HEART DISEASE PREDICTION USING LOGISTIC REGRESSION.

Introduction

World Health Organization has estimated 12 million deaths occur worldwide, every year due to Heart diseases. Half the deaths in the United States and other developed countries are due to cardio vascular diseases. The early prognosis of cardiovascular diseases can aid in making decisions on lifestyle changes in high risk patients and in turn reduce the complications. This research intends to pinpoint the most relevant/risk factors of heart disease as well as predict the overall risk using logistic regression.

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
```

Data Preparation

Source:

The dataset is publically available on the Kaggle website, and it is from an ongoing ongoing cardiovascular study on residents of the town of Framingham, Massachusetts. 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.

In [2]:

```
heart_df=pd.read_csv("D:\\Semester 7\\ML Lab\\Project\\MLProject\\Heart\\framingham_neisha.
heart_df.drop(['education'],axis=1,inplace=True)
heart_df.head()
```

Out[2]:

	male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp	diabetes	to
0	1	39	0	0.0	0.0	0	0	0	
1	0	46	0	0.0	0.0	0	0	0	
2	1	48	1	20.0	0.0	0	0	0	
3	0	61	1	30.0	0.0	0	1	0	
4	0	46	1	23.0	0.0	0	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 [3]:

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

Missing values

In [4]:

```
heart_df.isnull().sum()
```

Out[4]:

```
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 [5]:

```
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 dat
```

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

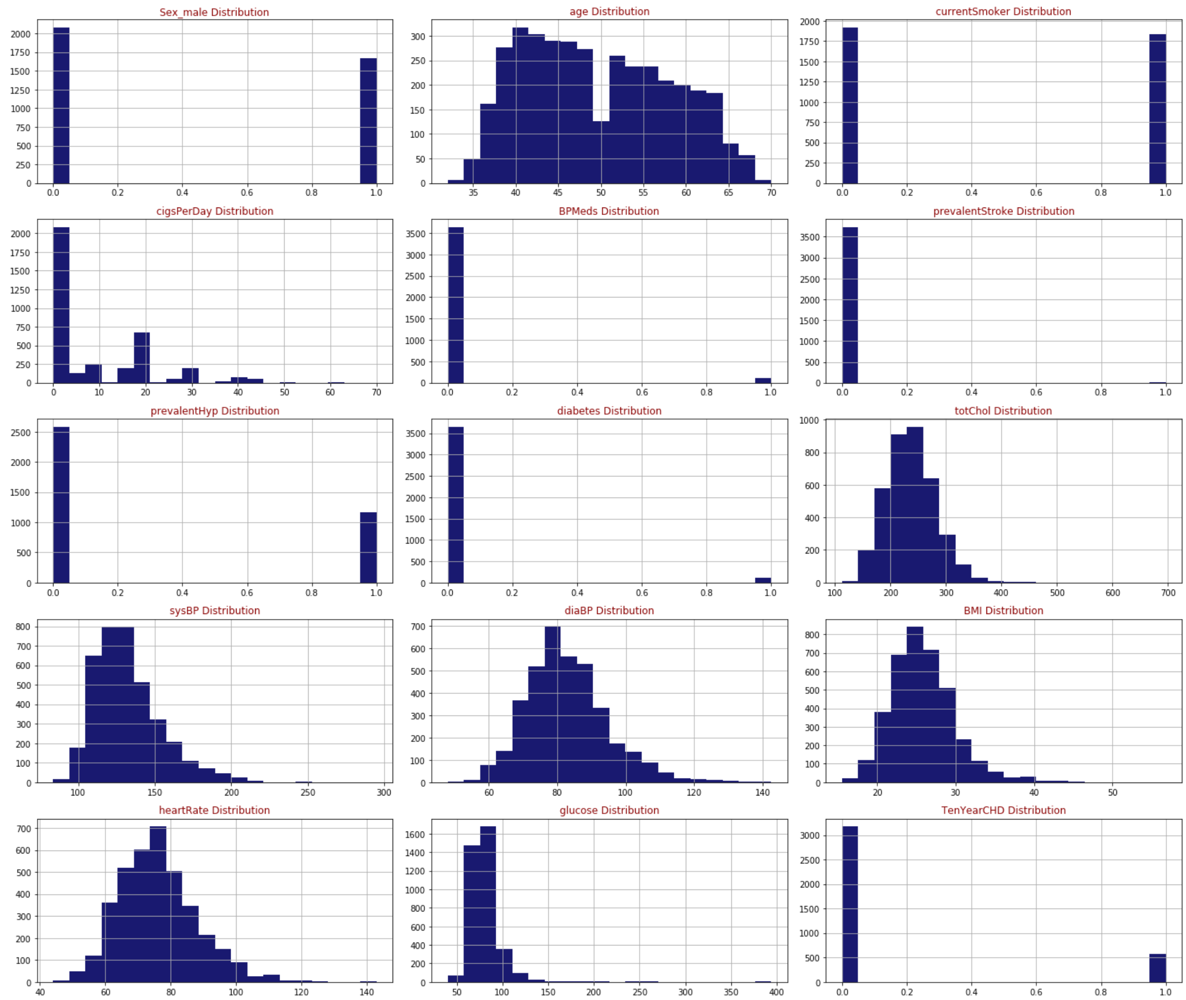
In [6]:

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

Exploratory Analysis

In [7]:

```
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 [8]:

```
heart_df.TenYearCHD.value_counts()
```

Out[8]:

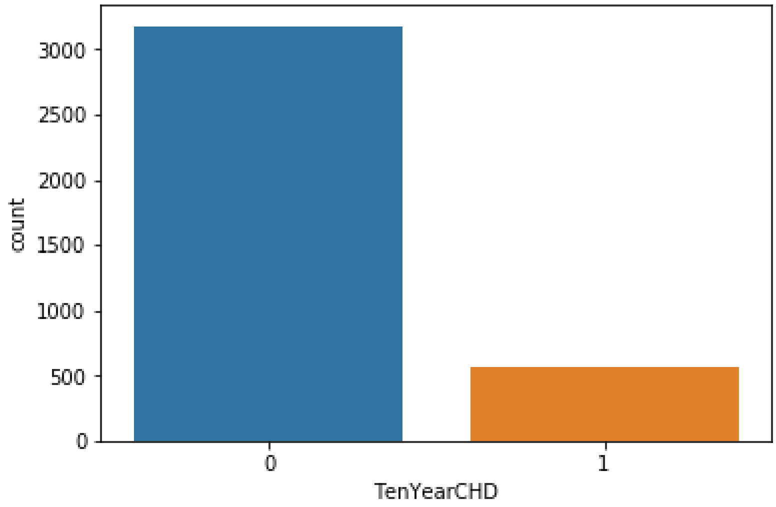
```
0    3179
1     572
Name: TenYearCHD, dtype: int64
```

In [9]:

```
sn.countplot(x='TenYearCHD',data=heart_df)
```

Out[9]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x21a23fe2c18>
```



