Title: Heart Failure Prediction with ML

Patient Data Understanding course Project by Kamal M. Shaik

Rowan University - Masters in Data Science

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1. About Data Set:

Cardiovascular diseases (CVDs) are the leading cause of death globally, resulting in 17.9 million deaths each year, representing about 31% of all fatalities. Heart attacks and strokes account for four in every five cardiovascular deaths, with one-third of these fatalities occurring before the age of 70. CVDs are a common cause of cardiac arrest, and this dataset contains 11 variables that can be used to predict heart disease. Patients with heart disease or those at high risk of stroke (due to conditions such as heart disease, diabetes, hyperlipidemia, or other pre-existing conditions) require early identification and care, which can be aided by a machine learning model. There are 918 observations and 12 columns in the dataset.

2. Data Collection:

- This dataset is sourced from Kaggle.
- URL: Heart Failure Prediction Dataset
- This dataset is a hybrid dataset built from various sources listed below.

Source:

This dataset was created by combining different datasets that were previously available independently but not combined. In this dataset, five heart datasets are combined over 11 common features, making it the largest heart disease dataset available for research purposes. The five datasets used for its curation are:

- Cleveland: 303 observations
- Hungarian: 294 observations
- Switzerland: 123 observations
- Long Beach VA: 200 observations
- Stalog (Heart) DataSet: 270 observations

Total: 1190 observations
Duplicated: 272 observations
Final dataset: 918 observations

Every dataset used can be found under the Index of heart disease datasets from the UCI Machine Learning Repository at the following link: UCI Machine Learning Repository - Heart Disease Datasets

3. Data Pre-Processing:

- There are 0 null values and 0 duplicated values, so we can consider this a clean dataset.
- Feature scaling is used in this project to equalize the range of variables. This is done during the data pre-processing stage.
- Features should be normalized so that no feature is unnecessarily large (centering) and all features are on the same scale (scaling).
- As there are 3 different data types in our dataset (i.e., float64 (1), int64 (6), object (5)), I had to implement label encoding to convert non-numeric data to numeric data.
- K-NN, for example, is sensitive to feature transformations since it relies on distances or similarities between data samples. As a result, it is advantageous for solving a system of equations, least squares, or other problems where rounding mistakes might cause major issues.

Importing required libraries and dataset initially

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import plotly.express as px
import seaborn as sns
import matplotlib as mlt
%matplotlib inline
df=pd.read_csv('/Users/kamal/Downloads/heart.csv')
```

------------------------- Data Exploration ----------------------------

Dataset value counts

```
print("Dataset Row count is", df.shape[0], ", Dataset Column count
is", df.shape[1])

Dataset Row count is 918 , Dataset Column count is 12
```

Analyzing datatypes of each attribute

```
df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
```

```
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   Age             918 non-null    int64  
 1   Sex             918 non-null    object 
 2   ChestPainType   918 non-null    object 
 3   RestingBP       918 non-null    int64  
 4   Cholesterol     918 non-null    int64  
 5   FastingBS       918 non-null    int64  
 6   RestingECG      918 non-null    object 
 7   MaxHR           918 non-null    int64  
 8   ExerciseAngina  918 non-null    object 
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    object 
 11  HeartDisease    918 non-null    int64  
dtypes: float64(1), int64(6), object(5)
memory usage: 86.2+ KB
```

Taking a look at random 10 samples of data

```
df.sample(10)
```

```
     Age Sex ChestPainType  RestingBP  Cholesterol  FastingBS 
RestingECG  \
103   40   M           ASY        120          466          1 
Normal   
767   54   F           NAP        108          267          0 
LVH   
776   62   F           ASY        150          244          0 
Normal   
449   55   M           NAP          0            0          0 
Normal   
515   63   M           NAP        130            0          1 
ST   
403   52   M           ASY        135            0          1 
Normal   
792   46   M           NAP        150          231          0 
Normal   
10    37   F           NAP        130          211          0 
Normal   
152   40   M           ATA        130          275          0 
Normal   
20    43   F            TA        100          223          0 
Normal   

     MaxHR ExerciseAngina  Oldpeak ST_Slope  HeartDisease  
103    152              Y      1.0     Flat             1  
767    167              N      0.0       Up             0  
776    154              Y      1.4     Flat             1  
449    155              N      1.5     Flat             1  
515    160              N      3.0     Flat             0  
```

```
403     128               Y      2.0     Flat              1
792     147               N      3.6     Flat              1
10      142               N      0.0       Up              0
152     150               N      0.0       Up              0
20      142               N      0.0       Up              0
```

observing value ranges of columns with interger type data

```
df.describe(include=int).T
```

```
              count        mean         std   min     25%    50%
75%    max
Age           918.0   53.510893    9.432617  28.0   47.00   54.0
60.0   77.0
RestingBP     918.0  132.396514   18.514154   0.0  120.00  130.0
140.0  200.0
Cholesterol   918.0  198.799564  109.384145   0.0  173.25  223.0
267.0  603.0
FastingBS     918.0    0.233115    0.423046   0.0    0.00    0.0
0.0    1.0
MaxHR         918.0  136.809368   25.460334  60.0  120.00  138.0
156.0  202.0
HeartDisease  918.0    0.553377    0.497414   0.0    0.00    1.0
1.0    1.0
```

observing value ranges of columns with object type data

```
df.describe(include=object).T
```

```
               count unique     top freq
Sex              918      2       M  725
ChestPainType    918      4     ASY  496
RestingECG       918      3  Normal  552
ExerciseAngina   918      2       N  547
ST_Slope         918      3    Flat  460
```

Checking for missing values

```
df.isnull().sum()
```

```
Age                 0
Sex                 0
ChestPainType       0
RestingBP           0
Cholesterol         0
FastingBS           0
RestingECG          0
MaxHR               0
ExerciseAngina      0
Oldpeak             0
```

