task-2-meriskill

June 20, 2024

1 Diabetes Prediction Using Machine Learning with Python

1.0.1 Objective:

Develop a machine learning model that can predict whether a patient has diabetes or not based on various medical parameters such as blood glucose levels, insulin levels, BMI, and more.

1.0.2 Key Technologies:

Python: Used for data preprocessing, feature selection, model implementation, and deployment.

Streamlit: Used for creating a user-friendly web interface for diabetes prediction.

Scikit-learn: Used for implementing machine learning algorithms.

Pandas: Used for data manipulation and analysis.

Matplotlib and Seaborn: Used for data visualization.

1.0.3 Benefits:

Early Detection: The model can help detect diabetes at an early stage, enabling timely interventions and improving patient outcomes.

Personalized Medicine: The model can provide personalized predictions based on individual medical parameters, enabling more targeted treatment plans.

Cost Savings: The model can reduce healthcare costs by identifying high-risk patients and enabling preventive measures.

1.0.4 Summary of the dataset:

This dataset seems to contain information related to diabetes risk. The variables include :

*** Pregnancies : The number of pregnencies an individual has had.**

*** Glucose : Glucose levels in the blood.**

*** BloodPressure : Blood pressure readings.**

*** SkinThickness : Thickness of a skinfold at a certain location on the body.**

*** Insulin : Levels of insulin in the blood.**

*** BMI (BODY Mass Index) : A measure of body fat based on height and weight.**

*** DiabetesPredictionFunction: A Function that scores the likelihood of diabetes based on family history.**

*** Age: Age of the individuals**

*** Outcome: abinary variable indicating the presence (1) or absence(0) of a diabetes outcome.**

[2]:
```
#Importing the required Libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

[3]:
```
#Load the Dataset
dia=pd.read_csv("D:\chrome (downloads)\Project 2 MeriSKILL\diabetes.csv")
```

[4]:
```
dia
```

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

     DiabetesPedigreeFunction  Age  Outcome
0                       0.627   50        1
1                       0.351   31        0
2                       0.672   32        1
```

```
3                       0.167   21        0
4                       2.288   33        1
..                        …   …       …
763                     0.171   63        0
764                     0.340   27        0
765                     0.245   30        0
766                     0.349   47        1
767                     0.315   23        0

[768 rows x 9 columns]
```

[18]:
```
pip install matplotlib
```

```
Requirement already satisfied: matplotlib in c:\users\venky\anaconda3\lib\site-
packages (3.8.0)
Requirement already satisfied: contourpy>=1.0.1 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (1.2.0)
Requirement already satisfied: cycler>=0.10 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (0.11.0)
Requirement already satisfied: fonttools>=4.22.0 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (4.25.0)
Requirement already satisfied: kiwisolver>=1.0.1 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (1.4.4)
Requirement already satisfied: numpy<2,>=1.21 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (1.26.4)
Requirement already satisfied: packaging>=20.0 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (23.1)
Requirement already satisfied: pillow>=6.2.0 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (10.2.0)
Requirement already satisfied: pyparsing>=2.3.1 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (3.0.9)
Requirement already satisfied: python-dateutil>=2.7 in
c:\users\venky\anaconda3\lib\site-packages (from matplotlib) (2.8.2)
Requirement already satisfied: six>=1.5 in c:\users\venky\anaconda3\lib\site-
packages (from python-dateutil>=2.7->matplotlib) (1.16.0)
Note: you may need to restart the kernel to use updated packages.
```

dataset outline: This contains 768 observations with 8 feature columns an a target variable ‘outcome’

[4]:
```
#checking the outline of the dataset
dia.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
```

[5]:
```
#checking for null values
dia.isnull().sum()
```

[5]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[6]:
```
#Checking the dupilcate
dia.duplicated().sum
```

[6]:
```
<bound method Series.sum of 0      False
1      False
2      False
3      False
4      False
       …
763    False
764    False
765    False
766    False
767    False
Length: 768, dtype: bool>
```

[7]:
```
dia.duplicated().sum()
```

[7]:
```
0
```

[8]:
```
#Analysing the summary of the dataset
dia.describe()
```

[8]:

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

\

	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000
mean	31.992578	0.471876	33.240885	0.348958
std	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.078000	21.000000	0.000000
25%	27.300000	0.243750	24.000000	0.000000
50%	32.000000	0.372500	29.000000	0.000000
75%	36.600000	0.626250	41.000000	1.000000
max	67.100000	2.420000	81.000000	1.000000

