In [1]:
```
import pandas as pd
import numpy as np
import statsmodels.api as sm
import scipy.stats as st
import matplotlib.pyplot as plt
import seaborn as sn
from sklearn.metrics import confusion_matrix
import matplotlib.mlab as mlab
%matplotlib inline
```

In [4]:
```
heart_df=pd.read_csv(r"C:\Users\shali\Downloads\archive (3)\framingham.csv")
heart_df.drop(['education'],axis=1,inplace=True)
heart_df.head()
```

Out[4]:

	male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp	diabetes	totChol	sysBP	diaBP	BMI	heartRate	glucose	TenYearCHD
0	1	39	0	0.0	0.0	0	0	0	195.0	106.0	70.0	26.97	80.0	77.0	0
1	0	46	0	0.0	0.0	0	0	0	250.0	121.0	81.0	28.73	95.0	76.0	0
2	1	48	1	20.0	0.0	0	0	0	245.0	127.5	80.0	25.34	75.0	70.0	0
3	0	61	1	30.0	0.0	0	1	0	225.0	150.0	95.0	28.58	65.0	103.0	1
4	0	46	1	23.0	0.0	0	0	0	285.0	130.0	84.0	23.10	85.0	85.0	0

Variables : 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):

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

In [9]:
```
heart_df.rename(columns={'male':'Sex_male'},inplace=True)
```

In [6]:
```
heart_df.isnull().sum()
```

Out[6]:
```
Sex_male             0
age                  0
currentSmoker        0
cigsPerDay          29
BPMeds              53
prevalentStroke      0
prevalentHyp         0
diabetes             0
totChol             50
sysBP                0
diaBP                0
BMI                 19
heartRate            1
glucose            388
TenYearCHD           0
dtype: int64
```

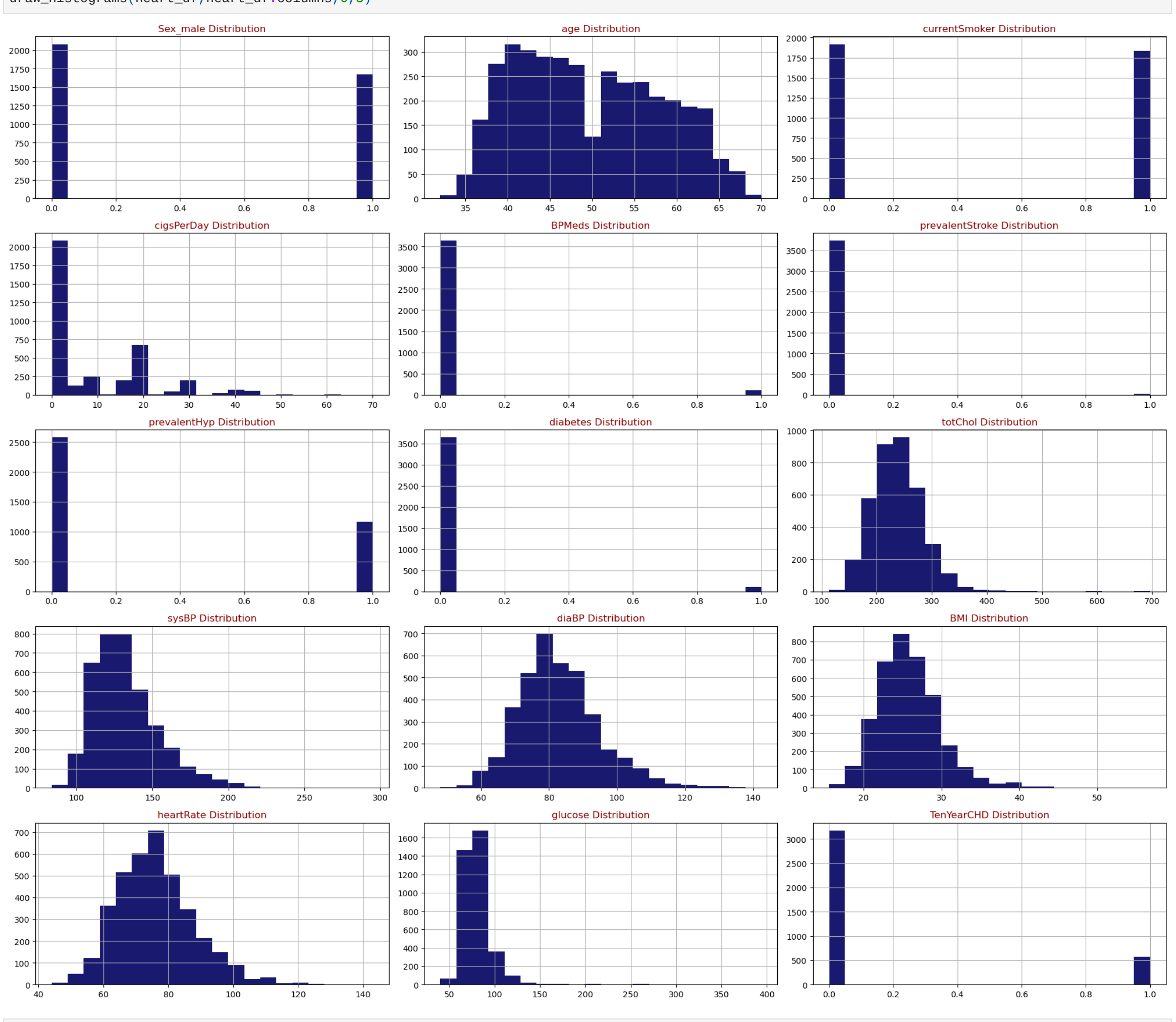
In [7]:
```
count=0
for i in heart_df.isnull().sum(axis=1):
    if i>0:
        count=count+1
print('Total number of rows with missing values is ', count)
print('since it is only',round((count/len(heart_df.index))*100), 'percent of the entire dataset the rows with missing values are excluded.')
```

```
Total number of rows with missing values is  489
since it is only 12 percent of the entire dataset the rows with missing values are excluded.
```

