Classification of Iris Dataset using Support Vector Machine (SVM)

Programming Assignment
CSE: 4739 Data Mining
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November 27 2022

1 Introduction

The programming assignment of classification of the Iris dataset using Support Vector Machines (SVMs) is a simple data analysis task implemented in the Python programming language. This assignment's objective is to analyze a dataset and implement an algorithm suitable for solving the analytical goal of the given dataset, which happens to be classifying Iris species based on a set of features. The Iris dataset [1] is one of the most popular datasets used for data analytical work and the best-known dataset for pattern recognition. The report will delve into the details of the dataset, the model, and the algorithm used on the dataset, and also provide a comprehensive view of each step of data analysis along with its implementation coded in Python.

2 Knowing the Iris Dataset

The first step of any data analysis task is getting to know the dataset and to do so, we will be visiting the description of the dataset provided on the official website [1]. As stated above, the Iris dataset happens to be one of the most popular datasets out there for any kind of data analytical work including classification, clustering, and pattern recognition. Created by R.A. Fisher, the dataset was primarily used for pattern recognition and has been a classic dataset for that domain. The dataset, however, is very simple. There are four features and a single target class. The features are – sepal length, septal width, petal length, and petal width. The target class has three values of Iris species - Iris Setosa, Iris Versicolour, and Iris Virginica. In total, 150 samples have been provided in the dataset – each class containing 50 samples.
We are given datasets in different forms - some might be thoroughly preprocessed and cleaned, some might need manual filling of missing values, and so on. Our Iris dataset, collected from the official website of the Iris Dataset [1], has already been cleaned with no missing values in the dataset. This makes our job in analyzing the dataset much easier. Hence, in this section, we will not try to quantify the missing values or clean the dataset any further. We will simply have a look at the summary statistics and visualize our dataset.

2.1 Importing the Libraries

Using built-in libraries is essential for any kind of work in Python. These libraries provide additional functionality to Python and save a lot of time for programmers. For our assignment, we will be primarily relying on five libraries – Pandas, NumPy, Scikit-learn, Matplotlib, and Seaborn. NumPy is primarily used for working with arrays efficiently. Pandas expand on the functionality of NumPy arrays by adding data frames that are similar to tables in SQL. Scikit-learn will be used for implementing basic transformations on our dataset like splitting and scaling. It will also be used to implement SVM and Grid Search. Finally, for visualization, we will be relying on Matplotlib and Seaborn.

Code:

```python
import pandas as pd
import numpy as np
from sklearn.svm import SVC
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV
import seaborn as sns
import matplotlib.pyplot as plt
```

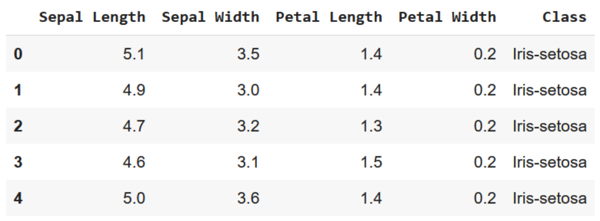
2.2 Loading the Dataset

After importing the libraries, we collect our dataset and other required files. We download two files - iris.names and iris.data. The iris.names file contains the description of our dataset where we can find the headers for the columns. The iris.data file is our raw dataset with the values only. The dataset is loaded to a Pandas Dataframe using the pandas built-in read_csv() function. While loading the dataset, we pass the column names as an argument. We have a look at the first five rows of our dataset using the head() function.

Code:

```
#The names are collected from the iris.names file of the official iris dataset
names = ['Sepal Length','Sepal Width','Petal Length','Petal Width','Class']
#The iris.data file is collected from the official iris dataset
df = pd.read_csv("iris.data", names = names)
df.head()
```

Output:



	Sepal Length	Sepal Width	Petal Length	Petal Width	Class
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa

2.3 Summary Statistics

In the description of Iris dataset, it has been mentioned that our dataset is been cleaned and there are no missing values. So, no further preprocessing is required except scaling. We first have a look at the number of rows and columns in our dataset by accessing the ‘shape‘ attribute of our Pandas Dataframe. We can see our dataset is relatively small with 150 rows and 5 columns which have been labeled before.

