Data Visualization and Exploration

1. Print 2 rows for sanity check to identify all the features present in the dataset and if the target matches with them.

```
import numpy as np
import pandas as pd
import seaborn as sns
import statsmodels.api as sm
import scipy.stats as st
import matplotlib.pyplot as plt
from sklearn.metrics import confusion_matrix
import matplotlib.mlab as mlab
import math
heart_data= pd.read_csv("/content/drive/MyDrive/Sem-2/ML/framingham.csv")
heart_data.head(15)
```

	male	age	education	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevale
0	1	39	4.0	0	0.0	0.0	0	
1	0	46	2.0	0	0.0	0.0	0	
2	1	48	1.0	1	20.0	0.0	0	
3	0	61	3.0	1	30.0	0.0	0	
4	0	46	3.0	1	23.0	0.0	0	
5	0	43	2.0	0	0.0	0.0	0	
6	0	63	1.0	0	0.0	0.0	0	
7	0	45	2.0	1	20.0	0.0	0	
8	1	52	1.0	0	0.0	0.0	0	
9	1	43	1.0	1	30.0	0.0	0	
10	0	50	1.0	0	0.0	0.0	0	
11	0	43	2.0	0	0.0	0.0	0	
12	1	46	1.0	1	15.0	0.0	0	
13	0	41	3.0	0	0.0	1.0	0	
14	0	39	2.0	1	9.0	0.0	0	

```
heart_data.shape
```

```
(4238, 16)
```

```
print(heart_data.head(2))
```

```
   male  age  education  currentSmoker  cigsPerDay  BPMeds  prevalentStroke  \
0     1   39        4.0              0         0.0     0.0                0
1     0   46        2.0              0         0.0     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

   TenYearCHD
0           0
1           0
```

```
heart_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4238 entries, 0 to 4237
Data columns (total 16 columns):
 #   Column           Non-Null Count  Dtype  
---  ------           --------------  -----  
 0   male             4238 non-null   int64  
 1   age              4238 non-null   int64  
 2   education        4133 non-null   float64
 3   currentSmoker    4238 non-null   int64  
 4   cigsPerDay       4209 non-null   float64
 5   BPMeds           4185 non-null   float64
 6   prevalentStroke  4238 non-null   int64  
 7   prevalentHyp     4238 non-null   int64  
 8   diabetes         4238 non-null   int64  
 9   totChol          4188 non-null   float64
 10  sysBP            4238 non-null   float64
 11  diaBP            4238 non-null   float64
 12  BMI              4219 non-null   float64
 13  heartRate        4237 non-null   float64
 14  glucose          3850 non-null   float64
 15  TenYearCHD       4238 non-null   int64  
dtypes: float64(9), int64(7)
memory usage: 529.9 KB
```

2. Comment on class imbalance with appropriate visualization method.

It is from an ongoing ongoing cardiovascular study on residents of the town of Framingham. The classification goal is to predict whether the patient has 10-year risk of future coronary heart disease (CHD).The dataset provides the patients' information. It includes over 4,000 records and 15 attributes.

3. Provide appropriate visualizations to get an insight about the dataset.

```
count=0
for i in heart_data.isnull().sum(axis=1):
    if i>0:
        count=count+1
print('Total number of rows with missing values is ', count)
print('since it is only',round((count/len(heart_data.index))*100), 'percent of the entire
```

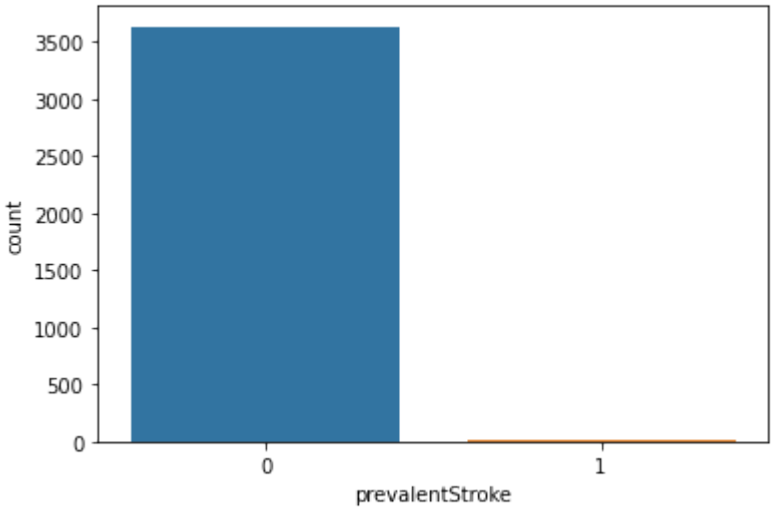
```
Total number of rows with missing values is  582
since it is only 14 percent of the entire dataset the rows with missing values are ex
```

```
heart_data.dropna(axis=0,inplace=True)


# checking for missing values
heart_data.isnull().sum()
```

```
male               0
age                0
education          0
currentSmoker      0
cigsPerDay         0
BPMeds             0
prevalentStroke    0
prevalentHyp       0
diabetes           0
totChol            0
sysBP              0
diaBP              0
BMI                0
heartRate          0
glucose            0
TenYearCHD         0
dtype: int64
```

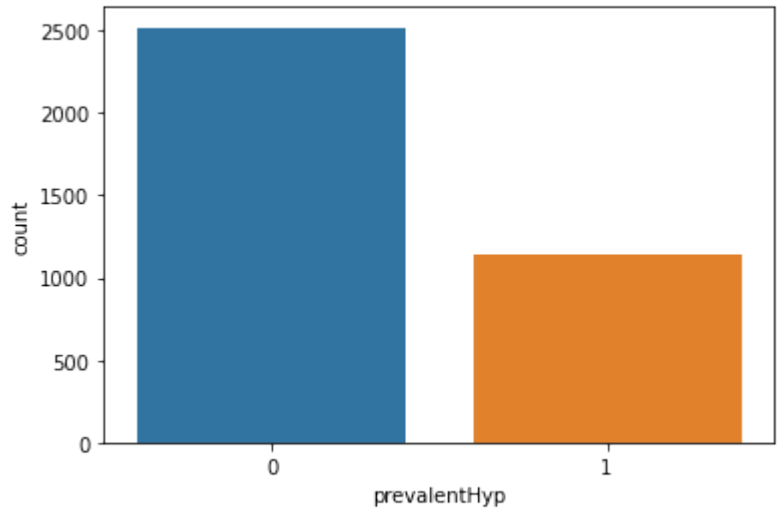
```
sns.countplot(x="prevalentStroke", data=heart_data)
# prevalentStroke positiveness is less as per study
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9168aed690>
```