In [8]:
```
heart_df.dropna(axis=0,inplace=True)
```

Exploratory Analysis

In [10]:
```
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_df,heart_df.columns,6,3)
```

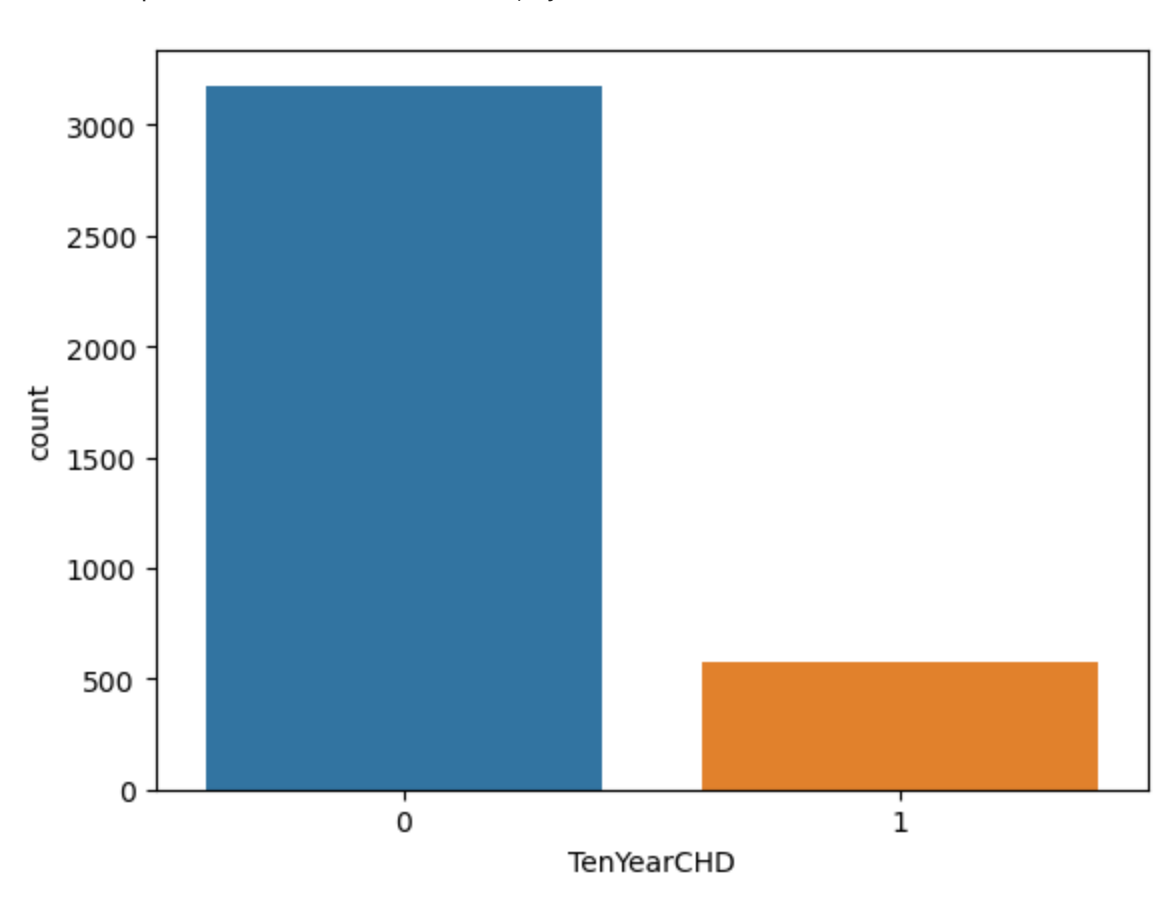


In [11]:
```
heart_df.TenYearCHD.value_counts()
