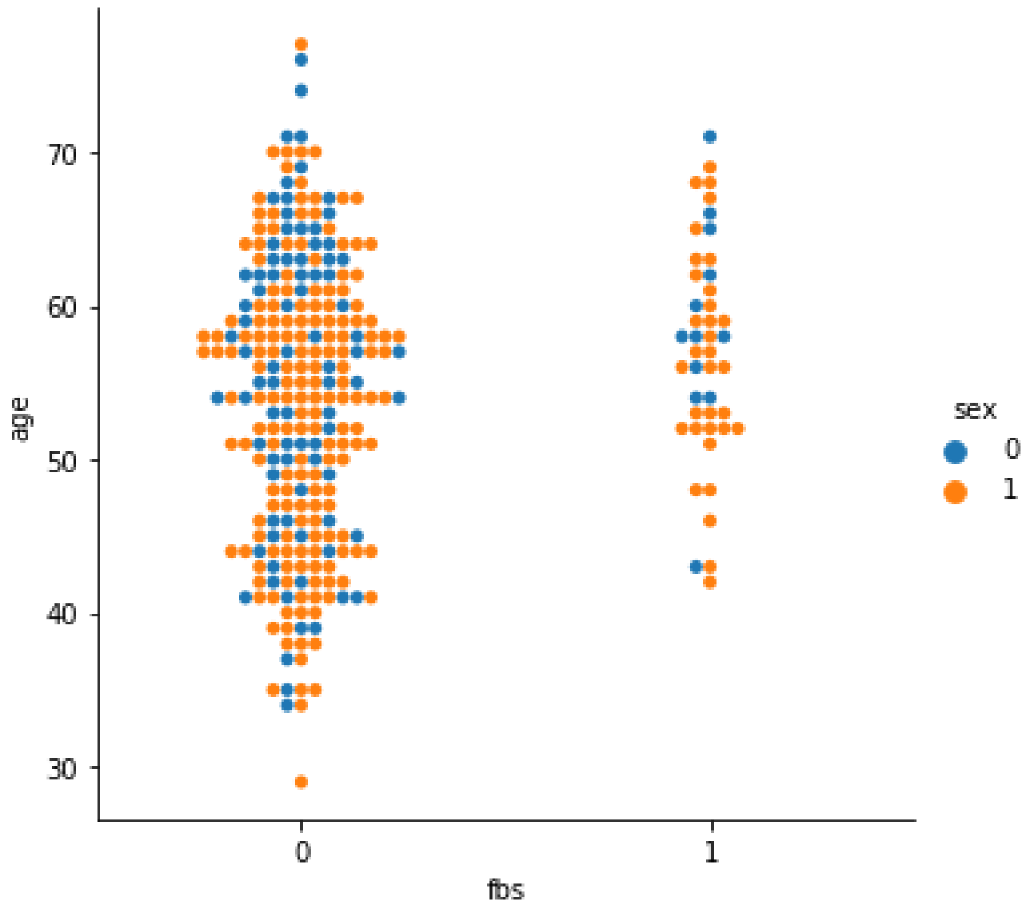
```
In [43]: # Visualizing the given categorical data such as  :
         # exang: exercise induced angina (1 = yes; 0 = no)
         # Recall 0 : stands for male and 1 stands for female

         sns.catplot(x="exng", y="age", hue="sex", kind="swarm", data=data_heart)

