

```
In [1]: 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
```

```
In [5]: # Loading the Dataset
```

```
disease_df = pd.read_csv("Downloads/framingham.csv")
disease_df.drop(['education'], inplace = True, axis = 1)
disease_df.rename(columns = {'male':'Sex_male'}, inplace = True)
```

```
In [7]: # Handling missing values (NAN / NULL removing)
```

```
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	1	39	0	0.0	0.0	0	
1	0	46	0	0.0	0.0	0	
2	1	48	1	20.0	0.0	0	
3	0	61	1	30.0	0.0	0	
4	0	46	1	23.0	0.0	0	

	prevalentHyp	diabetes	totChol	sysBP	diaBP	BMI	heartRate	glucose	\
0	0	0	195.0	106.0	70.0	26.97	80.0	77.0	
1	0	0	250.0	121.0	81.0	28.73	95.0	76.0	
2	0	0	245.0	127.5	80.0	25.34	75.0	70.0	
3	1	0	225.0	150.0	95.0	28.58	65.0	103.0	
4	0	0	285.0	130.0	84.0	23.10	85.0	85.0	

	TenYearCHD
0	0
1	0
2	0
3	1
4	0

(3751, 15)

TenYearCHD

0	3179
1	572

Name: count, dtype: int64

```
In [21]: # Splitting the Dataset into Test and Train Sets
```

```
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_sta

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,)

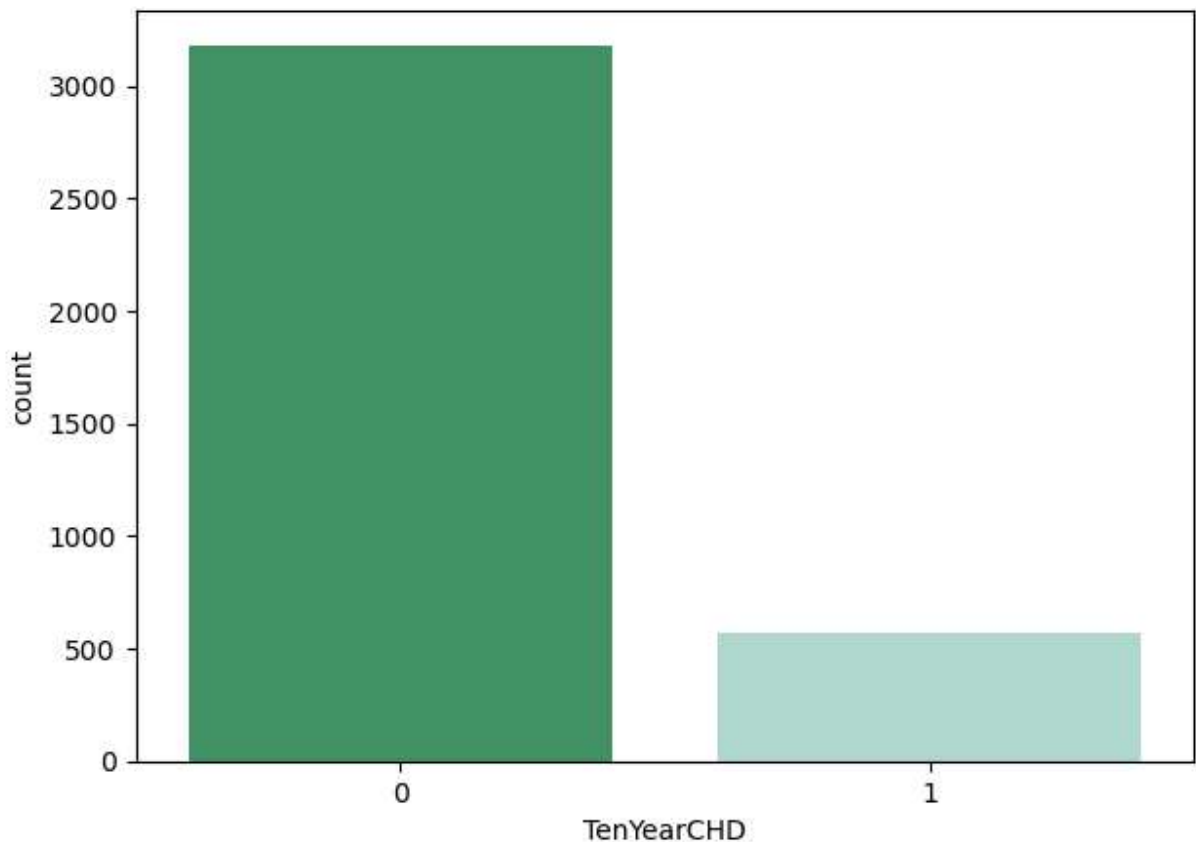
```
In [23]: # Exploratory Data Analysis #

# counting no. of patients affected with CHD
plt.figure(figsize=(7,5))
sns.countplot(x="TenYearCHD", data=disease_df, palette="BuGn_r")
plt.show()
```