```

Out[11]:
```
0    3177
1     572
Name: TenYearCHD, dtype: int64
```

In [12]:
```
sn.countplot(x='TenYearCHD',data=heart_df)
```

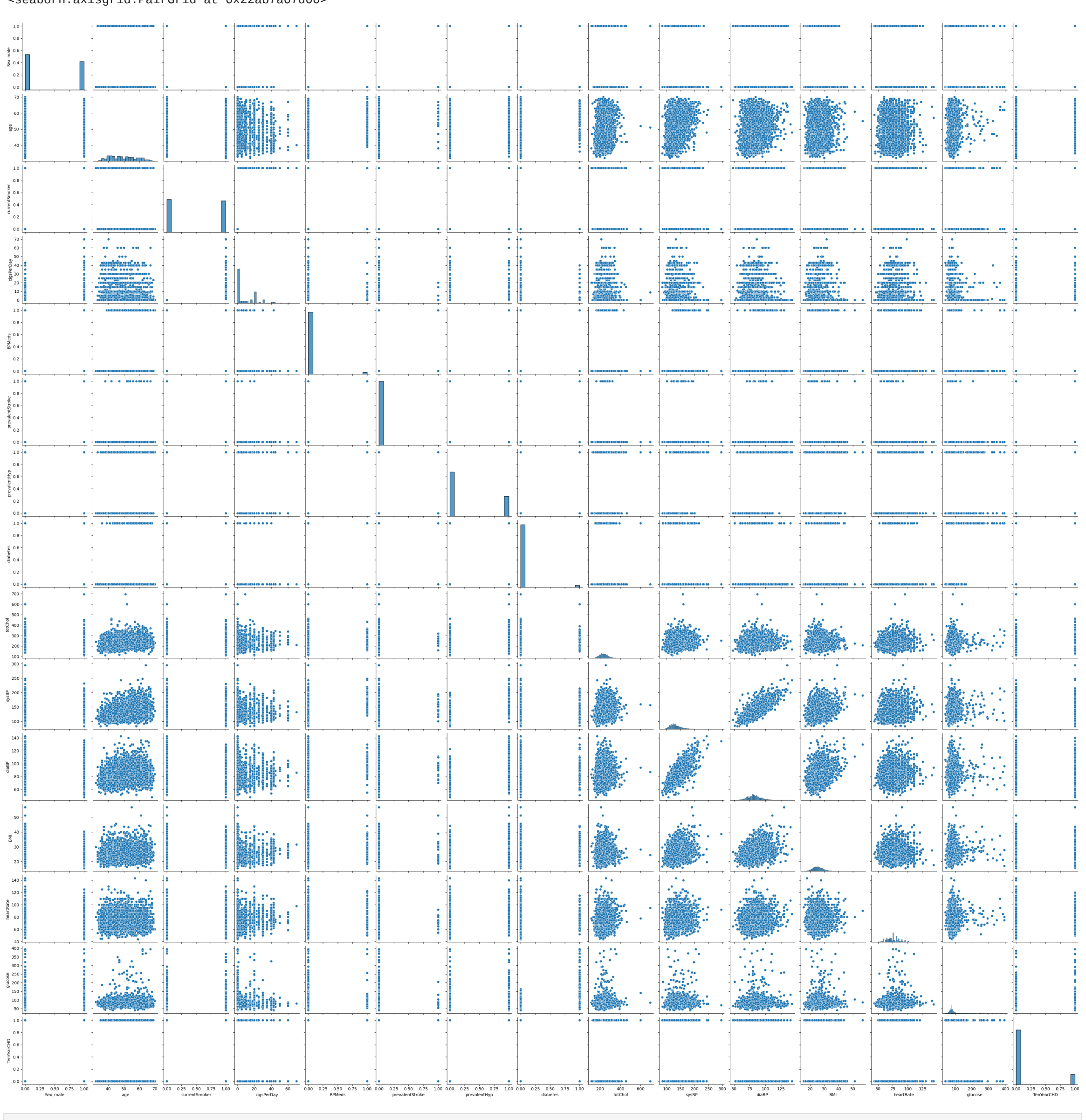
Out[12]: <AxesSubplot:xlabel='TenYearCHD', ylabel='count'>



