

# **Diabetes Prediction using Machine Learning**

*Submitted by*

**CHINTAPALLIDINESH(RA2111027010002)  
SNEHAL SUKUNDARI(RA2111027010049)  
RATAN PRIYA SINGH(RA2111027010065)**

*Under the Guidance of*

**Dr.E.SASIKALA**

**Department of Data Science And Business Systems**

*In partial satisfaction of the requirements for the degree of*

**BACHELOR OF TECHNOLOGY  
in  
COMPUTER SCIENCE ENGINEERING**

**with specialization in Big Data Analytics**



**SCHOOL OF COMPUTING**

**COLLEGE OF ENGINEERING AND TECHNOLOGY  
SRM INSTITUTE OF SCIENCE AND TECHNOLOGY**

**KATTANKULATHUR - 603203**

**NOV 2023**



COLLEGE OF ENGINEERING & TECHNOLOGY  
SRM INSTITUTE OF SCIENCE & TECHNOLOGY  
S.R.M. NAGAR, KATTANKULATHUR – 603 203  
Chengalpattu District

## BONAFIDE CERTIFICATE

Register No. RA2111027010065 Certified to be the bonafide work done  
by RATAN PTIYA SINGH of III Year/V Sem B.Tech Degree  
Course in the **MACHINE LEARNING I [18CSE392T]** in **SRM  
INSTITUTE OF SCIENCE AND TECHNOLOGY**, Kattankulathur during  
the academic year 2023 – 2024.

**Name of the Faculty: Dr.E.SASIKALA**

**Professor Department of Computing**

**Technologies SRMIST – KTR.**

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## **INTRODUCTION:**

Diabetes is a chronic metabolic disorder characterized by elevated blood sugar levels, which can lead to serious health complications if not managed effectively. Early detection and prediction of diabetes risk are crucial for preventing its onset and providing timely intervention. Machine learning, a subfield of artificial intelligence, has emerged as a powerful tool for diabetes prediction. By analyzing various factors and patterns in medical data, machine learning algorithms can assist healthcare professionals in identifying individuals at risk of developing diabetes. This application of machine learning holds great promise in improving the prevention and management of diabetes, ultimately enhancing the quality of healthcare and the overall well-being of individuals.

Diabetes prediction involves using historical patient data to develop models that can forecast the likelihood of an individual developing diabetes in the future. Early prediction of diabetes can lead to timely interventions, lifestyle adjustments, and personalized medical care, which are crucial for managing the disease effectively.

There are two main types of diabetes:

- Type 1: Diagnosed in childhood
- Type 2: Diagnosed in adulthood

## **ABSTRACT:**

Diabetes is a chronic metabolic disorder characterized by elevated blood sugar levels, which can lead to serious health complications if not managed effectively. Early detection and prediction of diabetes risk are crucial for preventing its onset and providing timely intervention. Machine learning, a subfield of artificial intelligence, has emerged as a powerful tool for diabetes prediction. By analyzing various factors and patterns in medical data, machine learning algorithms can assist healthcare professionals in identifying individuals at risk of developing diabetes. This application of machine learning holds great promise in improving the prevention and management of diabetes, ultimately enhancing the quality of healthcare and the overall well-being of individuals. In this discussion, we will explore the role of machine learning in predicting diabetes and its potential to transform the healthcare landscape.

## **PROBLEM STATEMENT:**

- To Develop a machine learning model that predicts the likelihood of an individual developing diabetes based on a set of clinical and lifestyle attributes.
- The goal is to create an accurate and interpretable predictive tool that aids healthcare professionals in identifying individuals at risk of diabetes and providing timely interventions.

## LITEATURE REVIEW:

S. No.	Title of the Work/Authors	Techniques	Results/Limitations
1.	Tao et al.[2]	KNN, Naïve Bayes, Decision Tree, Random Forest, SVM and Logistic Regression	Concentrated on the accuracy of recall and got better result. Filtering criteria can be improved
2.	Loannis et al..[1]	Naïve Bayes, Logistic regression, and Svm	From the three algorithm Svm provided high accuracy of 84%
3.	Weifeng Xu et al.[3]	ID3Naïv Bayes, Randomforest, Adaboost	Random forest classifier method better relative to other in contrast ID3 provided the least accuracy than others.
4.	Yunsheng et al. [4]	DISKR and KNN	Accuracy increase can be increase by removing outliers. Space complexity decreased.
5.	Messan et al.[5]	GMM, ELM, ANN LR, and SVM	Comparison of algorithm were done from those method artificial neural network provide better accuracy than other classifier.
6.	Ramiro et al.[6]	Fuzzy rule	Wrong treatment was reduced using fuzzy rule and recommendation system was developed for doctor.

S. No.	Title of the Work/Authors	Techniques	Results/Limitations
7.	Swarupa et al.[7]	KNN,J48, ANN, zeroR, NB, evparameter selection, Filtered classifier and simple cart	Various dataset applied containing diabetes dataset. Cross validation not applied. NBshown high accuracy by providing accuracy of 77,01%.
8.	Pradeep & Dr.Naveen [8]	Decision tree(J48)	J48 is noted as good accuracy provider algorithm. Feature selection has high role in the prediction area.
9.	Sajida et al.[9]	Adaboost, j48,and Bagging	Adaboost was shown improved accuracy than other method.



## **INFERENCE FROM LITERATURE REVIEW:**

### **1. Data Sources and Features:**

- Researchers commonly use various data sources, including electronic health records, medical databases, and wearable devices, to collect data for diabetic prediction models.

### **2. Machine Learning Algorithms:**

- Machine learning algorithms like logistic regression, decision trees, random forests, support vector machines, and neural networks are frequently applied to predict diabetes.

