<pre>import numpy as np import pandas as pd import matplotlib.pyplot as plt import seaborn as sns from sklearn.preprocessing import StandardScaler from sklearn.model_selection import train_test_split from sklearn import svm from sklearn.metrics import accuracy_score</pre>			
<pre>#data collection from csv file #loadingg the diabetes dataset to panda Dataframe dataset=pd.read_csv("D:\diabetes prediction dataset.csv") dataset Pregnancies Glucose BloodPressure SkinThickness Insulin BMI</pre>	0.627 50 1		
2 8 183 64 0 0 23.3 3 1 89 66 23 94 28.1 4 0 137 40 35 168 43.1	0.672 32 1 0.167 21 0 2.288 33 1 0.171 63 0 0.340 27 0		
765 5 121 72 23 112 26.2 766 1 126 60 0 0 30.1 767 1 93 70 31 0 30.4 768 rows × 9 columns [4]: #printing the first 5 rows of the dataset dataset.head()	0.349 47 1		
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	DiabetesPedigreeFunction Age Outcome 0.627 50 1 0.351 31 0 0.672 32 1 0.167 21 0 2.288 33 1		
<pre>[5]: #number odf rows and coloumns in this dataset dataset.shape [5]: (768, 9) [6]: #getting the statistical measures of the data dataset.describe() [6]: Pregnancies Glucose BloodPressure SkinThickness Inst</pre>	ulin BMI DiabetesPedigreeFunction Age Outcome		
	000 768.000000 768.000000 768.000000 768.000000 479 31.992578 0.471876 33.240885 0.348958 002 7.884160 0.331329 11.760232 0.476951 000 0.000000 0.078000 21.000000 0.000000 000 27.300000 0.243750 24.000000 0.000000		
75% 6.000000 117.000000 72.000000 23.000000 30.5000 75% 6.000000 140.250000 80.000000 32.000000 127.2500 max 17.000000 199.000000 122.000000 99.000000 846.0000 [7]: dataset['Outcome'].value_counts() #0>Non-Diabetic #1>Diabetic	000 36.600000		
<pre>[7]: 0 500 1 268 Name: Outcome, dtype: int64 [8]: # Adding the correlation matrix to the code # Get the correlation matrix correlation_matrix = dataset.corr() # Print the correlation matrix</pre>			
<pre>print("Correlation Matrix:") print(correlation_matrix) # Plotting the correlation matrix as a heatmap plt.figure(figsize=(10, 8)) plt.title('Correlation Matrix') plt.imshow(correlation_matrix, cmap='pink') plt.colorbar() plt.xticks(range(len(dataset.columns)), dataset.columns,rotati plt.yticks(range(len(dataset.columns)), dataset.columns)</pre>	ion=90)		
plt.show() Pregnancies Glucose BloodPressure Pregnancies 1.000000 0.129459 0.141282 Glucose 0.129459 1.000000 0.152590 BloodPressure 0.141282 0.152590 1.000000 SkinThickness -0.081672 0.057328 0.207371 Insulin -0.073535 0.331357 0.088933 BMI 0.017683 0.221071 0.281805 DiabetesPedigreeFunction -0.033523 0.137337 0.041265	SkinThickness \ -0.081672 0.057328 0.207371 1.000000 0.436783 0.392573 0.183928		
Glucose 0.331357 0.221071 0 BloodPressure 0.088933 0.281805 0 SkinThickness 0.436783 0.392573 0 Insulin 1.000000 0.197859 0 BMI 0.197859 1.000000 0	.033523 .137337 .041265 .183928 .185071 .140647		
Age -0.042163 0.036242 0 Outcome 0.130548 0.292695 0 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	.000000 .033561 .173844		
BMI 0.036242 0.292695 DiabetesPedigreeFunction 0.033561 0.173844 Age 1.000000 0.238356 Outcome 0.238356 1.000000 Correlat Pregnancies -	tion Matrix		
Glucose - BloodPressure - SkinThickness -	- 0.8		
Insulin -	- 0.4		
Age - Outcome -	- 0.2		
Pregnancies - Glucose - SkinThickness -	BMI - betesPedigreeFunction - Age -		
<pre>[9]: plt.figure(figsize=(10, 6)) sns.histplot(x='Glucose', hue='Outcome', data=dataset, bins=20 plt.title('Glucose Distribution by Outcome') plt.xlabel('Glucose Level') plt.ylabel('Count') plt.show()</pre> Glucose Distribution by			
80 -	Outcome Outcome 1		
60 - tino 40 -			
20 - 25 50 75 100 Glucose Level	125 150 175 200		
plt.figure(figsize=(8, 5)) sns.countplot(x='Pregnancies', hue='Outcome', data=dataset, paper plt.title('Pregnancies Distribution by Outcome') plt.xlabel('Number of Pregnancies') plt.ylabel('Count') plt.show() Pregnancies Distribution by Outcome'			