         # We see that excercise induced angina more likely in females than in males.
         # Excercise induced angina less in males (as compared to females)

Out[43]: <seaborn.axisgrid.FacetGrid at 0x11733240>
```



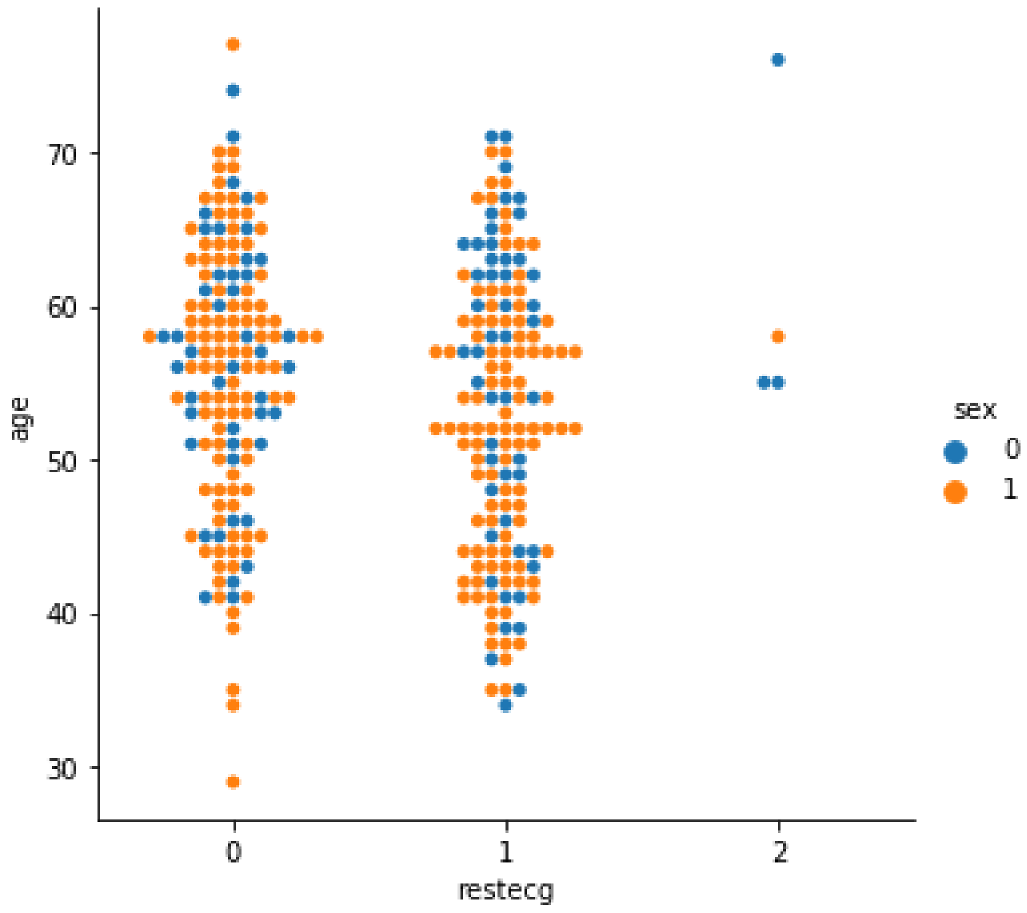
```
In [59]: # Visualizing cp vs age : with males/females :

         # cp : Chest Pain type chest pain type

         # Value 1: typical angina
         # Value 2: atypical angina
         # Value 3: non-anginal pain
         # Value 4: asymptomatic

         sns.catplot(x="cp", y="age", hue="sex", kind="swarm", data=data_heart)

         # vertical positioning of the categorical labels :
         #sns.catplot(x="age", y="cp", hue="sex", kind="swarm", data=data_heart)

Out[59]: <seaborn.axisgrid.FacetGrid at 0x13eff240>
```



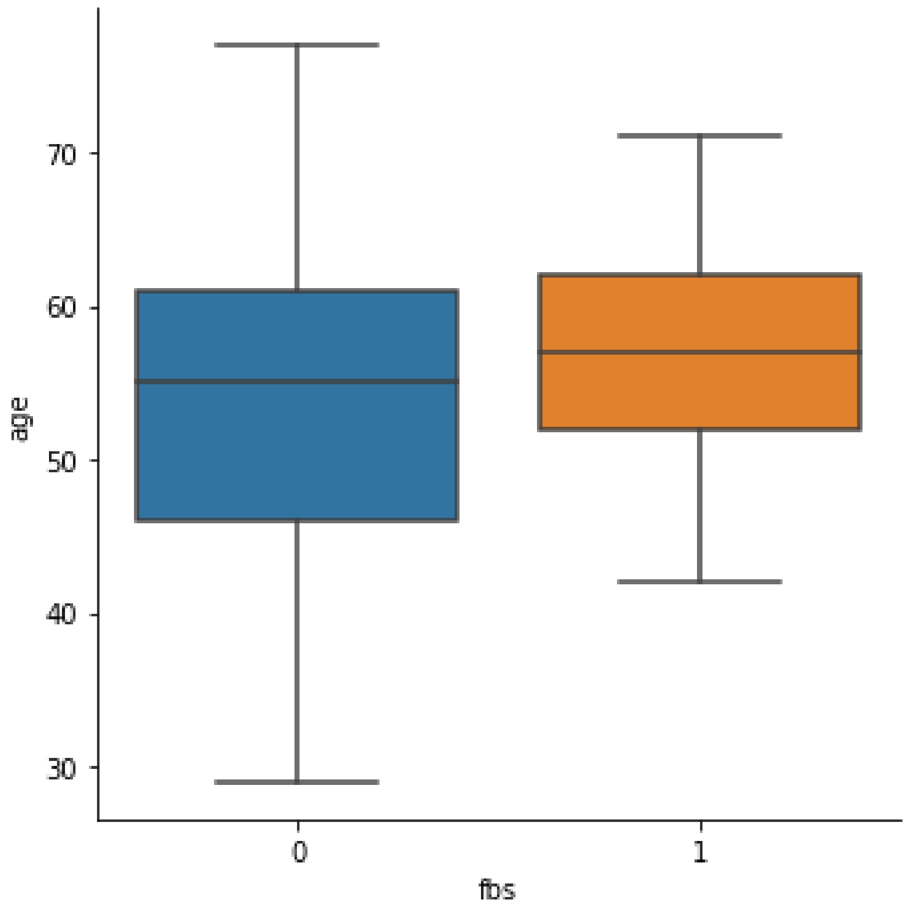
```
In [56]: # Visualizing fasting blood sugar in males vs females with age on x-axis :
         # fbs : (fasting blood sugar > 120 mg/dl) (1 = true; 0 = false)

         sns.catplot(x="fbs", y="age", hue="sex", kind = "swarm", data=data_heart)

         # majority of the population resides in the fasting blood sugar < 120 mg/dL

Out[56]: <seaborn.axisgrid.FacetGrid at 0x12e657b8>
```



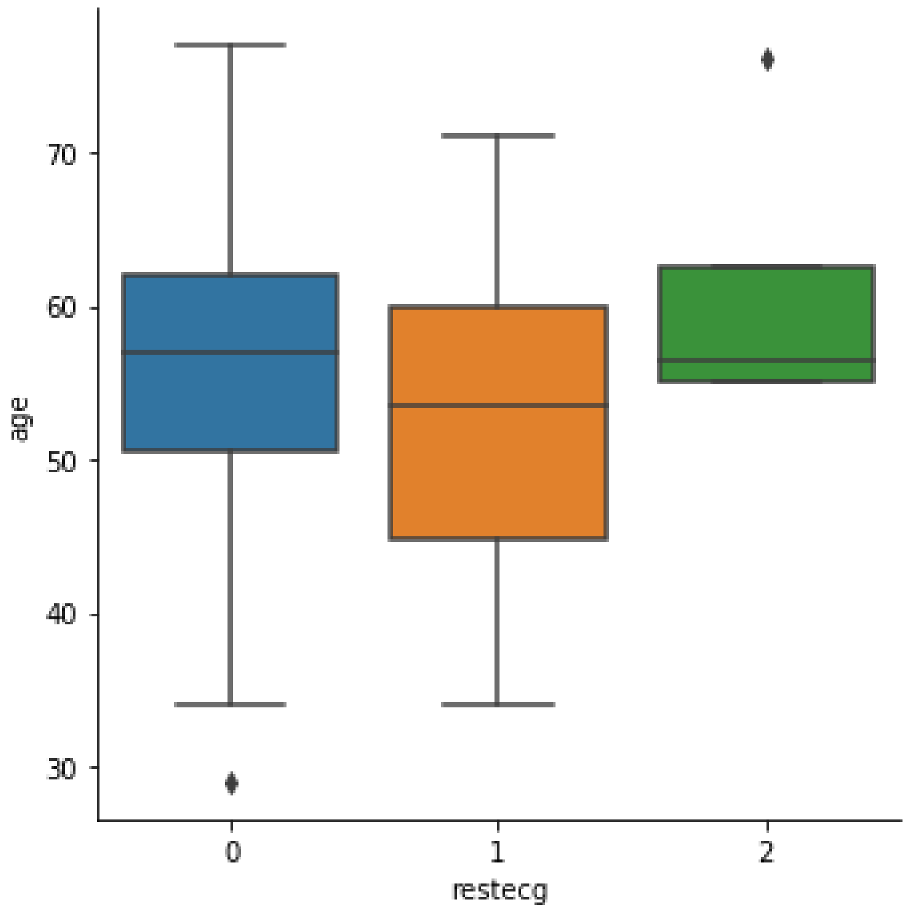
```
In [61]: # visualizing the rest_ecg with respect to age

         # rest_ecg : resting electrocardiographic results

         # Value 0: normal
         # Value 1: having ST-T wave abnormality (T wave inversions and/or ST elevation or depre
         # Value 2: showing probable or definite left ventricular hypertrophy by Estes' criteria

         sns.catplot(x="restecg" , y = "age" , hue = "sex" , kind = "swarm" , data=data_heart)

Out[61]: <seaborn.axisgrid.FacetGrid at 0x140a8240>
```



```
In [67]: # fbs boxplot
         sns.catplot(x="fbs", y="age", kind="box", data=data_heart)

         # fbs with respect to males
         # sns.catplot(x="fbs", y="age", kind="box",data=data_heart_male)
         # sns.catplot(x="fbs", y="age", kind="box",data=data_heart_female)

Out[67]: <seaborn.axisgrid.FacetGrid at 0x132eef60>
```



```
In [74]: sns.catplot(x="restecg", y="age", kind="box",data=data_heart)

