

importing the dependencies

```
In [70]: import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix
from matplotlib.pyplot import figure
import seaborn as sns
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
import plotly.express as px
```

Data Collection And Analysis

PIMA Diabeyes Dataset

```
In [71]: data=pd.read_csv("diabetes_data.csv")
```

```
In [72]: #printing first 5 rows of dataset
data.head()
```

```
Out[72]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	A
0	6	148	72	35	0	33.6		0.627
1	1	85	66	29	0	26.6		0.351
2	8	183	64	0	0	23.3		0.672
3	1	89	66	23	94	28.1		0.167
4	0	137	40	35	168	43.1		2.288

In [73]: *# information of dataset*
data.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
```

In [6]: data.shape

Out[6]: (768, 9)

In [74]: data.describe()

Out[74]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPe
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	

Check Missing Values

```
In [12]: data.isnull().sum()
```

```
Out[12]: Pregnancies      0
          Glucose          0
          BloodPressure    0
          SkinThickness     0
          Insulin           0
          BMI               0
          DiabetesPedigreeFunction  0
          Age              0
          Outcome          0
          dtype: int64
```

```
In [14]: # Handle Missing Values
          data.isnull().sum()*100/len(data)
```

```
Out[14]: Pregnancies      0.0
          Glucose          0.0
          BloodPressure    0.0
          SkinThickness     0.0
          Insulin           0.0
          BMI               0.0
          DiabetesPedigreeFunction  0.0
          Age              0.0
          Outcome          0.0
          dtype: float64
```

```
In [48]: data['Outcome'].value_counts()
```

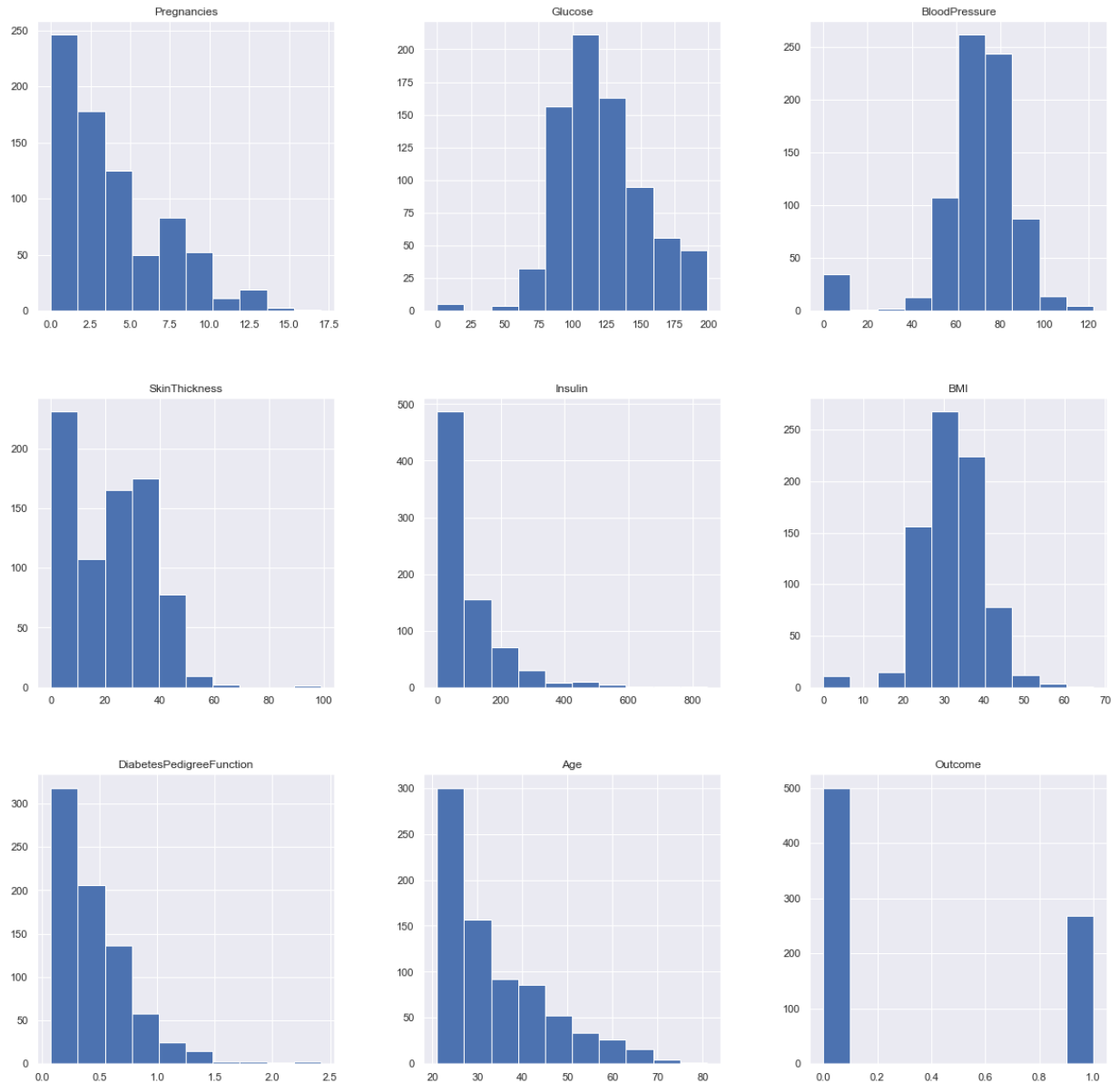
```
Out[48]: 0    500
          1    268
          Name: Outcome, dtype: int64
```