Code:

```
print('The data frame has', df.shape[0], 'rows and', df.shape[1], 'columnns')
```

Output:

```
The data frame has 150 rows and 5 columnns
```

To get a better idea of our dataset, we can check its summary statistics by using Pandas built-in function ‘describe()‘. The summary statistics give us a numerical estimation of all the important statistical measures. The class attribute of our dataset is categorical and hence, will not be shown in the summary statistics.

Code:

```
df.describe()
```

Output:

	Sepal Length	Sepal Width	Petal Length	Petal Width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000
75%	6.400000	3.300000	5.100000	1.800000
max	7.900000	4.400000	6.900000	2.500000

2.4 Data Visualization

Using summary statistics give us a numerical view on our dataset. But humans are better at retaining information visually. We will use some simple boxplots to visualize our dataset. Using Seaborn's built-in boxplot() and stripplot() function, we can easily plot our boxplots and the datapoints in the same visualization.

2.4.1 Sepal Length vs Class

Code:

```
sns.set(rc={'figure.figsize':(8,8.5)})
sns.set(style="white", color_codes=True)
ax = sns.boxplot(x="Class", y="Sepal Length", data=df).set(title='Sepal Length vs Class')
ax = sns.stripplot(x="Class", y="Sepal Length", data=df, jitter=True, edgecolor="gray")
```

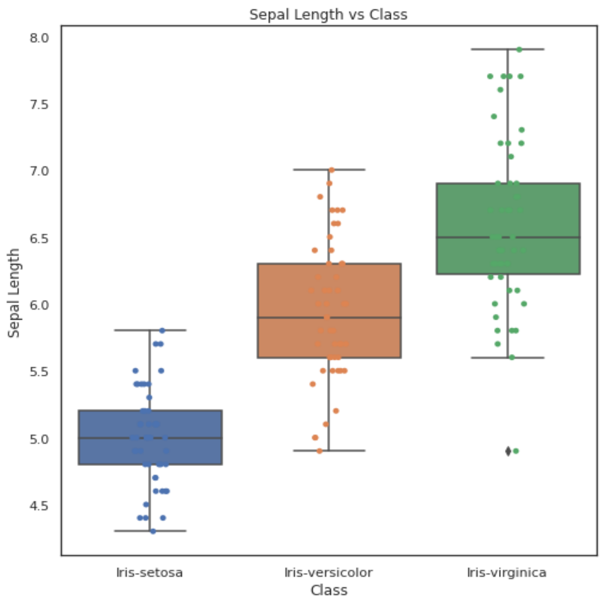


Figure 1: Relationship between Sepal Length and Class

Iris-setosa has the least median sepal length followed by Iris-versicolor and Iris-virginica. However, Iris-virginica has an outlier with a sepal length of around 5 cm which falls way behind the median sepal length of 6.5 cm.

2.4.2 Sepal Width vs Class

Code:

```
ax = sns.boxplot(x="Class", y="Sepal Width", data=df).set(title='Sepal Width vs Class')
ax = sns.stripplot(x="Class", y="Sepal Width", data=df, jitter=True, edgecolor="gray")
```