### **3. Feature Selection and Engineering:**

- Feature selection techniques, such as Recursive Feature Elimination (RFE) and feature importance ranking, are used to identify the most relevant features.

### **4. Data Preprocessing:**

- Data preprocessing steps, including handling missing values, normalization, and scaling, are essential for improving the robustness of machine learning models.

### **5. Model Evaluation:**

- Common evaluation metrics include accuracy, sensitivity, specificity, ROC-AUC, and F1-score.

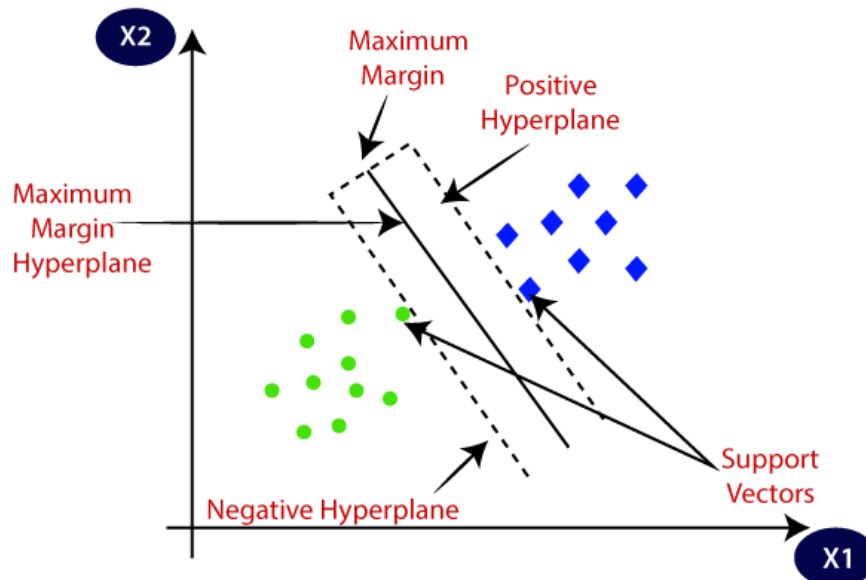
- Cross-validation techniques like k-fold cross-validation help assess model generalizability.

### **6. Challenges and Limitations:**

- Imbalanced datasets, where non-diabetic cases significantly outnumber diabetic cases, are a common challenge. Researchers often employ techniques like oversampling or synthetic data generation to address this issue.

## ALGORITHM:

### Support Vector Machine:



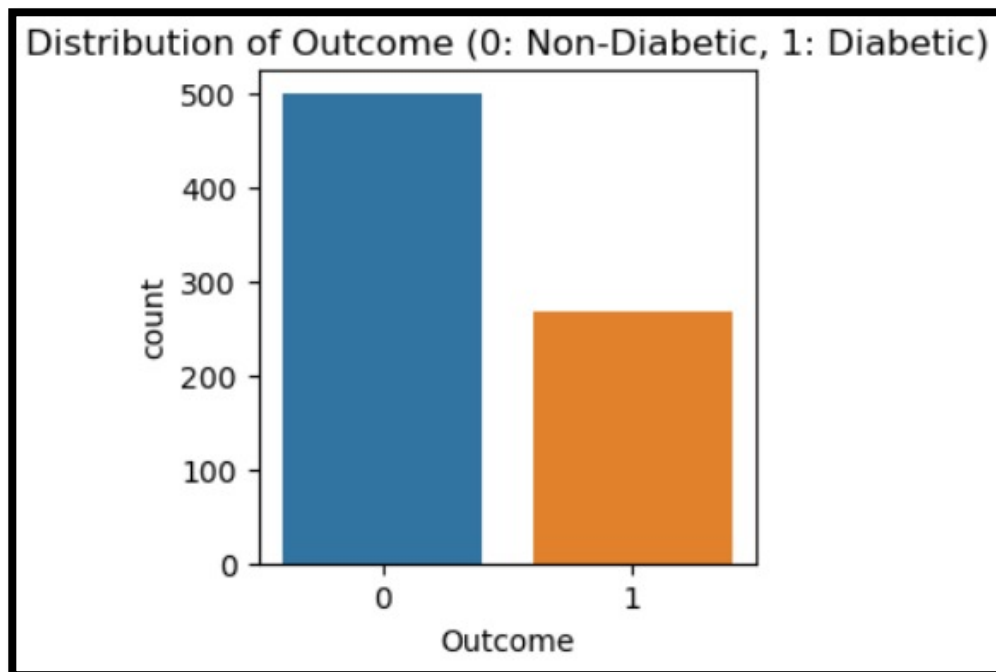
- SVMs work well with high-dimensional data, making them suitable for applications where there are many features associated with the data. In the case of diabetic prediction, there could be numerous parameters and features to consider, such as age, weight, blood pressure, glucose levels, etc. SVMs can effectively handle this complexity.
- SVMs can handle non-linear relationships between features. In the case of diabetes prediction, the relationship between different health parameters might not be linear.
- SVMs can model complex patterns in the data, making them useful in capturing the intricate relationships between various factors associated with diabetes.
- SVMs use a subset of training points in the decision function (called support vectors), so they are memory efficient, especially in high-dimensional spaces. This is particularly important when dealing with a large number of features, as is often the case in medical (Diabetic) datasets.

