Diabetes Prediction using Supervised Learning Techniques

By
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Introduction

This project applied supervised learning techniques to a real-world "Diabetes" dataset from the National Institute of Diabetes and Digestive and Kidney Diseases,
and use data visualization tools to communicate the insights gained from the analysis.
The objective of the dataset is to diagnostically predict whether a patient has diabetes based on certain diagnostic measurements included in the dataset.

Project Goals

The ultimate goal of the project is to gain insights from the data sets and communicate these insights to stakeholders using appropriate visualizations and metrics to make informed decisions based on the business questions asked.

Process

A **Importing the data**

Kaggle_Diabetes data set

B **Exploratory Data Analysis**

Visualization to understand data

C **Preprocessing & Feature Engineering**

Handling missing values,outliers, scaling etc

D **Training ML model**

Evaluation metrics (accuracy, precision, recall, F1-score, and ROC-AUC)

E **Model Tuning**

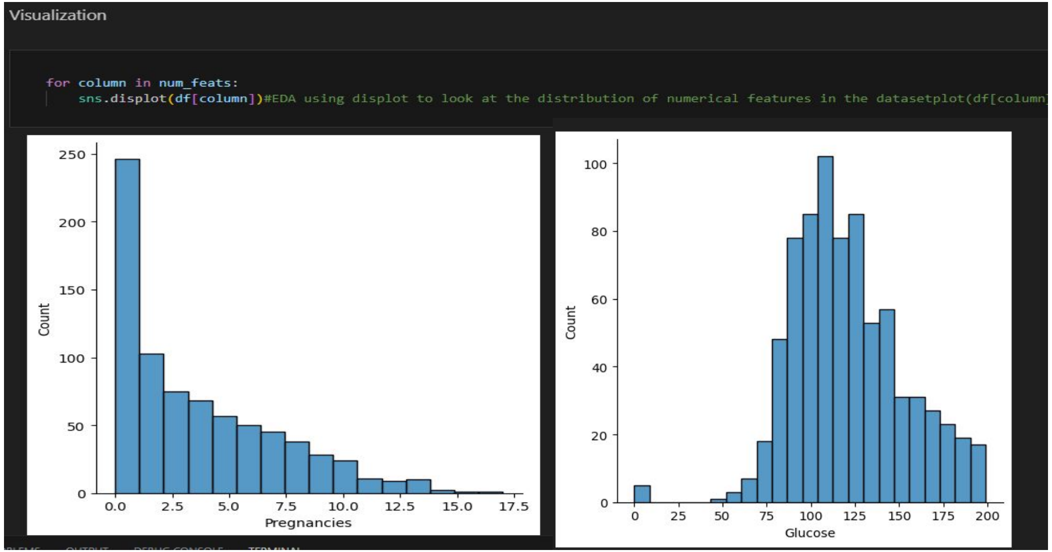
Hyperparameter Tuning & Cross validation

EDA QUESTIONS ANSWERED.

Are there any missing values in the dataset?

- How are the predictor variables related to the outcome variable?
- What is the correlation between the predictor variables?
- What is the distribution of each predictor variable?
- Are there any outliers in the predictor variables?
- How are the predictor variables related to each other?
- Is there any interaction effect between the predictor variables?
- What is the average age of the individuals in the dataset?
- What is the average glucose level for individuals with diabetes and without diabetes?
- What is the average BMI for individuals with diabetes and without diabetes?
- How does the distribution of the predictor variables differ for individuals with diabetes and without diabetes?
- Are there any differences in the predictor variables between males and females (if gender information is available)?