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

In [13]:
```
sn.pairplot(data=heart_df)
```

Out[13]: <seaborn.axisgrid.PairGrid at 0x22ab7a07d00>



In [14]:
```
heart_df.describe()
```

Out[14]:

	Sex_male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp	diabetes	totChol	sysBP	diaBP	BMI	heartRate
count	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000
mean	0.445185	49.578821	0.488397	9.005335	0.030408	0.005601	0.311816	0.027207	236.952787	132.365964	82.933716	25.809651	75.703921
std	0.497053	8.569322	0.499932	11.922440	0.171730	0.074643	0.463297	0.162709	44.610417	22.051951	11.933321	4.065894	11.957763
min	0.000000	32.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	113.000000	83.500000	48.000000	15.540000	44.000000
25%	0.000000	42.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	206.000000	117.000000	75.000000	23.090000	68.000000
50%	0.000000	49.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	234.000000	128.000000	82.000000	25.410000	75.000000
75%	1.000000	56.000000	1.000000	20.000000	0.000000	0.000000	1.000000	0.000000	264.000000	144.000000	90.000000	28.060000	82.000000
max	1.000000	70.000000	1.000000	70.000000	1.000000	1.000000	1.000000	1.000000	696.000000	295.000000	142.500000	56.800000	143.000000

Logistic Regression

Logistic regression is a type of regression analysis in statistics used for prediction of outcome of a categorical dependent variable from a set of predictor or independent variables. In logistic regression the dependent variable is always binary. Logistic regression is mainly used to for prediction and also calculating the probability of success.

In [15]:
```
from statsmodels.tools import add_constant as add_constant
heart_df_constant = add_constant(heart_df)
heart_df_constant.head()
```

Out[15]:

	const	Sex_male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp	diabetes	totChol	sysBP	diaBP	BMI	heartRate	glucose	TenYearCHD
0	1.0	1	39	0	0.0	0.0	0	0	0	195.0	106.0	70.0	26.97	80.0	77.0	0
1	1.0	0	46	0	0.0	0.0	0	0	0	250.0	121.0	81.0	28.73	95.0	76.0	0
2	1.0	1	48	1	20.0	0.0	0	0	0	245.0	127.5	80.0	25.34	75.0	70.0	0
3	1.0	0	61	1	30.0	0.0	0	1	0	225.0	150.0	95.0	28.58	65.0	103.0	1
4	1.0	0	46	1	23.0	0.0	0	0	0	285.0	130.0	84.0	23.10	85.0	85.0	0

In [16]:
```
st.chisqprob = lambda chisq, df: st.chi2.sf(chisq, df)
cols=heart_df_constant.columns[:-1]
model=sm.Logit(heart_df.TenYearCHD,heart_df_constant[cols])
result=model.fit()
result.summary()
```

```
Optimization terminated successfully.
         Current function value: 0.377199
         Iterations 7
```

Out[16]:

Logit Regression Results

Dep. Variable:	TenYearCHD	No. Observations:	3749
Model:	Logit	Df Residuals:	3734
Method:	MLE	Df Model:	14
Date:	Sat, 09 Sep 2023	Pseudo R-squ.:	0.1169
Time:	20:19:56	Log-Likelihood:	-1414.1
converged:	True	LL-Null:	-1601.4
Covariance Type:	nonrobust	LLR p-value:	2.922e-71

	coef	std err	z	P>|z|	[0.025	0.975]
const	-8.6463	0.687	-12.577	0.000	-9.994	-7.299
Sex_male	0.5740	0.107	5.343	0.000	0.363	0.785
age	0.0640	0.007	9.787	0.000	0.051	0.077
currentSmoker	0.0732	0.155	0.473	0.636	-0.230	0.376
cigsPerDay	0.0184	0.006	3.003	0.003	0.006	0.030
BPMeds	0.1446	0.232	0.622	0.534	-0.311	0.600
prevalentStroke	0.7191	0.489	1.471	0.141	-0.239	1.677
prevalentHyp	0.2146	0.136	1.574	0.116	-0.053	0.482
diabetes	0.0025	0.312	0.008	0.994	-0.609	0.614
totChol	0.0022	0.001	2.074	0.038	0.000	0.004
sysBP	0.0153	0.004	4.080	0.000	0.008	0.023
diaBP	-0.0039	0.006	-0.619	0.536	-0.016	0.009
BMI	0.0103	0.013	0.820	0.412	-0.014	0.035
heartRate	-0.0023	0.004	-0.550	0.583	-0.010	0.006
glucose	0.0076	0.002	3.408	0.001	0.003	0.012

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.

