Diabetes_classification_with_LogisticRegression_SVC_DecisionTree_NaiveB

[1]:
```
#let's start with importing necessary libraries
import pandas as pd
import numpy as np
from sklearn.preprocessing import StandardScaler #scaling dataset

## all models/aglorithm for classification
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.svm import SVC
#from sklearn.naive_bayes import BernoulliNB
from sklearn.naive_bayes import GaussianNB

from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns
```

[3]:
```
#read the data file from folder
data = pd.read_csv('diabetes.csv')
data.head(2)
```

[3]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
```

[3]:
```
## for EDA
data.describe()

## if we had any categorical variable column then we would use OneHot-encoding,␣
↪ordinal-encoding or target-guided encoding
```

```python
## for now we mostly have numerical column

### we can see minimum values as 0, but it can't be real,like gulcose can␣
↪nerver be 0 of any person
```

[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin
count	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479
std	3.369578	31.972618	19.355807	15.952218	115.244002
min	0.000000	0.000000	0.000000	0.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000
75%	6.000000	140.250000	80.000000	32.000000	127.250000
max	17.000000	199.000000	122.000000	99.000000	846.000000

	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000
mean	31.992578	0.471876	33.240885	0.348958
std	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.078000	21.000000	0.000000
25%	27.300000	0.243750	24.000000	0.000000
50%	32.000000	0.372500	29.000000	0.000000
75%	36.600000	0.626250	41.000000	1.000000
max	67.100000	2.420000	81.000000	1.000000

[4]:

```python
data.isnull().sum()
## no null value
```

[4]:

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

We can see there few data for columns Glucose, Insulin, skin thickness, BMI and Blood Pressure which have value as 0. That's not possible, right? you can do a quick search to see that one cannot have 0 values for these. Let's deal with that. we can either remove such data or simply replace it with their respective mean values. Let's do the latter.

[4]:

```python
## trying to get all 0 values of these particular columns
```

[5]:

```python
data[(data==0).any(axis=1)][0:2] ## outcome column is also returning
```

[5]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
```

[ ]:
```
data[(data['Glucose']==0) | (data['BloodPressure']==0) |␣
↪(data['SkinThickness']==0) | (data['Insulin']==0) | (data['BMI']==0)]
```

[ ]:
```
     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
5              5      116             74              0        0  25.6
7             10      115              0              0        0  35.3
..           …        …              …              …       …   …
761            9      170             74             31        0  44.0
762            9       89             62              0        0  22.5
764            2      122             70             27        0  36.8
766            1      126             60              0        0  30.1
767            1       93             70             31        0  30.4

     DiabetesPedigreeFunction  Age  Outcome
0                       0.627   50        1
1                       0.351   31        0
2                       0.672   32        1
5                       0.201   30        0
7                       0.134   29        0
..                        …  …      …
761                     0.403   43        1
762                     0.142   33        0
764                     0.340   27        0
766                     0.349   47        1
767                     0.315   23        0

[376 rows x 9 columns]
```

[18]:
```
data[(data['Glucose']==0) | (data['BloodPressure']==0) |␣
↪(data['SkinThickness']==0) | (data['Insulin']==0) | (data['BMI']==0)].shape
```