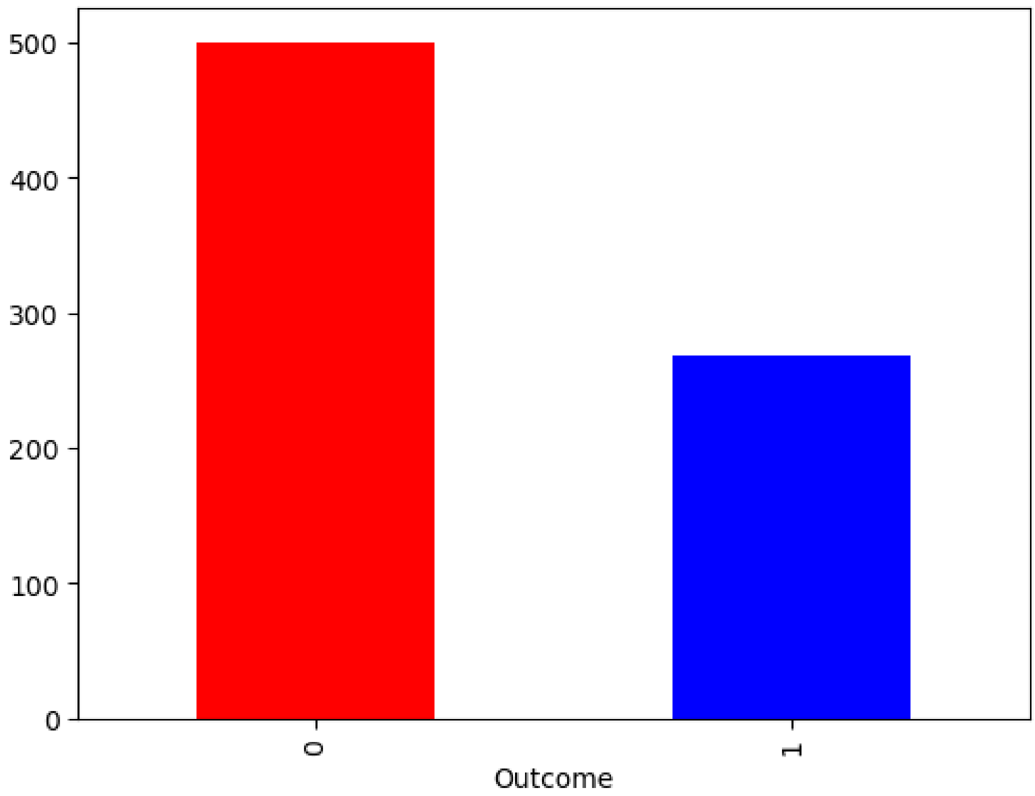
[9]:
```
dia['Outcome'].value_counts()
```

[9]:
```
Outcome
0    500
1    268
Name: count, dtype: int64
```

1.1 Exploratory Data Analysis

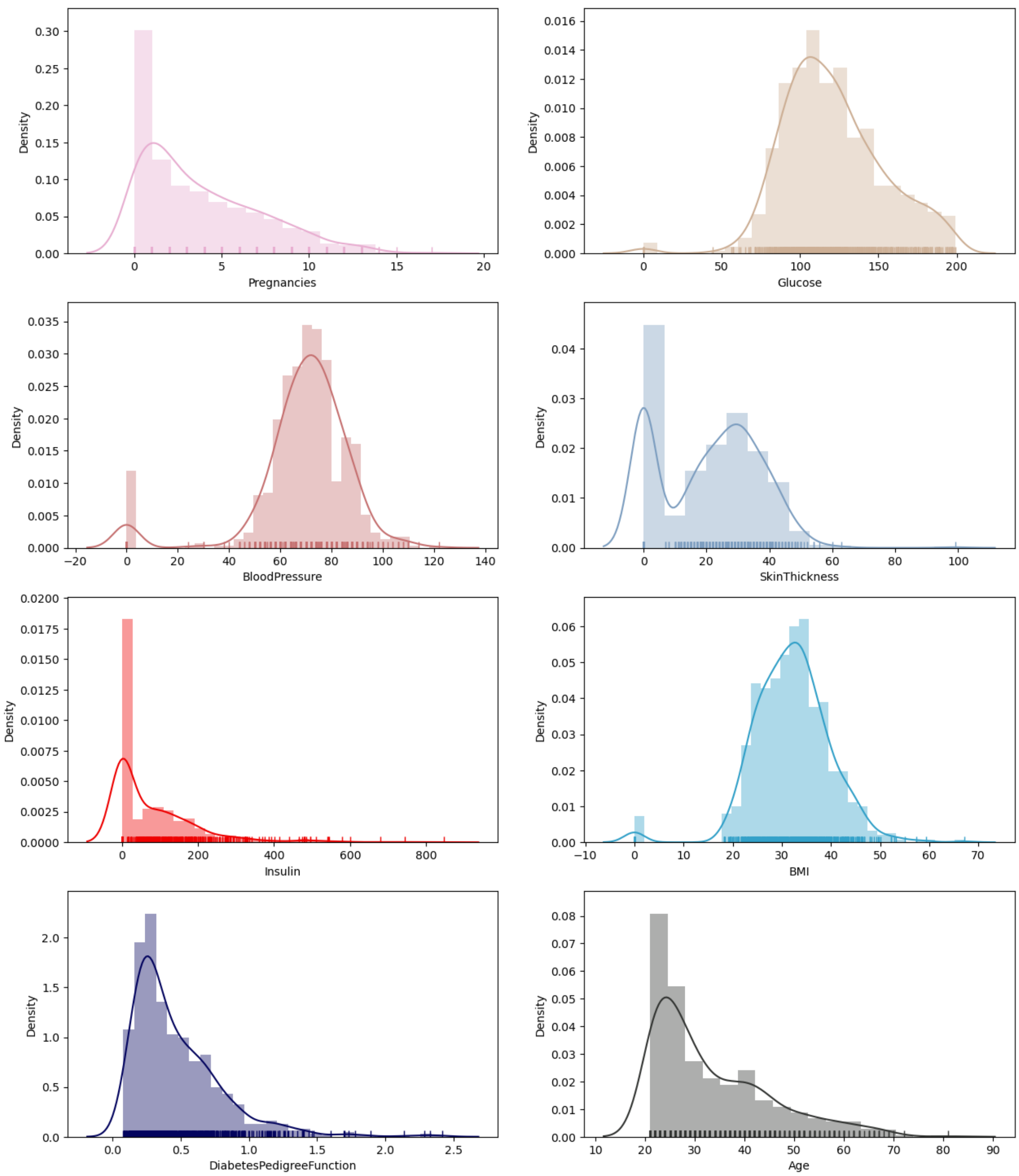
[10]:
```
#visualizing bar graph of the outcome
# 1 means diabetes patient and 0 means no diabetes patient
dia['Outcome'].value_counts().plot(kind='bar', color= ['red','blue'])
```

