Importing Required Libraries

```
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
```

```
data = pd.read_csv('/content/diabetes.csv')
```

```
data
```

	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
...	...	...	...	...	...	...	...	...	...
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

768 rows × 9 columns

```
data.head(5)
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigre
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	

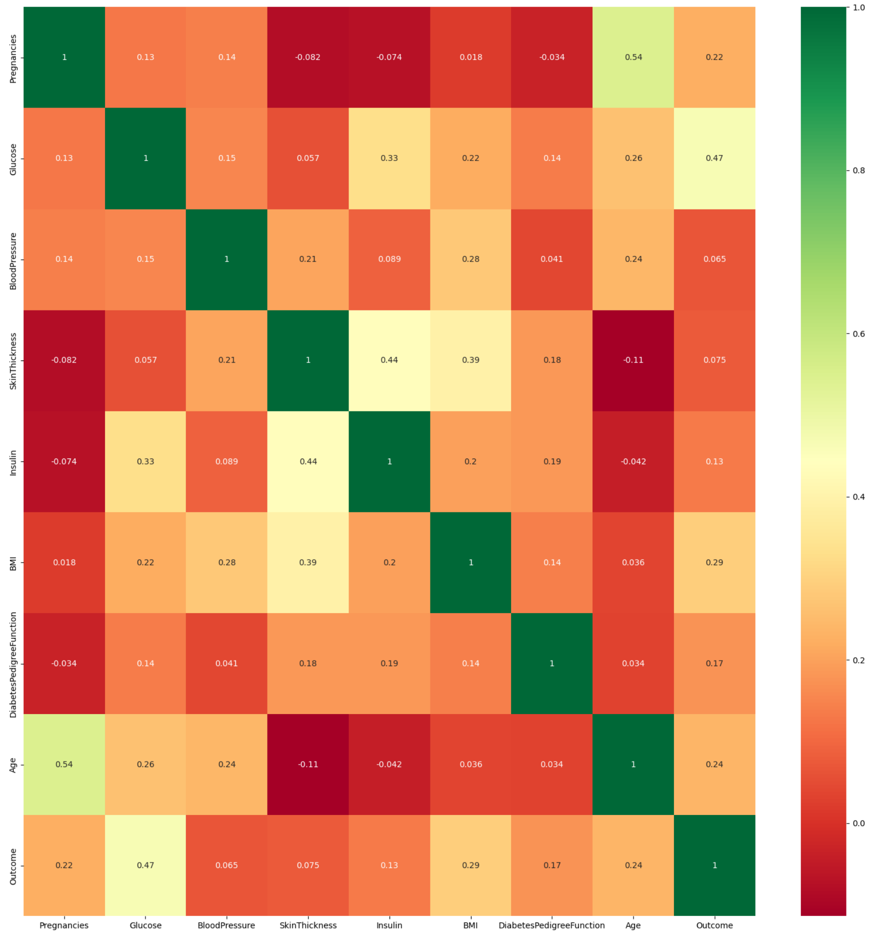
```
data.shape
```

```
(768, 9)
```

```
#Check if any null value is present
data.isnull().values.any()
```

```
False
```

```
# Correlation
import seaborn as sns
import matplotlib.pyplot as plt
# get correlation of each features in dataset
corrmat = data.corr()
top_corr_features = corrmat.index
plt.figure(figsize=(20,20))
# Plot Heat Map
g = sns.heatmap(data[top_corr_features].corr(),annot=True,cmap="RdYlGn")
```



```
data.corr()
```

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

```
data['Outcome'].value_counts()
```

```
0    500
1    268
Name: Outcome, dtype: int64
```

```
data.groupby('Outcome').mean()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI
1	4.865672	141.257463	70.824627	22.164179	100.335821	35.142537

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

```
X
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedig
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	

768 rows × 8 columns

```
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
```

Data Standardization

```
scaler = StandardScaler()
```

```
scaler.fit(X)
```

```
▾ StandardScaler
StandardScaler()
```

```
standardized_data = scaler.transform(X)
```

```
print(standardized_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]]
```

```
X = standardized_data
Y = data['Outcome']
```

```
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]
 ...
 [ 0.3429808   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
```

Check how many other missing(zero) values

```
print("Total no of rows : {0}".format(len(data)))
print("Number of rows missing Pregnancies: {0}".format(len(data.loc[data['Pregnancies']== 0])))
print("Number of rows missing Glucose: {0}".format(len(data.loc[data['Glucose']== 0])))
print("Number of rows missing BloodPressure: {0}".format(len(data.loc[data['BloodPressure']== 0])))
print("Number of rows missing SkinThickness: {0}".format(len(data.loc[data['SkinThickness']== 0])))
print("Number of rows missing Insulin: {0}".format(len(data.loc[data['Insulin']== 0])))
print("Number of rows missing BMI: {0}".format(len(data.loc[data['BMI']== 0])))
print("Number of rows missing DiabetesPedigreeFunction: {0}".format(len(data.loc[data['DiabetesPedigreeFunction']== 0])))
print("Number of rows missing Age: {0}".format(len(data.loc[data['Age']== 0])))
```

```
Total no of rows : 768
Number of rows missing Pregnancies: 111
Number of rows missing Glucose: 5
Number of rows missing BloodPressure: 35
Number of rows missing SkinThickness: 227
Number of rows missing Insulin: 374
Number of rows missing BMI: 11
Number of rows missing DiabetesPedigreeFunction: 0
Number of rows missing Age: 0
```

Train Test Split

```
X_train, X_test, Y_train, Y_test = train_test_split(X,Y, test_size = 0.2, stratify=Y, random_state=2)
```

```
print(X.shape, X_train.shape, X_test.shape)
```

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

Training the model

```
classifier = svm.SVC(kernel='linear')
```

```
#training the support vector Machine Classifier
classifier.fit(X_train, Y_train)
```

```
▾       SVC
SVC(kernel='linear')
```

Accuracy Score

```
# accuracy score on the training data
X_train_prediction = classifier.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)
```

```
print('Accuracy score of the training data : ', training_data_accuracy)
```

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

```
# accuracy score on the test data
X_test_prediction = classifier.predict(X_test)
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 :  0.7727272727272727
```

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

# changing the input_data to numpy array
input_data_as_numpy_array = np.asarray(input_data)

# reshape the array as we are predicting for one instance
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

# standardize the input data
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')
```

```
    [[ 0.3429808   1.41167241  0.14964075 -0.09637905  0.82661621 -0.78595734
       0.34768723  1.51108316]]
    [1]
    The person is diabetic
    /usr/local/lib/python3.10/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but StandardScaler w
      warnings.warn(
```