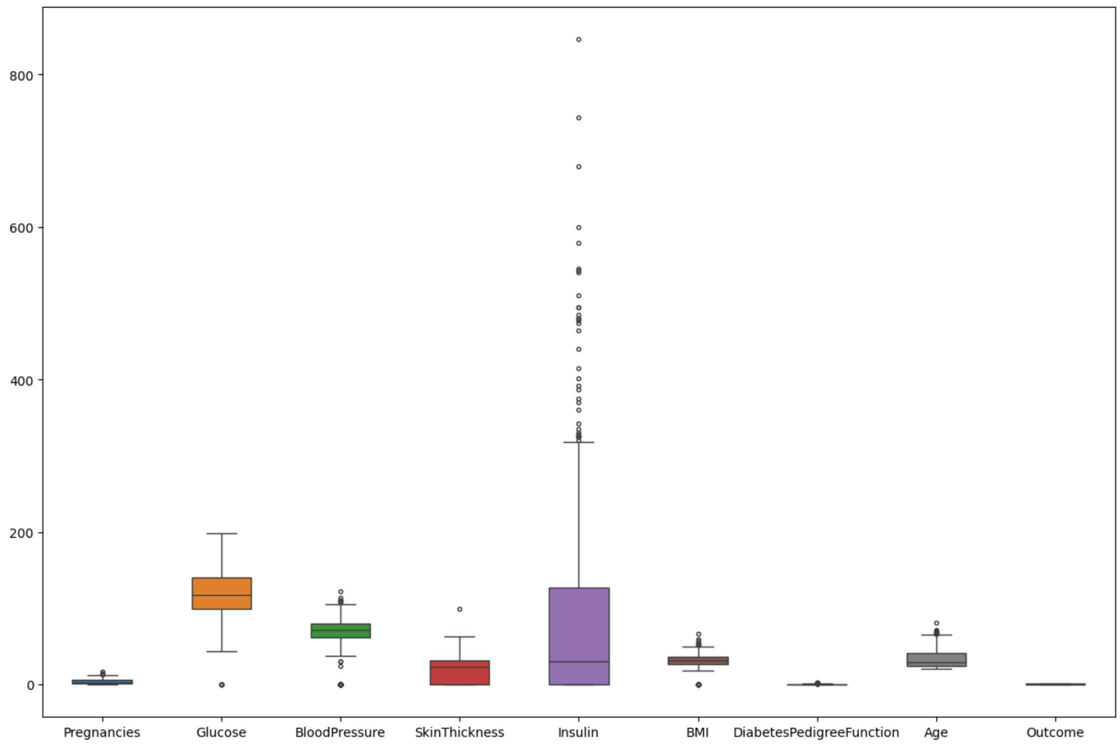
[18]:
```
(376, 9)
```

[20]:
```
## so many rows have 0 (50% rows), we'll replace it with mean or median(if␣
↪distribution have outlier)
data.shape
```

[20]: (768, 9)

[23]:
```
##there are outliers present in some columns.
# lets visualize
fig, ax = plt.subplots(figsize=(15,10))
sns.boxplot(data=data, width=0.5, ax=ax, fliersize=3)
```

[23]: <Axes: >

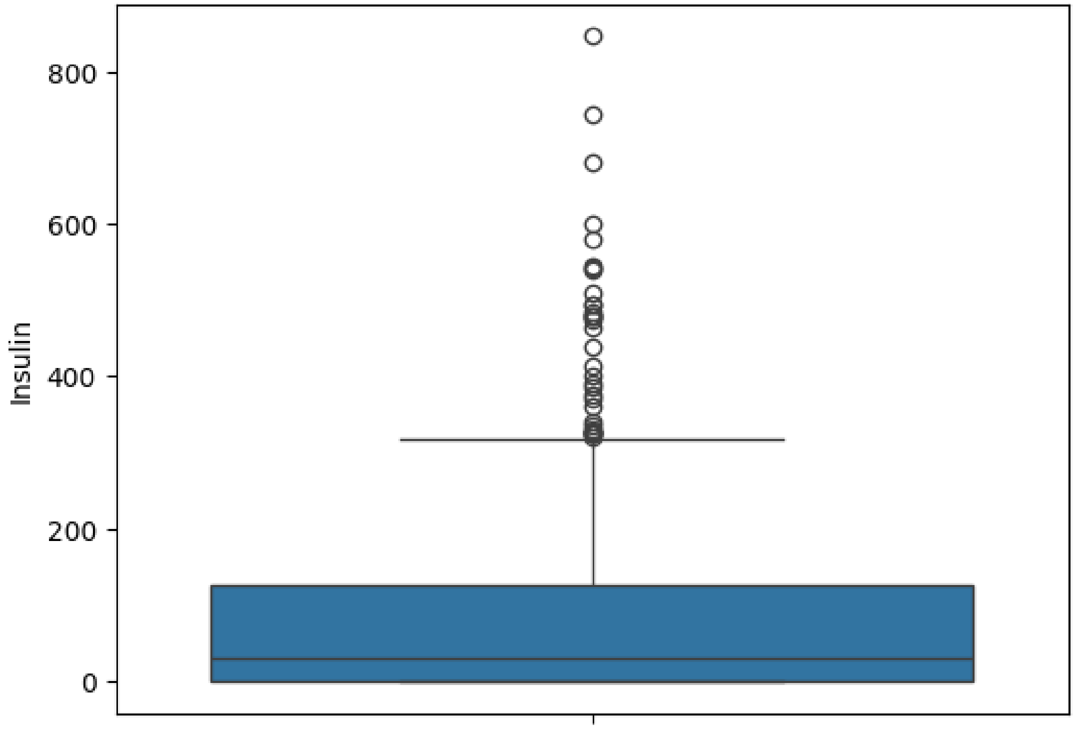


[30]:
```
print(data['Insulin'].mean())
print(data.Insulin.median())
## 79 insulin is under normal
```

```
79.79947916666667
30.5
```