C:\Users\Computer\AppData\Local\Temp\ipykernel_5456\3424366598.py:5: FutureWarning:

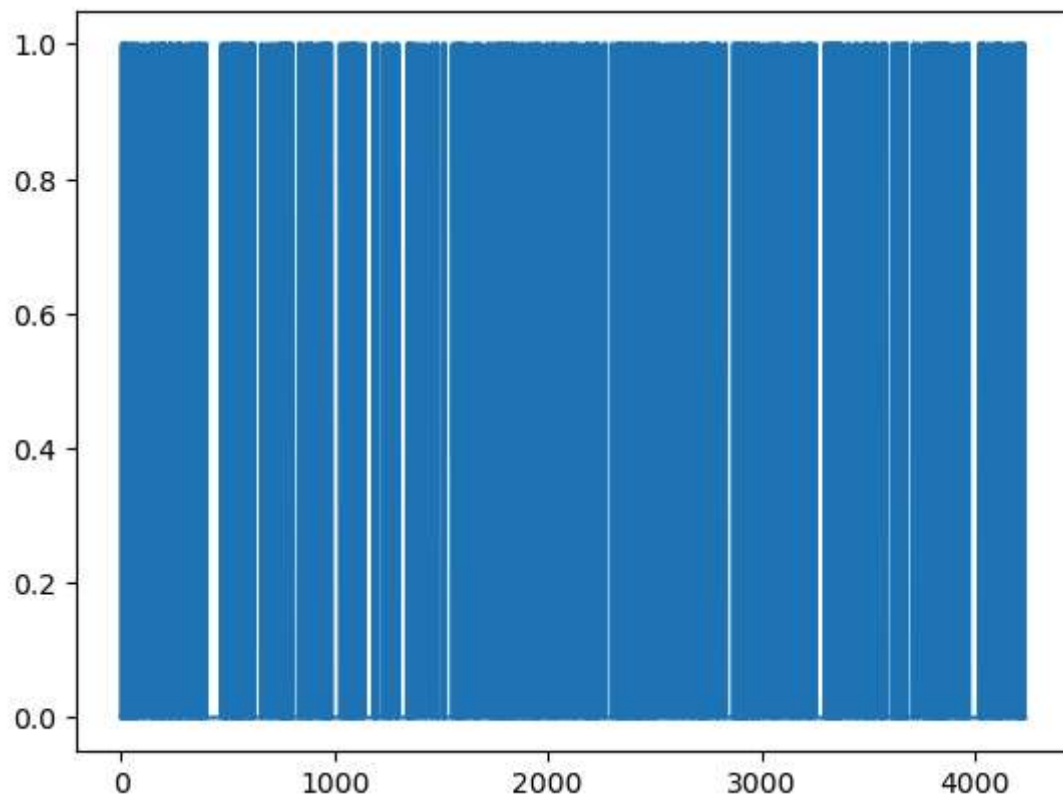
Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

```
sns.countplot(x="TenYearCHD", data=disease_df, palette="BuGn_r")
```



```
In [31]: laste = disease_df['TenYearCHD'].plot()
```

```
plt.show(laste)
```