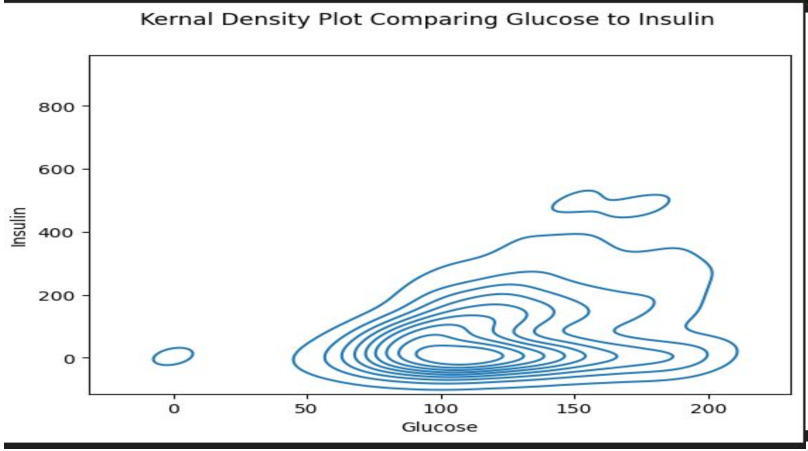
Exploratory Data Analysis Visualization



Displot showing distribution of pregnancy and Glucose variables..

Visualizations showing relationship between Glucose level and Insulin.

```python
import matplotlib.pyplot as plt
sns.kdeplot(data=df,
            x='Glucose',
            y='Insulin')
plt.suptitle("Kernal Density Plot Comparing Glucose to Insulin")
plt.show()
```




```python
import seaborn as sns
import matplotlib.pyplot as plt
sns.histplot(data=df,
             x="Glucose",
             y="Insulin")

plt.suptitle("2 Variable Histogram = Density Plot")

plt.show()
```

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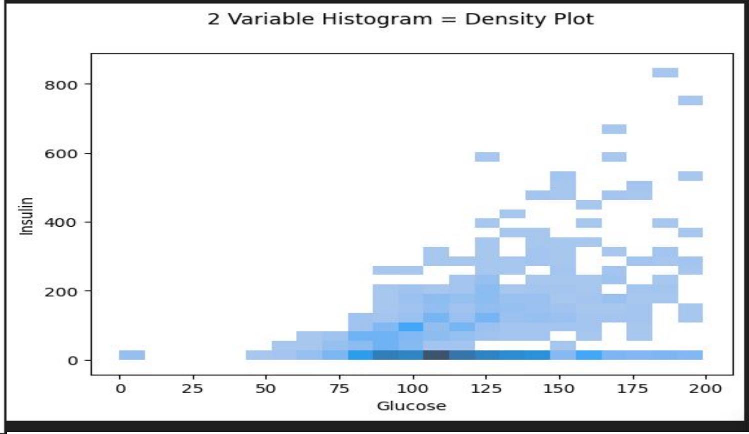
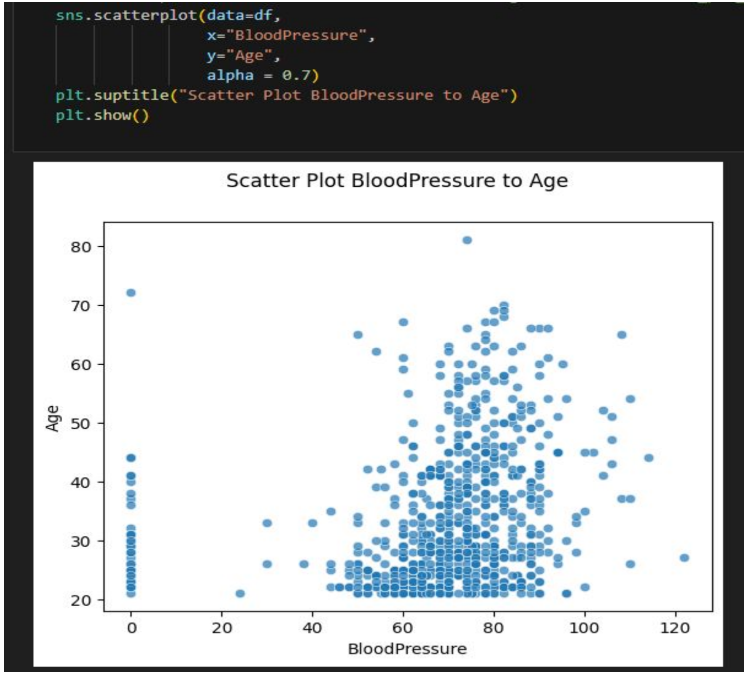
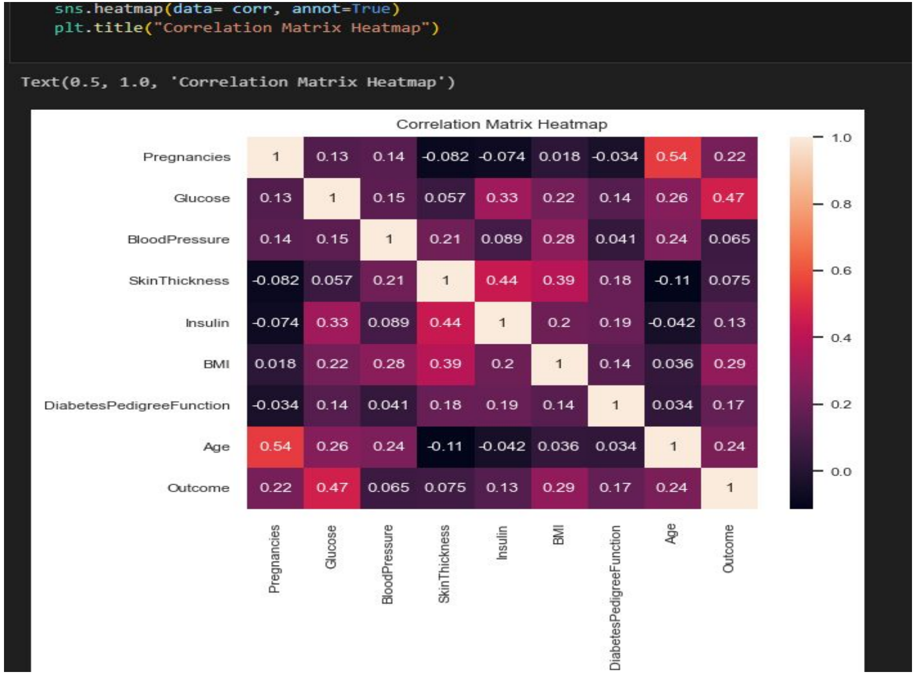