```
ST_Slope          0
HeartDisease      0
dtype: int64
```

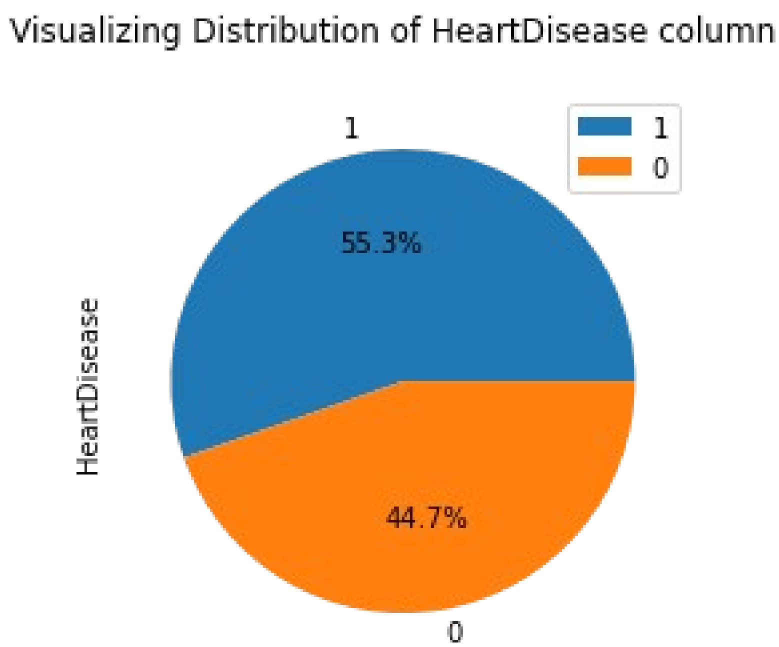
Checking for duplicated values

```
df.duplicated().sum()

0
```

---------------------- VISUALIZATION --------------------------

As our target variable column is 'HeartDisease', let's visualize it

```
hd = pd.DataFrame(df['HeartDisease'].value_counts())
hd

   HeartDisease
1           508
0           410

hd.plot(kind='pie', title='Visualizing Distribution of HeartDisease
column', figsize=[4,4],
          autopct='%.1f%%', subplots=True,fontsize =10)
plt.show()
```



we have 55.3% of positive cases and 44.7% negative cases w.r.t HeartDisease,

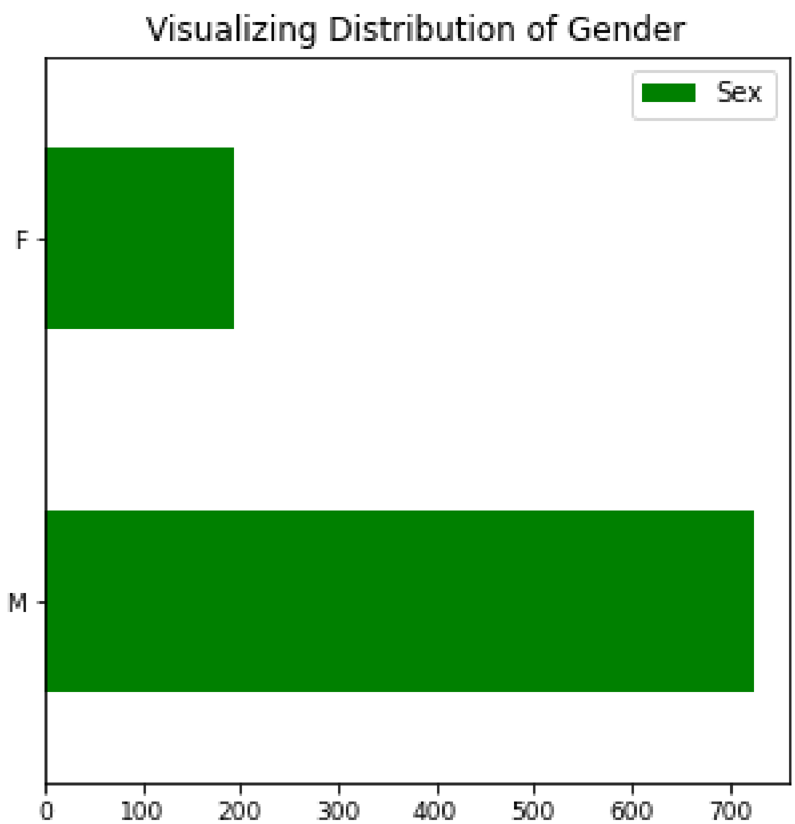
So, we can conclude this as a very balanced dataset

Visualizing plot to see Gender Distribution

```
gender = pd.DataFrame(df['Sex'].value_counts())
gender
```

	Sex
M	725
F	193

```
gender.plot.barh( title='Visualizing Distribution of Gender',
figsize=[5,5],fontsize=9,color='green')
plt.show()
```



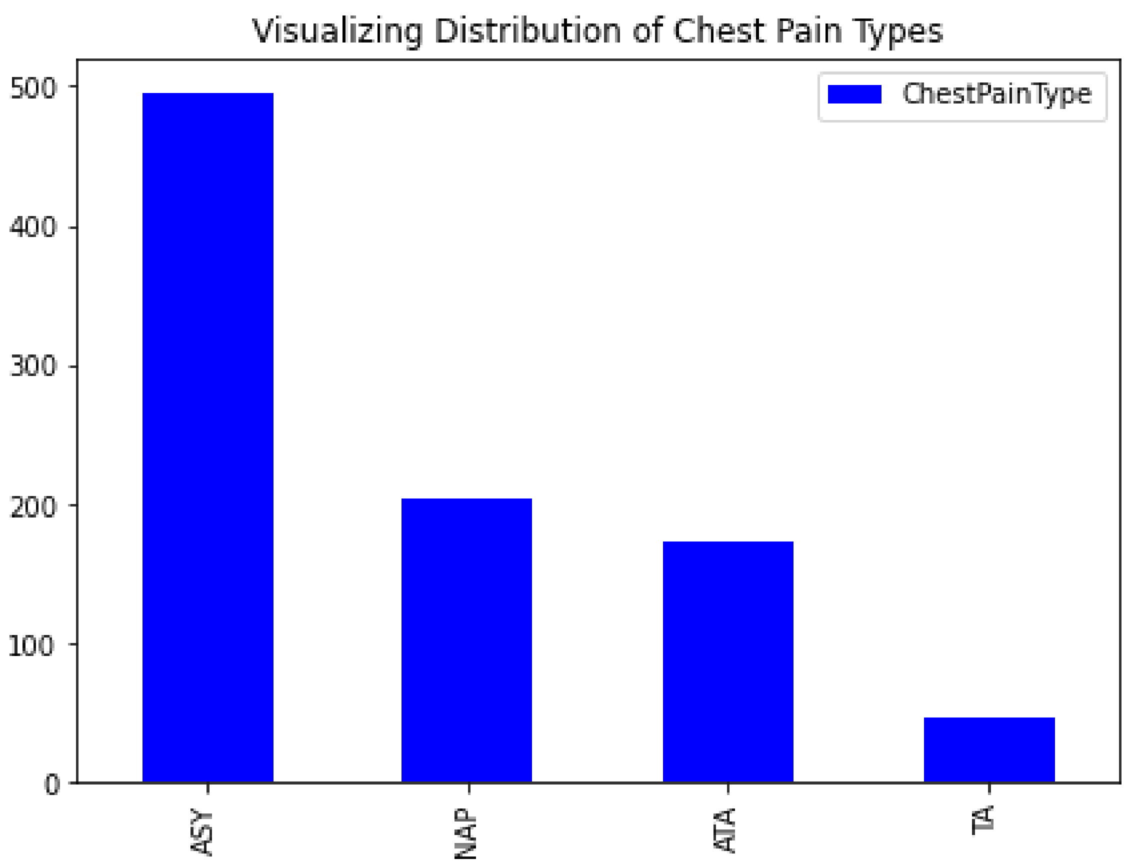
Male patients are dominant in number of this dataset

Now, Making a plot to see which Chest Pain Type is prominent among Heart Disease Patients