[29]:
```
sns.boxplot(data=data.Insulin)
```

[29]: <Axes: ylabel='Insulin'>



[31]:
```
# here few misconception is, there like BMI can not be zero, BP can't be zero,␣
↪glucose, insuline can't be zero so lets
## try to
## now replacing zero values with the mean of the column
data['BMI']=data['BMI'].replace(0,data['BMI'].mean())
data['BloodPressure']=data['BloodPressure'].replace(0,data['BloodPressure'].
↪mean())
data['Glucose']=data['Glucose'].replace(0,data['Glucose'].mean())
data['Insulin']=data['Insulin'].replace(0,data['Insulin'].mean())
data['SkinThickness']=data['SkinThickness'].replace(0,data['SkinThickness'].
↪mean())
```

[33]:
```
data[(data['Glucose']==0) | (data['BloodPressure']==0) |␣
↪(data['SkinThickness']==0) | (data['Insulin']==0) | (data['BMI']==0)]
## removed all 0 value from these columns
```

[33]:
```
Empty DataFrame
Columns: [Pregnancies, Glucose, BloodPressure, SkinThickness, Insulin, BMI,
DiabetesPedigreeFunction, Age, Outcome]
Index: []
```

[38]:
```
data.describe()
```

[38]:
```
       Pregnancies     Glucose  BloodPressure  SkinThickness     Insulin  \
count   768.000000  768.000000     768.000000     768.000000  768.000000
mean      3.845052  121.681605      72.254807      26.606479  118.660163
std       3.369578   30.436016      12.115932       9.631241   93.080358
min       0.000000   44.000000      24.000000       7.000000   14.000000
25%       1.000000   99.750000      64.000000      20.536458   79.799479
50%       3.000000  117.000000      72.000000      23.000000   79.799479
75%       6.000000  140.250000      80.000000      32.000000  127.250000
max      17.000000  199.000000     122.000000      99.000000  846.000000

              BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    32.450805                  0.471876   33.240885    0.348958
std      6.875374                  0.331329   11.760232    0.476951
min     18.200000                  0.078000   21.000000    0.000000
25%     27.500000                  0.243750   24.000000    0.000000
50%     32.000000                  0.372500   29.000000    0.000000
75%     36.600000                  0.626250   41.000000    1.000000
max     67.100000                  2.420000   81.000000    1.000000
```

[ ]:
```

```

[6]:
```
data.head(2)
```

[6]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
```

[35]:
```
#segregate the dependent and independent variable
X = data.drop(columns=['Outcome'])
y = data['Outcome']
```

[42]:
```
## seperate dataset into train and test
X_train, X_test, y_train, y_test = train_test_split(X,y, test_size=0.25,␣
↪random_state=0)
X_train.shape, X_test.shape
```

[42]:
```
((576, 8), (192, 8))
```

since we have lot of outliers we can do standard scaling bring all mean=0 and standard_deviation=1 (using z-score)

[43]:
```
import pickle
## Standard Scaling - Standardization
def scaler_standard(X_train,X_test):
    #scaling the data
    scaler = StandardScaler()
    X_train_scaled = scaler.fit_transform(X_train)
    X_test_scaled = scaler.transform(X_test)

    #saving the model
    file = open('/config/workspace/Model/standardScaler.pkl','wb')
    pickle.dump(scaler,file)
    file.close()

    return X_train_scaled, X_test_scaled
```

[46]:
```
X_train_scaled, X_test_scaled = scaler_standard(X_train, X_test)
```

[47]:
```
X_train_scaled
```

[47]:
```
array([[ 1.50755225, -1.09947934, -0.89942504, …, -1.45561965,
        -0.98325882, -0.04863985],
       [-0.82986389, -0.1331471 , -1.23618124, …,  0.09272955,
        -0.62493647, -0.88246592],
       [-1.12204091, -1.03283573,  0.61597784, …, -0.03629955,
         0.39884168, -0.5489355 ],
       …,
       [ 0.04666716, -0.93287033, -0.64685789, …, -1.14021518,
        -0.96519215, -1.04923114],
       [ 2.09190629, -1.23276654,  0.11084355, …, -0.36604058,
        -0.5075031 ,  0.11812536],
       [ 0.33884418,  0.46664532,  0.78435594, …, -0.09470985,
         0.51627505,  2.953134  ]])
```

[41]:
```
## ignore warning because of some deprecated function
import warnings
warnings.filterwarnings('ignore')
```

[ ]:
```
```

Logistic Regression Model Training With Hyperparameter Tuning

[48]:
```
## Hyperparameter Tuning
## GridSearch CV
from sklearn.model_selection import GridSearchCV
import numpy as np
```

[110]:
```
# parameter grid
parameters = {
    'penalty' : ['l1','l2'],
    'C'       : np.logspace(-3,3,7),
    'solver'  : ['newton-cg', 'lbfgs', 'liblinear'],
}
```

[111]:
```
logreg = LogisticRegression()
clf = GridSearchCV(logreg,                    # model
                   param_grid = parameters,   # hyperparameters
                   scoring='accuracy',        # metric for scoring
                   cv=5)                     # number of folds

clf.fit(X_train_scaled,y_train)
```

[111]:
```
GridSearchCV(cv=5, estimator=LogisticRegression(),
             param_grid={'C': array([1.e-03, 1.e-02, 1.e-01, 1.e+00, 1.e+01,
1.e+02, 1.e+03]),
                         'penalty': ['l1', 'l2'],
                         'solver': ['newton-cg', 'lbfgs', 'liblinear']},
             scoring='accuracy')
```

[112]:
```
clf.best_params_
```

[112]:
```
{'C': 1.0, 'penalty': 'l1', 'solver': 'liblinear'}
```

[113]:
```
clf.best_score_
```

[113]:
```
0.7725487256371812
```

[134]:
```
## we can directly use clf() for prediction
## but for now again instantiating logisticRegression
## with best_params_ (best combination of parameters from GridSearchCV)
log_clf = LogisticRegression(C= 1.0, penalty='l1', solver='liblinear') ##can␣
 ↪usepenalty ='l2' because on other project it was given better recall
log_clf.fit(X_train,y_train)
```

[134]:
```
LogisticRegression(penalty='l1', solver='liblinear')
```

[ ]:
```
```

Decision Tree Model Training With Hyperparameter Tuning

[54]:
```
parameter={
 'criterion':['gini','entropy','log_loss'],
  'splitter':['best','random'],
  'max_depth':[1,2,3,4,5],
```

```
    'max_features':['auto', 'sqrt', 'log2']

}
```

- verbose is the verbosity: the higher, the more messages; in this case, it is set to 3.
- cv is the cross-validation generator or an iterable, in this case, there is a 3-fold cross-validation

[57]:
```
dtclassifier = DecisionTreeClassifier()
clf=GridSearchCV(dtclassifier,param_grid=parameter,cv=3,scoring='accuracy',verbose=3)

clf.fit(X_train,y_train)
```

```
Fitting 3 folds for each of 90 candidates, totalling 270 fits
[CV 1/3] END criterion=gini, max_depth=1, max_features=auto, splitter=best;,
score=nan total time=   0.0s
[CV 2/3] END criterion=gini, max_depth=1, max_features=auto, splitter=best;,
score=nan total time=   0.0s
[CV 3/3] END criterion=gini, max_depth=1, max_features=auto, splitter=best;,
score=nan total time=   0.0s
[CV 1/3] END criterion=gini, max_depth=1, max_features=auto, splitter=random;,
score=nan total time=   0.0s
[CV 2/3] END criterion=gini, max_depth=1, max_features=auto, splitter=random;,
score=nan total time=   0.0s
[CV 3/3] END criterion=gini, max_depth=1, max_features=auto, splitter=random;,
score=nan total time=   0.0s
[CV 1/3] END criterion=gini, max_depth=1, max_features=sqrt, splitter=best;,
score=0.667 total time=   0.0s
[CV 2/3] END criterion=gini, max_depth=1, max_features=sqrt, splitter=best;,
score=0.583 total time=   0.0s
[CV 3/3] END criterion=gini, max_depth=1, max_features=sqrt, splitter=best;,
score=0.641 total time=   0.0s
[CV 1/3] END criterion=gini, max_depth=1, max_features=sqrt, splitter=random;,
score=0.661 total time=   0.0s
[CV 2/3] END criterion=gini, max_depth=1, max_features=sqrt, splitter=random;,
score=0.724 total time=   0.0s
[CV 3/3] END criterion=gini, max_depth=1, max_features=sqrt, splitter=random;,
score=0.651 total time=   0.0s
[CV 1/3] END criterion=gini, max_depth=1, max_features=log2, splitter=best;,
score=0.708 total time=   0.0s
[CV 2/3] END criterion=gini, max_depth=1, max_features=log2, splitter=best;,
score=0.641 total time=   0.0s
[CV 3/3] END criterion=gini, max_depth=1, max_features=log2, splitter=best;,
score=0.641 total time=   0.0s
[CV 1/3] END criterion=gini, max_depth=1, max_features=log2, splitter=random;,
score=0.646 total time=   0.0s
[CV 2/3] END criterion=gini, max_depth=1, max_features=log2, splitter=random;,
score=0.641 total time=   0.0s
[CV 3/3] END criterion=gini, max_depth=1, max_features=log2, splitter=random;,
```

```
splitter=random;, score=nan total time=   0.0s
[CV 1/3] END criterion=log_loss, max_depth=5, max_features=sqrt, splitter=best;,
score=0.719 total time=   0.0s
[CV 2/3] END criterion=log_loss, max_depth=5, max_features=sqrt, splitter=best;,
score=0.672 total time=   0.0s
[CV 3/3] END criterion=log_loss, max_depth=5, max_features=sqrt, splitter=best;,
score=0.651 total time=   0.0s
[CV 1/3] END criterion=log_loss, max_depth=5, max_features=sqrt,
splitter=random;, score=0.693 total time=   0.0s
[CV 2/3] END criterion=log_loss, max_depth=5, max_features=sqrt,
splitter=random;, score=0.630 total time=   0.0s
[CV 3/3] END criterion=log_loss, max_depth=5, max_features=sqrt,
splitter=random;, score=0.620 total time=   0.0s
[CV 1/3] END criterion=log_loss, max_depth=5, max_features=log2, splitter=best;,
score=0.740 total time=   0.0s
[CV 2/3] END criterion=log_loss, max_depth=5, max_features=log2, splitter=best;,
score=0.734 total time=   0.0s
[CV 3/3] END criterion=log_loss, max_depth=5, max_features=log2, splitter=best;,
score=0.677 total time=   0.0s
[CV 1/3] END criterion=log_loss, max_depth=5, max_features=log2,
splitter=random;, score=0.703 total time=   0.0s
[CV 2/3] END criterion=log_loss, max_depth=5, max_features=log2,
splitter=random;, score=0.719 total time=   0.0s
[CV 3/3] END criterion=log_loss, max_depth=5, max_features=log2,
splitter=random;, score=0.661 total time=   0.0s
```

[57]:
```
GridSearchCV(cv=3, estimator=DecisionTreeClassifier(),
             param_grid={'criterion': ['gini', 'entropy', 'log_loss'],
                         'max_depth': [1, 2, 3, 4, 5],
                         'max_features': ['auto', 'sqrt', 'log2'],
                         'splitter': ['best', 'random']},
             scoring='accuracy', verbose=3)
```

[58]:
```python
clf.best_params_
```

[58]:
```
{'criterion': 'entropy',
 'max_depth': 4,
 'max_features': 'log2',
 'splitter': 'random'}
```

[59]:
```python
## passing best parameter to DTC, we can even use above clf() to predict␣
↪directly
dt_clf = DecisionTreeClassifier(criterion= 'entropy',
 max_depth= 4,
 max_features= 'log2',
 splitter= 'random')
```

```
dt_clf.fit(X_train,y_train)
```

[59]:
```
DecisionTreeClassifier(criterion='entropy', max_depth=4, max_features='log2',
                       splitter='random')
```

[ ]:

Support Vector Classifier With Hyperparameter Tuning

[60]:
```
# defining parameter range
param_grid = {'C': [0.1, 1, 10],
              'gamma': [1, 0.1, 0.01, 0.001, 0.0001],
              'kernel':['linear','rbf','polynomial']
              }
```

[62]:
```
## directly passing classifier in GridSearchCV
grid=GridSearchCV(SVC(),param_grid=param_grid,refit=True,cv=2,verbose=3,scoring='accuracy')

grid.fit(X_train,y_train)
```

```
Fitting 2 folds for each of 45 candidates, totalling 90 fits
[CV 1/2] END …C=0.1, gamma=1, kernel=linear;, score=0.771 total time=   0.2s
[CV 2/2] END …C=0.1, gamma=1, kernel=linear;, score=0.740 total time=   0.2s
[CV 1/2] END …C=0.1, gamma=1, kernel=rbf;, score=0.642 total time=   0.0s
[CV 2/2] END …C=0.1, gamma=1, kernel=rbf;, score=0.642 total time=   0.0s
[CV 1/2] END …C=0.1, gamma=1, kernel=polynomial;, score=nan total time=   0.0s
[CV 2/2] END …C=0.1, gamma=1, kernel=polynomial;, score=nan total time=   0.0s
[CV 1/2] END …C=0.1, gamma=0.1, kernel=linear;, score=0.771 total time=   0.2s
[CV 2/2] END …C=0.1, gamma=0.1, kernel=linear;, score=0.740 total time=   0.2s
[CV 1/2] END …C=0.1, gamma=0.1, kernel=rbf;, score=0.642 total time=   0.0s
[CV 2/2] END …C=0.1, gamma=0.1, kernel=rbf;, score=0.642 total time=   0.0s
[CV 1/2] END .C=0.1, gamma=0.1, kernel=polynomial;, score=nan total time=   0.0s
[CV 2/2] END .C=0.1, gamma=0.1, kernel=polynomial;, score=nan total time=   0.0s
[CV 1/2] END ..C=0.1, gamma=0.01, kernel=linear;, score=0.771 total time=   0.1s
[CV 2/2] END ..C=0.1, gamma=0.01, kernel=linear;, score=0.740 total time=   0.2s
[CV 1/2] END …C=0.1, gamma=0.01, kernel=rbf;, score=0.642 total time=   0.0s
[CV 2/2] END …C=0.1, gamma=0.01, kernel=rbf;, score=0.642 total time=   0.0s
[CV 1/2] END C=0.1, gamma=0.01, kernel=polynomial;, score=nan total time=   0.0s
[CV 2/2] END C=0.1, gamma=0.01, kernel=polynomial;, score=nan total time=   0.0s
[CV 1/2] END .C=0.1, gamma=0.001, kernel=linear;, score=0.771 total time=   0.1s
[CV 2/2] END .C=0.1, gamma=0.001, kernel=linear;, score=0.740 total time=   0.2s
[CV 1/2] END …C=0.1, gamma=0.001, kernel=rbf;, score=0.642 total time=   0.0s
[CV 2/2] END …C=0.1, gamma=0.001, kernel=rbf;, score=0.660 total time=   0.0s
[CV 1/2] END C=0.1, gamma=0.001, kernel=polynomial;, score=nan total time=
0.0s
[CV 2/2] END C=0.1, gamma=0.001, kernel=polynomial;, score=nan total time=
0.0s
[CV 1/2] END C=0.1, gamma=0.0001, kernel=linear;, score=0.771 total time=   0.2s
```

```
[CV 2/2] END ..C=10, gamma=0.1, kernel=polynomial;, score=nan total time=   0.0s
[CV 1/2] END …C=10, gamma=0.01, kernel=linear;, score=0.764 total time=  15.6s
[CV 2/2] END …C=10, gamma=0.01, kernel=linear;, score=0.733 total time=   7.1s
[CV 1/2] END …C=10, gamma=0.01, kernel=rbf;, score=0.660 total time=   0.0s
[CV 2/2] END …C=10, gamma=0.01, kernel=rbf;, score=0.639 total time=   0.0s
[CV 1/2] END .C=10, gamma=0.01, kernel=polynomial;, score=nan total time=   0.0s
[CV 2/2] END .C=10, gamma=0.01, kernel=polynomial;, score=nan total time=   0.0s
[CV 1/2] END ..C=10, gamma=0.001, kernel=linear;, score=0.764 total time=  15.6s
[CV 2/2] END ..C=10, gamma=0.001, kernel=linear;, score=0.733 total time=   7.1s
[CV 1/2] END …C=10, gamma=0.001, kernel=rbf;, score=0.705 total time=   0.0s
[CV 2/2] END …C=10, gamma=0.001, kernel=rbf;, score=0.691 total time=   0.0s
[CV 1/2] END C=10, gamma=0.001, kernel=polynomial;, score=nan total time=   0.0s
[CV 2/2] END C=10, gamma=0.001, kernel=polynomial;, score=nan total time=   0.0s
[CV 1/2] END .C=10, gamma=0.0001, kernel=linear;, score=0.764 total time=  15.6s
[CV 2/2] END .C=10, gamma=0.0001, kernel=linear;, score=0.733 total time=   7.1s
[CV 1/2] END …C=10, gamma=0.0001, kernel=rbf;, score=0.767 total time=   0.0s
[CV 2/2] END …C=10, gamma=0.0001, kernel=rbf;, score=0.726 total time=   0.0s
[CV 1/2] END C=10, gamma=0.0001, kernel=polynomial;, score=nan total time=
0.0s
[CV 2/2] END C=10, gamma=0.0001, kernel=polynomial;, score=nan total time=
0.0s
```

[62]:
```
GridSearchCV(cv=2, estimator=SVC(),
             param_grid={'C': [0.1, 1, 10],
                         'gamma': [1, 0.1, 0.01, 0.001, 0.0001],
                         'kernel': ['linear', 'rbf', 'polynomial']},
             scoring='accuracy', verbose=3)
```

[63]:
```
grid.best_params_
```

[63]:
```
{'C': 1, 'gamma': 1, 'kernel': 'linear'}
```

[64]:
```
svc_clf=SVC(C=0.1,gamma=1,kernel='linear')
svc_clf.fit(X_train,y_train)
```

[64]:
```
SVC(C=0.1, gamma=1, kernel='linear')
```

[ ]:
```

```

Naive Baye's Implementation

[ ]:
```
## hyperparameter tuning
param_grid_nb = {
    'var_smoothing': np.logspace(0,-9, num=100)
}
```

- var_smoothing is a stability calculation to widen (or smooth) the curve and therefore account for more samples that are further away from the distribution mean. In this case, np.logspace returns numbers spaced evenly on a log scale, starts from 0, ends at -9, and generates 100 samples.

- Why this step: To set the selected parameters used to find the optimal combination.

[ ]:
```
nbModel_grid = GridSearchCV(estimator=GaussianNB(), param_grid=param_grid_nb, verbose=1, cv=2, n_jobs=-1)
nbModel_grid.fit(X_train, y_train)
```

- verbose is the verbosity: the higher, the more messages; in this case, it is set to 1.
- cv is the cross-validation generator or an iterable, in this case, there is a 2-fold cross-validation
- n_jobs is the maximum number of concurrently running workers; in this case, it is set to -1 which implies that all CPUs are used.

[66]:
```
## directly using Gaussian Naive bayes with Hyperparameter Tuning
gnb = GaussianNB()
```

[67]:
```
gnb.fit(X_train,y_train)
```

[67]:
```
GaussianNB()
```

[ ]:
```

```

let's see how well our model performs on the test data set.

[135]:
```
## Logistic Regression prediction
y_pred_logre = log_clf.predict(X_test_scaled)
```

[69]:
```
## Decision Tree prediction
y_pred_dtc = dt_clf.predict(X_test_scaled)
```

[70]:
```
## Support Vector Classifier prediction
y_pred_svc = svc_clf.predict(X_test_scaled)
```

[71]:
```
## Gaussian Naive Bayes prediction
y_pred_gnb = gnb.predict(X_test_scaled)
```

[ ]:
```

```

Confusion Matrix

[116]:
```
## Logistic Regression confusion matrix
print(confusion_matrix(y_pred_logre,y_test))
```