Out[74]: <seaborn.axisgrid.FacetGrid at 0x152d6be0>
```



```
In [66]: # correlation plot between the features/variables :

Out[66]: Index([u'age', u'sex', u'cp', u'trtbps', u'chol', u'fbs', u'restecg',
                u'thalachh', u'exng', u'oldpeak', u'slp', u'caa', u'thall', u'output'],
               dtype='object')

In [241]: # Predicting heart risk based on these features :
          # cholestrol, resting blood pressure and maximum heart rate achieved

          #data_heart.columns
          #data_heart.head(40)

In [75]: # Prediction/Classification of heart attack on the basis of following features :

         feature_cols = ['trtbps', 'chol', 'thalachh']
         #target_cols = ['output']

         X = data_heart[feature_cols]
         # recall y has to be a pandas series
         Y = data_heart.output

         from sklearn.cross_validation import train_test_split
         X_train, X_test, Y_train, Y_test = train_test_split(X,Y, random_state=1)

         # import model
         from sklearn.linear_model import LogisticRegression

         # instantiate model
         logreg = LogisticRegression()
```

```
C:\ProgramData\Anaconda2\lib\site-packages\sklearn\cross_validation.py:41: DeprecationWarning: T
  "This module will be removed in 0.20.", DeprecationWarning)
```

```
In [76]: #X_train.shape
         #Y_train.shape
         #X_test.shape
         #Y_test.shape

         # fit the model on the data
         logreg.fit(X_train, Y_train)
```

```
Out[76]: LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, max_iter=100, multi_class='ovr', n_jobs=1,
                   penalty='l2', random_state=None, solver='liblinear', tol=0.0001,
                   verbose=0, warm_start=False)
```

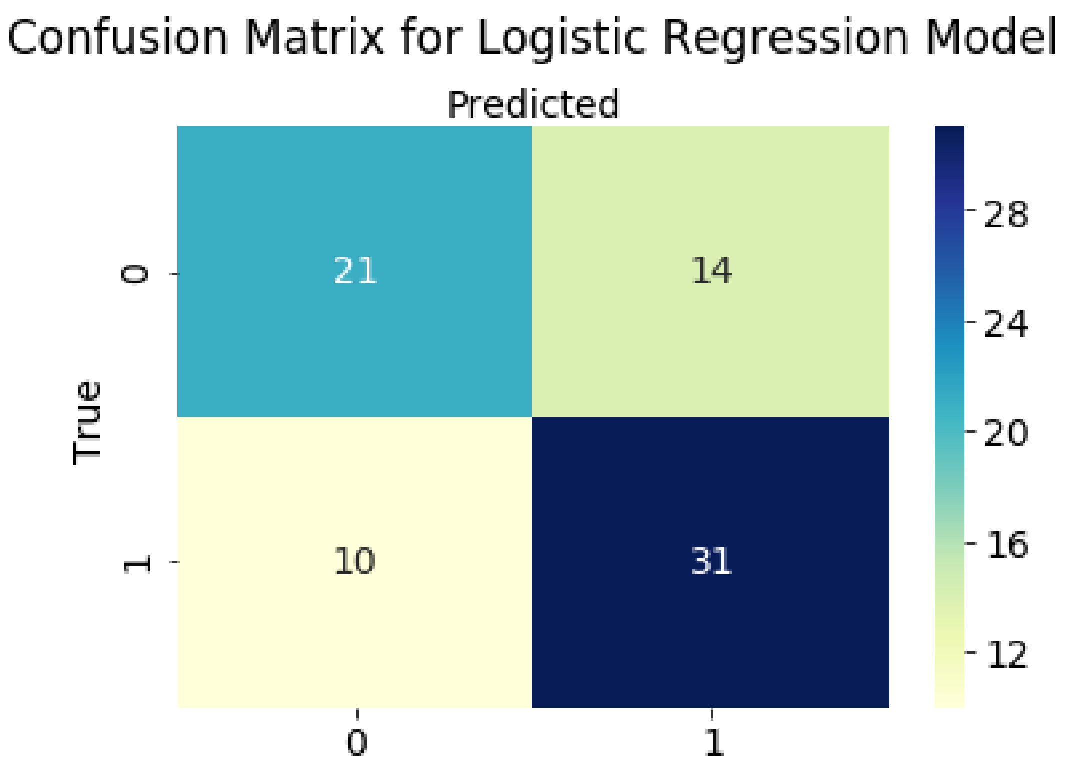
```
In [77]: # perform prediction
         Y_pred = logreg.predict(X_test)
```

```
In [78]: # calculate RMSE error between Y_test and Y_pred
         # and see how it changes if you remove one feature from the feature_cols

         from sklearn import metrics
         import numpy as np
         # print(np.sqrt(metrics.mean_squared_error(Y_test,Y_pred)))
