AI based diabetes prediction system

Introduction:

A system is used to predict whether a patient has diabetes based on some of its health-related details such as BMI (Body Mass Index), blood pressure, Insulin, etc.

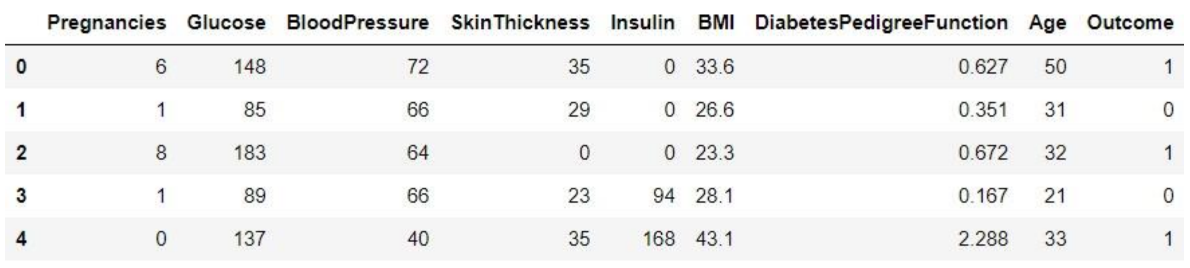
Importing Libraries

```
import numpy as np

import pandas as pd

import matplotlib.pyplot as plt

import seaborn as sns sns.set() from mlxtend.plotting

import plot_decision_regions

import missingno as  msno  from  pandas.plotting

import scatter_matrix from sklearn.preprocessing

import StandardScaler from sklearn.model_selection

import train_test_split from sklearn.neighbors

import KNeighborsClassifier  from  sklearn.metrics

import confusion_matrix from  sklearn

import  metrics  from  sklearn.metrics

import  classification_report

import   warnings   warnings.filterwarnings('ignore')   %matplotlib
inline
```

Here we will be reading the dataset which is in the CSV format

```
diabetes_df = pd.read_csv('diabetes.csv') diabetes_df.head()
```

Output:



	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

Exploratory Data Analysis (EDA)

Now let' see that what are columns available in our dataset.

```
diabetes_df.columns
```

Output:

```
Index(['Pregnancies','Glucose','BloodPressure','SkinThickness','I

nsulin','BMI','DiabetesPedigreeFunction', 'Age', 'Outcome'],

dtype='object')
```

Information about the dataset

```
diabetes_df.info()
```

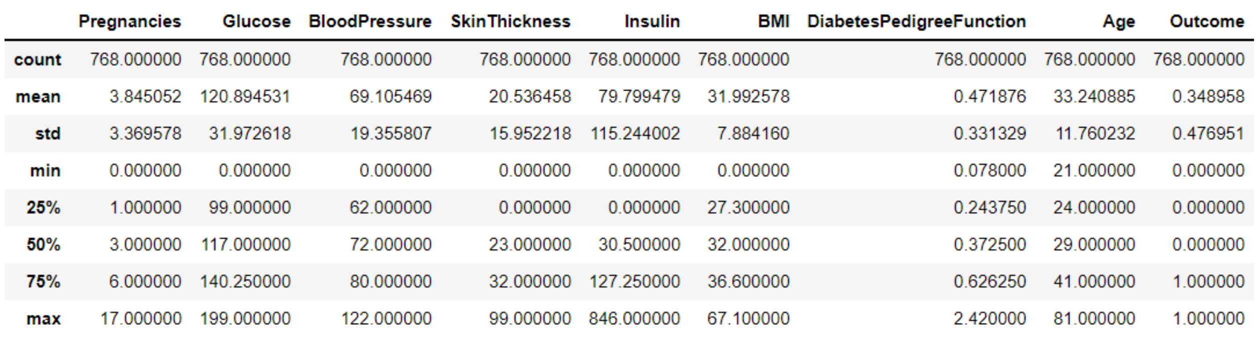
Output:

```
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

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
```

To know more about the dataset

```
diabetes_df.describe()
```

Output:



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	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	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

To know more about the dataset with transpose – here T is for the transpose

```
diabetes_df.describe().T
```

To check that if our dataset have null values or not

```
diabetes_df.isnull().head(10)
```

Now let’s check the number of null values our dataset has.

```
diabetes_df.isnull().sum()
```

Output:

```
Pregnancies 0 Glucose 0 BloodPressure 0 SkinThickness 0 Insulin 0

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

Here from the above code we first checked that is there any null values from the **IsNull()** function then we are going to take the sum of all those missing values from the **sum()** function and the inference we now get is that there are no missing values but that is actually not a true story as in **this particular dataset all the missing values were given the 0 as a value which is not good for the authenticity of the dataset.** Hence we will first **replace the 0 value with the NAN** value then start the imputation process.