0--> Non Diabetic

1--> Diabetic

Histogram

```
In [20]: #histogram  
p = data.hist(figsize = (20,20))
```



PairPlot

```
In [21]: #pairplot
sns.pairplot(data)
```

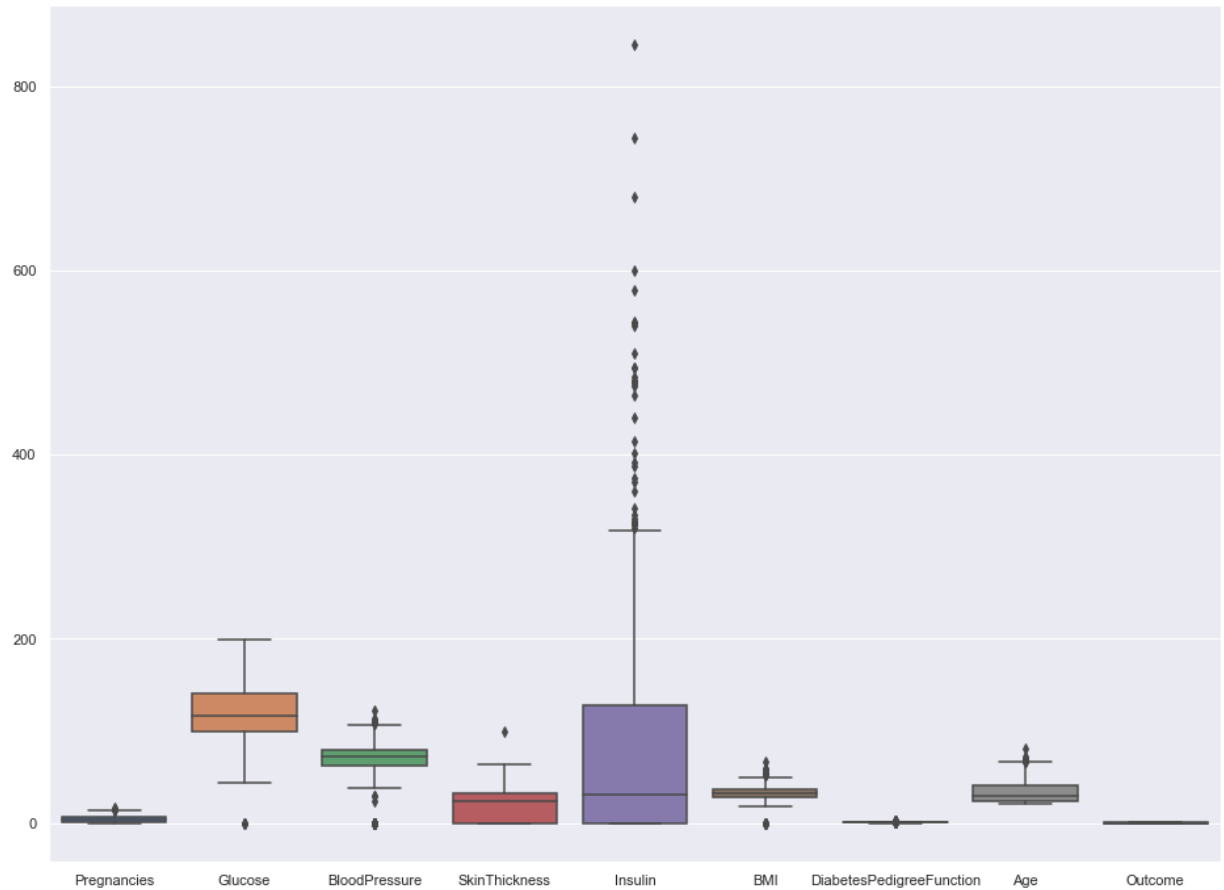
```
Out[21]: <seaborn.axisgrid.PairGrid at 0x17c523b69a0>
```