```
cp = pd.DataFrame(df['ChestPainType'].value_counts())
cp
```

	ChestPainType
ASY	496
NAP	203
ATA	173
TA	46

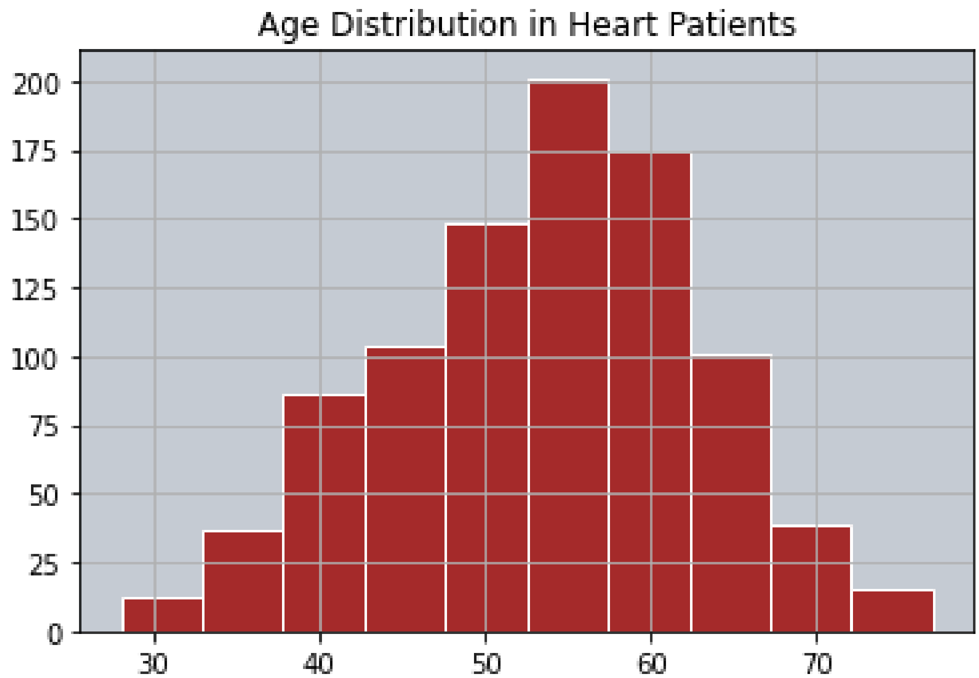
```
cp.plot.bar(title='Visualizing Distribution of Chest Pain Types',
figsize=[7,5],fontsize=10,color='b')
plt.show()
```



We see that the most common type of Chest Pain in Heart Patients is Asymptomatic with around 400 patients.

```
df.hist(column='Age',grid=1,color='Brown',edgecolor='white');
ax=plt.gca()
```

```
ax.set_facecolor('#C5CBD3')
plt.title('Age Distribution in Heart Patients');
```

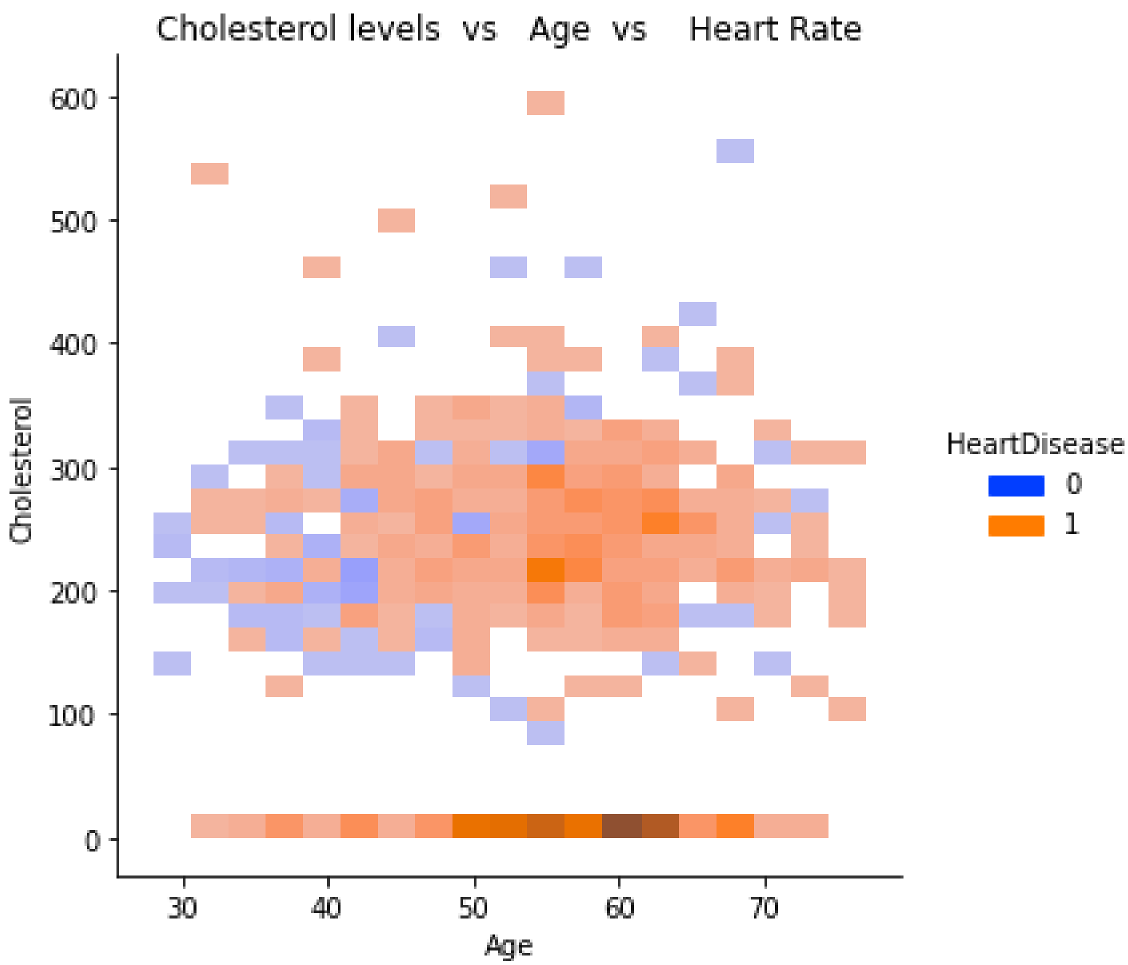


We could observe that adults around the age of 60 seem to be the most vulnerable to heart disease

