

A-I BASED DIABETES PREDICTION SYSTEM



Phase4:

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.

Medical diagnosis is a very essential and critical aspect for healthcare professionals. In particular, AI classification of diabetics is very complex. An early identification of diabetes is much important in controlling diabetes. A patient has to go through several tests and later it is very difficult for the professionals to keep track of multiple factors at the time of diagnosis process which can lead to inaccurate results which makes the detection very challenging. Due to most advance technologies especially machine learning algorithms are very beneficial for the fast and accurate prediction of the disease in the healthcare industries.

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	33.6	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	0.288	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.s
hape[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 Total missing Values'+ '\t\t\t % of missing values')
```

```
#print("\n")
```

```
for i in df.columns:
```

```
    print(f"{i:
```

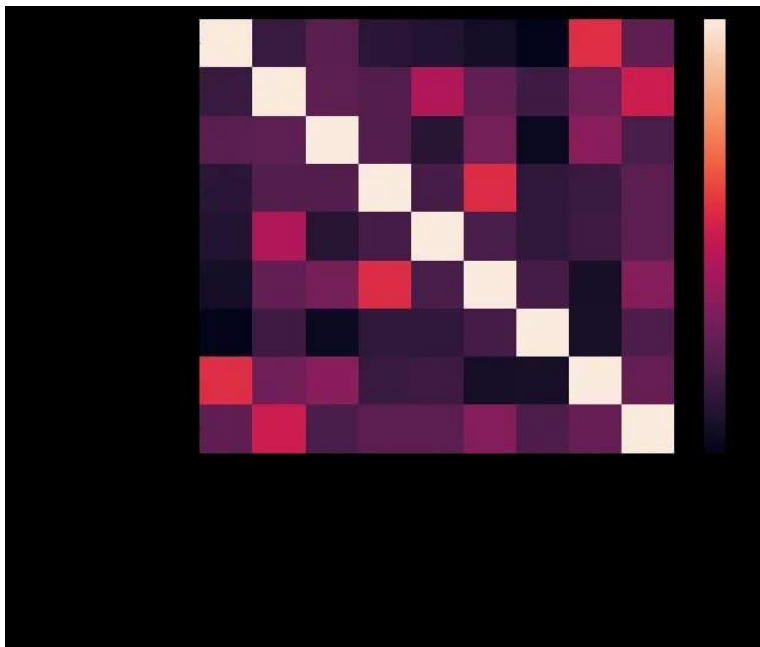
```
<50}{df[i].isnull().sum():<30}{((df[i].isnull().sum())*100)/df.shape[0]: .2f}")
```

