In [1]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
```

Importing the Data

In [2]:

```
Df=pd.read_csv('health care diabetes.csv')
Df.head()
```

Out[2]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

In [3]:

```
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
```

In [4]:

```
Df['Outcome'].value_counts()
```

Out[4]:

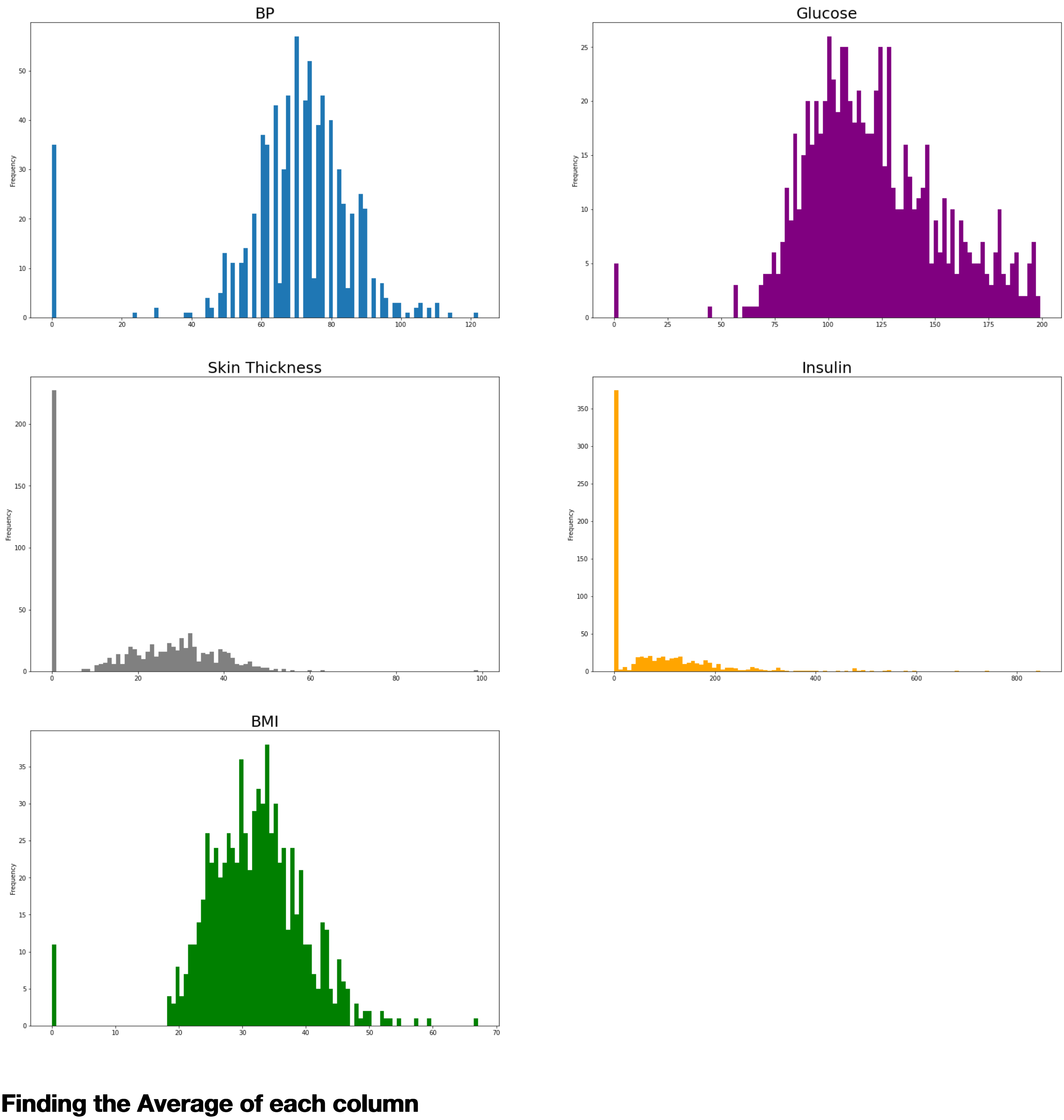
```
0    500
1    268
Name: Outcome, dtype: int64
```

Histogram to see the distribution of the data

In [5]:

```
plt.figure(figsize=(30,30))
plt.subplot(3,2,1)
Df['BloodPressure'].plot(kind='hist',bins=100)
```

```
plt.title('BP',fontsize=25)

plt.subplot(3,2,2)
Df['Glucose'].plot(kind='hist',bins=100,color='Purple')
plt.title('Glucose',fontsize=25)

plt.subplot(3,2,3)
Df['SkinThickness'].plot(kind='hist',bins=100,color='Grey')
plt.title('Skin Thickness',fontsize=25)

plt.subplot(3,2,4)
Df['Insulin'].plot(kind='hist',bins=100,color='orange')
plt.title('Insulin',fontsize=25)

plt.subplot(3,2,5)
Df['BMI'].plot(kind='hist',bins=100,color='green')
plt.title('BMI',fontsize=25)

plt.show()
```



Finding the Average of each column

In [6]:

```
BpAvg=Df['BloodPressure'].mean()
```

```
BpAvg=Df['BloodPressure'].mean()
GlucoseAvg=Df['Glucose'].mean()
SkinThicknessAvg=Df['SkinThickness'].mean()
InsulinAvg=Df['Insulin'].mean()
BMIAvg=Df['BMI'].mean()

print(BpAvg)
print(GlucoseAvg)
print(SkinThicknessAvg)
print(InsulinAvg)
print(BMIAvg)
```

```
69.10546875
120.89453125
20.536458333333332
79.79947916666667
31.992578124999977
```

Converting Int and Float to Object for replacing the '0' values with the mean.

In [7]:

```
Df['BloodPressure']=Df['BloodPressure'].map(str)
Df['Glucose']=Df['Glucose'].map(str)
Df['SkinThickness']=Df['SkinThickness'].map(str)
Df['Insulin']=Df['Insulin'].map(str)
Df['BMI']=Df['BMI'].map(str)
```

In [8]:

```
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    object
 2   BloodPressure             768 non-null    object
 3   SkinThickness             768 non-null    object
 4   Insulin                   768 non-null    object
 5   BMI                       768 non-null    object
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64
 8   Outcome                   768 non-null    int64
dtypes: float64(1), int64(3), object(5)
memory usage: 54.1+ KB
```

Replacing '0' with the Average

In [9]:

```
Df['BloodPressure']=Df['BloodPressure'].replace('0',BpAvg)
Df['Glucose']=Df['Glucose'].replace('0',GlucoseAvg)
Df['SkinThickness']=Df['SkinThickness'].replace('0',SkinThicknessAvg)
Df['Insulin']=Df['Insulin'].replace('0',InsulinAvg)
Df['BMI']=Df['BMI'].replace('0',BMIAvg)
```

Converting again Object type to Int & Float for Model training

In [10]:

```
Df['BloodPressure']=Df['BloodPressure'].map(int)
Df['Glucose']=Df['Glucose'].map(int)
Df['SkinThickness']=Df['SkinThickness'].map(int)
Df['Insulin']=Df['Insulin'].map(int)
Df['BMI']=Df['BMI'].map(float)
```

In [11]:

```
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
```

Correlation among the variables

In [12]:

```
correlation=Df.corr()
correlation
```

Out[12]:

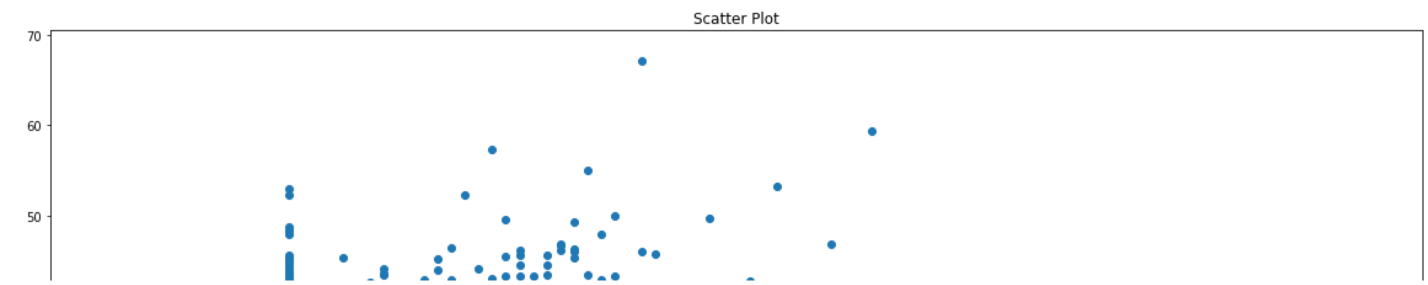
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
Pregnancies	1.000000	0.128022	0.208987	0.009393	-0.018780	0.017683	-0.03352
Glucose	0.128022	1.000000	0.219765	0.158060	0.396137	0.235123	0.13715
BloodPressure	0.208987	0.219765	1.000000	0.130403	0.010492	0.242947	0.00047
SkinThickness	0.009393	0.158060	0.130403	1.000000	0.245410	0.499700	0.15719
Insulin	-0.018780	0.396137	0.010492	0.245410	1.000000	0.189561	0.15824
BMI	0.017683	0.235123	0.242947	0.499700	0.189561	1.000000	0.14064
DiabetesPedigreeFunction	-0.033523	0.137158	0.000471	0.157196	0.158243	0.140647	1.00000
Age	0.544341	0.266673	0.326791	0.020582	0.037676	0.036242	0.03356
Outcome	0.221898	0.492884	0.162879	0.171857	0.178696	0.292695	0.17384

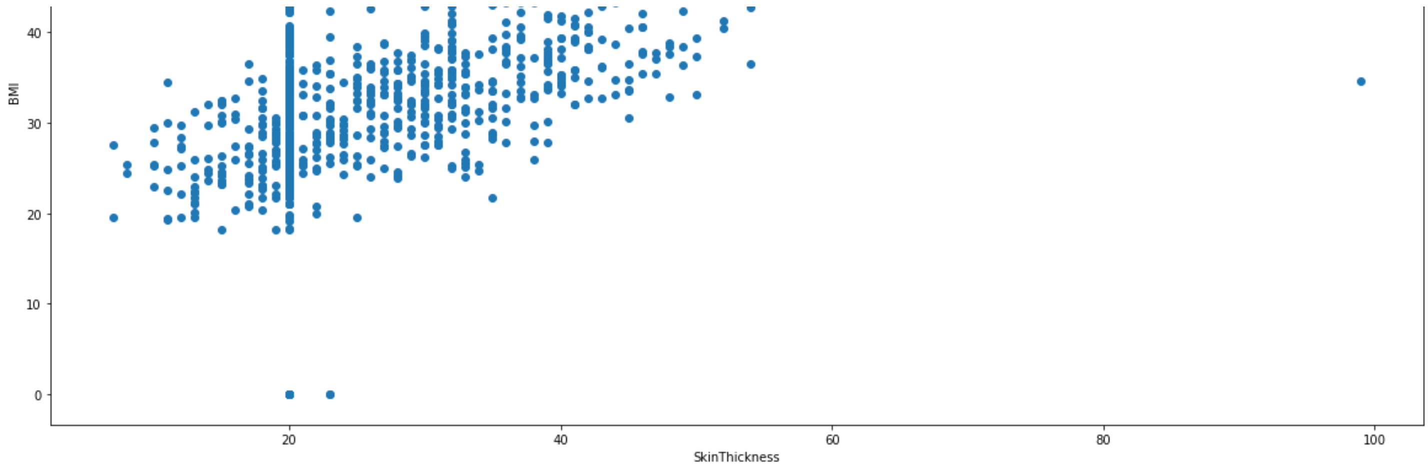
In [13]:

```
plt.figure(figsize=(20,10))
plt.scatter(Df['SkinThickness'],Df['BMI'])
plt.title('Scatter Plot')
plt.xlabel('SkinThickness')
plt.ylabel('BMI')
```

Out[13]:

```
Text(0, 0.5, 'BMI')
```

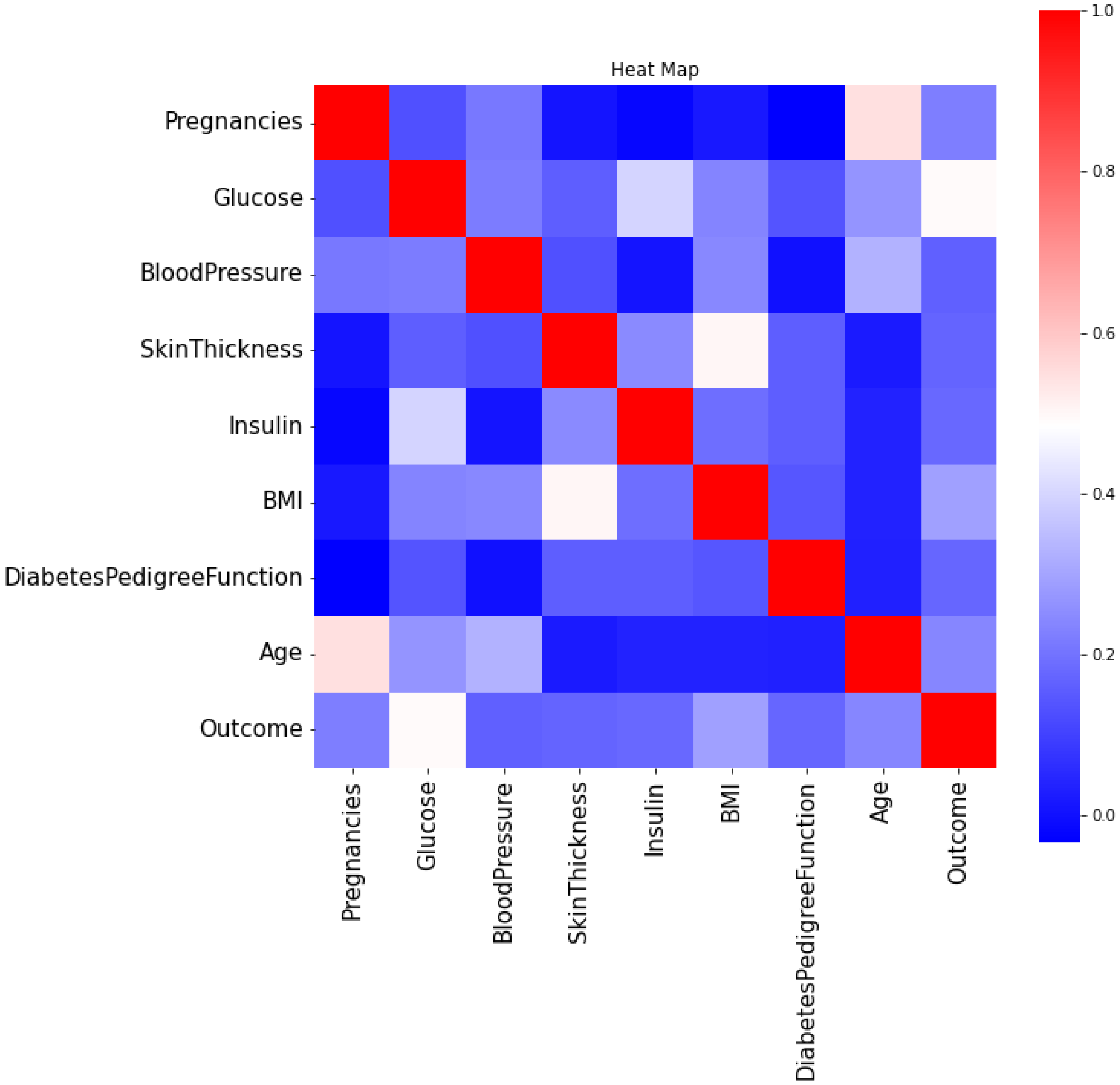




We can conclude that more the BMI, more the Skin Thickness

In [14]:

```
plt.figure(figsize=(10,10))
sns.heatmap(data=correlation,square=True,cmap='bwr')
plt.yticks(size=15,rotation=0)
plt.xticks(size=15,rotation=90)
plt.title('Heat Map')

plt.show()
```



Model Building

In [15]:

```
from sklearn.svm import SVC
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
from sklearn.metrics import f1_score
from sklearn.metrics import classification_report
from sklearn import metrics
```

In [16]:

```
X=Df.drop('Outcome',axis=1)
y=Df['Outcome']
```

In [17]:

```
Xtrain,Xtest,ytrain,ytest=train_test_split(X,y,test_size=0.3,random_state=15)
```

In [18]:

```
svc=SVC()
```

In [19]:

```
svc.fit(Xtrain,ytrain)
```

Out[19]:

```
SVC()
```

In [20]:

```
ypredicted=svc.predict(Xtest)
```

In [21]:

```
metrics.confusion_matrix(ytest,ypredicted)
```

Out[21]:

```
array([[142,  18],
       [ 35,  36]], dtype=int64)
```

In [22]:

```
pd.crosstab(ytest, ypredicted, rownames=['True'], colnames=['Predicted'], margins=True)
```

Out[22]:

Predicted	0	1	All
True			
0	142	18	160
1	35	36	71
All	177	54	231

In [23]:

```
metrics.accuracy_score(ytest,ypredicted)
```

Out[23]:

```
0.7705627705627706
```

In [24]:

```
print(classification_report(ytest, ypredicted))
```

```
              precision    recall  f1-score   support

           0       0.80      0.89      0.84       160
           1       0.67      0.51      0.58        71

    accuracy                           0.77       231
   macro avg       0.73      0.70      0.71       231
weighted avg       0.76      0.77      0.76       231
```

We can conclude that our model test accuracy is not bad. Now we will check if the model is generalised or not.

In [25]:

```
ytrainpred=svc.predict(Xtrain)
```

In [26]:

```
metrics.accuracy_score(ytrain,ytrainpred)
```

Out[26]:

```
0.7616387337057728
```

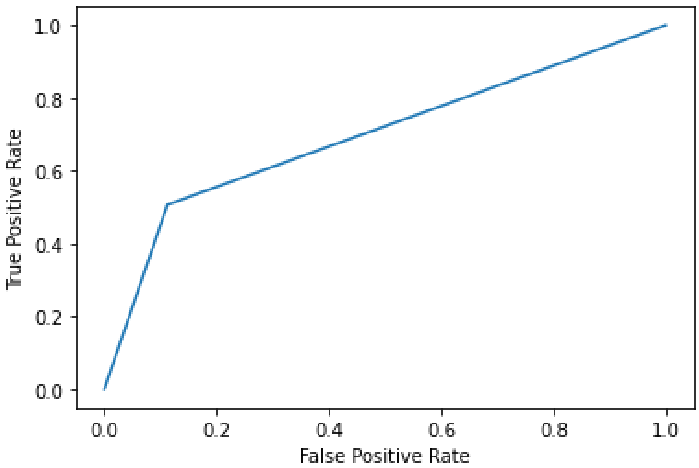
From the above test we saw that the model is working fine and has got Low Bias and Low Variance.

In [27]:

```
fpr, tpr, _ = metrics.roc_curve(ytest, ypredicted)
```

In [28]:

```
plt.plot(fpr,tpr)
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.show()
```



ROC curve shows the best threshold value for the classification

Lets try to build the Logistic Regression model and check whether it will give more accuracy or not

In [29]:

```
from sklearn.linear_model import LogisticRegression
```

In [30]:

```
lr=LogisticRegression()
```

In [31]:

```
lr.fit(Xtrain,ytrain)
```

```
C:\Users\NAVAL\anaconda3\lib\site-packages\sklearn\linear_model\_logistic.py:763: Converg
enceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
```

Out[31]:

```
LogisticRegression()
```

In [32]:

```
ypred=lr.predict(Xtest)
```

In [33]:

```
metrics.accuracy_score(ytest,ypred)
```

Out[33]:

```
0.7575757575757576
```

In [34]:

```
metrics.confusion_matrix(ytest,ypred)
```

Out[34]:

```
array([[136,  24],
       [ 32,  39]], dtype=int64)
```

In [35]:

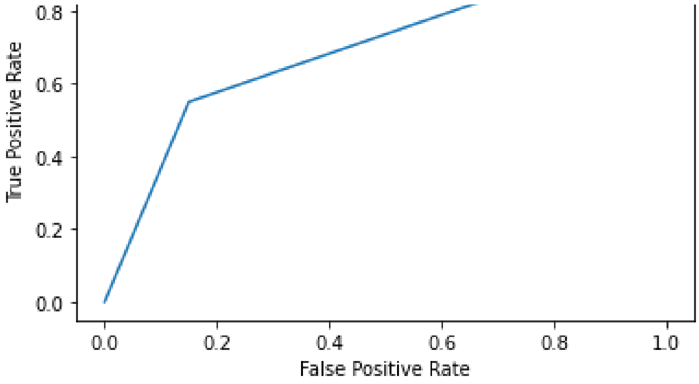
```
pd.crosstab(ytest, ypred, rownames=['True'], colnames=['Predicted'], margins=True)
```

Out[35]:

Predicted	**0**	**1**	**All**
True			
0	136	24	160
1	32	39	71
All	168	63	231

In [36]:

```
fpr, tpr, _ = metrics.roc_curve(ytest, ypred)
plt.plot(fpr,tpr)
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.show()
```



We will go for the SVM model as it gave us more accuracy

KMeans Clustering

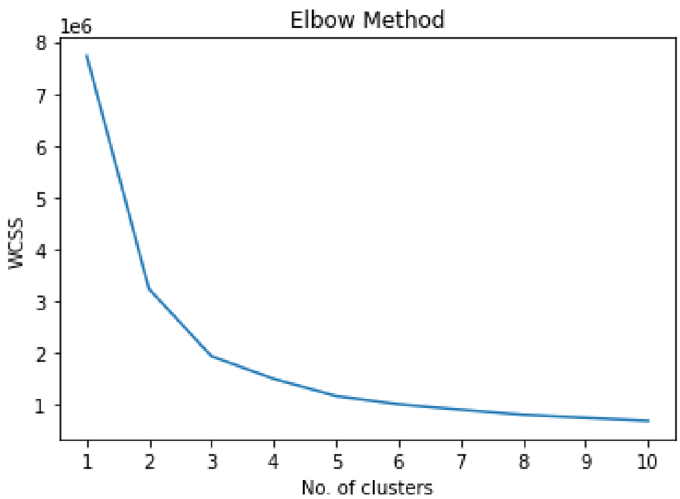
In [37]:

```
from sklearn.cluster import KMeans
```

In [38]:

```
wcss=[]
for i in range(1,11):
    kmeans=KMeans(n_clusters=i,init='k-means++',random_state=0)
    kmeans.fit(X)
    wcss.append(kmeans.inertia_)

plt.plot(range(1,11),wcss)
plt.title('Elbow Method')
plt.xlabel('No. of clusters')
plt.ylabel('WCSS')
plt.xticks(range(1, 11))
plt.show()
```

```
C:\Users\NAVAL\anaconda3\lib\site-packages\sklearn\cluster\_kmeans.py:881: UserWarning: K
Means is known to have a memory leak on Windows with MKL, when there are less chunks than
available threads. You can avoid it by setting the environment variable OMP_NUM_THREADS=3
.
  warnings.warn(
```



With the help of elbow method we concluded that we should use 2 clusters

In [39]:

```
clusters=KMeans(n_clusters=2,random_state=0)
```

In [40]:

```
clusters.fit(Xtrain,ytrain)
```

Out[40]:

```
KMeans(n_clusters=2, random_state=0)
```

In [41]:

```
yknn=clusters.predict(Xtest)
```

In [42]:

```
metrics.accuracy_score(ytest,yknn)
```

Out[42]:

```
0.7186147186147186
```

In [43]:

```
metrics.confusion_matrix(ytest,yknn)
```

Out[43]:

```
array([[152,   8],
       [ 57,  14]], dtype=int64)
```

In [44]:

```
pd.crosstab(ytest, yknn, rownames=['True'], colnames=['Predicted'], margins=True)
```

Out[44]:

Predicted	0	1	All
True			
0	152	8	160
1	57	14	71
All	209	22	231

We are getting higher TN but lower TP from KNN clustering as compared to the SVM model

In [45]:

```
print(classification_report(ytest, yknn))
```

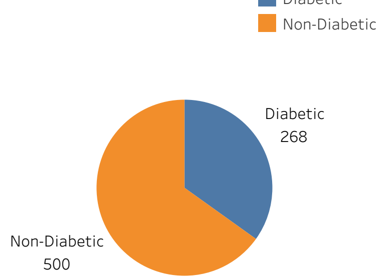
```
              precision    recall  f1-score   support

           0       0.73      0.95      0.82       160
           1       0.64      0.20      0.30        71

    accuracy                           0.72       231
   macro avg       0.68      0.57      0.56       231
weighted avg       0.70      0.72      0.66       231
```

In [46]:

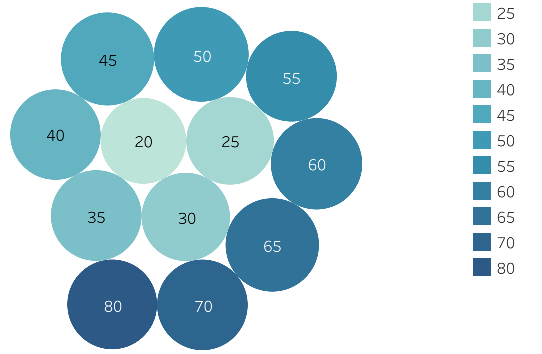
```
Df.to_csv(r'C:\Users\NAVAL\Downloads\Healthcare_diabetes.csv')
```

Converting the preprocessed dataframe to CSV file for Tableau Visualization.

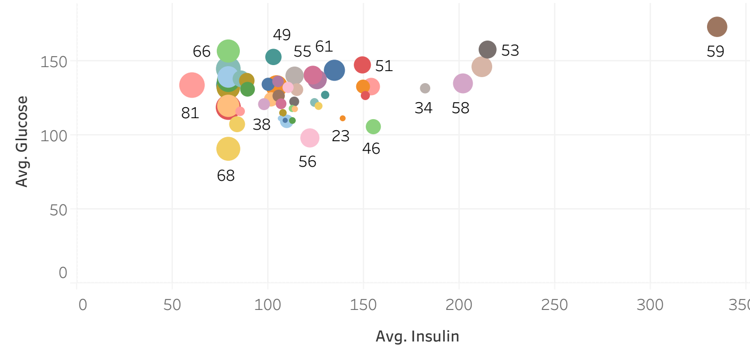
Non-Diabetic vs Diabetic



Age Bins and Avg BP



Avg. Insulin And Avg Glucose With Age Group



Distribution Of Diabetic And Non Diabetic