```
diabetes_df_copy=diabetes_df.copy(deep=True)

diabetes_df_copy[['Glucose','BloodPressure','SkinThickness','Insu

lin','BMI']]=diabetes_df_copy[['Glucose','BloodPressure','SkinThi

ckness','Insulin','BMI']].replace(0,np.NaN) # Showing the Count of

NANs print(diabetes_df_copy.isnull().sum())
```

Output:

```
Pregnancies 0 Glucose 5 BloodPressure 35 SkinThickness 227 Insulin
```

```
374 BMI 11 DiabetesPedigreeFunction 0 Age
0 Outcome 0 dtype: int64
```

As mentioned above that now **we will be replacing the zeros with the NAN values** so that we can impute it later to maintain the authenticity of the dataset as well as trying to have a better Imputation approach i.e **to apply mean values of each column to the null values of the respective columns.**

Data Visualization

Plotting the data distribution plots before removing null values

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

Inference: So here we have seen the distribution of each features whether it is dependent data or independent data and one thing which could always strike that **why do we need to see the distribution of data?** So the answer is simple it is the best way to start the analysis of the dataset as **it shows the occurrence of every kind of value in the graphical structure which in turn lets us know the range of the data.**

Now we will be imputing the mean value of the column to each missing value of that particular column.

```
diabetes_df_copy['Glucose'].fillna(diabetes_df_copy['Glucose'].me
an(),inplace=True)
diabetes_df_copy['BloodPressure'].fillna(diabetes_df_copy['BloodP
ressure'].mean(),inplace=True)
diabetes_df_copy['SkinThickness'].fillna(diabetes_df_copy['SkinTh
ickness'].median(),inplace=True)
diabetes_df_copy['Insulin'].fillna(diabetes_df_copy['Insulin'].me
dian(),inplace=True)
diabetes_df_copy['BMI'].fillna(diabetes_df_copy['BMI'].median(),
inplace = True)
```

Plotting the distributions after removing the NAN values.

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

Inference: Here we are again using the hist plot to **see the distribution of the dataset** but this time we are using this visualization to see the changes that we can see after those null values are removed from the dataset and we can clearly see the difference **for example –** In age column after removal of the null values, **we can see that there is a spike at the range of 50 to 100 which is quite logical as well.**

Plotting Null Count Analysis Plot

```
p = msno.bar(diabetes_df)
```

Inference: Now in the above graph also we can clearly see that there are **no null** values in the dataset.

Now, let's check that how well our outcome column is balanced

```
color_wheel = {1: "#0392cf", 2: "#7bc043"}
colors = diabetes_df["Outcome"].map(lambda x: color_wheel.get(x
+1)) print(diabetes_df.Outcome.value_counts())
 p=diabetes_df.Outcome.value_counts().plot(kind="bar")
```

Output:

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

Inference: Here from the above visualization it is clearly visible that our **dataset is completely imbalanced**
in fact the number of patients who are **diabetic is half of the patients who are non-diabetic.**

```
plt.subplot(121),
sns.distplot(diabetes_df['Insulin'])plt.subplot(122),
 diabetes_df['Insulin'].plot.box(figsize=(16,5))
 plt.show()
```

Inference: That's how **Distplot** can be helpful where one will able to see the distribution of the data as well as with the help of **boxplot one can see the outliers in that column** and other information too which can be derived by the **box and whiskers plot.**

Correlation between all the features

Correlation between all the features before cleaning

```
plt.figure(figsize=(12,10))
# seaborn has an easy method to showcase heatmap
p  = sns.heatmap(diabetes_df.corr(), annot=True,cmap ='RdYlGn')
```

Scaling the Data

Before scaling down the data let’s have a look into it

```
diabetes_df_copy.head()
```

After Standard scaling

```
sc_X=StandardScaler()X=pd.DataFrame(sc_X.fit_transform(diabetes_d
f_copy.drop(["Outcome"],axis=1),),
columns=['Pregnancies','Glucose','BloodPressure','SkinThickness',
'Insulin','BMI','DiabetesPedigreeFunction','Age'])
X.head()
```

That’s how our dataset will be looking like when it is scaled down or we can see every value now is on thesame scale which will help our **ML model to give a better result.**

Let’s explore our target column

```
y = diabetes_df_copy.Outcome y
```

Output:

```
0 1 1 0 2 1 3 0 4 1 .. 763 0 764 0 765 0 766 1 767 0 Name: Outcome,
Length: 768, dtype: int64
```

Model Building

Splitting the dataset

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

Now we will split the data into training and testing data using the train_test_split function

```
from sklearn.model_selection import train_test_split X_train,
X_test, y_train, y_test = train_test_split(X,y,test_size=0.33,
random_state=7)
```

Random Forest

Building the model using RandomForest

```
from sklearn.ensemble
importRandomForestClassifier
rfc=RandomForestClassifier(n_estimators=200) rfc.fit(X_train,
y_train)
```

Now after building the model let's check the accuracy of the model on the training dataset.