## WHY SVM

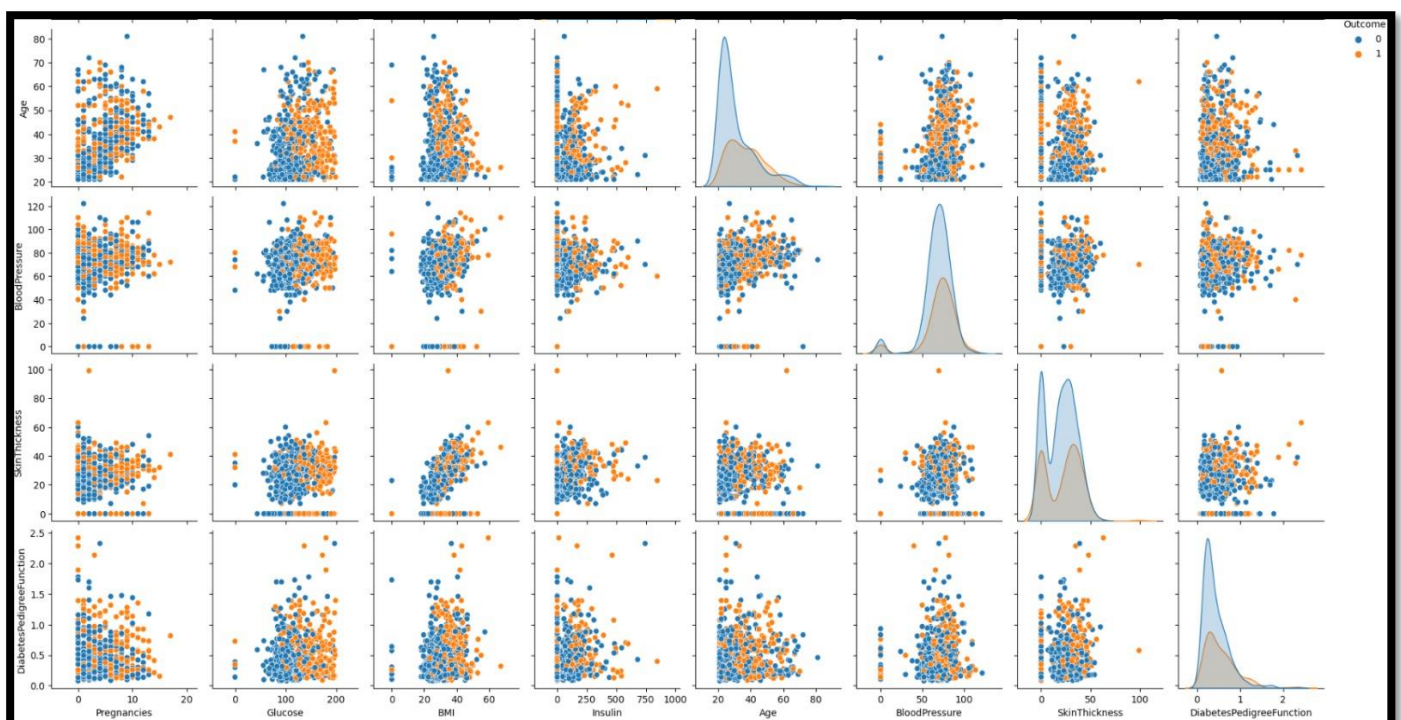
- For predicting blood pressure status, they used conditional decision making and for predicting diabetes, they used SVM, KNN, and decision tree. Among these models, SVM worked better as they got 75% accuracy which is better than other classifier algorithms.
- Maximizes the distance from the nearest data points.
- They can be used to avoid the difficulties of using linear functions in the high-dimensional feature space.
- Robustness to overfitting.
- SVMs aim to find the hyperplane that maximizes the margin between classes. This results in a decision boundary that is less prone to errors and is more robust, which often leads to better generalization performance.