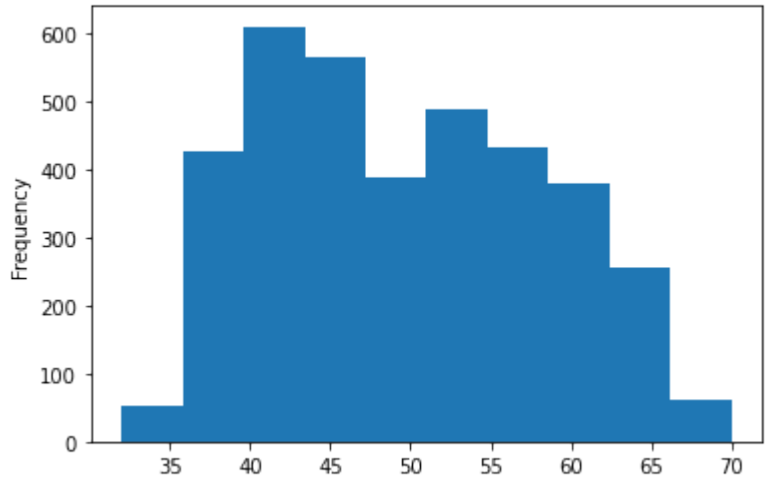
```
sns.countplot(x="prevalentHyp", data=heart_data)
# prevalentHyp is approx. half of the possibility of positiveness.
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9165c91e50>
```



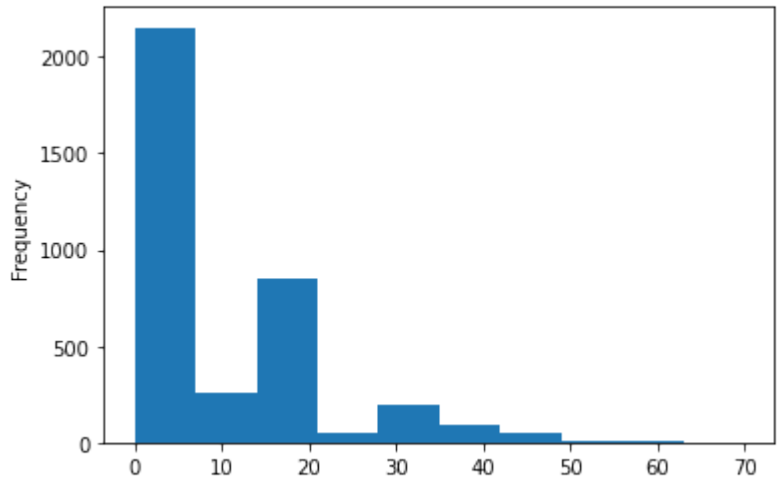

```
heart_data["age"].plot.hist(x="Age")
# Peaople with age approx. 40 are having high risk of heart attack
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9165c6e310>
```



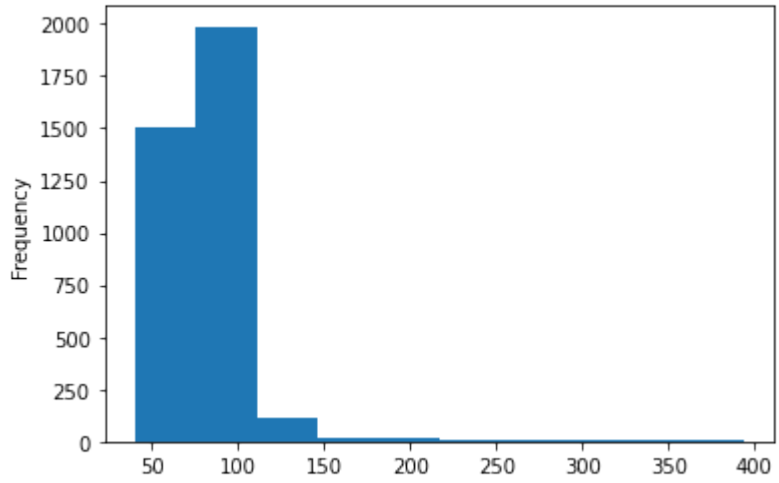

```
heart_data["cigsPerDay"].plot.hist()
#People with smoking habit 0 to (approx.)8 is more
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9165b95210>
```



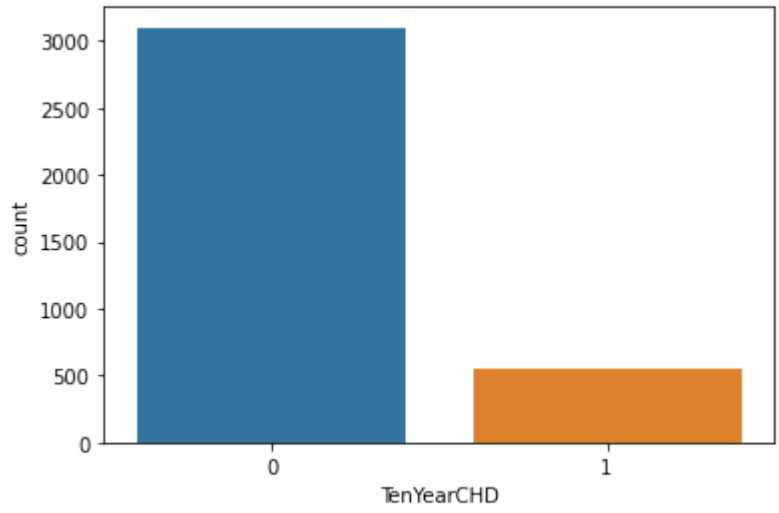

```
heart_data["glucose"].plot.hist()
# Count of glucose mostly displays between 80 to 120
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9165b72f90>
```




```
sns.countplot(x="TenYearCHD", data=heart_data)
# Over 10 years of duration the risk of Coronary Heart disease
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9165a38ed0>
```



4. Do the correlational analysis on the dataset. Provide a visualization for the same. Will this correlational analysis have an effect on feature selection that you will perform in the next step? Justify your answer.