```

```

Plotting a Distribution plot to verify if Age affects Cholesterol levels

```
dp=df[df['HeartDisease']==1]
sns.displot(data=df,y='Cholesterol',x='Age',
hue='HeartDisease',palette='bright',cmap='coolwarm', height=5);
plt.title('Cholesterol levels  vs   Age  vs    Heart Rate');
```

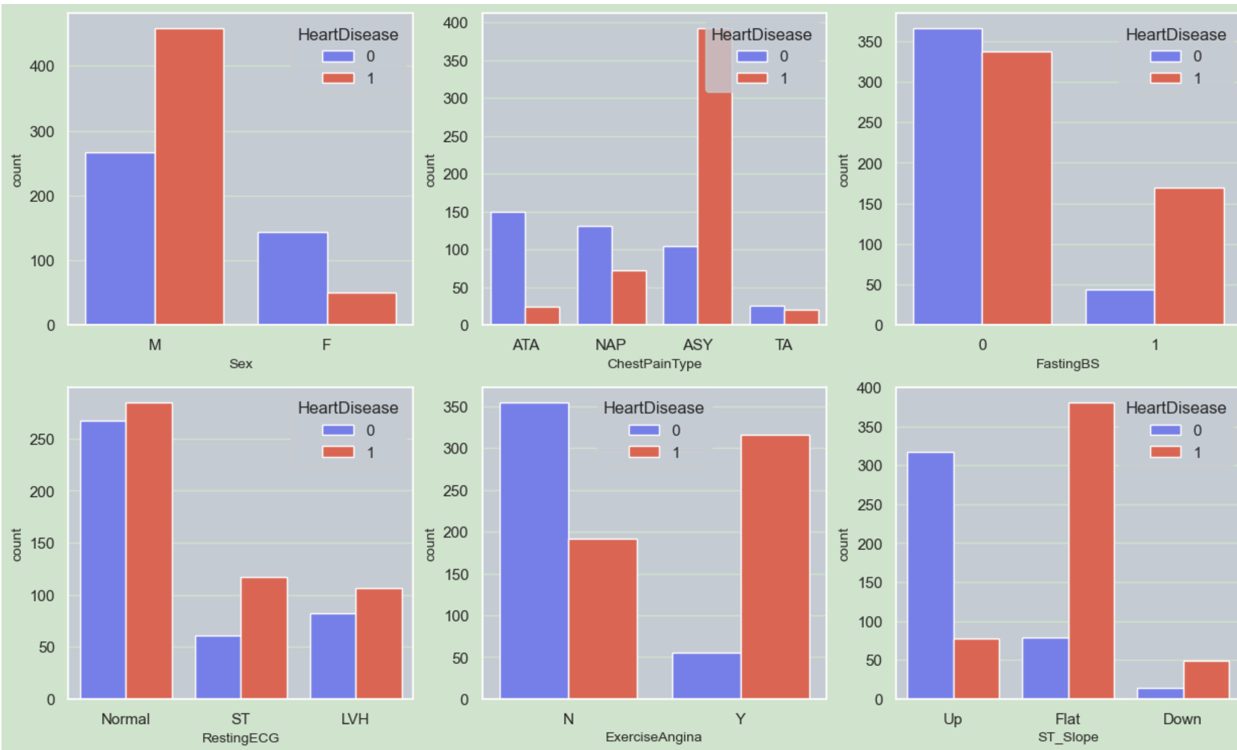


age has little impact on our cholesterol statistics.

Plotting a barplot with other attributes vs 'HeartDisease' column.

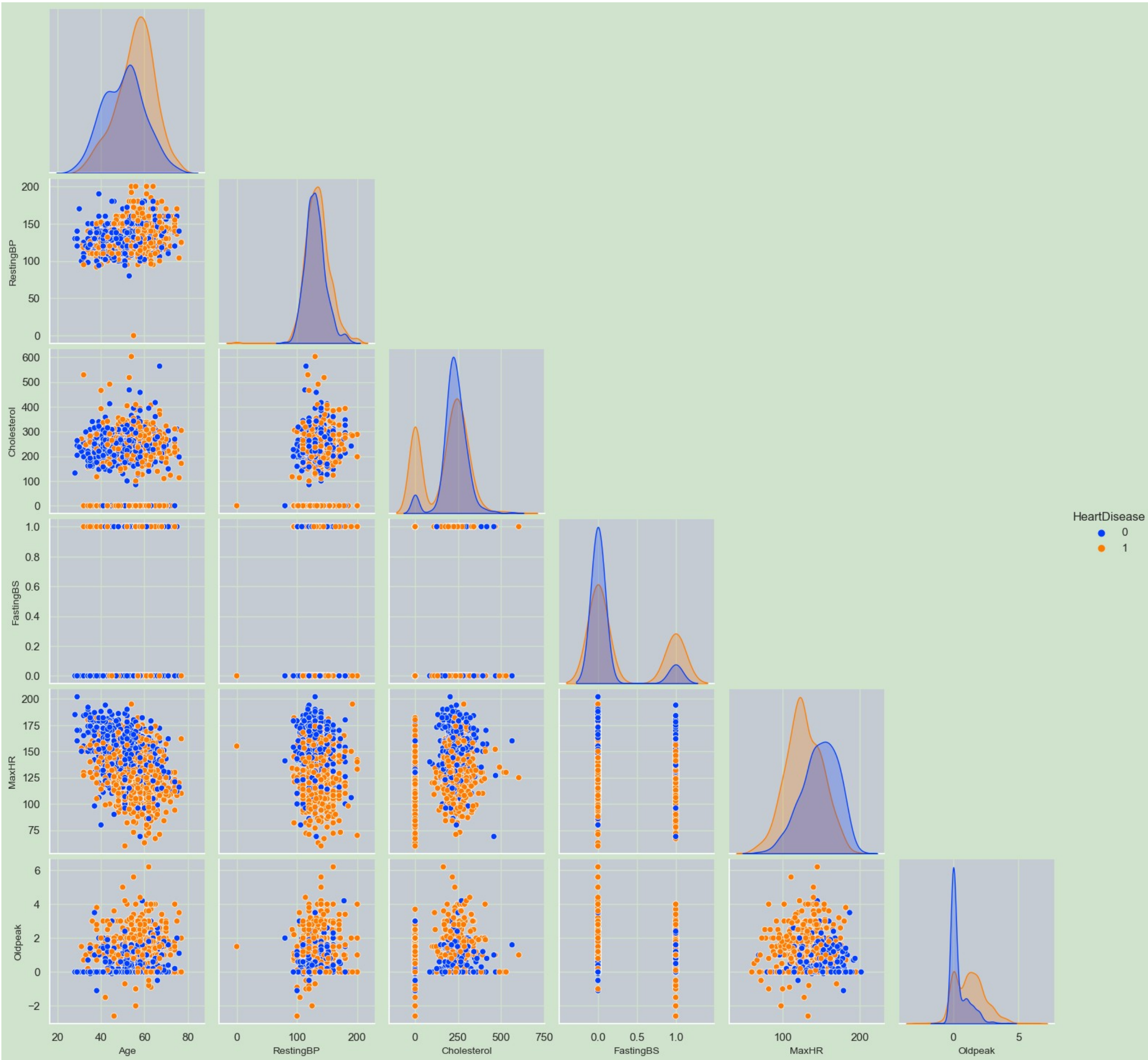
```
categorical = ['Sex', 'ChestPainType','FastingBS','RestingECG',
                          'ExerciseAngina',
'ST_Slope','HeartDisease']
numeric = ['Age','RestingBP','Cholesterol','MaxHR','Oldpeak']

