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20BTRCD014

Pima Indians Diabetes Database

Problem Statement :

1. Perform the Data Exploratory Analysis. on the given Dataset.
2. Can you build a machine learning model { Any Model } to accurately predict whether or not the patients in the dataset have diabetes or not?

In [1]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, confusion_matrix, f1_score
```

In [2]:

```
lab = pd.read_csv("diabetes.csv")
```

A DataFrame has been created using 'Pandas' by importing our .csv file

In [3]:

```
lab
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunct
0	6	148	72	35	0	33.6	0.
1	1	85	66	29	0	26.6	0.
2	8	183	64	0	0	23.3	0.
3	1	89	66	23	94	28.1	0.
4	0	137	40	35	168	43.1	2.
...	...	...	...	...	...	...	
763	10	101	76	48	180	32.9	0.
764	2	122	70	27	0	36.8	0.
765	5	121	72	23	112	26.2	0.
766	1	126	60	0	0	30.1	0.
767	1	93	70	31	0	30.4	0.

768 rows × 9 columns

In [4]:

```
lab.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

1.Exploratory Data Analysis

In [5]:

```
lab.shape
```

Out[5]:

```
(768, 9)
```

Our dataset has 768 rows and 9 columns or features

In [6]:

```
lab.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 [7]:

```
lab.isna().sum()
```

Out[7]:

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

As we don't have any null values in our dataset, no need to change anything

In [8]:

```
lab.corr()
```

Out[8]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.0
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.2
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.2
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.3
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.1
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.0
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.1
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.0
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.2

'Glucose' has the maximum and 'BloodPressure' has the minimum positive linear correlation with 'Outcome'.

There is no feature that has a negative linear correlation with 'Outcome'

In [9]:

```
lab.describe()
```

Out[9]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diabet
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

The minimum value of the features 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin' and 'BMI' is 0. These values cannot be 0. Thus, this can be called as "missing data" in our case. We need to either drop the 0-valued rows or we need to replace them with the "mean" or "median" value of that feature.

In [10]:

```
lab = lab[['Pregnancies','Glucose','BMI','DiabetesPedigreeFunction','Insulin','Age','Outcom
lab = lab.sort_values(by='Age')
lab
```

Out[10]:

	Pregnancies	Glucose	BMI	DiabetesPedigreeFunction	Insulin	Age	Outcome
255	1	113	33.6	0.543	0	21	1
60	2	84	0.0	0.304	0	21	0
102	0	125	22.5	0.262	0	21	0
182	1	0	27.7	0.299	23	21	0
623	0	94	43.5	0.347	115	21	0
...	...	...	...	...	...	...	...
123	5	132	26.8	0.186	0	69	0
684	5	136	0.0	0.640	0	69	0
666	4	145	32.5	0.235	0	70	1
453	2	119	19.6	0.832	0	72	0
459	9	134	25.9	0.460	60	81	0

768 rows × 7 columns

In [11]:

```
lab.describe()
```

Out[11]:

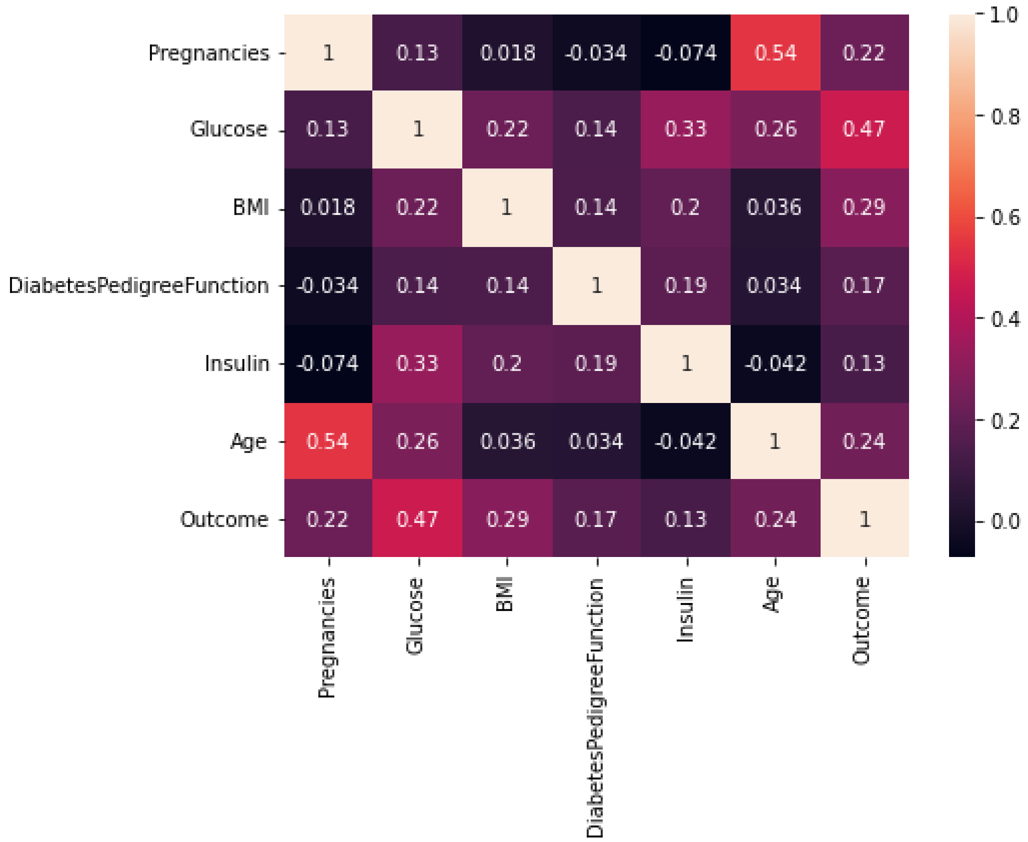
	Pregnancies	Glucose	BMI	DiabetesPedigreeFunction	Insulin	Age
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	31.992578	0.471876	79.799479	33.240885
std	3.369578	31.972618	7.884160	0.331329	115.244002	11.760232
min	0.000000	0.000000	0.000000	0.078000	0.000000	21.000000
25%	1.000000	99.000000	27.300000	0.243750	0.000000	24.000000
50%	3.000000	117.000000	32.000000	0.372500	30.500000	29.000000
75%	6.000000	140.250000	36.600000	0.626250	127.250000	41.000000
max	17.000000	199.000000	67.100000	2.420000	846.000000	81.000000

In [12]:

```
conf_mat = lab.corr()
plt.figure(figsize=(7,5))
sns.heatmap(conf_mat, annot=True)
```

Out[12]:

```
<AxesSubplot:>
```



Let's fill those features containing '0' values with mean or median values

To decide which method to use, let's visualize the data

```
Mean-It is preferred if data is numeric and not skewed.
Median-It is preferred if data is numeric and skewed.
Mode-It is preferred if the data is a string(object) or numeric.
```

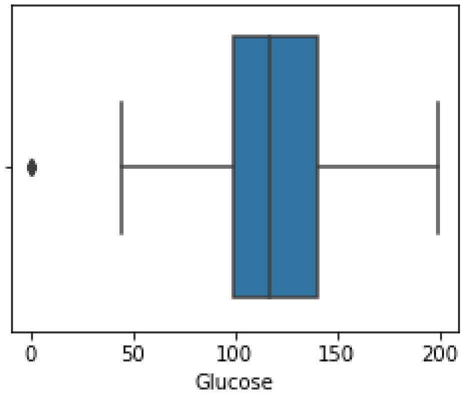
In [13]:

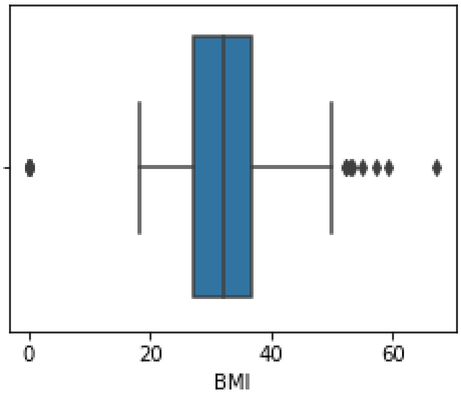
```
fig, ax = plt.subplots(figsize=(4,3))
sns.boxplot(lab.Glucose)

fig, ax = plt.subplots(figsize=(4,3))
sns.boxplot(lab.BMI)

fig, ax = plt.subplots(figsize=(4,3))
sns.boxplot(lab.Insulin)
```

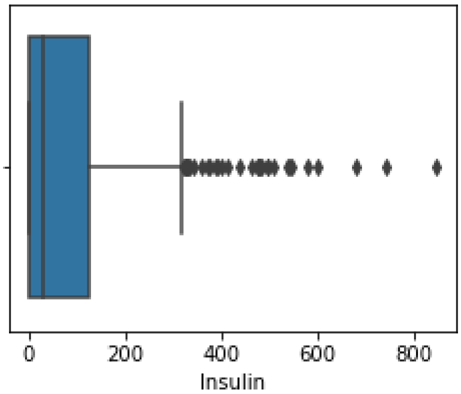
```
C:\Users\Radha Krishna\anaconda3\lib\site-packages\seaborn\_decorators.py:3
6: FutureWarning: Pass the following variable as a keyword arg: x. From vers
ion 0.12, the only valid positional argument will be `data`, and passing oth
er arguments without an explicit keyword will result in an error or misinter
pretation.
  warnings.warn(
C:\Users\Radha Krishna\anaconda3\lib\site-packages\seaborn\_decorators.py:3
6: FutureWarning: Pass the following variable as a keyword arg: x. From vers
ion 0.12, the only valid positional argument will be `data`, and passing oth
er arguments without an explicit keyword will result in an error or misinter
pretation.
  warnings.warn(
C:\Users\Radha Krishna\anaconda3\lib\site-packages\seaborn\_decorators.py:3
6: FutureWarning: Pass the following variable as a keyword arg: x. From vers
ion 0.12, the only valid positional argument will be `data`, and passing oth
er arguments without an explicit keyword will result in an error or misinter
pretation.
  warnings.warn(
```

Out[13]:

```
<AxesSubplot:xlabel='Insulin'>
```







As the box-plots of 'Glucose' and 'Insulin' tells us that the data is skewed --> So, we can use medium method to fill missing values

As box plot of 'BMI' is showing that the data is not skewed --> we can use mean method to fill missing values

In [14]:

```
lab.fillna(lab.mean)
```

Out[14]:

	Pregnancies	Glucose	BMI	DiabetesPedigreeFunction	Insulin	Age	Outcome
255	1	113	33.6	0.543	0	21	1
60	2	84	0.0	0.304	0	21	0
102	0	125	22.5	0.262	0	21	0
182	1	0	27.7	0.299	23	21	0
623	0	94	43.5	0.347	115	21	0
...	...	...	...	...	...	...	...
123	5	132	26.8	0.186	0	69	0
684	5	136	0.0	0.640	0	69	0
666	4	145	32.5	0.235	0	70	1
453	2	119	19.6	0.832	0	72	0
459	9	134	25.9	0.460	60	81	0

768 rows × 7 columns

In [15]:

```
median = []
features = ['Glucose', 'Insulin']
for f in features:
    median.append(lab[f].median())

def replace_with_median(lab, f, value):
    lab[f] = lab[f].replace(0, value)

for i, f in enumerate(features):
    replace_with_median(lab, f, median[i])


mean = []
features_ = ['BMI']
for f1 in features_:
    mean.append(lab[f1].mean())

def replace_with_mean(lab, f1, value):
    lab[f1] = lab[f1].replace(0, value)

for i, f1 in enumerate(features_):
    replace_with_mean(lab, f1, mean[i])
```