Feature Selection: Backward elemination (P-value approach)

In [17]:
```
def back_feature_elem (data_frame,dep_var,col_list):
    """ Takes in the dataframe, the dependent variable and a list of column names, runs the regression repeatedly eliminating feature with the highe
    P-value above alpha one at a time and returns the regression summary with all p-values below alpha"""

    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_df_constant,heart_df.TenYearCHD,cols)
```

In [18]:
```
result.summary()
```

Out[18]:

Logit Regression Results

Dep. Variable:	TenYearCHD	No. Observations:	3749
Model:	Logit	Df Residuals:	3742
Method:	MLE	Df Model:	6
Date:	Sat, 09 Sep 2023	Pseudo R-squ.:	0.1148
Time:	20:26:22	Log-Likelihood:	-1417.6
converged:	True	LL-Null:	-1601.4
Covariance Type:	nonrobust	LLR p-value:	2.548e-76

	coef	std err	z	P>|z|	[0.025	0.975]
const	-9.1211	0.468	-19.491	0.000	-10.038	-8.204
Sex_male	0.5813	0.105	5.521	0.000	0.375	0.788
age	0.0654	0.006	10.330	0.000	0.053	0.078
cigsPerDay	0.0197	0.004	4.803	0.000	0.012	0.028
totChol	0.0023	0.001	2.099	0.036	0.000	0.004
sysBP	0.0174	0.002	8.166	0.000	0.013	0.022
glucose	0.0076	0.002	4.573	0.000	0.004	0.011

- Logistic regression equation
- $P=e^{\beta_0+\beta_1X_1}/1+e^{\beta_0+\beta_1X_1}$

When all features plugged in:

$logit(p)=log(p/(1-p))=\beta_0+\beta_1 * Sexmale+\beta_2 * age+\beta_3 * cigsPerDay+\beta_4 * totChol+\beta_5 * sysBP+\beta_6 * glucose$