import seaborn as sns
colors = px.colors.qualitative.Plotly
sns.set_theme(rc = {'figure.dpi': 100, 'axes.labelsize': 10,
                    'axes.facecolor': '#C5CBD3', 'grid.color':
'#D0E3CC',
                    'figure.facecolor': '#D0E3CC'}, font_scale = 1)
fig, ax = plt.subplots(2, 3, figsize = (15, 9))
for indx, (column, axes) in list(enumerate(list(zip(categorical,
ax.flatten())))):
    if column not in 'HearDisease':
```

```
        sns.countplot(ax = axes, x = df[column], hue =
df['HeartDisease'], palette = colors, alpha = 1)
else:
    [axes.set_visible(False) for axes in ax.flatten()[indx + 1:]]
axes_legend = ax.flatten()
axes_legend[1].legend(title = 'HeartDisease', loc = 'upper right')
axes_legend[2].legend(title = 'HeartDisease', loc = 'upper right')
plt.show()
```



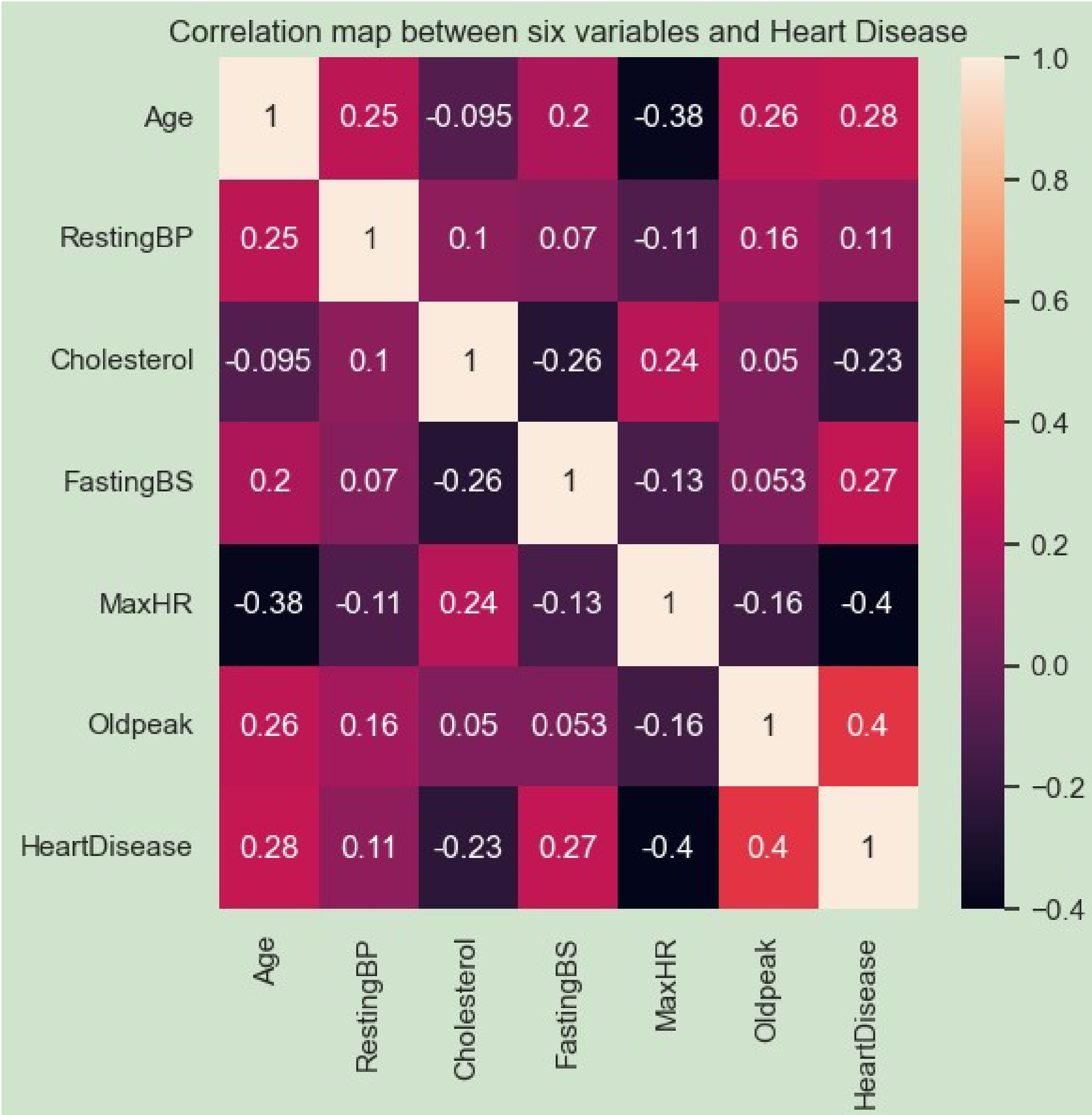
Pair plot can also be used to understand the best set of features to explain a relationship between two variables.

