# Project On HealthCare

Importing the Necessary libraries

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn import metrics
from sklearn.neighbors import KNeighborsClassifier
import warnings
warnings.filterwarnings('ignore')
```

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

```
df.head()
```

```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   
BMI  \
0            6      148             72             35        0  33.6   

1            1       85             66             29        0  26.6   

2            8      183             64              0        0  23.3   

3            1       89             66             23       94  28.1   

4            0      137             40             35      168  43.1   


   DiabetesPedigreeFunction  Age  Outcome  
0                     0.627   50        1  
1                     0.351   31        0  
2                     0.672   32        1  
3                     0.167   21        0  
4                     2.288   33        1  
```

```
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
```

```
df.describe()
```

```
       Pregnancies     Glucose  BloodPressure  SkinThickness
Insulin  \
count   768.000000  768.000000     768.000000     768.000000
768.000000
mean      3.845052  120.894531      69.105469      20.536458
79.799479
std       3.369578   31.972618      19.355807      15.952218
115.244002
min       0.000000    0.000000       0.000000       0.000000
0.000000
25%       1.000000   99.000000      62.000000       0.000000
0.000000
50%       3.000000  117.000000      72.000000      23.000000
30.500000
75%       6.000000  140.250000      80.000000      32.000000
127.250000
max      17.000000  199.000000     122.000000      99.000000
846.000000

              BMI  DiabetesPedigreeFunction        Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    31.992578                  0.471876   33.240885    0.348958
std      7.884160                  0.331329   11.760232    0.476951
min      0.000000                  0.078000   21.000000    0.000000
25%     27.300000                  0.243750   24.000000    0.000000
50%     32.000000                  0.372500   29.000000    0.000000
75%     36.600000                  0.626250   41.000000    1.000000
max     67.100000                  2.420000   81.000000    1.000000
```

## Data Exploration :-

1. Descriptive Analysis

```
df.corr()
```

```
                          Pregnancies   Glucose  BloodPressure
SkinThickness  \
Pregnancies                  1.000000  0.129459       0.141282      -
```

```
0.081672
Glucose                    0.129459  1.000000       0.152590
0.057328
BloodPressure              0.141282  0.152590       1.000000
0.207371
SkinThickness             -0.081672  0.057328       0.207371
1.000000
Insulin                   -0.073535  0.331357       0.088933
0.436783
BMI                        0.017683  0.221071       0.281805
0.392573
DiabetesPedigreeFunction  -0.033523  0.137337       0.041265
0.183928
Age                        0.544341  0.263514       0.239528      -
0.113970
Outcome                    0.221898  0.466581       0.065068
0.074752

                           Insulin       BMI  DiabetesPedigreeFunction
\
Pregnancies              -0.073535  0.017683                 -0.033523

Glucose                   0.331357  0.221071                  0.137337

BloodPressure             0.088933  0.281805                  0.041265

SkinThickness             0.436783  0.392573                  0.183928

Insulin                   1.000000  0.197859                  0.185071

BMI                       0.197859  1.000000                  0.140647

DiabetesPedigreeFunction  0.185071  0.140647                  1.000000

Age                      -0.042163  0.036242                  0.033561

Outcome                   0.130548  0.292695                  0.173844


                               Age   Outcome
Pregnancies               0.544341  0.221898
Glucose                   0.263514  0.466581
BloodPressure             0.239528  0.065068
SkinThickness            -0.113970  0.074752
Insulin                  -0.042163  0.130548
BMI                       0.036242  0.292695
DiabetesPedigreeFunction  0.033561  0.173844
Age                       1.000000  0.238356
Outcome                   0.238356  1.000000
```

```
df.columns
```

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness',
'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

```
df.isnull().sum()
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

```
#Value of zero does not make sense and thus indicates missing value
#lets count zero in each
```

```
df[df[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']]==0]
.count()
```

```
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64
```

```
#lets replace zero with nan
```

```
df.loc[df['Glucose']==0,'Glucose']=np.nan
df.loc[df['BloodPressure']==0,'BloodPressure']=np.nan
df.loc[df['SkinThickness']==0,'SkinThickness']=np.nan
df.loc[df['Insulin']==0,'Insulin']=np.nan
df.loc[df['BMI']==0,'BMI']=np.nan
df.isnull().sum()
```

```
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
```

```
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64
```

```
#finding missing value %

missing_val_per=(df.isnull().sum()*100)/len(df)
missing_val_per
```

```
Pregnancies                  0.000000
Glucose                      0.651042
BloodPressure                4.557292
SkinThickness               29.557292
Insulin                     48.697917
BMI                          1.432292
DiabetesPedigreeFunction     0.000000
Age                          0.000000
Outcome                      0.000000
dtype: float64
```

"Insuline" having more aprrox 50% of missing values, and is one of the most important feature for diabetes lets fix it

```
df.describe()
```

```
       Pregnancies     Glucose  BloodPressure  SkinThickness
Insulin  \
count   768.000000  763.000000     733.000000     541.000000
394.000000
mean      3.845052  121.686763      72.405184      29.153420
155.548223
std       3.369578   30.535641      12.382158      10.476982
118.775855
min       0.000000   44.000000      24.000000       7.000000
14.000000
25%       1.000000   99.000000      64.000000      22.000000
76.250000
50%       3.000000  117.000000      72.000000      29.000000
125.000000
75%       6.000000  141.000000      80.000000      36.000000
190.000000
max      17.000000  199.000000     122.000000      99.000000
846.000000

              BMI  DiabetesPedigreeFunction         Age     Outcome
count  757.000000                768.000000  768.000000  768.000000
mean    32.457464                  0.471876   33.240885    0.348958
std      6.924988                  0.331329   11.760232    0.476951
min     18.200000                  0.078000   21.000000    0.000000
25%     27.500000                  0.243750   24.000000    0.000000
```

```
50%     32.300000                   0.372500   29.000000    0.000000
75%     36.600000                   0.626250   41.000000    1.000000
max     67.100000                   2.420000   81.000000    1.000000
```

```
Median=df['Insulin'].median()
Median
```

```
125.0
```

```
Mode=df['Insulin'].mode()
Mode
```

```
0    105.0
Name: Insulin, dtype: float64
```

