AI BASED DIABETES PREDICTION SYSTEM -DEVELOPMENT PART 2

Problem Statement:

There is a pressing need for an AI-based diabetes prediction system to address the growing global burden of diabetes. Despite advancements in healthcare, diabetes remains a major public health concern, with millions of people at risk of developing the condition. Current diagnostic methods are often reactive and lack precision, leading to delayed interventions and increased healthcare costs. An AI-based prediction system is required to accurately identify individuals at risk of diabetes, allowing for early interventions, personalized care, and improved healthcare resource allocation. Such a system should leverage data from various sources, including medical records, lifestyle factors, and genetic information, to provide accurate and timely predictions, ultimately reducing the prevalence and impact of diabetes on individuals and healthcare systems.

Overview :

1.Data gathering and analysis:

The dataset is originally collected and circulated by “National Institute of Diabetes and Digestive and Kidney Diseases” which is available at Kaggle in the name of Pima Indians Diabetes Database. The main objective is to predict whether a patient has diabetics or not, based on the diagnostic measurements gathered in the database. All patients belong to the Pima Indian heritage, and are females of ages 21 and above.

We’ll start with importing Pandas and NumPy into our python environment and loading a .csv dataset into a pandas dataframe named df. To see the first five records from the dataset we use pandas df.head() function. We’ll also use seaborn and matplotlib for visualization. Each and every examples shown in this article are verified on a Jupyter notebook.

In[1]:

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

In[2]:
#importing dataset
df = pd.read_csv('../input/pima-indians-diabetes-database/diabetes.csv')
df.head()

Out[2]:
Pregnancies  Glucose BloodPressure  SkinThickness  Insulin  BMI DiabetesPedigreeFunction Age  Outcome
0  6  148 72  35  0  33.60.627  50  1
1  1  85  66  29  0  26.60.351  31  0
2  8  183 64  0  0  23.30.672  32  1
3  1  89  66  23  94  28.10.167  21  0
4  0  137 40  35  168 43.12.288  33  1
```

The dataset contains 768 observable with eight feature variables and one target variable. Before starting to analyze the data and draw any conclusions, it is essential to

understand the presence of missing values in any dataset. To do so the simplest way is to use df.info() function which will provide us the column names with the number of non-null values in each column.

In[3]:

```
df.dtypes
```

Out[3]:

```
Pregnancies                 int64
Glucose                     int64
BloodPressure               int64
SkinThickness               int64
Insulin                     int64
BMI                       float64
DiabetesPedigreeFunction    float64
Age                         int64
Outcome                     int64
dtype: object
```

In[4]:

```
df.info()
```

Out[4]:

```
<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
```

According to the output we don't observe any null values. But there are five features such as Glucose, BloodPressure, SkinThickness, Insulin and BMI contains zero values which is not possible in the medical history. We will consider these values as missing values.We'll replace the zero values to NaN and then impute them with their mean value.

In[5]:

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

In[6]:

```
# making a list of columns with total number of missing values
print('Column'+ '\t\t\t\t Total missing Values'+'\t\t\t\t % of missing values')
#print("\n")
for i in df.columns:
print(f"{i:
<50}{df[i].isnull().sum():<30}{((df[i].isnull().sum())*100)/df.shape[0]: .2f}")
```

Column	Total missing Values	% of missing values
Pregnancies	0	0.00
Glucose	5	0.65
BloodPressure	35	4.56
SkinThickness	227	29.56
Insulin	374	48.70
BMI	11	1.43
DiabetesPedigreeFunction	0	0.00
Age	0	0.00
Outcome	0	0.00

In[7]

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

In[8]