```
sns.pairplot(df, hue='HeartDisease', palette='bright', corner=True);
```



Examining the correlation between variables using HEATMAP.

```
plt.figure(figsize=(6, 6))
sns.heatmap(df.corr(), annot=True)
plt.xticks(rotation=90);
plt.title('Correlation map between six variables and Heart Disease');
```



Here we can observe that AGE and FASTING BLOOD SUGAR are the two variables that have the greatest impact on heart disease. While Max Heart Rate seems to have the least impact.

Before going for Data Preperation, Let's see if we got any outliers in Numeric data that can make impact on Model predictions

```
def outliers(data,col):
        q1 = data[col].quantile(0.25,interpolation='nearest')
        q2 = data[col].quantile(0.5,interpolation='nearest')
        q3 = data[col].quantile(0.75,interpolation='nearest')
        q4 = data[col].quantile(1,interpolation='nearest')
        IQR = q3 -q1
        global LLP
```

```
        global ULP
        LLP = q1 - 1.5*IQR
        ULP = q3 + 1.5*IQR
        if data[col].min() > LLP and data[col].max() < ULP:
            print("No outlier values in",i)
        else:
            print("There are outlier values in",i)
            x = data[data[col]<LLP][col].size
            y = data[data[col]>ULP][col].size
            a.append(i)
            print('Count of outlier values :',x+y)
global a
a = []
for i in numeric:
    outliers(df,i)
```

```
No outlier values in Age
There are outlier values in RestingBP
Count of outlier values : 28
There are outlier values in Cholesterol
Count of outlier values : 183
There are outlier values in MaxHR
Count of outlier values : 2
There are outlier values in Oldpeak
Count of outlier values : 16
```

To avoid outlier infulence on our models we have to pre process our data with feature scaling after converting them to numerical labels.

------------------------------ PRE PROCESSING OF DATA -----------------------------------

LABEL ENCODING

to convert non-numerical columns to numerical labels.

Label Encoding helps in converting the labels into a numeric form so as to convert them into the machine-readable form. Machine learning algorithms can then decide in a better way how those labels must be operated. It is an important pre-processing step for the structured dataset in supervised learning.

```
def LE(c1):
    from sklearn import preprocessing
    l_encode = preprocessing.LabelEncoder()
    df[c1]= l_encode.fit_transform(df[c1])
    df[c1].unique()
```

```python
LE("Sex")
LE("ChestPainType")
LE("RestingECG")
LE("ExerciseAngina")
LE("ST_Slope")
df
```

```
     Age  Sex  ChestPainType  RestingBP  Cholesterol  FastingBS  
RestingECG  \
0     40    1              1        140          289          0  
1  
1     49    0              2        160          180          0  
1  
2     37    1              1        130          283          0  
2  
3     48    0              0        138          214          0  
1  
4     54    1              2        150          195          0  
1  
..   ...  ...            ...        ...          ...        ...  
...  
913   45    1              3        110          264          0  
1  
914   68    1              0        144          193          1  
1  
915   57    1              0        130          131          0  
1  
916   57    0              1        130          236          0  
0  
917   38    1              2        138          175          0  
1  

     MaxHR  ExerciseAngina  Oldpeak  ST_Slope  HeartDisease  
0      172               0      0.0         2             0  
1      156               0      1.0         1             1  
2       98               0      0.0         2             0  
3      108               1      1.5         1             1  
4      122               0      0.0         2             0  
..     ...             ...      ...       ...           ...  
913    132               0      1.2         1             1  
914    141               0      3.4         1             1  
915    115               1      1.2         1             1  
916    174               0      0.0         1             1  
917    173               0      0.0         2             0  

[918 rows x 12 columns]
```

Scaling using StandardScaler

StandardScaler removes the mean and scales the data to unit variance. The scaling shrinks the range of the feature values for appropriate model training.

```
f_scaler = StandardScaler()
f_scaler.fit(df.drop('HeartDisease',axis = 1))
```

```
<IPython.core.display.Javascript object>
```

```
StandardScaler()
```

```
features_scaled = f_scaler.transform(df.drop('HeartDisease',axis = 1))
df_scaled = pd.DataFrame(features_scaled,columns = df.columns[:-1])
df_scaled.head()
```

```
        Age       Sex  ChestPainType  RestingBP  Cholesterol  
FastingBS  \
0 -1.433140  0.515952       0.229032   0.410909     0.825070  -
0.551341   
1 -0.478484 -1.938163       1.275059   1.491752    -0.171961  -
0.551341   
2 -1.751359  0.515952       0.229032  -0.129513     0.770188  -
0.551341   
3 -0.584556 -1.938163      -0.816995   0.302825     0.139040  -
0.551341   
4  0.051881  0.515952       1.275059   0.951331    -0.034755  -
0.551341   

   RestingECG     MaxHR  ExerciseAngina   Oldpeak  ST_Slope  
0    0.017255  1.382928       -0.823556 -0.832432  1.052114  
1    0.017255  0.754157       -0.823556  0.105664 -0.596078  
2    1.601219 -1.525138       -0.823556 -0.832432  1.052114  
3    0.017255 -1.132156        1.214246  0.574711 -0.596078  
4    0.017255 -0.581981       -0.823556 -0.832432  1.052114  
```

Splitting Data for Model Evaluation by using Train Test Split Method

```
X = df_scaled
y = df['HeartDisease']
X_train, X_test, y_train, y_test = train_test_split(X, y, 
test_size=0.3, random_state=108)
```