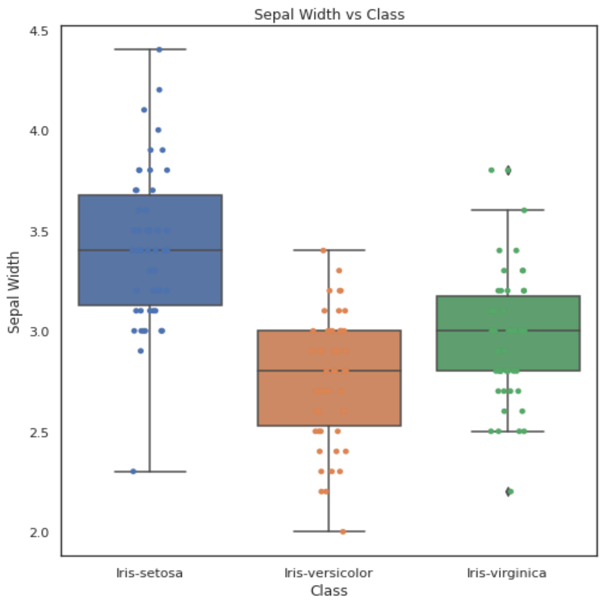


Figure 2: Relationship between Sepal Width and Class

The sepal width shows a different distribution with Iris-setosa having the highest median width but also having a wider range of values. Iris-virginica has a couple of outliers at the top and bottom.

2.4.3 Petal Length vs Class

Code:

```
ax = sns.boxplot(x="Class", y="Petal Length", data=df).set(title='Petal Length vs Class')
ax = sns.stripplot(x="Class", y="Petal Length", data=df, jitter=True, edgecolor="gray")
```

Iris-setosa has a very narrow range of petal length and also has the least median petal length. The median petal length of the other two classes are considerably higher. Iris-setosa and Iris-versicolor has some outliers at the bottom.

2.4.4 Petal Width vs Class

Code:

```
ax = sns.boxplot(x="Class", y="Petal Width", data=df).set(title='Petal Width vs Class')
ax = sns.stripplot(x="Class", y="Petal Width", data=df, jitter=True, edgecolor="gray")
```

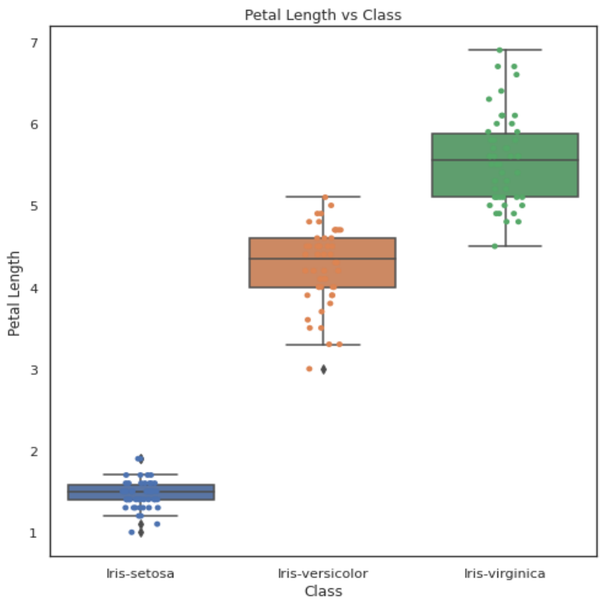


Figure 3: Relationship between Petal Length and Class

Similar to the petal length, the petal width of Iris-setosa has a narrow range and also has the least median length. However, it has outliers at the top. The other two classes have considerably higher median petal width with no outliers.

3 Data Preprocessing

Before feeding our dataset to our model, we need to transform it into an appropriate form. Data Preprocessing involves - Data Cleaning, Data Integration, Data Reduction, and Data Transformation. As mentioned earliar, our dataset has already been cleaned and is from a single source. So, the first two steps can be skipped. We would first perform correlation analysis on our dataset, and then scale the dataset. Apart from that, we need to map categorical values to numerical ones, extract features and target class from our dataset, and make train-test splits.

3.1 Mapping Categorical to Numerical Values

Our model can not interpret categorical values. So, we feed these values to our model by simply mapping them to a numerical value. Our class attribute is a categorical attribute and needs to be mapped. Using the unique() command, we can find the list of unique values for any attribute.

