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Date : 14/12/2024

Topic : Diabetes Prediction Model

Data Source : https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database Credits : Lex Fridman, Jeremy Howards, Siddharthan

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 from matplotlib import pyplot as plt

import pickle

Providing Data (diabetes.csv)

Importing the data

DiabetesData_1 = pd.read_csv('/content/diabetes.csv')

Check the Number of rows and columns in the data set

DiabetesData_1.shape

→ (768, 9)

We have 768 rows and 9 columns. to check the column name..

#displaying the 5 rows of the data DiabetesData_1.head()

₹		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

Checking the basic Statistics of the Data using description()

DiabetesData_1.describe()

		Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	0u
	count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.0
	mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.0
	std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.4
	min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.0
	25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.0
	50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.0
	75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.0
	max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.0
	4									•

DiabetesData_1.mean()



Grouping the Outcome and getting mean value of those will give us a Idea that how the Prediction is going to be.

Here the 0 is the "Non Diabetic people" and the 1 is the Diabetic people".

DiabetesData_1.groupby("Outcome").mean()

₹		Pregnancies Glucos		BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	
	Outcome									
	0	3.298000	109.980000	68.184000	19.664000	68.792000	30.304200	0.429734	31.190000	
	1	4.865672	141.257463	70.824627	22.164179	100.335821	35.142537	0.550500	37.067164	
	4									>

Dividing the data set into features and labesl and store them into the variables "Features" and "Label" respectively

Features = DiabetesData_1.drop(columns='Outcome', axis=1)
Label = DiabetesData_1['Outcome']

Features.head()

₹		Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesP	edigreeFunct	tion	Age
	0	6	148	72	35	0	33.6		0	.627	50
	1	1	85	66	29	0	26.6		0	.351	31
	2	8	183	64	0	0	23.3		0	0.672	32
	3	1	89	66	23	94	28.1		0	0.167	21
	4	0	137	40	35	168	43.1		2	2.288	33
	4										

Label.head()

7	Outcome	9
0	1	L
1	()
2	1	L
3	()
4	1	L
dtvi	ne: int64	
	ie. IIII04	

Now lets do standardize the data. In the next few steps, we are going to 1). Fit the data 2). Standardize (transform the data into a small range) these steps will make our model to predict high

Stool = StandardScaler()

Stool.fit_transform(Features)

```
\Rightarrow array([[ 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],
             \hbox{$[-0.84488505,}\quad 0.1597866\ ,\ -0.47073225,\ \dots,\ -0.24020459,
               0.37110101, 1.17073215],
             [-0.84488505, -0.8730192
                                            0.04624525, ..., -0.20212881,
              -0.47378505, -0.87137393]])
Standarized_Features = Stool.fit_transform(Features)
Features = Standarized_Features
Label = Label
Now all the basic data standardization is completed, Let's move to the Training section.
before that, we need to spllit the data into training portion and testing portion. Here is the steps..
Features_train, Features_test, Label_train, Label_test = train_test_split(Features, Label, test_size=0.2, stratify=Label, ra
print(Features.shape, Features_train.shape, Features_test.shape)
→ (768, 8) (614, 8) (154, 8)
print(Label.shape, Label_train.shape, Label_test.shape)
→ (768,) (614,) (154,)
The data splitted successfully, now get into the training session
Classifier = svm.SVC(kernel='linear')
Classifier.fit(Features train, Label train)
₹
              SVC
                       (i) (?)
     SVC(kernel='linear')
Hello shiva sir, since we have a small data set. the training wont take much time to complete
#Testing and evaluvating
Features_train_prediction = Classifier.predict(Features_train)
Training_data_accuracy = accuracy_score(Features_train_prediction, Label_train)
print("Traning data accuracy is", Training_data_accuracy)
> Traning data accuracy is 0.7866449511400652
Features test prediction = Classifier.predict(Features test)
Testing_data_accuracy = accuracy_score(Features_test_prediction, Label_test)
print("Testing data accuracy is", Testing data accuracy)
→ Testing data accuracy is 0.7727272727272727
We evaluated our modal and that is performing good after some oprimization in data.
Now lets build a predictive system by user's input
input data = (2,112,66,22,0,25,0.307,24)
input_data_as_numpy_array = np.asarray(input_data)
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)
Stooled_data = Stool.transform(input_data_reshaped)
print(Stooled_data)
```

prediction = Classifier.predict(Stooled_data)

print(prediction)

if (prediction[0] == 0):

The person is not diabetic

warnings.warn(

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```
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                                                             MLmodelfordiabetes.ipynb - Colab
     print('The person is not diabetic')
   else:
     print('The person is diabetic')
    ⋽ [[-0.54791859 -0.27837344 -0.16054575 0.09180513 -0.69289057 -0.88749274
          -0.497946
                     -0.78628618]]
        The person is not diabetic
        /usr/local/lib/python3.10/dist-packages/sklearn/base.py:493: UserWarning: X does not have valid feature names, but Stand
          warnings.warn(
    Saving the Model
   file name = "trained model.sav"
   pickle.dump(Classifier, open(file_name,"wb"))
   loaded_model = pickle.load(open("trained_model.sav","rb"))
   input_data = (2,112,66,22,0,25,0.307,24)
   input_data_as_numpy_array = np.asarray(input_data)
   input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)
   Stooled data = Stool.transform(input data reshaped)
   print(Stooled_data)
   prediction = loaded_model.predict(Stooled_data)
   print(prediction)
   if (prediction[0] == 0):
     print('The person is not diabetic')
   else:
     print('The person is diabetic')
       [[-0.54791859 -0.27837344 -0.16054575 0.09180513 -0.69289057 -0.88749274
          -0.497946 -0.78628618]]
        [0]
```

/usr/local/lib/python3.10/dist-packages/sklearn/base.py:493: UserWarning: X does not have valid feature names, but Stand