[10]: <Axes: xlabel='Outcome'>



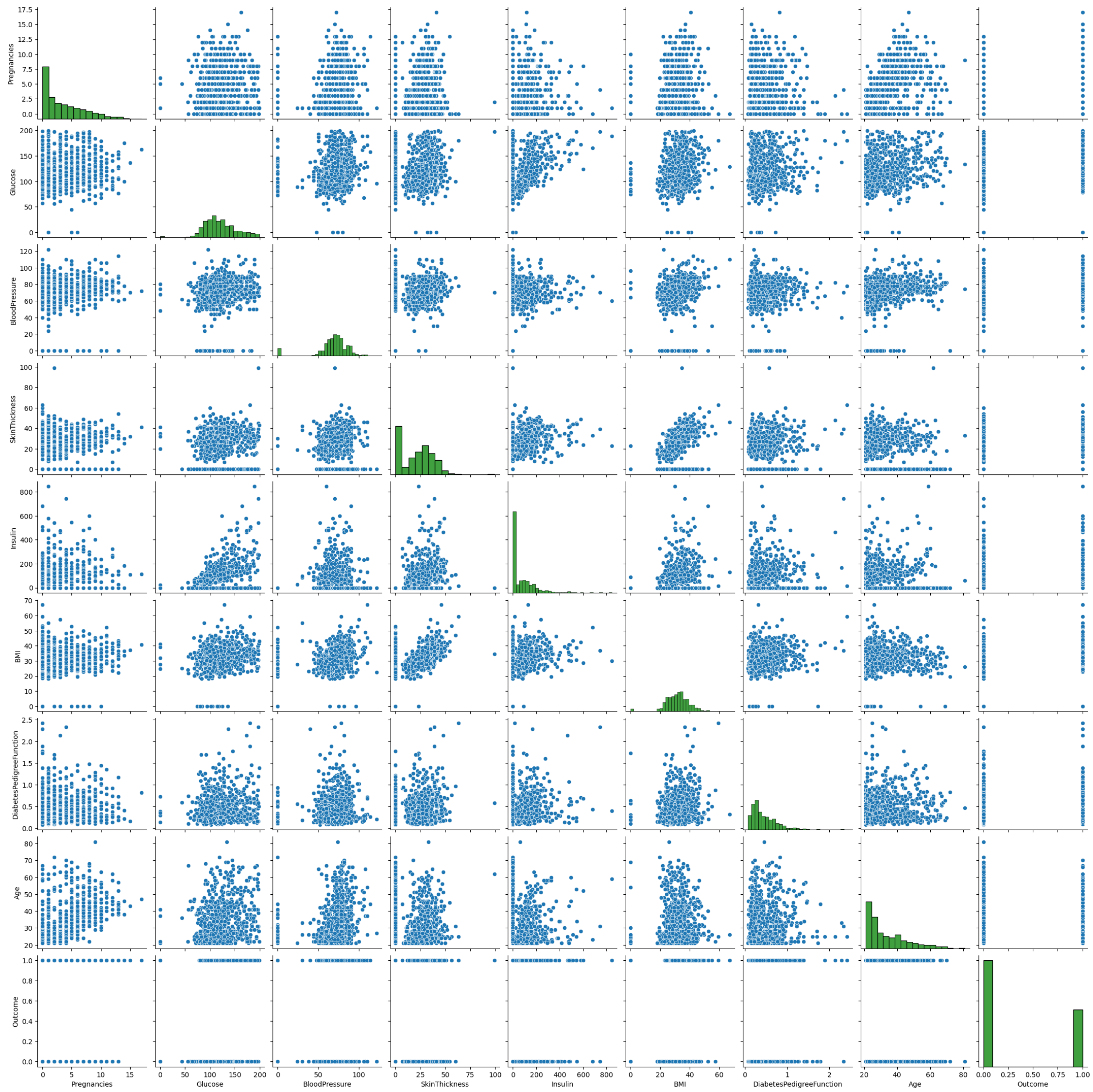
[25]:
```
fig, axs = plt.subplots(4, 2, figsize=(15, 18))
axs = axs.flatten()
sns.distplot(dia['Pregnancies'],rug=True, color='#E8AED1', ax=axs[0])
sns.distplot(dia['Glucose'],rug=True, color='#CDAF95', ax=axs[1])
sns.distplot(dia['BloodPressure'],rug=True, color='#C67171', ax=axs[2])
sns.distplot(dia['SkinThickness'],rug=True, color='#7D9EC0', ax=axs[3])
sns.distplot(dia['Insulin'],rug=True, color='#EE0000', ax=axs[4])
sns.distplot(dia['BMI'],rug=True, color='#33A1C9', ax=axs[5])
sns.distplot(dia['DiabetesPedigreeFunction'],rug=True, color='#03045e',␣
↪ax=axs[6])
sns.distplot(dia['Age'],rug=True, color='#333533', ax=axs[7])
```