The coefficient for age says that, holding all others constant, we will see 7% increase in the odds of getting diagnosed with CDH for a one year increase in age since exp(0.0655) = 1.067644.

Each attribute is a potential risk factor. There are both demographic, behavioural and medical risk factors.

Demographic: sex: male or female;(Nominal)

age: age of the patient;(Continuous - Although the recorded ages have been truncated to whole numbers, the concept of age is continuous)

Behavioural

currentSmoker: whether or not the patient is a current smoker (Nominal)

cigsPerDay: the number of cigarettes that the person smoked on average in one day.(can be considered continuous as one can have any number of cigarretts, even half a cigarette.)

Medical(history):

BPMeds: whether or not the patient was on blood pressure medication (Nominal)

prevalentStroke: whether or not the patient had previously had a stroke (Nominal)

prevalentHyp: whether or not the patient was hypertensive (Nominal)

diabetes: whether or not the patient had diabetes (Nominal)

Medical(current):

totChol: total cholesterol level (Continuous)

sysBP: systolic blood pressure (Continuous)

diaBP: diastolic blood pressure (Continuous)

BMI: Body Mass Index (Continuous)

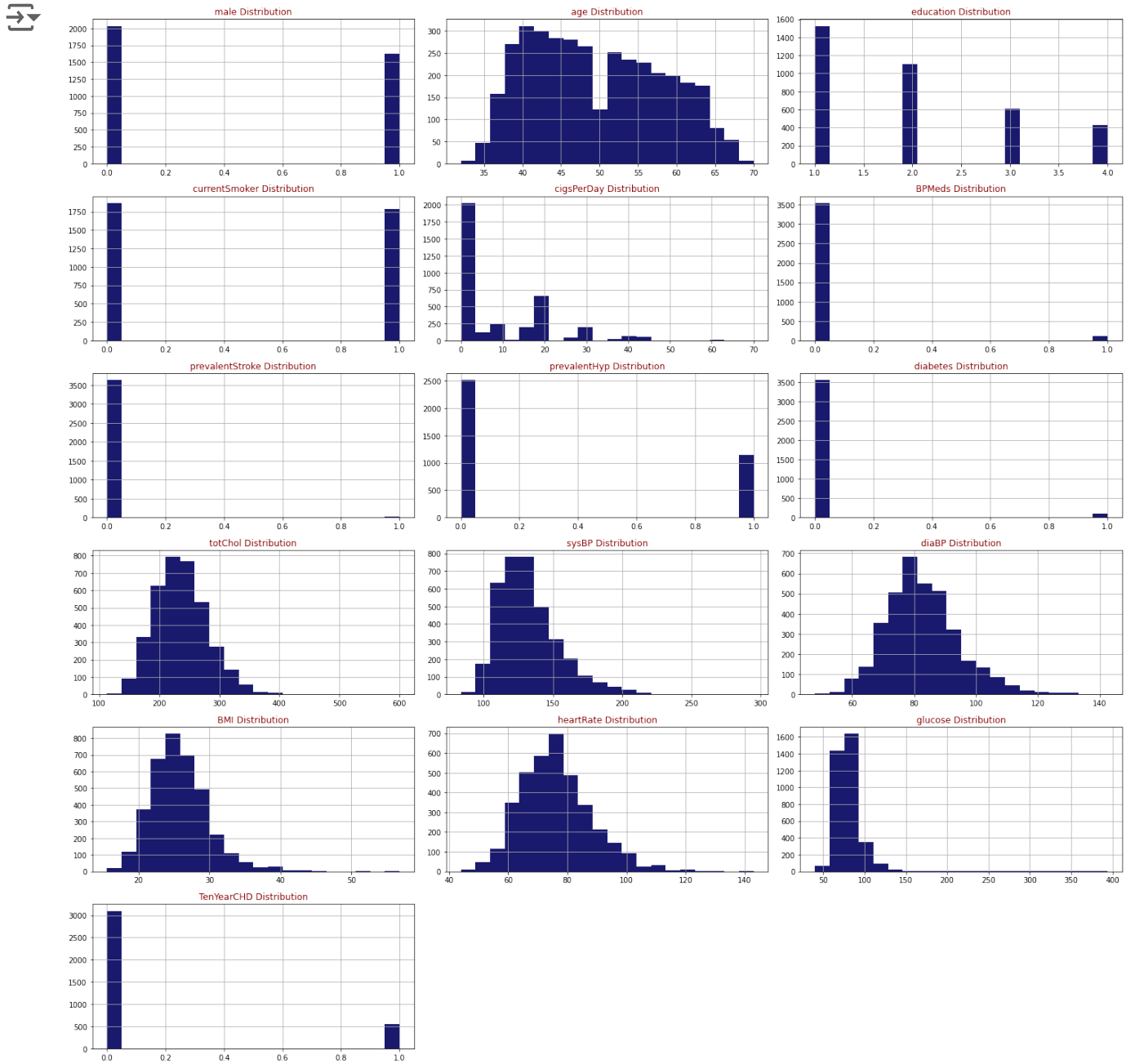
heartRate: heart rate (Continuous - In medical research, variables such as heart rate though in fact discrete, yet are considered continuous because of large number of possible values.)

glucose: glucose level (Continuous)

Predict variable (desired target):

TenYearCHD: 10 year risk of coronary heart disease CHD (binary: “1”, means “Yes”, “0” means “No”)

```
def draw_histograms(dataframe, features, rows, cols):
    fig=plt.figure(figsize=(20,20))
    for i, feature in enumerate(features):
        ax=fig.add_subplot(rows,cols,i+1)
        dataframe[feature].hist(bins=20,ax=ax,facecolor='midnightblue')
        ax.set_title(feature+" Distribution",color='DarkRed')

    fig.tight_layout()
    plt.show()
draw_histograms(heart_data,heart_data.columns,6,3)
```