Interpreting the results: Odds Ratio, Confidence Intervals and Pvalues

In [19]:
```
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           0.000044       0.000274    0.000109   0.000
Sex_male        1.454877       2.198166    1.788313   0.000
age             1.054409       1.080897    1.067571   0.000
cigsPerDay      1.011730       1.028128    1.019896   0.000
totChol         1.000150       1.004386    1.002266   0.036
sysBP           1.013299       1.021791    1.017536   0.000
glucose         1.004343       1.010895    1.007614   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.

Splitting data to train and test split

In [23]:
```
import sklearn
new_features=heart_df[['age','Sex_male','cigsPerDay','totChol','sysBP','glucose','TenYearCHD']]
x=new_features.iloc[:,:-1]
y=new_features.iloc[:,-1]
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=.20,random_state=5)
```

In [24]:
```
from sklearn.linear_model import LogisticRegression
logreg=LogisticRegression()
logreg.fit(x_train,y_train)
y_pred=logreg.predict(x_test)
```

Model Evaluation

Model accuracy

In [25]:
```
sklearn.metrics.accuracy_score(y_test,y_pred)
```

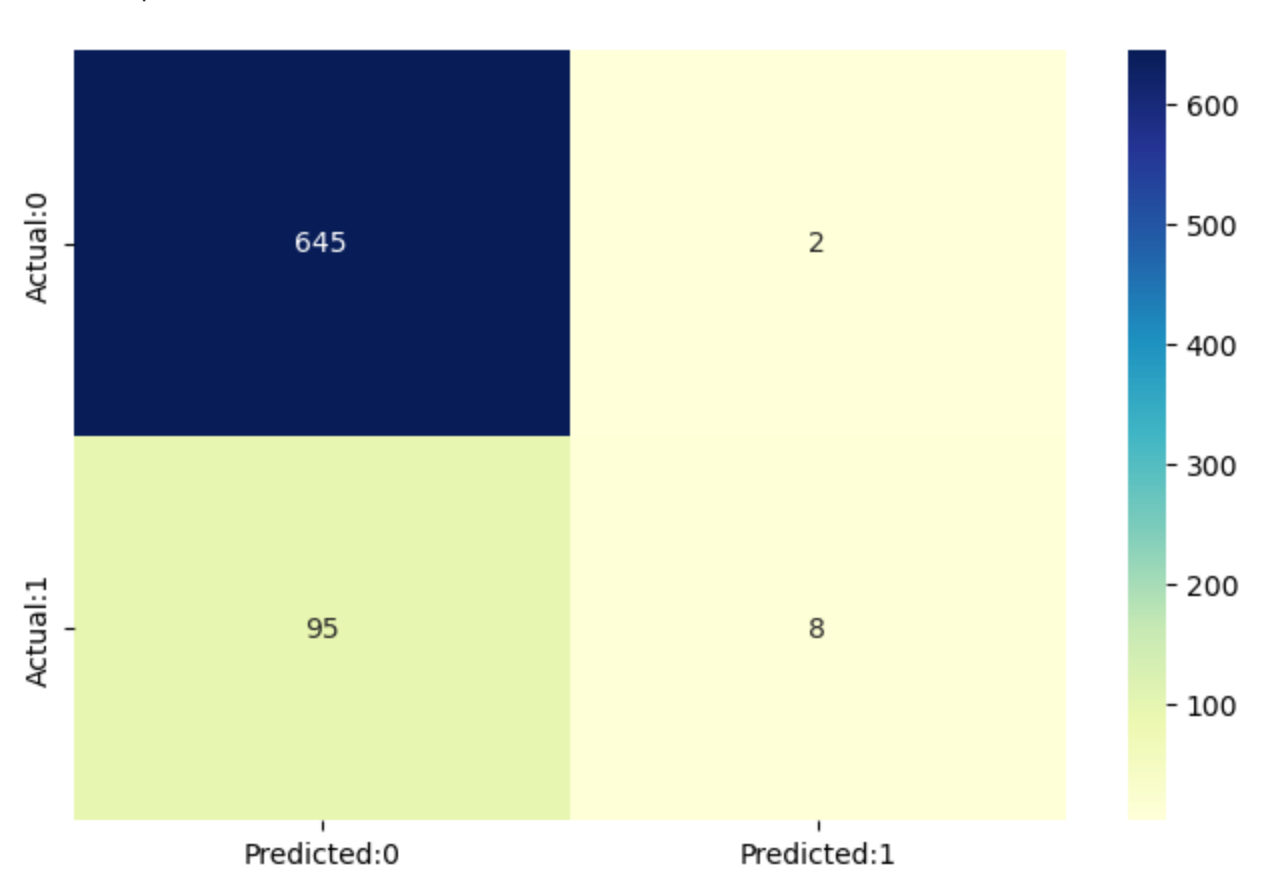
Out[25]: 0.8706666666666667

Accuracy of the model is 0.88

Confusion matrix

In [26]:
```
from sklearn.metrics import confusion_matrix
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))
sn.heatmap(conf_matrix, annot=True,fmt='d',cmap="YlGnBu")
```

Out[26]: <AxesSubplot:>



The confusion matrix shows 658+4 = 662 correct predictions and 88+1= 89 incorrect ones.

- True Positives: 4
- True Negatives: 658
- False Positives: 1 (Type I error)
- False Negatives: 88 (Type II error)

In [27]:
```
TN=cm[0,0]
TP=cm[1,1]
FN=cm[1,0]
FP=cm[0,1]
sensitivity=TP/float(TP+FN)
specificity=TN/float(TN+FP)
```

Model Evaluation - Statistics

In [28]:
```
print('The acuuracy of the model = TP+TN/(TP+TN+FP+FN) = ',(TP+TN)/float(TP+TN+FP+FN),'\n',

'The Missclassification = 1-Accuracy = ',1-((TP+TN)/float(TP+TN+FP+FN)),'\n',

'Sensitivity or True Positive Rate = TP/(TP+FN) = ',TP/float(TP+FN),'\n',

'Specificity or True Negative Rate = TN/(TN+FP) = ',TN/float(TN+FP),'\n',

'Positive Predictive value = TP/(TP+FP) = ',TP/float(TP+FP),'\n',

'Negative predictive Value = TN/(TN+FN) = ',TN/float(TN+FN),'\n',

'Positive Likelihood Ratio = Sensitivity/(1-Specificity) = ',sensitivity/(1-specificity),'\n',