[25]: <Axes: xlabel='Age', ylabel='Density'>

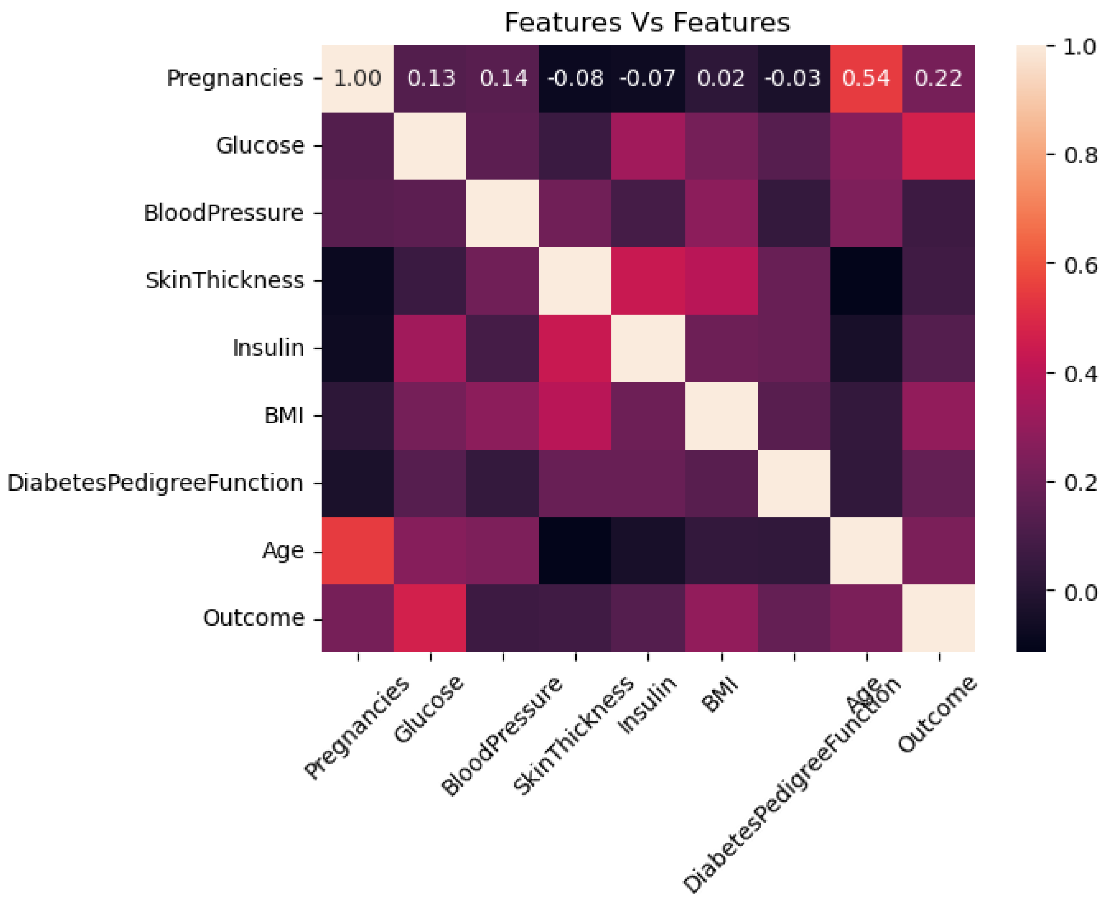


[28]:
```
sns.pairplot(dia , diag_kws={'color':'green'})
```

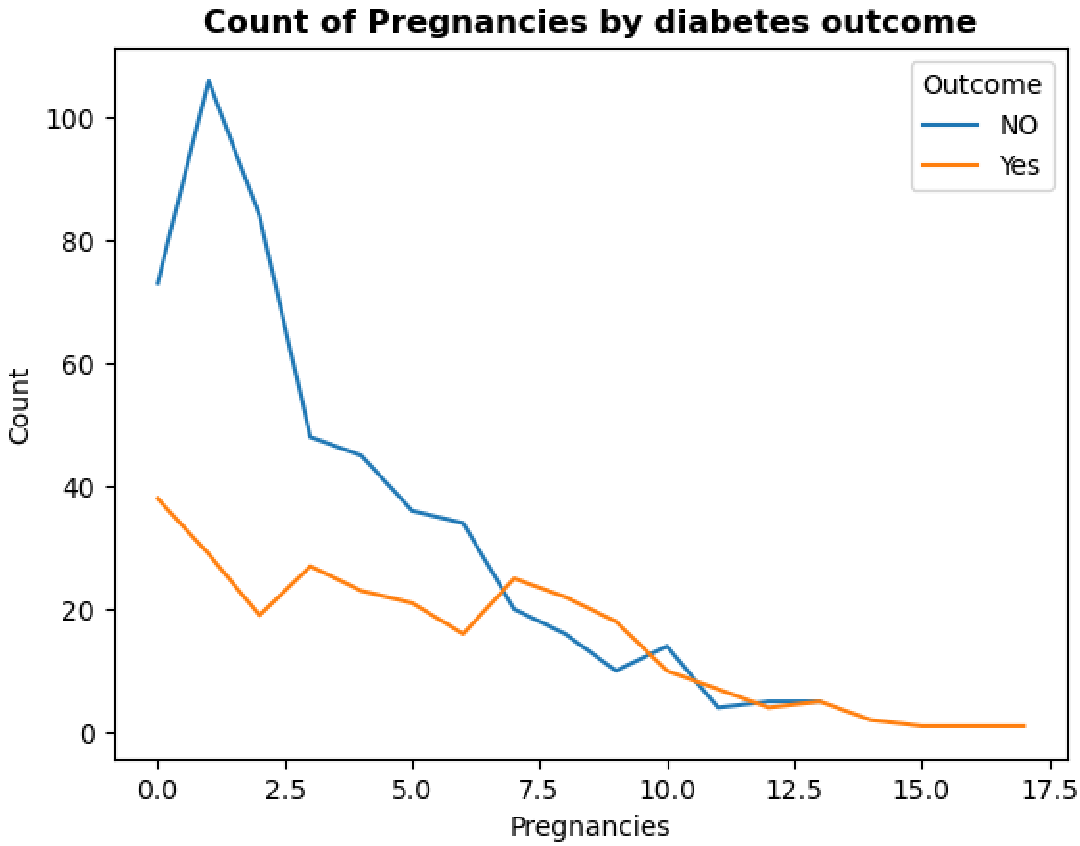
[28]: <seaborn.axisgrid.PairGrid at 0x26827d2dc90>



