Lab 6 - Predicting Breast Cancer - III-PART-B

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Lab Overview

Objectives

A) Compare and understand the difference SVM and anyother two classification algorithm result with respect to Breast cancer Dataset

B)Find a Dataset and Demonstrate SVM Algorithm on it.

Problem Definition

A) Compare and contrast the different evaluation metrices, effect of classification with respect to change in trainingtest split, random state, pre-processing labels, hyper parameters, alogrithm parameter of decision tree and random forest and interpret the change in result using visualization. List the advantages and Disadvantages of SVM

B) Enumerate your findings/observations on SVM Algorithm

Approach

Imported the Dataset using required libraries from Kaggle(https://www.kaggle.com/uciml/breast-cancer-wisconsin-data(https://www.kaggle.com/uciml/breast-cancer-wisconsin-data)) to python. Did some pre-processing technique and then build the model using SVM, Decision tree Random forest and compare the difference in the classification metrics and other parameters and after than did hyperparameter tuning for checking the model which gives the highest accuaracy with all the parameter. At the end did some visualization on the results. Liest out the advantages and disadvantages of SVM.

After a thorough understanding in SVM took a dataset(Prima India Diabetics)dataset from kaggle and perfomed SVM.

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References

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- 2. https://scikit-learn.org/stable/modules/generated/sklearn.tree.DecisionTreeClassifier.html (https://scikit-learn.org/stable/modules/generated/sklearn.tree.DecisionTreeClassifier.html (https://scikit-learn.org/stable/modules/generated/sklearn.tree.DecisionTreeClassifier.html)
- 3. https://www.datacamp.com/community/tutorials/svm-classification-scikit-learn-python)

 (https://www.datacamp.com/community/tutorials/svm-classification-scikit-learn-python)
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- 5. https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html (https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html (https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html (https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html)
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- 7. https://www.kaggle.com/uciml/pima-indians-diabetes-database (https://www.kaggle.com/uciml/pima-indians-database (https://www.kaggle.com/uciml/pima-indians-database (https://www.kaggle.com/uciml/pima-indians-database (https://www.kaggle.com/uciml/pima-indians-database (<a href="https://www.kaggle.com/uciml/pima-indians-database (<a href="https://www.kagg

About The Datset

The datasets consist of several medical predictor (independent) variables and one target (dependent) variable, Outcome.

Independent variables include the number of pregnancies the patient has had, their BMI, insulin level, age, and so on.

Pregnancies-Number of times pregnant

Glucose-Plasma glucose concentration a 2 hours in an oral glucose tolerance test

BloodPressure-Diastolic blood pressure (mm Hg)

SkinThickness-Triceps skin fold thickness (mm)

Insulin-2-Hour serum insulin (mu U/ml)

BMI-Body mass index (weight in kg/(height in m)^2)

DiabetesPedigreeFunction-Diabetes pedigree function

Age-Age (years)

Outcome-Class variable (0 or 1) 268 of 768 are 1, the others are 0

Importing Required Libraries

```
In [49]: | import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
import seaborn as sns
import matplotlib.pyplot as plt
```

Loading the Dataset

```
In [11]:  M df = pd.read_csv("diabetes.csv")
```

In [12]:												
	Out[12]:			Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	DiabetesPedigreeFunction	Age	Outco
			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	0.672	32	
			3	1	89	66	23	94	28.1	0.167	21	
			4	0	137	40	35	168	43.1	2.288	33	
			763	10	101	76	48	180	32.9	0.171	63	
			764	2	122	70	27	0	36.8	0.340	27	
			765	5	121	72	23	112	26.2	0.245	30	
			766	1	126	60	0	0	30.1	0.349	47	
			767	1	93	70	31	0	30.4	0.315	23	

768 rows × 9 columns

Basic Inference from Data (Data Wrangling)

Dimension of Dataset

```
In [38]: M df.shape
Out[38]: (768, 9)
```

Getting the Concise summary of Dataframe

```
In [39]: ► df.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
                                        768 non-null int64
                Glucose
                BloodPressure
                                        768 non-null int64
                SkinThickness
                                        768 non-null
                                                       int64
                Insulin
                                        768 non-null
                                                       int64
                BMI
                                        768 non-null
                                                       float64
                DiabetesPedigreeFunction 768 non-null
                                                       float64
            7
                                        768 non-null
                                                       int64
                Age
            8 Outcome
                                        768 non-null
                                                       int64
            dtypes: float64(2), int64(7)
            memory usage: 54.1 KB
```

Checking the no of null values

```
    df.isnull().sum()

In [41]:
             df.isna().sum()
   Out[41]: Pregnancies
                                          0
                                          0
             Glucose
             BloodPressure
                                          0
             SkinThickness
                                          0
             Insulin
                                          0
             BMI
             DiabetesPedigreeFunction
                                          0
             Age
                                          0
             Outcome
             dtype: int64
```

Finding the unique values of Dependent varaiable and counting them

Description of Datset

```
In [47]:  
#Getting a statistical decription of our data
df.describe()

Out[47]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	ВМІ	DiabetesPedigreeFuncti
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.0000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.4718
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.3313
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.0780
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.2437
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.3725
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.6262
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.4200

Getting to view the correlation on our data set

Out[51]: <matplotlib.axes._subplots.AxesSubplot at 0x1d1a8915640>



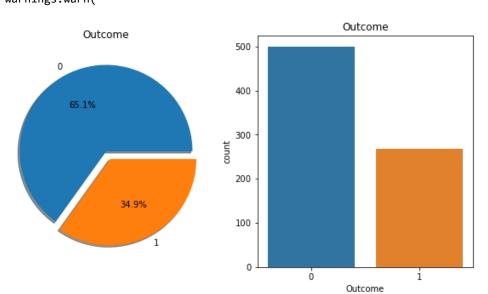
Dividing the Columns into Dependent(Y) and Independent One(X)

Plotting target column