## OUTPUT:

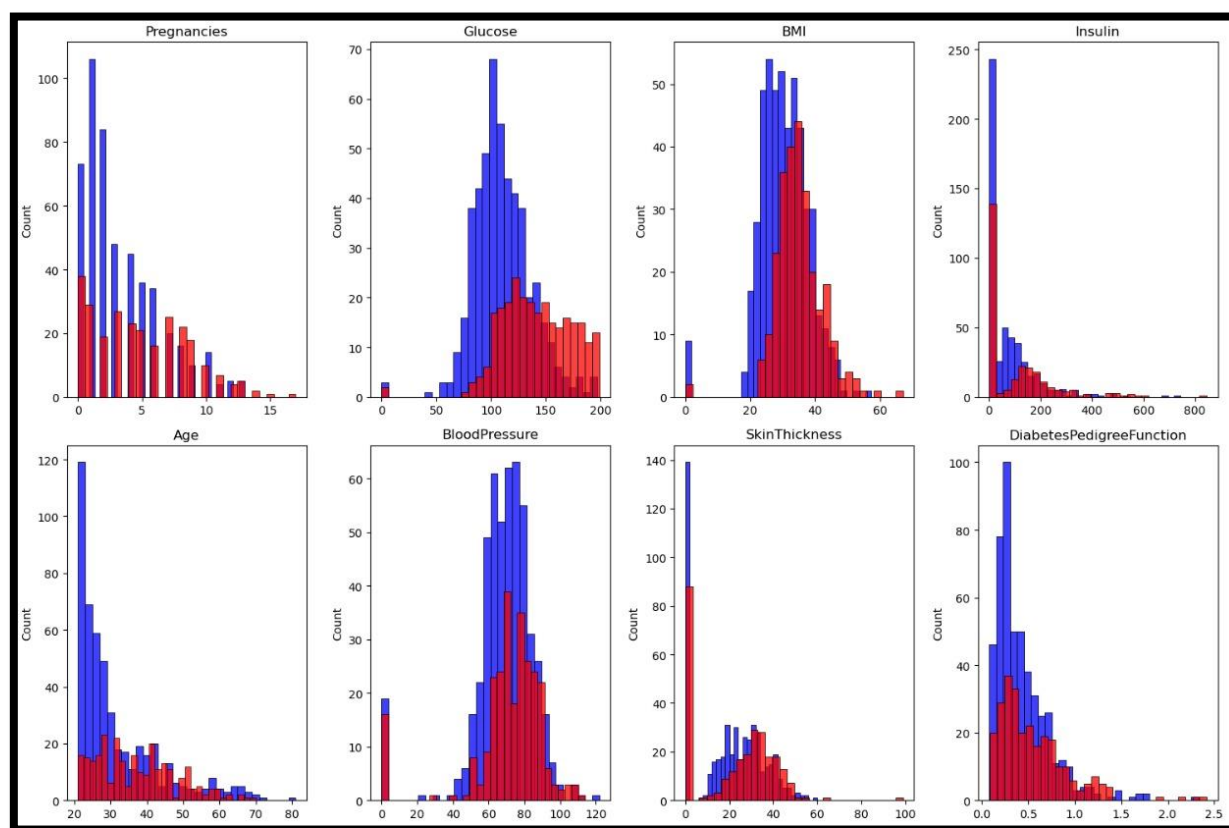
### BAR GRAPH



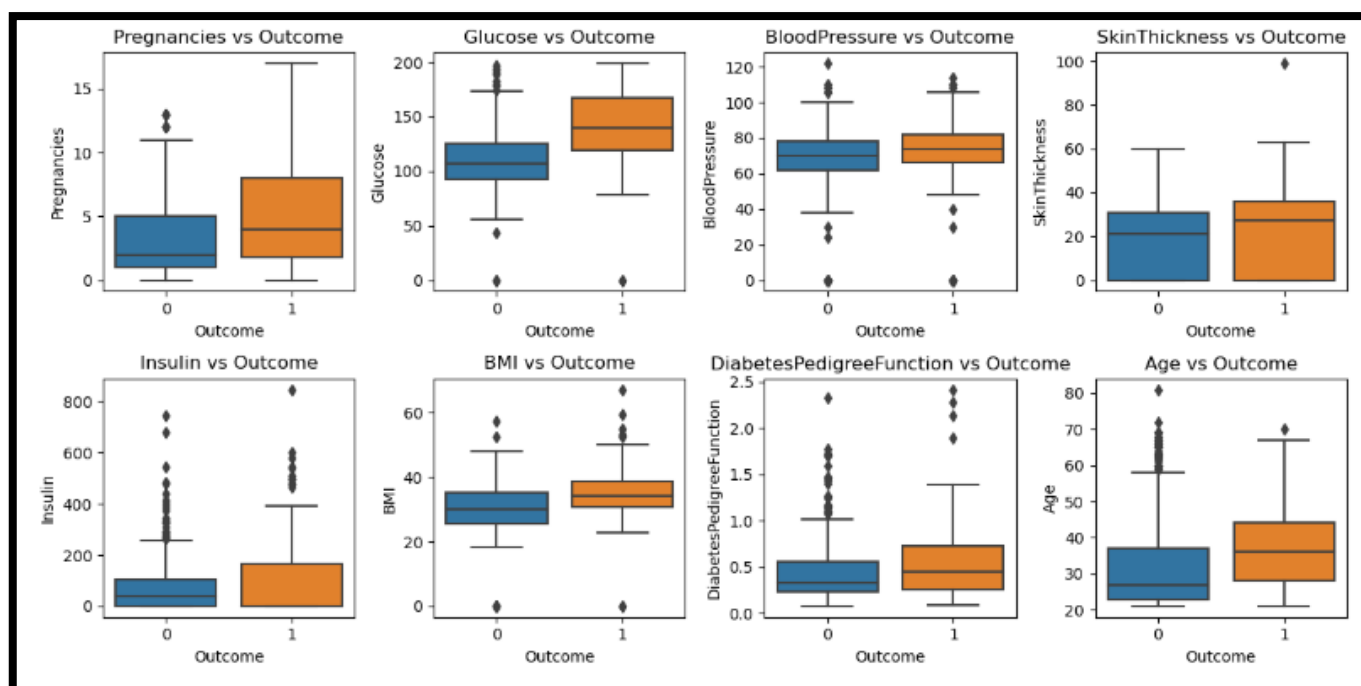
### PAIR PLOT OF FEATURES



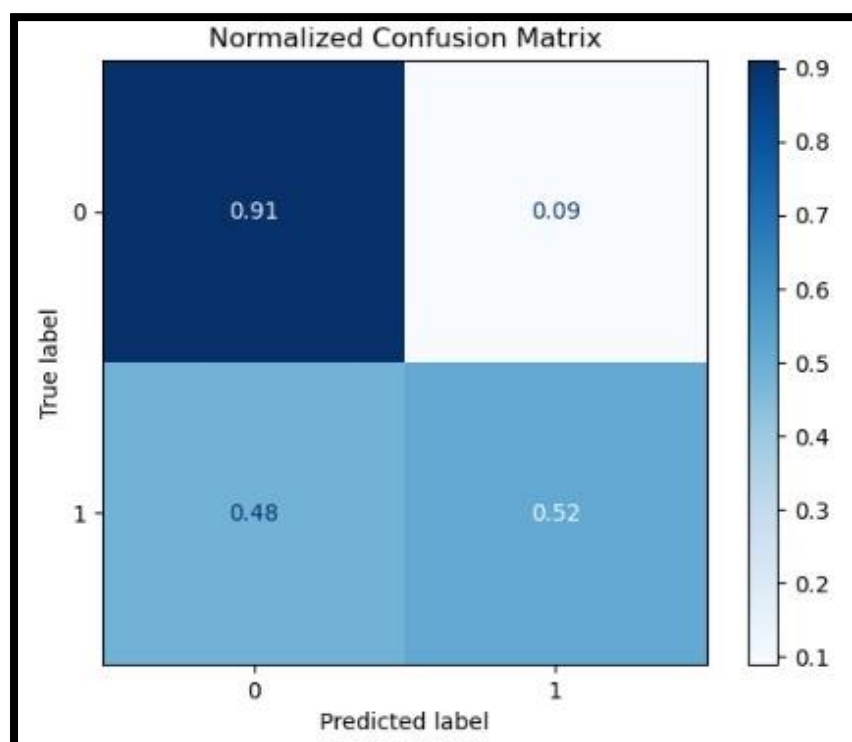
## HISTOGRAM OF ATTRIBUTES:



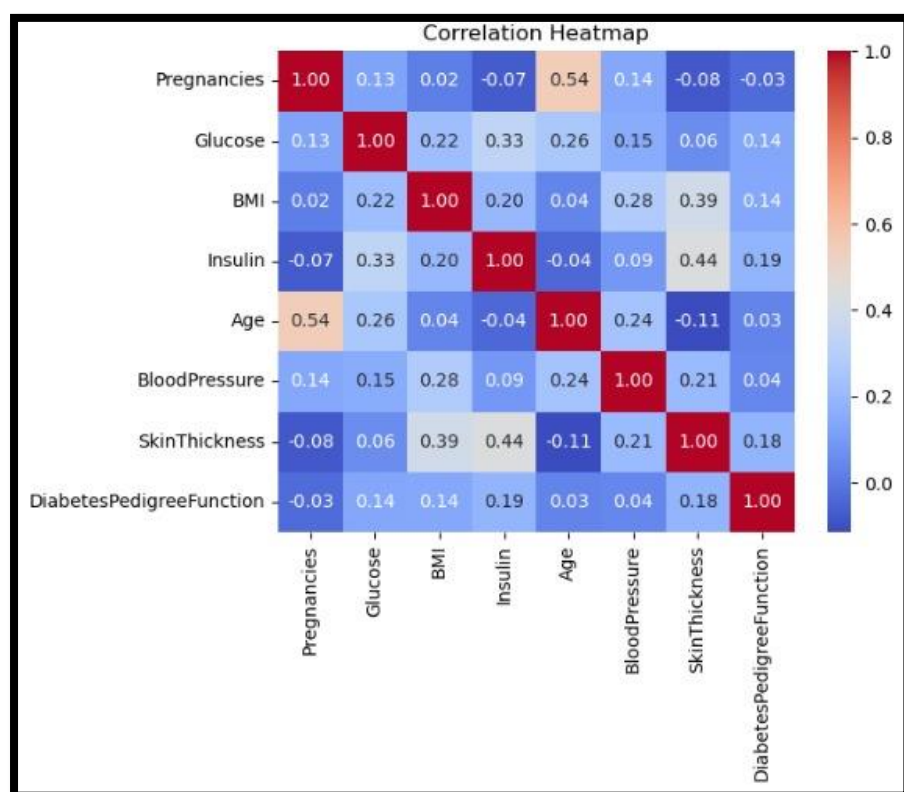
## BOX PLOT:



## CONFUSION MATRIX:



## CORRELATION MATRIX:



## RESULT:

```
# accuracy score on the test data
print('Accuracy score of test data : ', test_data_accuracy)
```

```
Accuracy score of test data : 0.7727272727272727
```

```
#Making a Predictive System
```

```
input_data = (5,166,72,19,175,25.8,0.587,51)
```

```
input_data_as_numpy_array = np.asarray(input_data)
```

```
input_data_resaped = input_data_as_numpy_array.reshape(1,-1)
```

```
std_data = scaler.transform(input_data_resaped)
```

```
print(std_data)
```

```
prediction = classifier.predict(std_data)
```

```
print(prediction)
```

```
if (prediction[0] == 0):
```

```
    print('The person is not diabetic')
```

```
else:
```

```
    print('The person is diabetic')
```

```
[[ 0.3429808  1.41167241  0.14964075 -0.09637905  0.82661621 -0.78595734
  0.34768723  1.51108316]]
```

```
[1]
```

```
The person is diabetic
```

## **CONCLUSION:**

- In this project, we successfully developed a machine learning model for diabetes prediction using Python. We started by collecting and preprocessing a dataset containing various patient attributes, including age, BMI, and glucose levels, and the binary diabetes label.
- This project demonstrates the effectiveness of machine learning in diabetes prediction. The model can be a valuable tool in helping to identify individuals at risk of diabetes, potentially leading to early interventions and improved patient outcomes.
- SVMs are particularly well-suited to scenarios where high-dimensional data, robustness, and generalization performance are essential. However, as with any machine learning tool, their effectiveness depends on the nature of the data and the problem at hand.



## REFERENCES:

➤Gauri D. Kalyankar, Shivananda R. Poojara and Nagaraj V. Dharwadkar,” Predictive Analysis of Diabetic Patient Data Using Machine Learning and Hadoop”, International Conference.

➤B. Nithya and Dr. V. Ilango,” Predictive Analytics in Health Care Using Machine Learning Tools and Techniques”, International Conference on Intelligent Computing and Control Systems.

➤P. Suresh Kumar and S. Pranavi “Performance Analysis of Machine Learning Algorithms on Diabetes Dataset using Big Data Analytics”, International Conference on Infocom Technologies and Unmanned Systems, 978-1-5386-0514-1, Dec. 18-20, 2017.

➤Tejas N. Joshi, Prof. Pramila M. Chawan, "Diabetes Prediction Using Machine Learning Techniques". Int. Journal of Engineering Research and Application, Vol. 8, Issue 1, (Part -II) January 2018.