```
[[130  62]
 [  0   0]]
```

[96]:
```
## Decision Tree confusion matrix
```

```
conf_mat_dtc = confusion_matrix(y_test,y_pred_dtc) ## doesn't matter in which␣
↪order we write
## even if we calculate accuracy score manually and use confusion matrix, order␣
↪of 'y_test' and 'y_pred'
## doesn't affect accuracy score result
conf_mat_dtc
```

[96]:
```
array([[126,   4],
       [ 55,   7]])
```

[77]:
```
## Support Vector Classifier confusion matrix
conf_mat = confusion_matrix(y_pred_svc,y_test)
conf_mat
```

[77]:
```
array([[130,  62],
       [  0,   0]])
```

[78]:
```
## Gaussian Naive Bayes confusion matrix
conf_mat = confusion_matrix(y_pred_gnb,y_test)
conf_mat
```

[78]:
```
array([[127,  57],
       [  3,   5]])
```

[ ]:
```

```

Accuracy Score

[128]:
```
## Logistic Regression accuracy score
accuracy_score(y_pred_logre,y_test)
```

[128]:
```
0.6770833333333334
```

[82]:
```
## Decision Tree accuracy score
accuracy_score(y_pred_dtc,y_test)
```

[82]:
```
0.6927083333333334
```

[83]:
```
## Support Vector Classifier accuracy score
accuracy_score(y_pred_svc,y_test)
```

[83]:
```
0.6770833333333334
```

[84]:
```
## Gaussian Naive Bayes accuracy score
print(accuracy_score(y_pred_gnb,y_test))
```

```
0.6875
```

[ ]:

```

```

manually calculating accuracy score of Decision Tree

[97]:
```
true_positive = conf_mat_dtc[0][0]
false_positive = conf_mat_dtc[0][1]
false_negative = conf_mat_dtc[1][0]
true_negative = conf_mat_dtc[1][1]
```

[98]:
```
Accuracy = (true_positive + true_negative) / (true_positive +false_positive +
 ↪false_negative + true_negative)
Accuracy
```

[98]: 0.6927083333333334

[99]:
```
Precision = true_positive/(true_positive+false_positive)
Precision
```

[99]: 0.9692307692307692

[107]:
```
Recall = true_positive/(true_positive+false_negative)
Recall
```

[107]: 0.6961325966850829

[101]:
```
F1_Score = 2*(Recall * Precision) / (Recall + Precision)
F1_Score
```

[101]: 0.8102893890675241

[124]:
```
## or we can directly use this method to get all report
## for Decision Tree Classifier
from sklearn.metrics import classification_report
print(classification_report(y_pred_dtc,y_test))
```

```
              precision    recall  f1-score   support

           0       0.97      0.70      0.81       181
           1       0.11      0.64      0.19        11

    accuracy                           0.69       192
   macro avg       0.54      0.67      0.50       192
weighted avg       0.92      0.69      0.77       192
```

[ ]:

```

```

[136]:
```
## Logistic Regression confusion matrix
conf_mat_log =confusion_matrix(y_pred_logre,y_test)
conf_mat_log
```

[136]:
```
array([[130,  62],
       [  0,   0]])
```

[137]:
```
true_positive = conf_mat_log[0][0]
false_positive = conf_mat_log[0][1]
false_negative = conf_mat_log[1][0]
true_negative = conf_mat_log[1][1]
```

[142]:
```
Recall = true_positive/(true_positive+false_negative)
Recall
```

[142]:
```
1.0
```

[143]:
```
Accuracy = (true_positive + true_negative) / (true_positive +false_positive +␣
 ↪false_negative + true_negative)
Accuracy
```

[143]:
```
0.6770833333333334
```

[144]:
```
##for logistic Regression
print(classification_report(y_pred_logre,y_test))
```

```
              precision    recall  f1-score   support

           0       1.00      0.68      0.81       192
           1       0.00      0.00      0.00         0

    accuracy                           0.68       192
   macro avg       0.50      0.34      0.40       192
weighted avg       1.00      0.68      0.81       192
```

- for diabetes Recall is important because our False-Negative is important
- if person have diabetes and result is showing Non-Diabetic then it's a blunder because may be he/she wouldn't re-do the test
- so False-Negative is important in this scenario

[ ]:
```

```

[104]:
```
## using Decision Tree classifier model to save and use it on flask app
## because it's giving higher accuracy/ recall (false-negative)

import pickle
file = open('/config/workspace/Model/modelForPrediction.pkl','wb')
```

```
pickle.dump(dt_clf,file)
file.close()
```

[ ]:

```

```