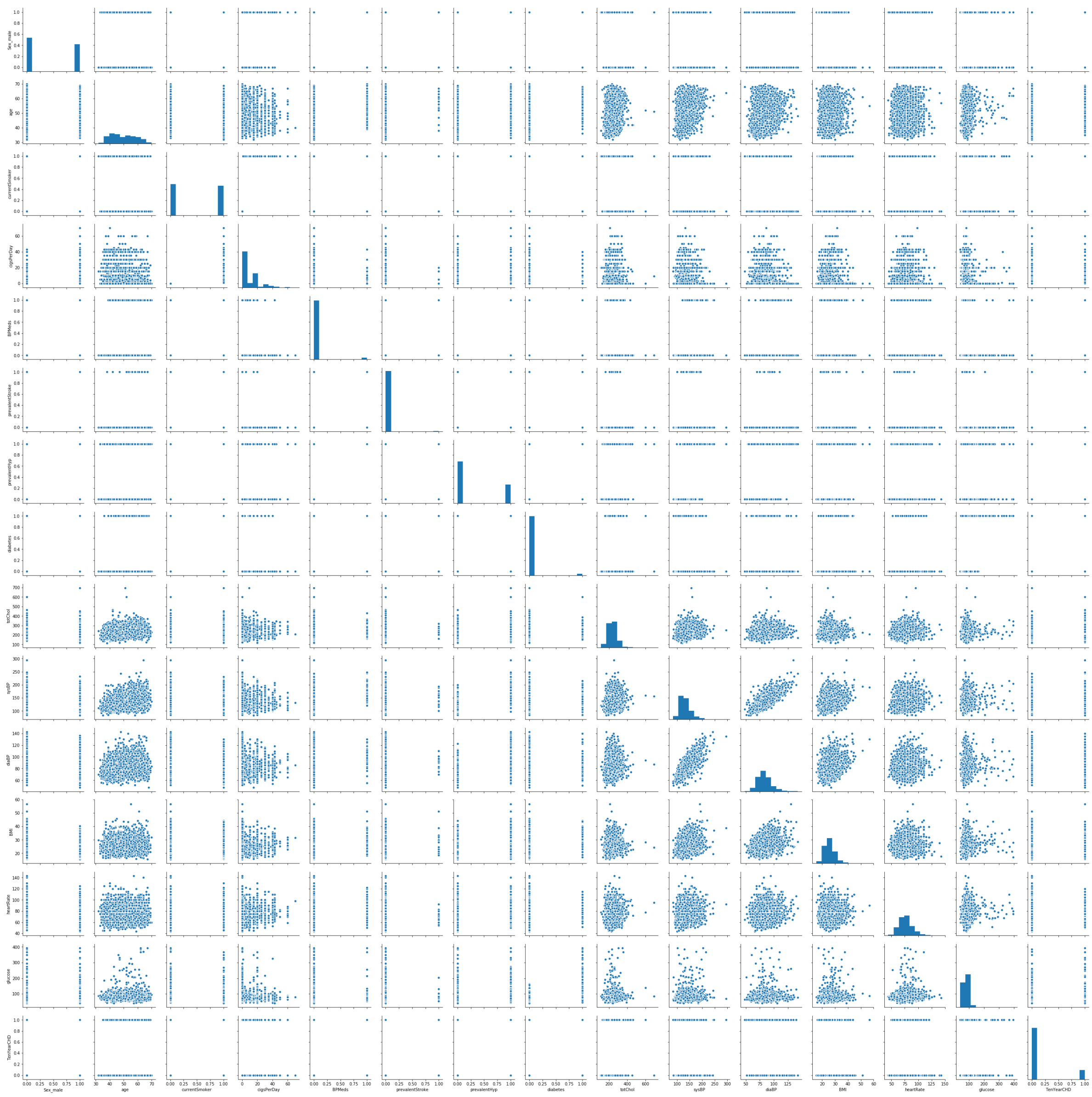
There are 3179 patents with no heart disease and 572 patients with risk of heart disease.