## CODE:-

In [1]: *#Importing the Dependencies*

```
import numpy as np
import pandas as pd
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn import svm
from sklearn.metrics import accuracy_score, plot_confusion_matrix, classification_report, confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]: *#Dataset source :Kaggle [PIMA(Pima Indians Diabetes Database) Diabetes]*

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

In [3]: diabetes.head()

Out[3]:

	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

In [4]: diabetes.shape

Out[4]: (768, 9)

In [5]: diabetes.describe()

Out[5]:

	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

In [6]: diabetes.isnull()

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	False	False	False	False	False	False	False	False	False
1	False	False	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False	False	False
...	...	...	...	...	...	...	...	...	...
763	False	False	False	False	False	False	False	False	False
764	False	False	False	False	False	False	False	False	False
765	False	False	False	False	False	False	False	False	False
766	False	False	False	False	False	False	False	False	False
767	False	False	False	False	False	False	False	False	False

768 rows × 9 columns

```
In [7]: diabetes.isna().any()
```

```
Out[7]: Pregnancies      False
         Glucose          False
         BloodPressure    False
         SkinThickness    False
         Insulin          False
         BMI              False
         DiabetesPedigreeFunction False
         Age              False
         Outcome          False
         dtype: bool
```

```
In [8]: diabetes.duplicated()
```

```
Out[8]: 0      False
         1      False
         2      False
         3      False
         4      False
         ...
         763    False
         764    False
         765    False
         766    False
         767    False
         Length: 768, dtype: bool
```

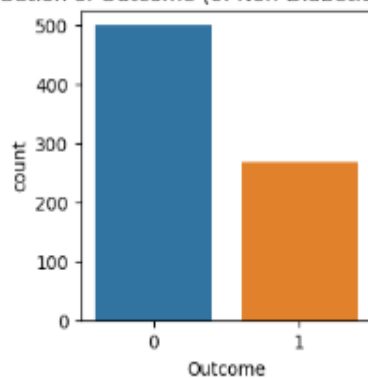
```
In [9]: diabetes['Outcome'].value_counts()
```

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

Data Visualization

```
In [10]: plt.figure(figsize=(3,3))
         sns.countplot(x='Outcome', data=diabetes)
         plt.title('Distribution of Outcome (0: Non-Diabetic, 1: Diabetic)')
         plt.show()
```

Distribution of Outcome (0: Non-Diabetic, 1: Diabetic)



```
In [11]: sns.pairplot(diabetes, vars=['Pregnancies', 'Glucose', 'BMI', 'Insulin', 'Age', 'BloodPressure', 'SkinThickness', 'DiabetesPedigreeFunction', 'Outcome'])
```



```
In [12]: diabetes.groupby('Outcome').mean()
```

```
Out[12]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
Outcome								
0	3.298000	109.980000	68.184000	19.664000	68.792000	30.304200	0.429734	31.190000
1	4.865672	141.257463	70.824627	22.164179	100.335821	35.142537	0.550500	37.067164

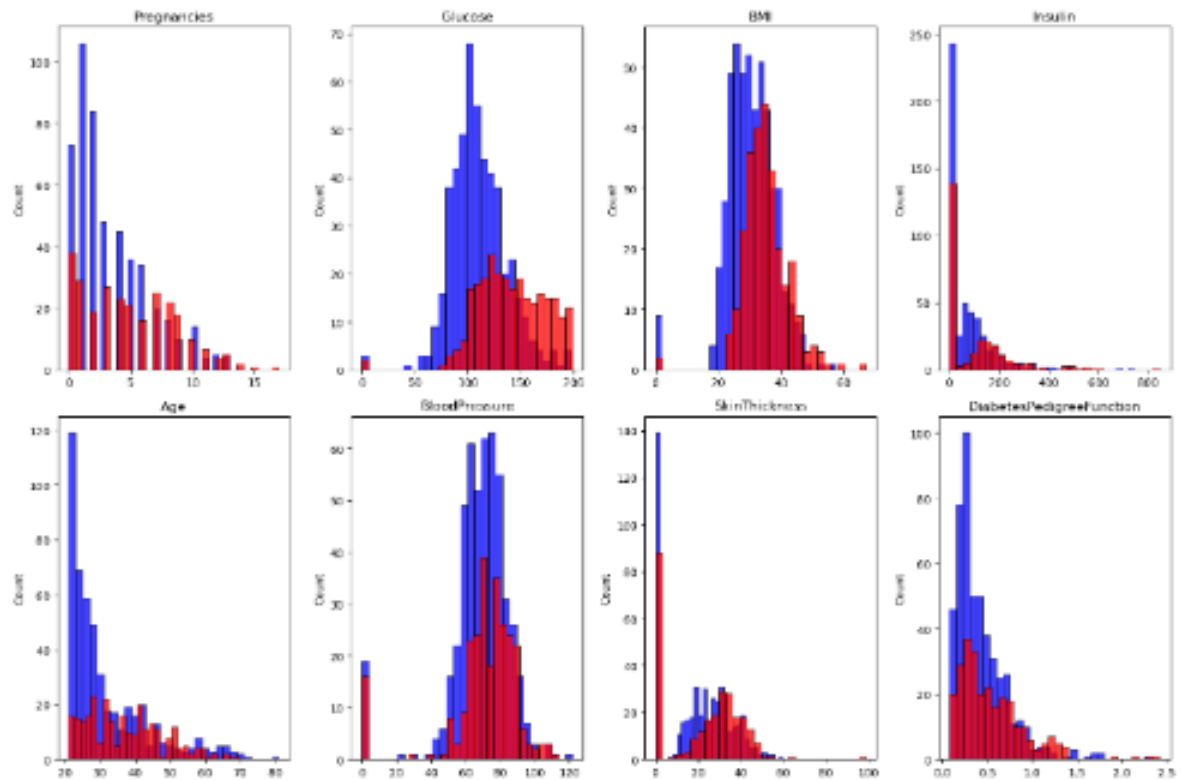
```
In [13]: # separating the data and labels
X = diabetes.drop(columns = 'Outcome', axis=1)
Y = diabetes['Outcome']
```

```
In [14]: print(Y)
```

```
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
```

```
In [15]: features = ['Pregnancies', 'Glucose', 'BMI', 'Insulin', 'Age', 'BloodPressure', 'SkinThickness', 'DiabetesPedigreeFunction']
plt.figure(figsize=(15, 10))
for i, feature in enumerate(features, 1):
    plt.subplot(2, 4, i)
    sns.histplot(diabetes[feature][diabetes['Outcome']==0], bins=30, color='b', label='No Diabetes')
    sns.histplot(diabetes[feature][diabetes['Outcome']==1], bins=30, color='r', label='Diabetes')
    plt.xlabel(feature)
    plt.title(feature)
    plt.ylabel('Count')

plt.tight_layout()
plt.show()
```