```
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

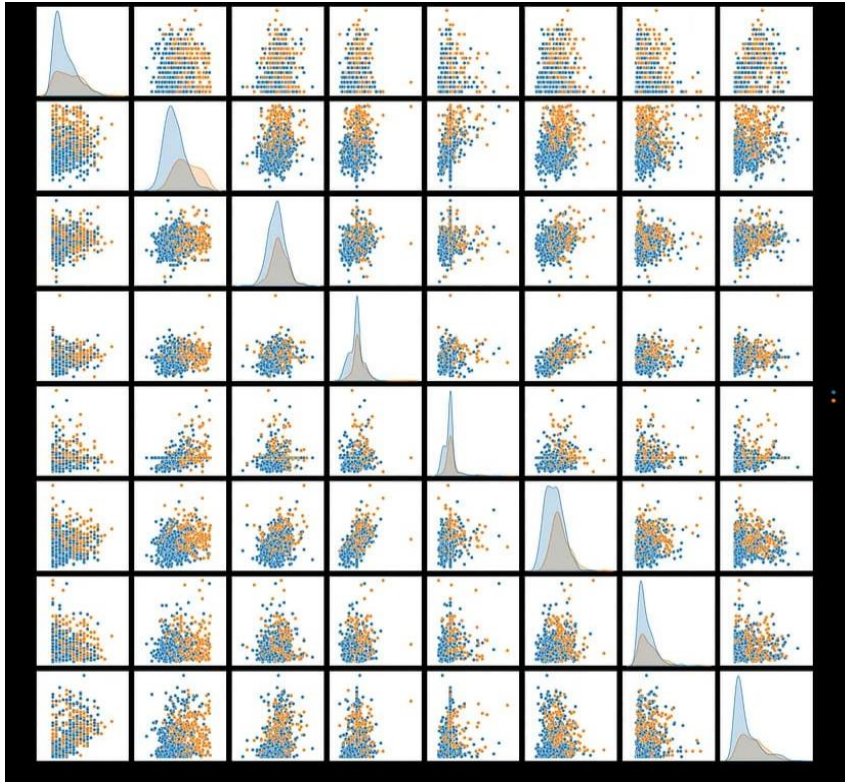
2.Data Visualization

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')
```

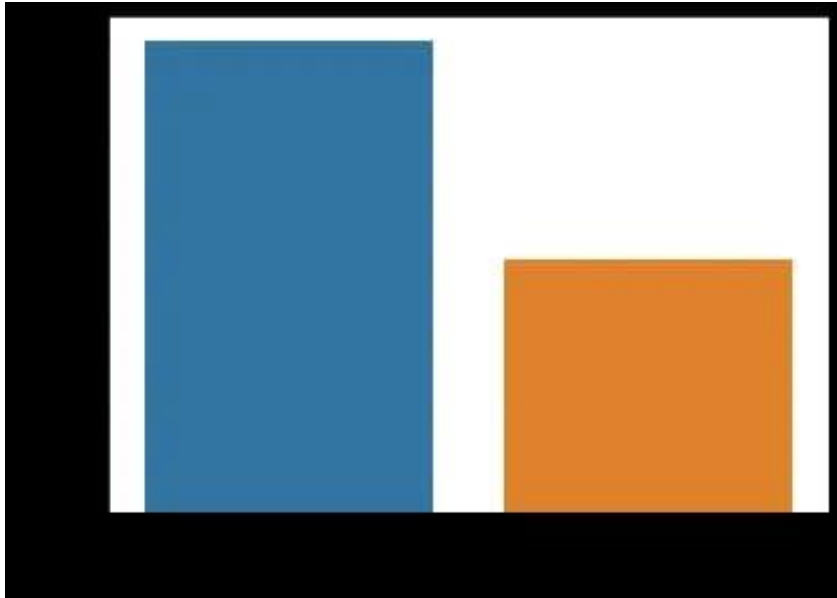


3. Classification

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()
```