         # 0.5619514869490163

         print(metrics.accuracy_score(Y_test,Y_pred))
```

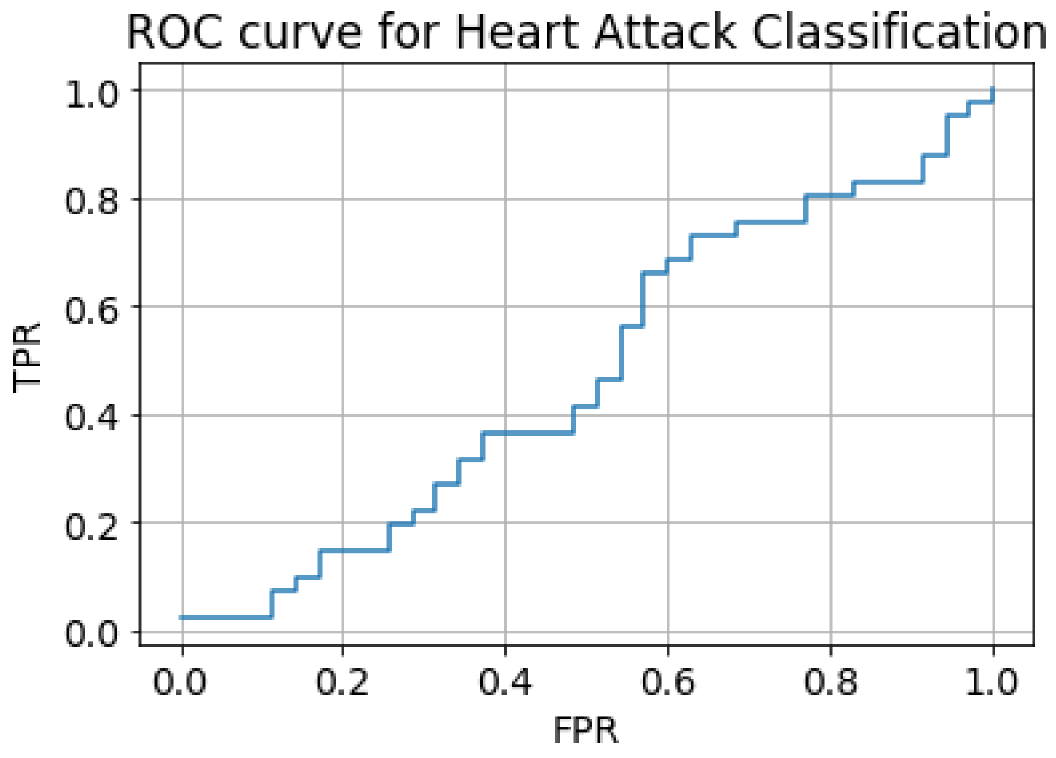
```
0.6842105263157895
```

```
In [79]: # remove chol and see how the rmse value changes :
         feature_cols = ['trtbps', 'thalachh', 'age']

         X = data_heart[feature_cols]
         Y = data_heart.output
         # train_test split
         from sklearn.cross_validation import train_test_split

         X_train, X_test, Y_train, Y_test = train_test_split(X,Y,random_state=1)

         # import
         from sklearn.linear_model import LogisticRegression

         # instantiate
         logreg = LogisticRegression()

In [80]: #fit the model
         logreg.fit(X_train,Y_train)

Out[80]: LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, max_iter=100, multi_class='ovr', n_jobs=1,
                   penalty='l2', random_state=None, solver='liblinear', tol=0.0001,
                   verbose=0, warm_start=False)

In [81]: Y_pred_new = logreg.predict(X_test)

In [165]: # For the logistic regression model print the confusion matrix
          metrics.confusion_matrix(Y_test,Y_pred)

Out[165]: array([[21, 14],
                 [10, 31]], dtype=int64)

In [223]: # splice the confusion matrix into 4 parts : TP,TN,FP,FN

          confusion_heartmat = metrics.confusion_matrix(Y_test,Y_pred)
          TP = confusion_heartmat[1,1]
          TN = confusion_heartmat[0,0]
          FP = confusion_heartmat[0,1]
          FN = confusion_heartmat[1,0]

In [168]: # calculate RMSE error between Y_test and Y_pred_new
          # print(np.sqrt(metrics.mean_squared_error(Y_test,Y_pred_new)))
          # 0.5735393346764044

          print(metrics.accuracy_score(Y_test,Y_pred_new))

0.6710526315789473


In [227]: # accuracy : TP+TN/TP+TN+FP+FN
          print(1-metrics.accuracy_score(Y_test,Y_pred))

0.3157894736842105
```

```
In [220]: # when actual value is positive, how often is the prediction correct :
          #TP/TP+FN

          # TPR  = sensitivity = Recall :
          metrics.recall_score(Y_test,Y_pred)

Out[220]: 0.7560975609756098

In [224]: # FPR - specificity
          print(FP/float(FP+TN))