#### Data Standardization

```
In [16]: scaler = StandardScaler()

In [17]: scaler.fit(X)

Out[17]: StandardScaler()

In [18]: standardized = scaler.transform(X)

In [19]: print(standardized)

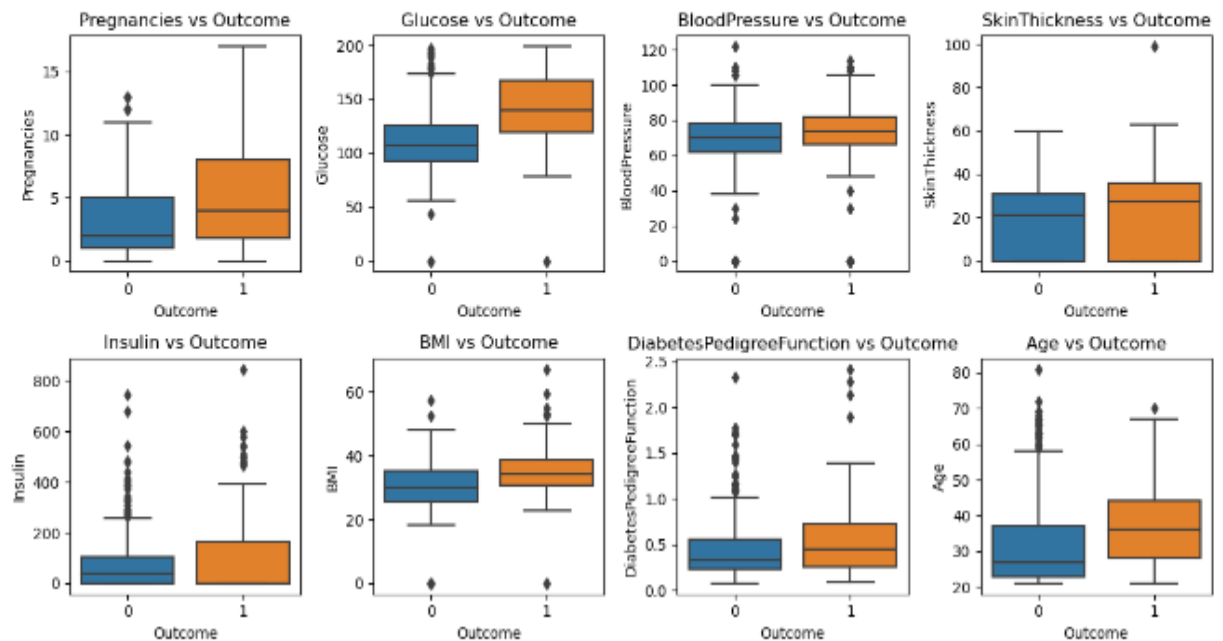
[[ 0.63994726  0.84832379  0.14964075 ...  0.20401277  0.46849198
    1.4259954 ]
 [-0.84488505 -1.12339636 -0.16054575 ... -0.68442195 -0.36506078
   -0.19067191]
 [ 1.23388019  1.94372388 -0.26394125 ... -1.10325546  0.60439732
   -0.10558415]
 ...
 [ 0.3429808  0.00330087  0.14964075 ... -0.73518964 -0.68519336
   -0.27575966]
 [-0.84488505  0.1597866  -0.47073225 ... -0.24020459 -0.37110101
    1.17073215]
 [-0.84488505 -0.8730192  0.04624525 ... -0.20212881 -0.47378505
   -0.87137393]]
```

```
In [20]: X = standardized
Y = diabetes['Outcome']
```

```
In [21]: print(X)
print(Y)

[[ 0.63994726  0.84832379  0.14964075 ...  0.20401277  0.46849198
  1.4259954 ]
 [-0.84488505 -1.12339636 -0.16054575 ... -0.68442195 -0.36506078
 -0.19067191]
 [ 1.23388019  1.94372388 -0.26394125 ... -1.10325546  0.60439732
 -0.10558415]
 ...
 [ 0.34298088  0.00330087  0.14964075 ... -0.73518964 -0.68519336
 -0.27575966]
 [-0.84488505  0.1597866  -0.47073225 ... -0.24020459 -0.37110101
  1.17073215]
 [-0.84488505 -0.8730192  0.04624525 ... -0.20212881 -0.47378505
 -0.87137393]]
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
```

```
In [22]: plt.figure(figsize=(12, 6))
for i, column in enumerate(diabetes.columns[1:]):
    plt.subplot(2, 4, i+1)
    sns.boxplot(x='Outcome', y=column, data=diabetes)
    plt.title(f'{column} vs Outcome')
plt.tight_layout()
plt.show()
```



#### Train Test Split

```
In [23]: X_train, X_test, Y_train, Y_test = train_test_split(X,Y, test_size = 0.2, stratify=Y, random_state=2)
```

```
In [24]: print(X.shape, X_train.shape, X_test.shape)
```

```
(768, 8) (614, 8) (154, 8)
```