[31]:
```python
# Visualizing HeatMap
sns.heatmap(dia.corr(), annot=True ,fmt='.2f')
plt.title('Features Vs Features')
plt.xticks(rotation=45)
plt.show()
```

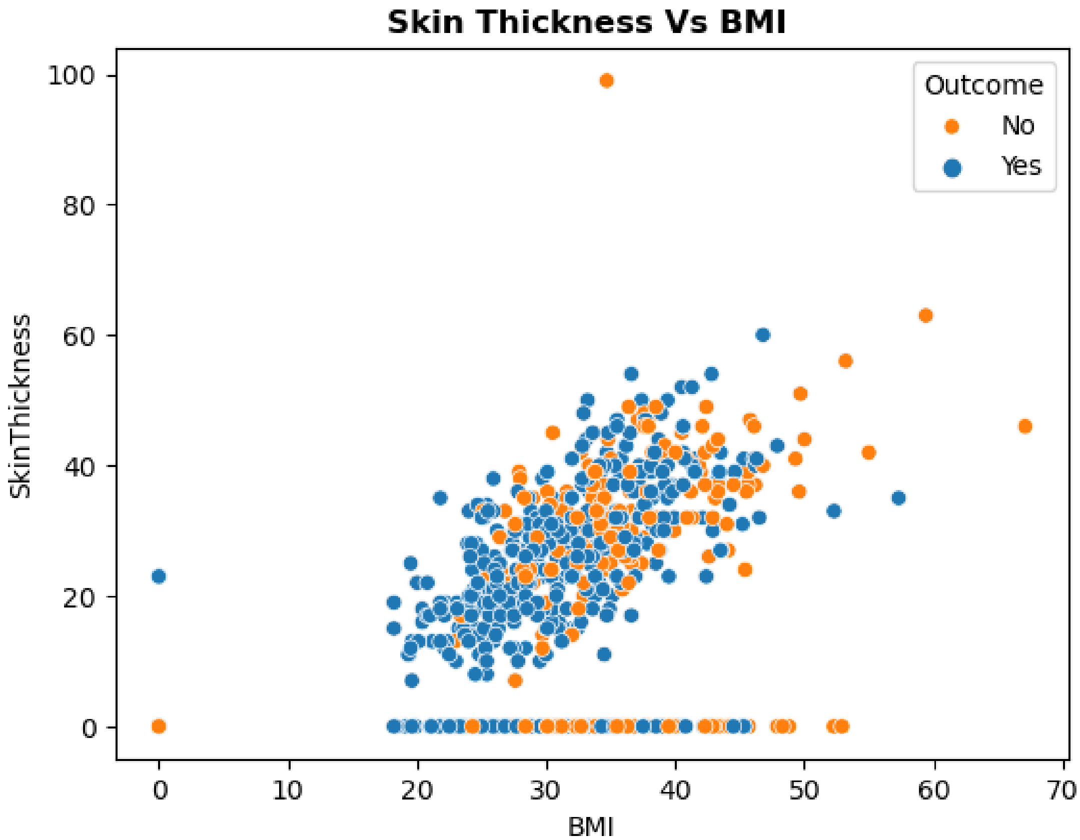



```
[40]: dia.groupby(['Pregnancies','Outcome']).size().unstack(level=1).plot(kind='line')
plt.ylabel('Count')
plt.legend(title='Outcome', labels= ['NO','Yes'])
plt.title('Count of Pregnancies by diabetes outcome', weight='bold')
plt.show()
```

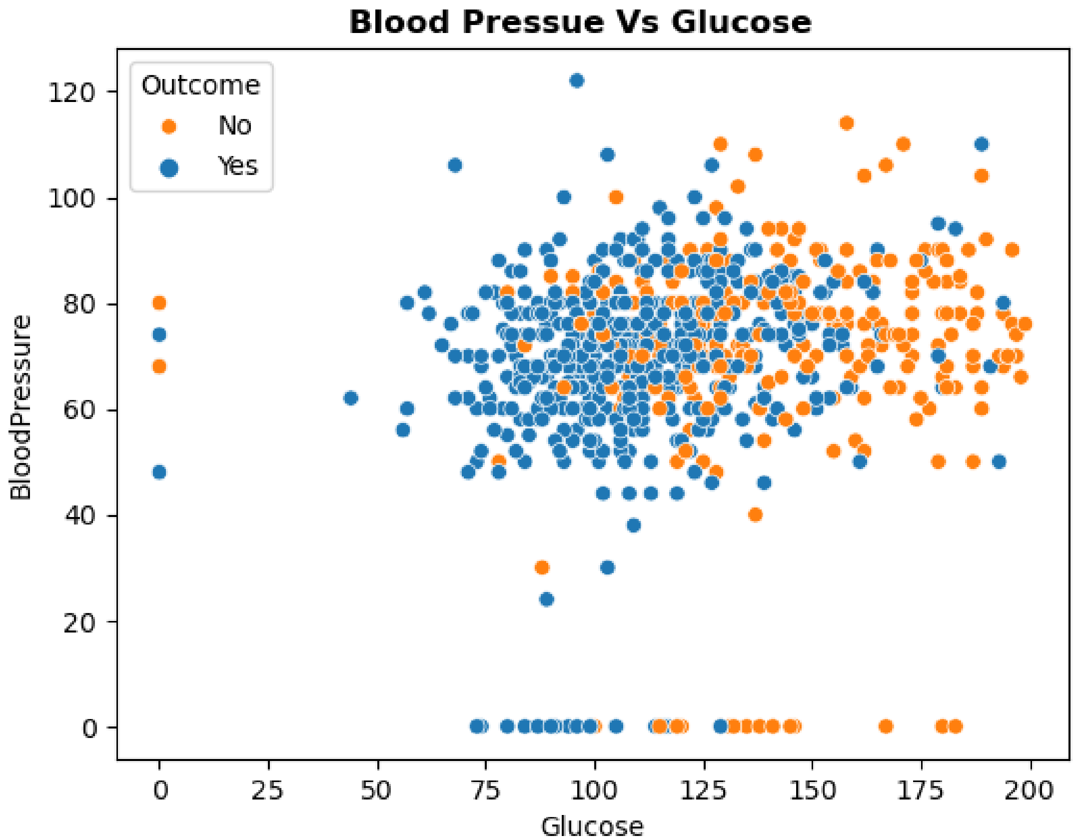


[41]:
```
#Insight:
# The number of having diabetesbis less when the number of pregnancies is low
# The Possibility of having diabetes increses as the number of pregnancies is␣
↪low
```