```
# making a list of columns with total number of missing
values
print('Column'+ '\t\t\t\t Total missing Values'+'\t\t\t\t % of
missing values')
#print("\n")
for i in df.columns:
    print(f"{i:
<50}{df[i].isnull().sum():<30}{((df[i].isnull().sum())*100)/df.s
hape[0]: .2f}")
```

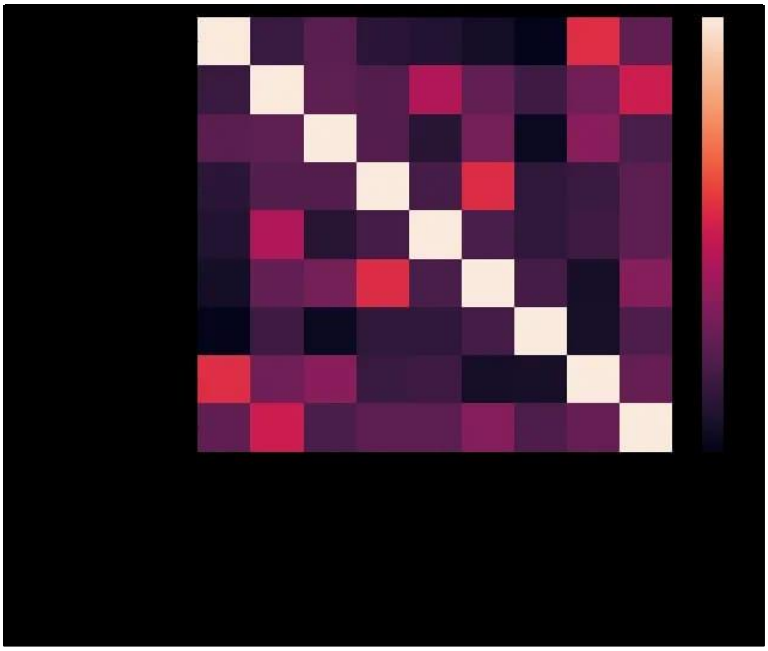
Out[8]:

Column	Total missing Values	% of missing values
Pregnancies	0	0.00
Glucose	0	0.00

BloodPressure	0	0.00
SkinThickness	0	0.00
Insulin	0	0.00
BMI	0	0.00
DiabetesPedigreeFunction	0	0.00
Age	0	0.00
Outcome	0	0.00

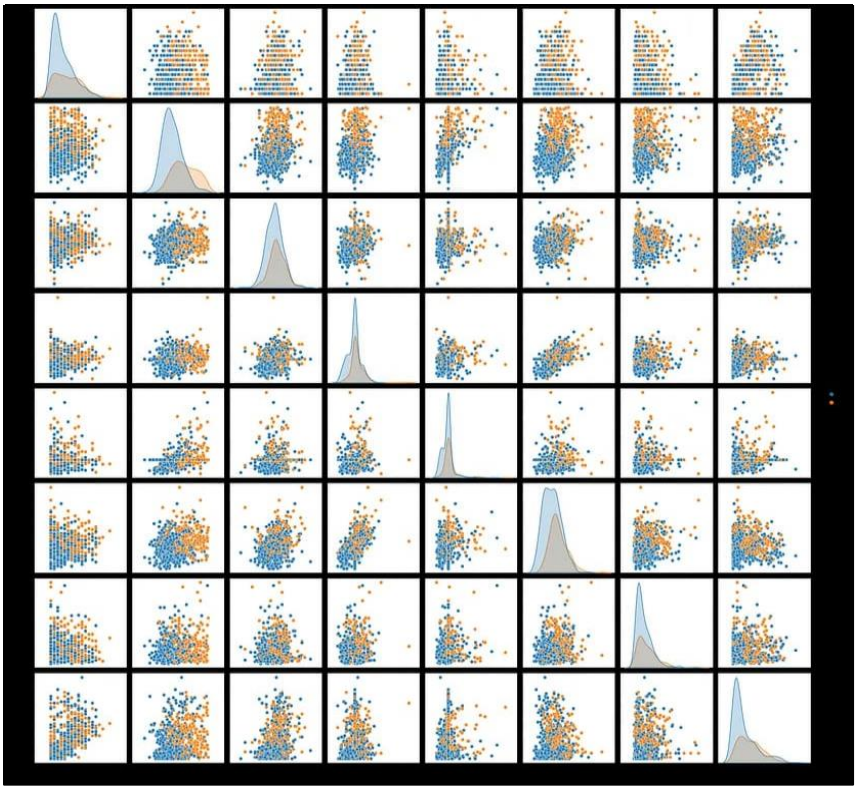
2.Data Visualization

The correlation between each columns are visualized using heatmap. From the output, the lighter colors indicate more correlation. We notice the correlation between pairs of features, like age and pregnancies, or BMI and skin thickness, etc.



To plot pairwise relationships in a dataset we use sns.pairplot() function and labeled the datapoints based on the target variable classes..

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

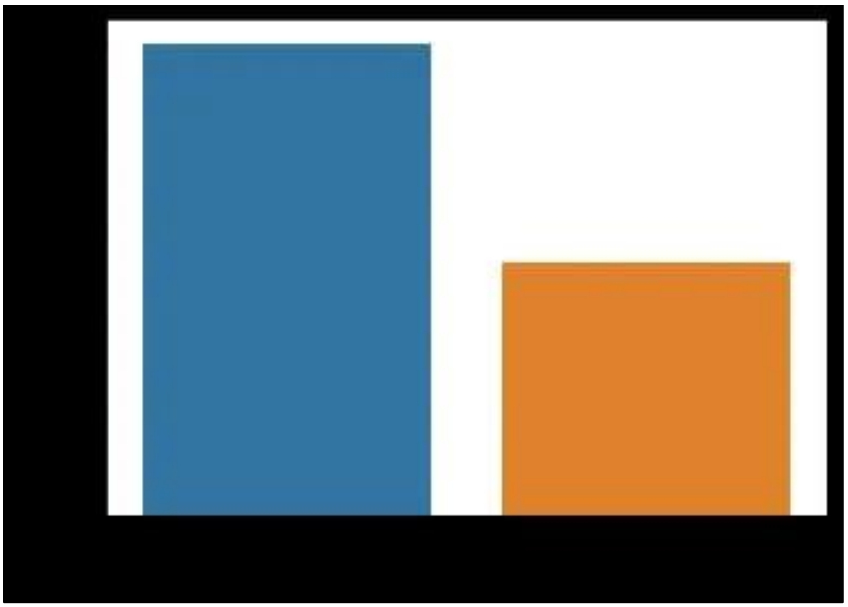


3.Classification

We need to separate the dataset into features and target variables. Following the popular convention, we call the dataframe with feature variables as X and the one with target variable as y.

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

Let’s visualize the target variable and have a look at how many people in the dataset are diabetic and how many are not.



Using sklearn’s train_test_split, we split the feature (X) and target (y) dataframes into a training set (80%) and testing set (20%). Training set is used for building classification model and testing set is used for evaluating the performance of the model.