1. Min = 14.0
2. Max = 846.0
3. Mean = 155.5
4. Median = 125.0
5. Mode = 105.0

Lets Proceed with Mean method

```
df['Glucose'].fillna(value=df['Glucose'].mean(),inplace=True)
df['BloodPressure'].fillna(value=df['BloodPressure'].mean(),inplace=Tr
ue)
df['SkinThickness'].fillna(value=df['SkinThickness'].mean(),inplace=Tr
ue)
df['Insulin'].fillna(value=df['Insulin'].mean(),inplace=True)
df['BMI'].fillna(value=df['BMI'].mean(),inplace=True)
```

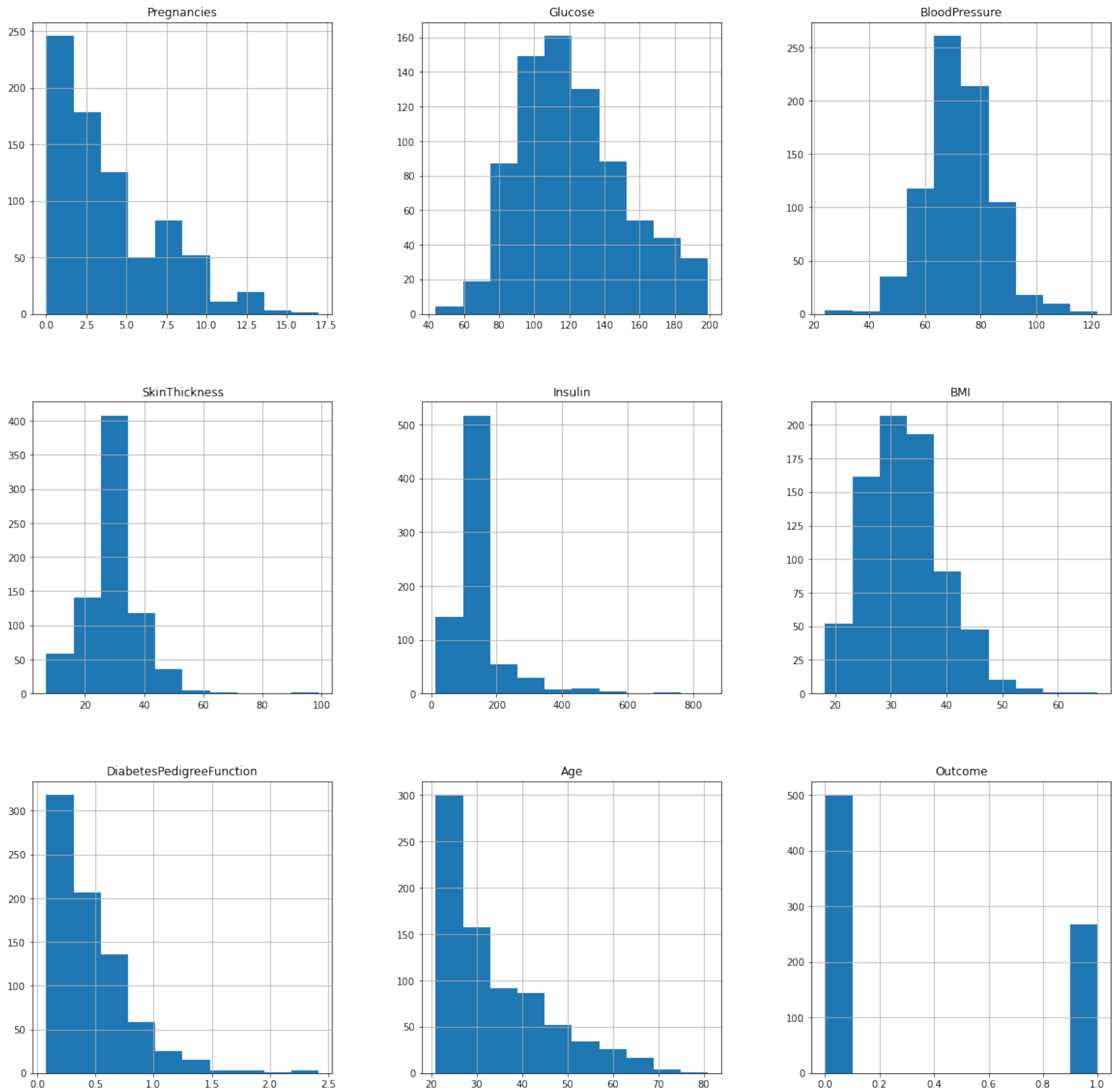
```
df.isnull().sum()
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

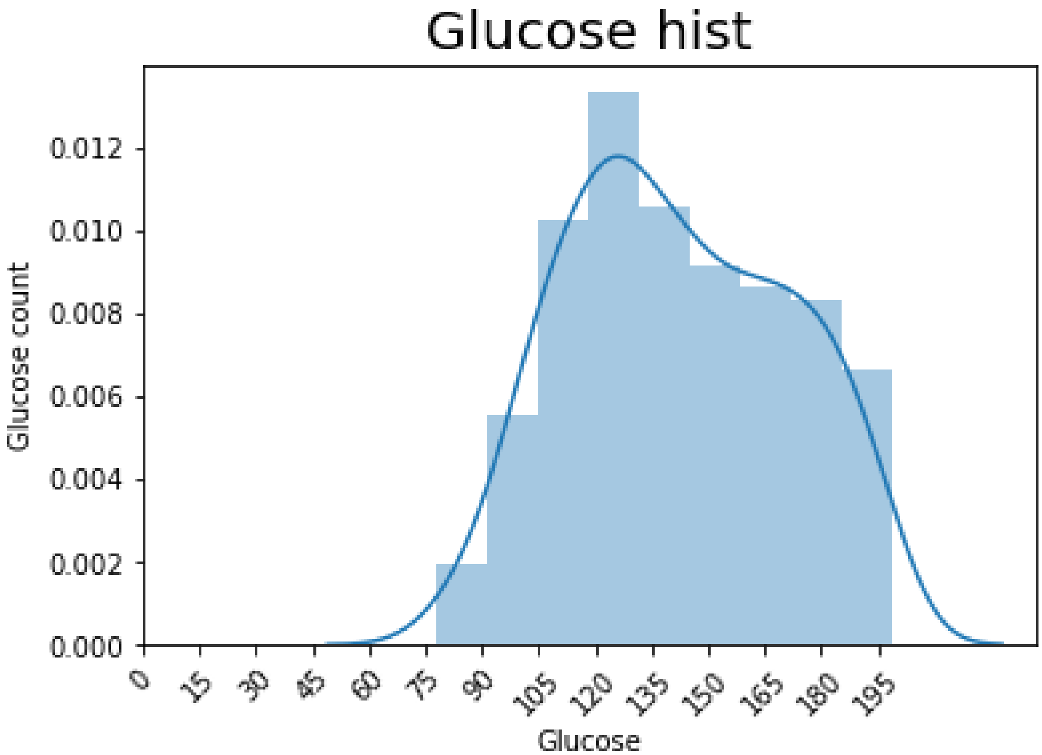
No Null Values remain

## 2.Exploring these values using Histogram

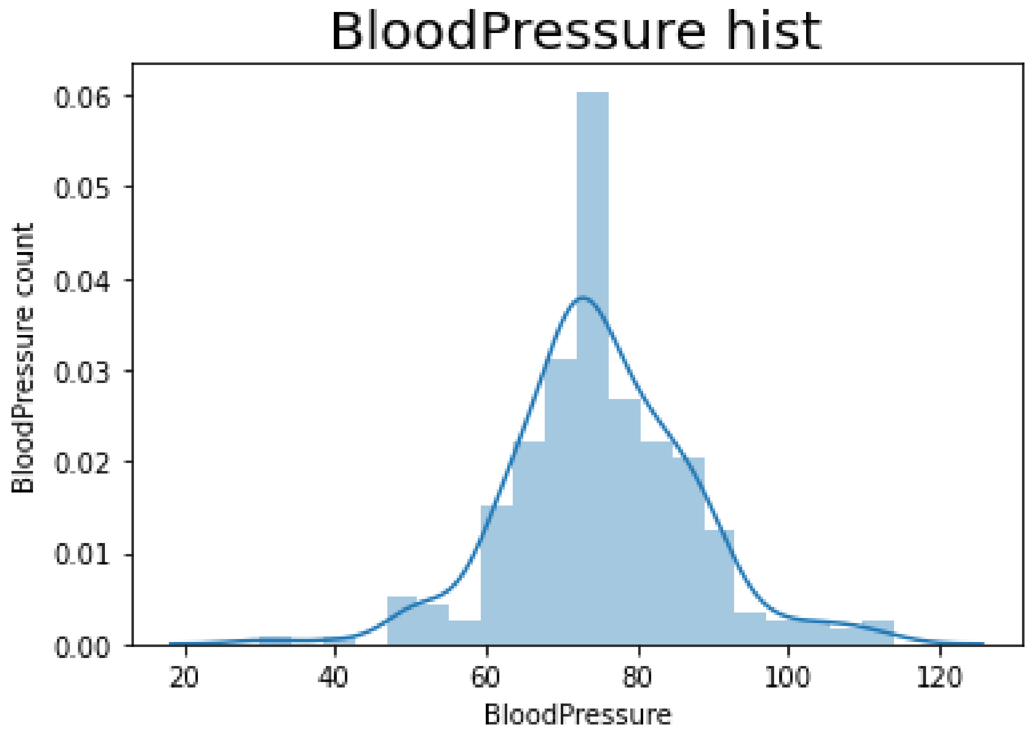
```
p=df.hist(figsize = (20,20))
```



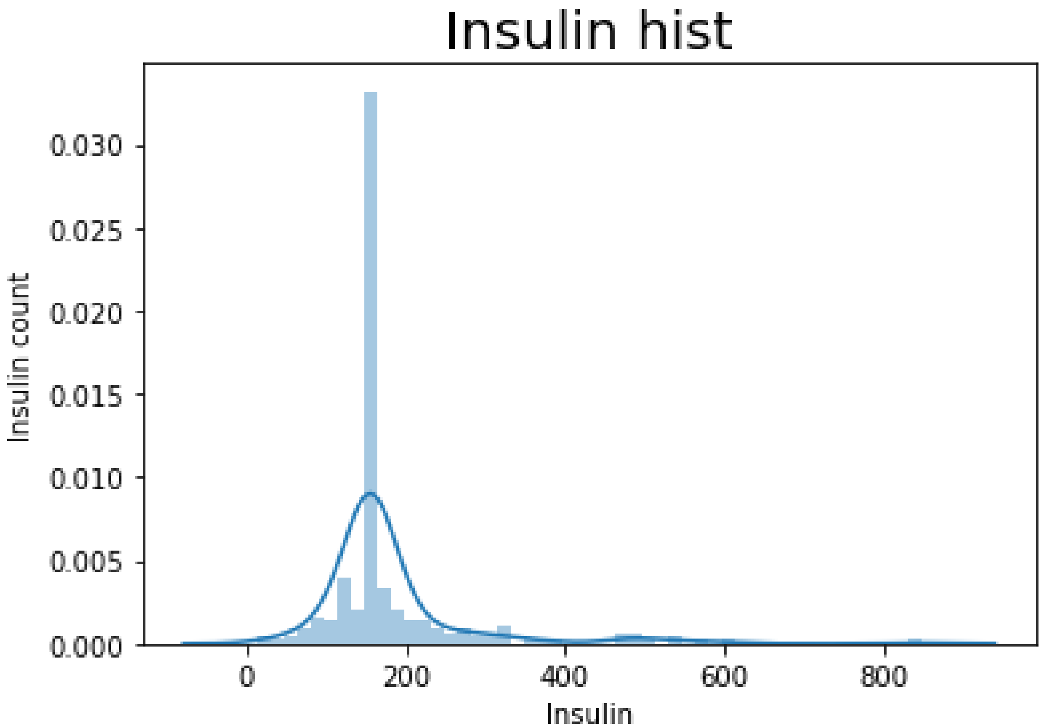