Kernel Density plot   and Histogram Density plot comparing Glucose to insulin showing outliers.

Scattered plot and Correlation matrix map showing correlation between different variables.





Predictor variables Average grouped by Outcome showing individuals with or without Diabetes.

```python
import pandas as pd
# define the columns to be grouped and calculated
columns_to_groupby = ['Outcome']
columns_to_calculate = ['SkinThickness', 'Insulin', 'Glucose', 'BloodPressure', 'BMI', 'DiabetesPedigreeFunction',  'Age']

# Calculate the average (mean) values for the specified columns for each group
Predictorvariables_average_results = df.groupby(columns_to_groupby)[columns_to_calculate].mean().reset_index()

print(Predictorvariables_average_results)
```

```
   Outcome  SkinThickness     Insulin     Glucose  BloodPressure        BMI  \
0        0      19.664000   68.792000  109.980000      68.184000  30.304200
1        1      22.164179  100.335821  141.257463      70.824627  35.142537

   DiabetesPedigreeFunction        Age
0                  0.429734  31.190000
1                  0.550500  37.067164
```

From this column calculation grouping by Outcome,Average glucose level of individuals without diabetes is 109.98 while the average glucose level with diabetes is 141.257463.
Average BMI for individuals without Diabetes is 30.30while Average BMI of individuals with Diabetes is 35.14

Distribution statistics showing statistical significant correlation between the feature variables

```
#Distribution statistics showing if there is a statistical significant correlation
# Calculate the correlation matrix
corr = df.corr()
corr
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.017683	-0.033523	0.544341	0.221898
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	0.137337	0.263514	0.466581
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	0.041265	0.239528	0.065068
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	0.183928	-0.113970	0.074752
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.197859	0.185071	-0.042163	0.130548
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.000000	0.140647	0.036242	0.292695
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.140647	1.000000	0.033561	0.173844
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.036242	0.033561	1.000000	0.238356
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.292695	0.173844	0.238356	1.000000

Summary statistics of each variable showing anomalies and potential outliers