Code:

```
df['Class'].unique()
```

In the output, we will find the names of the three Iris species. Then, we perform the mapping:

- Iris-setosa : 0
- Iris-versicolor : 1
- Iris-virginica : 2

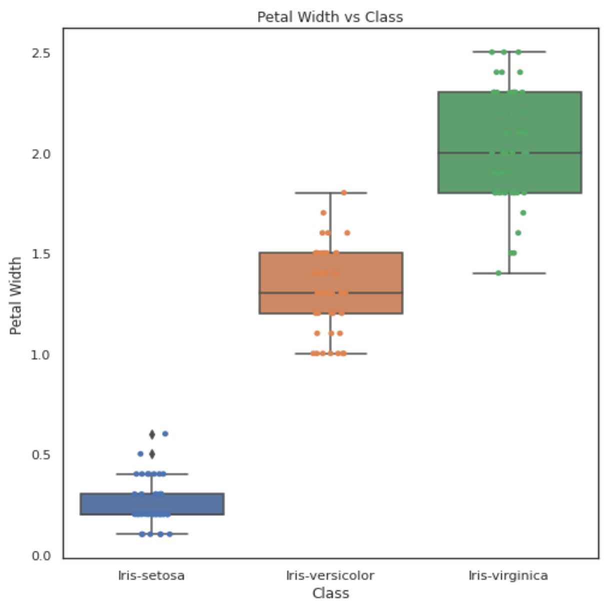


Figure 4: Relationship between Petal Width and Class

Code:

```
mapping = {'Iris-setosa': 0, 'Iris-versicolor':1, 'Iris-virginica':2}
df['Class'] = df['Class'].map(mapping)
df['Class'].unique()
```

The Pandas built-in map() function can be used to perform our mapping. Afterward, we check the unique values and find that they are 0, 1, and 2.

3.2 Correlation Analysis

Before extracting our features from the dataset, let's perform correlation analysis and remove all the redundant and derived columns from our dataset. To check the correlation between the columns we can use a heatmap from Seaborn.

Code:

```
sns.heatmap(abs(round(df.corr(),2)), annot = True, square=True)
plt.show()
```

Petal Width and Petal Length has a very high correlation. Hence, simply taking one of them should give us a better feature vector. Again, there is a high correlation between the target class and petal width. So, just using the petal width might be enough to predict our target class at a considerably high accuracy. As petal width has a higher correlation with the target class than petal length, we will keep petal width instead of petal length.

3.3 Extracting Features and Target class

We need to extract the feature vector, X, and target vector, y from our dataset (Capital X is used to denote matrix/ 2D vector and small y is used to denote 1D vector). Our reduced feature set has Sepal Length,

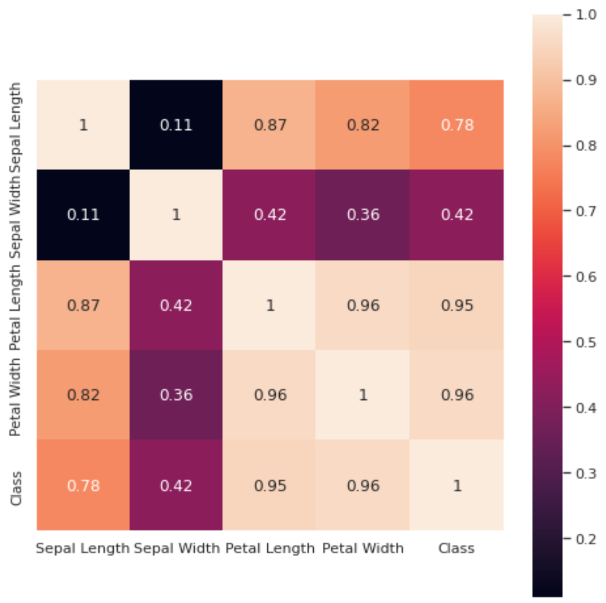


Figure 5: Correlation between the Features

Sepal Width, and Petal Width. Our target class has the Class attribute only.