#### Training the Model

```
In [25]: classifier = svm.SVC(kernel='linear')
```

```
In [26]: classifier.fit(X_train, Y_train)
```

```
Out[26]: SVC(kernel='linear')
```

#### Model Evaluation

```
In [27]: X_train_prediction = classifier.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)
```

#### Accuracy Score

```
In [28]: # accuracy score on the train data
print('Accuracy score of the training data : ', training_data_accuracy)
```

```
Accuracy score of the training data : 0.7866449511400652
```

```
In [29]: X_test_prediction = classifier.predict(X_test)
test_data_accuracy = accuracy_score(X_test_prediction, Y_test)
```

```
In [30]: # accuracy score on the test data
print('Accuracy score of test data : ', test_data_accuracy)
```

```
Accuracy score of test data : 0.7727272727272727
```

```
In [31]: conf_matrix = confusion_matrix(X_test_prediction, Y_test)
class_report = classification_report(X_test_prediction, Y_test)

print("\nConfusion Matrix:")
print(conf_matrix)
print("\nClassification Report:")
print(class_report)
```

#### Confusion Matrix:

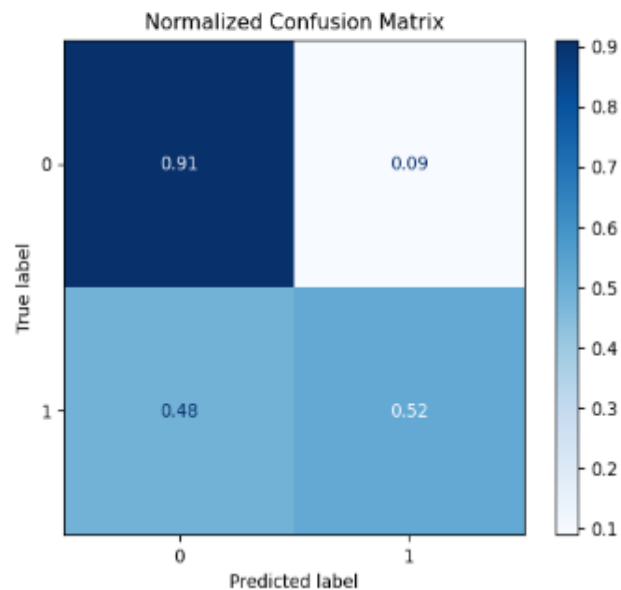
```
[[91 26]
 [ 9 28]]
```

#### Classification Report:

	precision	recall	f1-score	support
0	0.91	0.78	0.84	117
1	0.52	0.76	0.62	37
accuracy			0.77	154
macro avg	0.71	0.77	0.73	154
weighted avg	0.82	0.77	0.79	154

```
In [32]: disp = plot_confusion_matrix(classifier, X_test, Y_test, cmap=plt.cm.Blues, normalize='true')
disp.ax_.set_title('Normalized Confusion Matrix')
plt.show()
```

C:\Users\chint\anaconda3\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot\_confusion\_matrix is deprecated; Function 'plot\_confusion\_matrix' is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: ConfusionMatrixDisplay.from\_predictions or ConfusionMatrixDisplay.from\_estimator.  
warnings.warn(msg, category=FutureWarning)



```
In [33]: #Making a Predictive System
```

```
input_data = (5,166,72,19,175,25.8,0.587,51)

input_data_as_numpy_array = np.asarray(input_data)

input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

std_data = scaler.transform(input_data_reshaped)
print(std_data)

prediction = classifier.predict(std_data)
print(prediction)

if (prediction[0] == 0):
    print('The person is not diabetic')
else:
    print('The person is diabetic')
```

[[ 0.3429888 1.41167241 0.14964075 -0.09637905 0.82661621 -0.78595734  
 0.34768723 1.51108316]]

[1]  
The person is diabetic

C:\Users\chint\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but StandardScaler was fitted with feature names  
warnings.warn(



```
In [34]: correlation_matrix = diabetes.corr()
print(correlation_matrix)
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	\
Pregnancies	1.000000	0.129459	0.141282	-0.081672	
Glucose	0.129459	1.000000	0.152590	0.057328	
BloodPressure	0.141282	0.152590	1.000000	0.207371	
SkinThickness	-0.081672	0.057328	0.207371	1.000000	
Insulin	-0.073535	0.331357	0.088933	0.436783	
BMI	0.017683	0.221071	0.281805	0.392573	
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	
Age	0.544341	0.263514	0.239528	-0.113970	
Outcome	0.221898	0.466581	0.065068	0.074752	

	Insulin	BMI	DiabetesPedigreeFunction	\
Pregnancies	-0.073535	0.017683	-0.033523	
Glucose	0.331357	0.221071	0.137337	
BloodPressure	0.088933	0.281805	0.041265	
SkinThickness	0.436783	0.392573	0.183928	
Insulin	1.000000	0.197859	0.185071	
BMI	0.197859	1.000000	0.140647	
DiabetesPedigreeFunction	0.185071	0.140647	1.000000	
Age	-0.042163	0.036242	0.033561	
Outcome	0.130548	0.292695	0.173844	

	Age	Outcome
Pregnancies	0.544341	0.221898
Glucose	0.263514	0.466581
BloodPressure	0.239528	0.065068
SkinThickness	-0.113970	0.074752
Insulin	-0.042163	0.130548
BMI	0.036242	0.292695
DiabetesPedigreeFunction	0.033561	0.173844
Age	1.000000	0.238356
Outcome	0.238356	1.000000

```
In [35]: sns.heatmap(diabetes[['Pregnancies', 'Glucose', 'BMI', 'Insulin', 'Age', 'BloodPressure', 'SkinThickness', 'DiabetesPedigreeFunction']],
plt.title('Correlation Heatmap')
plt.show()
```