```
fig = plt.figure(figsize=(6,4))

sns.distplot(df['Glucose'][df['Outcome']==1])
plt.xticks([i for i in range(0,201,15)],rotation=45)
plt.ylabel('Glucose count')
plt.title('Glucose hist',fontsize=20)
plt.show()
```



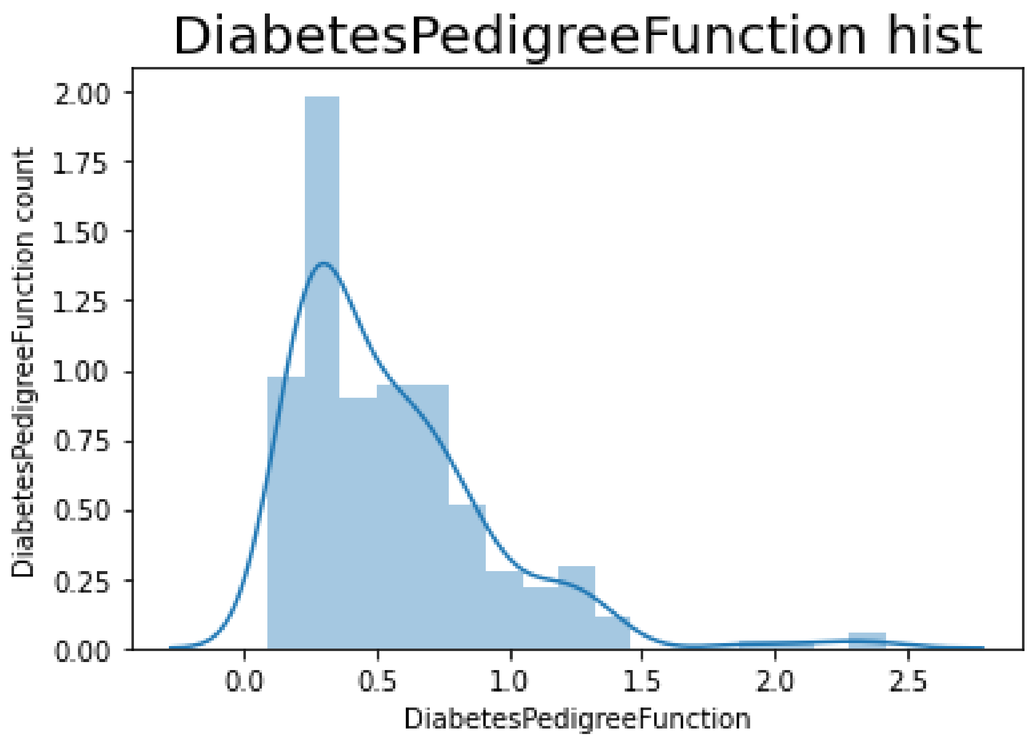

```
fig = plt.figure(figsize=(6,4))

sns.distplot(df['BloodPressure'][df['Outcome']==1])
plt.xticks()
plt.ylabel('BloodPressure count')
plt.title('BloodPressure hist',fontsize=20)
plt.show()
```