```
#The summary statistics of each of the variables, we can  identify anomalies and potential outliers.
df.describe()
```

	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

E.g BloodPressure cannot be zero except the patient is dead, same with Skin Thickness, BMI where mininum value is zero

This summary statistics shows the average age of the individuals in the dataset as
33 years,Overall Average glucose level as 120.89, Average BMI as 31.99.

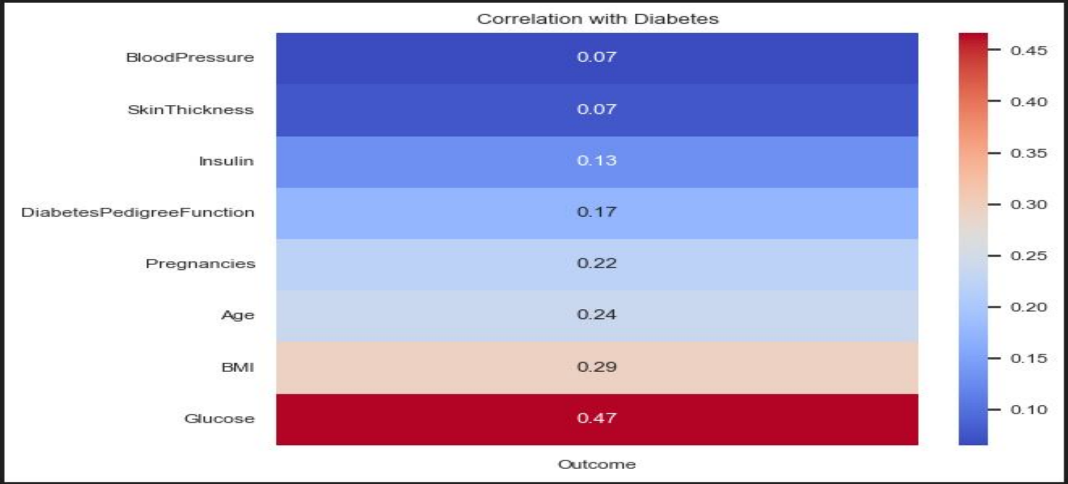
This statistics also show some anomalies eg Blood Pressure of a living being cannot be zero, same with Skin Thickness, BMI,Glucose level. This indicates outliers.

Various feature variable correlation indicating Diabetes in target variable(Outcome).

```python
corr = df.corr()
target_corr = corr['Outcome'].drop('Outcome')

target_corr_sorted = target_corr.sort_values(ascending=True)

sns.set(font_scale=0.8)
sns.set_style("white")
sns.set_palette("PuBuGn_d")
sns.heatmap(target_corr_sorted.to_frame(), cmap="coolwarm", annot=True, fmt='.2f')
plt.title('Correlation with Diabetes')
plt.show()
```



With a correlation of 0.47, Glucose is the most strongly correlated feature with the outcome. This suggests that higher glucose levels could be a significant indicator of diabetes.

BMI can also be an important factor in having diabetes.

Results showing no missing values in the dataset.

```
# check missing values in variables

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

✓ 0.0s

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

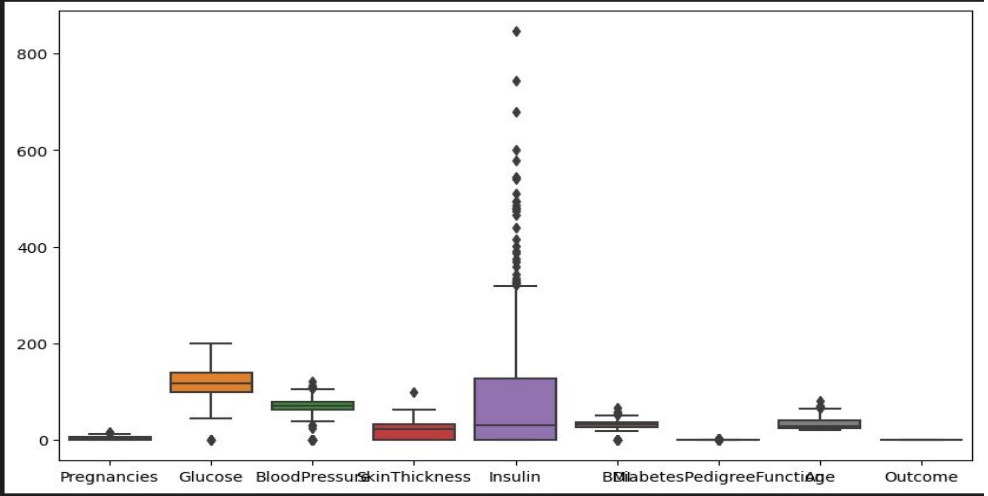
Answer: There are no missing values in the dataset.