```
from sklearn.metrics import confusion_matrix
mat = confusion_matrix(y_test, y_pred)
plt.figure(figsize=(7, 5))
sns.heatmap(mat, annot=True)
```

Before implementing classification algorithm, we scale the feature variables of our dataset using sklearn's StandardScaler() function. This function standardize the features by removing the mean and scaling to unit variance.

```
from sklearn.preprocessing import StandardScaler
scaling_x=StandardScaler()
X_train=scaling_x.fit_transform(X_train)
X_test=scaling_x.transform(X_test)
```

4.Training and Evaluating Model

We'll be using a machine simple learning model called Random Forest Classifier. We train the model with standard parameters using the training dataset. The trained model is saved as "rcf". We evaluate the performance of our model using test dataset. Our model has a classification accuracy of 80.5%.

```
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier()
rfc.fit(X_train, y_train)
rfc.predict(X_test)
rfc.score(X_test, y_test)
```

Output:

0.8051948051948052

5.Plotting decision boundaries

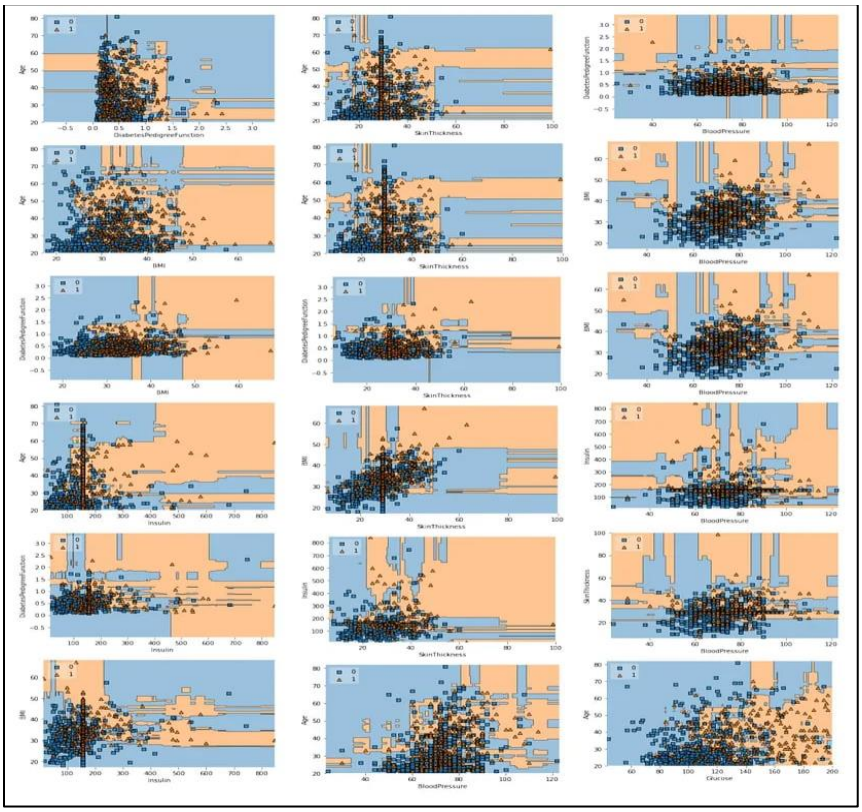
A decision boundaries plot works well only with two features. Our data has eight features, but we still can plot decision boundaries by choosing which features to use. We plot decision boundary for each two possible features and see how well the model classifies the patients.