```
fig = plt.figure(figsize=(6,4))

sns.distplot(df['Insulin'][df['Outcome']==1])
plt.xticks()
plt.ylabel('Insulin count')
plt.title('Insulin hist',fontsize=20)
plt.show()
```

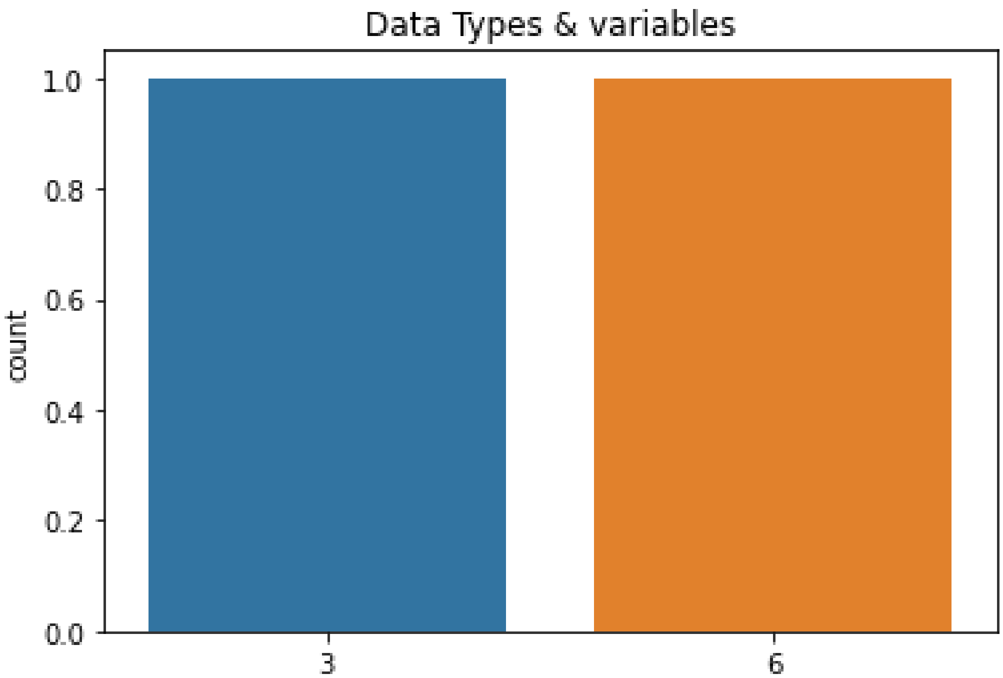



```
fig = plt.figure(figsize=(6,4))

sns.distplot(df['DiabetesPedigreeFunction'][df['Outcome']==1])
plt.xticks()
plt.ylabel('DiabetesPedigreeFunction count')
plt.title('DiabetesPedigreeFunction hist',fontsize=20)
plt.show()
```



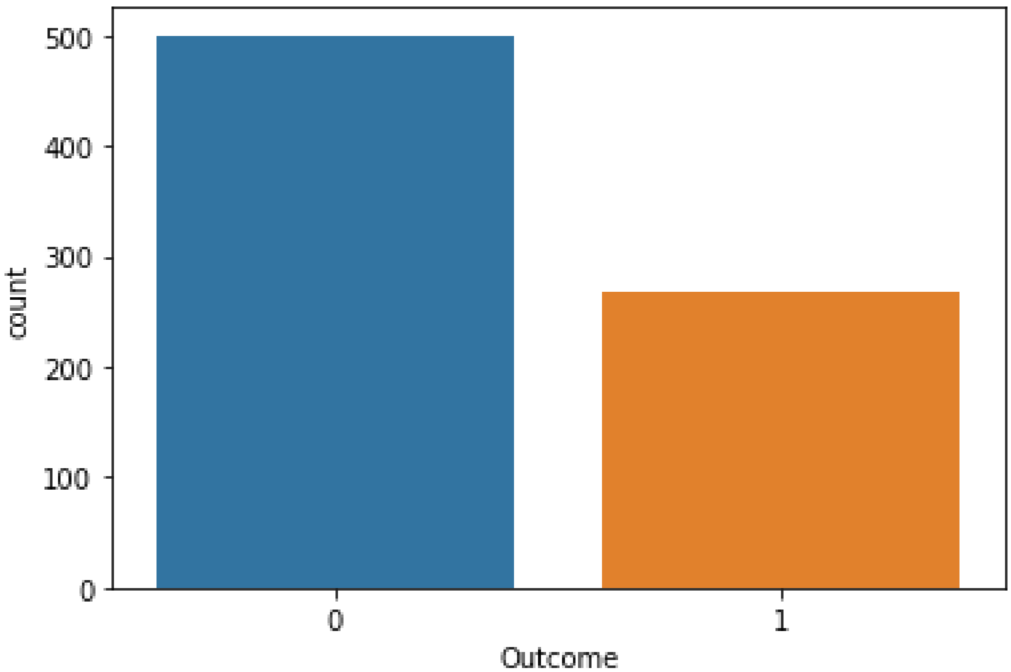

### 3.Create a Countplot descibing the count of variables

```
df.dtypes.value_counts()

float64    6
int64      3
dtype: int64

plt.title("Data Types & variables")
sns.countplot(x=df.dtypes.value_counts(),data=df)
plt.show()
```




Data Exploration:

```
#Check the balance of the data by plotting the count of outcomes by
their value.
#Describe your findings and plan future course of action.

df['Outcome'].value_counts()