There are no missing values in the dataset

Handling outliers in preprocessing and feature engineering

```
# Detecting outliers
plt.figure(figsize=(10, 6))
sns.boxplot(df)
```

<Axes: >



Insulin has many outliers

It can bee seen that Insulin has many outliers more than other feature variables, this was handled by transforming using log transformation.

```
cols_with_outliers = ['Glucose','Insulin', 'SkinThickness','BloodPressure', 'BMI', 'Age']
df[cols_with_outliers] = df[cols_with_outliers].apply(lambda x: np.log1p(x))
```

Logistic regression model showing evaluation metrics results

```python
#  Evaluate the model using various metrics
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)
f1 = f1_score(y_test, y_pred)
roc_auc = roc_auc_score(y_test, y_pred)
confusion_mat = confusion_matrix(y_test, y_pred)
classification_rep = classification_report(y_test, y_pred)

# Print the evaluation metrics
print("Evaluation Metrics:")
print(f"Accuracy: {accuracy}")
print(f"Precision: {precision}")
print(f"Recall: {recall}")
print(f"F1 Score: {f1}")
print(f"ROC-AUC: {roc_auc}")
print(f"Confusion Matrix:\n{confusion_mat}")
print(f"classification_report: {classification_rep}")
```

✓ 0.0s

```
Evaluation Metrics:
Accuracy: 0.7272727272727273
Precision: 0.6164383561643836
Recall: 0.5625
F1 Score: 0.5882352941176471
ROC-AUC: 0.6885347682119204
Confusion Matrix:
[[123  28]
 [ 35  45]]
```

```
Evaluation Metrics:
Accuracy: 0.7272727272727273
Precision: 0.6164383561643836
Recall: 0.5625
F1 Score: 0.5882352941176471
ROC-AUC: 0.6885347682119204
Confusion Matrix:
[[123  28]
 [ 35  45]]
classification_report:               precision    recall  f1-score   support

           0       0.78      0.81      0.80       151
           1       0.62      0.56      0.59        80

    accuracy                           0.73       231
   macro avg       0.70      0.69      0.69       231
weighted avg       0.72      0.73      0.72       231
```

Random Forest Classifier model with model Evaluation metrics Results

```python
#  RandomForestClassifier model evaluation metrics
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)
f1 = f1_score(y_test, y_pred)
roc_auc = roc_auc_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
classification_rep = classification_report(y_test, y_pred)

print('Model accuracy score with 10 decision-trees : {0:0.4f}'. format(accuracy_score(y_test, y_pred)))
print("Precision:", precision)
print("Recall:", recall)
print("F1-score:", f1)
print("ROC-AUC:", roc_auc)
print("\nConfusion Matrix:")
print(conf_matrix)
print("\nClassification Report:")
print(classification_rep)
```

✓ 0.1s

```
Model accuracy score with 10 decision-trees : 0.7316
Precision: 0.6097560975609756
Recall: 0.625
F1-score: 0.6172839506172839
ROC-AUC: 0.7065397350993378

Confusion Matrix:
[[119  32]
 [ 30  50]]
```


```
Model accuracy score with 10 decision-trees : 0.7316
Precision: 0.6097560975609756
Recall: 0.625
F1-score: 0.6172839506172839
ROC-AUC: 0.7065397350993378

Confusion Matrix:
[[119  32]
 [ 30  50]]
```


```
Classification Report:
              precision    recall  f1-score   support

           0       0.80      0.79      0.79       151
           1       0.61      0.62      0.62        80

    accuracy                           0.73       231
   macro avg       0.70      0.71      0.71       231
weighted avg       0.73      0.73      0.73       231
```

Result explanation

Based on these metrics, we can Random Forest Classifier model has a slightly higher accuracy score (0.7316), compared to Logistic Regression model with .07272 accuracy.The Random Forest Classifier has a higher ROC-AUC score (0.7065) compared to the Logistic Regression model (0.6885). Additionally, the Random Forest Classifier has slightly higher F1 score and recall values.