```
rfc_train =  rfc.predict(X_train)
fromsklearn import metrics
print("Accuracy_Score=",format(metrics.accuracy_score(y_train,
rfc_train)))
```

Output: Accuracy = 1.0

So here we can see that on the **training dataset our model is overfitted.**

Getting the accuracy score for Random Forest

```
from  sklearn  import  metrics  predictions =rfc.predict(X_test)
print("Accuracy_Score =",format(metrics.accuracy_score(y_test,
predictions)))
```

Output:

```
Accuracy_Score = 0.7677165354330708
```

Classification report and confusion matrix of random forest model

```
from  sklearn.metrics
importclassification_report,
confusion_matrix
print(confusion_matrix(y_test, predictions))
print(classification_report(y_test,predictions))
```

Decision Tree

Building the model using DecisionTree

```
from sklearn.tree import DecisionTreeClassifier dtree =
DecisionTreeClassifier() dtree.fit(X_train, y_train)
```

Now we will be making the predictions on the **testing data** directly as it is of more importance.

Getting the accuracy score for Decision Tree

```
from  sklearn  import  metrics  predictions=  dtree.predict(X_test)
print("AccuracyScore =",
format(metrics.accuracy_score(y_test,predictions)))
```

Output:

```
Accuracy Score = 0.7322834645669292
```

Classification report and confusion matrix of the decision tree model

```
from  sklearn.metrics
importclassification_report,
confusion_matrix
print(confusion_matrix(y_test, predictions))
print(classification_report(y_test,predictions))
```

XgBoost classifier

Building model using XGBoost

```
from xgboost import XGBClassifier xgb_model = XGBClassifier(gamma=0)
xgb_model.fit(X_train, y_train)
```

Now we will be making the predictions on the **testing data** directly as it is of more importance.

Getting the accuracy score for the XgBoost classifier

```
from sklearn import metrics xgb_pred =
       xgb_model.predict(X_test)
print("AccuracyScore =",format(metrics.accuracy_score(y_test,
xgb_pred)))
```

Output:

```
Accuracy Score = 0.7401574803149606
```

Classification report and confusion matrix of the XgBoost classifier

```
from sklearn.metrics import classification_report,
confusion_matrix print(confusion_matrix(y_test, xgb_pred))
print(classification_report(y_test,xgb_pred))
```

Support Vector Machine (SVM)

Building the model using Support Vector Machine (SVM)

```
from sklearn.svm import SVC svc_model = SVC()
svc_model.fit(X_train, y_train)
```

Prediction from support vector machine model on the testing data

```
svc_pred = svc_model.predict(X_test)
```

Accuracy score for SVM

```
from sklearn import metrics print("Accuracy Score =",
format(metrics.accuracy_score(y_test, svc_pred)))
```

Output:

```
Accuracy Score = 0.7401574803149606
```

Classification report and confusion matrix of the SVM classifier

```
from sklearn.metrics import classification_report,
confusion_matrix
print(confusion_matrix(y_test, svc_pred))
print(classification_report(y_test,svc_pred))
```

The Conclusion from Model Building

Therefore Random forest is the best model for this prediction since it has an accuracy_score of 0.76

Feature Importance

Knowing about the feature importance is quite necessary as it shows that how much weightage eachfeature provides in the model building phase.

Getting feature importances

```
rfc.feature_importances_
```

Output:

```
array([0.07684946, 0.25643635, 0.08952599, 0.08437176, 0.08552636,
0.14911634, 0.11751284, 0.1406609 ])
```

From the above output, it is not much clear that which feature is important for that reason **we will now make a visualization of the same.**

Plotting feature importances

```
(pd.Series(rfc.feature_importances_,
index=X.columns).plot(kind='barh'))
```

Here from the above graph, it is clearly visible that **Glucose as a feature is the most important in this dataset.**

Saving Model – Random Forest

```
import pickle
```

# Firstly we will be using the dump() function to save the model using pickle `saved_model = pickle.dumps(rfc)`

# Then we will be loading that saved model `rfc_from_pickle = pickle.loads(saved_model)`

# lastly, after loading that model we will use this to make predictions `rfc_from_pickle.predict(X_test)`

Now for the last time, I'll be looking at the head and tail of the dataset so that we can take any random set of features from both the head and tail of the data to test that if our model is good enough to give the right prediction.

```
diabetes_df.head()
diabetes_df.tail()
```

Putting data points in the model will either return 0 or 1 i.e. person suffering from diabetes or not.

```
rfc.predict([[0,137,40,35,168,43.1,2.228,33]]) #4th patient
```

Output:

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

Another one

```
rfc.predict([[10,101,76,48,180,32.9,0.171,63]]) # 763 th patient
```

Output:

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

Conclusion

After using all these patient records, we are able to build a machine learning model (random forest – best one) to accurately predict whether or not the patients in the dataset have diabetes or not along with that we were able to draw some insights from the data via data analysis and visualization.