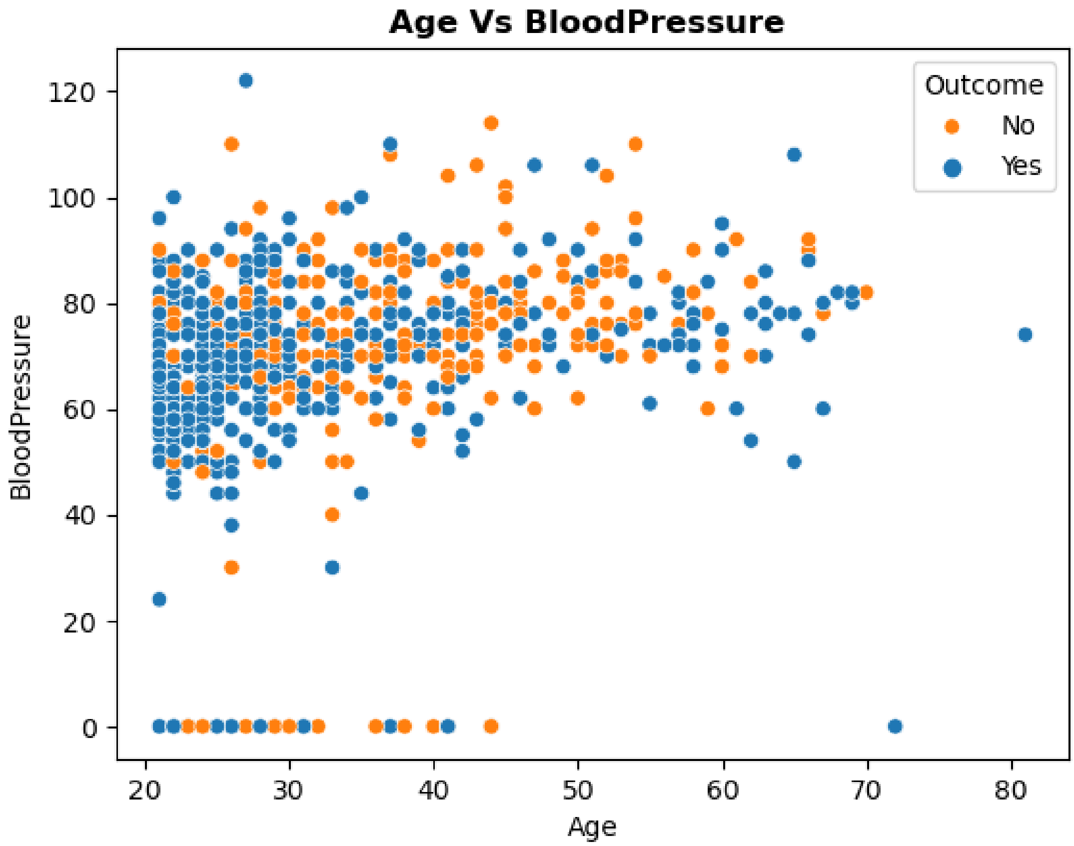
[43]:
```
sns.scatterplot(data=dia , x='BMI' , y='SkinThickness' , hue='Outcome')
plt.legend(title= 'Outcome', labels=['No', 'Yes'])
plt.title('Skin Thickness Vs BMI ', weight ='bold')
plt.show()
```