In [33]: *# Fitting Logistic regression model for heart disease prediction*

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

# Evaluation and accuracy

from sklearn.metrics import accuracy_score
print('Accuracy of the model is =', accuracy_score(y_test, y_pred))
```

Accuracy of the model is = 0.8490230905861457

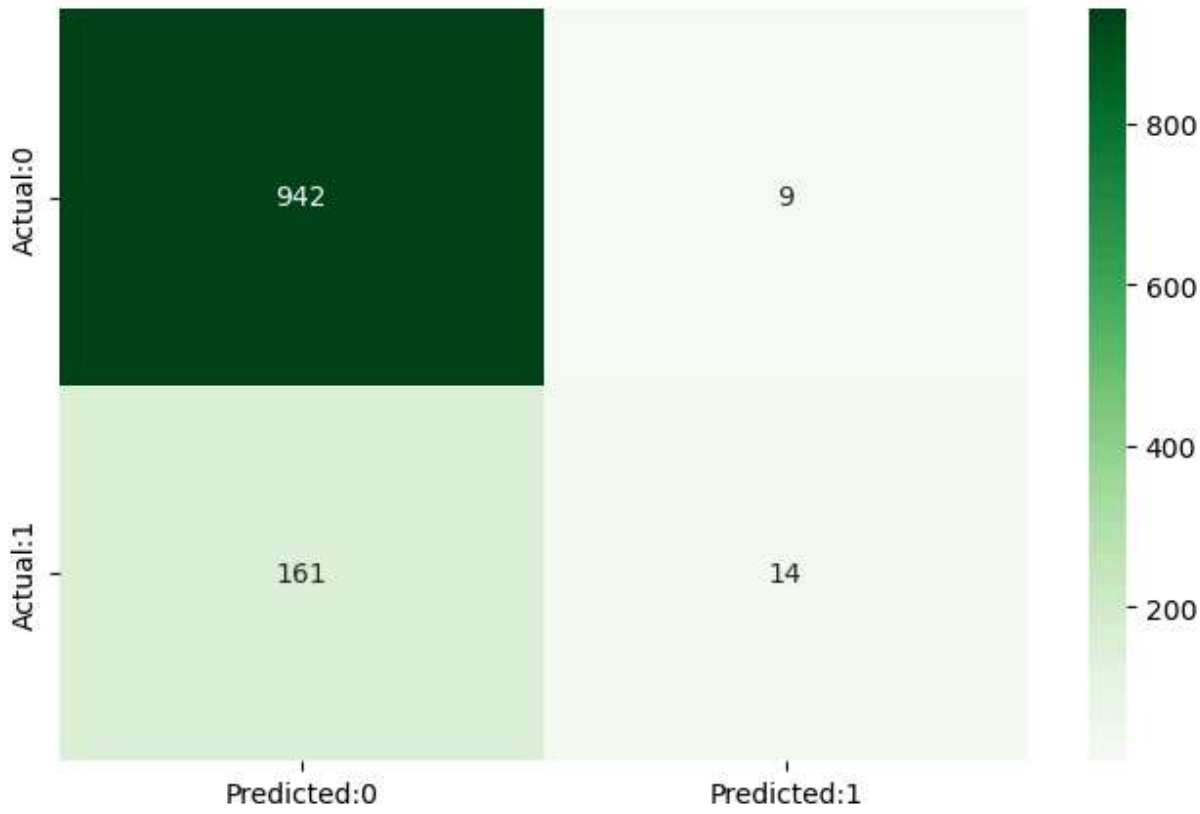
In [37]: *# confusion matrix*

```
from sklearn.metrics import confusion_matrix, classification_report

cm = confusion_matrix(y_test, y_pred)
conf_matrix = pd.DataFrame(data = cm, columns = ['Predicted:0', 'Predicted:1'],
                           index = ['Actual:0', 'Actual:1'])
plt.figure(figsize = (8, 5))
sns.heatmap(conf_matrix, annot = True, fmt = 'd', cmap = "Greens")

plt.show()

print('The details for confusion matrix is:')
print(classification_report(y_test, y_pred))
```



The details for confusion matrix is:

	precision	recall	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	0.73	0.54	0.53	1126
weighted avg	0.82	0.85	0.80	1126

```
In [ ]:
```