0.4


In [226]: from sklearn.metrics import classification_report
          print(classification_report(Y_test, Y_pred, labels=[0, 1]))

             precision    recall  f1-score   support

          0       0.68      0.60      0.64        35
          1       0.69      0.76      0.72        41

avg / total       0.68      0.68      0.68        76



In [242]: conf_matrix_logreg_model = metrics.confusion_matrix(Y_test, Y_pred)

          labels = [0, 1]
          fig, ax = plt.subplots()
          tick_marks = np.arange(len(labels))
          plt.xticks(tick_marks, labels)
          plt.yticks(tick_marks, labels)

          # create heatmap
          sns.heatmap(pd.DataFrame(conf_matrix_logreg_model), annot=True, cmap="YlGnBu", fmt='g'
          ax.xaxis.set_label_position("top")
          plt.title('Confusion Matrix for Logistic Regression Model', y=1.1)
          plt.ylabel('True')
          plt.xlabel('Predicted')

Out[242]: Text(0.5,11,'Predicted')
```



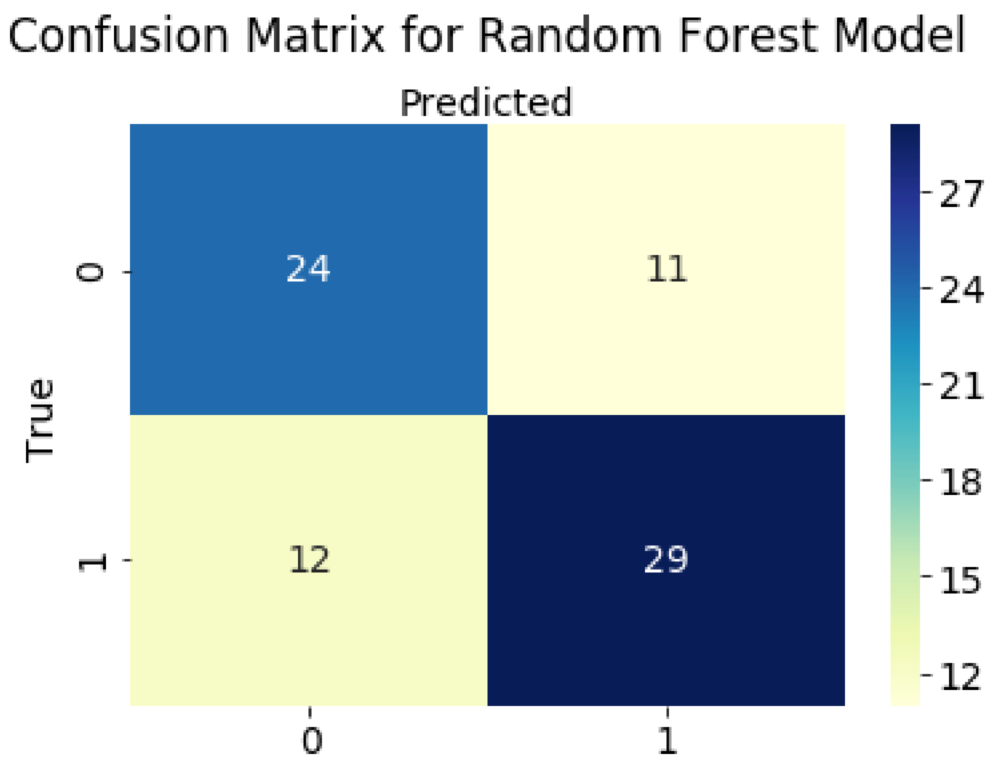
```
In [216]: # Draw the ROC-AUC-Curve :

          # calculate Y_pred_prob
          Y_pred_prob = logreg.predict_proba(X_test)[:,1]
          #Y_test.shape
          #Y_pred_prob.shape

          fpr, tpr, threshold = metrics.roc_curve(Y_test,Y_pred_prob)

In [219]: # allow plots to appear in the notebook
          %matplotlib inline
          import matplotlib.pyplot as plt
          plt.rcParams['font.size'] = 14

          plt.plot(fpr,tpr)
          plt.xlabel('FPR')
          plt.ylabel('TPR')
          plt.title('ROC curve for Heart Attack Classification')
          plt.grid(True)
```



```
In [232]: # Let us use a different model to see if the accuracy can be improved :
          # Let us use random forest classifier :

          from sklearn.ensemble import RandomForestClassifier

          # instantiate
          rf_model = RandomForestClassifier(max_depth=2, random_state=0)

          feature_cols = ['trtbps', 'chol', 'thalachh']
          #target_cols = ['output']

          X = data_heart[feature_cols]
          # recall y has to be a pandas series
          Y = data_heart.output