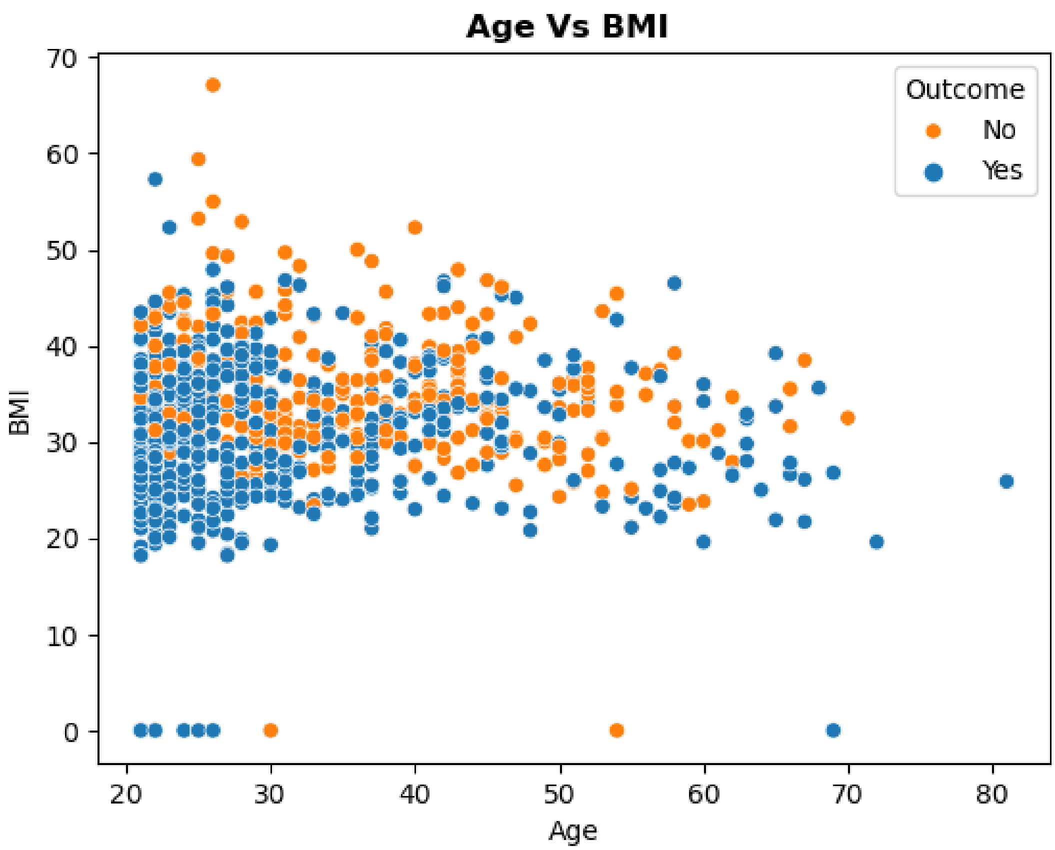
[48]:
```
sns.scatterplot(data=dia , x='Glucose' , y='BloodPressure' , hue='Outcome')
plt.legend(title= 'Outcome', labels=['No', 'Yes'])
plt.title('Blood Pressue Vs Glucose  ', weight ='bold')
plt.show()
```



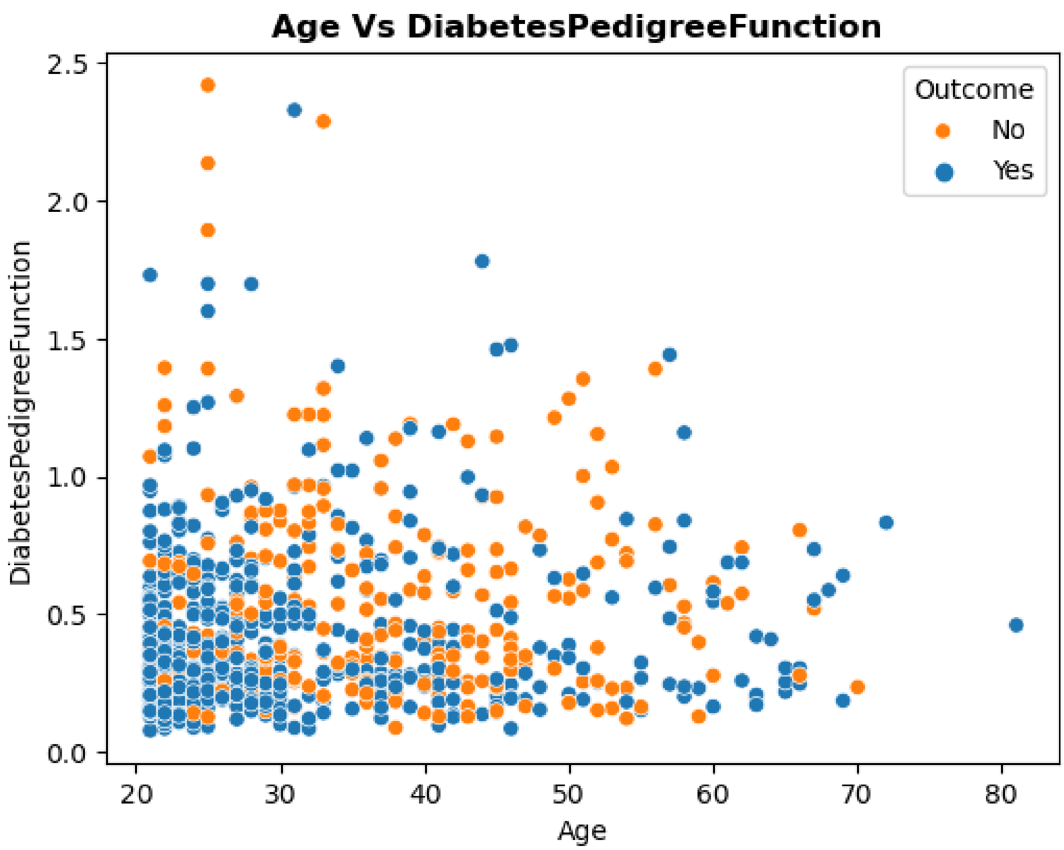
[49]:
```
sns.scatterplot(data=dia , x='Age' , y='BloodPressure' , hue='Outcome')
plt.legend(title= 'Outcome', labels=['No', 'Yes'])
plt.title('Age Vs BloodPressure ', weight ='bold')
plt.show()
```



[50]:
```
sns.scatterplot(data=dia , x='Age' , y='BMI' , hue='Outcome')
plt.legend(title= 'Outcome', labels=['No', 'Yes'])
plt.title('Age Vs BMI ', weight ='bold')
plt.show()
```



[51]:
```
sns.scatterplot(data=dia , x='Age' , y='DiabetesPedigreeFunction' ,␣
    ↪hue='Outcome')
plt.legend(title= 'Outcome', labels=['No', 'Yes'])
plt.title('Age Vs DiabetesPedigreeFunction ', weight ='bold')
plt.show()
```



[5]:
```python
from sklearn import metrics
from sklearn.model_selection import train_test_split
```

[6]:
```python
#splitting data into features and target
x= dia.drop(["Outcome"], axis= "columns")
y= dia["Outcome"]
```

x.head()

