Importing the library

In [1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn import metrics
import seaborn as sns
%matplotlib inline
import warnings
warnings.filterwarnings('ignore')
```

In [2]:

```
import os
os.getcwd()
```

Out[2]:

```
'C:\\Users\\tiwarikrishna.ENTECNIA\\Desktop\\Capstone project\\Capstone Proj
ect\\Data-Science-Capstone-Projects-master\\Project 2\\Healthcare - Diabete
s'
```

In [3]:

```
#importing the dataset
df = pd.read_csv('health care diabetes.csv')
df.shape
```

Out[3]:

```
(768, 9)
```

In [4]:

```
df.head()
```

Out[4]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
0	6	148	72	35	0	33.6	0.62
1	1	85	66	29	0	26.6	0.35
2	8	183	64	0	0	23.3	0.67
3	1	89	66	23	94	28.1	0.16
4	0	137	40	35	168	43.1	2.28

Descriptive Analysis

In [5]:

```
df.isnull().values.any()
```

Out[5]:

```
False
```

In [6]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   768 non-null    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64  
 8   Outcome                   768 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

Data Exploration

1. Perform descriptive analysis. Understand the variables and their corresponding values.On the columns below, a value of zero does not make sense and thus indicates missing value.

In [7]:

```
# Getting the statistical measures of the data
df.describe().T
```

Out[7]:

	count	mean	std	min	25%	50%	75%
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000

**Insights from Descriptive Analysis

It seems in above results, there is 768 observations of 9 variable. Above we see the basic statistics about the diabetes dataframe some point to note

- For Pregnancy we have min of 0 and max of 17 with a mean of 3.8
- one thing to note is that for many of the predictors (Glucose, BP, Skinthickness, Insulin, BMI) we have min, reading of 0 which is not possible, so it is most like be the missing values which needs to be imputes based on the distribution of these predictors
- For age values ranges from 21-81 with a means of 33.24 which is somewhat normal distributes

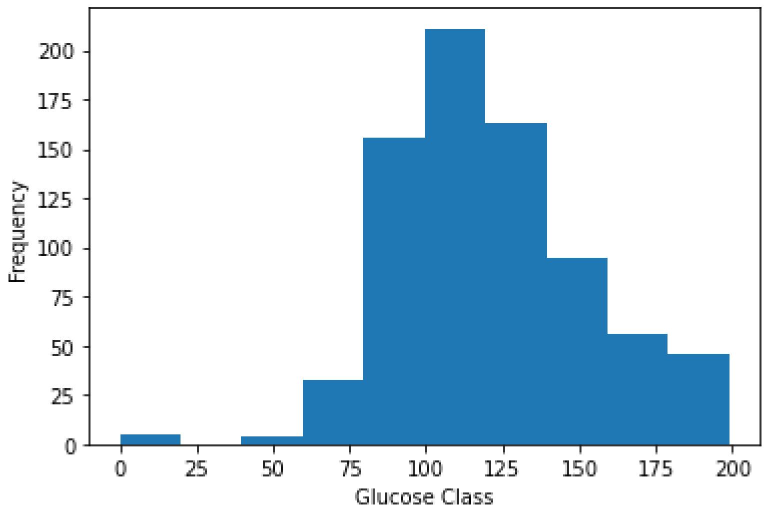
Treating Missing values and Analysing Distribution of the data

2. Visually explore these variables using histograms. Treat the missing values accordingly.

In [8]:

```
plt.xlabel('Glucose Class')
df['Glucose'].plot.hist()
print("Mean of Glucose level is :-", df['Glucose'].mean())
print("Datatype of Glucose Variable is:",df['Glucose'].dtypes)
```

```
Mean of Glucose level is :- 120.89453125
Datatype of Glucose Variable is: int64
```



Now i am going to treat here missing values which is basically 0 by means of Glucose level, as 0 Glucose level is not possible in living person. This is because we can see from histogram most of observations have Glucose level between 100 and 120.

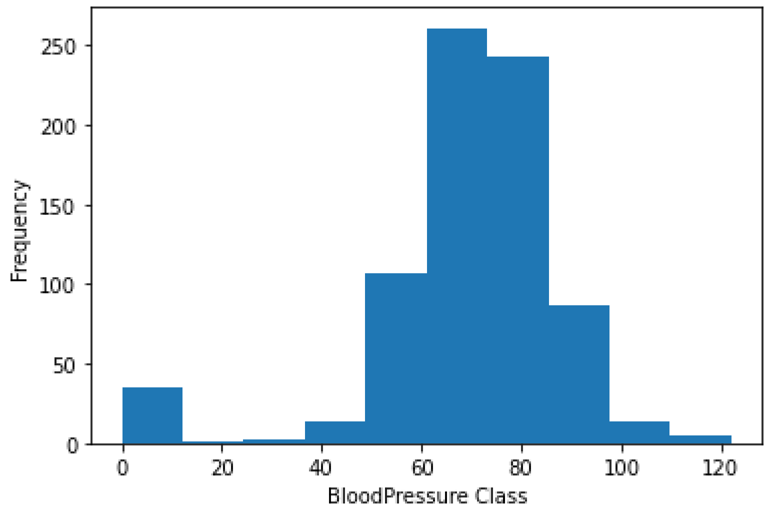
In [9]:

```
df['Glucose']=df['Glucose'].replace(0,df['Glucose'].mean())
```

In [10]:

```
plt.xlabel('BloodPressure Class')
df['BloodPressure'].plot.hist()
print("Mean of BloodPressure level is :-", df['BloodPressure'].mean())
print("Datatype of BloodPressure Variable is:",df['BloodPressure'].dtypes)
```

```
Mean of BloodPressure level is :- 69.10546875
Datatype of BloodPressure Variable is: int64
```



I am treating missing values which is basically 0 by mean of BloodPressure level. This is because we can see from histogram most of observation have BP level between 70 and 80.

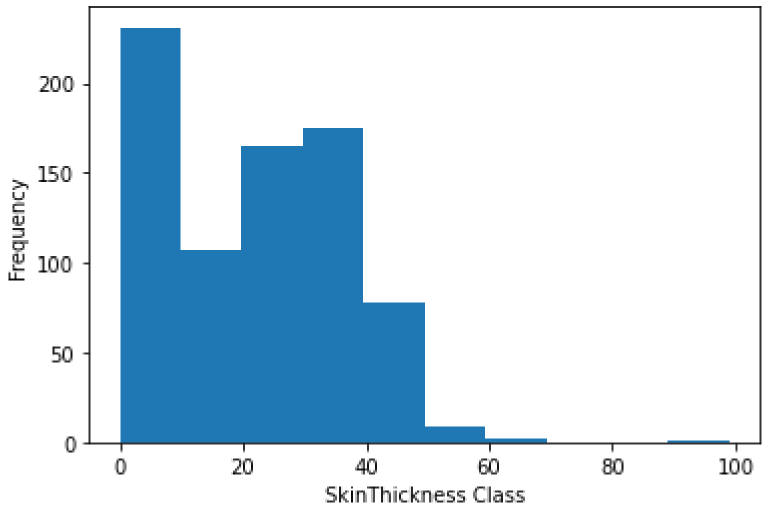
In [11]:

```
df['BloodPressure']=df['BloodPressure'].replace(0,df['BloodPressure'].mean())
```

In [12]:

```
plt.xlabel('SkinThickness Class')
df['SkinThickness'].plot.hist()
print("Mean of SkinThickness is :-", df['SkinThickness'].mean())
print("Datatype of SkinThickness Variable is:",df['SkinThickness'].dtypes)
```

```
Mean of SkinThickness is :- 20.536458333333332
Datatype of SkinThickness Variable is: int64
```



I am treating missing values which is basically 0 by mean of SkinThickness. This is because we can see from histogram most of observation have SkinThickness between 20 and 30.

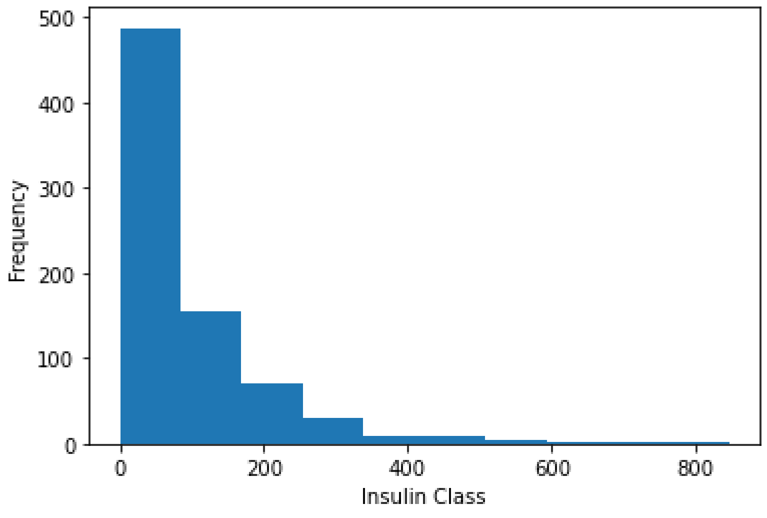
In [13]:

```
df['SkinThickness']=df['SkinThickness'].replace(0,df['SkinThickness'].mean())
```

In [14]:

```
plt.xlabel('Insulin Class')
df['Insulin'].plot.hist()
print("Mean of Insulin is :-", df['Insulin'].mean())
print("Datatype of Insulin Variable is:",df['Insulin'].dtypes)
```

```
Mean of Insulin is :- 79.79947916666667
Datatype of Insulin Variable is: int64
```



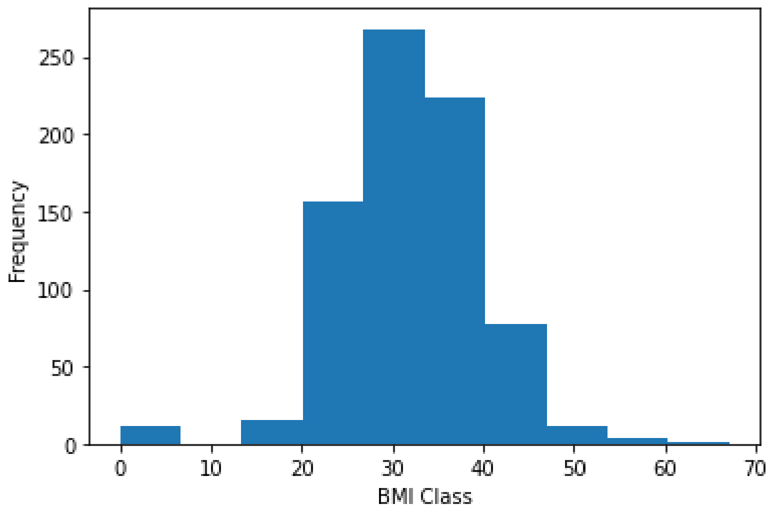
In [15]:

```
df['Insulin']=df['Insulin'].replace(0,df['Insulin'].mean())
```

In [16]:

```
plt.xlabel('BMI Class')
df['BMI'].plot.hist()
print("Mean of BMI is :-", df['BMI'].mean())
print("Datatype of BMI Variable is:",df['BMI'].dtypes)
```

```
Mean of BMI is :- 31.992578124999977
Datatype of BMI Variable is: float64
```



In [17]:

```
df['BMI']=df['BMI'].replace(0,df['BMI'].mean())
```

As Such we do not see Strong correlation between any predictor variable when look form the outcome point of view there are some what positive corr with Glucose level, BMI, Age, Preg in that order

So now we can move onto the model building part

In [18]:

```
df.head()
```

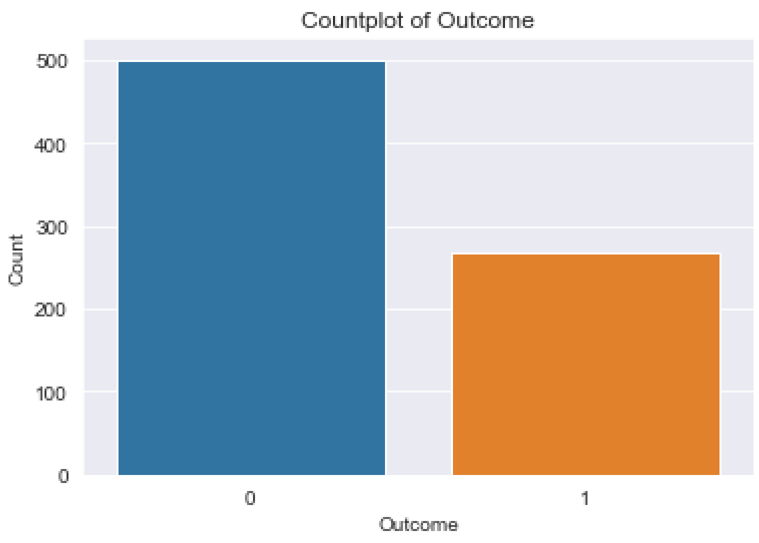
Out[18]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFun
0	6	148.0	72.0	35.000000	79.799479	33.6	
1	1	85.0	66.0	29.000000	79.799479	26.6	
2	8	183.0	64.0	20.536458	79.799479	23.3	
3	1	89.0	66.0	23.000000	94.000000	28.1	
4	0	137.0	40.0	35.000000	168.000000	43.1	

In [19]:

```
sns.set_style('darkgrid')
sns.countplot(df['Outcome'])
plt.title("Countplot of Outcome")
plt.xlabel('Outcome')
plt.ylabel("Count")
print("Count of class is:\n",df['Outcome'].value_counts())
```

```
Count of class is:
 0    500
1    268
Name: Outcome, dtype: int64
```



So we have about 65% non-diabetic and 35% diabetic

Now we have some idea about the dataset

Now lets deal with the missing values. Although in isna we dont have any missing values. we saw above that we have lot of zero values in many of the predictors (Glucose, BP, Skinthickness, Insulin, BMI) which is not possible. So we have to treat these zero as missing values and impute them in some manner

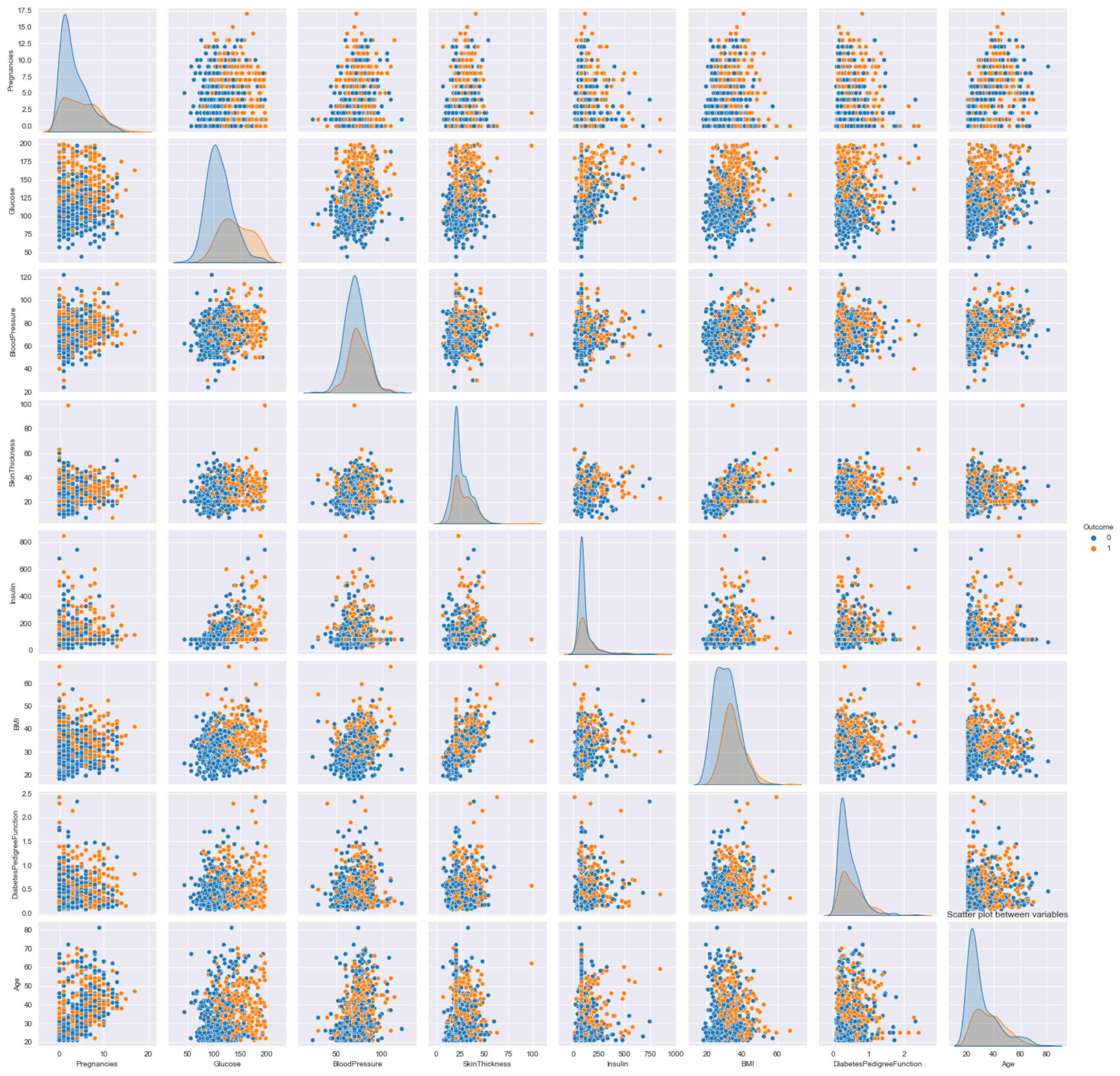
- Before dealing with them lets check the distribution of these variables

In [20]:

```
sns.pairplot(df, hue="Outcome")
plt.title('Scatter plot between variables')
```

Out[20]:

```
Text(0.5, 1.0, 'Scatter plot between variables')
```



We can see from scatter plot that there is no strong multicolinearity among features, but between skin thickness and BMI, Pregnancies and age it looks like there is small chance of positive correlation..i will explore more when analyzing correlation

In [21]:

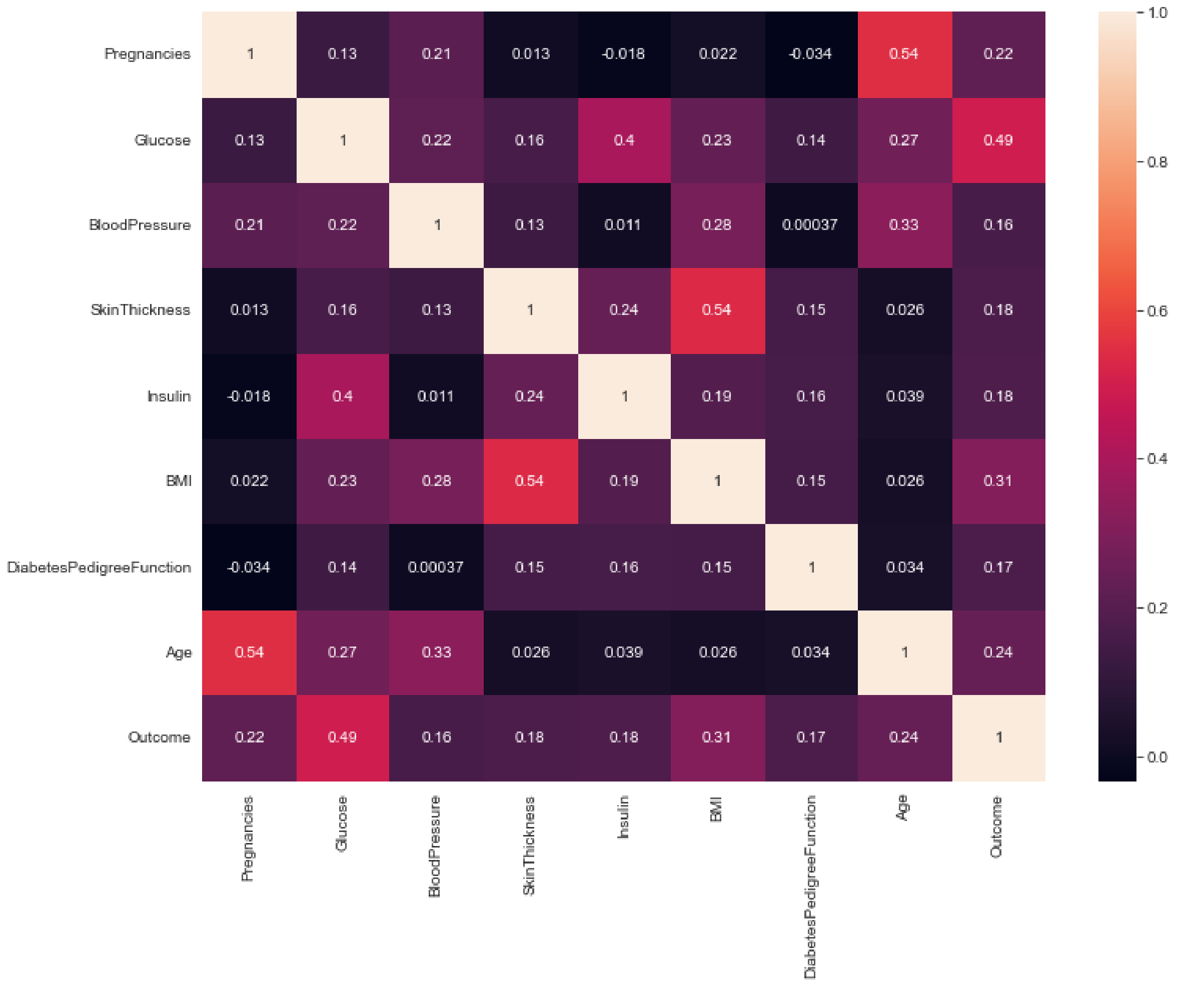
```
df.corr()
```

Out[21]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	
Pregnancies	1.000000	0.127964	0.208984	0.013376	-0.018082	0.0
Glucose	0.127964	1.000000	0.219666	0.160766	0.396597	0.2
BloodPressure	0.208984	0.219666	1.000000	0.134155	0.010926	0.2
SkinThickness	0.013376	0.160766	0.134155	1.000000	0.240361	0.5
Insulin	-0.018082	0.396597	0.010926	0.240361	1.000000	0.1
BMI	0.021546	0.231478	0.281231	0.535703	0.189856	1.0
DiabetesPedigreeFunction	-0.033523	0.137106	0.000371	0.154961	0.157806	0.1
Age	0.544341	0.266600	0.326740	0.026423	0.038652	0.0
Outcome	0.221898	0.492908	0.162986	0.175026	0.179185	0.3

In [22]:

```
plt.figure(figsize=(12,9))
sns.heatmap(df.corr(),annot=True)
plt.show()
```



As Such we do not see Strong correlation between any predictor variable when look form the outcome point of view there are some what positive corr with Glucose level, BMI, Age, Preg in that order

So now we can move onto the model building part

Model Building

Before we move on to the model building and comparing various model with KNN, we need to preprocess the data

First do the test train split

In [23]:

```
X = df.iloc[:,:-1].values
y = df.iloc[:,-1].values
```

In [24]:

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X,y, test_size=.25, random_state= 42)
```

In [25]:

```
print(X_train.shape)
print(y_train.shape)
print(X_test.shape)
print(y_test.shape)
```

```
(576, 8)
(576,)
(192, 8)
(192,)
```

In [26]:

```
from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
scaler.fit(X_train)
X_train_sc = scaler.transform(X_train)
X_test_sc = scaler.transform(X_test)
```

Applying the KNN Classification

In [27]:

```
from sklearn.neighbors import KNeighborsClassifier

knn_model = KNeighborsClassifier(n_neighbors=20)
knn_model.fit(X_train_sc, y_train)
knn_pred = knn_model.predict(X_test_sc)
```

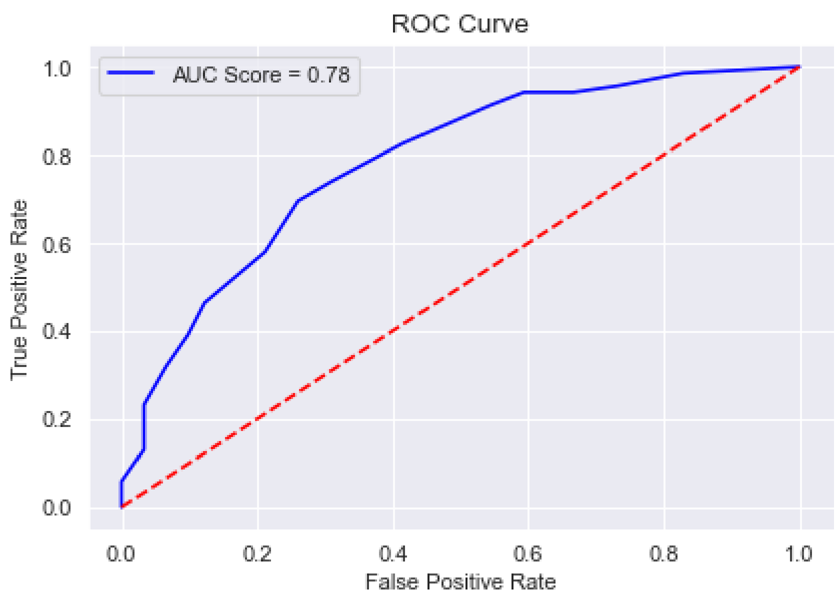
In [28]:

```
from sklearn import metrics
print("Model Validation ==>\n")
print("Accuracy Score of KNN Model::")
print(metrics.accuracy_score(y_test,knn_pred))
print("\n","Classification Report::")
print(metrics.classification_report(y_test,knn_pred),'\n')
print("\n", "Confusion Matrix")
print(metrics.confusion_matrix(y_test, knn_pred))
print("\n","ROC Curve")
knn_prob=knn_model.predict_proba(X_test_sc)
knn_prob1=knn_prob[:,1]
fpr,tpr,thresh=metrics.roc_curve(y_test,knn_prob1)
roc_auc_knn=metrics.auc(fpr,tpr)
plt.figure(dpi=80)
plt.title("ROC Curve")
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.plot(fpr,tpr,'b',label='AUC Score = %0.2f'%roc_auc_knn)
plt.plot(fpr,fpr,'r--',color='red')
plt.legend()
```

```
Model Validation ==>

Accuracy Score of KNN Model::
0.7291666666666666

 Classification Report::
              precision    recall  f1-score   support

           0       0.74      0.88      0.81       123
           1       0.68      0.46      0.55        69

    accuracy                           0.73       192
   macro avg       0.71      0.67      0.68       192
weighted avg       0.72      0.73      0.71       192



 Confusion Matrix
[[108  15]
 [ 37  32]]

 ROC Curve
```

Out[28]:

```
<matplotlib.legend.Legend at 0x2ca3b91f340>
```



- Here as we see that the precision for both positive and negetive is okay i.e. how many correctly predicted turned out to be positive
- but when we look at the recall values which is how many actual positive (on both diabetic and non diabetic) we are able to predict correctly. Here recall values is very low esp. for the diabetic class. Out of the total diabetic we are able to predict only 46% of the time
- Also the AUC score which is how much better we are able to differentiate between diabetic and non-diabetic class is 78% which is okay.

Now lets train other classifier to see if the position improves

Logistic Regression

In [29]:

```
from sklearn.linear_model import LogisticRegression

clf_log = LogisticRegression()
clf_log.fit(X_train_sc, y_train)
y_log_pred = clf_log.predict(X_test_sc)
```

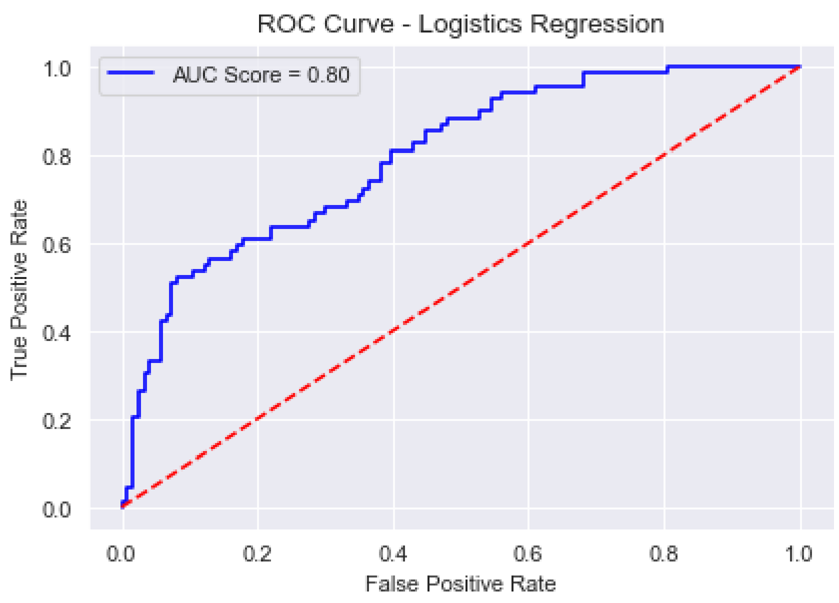
In [30]:

```
print("Logistics Regression Model Validation ==>\n")
print("Accuracy Score of Logistics Model::")
print(metrics.accuracy_score(y_test,y_log_pred))
print("\n","Classification Report::")
print(metrics.classification_report(y_test, y_log_pred),'\n')
print("\n", "Confusion Matrix")
print(metrics.confusion_matrix(y_test, y_log_pred))
print("\n","ROC Curve")
log_prob=clf_log.predict_proba(X_test_sc)
log_prob1=log_prob[:,1]
fpr,tpr,thresh=metrics.roc_curve(y_test,log_prob1)
roc_auc_log=metrics.auc(fpr,tpr)
plt.figure(dpi=80)
plt.title("ROC Curve - Logistics Regression")
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.plot(fpr,tpr,'b',label='AUC Score = %0.2f'%roc_auc_log)
plt.plot(fpr,fpr,'r--',color='red')
plt.legend()
```

```
Logistics Regression Model Validation ==>

Accuracy Score of Logistics Model::
0.734375

 Classification Report::
              precision    recall  f1-score   support

           0       0.79      0.80      0.80       123
           1       0.64      0.61      0.62        69

    accuracy                           0.73       192
   macro avg       0.71      0.71      0.71       192
weighted avg       0.73      0.73      0.73       192



 Confusion Matrix
[[99 24]
 [27 42]]

 ROC Curve
```

Out[30]:

```
<matplotlib.legend.Legend at 0x2ca3be5c340>
```



its performance is almost same as that of the basic KNN classifier . Some small improvement are shown

- Precision has decrease for positive class by about 5% point
- but Good news is that the recall value have increase as compared to the basic KNN model by 15% point which is a good
- Also the Ability to differentiate has only change by about 2%

Support Vector Machine

In [31]:

```
from sklearn.svm import SVC

clf_svc = SVC(kernel='rbf',random_state=42,probability=True)
clf_svc.fit(X_train_sc, y_train)
y_pred_svc = clf_svc.predict(X_test_sc)
```

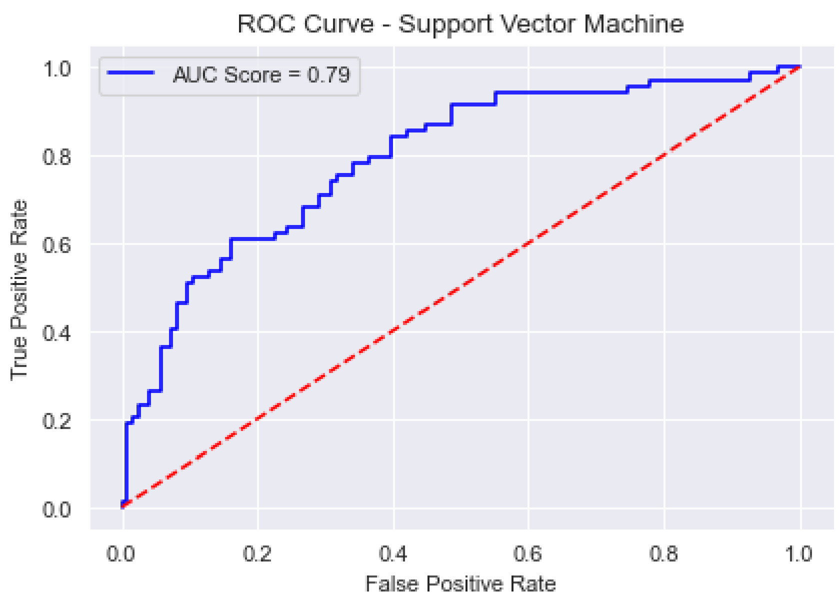
In [32]:

```
print("Support Vector Machine Model Validation ==>\n")
print("Accuracy Score of SVM Model::")
print(metrics.accuracy_score(y_test,y_pred_svc))
print("\n","Classification Report::")
print(metrics.classification_report(y_test, y_pred_svc),'\n')
print("\n", "Confusion Matrix")
print(metrics.confusion_matrix(y_test, y_pred_svc))
print("\n","ROC Curve")
svc_prob=clf_svc.predict_proba(X_test_sc)
svc_prob1=svc_prob[:,1]
fpr,tpr,thresh=metrics.roc_curve(y_test,svc_prob1)
roc_auc_svc=metrics.auc(fpr,tpr)
plt.figure(dpi=80)
plt.title("ROC Curve - Support Vector Machine")
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.plot(fpr,tpr,'b',label='AUC Score = %0.2f'%roc_auc_svc)
plt.plot(fpr,fpr,'r--',color='red')
plt.legend()
```

```
Support Vector Machine Model Validation ==>

Accuracy Score of SVM Model::
0.75

 Classification Report::
              precision    recall  f1-score   support

           0       0.79      0.83      0.81       123
           1       0.67      0.61      0.64        69

    accuracy                           0.75       192
   macro avg       0.73      0.72      0.72       192
weighted avg       0.75      0.75      0.75       192



 Confusion Matrix
[[102  21]
 [ 27  42]]

 ROC Curve
```

Out[32]:

```
<matplotlib.legend.Legend at 0x2ca3be459a0>
```



Not much has change with the using SVM model some parameter like accracy has increase but not much improvement

Lets see the Random Forest model

Random Forest

In [33]:

```
from sklearn.ensemble import RandomForestClassifier

clf_forest = RandomForestClassifier(n_estimators=1000,random_state = 42)
clf_forest.fit(X_train_sc, y_train)
y_pred_for = clf_forest.predict(X_test_sc)
```

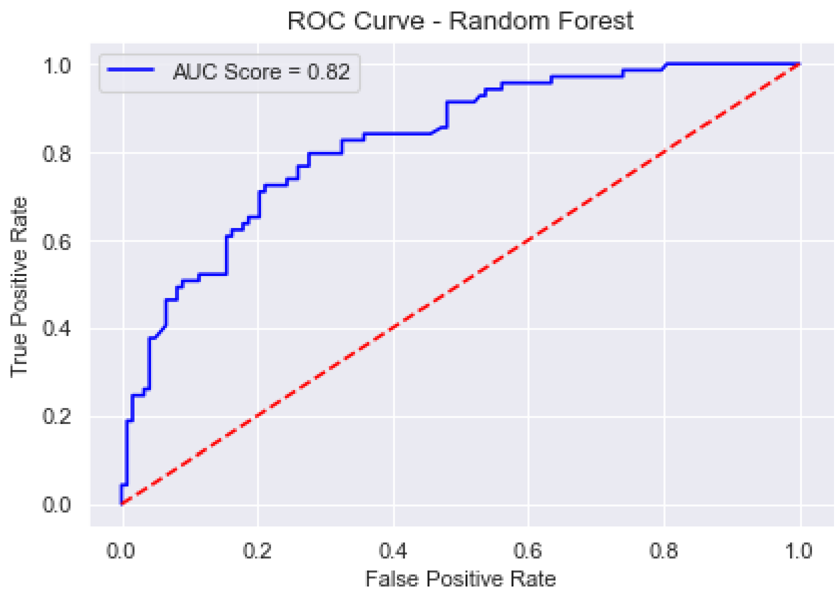
In [34]:

```
print("Random Forest Model Validation ==>\n")
print("Accuracy Score of Random Forest Model::")
print(metrics.accuracy_score(y_test,y_pred_for))
print("\n","Classification Report::")
print(metrics.classification_report(y_test, y_pred_for),'\n')
print("\n", "Confusion Matrix")
print(metrics.confusion_matrix(y_test, y_pred_for))
print("\n","ROC Curve")
for_prob=clf_forest.predict_proba(X_test_sc)
for_prob1=for_prob[:,1]
fpr,tpr,thresh=metrics.roc_curve(y_test,for_prob1)
roc_auc_for=metrics.auc(fpr,tpr)
plt.figure(dpi=80)
plt.title("ROC Curve - Random Forest")
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.plot(fpr,tpr,'b',label='AUC Score = %0.2f'%roc_auc_for)
plt.plot(fpr,fpr,'r--',color='red')
plt.legend()
```

```
Random Forest Model Validation ==>

Accuracy Score of Random Forest Model::
0.7604166666666666

 Classification Report::
              precision    recall  f1-score   support

           0       0.82      0.80      0.81       123
           1       0.66      0.70      0.68        69

    accuracy                           0.76       192
   macro avg       0.74      0.75      0.74       192
weighted avg       0.76      0.76      0.76       192



 Confusion Matrix
[[98 25]
 [21 48]]

 ROC Curve
```

Out[34]:

```
<matplotlib.legend.Legend at 0x2ca3bb40700>
```



As compared to the Basic KNN model we see following improvement

- Accuracy has increase from 73% to 76%
- precision
  - for non-diabetic it is showing much improvement from 74% to 82%
  - but for diabetic it has declined from 68 to 66% which means out of 100 total diabetic that it predict 66 are actually diabetic
- Recall
  - for non-diabetic it is showing the decline from 88% to 80% which means earlier out of total 100 non diabetic it is able to predict 88 correctly but now only 80 are correctly diagnosed as Non-diabetic
  - But Good news is that for diabetic values has increase from 46% to 70% which means earlier out of 100 diabetic KNN model was able to do correct prediction for only 46 person which has now increase to 70 people
- AUC (ROC) score has measly increase from 78% to 82%

Applying the oversampling techniques to balance the dataset

Earlier we saw that we have an imbalance data i.e. 65% of cases are of non-diabetic class and 35% are for the diabetic class. This is the big reason for not able to correctly predict the diabetic classification as compared to the Non diabetic classification

To solve this we will apply Oversampling techniques like SMOTE (Synthetic minority oversamping technique)

SMOTE is an oversampling technique where the synthetic samples are generated for the minority class. This algorithm helps to overcome the overfitting problem posed by random oversampling. It focuses on the feature space to generate new instances with the help of interpolation between the positive instances that lie together

In [35]:

```
from collections import Counter
from imblearn.over_sampling import SMOTE

counter = Counter(y_train)
print("Before Oversampling", counter)
smt = SMOTE()

X_train_sm, y_train_sm = smt.fit_resample(X_train_sc,y_train)
counter = Counter(y_train_sm)
print("After Oversampling", counter)
```

```
Before Oversampling Counter({0: 377, 1: 199})
After Oversampling Counter({1: 377, 0: 377})
```

Applying the Logistic regression on Oversampled data

In [36]:

```
clf_log_sm = LogisticRegression()
clf_log_sm.fit(X_train_sm, y_train_sm)
y_log_pred = clf_log.predict(X_test_sc)
```

In [37]:

```
print("Logistics Regression Model using smote ==>\n")
print("Accuracy Score of Logistics Model::")
print(metrics.accuracy_score(y_test,y_log_pred))
print("\n","Classification Report::")
print(metrics.classification_report(y_test, y_log_pred),'\n')
print("\n", "Confusion Matrix")
print(metrics.confusion_matrix(y_test, y_log_pred))
print("\n","ROC Curve")
log_prob=clf_log_sm.predict_proba(X_test_sc)
log_prob1=log_prob[:,1]
fpr,tpr,thresh=metrics.roc_curve(y_test,log_prob1)
roc_auc_log=metrics.auc(fpr,tpr)
plt.figure(dpi=80)
plt.title("ROC Curve - Logistics Regression using smote")
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.plot(fpr,tpr,'b',label='AUC Score = %0.2f'%roc_auc_log)
plt.plot(fpr,fpr,'r--',color='red')
plt.legend()
```

```
Logistics Regression Model using smote ==>

Accuracy Score of Logistics Model::
0.734375

 Classification Report::
              precision    recall  f1-score   support

           0       0.79      0.80      0.80       123
           1       0.64      0.61      0.62        69

    accuracy                           0.73       192
   macro avg       0.71      0.71      0.71       192
weighted avg       0.73      0.73      0.73       192



 Confusion Matrix
[[99 24]
```

Although we see a small decrease in accuracy but the recall values of diabetic is same

Applying SVM on Oversampled data

In [38]:

```
from sklearn.svm import SVC

clf_svc_sm = SVC(kernel='rbf',random_state=42,probability=True)
clf_svc_sm.fit(X_train_sm, y_train_sm)
y_pred_svc = clf_svc_sm.predict(X_test_sc)
```

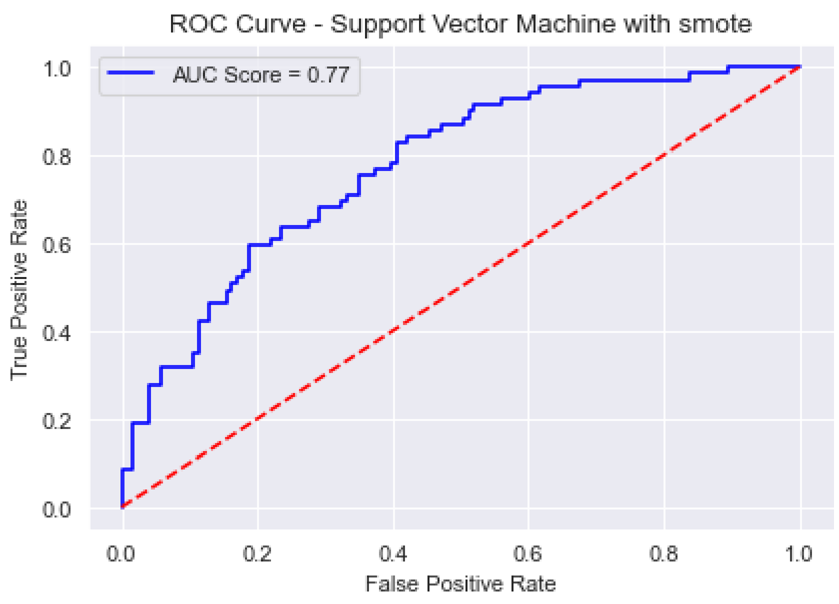
In [39]:

```
print("Support Vector Machine Model on Oversampled data ==>\n")
print("Accuracy Score of SVM Model::")
print(metrics.accuracy_score(y_test,y_pred_svc))
print("\n","Classification Report::")
print(metrics.classification_report(y_test, y_pred_svc),'\n')
print("\n", "Confusion Matrix")
print(metrics.confusion_matrix(y_test, y_pred_svc))
print("\n","ROC Curve")
svc_prob=clf_svc_sm.predict_proba(X_test_sc)
svc_prob1=svc_prob[:,1]
fpr,tpr,thresh=metrics.roc_curve(y_test,svc_prob1)
roc_auc_svc=metrics.auc(fpr,tpr)
plt.figure(dpi=80)
plt.title("ROC Curve - Support Vector Machine with smote")
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.plot(fpr,tpr,'b',label='AUC Score = %0.2f'%roc_auc_svc)
plt.plot(fpr,fpr,'r--',color='red')
plt.legend()
```

```
Support Vector Machine Model on Oversampled data ==>

Accuracy Score of SVM Model::
0.6822916666666666

 Classification Report::
              precision    recall  f1-score   support

           0       0.80      0.67      0.73       123
           1       0.54      0.71      0.62        69

    accuracy                           0.68       192
   macro avg       0.67      0.69      0.67       192
weighted avg       0.71      0.68      0.69       192



 Confusion Matrix
[[82 41]
 [20 49]]

 ROC Curve
```

Out[39]:

```
<matplotlib.legend.Legend at 0x2ca33d2d040>
```



Although we see a small decrease in the accuracy but the recall value of diabetic has increased 61 to 75%

Applying Random Forest on Oversampled data

In [40]:

```
from sklearn.ensemble import RandomForestClassifier

clf_forest_sm = RandomForestClassifier(n_estimators=1000,random_state = 42)
clf_forest_sm.fit(X_train_sm, y_train_sm)
y_pred_for = clf_forest_sm.predict(X_test_sc)
```

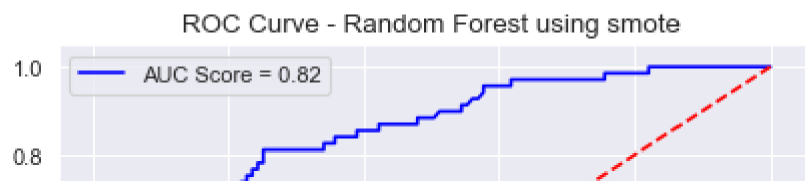
In [41]:

```
print("Random Forest Model Validation using smote ==>\n")
print("Accuracy Score of Random Forest Model using smote::")
print(metrics.accuracy_score(y_test,y_pred_for))
print("\n","Classification Report::")
print(metrics.classification_report(y_test, y_pred_for),'\n')
print("\n", "Confusion Matrix")
print(metrics.confusion_matrix(y_test, y_pred_for))
print("\n","ROC Curve")
for_prob=clf_forest_sm.predict_proba(X_test_sc)
for_prob1=for_prob[:,1]
fpr,tpr,thresh=metrics.roc_curve(y_test,for_prob1)
roc_auc_for=metrics.auc(fpr,tpr)
plt.figure(dpi=80)
plt.title("ROC Curve - Random Forest using smote")
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.plot(fpr,tpr,'b',label='AUC Score = %0.2f'%roc_auc_for)
plt.plot(fpr,fpr,'r--',color='red')
plt.legend()
```

```
Random Forest Model Validation using smote ==>

Accuracy Score of Random Forest Model using smote::
0.765625

 Classification Report::
              precision    recall  f1-score   support

           0       0.86      0.76      0.81       123
           1       0.64      0.78      0.71        69

    accuracy                           0.77       192
   macro avg       0.75      0.77      0.76       192
weighted avg       0.78      0.77      0.77       192



 Confusion Matrix
[[93 30]
 [15 54]]

 ROC Curve
```

Out[41]:

```
<matplotlib.legend.Legend at 0x2ca33dfe700>
```



AS we can see that with using the oversampled data we are able to incrase the recall values 70% to 80% at the cost of 3% point decrease in the accuracy.

That means that we are able to better identify the diabetic person at the cost of few non-diabetic that could be misclassified as diabetic.

In [ ]:

```

```