In [10]:

```
sn.pairplot(data=heart_df)
```

Out[10]:

<seaborn.axisgrid.PairGrid at 0x21a2410eac8>



In [11]:

```
heart_df.describe()
```

Out[11]:

	Sex_male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	pr
count	3751.000000	3751.000000	3751.000000	3751.000000	3751.000000	3751.000000	3
mean	0.445215	49.573447	0.488403	9.008531	0.030392	0.005599	
std	0.497056	8.570204	0.499932	11.925097	0.171686	0.074623	
min	0.000000	32.000000	0.000000	0.000000	0.000000	0.000000	
25%	0.000000	42.000000	0.000000	0.000000	0.000000	0.000000	
50%	0.000000	49.000000	0.000000	0.000000	0.000000	0.000000	
75%	1.000000	56.000000	1.000000	20.000000	0.000000	0.000000	
max	1.000000	70.000000	1.000000	70.000000	1.000000	1.000000	

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 [12]:

```
from statsmodels.tools import add_constant as add_constant
heart_df_constant = add_constant(heart_df)
heart_df_constant.head()
```

Out[12]:

	const	Sex_male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp
0	1.0	1	39	0	0.0	0.0	0	0
1	1.0	0	46	0	0.0	0.0	0	0
2	1.0	1	48	1	20.0	0.0	0	0
3	1.0	0	61	1	30.0	0.0	0	1
4	1.0	0	46	1	23.0	0.0	0	0

In [13]:

```
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: 0.377036
         Iterations 7
```

Out[13]:

Logit Regression Results

Dep. Variable:	TenYearCHD	**No. Observations:**	3751
Model:	Logit	**Df Residuals:**	3736
Method:	MLE	**Df Model:**	14
Date:	Fri, 26 Oct 2018	**Pseudo R-squ.:**	0.1170
Time:	21:36:24	**Log-Likelihood:**	-1414.3
converged:	True	**LL-Null:**	-1601.7
		LLR p-value:	2.439e-71

	coef	**std err**	**z**	**P>|z|**	**[0.025**	**0.975]**
const	-8.6532	0.687	-12.589	0.000	-10.000	-7.306
Sex_male	0.5742	0.107	5.345	0.000	0.364	0.785
age	0.0641	0.007	9.799	0.000	0.051	0.077
currentSmoker	0.0739	0.155	0.478	0.633	-0.229	0.377
cigsPerDay	0.0184	0.006	3.000	0.003	0.006	0.030
BPMeds	0.1448	0.232	0.623	0.533	-0.310	0.600
prevalentStroke	0.7193	0.489	1.471	0.141	-0.239	1.678
prevalentHyp	0.2142	0.136	1.571	0.116	-0.053	0.481
diabetes	0.0022	0.312	0.007	0.994	-0.610	0.614
totChol	0.0023	0.001	2.081	0.037	0.000	0.004
sysBP	0.0154	0.004	4.082	0.000	0.008	0.023
diaBP	-0.0040	0.006	-0.623	0.533	-0.016	0.009
BMI	0.0103	0.013	0.827	0.408	-0.014	0.035
heartRate	-0.0023	0.004	-0.549	0.583	-0.010	0.006
glucose	0.0076	0.002	3.409	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 [14]:

```
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
    P-value above alpha one at a time and returns the regression summary with all p-values

    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 [15]:

```
result.summary()
```

Out[15]:

Logit Regression Results

Dep. Variable:	TenYearCHD	**No. Observations:**	3751
Model:	Logit	**Df Residuals:**	3744
Method:	MLE	**Df Model:**	6
Date:	Fri, 26 Oct 2018	**Pseudo R-squ.:**	0.1149
Time:	21:36:24	**Log-Likelihood:**	-1417.7
converged:	True	**LL-Null:**	-1601.7
		LLR p-value:	2.127e-76

	coef	std err	z	P>|z|	[0.025	0.975]
const	-9.1264	0.468	-19.504	0.000	-10.043	-8.209
Sex_male	0.5815	0.105	5.524	0.000	0.375	0.788
age	0.0655	0.006	10.343	0.000	0.053	0.078
cigsPerDay	0.0197	0.004	4.805	0.000	0.012	0.028
totChol	0.0023	0.001	2.106	0.035	0.000	0.004
sysBP	0.0174	0.002	8.162	0.000	0.013	0.022
glucose	0.0076	0.002	4.574	0.000	0.004	0.011

Logistic regression equation

$$P = \quad e^{\beta_0+\beta_1 X_1} \ \ / \ \ 1 + e^{\beta_0+\beta_1 X_1}$$

When all features plugged in:

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

Interpreting the results: Odds Ratio, Confidence Intervals and Pvalues

In [16]:

```
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       0.000272    0.000109   0.000
Sex_male        1.455242       2.198536    1.788687   0.000
age             1.054483       1.080969    1.067644   0.000
cigsPerDay      1.011733       1.028128    1.019897   0.000
totChol         1.000158       1.004394    1.002273   0.035
sysBP           1.013292       1.021784    1.017529   0.000
glucose         1.004346       1.010898    1.007617   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 [27]:

```
import sklearn
new_features=heart_df[['age','Sex_male','cigsPerDay','totChol','sysBP','glucose','TenYearCH
x=new_features.iloc[:,:-1]
y=new_features.iloc[:,-1]
#from sklearn.cross_validation import train_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=.20,random_state=5)
```

In [28]:

```
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 [29]:

```
sklearn.metrics.accuracy_score(y_test,y_pred)
```

Out[29]:

```
0.881491344873502
```

Accuracy of the model is 0.88

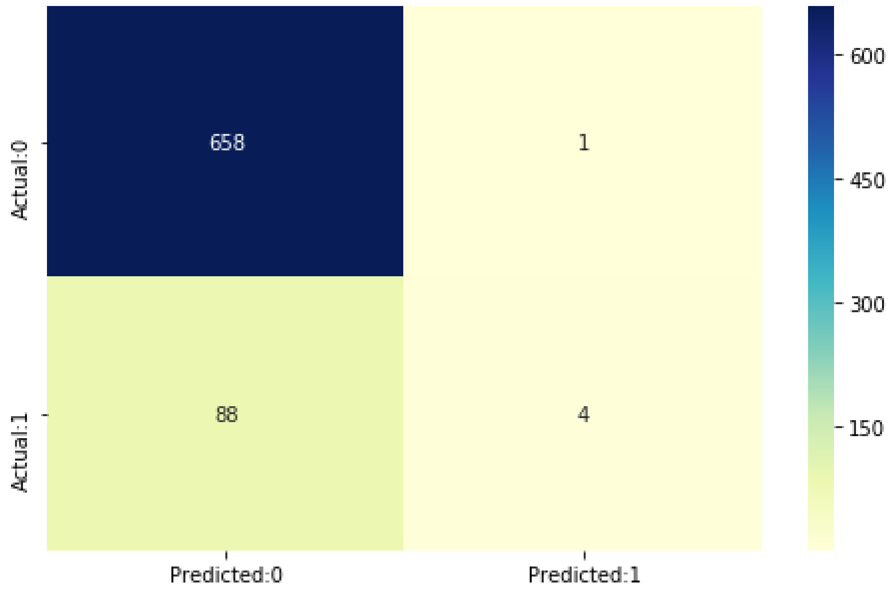
Confusion matrix

In [30]:

```
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','A
plt.figure(figsize = (8,5))
sn.heatmap(conf_matrix, annot=True,fmt='d',cmap="YlGnBu")
```

Out[30]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x21a304225c0>
```



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 [31]:

```
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 [32]:

```
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),'\

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

```
The acuuracy of the model = TP+TN/(TP+TN+FP+FN) =  0.8814913448735021
 The Missclassification = 1-Accuracy =  0.118508655126498
 Sensitivity or True Positive Rate = TP/(TP+FN) =  0.043478260869565216
 Specificity or True Negative Rate = TN/(TN+FP) =  0.9984825493171472
 Positive Predictive value = TP/(TP+FP) =  0.8
 Negative predictive Value = TN/(TN+FN) =  0.8820375335120644
 Positive Likelihood Ratio = Sensitivity/(1-Specificity) =  28.6521739130435
1
 Negative likelihood Ratio = (1-Sensitivity)/Specificity =  0.95797541958504
03
```