[7]:
```python
y.head()
```

[7]:
```
0    1
1    0
2    1
3    0
4    1
Name: Outcome, dtype: int64
```

[8]:
```python
#splitting the dataset into training and test set
```

```
x_test, x_train, y_test, y_train = train_test_split(x,y, test_size= 0.2,␣
 ↪train_size= 0.8,random_state=123,shuffle= True)
```

[9]:
```
x_test.shape,x_train.shape, y_test.shape, y_train.shape
```

[9]: ((614, 8), (154, 8), (614,), (154,))

2 Model building

2.0.1 Logistic Regression

[10]:
```
#import Logistic regression from sklearn module
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, classification_report,␣
 ↪accuracy_score
```

[19]:
```
LR=LogisticRegression()
```

[21]:
```
logistic_model = LogisticRegression()
logistic_model.fit(x_train,y_train)
```

[21]: LogisticRegression()

[25]:
```
LR.fit(x_train, y_train)
```

[25]: LogisticRegression()

[26]:
```
y_pred= LR.predict(x_test)
```

[27]:
```
accuracy= accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.754071661237785
```

[28]:
```
CM = confusion_matrix(y_test, y_pred)
print(CM)
```

```
[[344  60]
 [ 91 119]]
```

[29]:
```
class_report = classification_report(y_test, y_pred)
print(class_report)
```

```
              precision    recall  f1-score   support

           0       0.79      0.85      0.82       404
           1       0.66      0.57      0.61       210
```

```
    accuracy                           0.75       614
   macro avg       0.73      0.71      0.72       614
weighted avg       0.75      0.75      0.75       614
```

3 Decision Tree

[32]:
```python
from sklearn.tree import DecisionTreeClassifier
```

[33]:
```python
DT= DecisionTreeClassifier()
```

[34]:
```python
DT.fit(x_train, y_train)
```

[34]:
```
DecisionTreeClassifier()
```

[36]:
```python
y.pred = DT.predict(x_test)
```

[37]:
```python
DT.score(x_test, y_test)
```

[37]:
```
0.6775244299674267
```

[38]:
```python
accuracy_DT = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy_DT)
```

```
Accuracy: 0.754071661237785
```

[39]:
```python
CM_DT = confusion_matrix(y_test, y_pred)
print(CM_DT)
```

```
[[344  60]
 [ 91 119]]
```

[40]:
```python
class_report= classification_report(y_test, y_pred)
print(class_report)
```

```
              precision    recall  f1-score   support

           0       0.79      0.85      0.82       404
           1       0.66      0.57      0.61       210

    accuracy                           0.75       614
   macro avg       0.73      0.71      0.72       614
weighted avg       0.75      0.75      0.75       614
```

4 Random Forest Classifier

[41]:
```
from sklearn.ensemble import RandomForestClassifier
```

[42]:
```
random_forest = RandomForestClassifier(n_estimators=10)
```

[43]:
```
random_forest.fit(x_train, y_train)
```

[43]:
```
RandomForestClassifier(n_estimators=10)
```

[44]:
```
y_pred = random_forest.predict(x_test)
```

[45]:
```
random_forest.score(x_test, y_test)
```

[45]:
```
0.744299674267101
```

[46]:
```
accuracy_RF = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy_RF)
```

```
Accuracy: 0.744299674267101
```

[48]:
```
CM_RF = confusion_matrix(y_test, y_pred)
print(CM_RF)
```

```
[[344  60]
 [ 97 113]]
```

[49]:
```
class_report = classification_report(y_test, y_pred)
print(class_report)
```

```
              precision    recall  f1-score   support

           0       0.78      0.85      0.81       404
           1       0.65      0.54      0.59       210

    accuracy                           0.74       614
   macro avg       0.72      0.69      0.70       614
weighted avg       0.74      0.74      0.74       614
```

5 Gaussian Naive Bayes Classifier

[14]:
```
from sklearn.naive_bayes import GaussianNB
naive_bayes = GaussianNB()
```

[15]:
```
naive_bayes.fit(x_train, y_train)
```

[15]: GaussianNB()

[16]:
```
y_pred_NB = naive_bayes.predict(x_test)
```

[54]:
```
naive_bayes.score(x_test, y_test)
```

[54]: 0.741042345276873

[17]:
```
accuracy_NB = accuracy_score(y_test, y_pred_NB)
print("Accuracy:", accuracy_NB)
```

```
Accuracy: 0.741042345276873
```

[18]:
```
CM_NB = confusion_matrix(y_test, y_pred_NB)
print(CM_NB)
```

```
[[329  75]
 [ 84 126]]
```

[19]:
```
class_report = classification_report(y_test, y_pred_NB)
print(class_report)
```

```
              precision    recall  f1-score   support

           0       0.80      0.81      0.81       404
           1       0.63      0.60      0.61       210

    accuracy                           0.74       614
   macro avg       0.71      0.71      0.71       614
weighted avg       0.74      0.74      0.74       614
```

6 Interpretation and summary report

- Imported the necessary modules for the project and checked the data
- Performed Exploratory analysis to visualize the distribution of different features
- Preformed preprocessing steps to treat the missing values
- Used 4 Models (Logistic Regression , random Forest , Decision tree and Naive Bayes Classifier) to find the best model for prediction
- Evaluated the performance using the Accuracy, Pression, Recall, and F1 score
- Based on the performance evaluation, Logistic Regression performed well in predicting if someone has diabetes or not
- Logistic regression has the highest accuracy of 76%
- This model also exhibited reasonable precision and recall, indicating its ability to correctly classify both positive and negative cases of diabetes.
- So, The Machine learning approach , specifically the Logistic regression , can be a valuable tool for predicting diabetes outcomes based on health-related variables

```
[ ]:
```