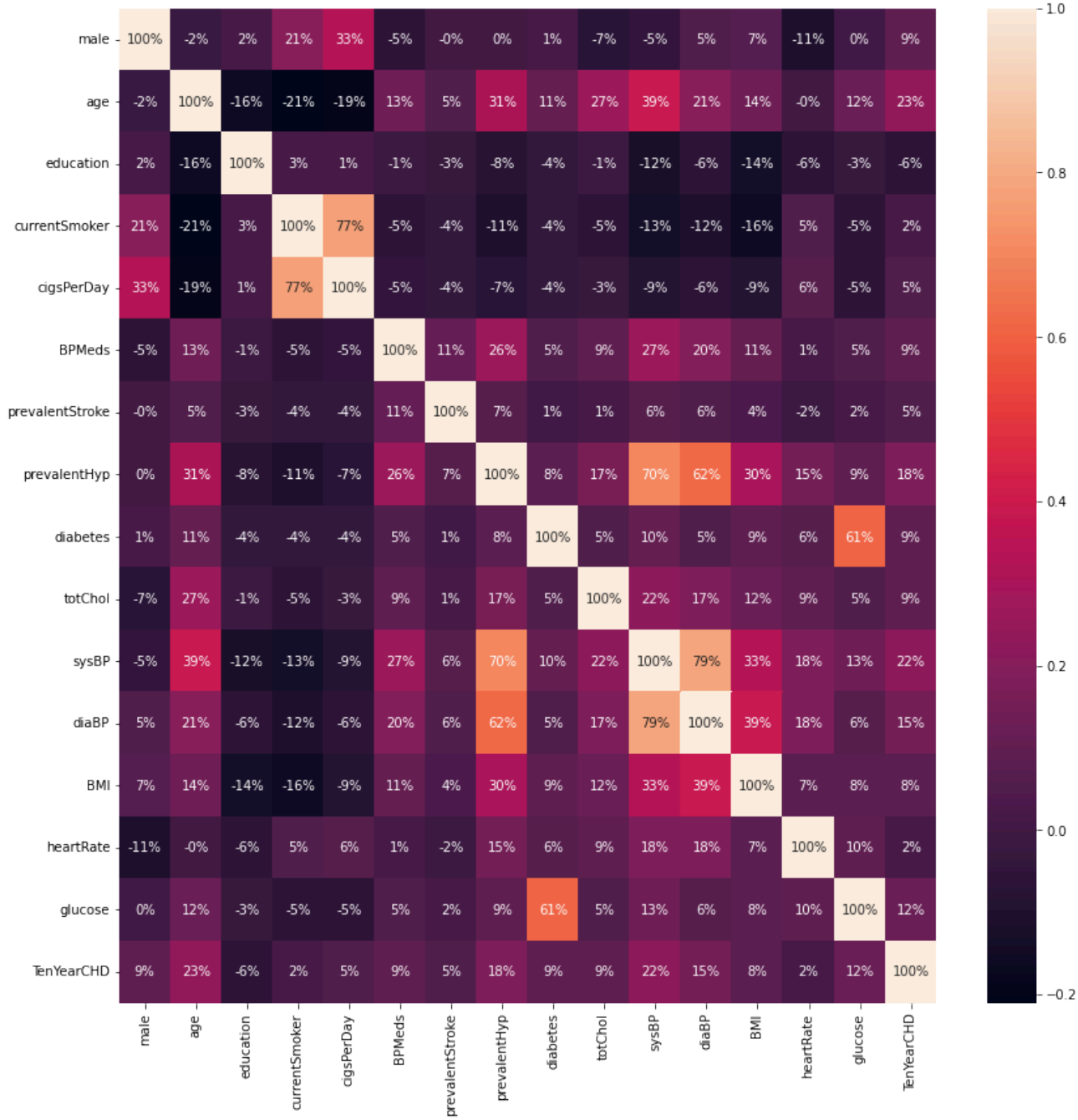



```
heart_data.TenYearCHD.value_counts()
```

```
0    3099
1     557
Name: TenYearCHD, dtype: int64
```

```
plt.figure(figsize=(14,14))
sns.heatmap(heart_data.corr(), annot=True, fmt='.0%')
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9165a09a50>
```



Strong Correlations found

currentSmoker & cigPerDay - 77%

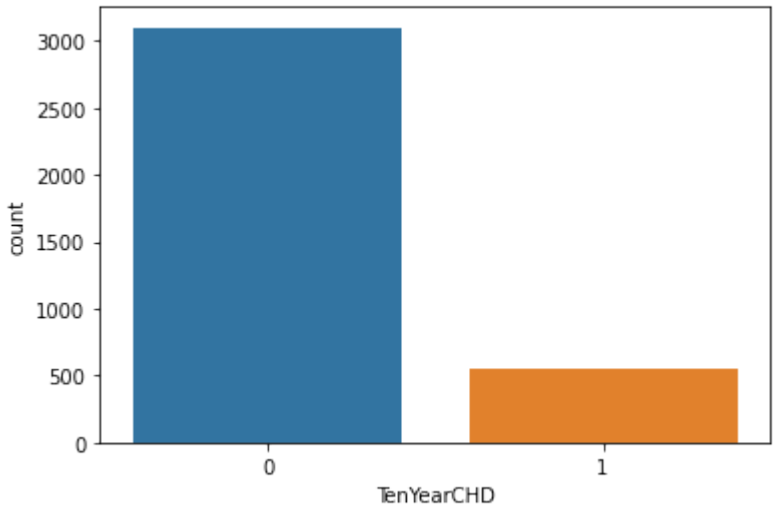
sysBP & diaBP - 79%

sysBP & prevalentHyp - 70%

diabetes & glucose - 61%

```
sns.countplot(x='TenYearCHD',data=heart_data)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f9164eec9d0>
```