```
from mlxtend.plotting import plot_decision_regions
def classify_with_rfc(X,Y):
    x = df[[X,Y]].values
    y = df['Outcome'].astype(int).values
    rfc = RandomForestClassifier()
    rfc.fit(x,y)
    # Plotting decision region
    plot_decision_regions(x, y, clf=rfc, legend=2)
    # Adding axes annotations
    plt.xlabel(X)
    plt.ylabel(Y)
    plt.show()
```

```
feat = ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin','BMI', 'DiabetesPedigreeFunction', 'Age']
```

```
size = len(feat)
for i in range(0,size):
    for j in range(i+1,size):
        classify_with_rfc(feat[i],feat[j])
```

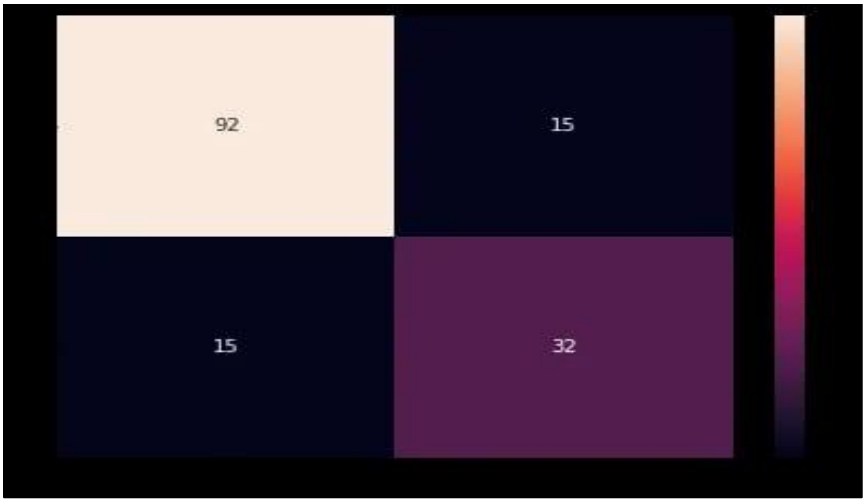
NB: 0 — Non Diabetic and 1 — Diabetic



The distributions shows our model classifies the patients really well. For a detailed evaluation of our model, we look at the confusion matrix.

```
from sklearn.metrics import confusion_matrix
mat = confusion_matrix(y_test, y_pred)
plt.figure(figsize=(7, 5))
```