'Negative likelihood Ratio = (1-Sensitivity)/Specificity = ',(1-sensitivity)/specificity)
```

```
The acuuracy of the model = TP+TN/(TP+TN+FP+FN) =  0.8706666666666667
 The Missclassification = 1-Accuracy =  0.1293333333333333
 Sensitivity or True Positive Rate = TP/(TP+FN) =  0.07766990291262135
 Specificity or True Negative Rate = TN/(TN+FP) =  0.9969088098918083
 Positive Predictive value = TP/(TP+FP) =  0.8
 Negative predictive Value = TN/(TN+FN) =  0.8716216216216216
 Positive Likelihood Ratio = Sensitivity/(1-Specificity) =  25.126213592232638
 Negative likelihood Ratio = (1-Sensitivity)/Specificity =  0.925190035372921
```

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.

Predicted probabilities of 0 (No Coronary Heart Disease) and 1 (Coronary Heart Disease: Yes) for the test data with a default classification threshold of 0.5

In [29]:
```
y_pred_prob=logreg.predict_proba(x_test)[:,:]
y_pred_prob_df=pd.DataFrame(data=y_pred_prob, columns=['Prob of no heart disease (0)','Prob of Heart Disease (1)'])
y_pred_prob_df.head()
```

Out[29]:

	Prob of no heart disease (0)	Prob of Heart Disease (1)
0	0.776132	0.223868
1	0.545785	0.454215
2	0.831962	0.168038
3	0.887940	0.112060
4	0.920553	0.079447

Lower the threshold

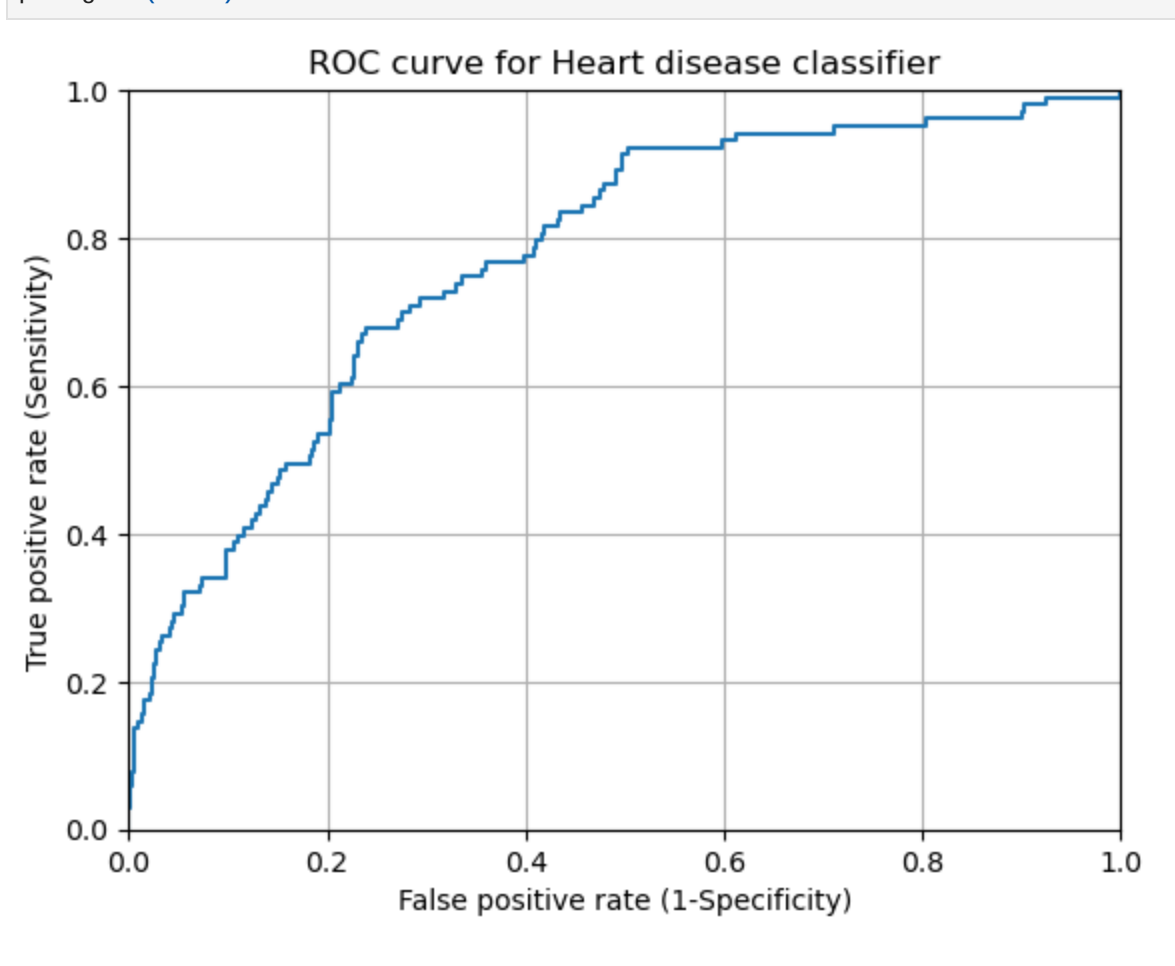
Since the model is predicting Heart disease too many type II errors is not advisable. A False Negative (ignoring the probability of disease when there actualy is one) is more dangerous than a False Positive in this case. Hence inorder to increase the sensitivity, threshold can be lowered.

In [37]:
```
from sklearn.preprocessing import binarize
for i in range(1,5):
    cm2=0
    y_pred_prob_yes=logreg.predict_proba(x_test)
    y_pred2 = binarize(y_pred_prob_yes, threshold=i/10)[:,1]