          from sklearn.cross_validation import train_test_split
          X_train, X_test, Y_train, Y_test = train_test_split(X,Y, random_state=1)

In [233]: # fit the model
          rf_model.fit(X_train, Y_train)

          # store prediction values
          Y_pred_rf_model = rf_model.predict(X_test)
```

```
        # test the accuracy score
        print(metrics.accuracy_score(Y_test,Y_pred_rf_model))

0.6973684210526315


In [248]: # use RandomizedSearchCV with random forest to tune the model to perform better :
          #print(rf_model.get_params)

          from sklearn.grid_search import RandomizedSearchCV
          # specify "parameter distributions" rather than a "parameter grid"

          max_values = range(2,40)
          estimators = range(2,20)

          param_dist = dict(max_depth = max_values, n_estimators=estimators)

          # n_iter controls the number of searches
          # instantiate the RandomizedSearchCV model
          rf_randcv_model = RandomizedSearchCV(rf_model,param_dist,cv=10,scoring='accuracy',n_it

          # train the model
          rf_randcv_model.fit(X_train,Y_train)

<bound method RandomForestClassifier.get_params of RandomForestClassifier(bootstrap=True, class_
            max_depth=2, max_features='auto', max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, n_estimators=10, n_jobs=1,
            oob_score=False, random_state=0, verbose=0, warm_start=False)>


Out[248]: <bound method RandomizedSearchCV.get_params of RandomizedSearchCV(cv=10, error_score='
                    estimator=RandomForestClassifier(bootstrap=True, class_weight=None, criterio
                      max_depth=2, max_features='auto', max_leaf_nodes=None,
                      min_impurity_decrease=0.0, min_impurity_split=None,
                      min_samples_leaf=1, min_samples_split=2,
                      min_weight_fraction_leaf=0.0, n_estimators=10, n_jobs=1,
                      oob_score=False, random_state=0, verbose=0, warm_start=False),
                    fit_params={}, iid=True, n_iter=10, n_jobs=1,
                    param_distributions={'n_estimators': [2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13