```
<IPython.core.display.Javascript object>
```

```
X_train.head()
```

```
          Age       Sex  ChestPainType  RestingBP  Cholesterol  
FastingBS  \
663  1.324756  0.515952       0.229032   1.491752     0.431746  -
```

```
0.551341
202 -1.220994  0.515952       1.275059   1.491752    -0.473815  -
0.551341
580 -0.266338  0.515952      -0.816995  -0.075471    -0.428079
1.813758
793  1.430829  0.515952      -0.816995  -0.399724     0.504923
1.813758
845  0.794391 -1.938163      -0.816995   0.681120     0.989718  -
0.551341

     RestingECG     MaxHR  ExerciseAngina   Oldpeak  ST_Slope
663    0.017255 -0.660578        1.214246 -0.832432 -0.596078
202    0.017255  0.361175       -0.823556 -0.832432  1.052114
580   -1.566710 -0.267596        1.214246  0.105664 -0.596078
793    0.017255  1.029244       -0.823556 -0.644813 -0.596078
845   -1.566710  0.361175        1.214246  0.105664 -0.596078

X_test.head()

          Age       Sex  ChestPainType  RestingBP  Cholesterol
FastingBS  \
491  2.279412  0.515952      -0.816995   2.032174     0.038422
1.813758
353  0.476173  0.515952      -0.816995  -0.129513    -1.818435  -
0.551341
655 -1.433140  0.515952      -0.816995   1.059415     0.221363  -
0.551341
657 -1.008848  0.515952       1.275059  -0.129513     0.312834  -
0.551341
805  0.051881  0.515952      -0.816995   0.410909     0.367716  -
0.551341

     RestingECG     MaxHR  ExerciseAngina   Oldpeak  ST_Slope
491    1.601219 -1.132156       -0.823556 -0.832432 -0.596078
353    1.601219 -1.446542        1.214246  0.105664 -0.596078
655    0.017255  1.736612       -0.823556 -0.832432  1.052114
657    0.017255  1.658016        1.214246 -0.457194  1.052114
805    0.017255  0.911350       -0.823556  0.293283  1.052114
```

---------------------------- MODEL TRAINING AND PREDICTION ------------------------------

We are going to train data with 4 classification models and predict results.

~ 1. DecisionTree Classifier

~ 2. RandomForest Classifier

~ 3. KNN Classification

~ 4. Logistic Regression

1. DecisionTree Classifier

A Decision Tree is a supervised Machine learning algorithm.

It is used in both classification and regression algorithms.

Decision trees and Random forest both belong to tree methods.

Decision trees make predictions by going through each and every feature in the data set, one-by-one.

```
from sklearn.tree import DecisionTreeClassifier
dt = DecisionTreeClassifier(random_state=40,max_depth=5)
dt.fit(X_train,y_train)
y_predicted_dt = dt.predict(X_test)
y_predicted_dt
```

```
array([1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 0, 1, 0, 0, 1, 1, 1,
1,
       1, 1, 0, 1, 1, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1,
1,
       0, 1, 1, 1, 0, 1, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 0, 0,
1,
       1, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1,
0,
       1, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 0, 0, 1, 0, 1,
1,
       0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0,
1,
       1, 0, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0,
1,
       0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1,
0,
```

```
       0, 0, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0,
1,
       1, 1, 0, 0, 1, 0, 1, 1, 1, 1, 0, 1, 1, 0, 0, 0, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 1, 1, 0, 1, 1, 1, 0, 0, 1])
```

```
dt.score(X_test,y_test)
```

```
0.8369565217391305
```

```
from sklearn.metrics import confusion_matrix
print(confusion_matrix(y_test,y_predicted_dt))
```

```
[[100  25]
 [ 20 131]]
```

```
from sklearn.metrics import classification_report
print(classification_report(y_test,y_predicted_dt))
```

```
              precision    recall  f1-score   support

           0       0.83      0.80      0.82       125
           1       0.84      0.87      0.85       151

    accuracy                           0.84       276
   macro avg       0.84      0.83      0.83       276
weighted avg       0.84      0.84      0.84       276
```

```
print("DecisionTree model
Accuracy:",round(dt.score(X_test,y_test)*100),'%')
```

```
DecisionTree model Accuracy: 84 %
```

2. RandomForest Classifier

Random forest is a Supervised Machine Learning Algorithm used for Classification and Regression problems.

It performs better results for classification problems.

It can handle the dataset containing categorical variables as in the case of classification.

Random forests are a collection of decision trees being grouped together and trained together that use random orders of the features in the given data sets.

```
from sklearn.ensemble import RandomForestClassifier
rf= RandomForestClassifier(n_estimators =20, random_state = 0)
rf.fit(X_train,y_train)
y_predicted_rf = rf.predict(X_test)
y_predicted_rf
```

```
array([1, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 0, 1, 0, 0, 1, 1, 1,
1,
       1, 1, 0, 1, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 1,
1,
       0, 1, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 0, 0,
1,
       1, 1, 1, 1, 0, 0, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1,
0,
       1, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 0, 0, 1, 0, 1,
0,
       0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0,
1,
       1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0,
1,
       0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1,
0,
       0, 0, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0,
1,
       1, 1, 0, 0, 1, 0, 1, 1, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 1, 1, 0, 1, 1, 1, 0, 0, 1])
```

```
rf.score(X_test,y_test)
```

```
0.8514492753623188
```

```
print(confusion_matrix(y_test,y_predicted_rf))
```

```
[[106  19]
 [ 22 129]]
```

```
print(classification_report(y_test,y_predicted_rf))
```

```
              precision    recall  f1-score   support

           0       0.83      0.85      0.84       125
           1       0.87      0.85      0.86       151

    accuracy                           0.85       276
   macro avg       0.85      0.85      0.85       276
weighted avg       0.85      0.85      0.85       276
```

```
print("RandomForest model
Accuracy:",round(rf.score(X_test,y_test)*100),'%')
```

```
RandomForest model Accuracy: 85 %
```

3. K-Nearest Neighbour Algorithm

K-Nearest Neighbour is simplest algorithm based on Supervised Learning.

It assumes the similarity between the new case and available cases and put the new case into the category that is most similar to the available categories.

K-NN is used for Regression and Classification but mostly used for Classification problems.