Boxplot

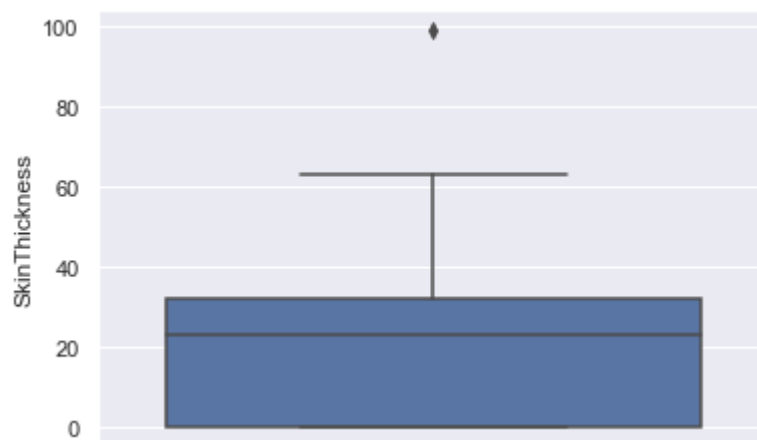
```
In [45]: plt.figure(figsize=(16,12))  
sns.boxplot(data=data)
```

Out[45]: <AxesSubplot:>



```
In [46]: sns.boxplot(y = 'SkinThickness', data = data)
```

```
Out[46]: <AxesSubplot:ylabel='SkinThickness'>
```



```
In [62]: from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
```

```
In [64]: scaler.fit(x)
```

```
Out[64]: StandardScaler()
```

```
In [27]: x = data.iloc[:, :-1]
y = data.iloc[:, -1]
```

```
In [28]: x.head()
```

```
Out[28]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	A
0	6	148	72	35	0	33.6	0.627	
1	1	85	66	29	0	26.6	0.351	
2	8	183	64	0	0	23.3	0.672	
3	1	89	66	23	94	28.1	0.167	
4	0	137	40	35	168	43.1	2.288	

```
In [29]: y.head()
```

```
Out[29]: 0    1
         1    0
         2    1
         3    0
         4    1
         Name: Outcome, dtype: int64
```

Train_Test_Split

```
In [76]: from sklearn.model_selection import train_test_split
         X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random
```

```
In [77]: print_score(X_train, X_test, y_train, y_test)
```

SVM:

Train score : 0.758957654723127
Test score : 0.7922077922077922


```
In [80]: X_train.shape
```

```
Out[80]: (614, 8)
```

```
In [82]: y_test.shape
```

```
Out[82]: (154,)
```

```
In [83]: X_train.shape
```

```
Out[83]: (614, 8)
```

```
In [84]: y_train.shape
```

```
Out[84]: (614,)
```

Model Evaluation

```
In [34]: from sklearn.svm import SVC
```

```
In [86]: svm=SVC(kernel='linear')
         svm
```

```
Out[86]: SVC(kernel='linear')
```



```
In [36]: svm.fit(X_train,y_train)
```

```
Out[36]: SVC(kernel='linear')
```

```
In [85]: y_svm=svm.predict(X_test)
y_svm
```

```
Out[85]: array([1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0,
                0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1,
                1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 1, 1,
                1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1,
                0, 0, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0],
                dtype=int64)
```

Confusion_Matrix

```
In [39]: svm_cm_test=confusion_matrix(y_test,y_svm)
svm_cm_test
```

```
Out[39]: array([[97, 10],
                [18, 29]], dtype=int64)
```

Accuracy

```
In [42]: from sklearn.metrics import accuracy_score
svm_acc_test=accuracy_score(y_test,y_svm)
```

```
In [47]: print(svm_acc_test)
```

```
0.8181818181818182
```

Making a Predictive System

```
In [75]: input_data=(4,110,92,0,0,37.6,0.191,30)

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

#reshape the array as we 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=svm.predict(std_data)
print(prediction)

[[ 0.04601433 -0.34096773  1.18359575 -1.28821221 -0.69289057  0.71168975
 -0.84827977 -0.27575966]]
[0]
```

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

```
In [68]: if(prediction[0]==0):
          print('non-diabetic')
        else:
          print('diabetic')
```

non-diabetic

Making pickle file

```
In [69]: import pickle
diabetes_pickle_file='svm.pkl'
pickle.dump(svm,open('diabetes_pickle_file','wb'))
pic=pickle.load(open('diabetes_pickle_file','rb'))
pic.predict([[4,110,92,0,0,37.6,0.191,30]])
```

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

```
Out[69]: array([0], dtype=int64)
```

```
In [ ]:
```