                    pre_dispatch='2*n_jobs', random_state=5, refit=True,
                    scoring='accuracy', verbose=0)>

In [251]: # get best parameters
          rf_randcv_model.best_params_

          # get best scores:
          rf_randcv_model.best_score_
```

```
Out[251]: 0.6696035242290749

In [237]: conf_matrix_rf_model = metrics.confusion_matrix(Y_test, Y_pred_rf_model)

          labels = [0, 1]
          fig, ax = plt.subplots()
          tick_marks = np.arange(len(labels))
          plt.xticks(tick_marks, labels)
          plt.yticks(tick_marks, labels)

          # create heatmap
          sns.heatmap(pd.DataFrame(conf_matrix_rf_model), annot=True, cmap="YlGnBu", fmt='g')
          ax.xaxis.set_label_position("top")
          plt.title('Confusion Matrix for Random Forest Model', y=1.1)
          plt.ylabel('True')
          plt.xlabel('Predicted')

Out[237]: Text(0.5,11,'Predicted')
```

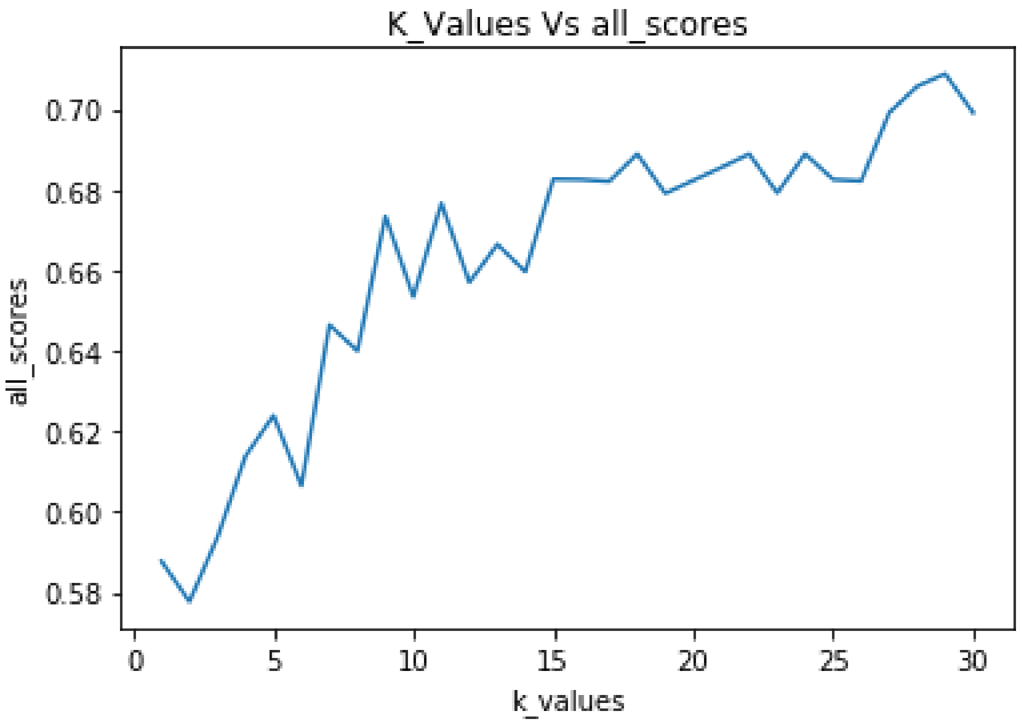


```
In [235]: metrics.confusion_matrix(Y_test,Y_pred_rf_model)

Out[235]: array([[24, 11],
                 [12, 29]], dtype=int64)
```

```
In [246]: # # Impelement NaiveBayes and check if accuracy can be improved or not.
          # from sklearn.naive_bayes import GaussianNB

          # # instantiate model
          # nb_model = GaussianNB()

          # # perform training
          # nb_model.fit(X_train,Y_train)

          # # perform testing
          # Y_pred_nb_model = nb_model.predict(X_test)

          # # check accuracy
          # print(metrics.accuracy_score(Y_test,Y_pred_nb_model))

          # #0.631578947368421
```

```
0.631578947368421
```

```
In [163]: # Future Work - Additional Improvements for accuracy to be tested in future :

          # # Use linear regression with cross validation to build model, do prediction and test

          # from sklearn.linear_model import LinearRegression
          # linreg = LinearRegression()

          # from sklearn.cross_validation import cross_val_score
          # mse_scores = cross_val_score(linreg,X,Y,cv=10,scoring = 'mean_squared_error')

          # pos_mse_scores = -mse_scores
          # # print(pos_mse_scores)