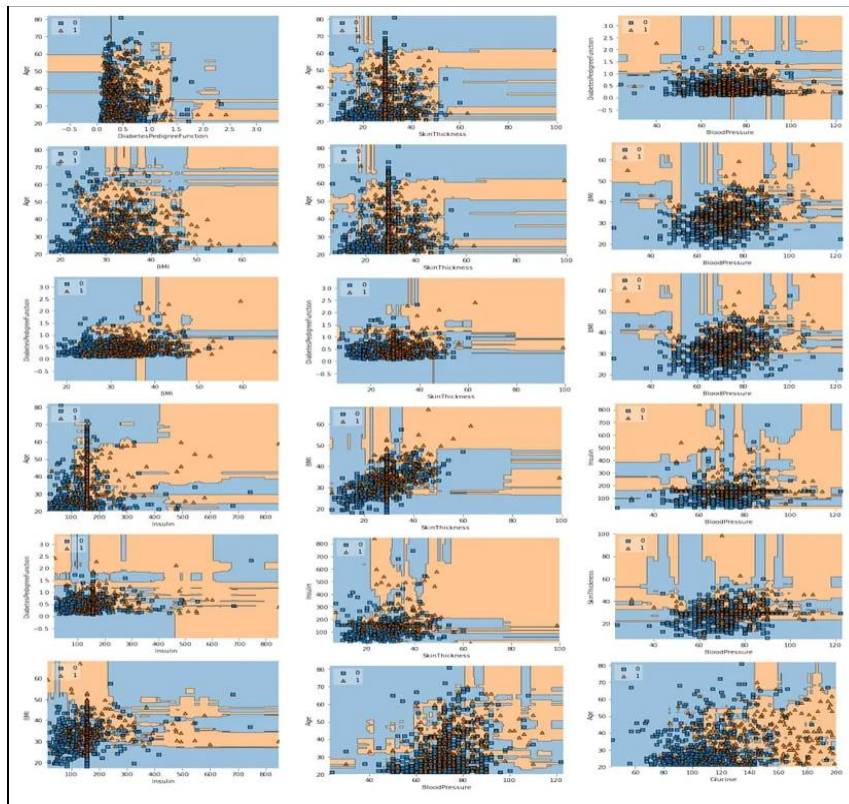
```
feat = ['Pregnancies', 'Glucose', 'BloodPressure',  
'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction',  
'Age']
```

```

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

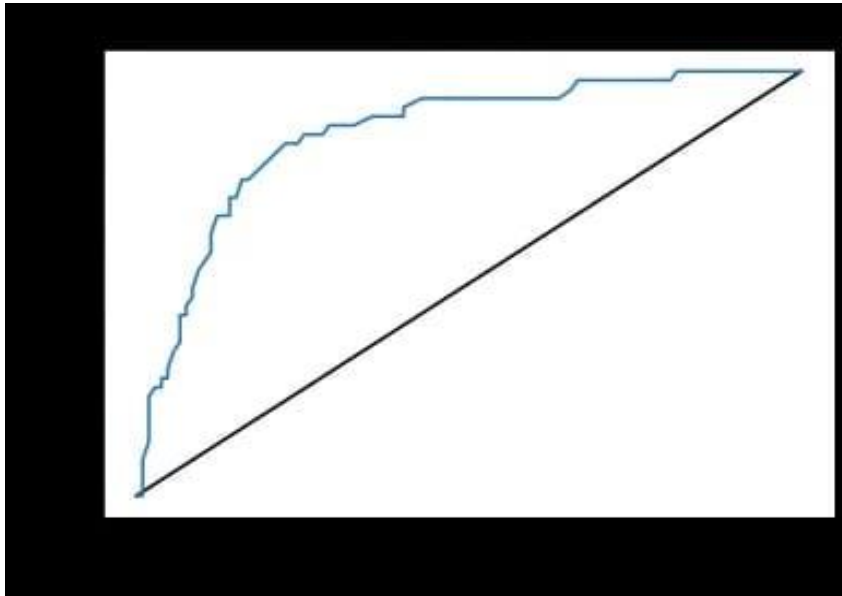
Output:

	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()
```

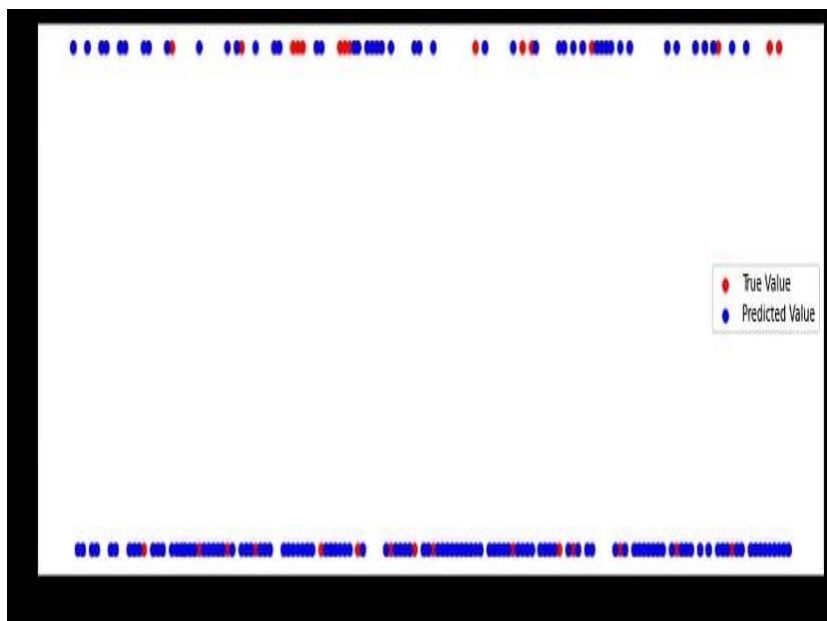
Output:



```
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.