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 [33]:

```
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
y_pred_prob_df.head()
```

Out[33]:

	Prob of no heart disease (0)	Prob of Heart Disease (1)
0	0.859991	0.140009
1	0.930990	0.069010
2	0.792031	0.207969
3	0.814827	0.185173
4	0.875303	0.124697

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 [34]:

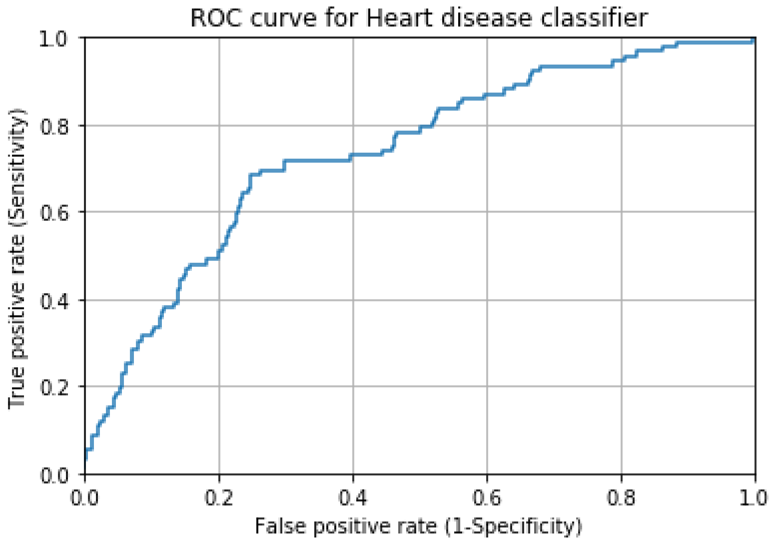
```
from sklearn.preprocessing import binarize
for i in range(1,5):
    cm2=0
    y_pred_prob_yes=logreg.predict_proba(x_test)
    y_pred2=binarize(y_pred_prob_yes,i/10)[:,1]
    cm2=confusion_matrix(y_test,y_pred2)
    print ('With',i/10,'threshold the Confusion Matrix is ','\n',cm2,'\n',
            'with',cm2[0,0]+cm2[1,1],'correct predictions and',cm2[1,0],'Type II errors( Fa
          'Sensitivity: ',cm2[1,1]/(float(cm2[1,1]+cm2[1,0])),'Specificity: ',cm2[0,0]/(flo
```

```
With 0.1 threshold the Confusion Matrix is
 [[240 419]
 [ 11  81]]
 with 321 correct predictions and 11 Type II errors( False Negatives)

 Sensitivity:  0.8804347826086957 Specificity:  0.36418816388467373



With 0.2 threshold the Confusion Matrix is
 [[519 140]
 [ 43  49]]
 with 568 correct predictions and 43 Type II errors( False Negatives)

 Sensitivity:  0.532608695652174 Specificity:  0.787556904400607



With 0.3 threshold the Confusion Matrix is
 [[617  42]
 [ 70  22]]
 with 639 correct predictions and 70 Type II errors( False Negatives)

 Sensitivity:  0.2391304347826087 Specificity:  0.936267071320182



With 0.4 threshold the Confusion Matrix is
 [[652   7]
 [ 86   6]]
 with 658 correct predictions and 86 Type II errors( False Negatives)

 Sensitivity:  0.06521739130434782 Specificity:  0.9893778452200304
```

ROC curve

In [25]:

```
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 [26]:

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

Out[26]:

```
0.7355182423962524
```

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/ (http://www.who.int/mediacentre/factsheets/fs317/en/)

Data Source References

https://www.kaggle.com/amanajmera1/framingham-heart-study-dataset/data (https://www.kaggle.com/amanajmera1/framingham-heart-study-dataset/data)

In [ ]:

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