    cm2=confusion_matrix(y_test,y_pred2)
    print ('With',i/10,'threshold the Confusion Matrix is ','\n',cm2,'\n',
            'with',cm2[0,0]+cm2[1,1],'correct predictions and',cm2[1,0],'Type II errors( False Negatives)','\n\n',
          'Sensitivity: ',cm2[1,1]/(float(cm2[1,1]+cm2[1,0])),'Specificity: ',cm2[0,0]/(float(cm2[0,0]+cm2[0,1])),'\n\n\n')
```

```
With 0.1 threshold the Confusion Matrix is
 [[311 336]
 [  8  95]]
 with 406 correct predictions and 8 Type II errors( False Negatives)

 Sensitivity:  0.9223300970873787 Specificity:  0.4806800618238022



With 0.2 threshold the Confusion Matrix is
 [[516 131]
 [ 46  57]]
 with 573 correct predictions and 46 Type II errors( False Negatives)

 Sensitivity:  0.5533980582524272 Specificity:  0.7975270479134466



With 0.3 threshold the Confusion Matrix is
 [[595  52]
 [ 68  35]]
 with 630 correct predictions and 68 Type II errors( False Negatives)

 Sensitivity:  0.33980582524271846 Specificity:  0.919629057187017



With 0.4 threshold the Confusion Matrix is
 [[638   9]
 [ 88  15]]
 with 653 correct predictions and 88 Type II errors( False Negatives)

 Sensitivity:  0.14563106796116504 Specificity:  0.9860896445131375
```

ROC curve

In [34]:
```
from sklearn.metrics import roc_curve
fpr, tpr, thresholds = roc_curve(y_test, y_pred_prob_yes[:,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.

The optimum position for roc curve is towards the top left corner where the specificity and sensitivity are at optimum levels

Area Under The Curve (AUC)

The area under the ROC curve quantifies model classification accuracy; the higher the area, the greater the disparity between true and false positives, and the stronger the model in classifying members of the training dataset. An area of 0.5 corresponds to a model that performs no better than random classification and a good classifier stays as far away from that as possible. An area of 1 is ideal. The closer the AUC to 1 the better.

In [35]:
```
sklearn.metrics.roc_auc_score(y_test,y_pred_prob_yes[:,1])
```

Out[35]: 0.7733227292507616

Conclusions:

- **All attributes selected after the elimination process show Pvalues lower than 5% and thereby suggesting significant role in the Heart disease prediction.**
- **Men seem to be more susceptible to heart disease than women.Increase in Age,number of cigarettes smoked per day and systolic Blood Pressure also show increasing odds of having heart disease.**
- **Total cholesterol shows no significant change in the odds of CHD. This could be due to the presence of 'good cholesterol(HDL) in the total cholesterol reading.Glucose too causes a very negligible change in odds (0.2%)**
- **The model predicted with 0.88 accuracy. The model is more specific than sensitive.**
- **The Area under the ROC curve is 73.5 which is somewhat satisfactory.**
- **Overall model could be improved with more data.**

- Appendix
  - http://www.who.int/mediacentre/factsheets/fs317/en/
- Data Source References
  - https://www.kaggle.com/amanajmera1/framingham-heart-study-dataset/data

In [ ]: