Verzeo Internship - Major Project - ML June Batch

Problem Statement :

Pima Indian Diabetes dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

Do classification by at least 2 Algorithms.

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import sklearn.metrics as metrics
from sklearn.metrics import classification_report
from sklearn.metrics import plot_confusion_matrix
from sklearn.metrics import average_precision_score
```

In [2]:
```
df = pd.read_csv("diabetes.csv")
```

In [3]:
```
df
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunc
0	6	148	72	35	0	33.6	0
1	1	85	66	29	0	26.6	0
2	8	183	64	0	0	23.3	0
3	1	89	66	23	94	28.1	0
4	0	137	40	35	168	43.1	2
...	...	...	...	...	...	...	
763	10	101	76	48	180	32.9	
764	2	122	70	27	0	36.8	0
765	5	121	72	23	112	26.2	0
766	1	126	60	0	0	30.1	0
767	1	93	70	31	0	30.4	0

768 rows × 9 columns

In [4]:
```
## statistic of dataset
diabetes = df[df['Outcome']==1].shape
```

```
non_diabetes = df[df['Outcome']==0].shape
print("Has Diabetes {}, Does not have Diabetes {}".format(diabetes,non_diabet
df.describe()
```

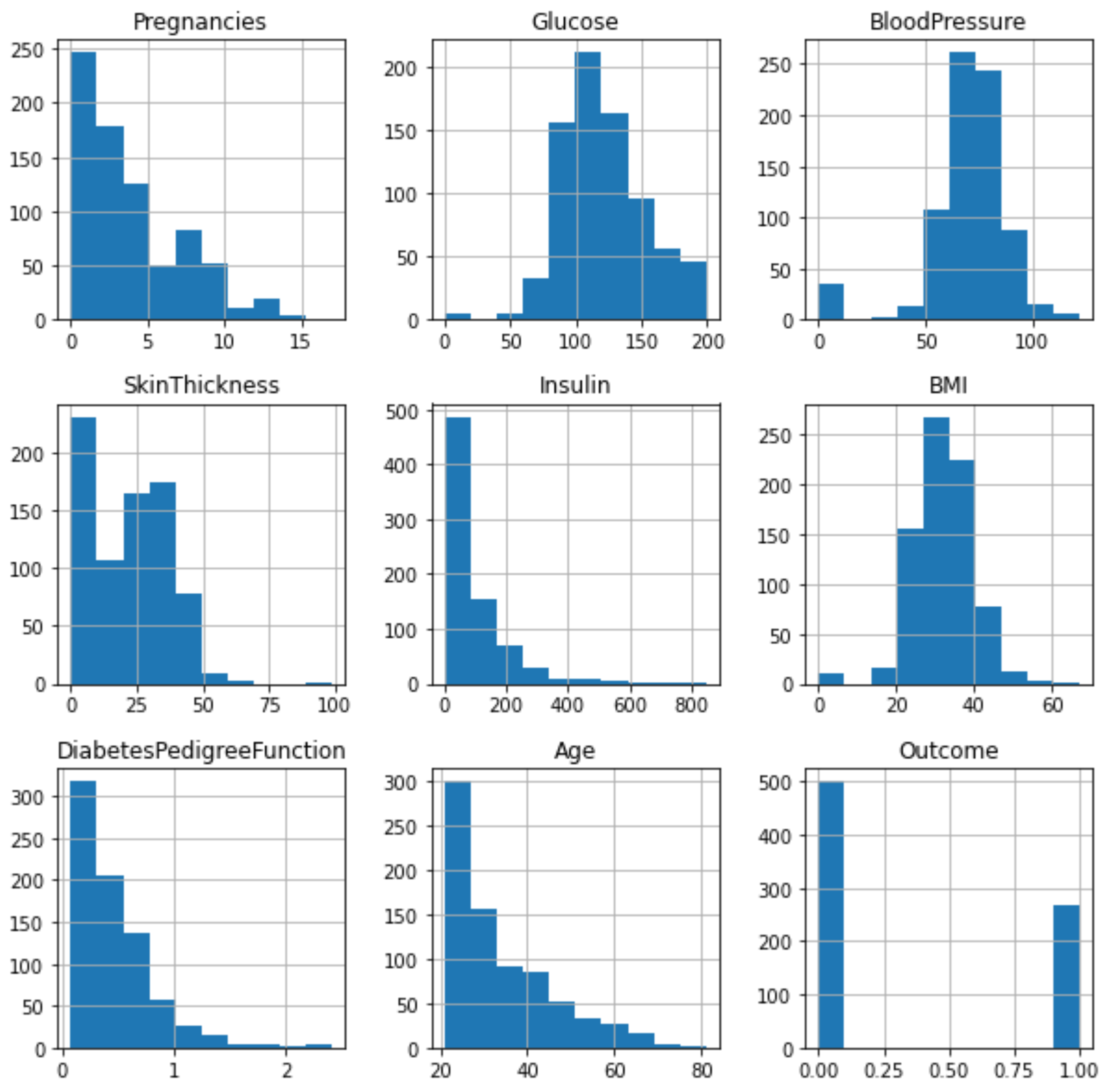
```
Has Diabetes (268, 9), Does not have Diabetes (500, 9)
```

Out[4]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diab
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 [5]:

```
# x-axis range , y-axis abundance
histo = df.hist(figsize = (10,10))
```



In [6]:
```
## count of zero entries
bp_zeros = df[df['BloodPressure']==0].shape
bmi_zeros = df[df['BMI']==0].shape
insulin_zeros = df[df['Insulin']==0].shape
glucose_zeros = df[df['Glucose']==0].shape
skin_zeros = df[df['SkinThickness']==0].shape
print('Zero Counts of BP :{},BMI : {} , Insulin : {} , Glucose : {} , skin :
      .format(bp_zeros,bmi_zeros,insulin_zeros,glucose_zeros,skin_zeros))
```

```
Zero Counts of BP :(35, 9),BMI : (11, 9) , Insulin : (374, 9) , Glucose : (5,
9) , skin : (227, 9)
```

In [7]:
```
#### pre-process Insulin & SkinThickness

df_copy = df.copy(deep=True)

df_copy[['Insulin','SkinThickness']] = df_copy[['Insulin','SkinThickness']].r
## The median is the middle point of a number set, in which half the numbers
## replace null value with median
df_copy['Insulin'].fillna(df_copy['Insulin'].median(),inplace=True)
df_copy['SkinThickness'].fillna(df_copy['SkinThickness'].median(),inplace=Tru
## test result
# print(df_copy[df_copy['Insulin']==0].shape,df_copy[df_copy['SkinThickness']
# pre-process Blood Pressure , BMI & Glucose invalid values
# as blood pressure & glucose are critical for determing diabeties it should
# their null fraction is very small so it should better to remove invalid ent
df_copy = df_copy[(df_copy['BloodPressure']!=0) & (df_copy['BMI']!=0) & (df_c
# test result
# print(df_copy[df_copy['BloodPressure']==0].shape,df_copy[df_copy['BMI']==0]
```

In [8]:
```
from sklearn.model_selection import train_test_split
```

In [9]:
```
## split dataset on outcome from 70% to 30%
X = df_copy.drop('Outcome',axis=1)
y = df_copy['Outcome']
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.30,random_st
print(X_train.shape)
print(X_test.shape)
print(y_train.shape)
print(y_test.shape)
```

```
(506, 8)
(218, 8)
(506,)
(218,)
```

Classification 1: Naive Bayes Classification

In [10]:
```
from sklearn.naive_bayes import GaussianNB
```

In [11]:
```
nb_model = GaussianNB()
```

In [12]:
```
nb_model.fit(X_train,y_train)
```

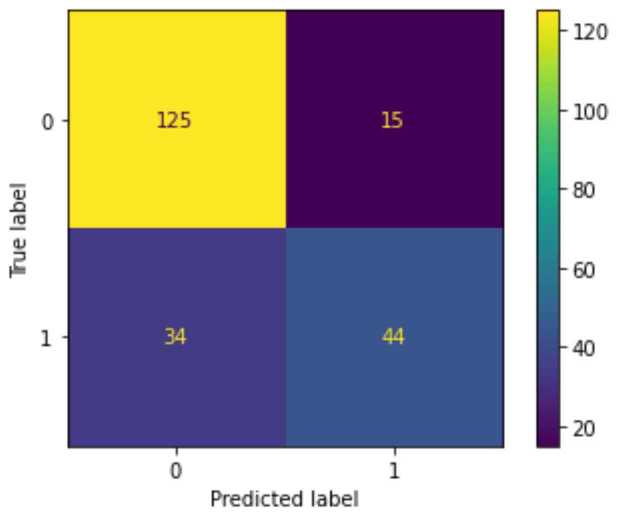
```
Out[12]: GaussianNB()
```

```
In [13]: predicted_nb_model = nb_model.predict(X_test)
```

```
In [14]: cm_nb_model = metrics.confusion_matrix(y_test,predicted_nb_model)
```

```
In [15]: accuracy_nb_model = metrics.accuracy_score(y_test,predicted_nb_model)
```

```
In [16]: plot_confusion_matrix(nb_model, X_test, y_test)
         plt.show()
```



```
In [17]: print("Confusion Matrix: \n",cm_nb_model)
         print("Accuracy: \n",accuracy_nb_model)
         average_precision = average_precision_score(y_test, predicted_nb_model)
         print("Average Precision = ",average_precision)
```

```
Confusion Matrix:
 [[125  15]
 [ 34  44]]
Accuracy:
 0.7752293577981652
Average Precision =  0.5766499607270872
```

```
In [18]: print(classification_report(y_test,nb_model.predict(X_test)))
```

```
              precision    recall  f1-score   support

           0       0.79      0.89      0.84       140
           1       0.75      0.56      0.64        78

    accuracy                           0.78       218
   macro avg       0.77      0.73      0.74       218
weighted avg       0.77      0.78      0.77       218
```

According to confusion matrix of Naive Bayes classifier, there are 44 who has Diabetes, 125 who does not have Diabetes and 49 which are misclassified.

Classification 2: Support Vector Machine Classification

In [19]:
```
from sklearn.svm import SVC
```

In [20]:
```
svc = SVC(random_state=0, kernel='rbf')
```

In [21]:
```
svc.fit(X_train, y_train)
```

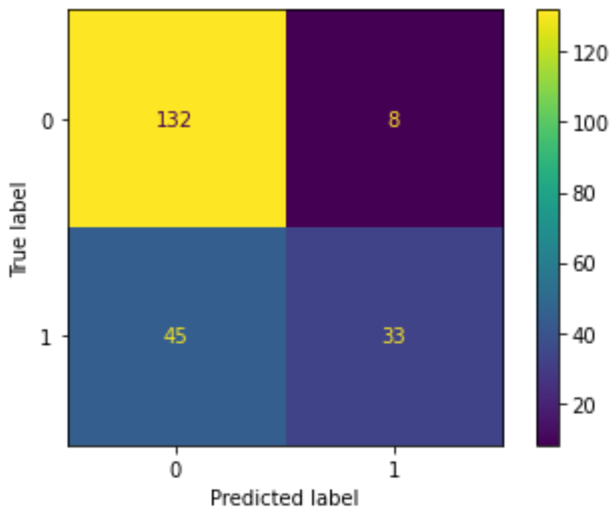
Out[21]:
```
SVC(random_state=0)
```

In [22]:
```
svm_y_pred = svc.predict(X_test)
```

In [23]:
```
cm_svc = metrics.confusion_matrix(y_test,svm_y_pred)
```

In [24]:
```
accuracy_svc = metrics.accuracy_score(y_test,svm_y_pred)
```

In [25]:
```
plot_confusion_matrix(svc, X_test, y_test)
plt.show()
```



In [26]:
```
print("Confusion Matrix: \n",cm_svc)
print("Accuracy: \n",accuracy_svc)
average_precision = average_precision_score(y_test, svm_y_pred)
print("Average Precision = ",average_precision)
```

```
Confusion Matrix:
 [[132   8]
 [ 45  33]]
Accuracy:
 0.7568807339449541
Average Precision =  0.5469473466788302
```

In [27]:
```
print(classification_report(y_test,svc.predict(X_test)))
```

```
              precision    recall  f1-score   support

           0       0.75      0.94      0.83       140
           1       0.80      0.42      0.55        78

    accuracy                           0.76       218
   macro avg       0.78      0.68      0.69       218
weighted avg       0.77      0.76      0.73       218
```

According to confusion matrix of Support Vector Machine classifier, there are 33 who has Diabetes, 132 who does not have Diabetes and 53 which are misclassified.