0    500
1    268
Name: Outcome, dtype: int64

sns.countplot(x='Outcome',data=df)
plt.show()
```

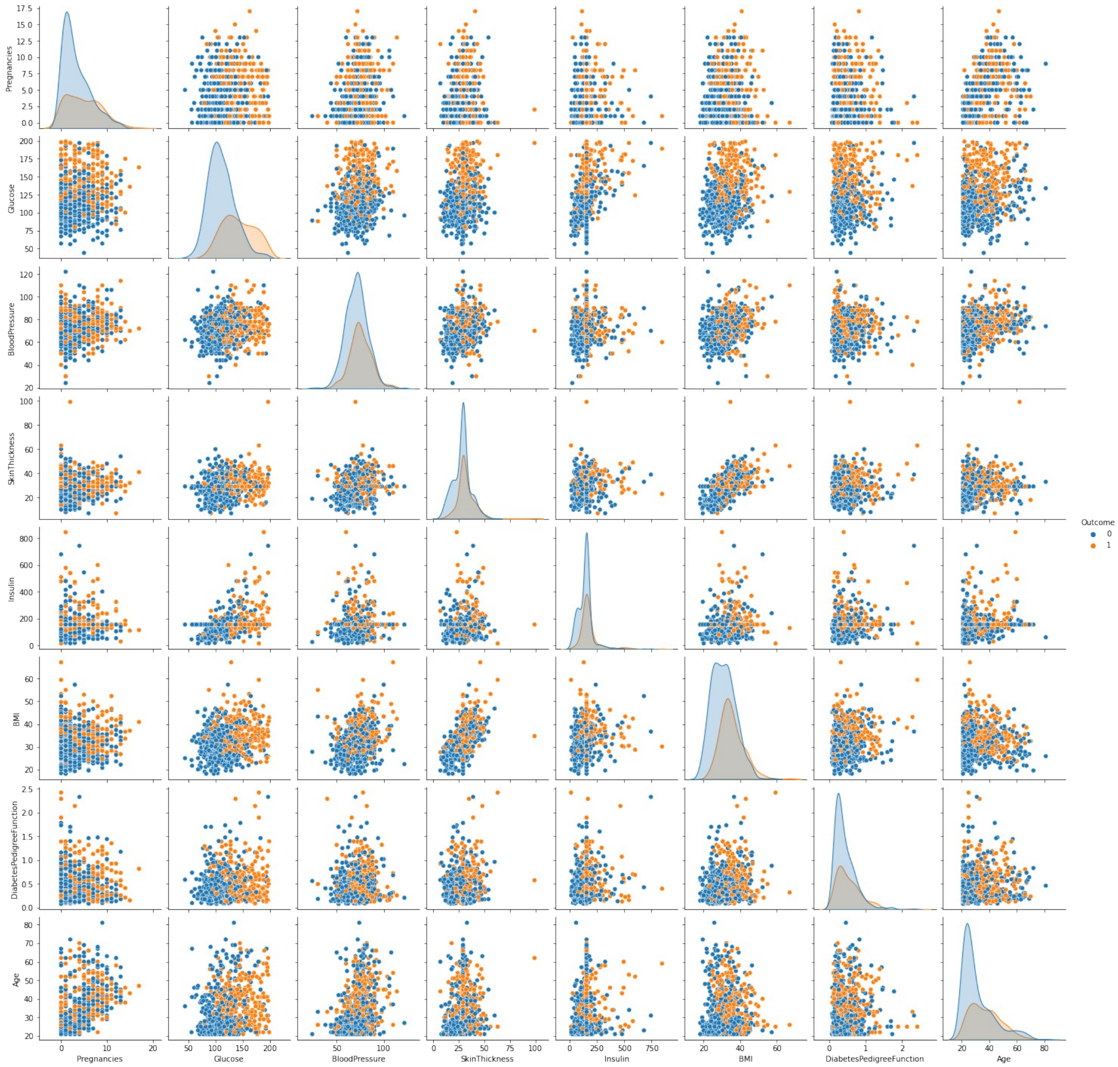



Create scatter charts between the pair of variables to understand the relationships

```
sns.pairplot(df)
plt.show()
```

Pair plot to know relationship between two variables

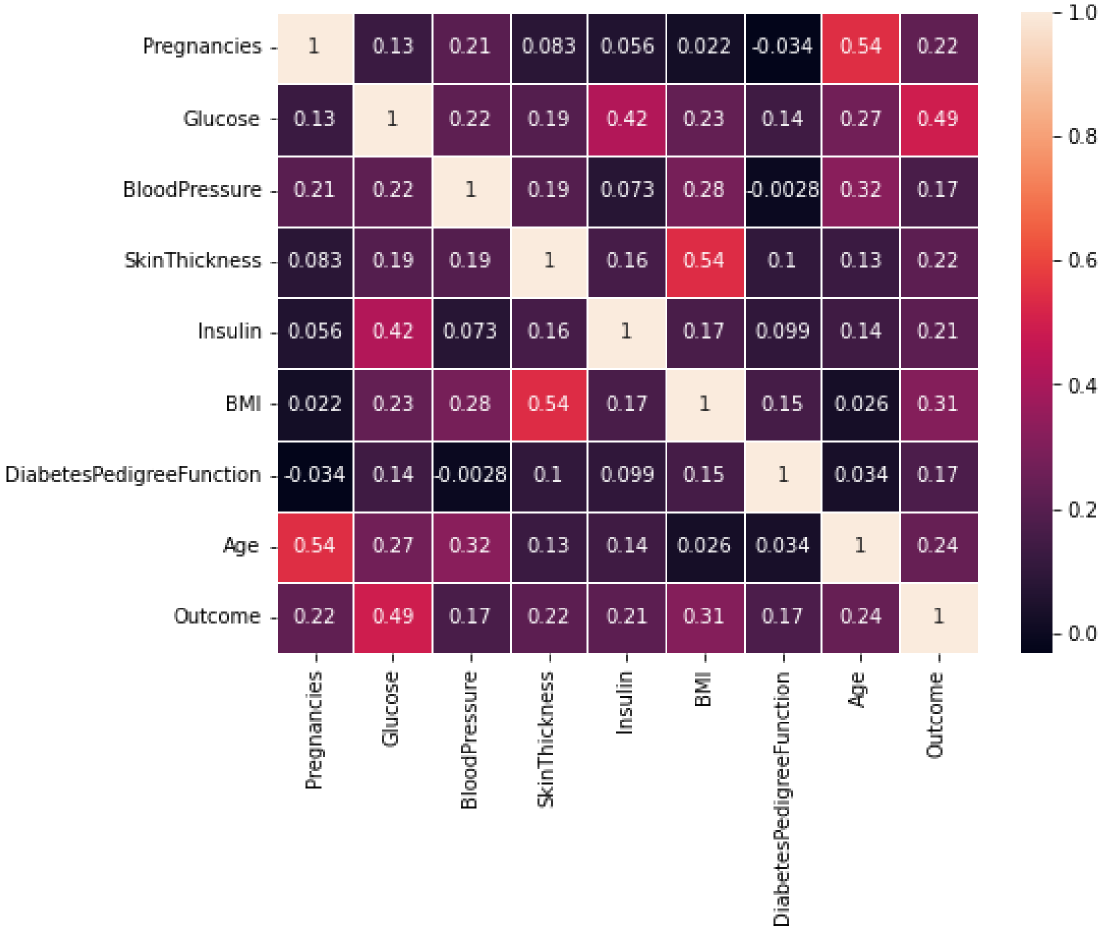
```
sns.pairplot(df,hue='Outcome')
plt.show()
```