100 -	Outcome 0 1		
40 - 20 -			
plt.figure(figsize=(8, 5)) sns.countplot(x='BloodPressure', hue='Outcome', data=dataset, plt.title('Blood Pressure Distribution by Outcome') plt.xlabel('Blood Pressure') plt.ylabel('Count')	12 13 14 15 17 palette='muted')		
Blood Pressure Distribution by Outc	ome Outcome 0 1		
25 - 10 -			
5 - 0 02 8084044645052545565666162645565807274757678808284838688 Blood Pressure	092949596980100120140180181101.1422		
<pre>sns.histplot(x='BMI', hue='Outcome', data=dataset, bins=20, pa plt.title('BMI Distribution by Outcome') plt.xlabel('BMI') plt.ylabel('Count') plt.show()</pre> BMI Distribution by	Outcome Outcome 0		
80 - 60 -			
20 -			
BMI #calculating mean for both diabetic and non diabetic dataset.groupby('Outcome').mean()	40 50 60 70		
Outcome 0 3.298000 109.980000 68.184000 19.664000 68.7	Insulin BMI DiabetesPedigreeFunction Age 792000 30.304200 0.429734 31.190000 335821 35.142537 0.550500 37.067164 alette='muted')		
plt.xlabel('Age') plt.ylabel('Count') plt.show() Age Distribution by	Outcome Outcome 0 1		
120 - 100 - 100 -			
60 - 40 - 20 -			
20 30 40 50 Age [15]: # Seperating the data and labels X=dataset.drop(columns='Outcome', axis=1)	60 70 80		
1 1 85 66 29	n BMI \ 0 33.6 0 26.6 0 23.3		
3 1 89 66 23 9 4 0 137 40 35 16 <t< td=""><td>4 28.1 8 43.1 0 32.9 0 36.8 2 26.2 0 30.1 0 30.4</td><td></td><td></td></t<>	4 28.1 8 43.1 0 32.9 0 36.8 2 26.2 0 30.1 0 30.4		
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] [17]: 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 [18]: #Data Standardization scaler=StandardScaler()			
<pre>scaler.fit(X) standarized_data=scaler.transform(X) print(standarized_data) [[0.63994726 0.84832379 0.14964075 0.20401277 0.468491</pre>	78		
[1.23388019	36 01		
Y=dataset['Outcome'] print(X) print(Y) [[0.63994726 0.84832379 0.14964075 0.20401277 0.468491	78		
-0.10558415] [0.3429808 0.00330087 0.14964075 0.73518964 -0.685193 -0.27575966] [-0.84488505 0.1597866 -0.47073225 0.24020459 -0.371101 1.17073215] [-0.84488505 -0.8730192	36 01		
2 1 3 0 4 1 763 0 764 0 765 0 766 1 767 0 Name: Outcome, Length: 768, dtype: int64			
<pre>[20]: # Train Test Split X_train, X_test, Y_train, Y_test=train_test_split(X,Y,test_size=6] [21]: print(X.shape, X_train.shape, X_test.shape) (768, 8) (614, 8) (154, 8) [22]: classifier=svm.SVC(kernel='linear') #training the support vector Machine Classifier</pre>	.2,stratify=Y,random_state=2)		
classifier.fit(X_train,Y_train) [22]: V SVC SVC(kernel='linear') [23]: # Accuracy of the training data			
<pre>X_train_prediction=classifier.predict(X_train) training_data_accuracy=accuracy_score(X_train_prediction,Y_tra print('Accuracy score of the training data:',training_data_acc Accuracy score of the training data: 0.7866449511400652 [24]: # Accuracy of the test data X_test_prediction=classifier.predict(X_test) test_data_accuracy=accuracy_score(X_test_prediction,Y_test)</pre>			
test_data_accuracy=accuracy_score(X_test_prediction,Y_test) print('Accuracy score of the test data:',test_data_accuracy) Accuracy score of the test data: 0.77272727272727 [25]: feature_names = ['Pregnancies', 'Glucose', 'BloodPressure', 'Sinput_data=(1,189,60,23,846,30.1,0.398,59) #changing the input_data to numpy array input_data_as_numpy_array=np.asarray(input_data)	SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Ag	2']	
<pre>#reshaping the array as we are predicting for one instance input_data_reshape=input_data_as_numpy_array.reshape(1,-1) #standardize the input data std_data=scaler.transform(input_data_reshape) print(std_data) prediction=classifier.predict(std_data)</pre>			
<pre>print(prediction) if (prediction[0]==0): print('The person is not diabetic') else: print('The person is diabetic') [[-0.84488505 2.13150675 -0.47073225 0.15453319 6.65283938 -0.2231152 2.19178518]]</pre>	0.24020459		

[1] The person is diabetic