In [16]:

```
lab
```

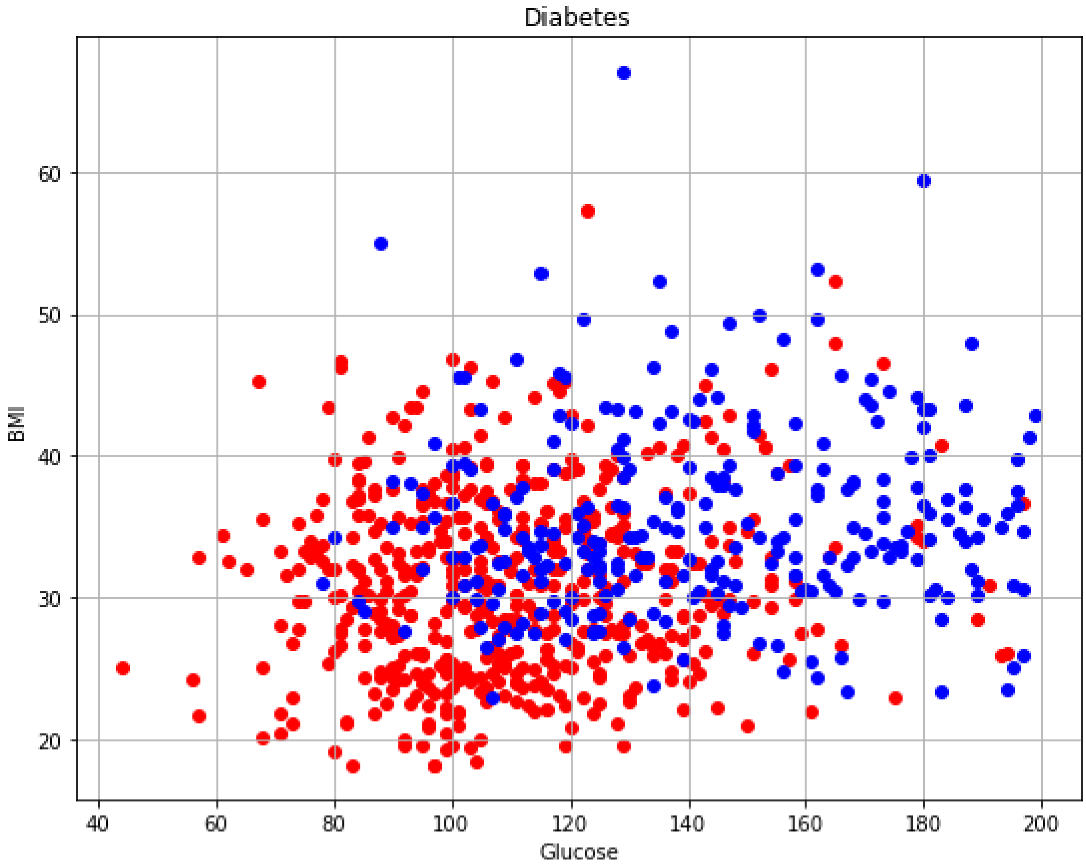
Out[16]:

	Pregnancies	Glucose	BMI	DiabetesPedigreeFunction	Insulin	Age	Outcome
255	1	113	33.600000	0.543	30.5	21	1
60	2	84	31.992578	0.304	30.5	21	0
102	0	125	22.500000	0.262	30.5	21	0
182	1	117	27.700000	0.299	23.0	21	0
623	0	94	43.500000	0.347	115.0	21	0
...	...	...	...	...	...	...	...
123	5	132	26.800000	0.186	30.5	69	0
684	5	136	31.992578	0.640	30.5	69	0
666	4	145	32.500000	0.235	30.5	70	1
453	2	119	19.600000	0.832	30.5	72	0
459	9	134	25.900000	0.460	60.0	81	0

768 rows × 7 columns

In [17]:

```
zero = lab[lab.Outcome == 0]
one = lab[lab.Outcome == 1]
fig, sub = plt.subplots()
fig.set_size_inches(9,7)

sub.scatter(zero['Glucose'],zero['BMI'], color='red')
sub.scatter(one['Glucose'],one['BMI'], color='blue')

sub.set_xlabel("Glucose")
sub.set_ylabel("BMI")
sub.grid()
sub.set_title("Diabetes")
plt.show()
```