```
corr_matrix=df.corr()
corr_matrix

                          Pregnancies   Glucose  BloodPressure
SkinThickness  \
Pregnancies                  1.000000  0.127911       0.208522
0.082989
Glucose                      0.127911  1.000000       0.218367
0.192991
BloodPressure                0.208522  0.218367       1.000000
0.192816
SkinThickness                0.082989  0.192991       0.192816
1.000000
Insulin                      0.056027  0.420157       0.072517
0.158139
BMI                          0.021565  0.230941       0.281268
0.542398
DiabetesPedigreeFunction    -0.033523  0.137060      -0.002763
```

```
0.100966
Age                        0.544341  0.266534       0.324595
0.127872
Outcome                    0.221898  0.492928       0.166074
0.215299

                          Insulin       BMI  DiabetesPedigreeFunction
\
Pregnancies              0.056027  0.021565                 -0.033523

Glucose                  0.420157  0.230941                  0.137060

BloodPressure            0.072517  0.281268                 -0.002763

SkinThickness            0.158139  0.542398                  0.100966

Insulin                  1.000000  0.166586                  0.098634

BMI                      0.166586  1.000000                  0.153400

DiabetesPedigreeFunction  0.098634  0.153400                  1.000000

Age                      0.136734  0.025519                  0.033561

Outcome                  0.214411  0.311924                  0.173844


                              Age   Outcome
Pregnancies              0.544341  0.221898
Glucose                  0.266534  0.492928
BloodPressure            0.324595  0.166074
SkinThickness            0.127872  0.215299
Insulin                  0.136734  0.214411
BMI                      0.025519  0.311924
DiabetesPedigreeFunction  0.033561  0.173844
Age                      1.000000  0.238356
Outcome                  0.238356  1.000000
```

```
plt.figure(figsize=(8,6))
sns.heatmap(corr_matrix,annot=True,linewidths=1)
plt.show()
```




## Observations or Findings

From the Correlation heatmap & Correlation Matrix we can see that there is strong correlation between "Outcome" and [Glucose,Insulin,BMI,Age] ,so we can select these feature to accept input from the user and predict the Outcome

The value of Pearson's Correlation Coefficient can be between -1 to +1. 1 means that they are highly correlated and 0 means no correlation.

This Correlation _matrix shows,there is 24% contribution of "Age" for the outcome,similarly Glucose level contributing highest for outcome i.e 49%.

Conclusion-If the glucose level is high then 49% chance of diabetes.

## Data Modeling:-

Model-1 Logistic Regreation:-

```
df.head()
```

```
   Pregnancies  Glucose  BloodPressure  SkinThickness     Insulin
BMI  \
0            6    148.0           72.0       35.00000  155.548223
33.6
1            1     85.0           66.0       29.00000  155.548223
26.6
2            8    183.0           64.0       29.15342  155.548223
23.3
3            1     89.0           66.0       23.00000   94.000000
28.1
4            0    137.0           40.0       35.00000  168.000000
43.1

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1
```

```
features=df.iloc[:,[0,1,2,3,4,5,6,7]].values
label = df.iloc[:,8].values
```

```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(features,label,test_siz
e=0.20,random_state=10)
```

```
model_1=LogisticRegression()
model_1.fit(x_train,y_train)
```

```
LogisticRegression()
```

```
model_2=DecisionTreeClassifier(max_depth=4)
model_2.fit(x_train,y_train)
```

```
DecisionTreeClassifier(max_depth=4)
```

```
model_3=RandomForestClassifier(n_estimators=4)
model_3.fit(x_train,y_train)
```

```
RandomForestClassifier(n_estimators=4)
```

```
model_4=SVC(kernel='linear',random_state=4)
model_4.fit(x_train,y_train)
```

```
SVC(kernel='linear', random_state=4)
```

```
model_5=KNeighborsClassifier(4)
model_5.fit(x_train,y_train)
```

```
KNeighborsClassifier(n_neighbors=4)
```

Making Predictions :-

```
y_predict_logistic=model_1.predict(x_test)
y_predict_decisiontree=model_2.predict(x_test)
y_predict_random=model_3.predict(x_test)
y_predict_svc=model_4.predict(x_test)
y_predict_KNn=model_5.predict(x_test)
```

Accuracy Evaluation :-