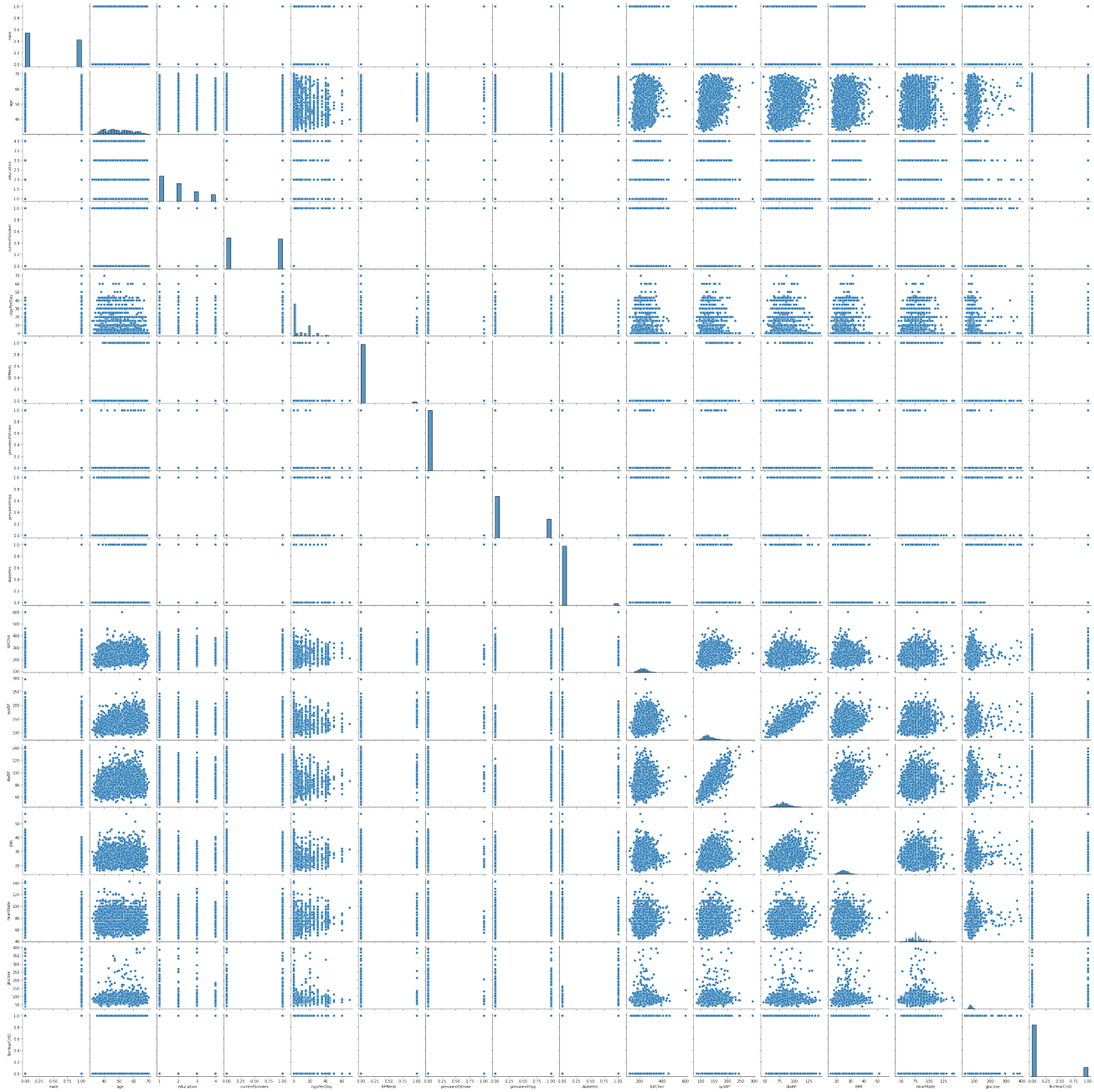


There are 3179 patents with no heart disease and 572 patients with risk of heart disease.

5. Any other visualization specific to the problem statement.

```
sns.pairplot(data=heart_data)
```

```
<seaborn.axisgrid.PairGrid at 0x7f9164cef990>
```



Data Pre-processing and cleaning

1. Do the appropriate pre-processing of the data like identifying NULL or Missing Values if any, handling of outliers if present in the dataset, skewed data etc. Mention the pre-

processing steps performed in the markdown cell. Explore a few latest data balancing tasks and its effect on model evaluation parameters.

```
# NULL values have been already being checked and taken care
heart_data.isnull().sum()
```

```
male               0
age                0
education          0
currentSmoker      0
cigsPerDay         0
BPMeds             0
prevalentStroke    0
prevalentHyp       0
diabetes           0
totChol            0
sysBP              0
diaBP              0
BMI                0
heartRate          0
glucose            0
TenYearCHD         0
dtype: int64
```

```
heart_data.describe()
```

	male	age	education	currentSmoker	cigsPerDay	BPMeds
count	3656.000000	3656.000000	3656.000000	3656.000000	3656.000000	3656.000000
mean	0.443654	49.557440	1.979759	0.489059	9.022155	0.030361
std	0.496883	8.561133	1.022657	0.499949	11.918869	0.171602
min	0.000000	32.000000	1.000000	0.000000	0.000000	0.000000
25%	0.000000	42.000000	1.000000	0.000000	0.000000	0.000000
50%	0.000000	49.000000	2.000000	0.000000	0.000000	0.000000
75%	1.000000	56.000000	3.000000	1.000000	20.000000	0.000000
max	1.000000	70.000000	4.000000	1.000000	70.000000	1.000000

```
#plot of age vs. TenYearCHD
print(stats.binned_statistic(heart_data.heartRate, heart_data.TenYearCHD))
```

```
BinnedStatisticResult(statistic=array([0.09090909, 0.13276231, 0.16345271, 0.1450253
       0.15319149, 0.21052632, 0.30769231, 0.        , 0.        ]), bin_edges=array(
       133.1, 143. ]), binnumber=array([4, 6, 4, ..., 3, 3, 4]))
```

Dropping Education column as it is outlier with respect to Chronic Heart Disease.

```
heart_data.drop(['education'],axis=1,inplace=True)
heart_data.head()
```

	male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp	diabe
0	1	39	0	0.0	0.0	0	0	
1	0	46	0	0.0	0.0	0	0	
2	1	48	1	20.0	0.0	0	0	
3	0	61	1	30.0	0.0	0	1	
4	0	46	1	23.0	0.0	0	0	

Class imbalance is when the number of samples is different for the different classes in the data. In real-world applications of machine learning, it's very common to encounter datasets with various degrees of class imbalance:

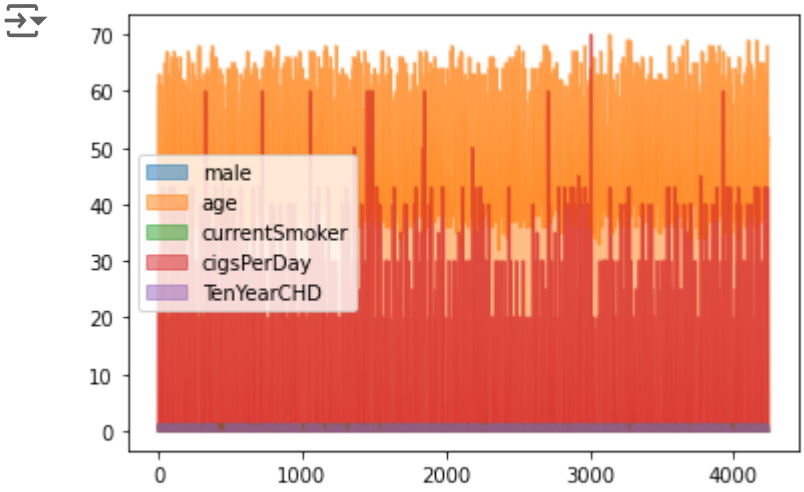
from moderate imbalance —

E.g. medical reports where 10% are diagnosed with having a disease and 90% are not even total Chlestrol, System BP, Dia BP, HeartRate, etc. is high—

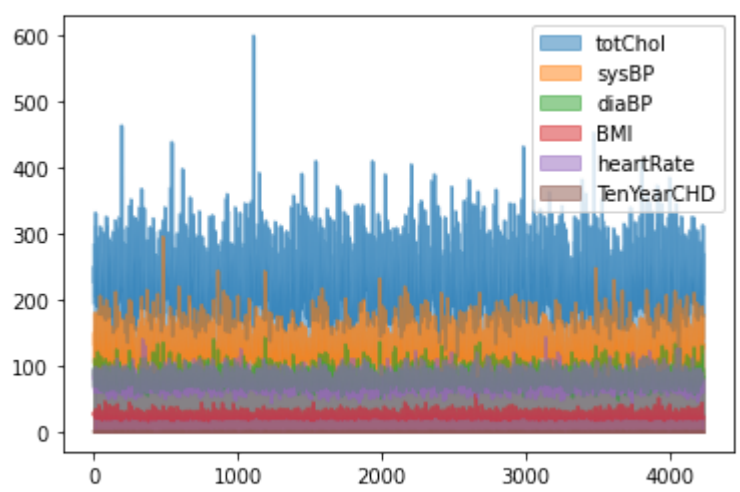
to extreme imbalance —

E.g. anomaly detection in an industrial plant, where perhaps 1 out of 10,000 TenYearCHD fails.

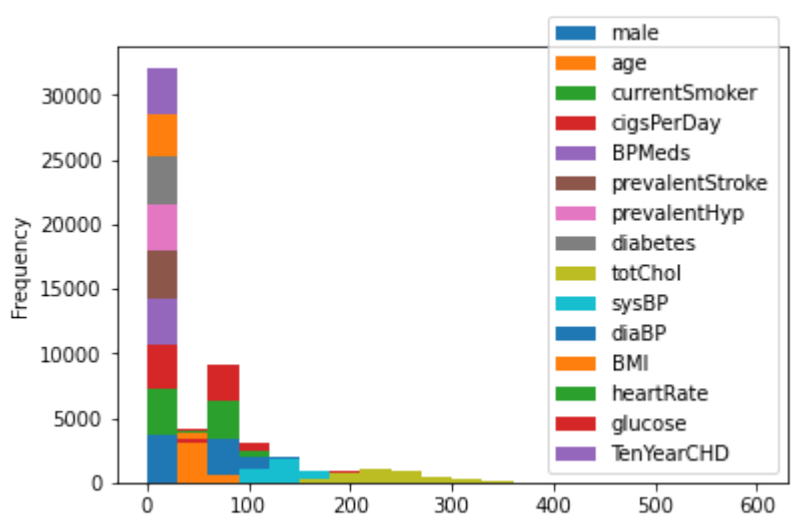
```
df = pd.DataFrame(heart_data, columns=["male", "age", "currentSmoker", "cigsPerDay", "Ten
df.plot.area(stacked=False);
```




```
df = pd.DataFrame(heart_data, columns=["totChol", "sysBP", "diaBP", "BMI", "heartRate", "
df.plot.area(stacked=False);
```




```
heart_data.plot.hist(stacked=True, bins=20);
```



2. Apply appropriate feature engineering techniques for them. Apply the feature transformation techniques like Standardization, Normalization, etc. You are free to apply the appropriate transformations depending upon the structure and the complexity of your dataset. Explore a few techniques for identifying feature importance for your feature engineering task.

```
from statsmodels.tools import add_constant as add_constant
heart_data_constant = add_constant(heart_data)
heart_data_constant.head()
```

```
st.chisqprob = lambda chisq, df: st.chi2.sf(chisq, df)
cols=heart_data_constant.columns[:-1]
model=sm.Logit(heart_data.TenYearCHD,heart_data_constant[cols])
result=model.fit()
result.summary()
```

The results above show some of the attributes with P value higher than the preferred alpha(5%) and thereby showing low statistically significant relationship with the probability of heart disease. Backward elemination approach is used here to remove those attributes with highest Pvalue one at a time follwed by running the regression repeatedly until all attributes have P Values less than 0.05.

```
def back_feature_elem (data_frame,dep_var,col_list):
    """ Takes in the dataframe, the dependent variable and a list of column names, runs t
    P-value above alpha one at a time and returns the regression summary with all p-value

    while len(col_list)>0 :
        model=sm.Logit(dep_var,data_frame[col_list])
        result=model.fit(disp=0)
        largest_pvalue=round(result.pvalues,3).nlargest(1)
        if largest_pvalue[0]<(0.05):
            return result
            break
        else:
            col_list=col_list.drop(largest_pvalue.index)

result=back_feature_elem(heart_data_constant,heart_data.TenYearCHD,cols)


result.summary()
```

