

Importing the dependencies

```
In [1]: 1 import numpy as np
        2 import pandas as pd
        3 from sklearn.preprocessing import StandardScaler
        4 from sklearn.model_selection import train_test_split
        5 from sklearn import svm
        6 from sklearn.metrics import accuracy_score
        7 %matplotlib inline
        8 import warnings
        9 warnings.filterwarnings('ignore')
       10 from sklearn.metrics import adjusted_rand_score
```

Data Collection and Analysis Diabetes dataset

```
In [2]: 1 #Load the Dataset to a pandas dataframe
        2 diabetes_data = pd.read_csv(r"C:\Users\user\Desktop\Machine learning p
```

```
In [3]: 1 # printing the first 10 rowa of the data
        2 diabetes_data.head(10)
```

Out[3]:

| | Pregnancies | Glucose | BloodPressure | SkinThickness | Insulin | BMI | DiabetesPedigreeFun |
|---|-------------|---------|---------------|---------------|---------|------|---------------------|
| 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 | |
| 5 | 5 | 116 | 74 | 0 | 0 | 25.6 | |
| 6 | 3 | 78 | 50 | 32 | 88 | 31.0 | |
| 7 | 10 | 115 | 0 | 0 | 0 | 35.3 | |
| 8 | 2 | 197 | 70 | 45 | 543 | 30.5 | |
| 9 | 8 | 125 | 96 | 0 | 0 | 0.0 | |

```
In [4]: 1 # Lets look at the number of rows and colums in the dataset
        2 diabetes_data.shape
```

Out[4]: (768, 9)

```
In [5]: 1 # statistical measures of the data
        2 diabetes_data.describe()
```

Out[5]:

| | Pregnancies | Glucose | BloodPressure | SkinThickness | Insulin | BMI | Diabetes |
|-------|-------------|------------|---------------|---------------|------------|------------|----------|
| count | 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 | |
| std | 3.369578 | 31.972618 | 19.355807 | 15.952218 | 115.244002 | 7.884160 | |
| min | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | |
| 25% | 1.000000 | 99.000000 | 62.000000 | 0.000000 | 0.000000 | 27.300000 | |
| 50% | 3.000000 | 117.000000 | 72.000000 | 23.000000 | 30.500000 | 32.000000 | |
| 75% | 6.000000 | 140.250000 | 80.000000 | 32.000000 | 127.250000 | 36.600000 | |
| max | 17.000000 | 199.000000 | 122.000000 | 99.000000 | 846.000000 | 67.100000 | |

```
In [6]: 1 # checking counts of output
        2 diabetes_data['Outcome'].value_counts()
```

Out[6]: 0 500
 1 268
 Name: Outcome, dtype: int64

0 --> Non-diabetic

1 --> diabetic

```
In [7]: 1 # mean value for both ccaes
        2 diabetes_data.groupby('Outcome').mean()
```

Out[7]:

| | Pregnancies | Glucose | BloodPressure | SkinThickness | Insulin | BMI | Diabetes |
|---------|-------------|------------|---------------|---------------|------------|-----------|----------|
| Outcome | | | | | | | |
| 0 | 3.298000 | 109.980000 | 68.184000 | 19.664000 | 68.792000 | 30.304200 | |
| 1 | 4.865672 | 141.257463 | 70.824627 | 22.164179 | 100.335821 | 35.142537 | |

```
In [8]: 1 # separating data and labels
        2 x = diabetes_data.drop(columns= 'Outcome', axis=1)
        3 y = diabetes_data['Outcome']
```

In [9]:

```
1 print(x)
2 print(y)
```

| | 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 |
|-----|--------------------------|-----|
| 0 | 0.627 | 50 |
| 1 | 0.351 | 31 |
| 2 | 0.672 | 32 |
| 3 | 0.167 | 21 |
| 4 | 2.288 | 33 |
| .. | ... | ... |
| 763 | 0.171 | 63 |
| 764 | 0.340 | 27 |
| 765 | 0.245 | 30 |
| 766 | 0.349 | 47 |
| 767 | 0.315 | 23 |

[768 rows x 8 columns]

| | |
|-----|---|
| 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

Data Standardization

In [10]:

```
1 # Performing standardization
2 scaler = StandardScaler()
```

In [11]:

```
1 scaler.fit(x)
```

Out[11]: StandardScaler()

In [12]:

```
1 Sd_data = scaler.transform(x)
```

```
In [13]: 1 print(Sd_data)
```

```
[[ 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 [14]: 1 x = Sd_data
        2 y = diabetes_data['Outcome']
```

```
In [15]: 1 print(x)
        2 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]
 ...
 [ 0.3429808  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]]
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
```

Train Test Split

Splitting dataset into train and test set

```
In [16]: 1 x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0
```

```
In [17]: 1 # Let's see the shapes
2 print(x.shape,x_train.shape, x_test.shape)

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

Training a model

```
In [18]: 1 classifier = svm.SVC(kernel='linear')
```

```
In [19]: 1 #training the suport vector Machine Classifier
2 classifier.fit(x_train, y_train)
```

```
Out[19]: SVC(kernel='linear')
```

Model Evaluation

Lets check classification report,confusion marix and accuracy score of above model

```
In [20]: 1 #importing tools
2 from sklearn.metrics import classification_report, accuracy_score, co
```

```
In [21]: 1 # prediction classes
2 y_pred = classifier.predict(x_test)
```

```
In [22]: 1 print("CLASSIFICATION REPORT: ")
2 print(classification_report(y_test, y_pred))
```

```
CLASSIFICATION REPORT:
              precision    recall  f1-score   support

     0           0.78       0.91      0.84         100
     1           0.76       0.52      0.62          54

   accuracy                   0.77         154
  macro avg           0.77       0.71      0.73         154
 weighted avg           0.77       0.77      0.76         154
```

