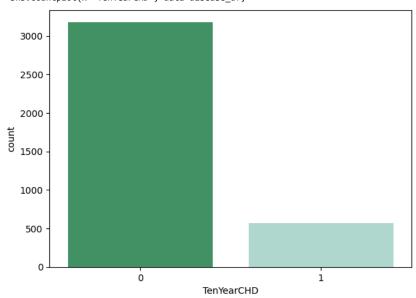
```
import pandas as pd
import pylab as pl
import numpy as np
import scipy.optimize as opt
import statsmodels.api as sm
from sklearn import preprocessing
'exec(% matplotlib inline)'
import matplotlib.pyplot as plt
import matplotlib.mlab as mlab
import seaborn as sns
# dataset
disease_df = pd.read_csv("/content/framingham.csv")
disease_df.drop(['education'], inplace = True, axis = 1)
disease_df.rename(columns ={'male':'Sex_male'}, inplace = True)
# removing NaN / NULL values
disease_df.dropna(axis = 0, inplace = True)
print(disease_df.head(), disease_df.shape)
print(disease_df.TenYearCHD.value_counts())
        Sex_male age currentSmoker
                                      cigsPerDay BPMeds prevalentStroke \
     0
                   39
                                             0.0
                                                     0.0
                                   0
                                   0
     1
               0
                   46
                                             0.0
                                                     0.0
                                                                        0
     2
               1
                   48
                                   1
                                            20.0
                                                     0.0
                                                                        0
     3
               0
                   61
                                   1
                                            30.0
                                                     0.0
                                                                        0
               0
                   46
                                            23.0
                                                     0.0
                                   1
        prevalentHyp
                      diabetes totChol sysBP
                                               diaBP
                                                         BMI
                                                             heartRate
                                                                         glucose
                                                 70.0 26.97
                                  195.0
                                        106.0
                                                                   80.0
                   0
                             0
                                                                   95.0
     1
                                  250.0
                                         121.0
                                                 81.0 28.73
                                                                             76.0
                                                                   75.0
     2
                   0
                             0
                                  245.0 127.5
                                                 80.0 25.34
                                                                            70.0
                   1
                                  225.0 150.0
                                                 95.0 28.58
                                                                   65.0
                                                                           103.0
     4
                   0
                                  285.0 130.0
                                                 84.0 23.10
                                                                   85.0
                                                                            85.0
        TenYearCHD
     0
                 0
                 0
     1
     2
                 0
     3
                 1
     4
                     (3751, 15)
     TenYearCHD
     0
          3179
           572
     Name: count, dtype: int64
X = np.asarray(disease_df[['age', 'Sex_male', 'cigsPerDay',
                            'totChol', 'sysBP', 'glucose']])
y = np.asarray(disease_df['TenYearCHD'])
# normalization of the dataset
X = preprocessing.StandardScaler().fit(X).transform(X)
# Train-and-Test -Split
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(
        X, y, test_size = 0.3, random_state = 4)
print ('Train set:', X_train.shape, y_train.shape)
print ('Test set:', X_test.shape, y_test.shape)
     Train set: (2625, 6) (2625,)
     Test set: (1126, 6) (1126,)
# counting no. of patients affected with CHD
plt.figure(figsize=(7, 5))
sns.countplot(x='TenYearCHD', data=disease_df,
             palette="BuGn_r",color='red')
plt.show()
```

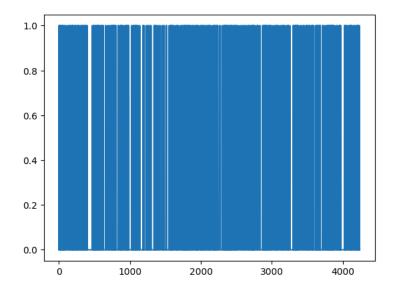
<ipython-input-18-0302d7529a5e>:3: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0.

 $\verb|sns.countplot(x='TenYearCHD', data=disease\_df, \\$ 



laste = disease\_df['TenYearCHD'].plot()
plt.show(laste)

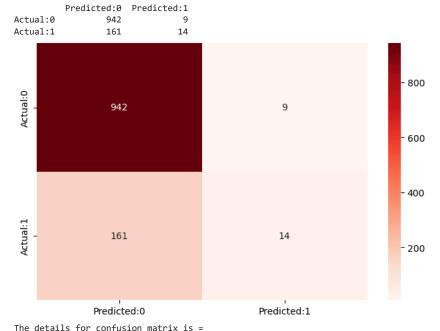


```
from sklearn.linear_model import LogisticRegression
logreg = LogisticRegression()
logreg.fit(X_train, y_train)
y_pred = logreg.predict(X_test)
```

Accuracy of the model is = 0.8490230905861457

```
# Confusion matrix
from sklearn.metrics import confusion_matrix, classification_report
```

cm = confusion matrix(v test v nred)



THE GECALIS	precision		f1-score	support
0	0.85	0.99	0.92	951
1	0.61	0.08	0.14	175
accuracy			0.85	1126
macro avg		0.54	0.53	1126
weighted avg	0.82	0.85	0.80	1126