```
In [52]: 

f,ax=plt.subplots(1,2,figsize=(10,5))
    df['Outcome'].value_counts().plot.pie(explode=[0,0.1],autopct='%1.1f%%',ax=ax[0],shadow=Traax[0].set_title('Outcome')
    ax[0].set_ylabel('')
    sns.countplot('Outcome',data=df,ax=ax[1])
    ax[1].set_title('Outcome')
    plt.show()
```

C:\Users\HP\anaconda3\anacondaorginal\lib\site-packages\seaborn_decorators.py:36: Future
Warning: Pass the following variable as a keyword arg: x. From version 0.12, the only val
id positional argument will be `data`, and passing other arguments without an explicit ke
yword will result in an error or misinterpretation.
warnings.warn(



Train-Test Split

```
In [15]: N X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size= 0.2)
In [53]: N # print(X_train.shape);
    print(Y_train.shape);
    print("\n\n");
    print(X_test.shape);
    print(Y_test.shape);

    (614,)

    (154, 8)
    (154,)
```

SVM

```
In [16]: M model = SVC(kernel = 'linear', C = 1)
```

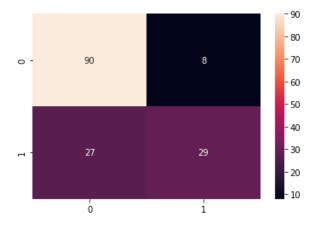
Accuracy Score

0.7727272727272727

Confusion Matrix

Out[22]: <matplotlib.axes._subplots.AxesSubplot at 0x1d1a8731190>

sns.heatmap(dataframe_conf_matrix, annot=True)



classification_report

	precision	recall	f1-score	support
0	0.77	0.92	0.84	98
1	0.78	0.52	0.62	56
accuracy			0.77	154
macro avg	0.78	0.72	0.73	154
weighted avg	0.77	0.77	0.76	154

Finding the Accuracy by changing the Parameter

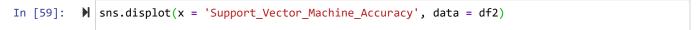
```
In [24]: ► def doSVC(X, Y, test_size = 0.20, randomstate = None, c = 1.0, Kernel = "rbf"):
               X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = test_size, rando
               cls1 = SVC(C = c, kernel = Kernel)
               cls1.fit(X_train,Y_train)
               pred = cls1.predict(X_test)
               acc_score1 = accuracy_score(pred,Y_test)
               return acc_score1
In [25]:
         ► test_size = [0.30, 0.25, 0.20, 0.10]
            random\_states = [8, 27, 42]
            Regularization Parameter = [1.0,50.0,100.0]
            kernels = ['linear', 'poly', 'rbf', 'sigmoid']
In [27]: ▶ for t_size in test_size:
               for r state in random states:
                   for RP in Regularization Parameter:
                      for ker in kernels:
                          a1 = doSVC(X, Y, t_size, r_state, RP, ker)
                          svd = \{\}
                          svd['Test_Size'] = t_size
                          svd['Random_States'] = r_state
                          svd['Support_Vector_Machine_Accuracy'] = a1
                          svd['RegularizationParameter'] = RP
                          svd['Kernel'] = ker
                          df2 = df2.append(svd, ignore_index = True)
```

In [58]: ► df2

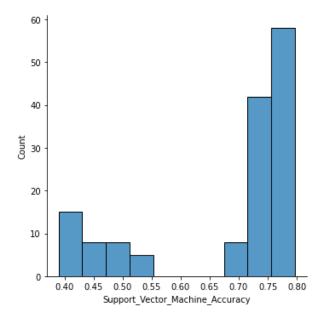
Out[58]:

	Test_Size	Random_States	RegularizationParameter	Kernel	Support_Vector_Machine_Accuracy
0	0.3	8	1.0	linear	0.796537
1	0.3	8	1.0	poly	0.757576
2	0.3	8	1.0	rbf	0.740260
3	0.3	8	1.0	sigmoid	0.519481
4	0.3	8	50.0	linear	0.779221
139	0.1	42	50.0	sigmoid	0.467532
140	0.1	42	100.0	linear	0.688312
141	0.1	42	100.0	poly	0.714286
142	0.1	42	100.0	rbf	0.714286
143	0.1	42	100.0	sigmoid	0.467532

144 rows × 5 columns



Out[59]: <seaborn.axisgrid.FacetGrid at 0x1d1a92dafa0>



Improving Model

Hyper Paramter Tuning

```
In [35]:
          ▶ from sklearn.model selection import GridSearchCV
             parameters = [{'C': [1.0,50.0,100.0], 'kernel' : ['linear', 'poly', 'rbf', 'sigmoid']}]
             oHe = OneHotEncoder()
             grid_search = GridSearchCV(estimator = model,
                                        param_grid = parameters,
                                        scoring = 'accuracy',
                                        cv = 10,
                                        n_{jobs} = -1)
             grid_search.fit(X_train, Y_train)
             best_accuracy_svc = grid_search.best_score_
             best parameters = grid search.best params
             print(best_accuracy_svc)
             print(best_parameters)
             0.7604442094130089
             {'C': 1.0, 'kernel': 'linear'}
```

Conclusion

In this Lab, for Diabetics Dataset accuracy range is around 75 to 80 per(max)

When the Kernel was "sigmoid" the accuracy value range below 50 %

Without changing random state and test size max accuracy is around 76%

When all of the given paramter are changed the max accuracy is around 80%

```
In [ ]: •|
```