Glucose and BMI will be good predictors as compared to others

In [18]:

```
X = lab.iloc[:,1:3].values
y = lab.iloc[:,-1].values
```

In [19]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
```

Splitting the dataset into train data and test data with 80:20 ratio.

In [20]:

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=0)
```

2. Model

a. Logistic Regression

In [21]:

```
log_reg = LogisticRegression()
log_reg.fit(X_train, y_train)
```

Out[21]:

```
LogisticRegression()
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [22]:

```
log_pred = log_reg.predict(X_test)
log_pred
```

Out[22]:

```
array([0, 1, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0,
       0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1,
       0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0,
       0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0,
       0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0],
      dtype=int64)
```

In [23]:

```
log_accuracy = log_reg.score(X_test, y_test)
log_accuracy
```

Out[23]:

```
0.7857142857142857
```

b. Decision Tree classifier

In [24]:

```
tree = DecisionTreeClassifier()
tree.fit(X_train, y_train)
```

Out[24]:

```
DecisionTreeClassifier()
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
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In [25]:

```
tree_pred = tree.predict(X_test)
tree_pred
```

Out[25]:

```
array([0, 1, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0,
       1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 1,
       1, 0, 1, 1, 0, 1, 1, 1, 0, 1, 0, 0, 0, 0, 1, 1, 1, 1, 0, 0, 0, 0,
       0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1,
       0, 1, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1, 1, 0, 0,
       0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 1,
       0, 0, 1, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0, 1, 1, 1, 0, 0, 1, 1, 0, 0],
      dtype=int64)
```

In [26]:

```
tree_accuracy = tree.score(X_test, y_test)
tree_accuracy
```

Out[26]:

```
0.6623376623376623
```

c. K Nearest Neighbors Classifier

In [27]:

```
knn = KNeighborsClassifier(n_neighbors=40)
knn.fit(X_train, y_train)
```

Out[27]:

```
KNeighborsClassifier(n_neighbors=40)
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.
On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

In [28]:

```
knn_pred = knn.predict(X_test)
knn_pred
```

Out[28]:

```
array([0, 1, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0,
       0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1,
       0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0,
       0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0],
      dtype=int64)
```

In [29]:

```
knn_accuracy = knn.score(X_test, y_test)
knn_accuracy
```

Out[29]:

```
0.8051948051948052
```

In [30]:

```
mc = pd.DataFrame({'Model': ['Logistic Regression','Decision Tree Classifier', 'K Nearest N
mc_s = mc.sort_values(by = 'Score', ascending = False)
mc_s = mc_s.set_index('Score')
mc_s
```

Out[30]:

	Model
Score	
0.805195	K Nearest Neighbors Classifier
0.785714	Logistic Regression
0.662338	Decision Tree Classifier

K Nearest Neighbors Classifier

Evaluation of model performance

In [31]:

```
print("Precision and recall are")
print(classification_report(y_test, knn_pred))
```

```
Precision and recall are
              precision    recall  f1-score   support

           0       0.79      0.95      0.86       100
           1       0.85      0.54      0.66        54

    accuracy                           0.81       154
   macro avg       0.82      0.74      0.76       154
weighted avg       0.81      0.81      0.79       154
```

Precision of a patient being detected with 'no diabetes' is more with recall value close to 1 i.e 0.95

In [32]:

```
print(confusion_matrix(y_test, knn_pred))
```

```
[[95  5]
 [25 29]]
```

we can tell from confusion matrix that, model is predicting 95 values correctly i.e, if patient had diabetes, then model is also predicting that patient has diabetes

```
95 - actual (diabetes) and predicted (diabetes)
5 - actual (no diabetes) and predicted (diabetes)
25 - actual (no diabetes) and predicted (diabetes)
29 - actual (no diabetes) and predicted (no diabetes)
```

Thank You