```
from sklearn.metrics import accuracy_score

accuracy_logistic=accuracy_score(y_test,y_predict_logistic)
accuracy_decisiontree=accuracy_score(y_test,y_predict_decisiontree)
accuracy_random=accuracy_score(y_test,y_predict_random)
accuracy_svc=accuracy_score(y_test,y_predict_svc)
accuracy_KNn=accuracy_score(y_test,y_predict_KNn)
```

Accuracy Test :-

```
print('Logistic Regression :', (accuracy_logistic*100))
print('Decision Tree Classifier :', (accuracy_decisiontree*100))
print('RandomForest :', (accuracy_random*100))
print('SVM :', (accuracy_svc*100))
print('KNn :', (accuracy_KNn*100))
```

```
Logistic Regression : 72.07792207792207
Decision Tree Classifier : 75.97402597402598
RandomForest : 72.72727272727273
SVM : 72.72727272727273
KNn : 69.48051948051948
```

"As compared with few algorithm we got highest accuracy as approx , "76%" in Decision Tree Classifier".

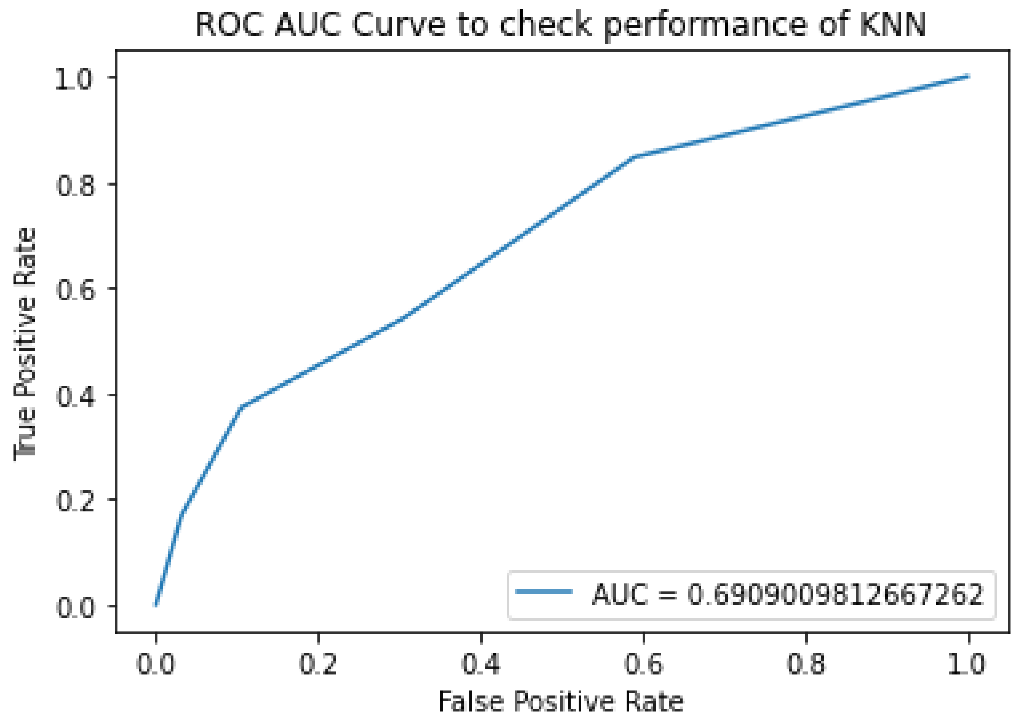
## Data Modeling : ROC AUC

Defining the metrics for :- "ROC AUC Curve".

```
from sklearn.metrics import roc_curve
y_predict_proba=model_5.predict_proba(x_test)[ : : ,1]
fpr,tpr,thresholds = roc_curve(y_test,y_predict_proba)
auc = metrics.roc_auc_score(y_test,y_predict_proba)
```

Create ROC Curve

```
plt.plot(fpr,tpr,label="AUC = "+str(auc))
plt.ylabel("True Positive Rate")
plt.xlabel("False Positive Rate")
plt.title("ROC AUC Curve to check performance of KNN")
plt.legend(loc=4)
plt.show()
```



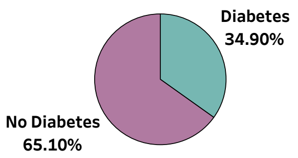

## Conclusion:-

AUC ROC useful when model is binary classification problem.

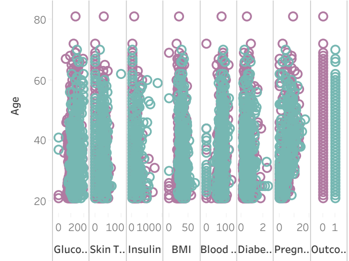
Better models can accurately distinguish between the two. Whereas, a poor model will have difficulties in distinguishing between the two in our case AUC Score is 69% ,for good model AUC must required more than 95%.

# Project-2 :- Healthcare

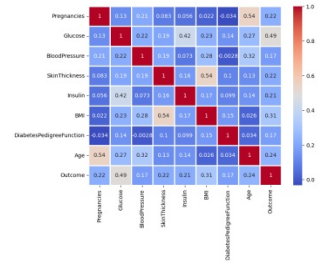
### Diabetes V/S NO Diabetes



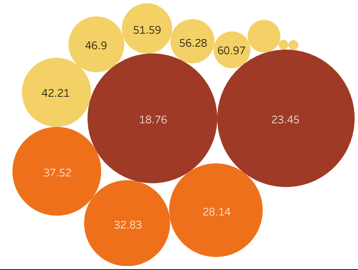

### Scatter Plot




### Heat Map




### Bubbles Map




### Histogram to analyze the distribution of the data