```
In [23]: 1 #Accuracy score of training data
2 x_train_prediction = classifier.predict(x_train)
3 training_data_accuracy = accuracy_score(x_train_prediction,y_train )*
```

```
In [24]: 1 print("ACCURACY OF TRAINING DATA: ",training_data_accuracy.round(2))
```

```
ACCURACY OF TRAINING DATA:  78.66
```

```
In [25]: 1 #Accuracy score of test data
2 x_test_prediction = classifier.predict(x_test)
3 test_data_accuracy = accuracy_score(x_test_prediction,y_test )*100
```

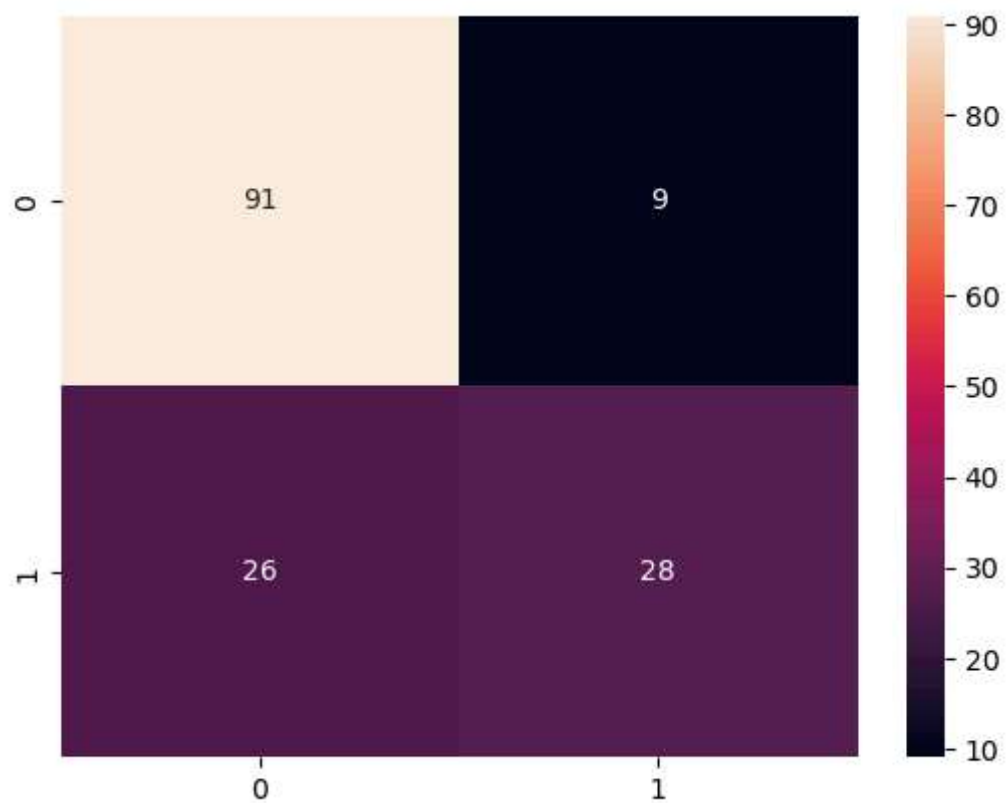
```
In [26]: 1 print("ACCURACY OF Test DATA: ",test_data_accuracy.round(2))
```

ACCURACY OF Test DATA: 77.27

Confusion Matrix

```
In [27]: 1 # Confusion Matrix
2 cm = confusion_matrix(y_test, y_pred)
3 #Visualizing the Confusion Matrix
4 import seaborn as sns
5 sns.heatmap(cm,annot=True)
```

Out[27]: <AxesSubplot:>



Making a predictive System

```

In [28]: 1 # input_data = (4,110,92,0,0,37.6,0.191,30) not diabetic
2 input_data = (5,166,72,19,175,25.8,0.587,51) # diabetic
3
4 # input data into numpy array
5 input_data_as_numpy_array = np.asarray(input_data)
6
7 # reshape the array as we are predicting for one instance
8 input_data_resaped = input_data_as_numpy_array.reshape(1,-1)
9
10 # standardize the inputdata
11 std_data = scaler.transform(input_data_resaped)
12 # print(std_data)
13
14 prediction = classifier.predict(std_data) # imp line
15 # print(prediction)
16
17 if (prediction[0]==0):
18     print('The person is not diabetic')
19 else:
20     print('The person is diabetic')

```

The person is diabetic

Saving the trained model

```

In [29]: 1 import pickle

```

```

In [30]: 1 filename = "trained_model.sav"
2 pickle.dump(classifier, open(filename, 'wb'))

```

```

In [31]: 1 #Loading the save model
2 loaded_model = pickle.load(open('trained_model.sav', 'rb'))

```

```

In [32]: 1 # input_data = (4,110,92,0,0,37.6,0.191,30) not diabetic
2 input_data = (5,166,72,19,175,25.8,0.587,51) # diabetic
3
4 # input data into numpy array
5 input_data_as_numpy_array = np.asarray(input_data)
6
7 # reshape the array as we are predicting for one instance
8 input_data_resaped = input_data_as_numpy_array.reshape(1,-1)
9
10 # standardize the inputdata
11 std_data = scaler.transform(input_data_resaped)
12 # print(std_data)
13
14 prediction = loaded_model.predict(std_data) # imp line
15 # print(prediction)
16
17 if (prediction[0]==0):
18     print('The person is not diabetic')
19 else:
20     print('The person is diabetic')

```

The person is diabetic

In []: ▶

1