Overall, the Random Forest Classifier appears to perform slightly better than the Logistic Regression model based on these evaluation metrics.

model tuning and cross-validation, to improve and optimize the model's performance.

```python
#Model performance evaluation matrics
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)
f1 = f1_score(y_test, y_pred)
roc_auc = roc_auc_score(y_test, y_pred)

# Print the evaluation metrics
print("Best Hyperparameters:", best_params)
print("Accuracy:", accuracy)
print("Precision:", precision)
print("Recall:", recall)
print("F1-score:", f1)
print("ROC-AUC:", roc_auc)
```

6] ✓ 0.0s

```
Best Hyperparameters: {'max_depth': None, 'min_samples_leaf': 1, 'min_samples_split': 10, 'n_estimators': 50}
Accuracy: 0.7402597402597403
Precision: 0.6190476190476191
Recall: 0.65
F1-score: 0.6341463414634146
ROC-AUC: 0.7190397350993377
```

This was done to improve and optimize the RandomForestClassifier
model's performance. By Hyperparameter Tuning the number of estimators to 50.
Evaluation metrics accuracy Increased.

Accuracy: 0.74025974
Precision: 0.61904761
Recall: 0.65
F1-score: 0.63414634
ROC-AUC: 0.71903973
Mean Cross-Validation Accuracy: 0.7820353
Mean cv precision:072295

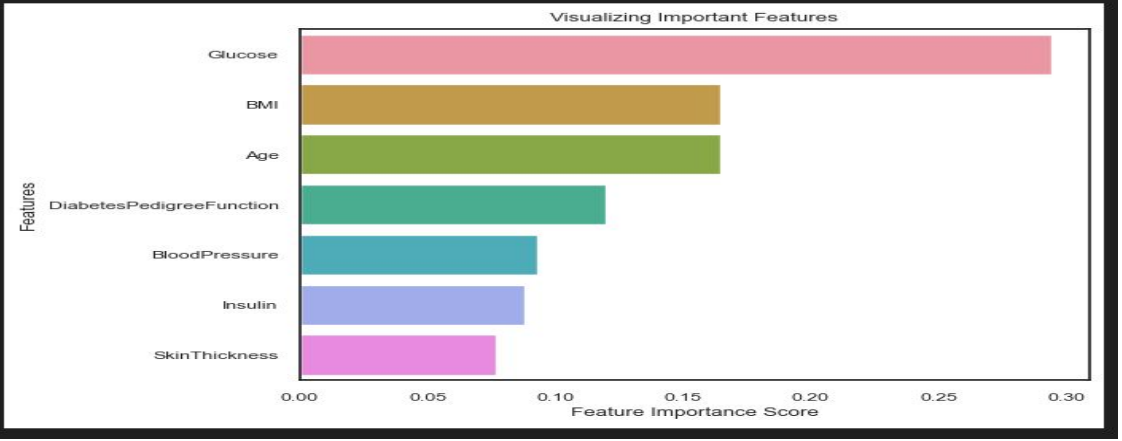
Feature scores showing the order of Importance or the diagnostic variables after tuning

```
sns.barplot(x=feature_scores, y=feature_scores.index)

# Add labels to the graph
plt.xlabel('Feature Importance Score')
plt.ylabel('Features')

# Add title to the graph
plt.title("Visualizing Important Features")

# Visualize the graph
plt.show()
```



It can be seen that Glucose level is the most important feature in this diagnostic model while skin Thickness is the least feature affecting the accuracy of this model.

conclusion

From the machine learning developed, and exploratory data analysis conducted,the following were observed.

- Random Forest Classifier appear to have a better accuracy than Logistic regression model in predicting whether a patient have Diabetes or not.
- Cross validation gave more robust estimate of the mode performances with increased accuracy as 0.782035306 and precision of 0.72297510.
- Glucose level is the most important feature in predicting whether a patient have Diabetes or not.
- The least important feature that doesn’t really affect the prediction is Skin thickness.

Challenges

- Time constraints to explore available data using other models

THANK YOU