```
sns.heatmap(mat, annot=True)
```




```
from sklearn.metrics import classification_report
target_names = ['Diabetes', 'Normal']
print(classification_report(y_test, y_pred,
target_names=target_names))
```

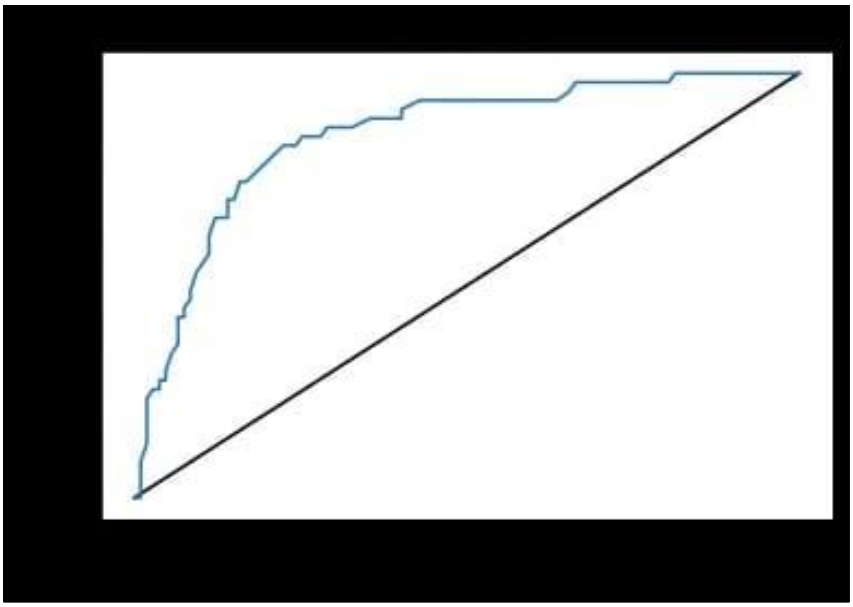
Output:

	precision	recall	f1-score	support
Diabetes	0.86	0.86	0.86	107
Normal	0.68	0.68	0.68	47
accuracy			0.81	154
macro avg	0.77	0.77	0.77	154
weighted avg	0.81	0.81	0.81	154

6.ROC curve

```
from sklearn.metrics import roc_curve
y_pred_proba = rfc.predict_proba(X_test)[:,1]
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba
plt.plot([0,1],[0,1],'k-')
plt.plot(fpr,tpr, label='Knn')
plt.xlabel('fpr')
plt.ylabel('tpr')
plt.title('ROC curve')
plt.show()
```

Output:



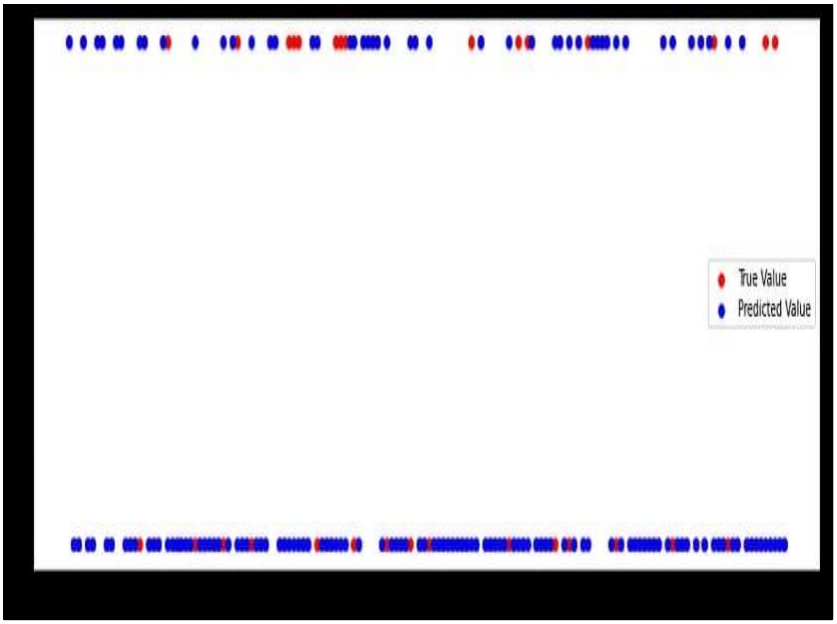
```
from sklearn.metrics import roc_auc_score
roc_auc_score(y_test,y_pred_proba)
```

Output:

0.8535494134022669

For our model, the Area Under the Receiver Operating Characteristic Curve (ROC AUC) score is 85%. This implies that the classification model is good enough to detect the diabetic patient.

True Value vs Predicted Value:



5.Conclusion

We built a machine learning-based classifier that predicts if a patient is diabetic or not, based on the information provided in the database.

While building this predictor, we learned about common preprocessing steps such as feature scaling and imputing missing values.

We implemented Random forest algorithm, evaluated the performance using the accuracy score, comparing the performance between train and test data. You can also tune the parameters and try improving the accuracy score, AUC.