Logit Regression Results

Dep. Variable:	TenYearCHD	**No. Observations:**	3656
Model:	Logit	**Df Residuals:**	3649
Method:	MLE	**Df Model:**	6
Date:	Sun, 26 Jun 2022	**Pseudo R-squ.:**	0.1147
Time:	13:53:37	**Log-Likelihood:**	-1381.2
converged:	True	**LL-Null:**	-1560.3
Covariance Type:	nonrobust	**LLR p-value:**	2.885e-74

	coef	std err	z	P>|z|	[0.025	0.975]
const	-9.1298	0.476	-19.199	0.000	-10.062	-8.198
male	0.5614	0.107	5.255	0.000	0.352	0.771
age	0.0659	0.006	10.254	0.000	0.053	0.078
cigsPerDay	0.0192	0.004	4.604	0.000	0.011	0.027
totChol	0.0023	0.001	2.024	0.043	7.16e-05	0.004
sysBP	0.0175	0.002	8.159	0.000	0.013	0.022
glucose	0.0073	0.002	4.342	0.000	0.004	0.011

Interpreting the results: Odds Ratio, Confidence Intervals and Pvalues

```
params = np.exp(result.params)
conf = np.exp(result.conf_int())
conf['OR'] = params
pvalue=round(result.pvalues,3)
conf['pvalue']=pvalue
conf.columns = ['CI 95%(2.5%)', 'CI 95%(97.5%)', 'Odds Ratio','pvalue']
print ((conf))
```

```
             CI 95%(2.5%)  CI 95%(97.5%)  Odds Ratio  pvalue
const            0.000043       0.000275    0.000108   0.000
male             1.421955       2.161623    1.753206   0.000
age              1.054747       1.081654    1.068116   0.000
cigsPerDay       1.011102       1.027789    1.019412   0.000
totChol          1.000072       1.004483    1.002275   0.043
sysBP            1.013411       1.021985    1.017689   0.000
glucose          1.004002       1.010623    1.007307   0.000
```

This fitted model shows that, holding all other features constant, the odds of getting diagnosed with heart disease for males (sex_male = 1)over that of females (sex_male = 0) is exp(0.5815) = 1.788687. In terms of percent change, we can say that the odds for males are 78.8% higher than the odds for females.

The coefficient for age says that, holding all others constant, we will see 7% increase in the odds of getting diagnosed with CDH for a one year increase in age since exp(0.0655) = 1.067644.

Similarly , with every extra cigarette one smokes thers is a 2% increase in the odds of CDH.

For Total cholosterol level and glucose level there is no significant change.

There is a 1.7% increase in odds for every unit increase in systolic Blood Pressure.

Model Building

1. Split the dataset into training and test sets. Answers without justification will not be awarded marks.

```
# Considering attributes withgood CI
import sklearn
from sklearn.model_selection import train_test_split
new_features=heart_data[['age','male','cigsPerDay','totChol','sysBP','glucose','TenYearCH
x=new_features.iloc[:,:-1]
y=new_features.iloc[:,-1]
```

Case 1: Train = 80 % Test = 20%

[x_train1, y_train1] = 80%;[x_test1, y_test1] = 20%.

```
x_train_1,x_test_1,y_train_1,y_test_1=train_test_split(x,y,test_size=.20,random_state=5)
```

Case 2: Train = 10 % Test = 90%

[x_train2, y_train2] = 10%;[x_test2, y_test2] = 90%

```
x_train_2,x_test_2,y_train_2,y_test_2=train_test_split(x,y,test_size=.90,random_state=5)
```

2. Explore k-fold cross validation.

```
# creates the dataset, then evaluates a logistic regression model on It using 10-fold cro

from numpy import mean
from numpy import std
from sklearn.datasets import make_classification
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.linear_model import LogisticRegression
# create dataset
X, y = make_classification(n_samples=1819, n_features=15, n_informative=7, n_redundant=8,
# prepare the cross-validation procedure
cv = KFold(n_splits=10, random_state=1, shuffle=True)
# create model
model = LogisticRegression()
# evaluate model
scores = cross_val_score(model, X, y, scoring='accuracy', cv=cv, n_jobs=-1)
# report performance
print('Accuracy: %.3f (%.3f)' % (mean(scores), std(scores)))
```

```
Accuracy: 0.772 (0.021)
```

3. Build Model/s using

1) Logistic Regression

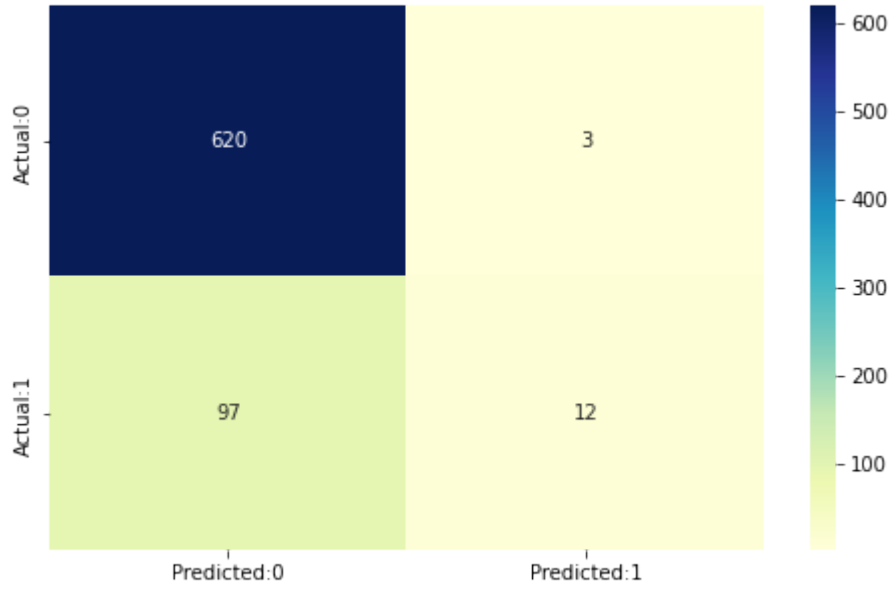
```
from sklearn.linear_model import LogisticRegression
logreg=LogisticRegression()
logreg.fit(x_train_1,y_train_1)
y_pred_1=logreg.predict(x_test_1)
```

```
# Model accuracy
sklearn.metrics.accuracy_score(y_test_1,y_pred_1)
```

```
0.8633879781420765
```

```
# Confusion matrix
from sklearn.metrics import confusion_matrix
cm_1=confusion_matrix(y_test_1,y_pred_1)
conf_matrix_1=pd.DataFrame(data=cm,columns=['Predicted:0','Predicted:1'],index=['Actual:0
plt.figure(figsize = (8,5))
sns.heatmap(conf_matrix, annot=True,fmt='d',cmap="YlGnBu")
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f915e080890>
```



The confusion matrix shows 620+12 = 632 correct predictions and 97+3= 100 incorrect ones.