          # import numpy as np
          # rmse_scores = np.sqrt(pos_mse_scores)
          # print(rmse_scores.mean())

          # # test model by removing cholestrol levels
          # feature_cols = ['trtbps', 'thalachh']
          # #target_cols = ['output']

          # X = data_heart[feature_cols]
          # # recall y has to be a pandas series
          # Y = data_heart.output

          # mse_scores_2 = cross_val_score(linreg,X,Y,cv=10,scoring = 'mean_squared_error')
          # print(mse_scores_2)

          # pos_mse_scores_2 = -mse_scores_2
          # rmse_scores_2 = np.sqrt(pos_mse_scores_2)
          # print(rmse_scores_2.mean())

          # # Use KNN for prediction

          # from sklearn.neighbors import KNeighborsClassifier

          # # find optimal value of k between 1 to 31 for this

          # k_values = range(1,31)
          # all_scores = []
          # for k in k_values :
          #     # instantiate
          #     knn = KNeighborsClassifier(n_neighbors=k)
          #     # score calculation
          #     scores = cross_val_score(knn,X,Y,cv=10,scoring='accuracy')
          #     # append
          #     all_scores.append(scores.mean())


          # # Very Very Very Intersting : I am achieving an accuracy of 70 % when input to cross
          # import numpy as np
          # #np.mean(all_scores)
          # #print(all_scores)
          # max(all_scores)

          # print(all_scores)

          # max(all_scores)

          # # plot K-value corresponding to accuracy
          # import matplotlib.pyplot as plt

          # plt.plot(k_values, all_scores)
          # plt.title('K_Values Vs all_scores')
          # plt.xlabel('k_values')
          # plt.ylabel('all_scores')
          # plt.show()

          # # n_neighbors = 29

          # knn = KNeighborsClassifier(n_neighbors=29)
          # knn.fit(X_train,Y_train)
          # Y_pred_best_knn_model = knn.predict(X_test)
          # print(metrics.accuracy_score(Y_test,Y_pred_best_knn_model))

          # ## Accuracy decreased for some reason.
```


K_Values Vs all_scores
all_scores
k_values
0.58
0.60
0.62
0.64
0.66
0.68
0.70
0
5
10
15
20
25
30