```
from sklearn.neighbors import KNeighborsClassifier

knn = KNeighborsClassifier(n_neighbors = 7)
knn.fit(X_train,y_train)
```

```
KNeighborsClassifier(n_neighbors=7)
```

How K value is selected in the K-NN :

There is no particular way to determine 'K', most preferred value for K is 5.

low K values like 1,2 can be noisy, has some outlier effects in model.

```
y_predicted_knn = knn.predict(X_test)
y_predicted_knn
```

```
array([1, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 1,
1,
       1, 1, 0, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1,
1,
       0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 0, 0,
1,
       1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1,
0,
       0, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 0, 0, 1, 0, 1,
0,
       0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 0, 0,
1,
       1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0,
1,
       0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1,
0,
       0, 0, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 1, 0,
1,
       0, 1, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 1, 1,
1,
       0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1])
```

```
knn.score(X_test,y_test)
```

```
0.8115942028985508
```

```
print(confusion_matrix(y_test,y_predicted_knn))
```

```
[[106  19]
 [ 33 118]]
```

```
print(classification_report(y_test,y_predicted_knn))
```

```
              precision    recall  f1-score   support

           0       0.76      0.85      0.80       125
           1       0.86      0.78      0.82       151

    accuracy                           0.81       276
   macro avg       0.81      0.81      0.81       276
weighted avg       0.82      0.81      0.81       276
```

```
print("k-NN model Accuracy:",round(knn.score(X_test,y_test)*100),'%')
```

```
k-NN model Accuracy: 81 %
```

4. Logistic Regression

Logistic Regression is a supervised learning classification algorithm used to predict the probability of a target variable.

It uses a logistic function to model the dependent variable.

There could only be two possible classes, for example in our case it’s either heart failure occurs or not.

```
from sklearn.linear_model import LogisticRegression

logistic = LogisticRegression(random_state=100, solver='liblinear')
logistic.fit(X_train,y_train)
y_predicted_lr = logistic.predict(X_test)

y_predicted_lr
```

```
array([1, 1, 0, 0, 0, 1, 1, 1, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 1,
1,
       1, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 1,
1,
       0, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 1, 0, 1, 1, 0, 0, 0,
1,
       1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1,
0,
       1, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 0, 0, 1, 0, 1,
1,
       0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1,
0,
       1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0,
1,
       0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1,
0,
       0, 0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 1, 0,
1,
       1, 1, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 1, 1,
1,
       0, 1, 1, 0, 1, 0, 0, 1, 1, 0, 1, 1, 1, 1, 0, 0, 0, 1, 1, 1, 1,
1,
       0, 1, 0, 1, 1, 0, 1, 1, 1, 0, 0, 1])
```

```
logistic.score(X_test,y_test)
```

```
0.8115942028985508
```

```
print(classification_report(y_test,y_predicted_lr))
```

```
              precision    recall  f1-score   support

           0       0.79      0.80      0.79       125
           1       0.83      0.82      0.83       151

    accuracy                           0.81       276
   macro avg       0.81      0.81      0.81       276
weighted avg       0.81      0.81      0.81       276
```

```
print("Logistic Regression model
Accuracy:",round(logistic.score(X_test,y_test)*100),'%')
```

```
Logistic Regression model Accuracy: 81 %
```

Let's compare all models accuracy scores

```
print("DecisionTree        :",round(dt.score(X_test,y_test)*100),'%'),
print("RandomForest        :",round(rf.score(X_test,y_test)*100),'%'),
print("k-
NN                :",round(knn.score(X_test,y_test)*100),'%'),
print("LogisticRegression  :",round(logistic.score(X_test,y_test)*100)
,'%')
```

```
DecisionTree        : 84 %
RandomForest        : 85 %
k-NN                : 81 %
LogisticRegression  : 81 %
```

We can obsereve Random Forest Classifier is performing better than others with accuracy of 85%

---------------------------- Feature Importances --------------------------------

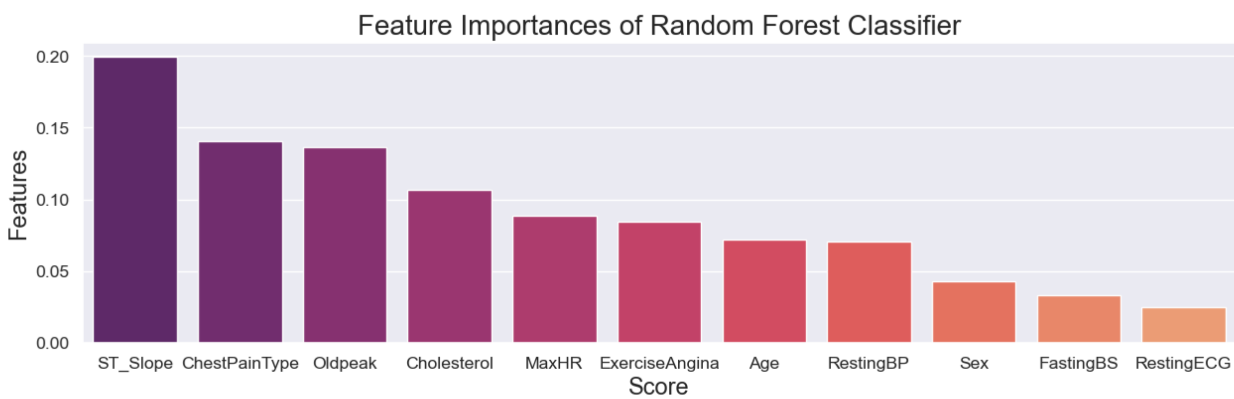
As RandomForest classifier is giving best score, let's see what features are influencing most for the decision

```
ft = pd.Series(rf.feature_importances_, index =
X_train.columns).sort_values(ascending = False)
print(ft)
```

```
ST_Slope          0.199108
ChestPainType     0.140650
Oldpeak           0.136305
```

```
Cholesterol       0.106668
MaxHR             0.088653
ExerciseAngina    0.084797
Age               0.072079
RestingBP         0.070365
Sex               0.043241
FastingBS         0.033259
RestingECG        0.024875
dtype: float64
```

```
sns.set_theme(style="darkgrid",font_scale=1.15)
plt.figure(figsize = (15,4))
sns.barplot(x = ft.index, y = ft,palette="flare_r", saturation =.99, )
plt.title('Feature Importances of Random Forest
Classifier',fontsize=20)
plt.xlabel('Score',fontsize=17)
plt.ylabel('Features',fontsize=17)
plt.show()
```



We can see ST_Slope, ChestPainType, Oldpeak are major features impacting model prediction.