True Positives: 12

True Negatives: 620

False Positives: 3 (Type I error)

False Negatives: 97 (Type II error)

```
TN_1=cm_1[0,0]
TP_1=cm_1[1,1]
FN_1=cm_1[1,0]
FP_1=cm_1[0,1]
sensitivity_1=TP_1/float(TP_1+FN_1)
specificity_1=TN_1/float(TN_1+FP_1)
```

```
# Model Evaluation - Statistics
print('The acuuracy of the model = TP_1+TN_1/(TP_1+TN_1+FP_1+FN_1) = ',(TP_1+TN_1)/float(

'The Missclassification = 1-Accuracy = ',1-((TP_1+TN_1)/float(TP_1+TN_1+FP_1+FN_1)),'\n',

'Sensitivity or True Positive Rate = TP_1/(TP_1+FN_1) = ',TP_1/float(TP_1+FN_1),'\n',

'Specificity or True Negative Rate = TN_1/(TN_1+FP_1) = ',TN_1/float(TN_1+FP_1),'\n',

'Positive Predictive value = TP_1/(TP_1+FP_1) = ',TP_1/float(TP_1+FP_1),'\n',

'Negative predictive Value = TN_1/(TN_1+FN_1) = ',TN_1/float(TN_1+FN_1),'\n',

'Positive Likelihood Ratio = Sensitivity/(1-Specificity) = ',(TP_1/float(TP_1+FN_1))/(1-(

'Negative likelihood Ratio = (1-Sensitivity)/Specificity = ',(1-(TP_1/float(TP_1+FN_1)))/
```

```
The acuuracy of the model = TP_1+TN_1/(TP_1+TN_1+FP_1+FN_1) =  0.8633879781420765
 The Missclassification = 1-Accuracy =  0.13661202185792354
 Sensitivity or True Positive Rate = TP_1/(TP_1+FN_1) =  0.11009174311926606
 Specificity or True Negative Rate = TN_1/(TN_1+FP_1) =  0.9951845906902087
 Positive Predictive value = TP_1/(TP_1+FP_1) =  0.8
 Negative predictive Value = TN_1/(TN_1+FN_1) =  0.8647140864714087
 Positive Likelihood Ratio = Sensitivity/(1-Specificity) =  22.86238532110109
 Negative likelihood Ratio = (1-Sensitivity)/Specificity =  0.894214264575318
```

From the above statistics it is clear that the model is highly specific than sensitive. The negative values are predicted more accurately than the positives.

```
y_pred_prob_1=logreg.predict_proba(x_test_1)[:,:]
y_pred_prob_df_1=pd.DataFrame(data=y_pred_prob_1, columns=['Prob of no heart disease (0)'
y_pred_prob_df_1.head()
```

	Prob of no heart disease (0)	Prob of Heart Disease (1)
0	0.932109	0.067891
1	0.979193	0.020807
2	0.807735	0.192265
3	0.810751	0.189249
4	0.898649	0.101351

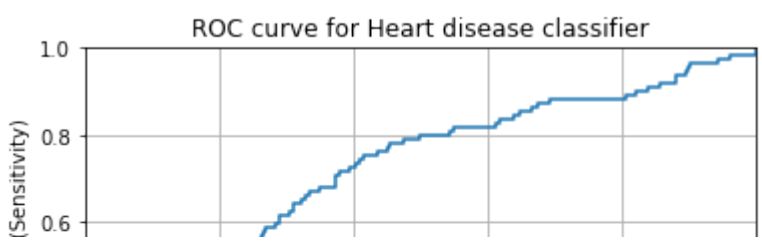
Lower the threshold

Since the model is predicting Heart disease too many type II errors is not advisable. A False Negative (ignoring the probability of disease when there actualy is one) is more dangerous than a False Positive in this case. Hence inorder to increase the sensitivity, threshold can be lowered.

```
from sklearn.preprocessing import binarize
for i in range(1,5):
    cm2_1=0
    y_pred_prob_yes_1=logreg.predict_proba(x_test_1)
    y_pred2_1=binarize(y_pred_prob_yes_1)[:,1]
    cm2_1=confusion_matrix(y_test_1,y_pred2_1)
    print ('With',i/10,'threshold the Confusion Matrix is ','\n',cm2_1,'\n',
            'with',cm2_1[0,0]+cm2_1[1,1],'correct predictions and',cm2_1[1,0],'Type II er
          'Sensitivity: ',cm2_1[1,1]/(float(cm2_1[1,1]+cm2_1[1,0])),'Specificity: ',cm2_1
```

```
With 0.1 threshold the Confusion Matrix is
 [[  0 623]
 [  0 109]]
 with 109 correct predictions and 0 Type II errors( False Negatives)

 Sensitivity:  1.0 Specificity:  0.0



With 0.2 threshold the Confusion Matrix is
 [[  0 623]
 [  0 109]]
 with 109 correct predictions and 0 Type II errors( False Negatives)

 Sensitivity:  1.0 Specificity:  0.0



With 0.3 threshold the Confusion Matrix is
 [[  0 623]
 [  0 109]]
 with 109 correct predictions and 0 Type II errors( False Negatives)

 Sensitivity:  1.0 Specificity:  0.0



With 0.4 threshold the Confusion Matrix is
 [[  0 623]
 [  0 109]]
 with 109 correct predictions and 0 Type II errors( False Negatives)

 Sensitivity:  1.0 Specificity:  0.0
```

```
# ROC Curve
from sklearn.metrics import roc_curve
fpr, tpr, thresholds = roc_curve(y_test_1, y_pred_prob_yes_1[:,1])
plt.plot(fpr,tpr)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.0])
plt.title('ROC curve for Heart disease classifier')
plt.xlabel('False positive rate (1-Specificity)')
plt.ylabel('True positive rate (Sensitivity)')
plt.grid(True)
```



A common way to visualize the trade-offs of different thresholds is by using an ROC curve, a plot of the true positive rate (# true positives/ total # positives) versus the false positive rate (# false positives / total # negatives) for all possible choices of thresholds. A model with good classification accuracy should have significantly more true positives than false positives at all thresholds.