Code:

```
x_names = ['Sepal Length','Sepal Width','Petal Width']
y_names = ['Class']
X = df[x_names]
y = df[y_names]
y = np.array(y)
y = y.reshape(y.shape[0])
```

3.4 Train-Test Splits

We will use 80% of our dataset to train the model and 20% for testing the model. The train_test_split() function can be used to split our feature vector, X, and target vector, y.
Code:

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=.2, random_state=0)
print("X_train shape:",X_train.shape)
print("X_test shape:",X_test.shape)
print("y_train shape:",y_train.shape)
print("y_test shape:",y_test.shape)
```

Output:

```
 X_train shape: (120, 3)
 X_test shape: (30, 3)
 y_train shape: (120,)
 y_test shape: (30,)
```

3.5 Data Transformation

Our dataset has a wide range of values and needs to be transformed so that the values fall within a suitable range. Models tend to converge faster when values are within suitable ranges such as [0,1]. There are many forms of transformation like min-max, Z-score, and so on. We perform Z-score standardization because our dataset contains a small number of outliers. The target class values are 0, 1, or 2 and hence don't need to be standardized.

Code:

```
sc = StandardScaler()
sc.fit(X_train)
X_train_std = sc.transform(X_train)
X_test_std = sc.transform(X_test)
print('Minimum and maximum values for the training dataset is:', np.round(np.min(X_train_std), 2),
    'and', np.round(np.max(X_train_std),2))
print('Minimum and maximum values for the testing dataset is:', np.round(np.min(X_test_std), 2),
    'and', np.round(np.max(X_test_std),2))
```

Output:

```
Minimum and maximum values for the training dataset is: -2.45 and 3.13
Minimum and maximum values for the testing dataset is: -1.98 and 2.67
```

4 Model: Support Vector Machine (SVM)

Our dataset is now ready to be fed to our model. Using scikitlearn's Support Vecotr Classifier (SVC) model, we will train our dataset and check the accuracy on the test dataset.

4.1 Description of the Model

Support Vector Machines are used for supervised learning or predicting labeled datasets. These models can be used for both classification and regression-based works. Support vector machines were first introduced in 1995 by Vapnik et al [2], and were very popular at the beginning due to their high accuracy on smaller datasets. Even now, SVMs tend to be a popular option for data analysts working with smaller datasets. For the Iris dataset, some of the models that achieved 100% accuracy happen to be ensembles of SVMs with other models.

The key idea of an SVM is to maximize the margin or the distance of data points from the decision boundary between contrasting classes. For a k-dimensional plane containing two classes, they can be separated by a (k-1) dimensional hyperplane. If that margin is somehow maximized then a more accurate decision boundary is obtained. If we look at the figure, the H3 line has the highest margin i.e., its distance from the contrasting class data points is the highest. However, H2 is also a valid decision boundary that separates the contrasting classes but doesn't seem to accurately predict the classes closer to the boundary. Hence, maximizing the margin should give us a better prediction for those values closer to the decision boundary. This is the rationale behind the construction of the maximum-margin hyperplane. Another, extension to this idea is that non-linear data points can't have a linear decision boundary but they can be projected to a higher dimensional space where they can be linearly separable and thus have a linear decision boundary. To do so, we often rely on the kernel trick for minimizing computational expenses. The kernel trick prevents actual mapping to the higher dimensional vector space but instead uses a kernel function to obtain similar results at a cheaper computational cost.

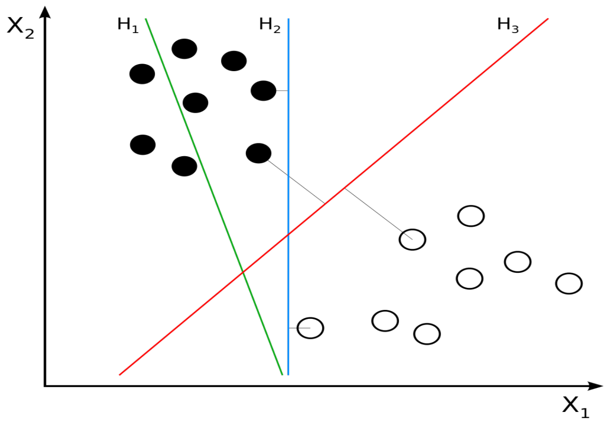


Figure 6: Different kinds of Decision Boundaries

4.2 Training the Model

We initialize an SVC model with the RBF kernel.

- RBF stands for radial basis function and is a function that will map the input feature space to another feature space. RBF is a standard kernel used for SVMs. There are other kernels like linear, polynomial, and sigmoid.
- The random_state parameter is used for generating the pseudorandom number used for shuffling the dataset.
- The hyperparameter C is used for regularization and is known as the penalty. Increasing C decreases the regularization effect and vice versa.
- The hyperparameter gamma is a kernel coefficient used for the polynomial, RBF, or gaussian, and sigmoid kernels. Higher values of gamma indicate the margin to be closer to the data points i.e., there will be a tighter boundary, while lower values of gamma give a more generalized boundary.

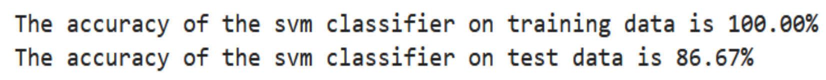
The hyperparameters c and gamma are randomly initialized at a value of 10.

Code:

```
svm = SVC(kernel='rbf', random_state=0, gamma= 10, C = 10)
svm.fit(X_train_std, y_train)

print('The accuracy of the svm classifier on training data is
    {:.2f}%'.format(svm.score(X_train_std, y_train)*100))
print('The accuracy of the svm classifier on test data is {:.2f}%'.format(svm.score(X_test_std,
    y_test)*100))
```

Output:



```
The accuracy of the svm classifier on training data is 100.00%
The accuracy of the svm classifier on test data is 86.67%
```

4.3 Hyperparameter Tuning

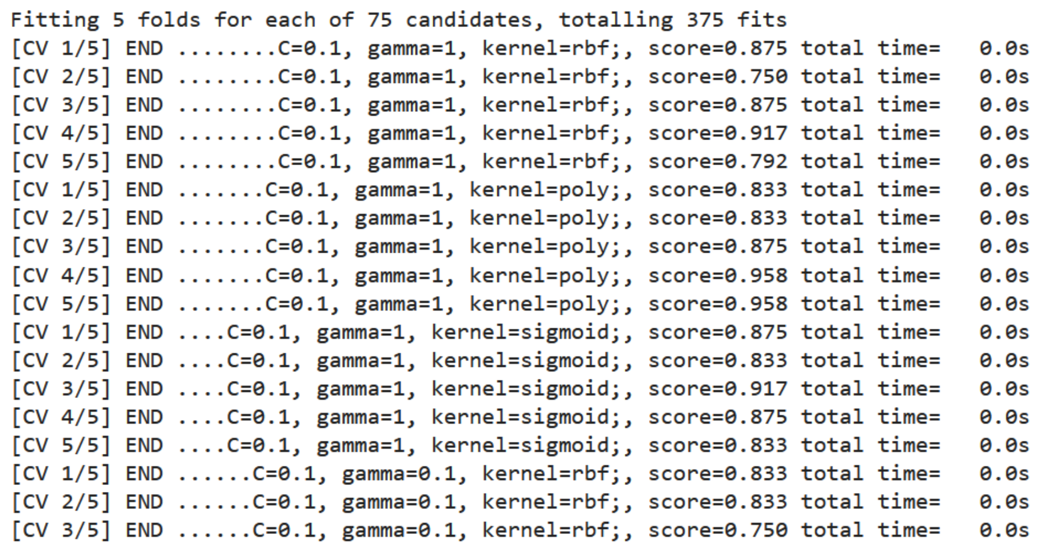
The score from the our previous instance of the SVM without the tuned hyperparameters wasn't bad but had a considerably higher training accuracy than testing accuracy. Hence, it faced overfitting. To prevent overfitting, we need to perform regularization which can be done by simply tuning the hyperparameters. The GridSearchCV() will be used to perform hyperparameter tuning which takes all possible combinations of hyperparameters when given a list of values for each hyperparameter. Afterward, it will give us the best hyperparameter values for our model.

Code:

```
# Defining the parameter range
param_grid = {'C': [0.1, 1, 10, 100, 1000],
             'gamma': [1, 0.1, 0.01, 0.001, 0.0001],
             'kernel': ['rbf','poly', 'sigmoid']}
grid = GridSearchCV(SVC(), param_grid, refit = True, verbose = 3)

# Fitting the model for grid search
grid.fit(X_train_std, y_train)
```

Output:

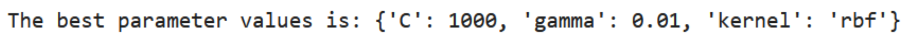


```
Fitting 5 folds for each of 75 candidates, totalling 375 fits
[CV 1/5] END ........C=0.1, gamma=1, kernel=rbf;, score=0.875 total time=   0.0s
[CV 2/5] END ........C=0.1, gamma=1, kernel=rbf;, score=0.750 total time=   0.0s
[CV 3/5] END ........C=0.1, gamma=1, kernel=rbf;, score=0.875 total time=   0.0s
[CV 4/5] END ........C=0.1, gamma=1, kernel=rbf;, score=0.917 total time=   0.0s
[CV 5/5] END ........C=0.1, gamma=1, kernel=rbf;, score=0.792 total time=   0.0s
[CV 1/5] END .......C=0.1, gamma=1, kernel=poly;, score=0.833 total time=   0.0s
[CV 2/5] END .......C=0.1, gamma=1, kernel=poly;, score=0.833 total time=   0.0s
[CV 3/5] END .......C=0.1, gamma=1, kernel=poly;, score=0.875 total time=   0.0s
[CV 4/5] END .......C=0.1, gamma=1, kernel=poly;, score=0.958 total time=   0.0s
[CV 5/5] END .......C=0.1, gamma=1, kernel=poly;, score=0.958 total time=   0.0s
[CV 1/5] END ....C=0.1, gamma=1, kernel=sigmoid;, score=0.875 total time=   0.0s
[CV 2/5] END ....C=0.1, gamma=1, kernel=sigmoid;, score=0.833 total time=   0.0s
[CV 3/5] END ....C=0.1, gamma=1, kernel=sigmoid;, score=0.917 total time=   0.0s
[CV 4/5] END ....C=0.1, gamma=1, kernel=sigmoid;, score=0.875 total time=   0.0s
[CV 5/5] END ....C=0.1, gamma=1, kernel=sigmoid;, score=0.833 total time=   0.0s
[CV 1/5] END ......C=0.1, gamma=0.1, kernel=rbf;, score=0.833 total time=   0.0s
[CV 2/5] END ......C=0.1, gamma=0.1, kernel=rbf;, score=0.833 total time=   0.0s
[CV 3/5] END ......C=0.1, gamma=0.1, kernel=rbf;, score=0.750 total time=   0.0s
```

Code:

```
print('The best parameter values is:' ,grid.best_params_)
```

Output:



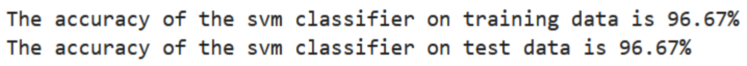
```
The best parameter values is: {'C': 1000, 'gamma': 0.01, 'kernel': 'rbf'}
```

Code:

```
svm = SVC(kernel='rbf', random_state=0, gamma = 0.01, C = 1000)
svm.fit(X_train_std, y_train)

print('The accuracy of the svm classifier on training data is
    {:.2f}%'.format(svm.score(X_train_std, y_train)*100))
print('The accuracy of the svm classifier on test data is {:.2f}%'.format(svm.score(X_test_std,
    y_test)*100))
```

Output:



```
The accuracy of the svm classifier on training data is 96.67%
The accuracy of the svm classifier on test data is 96.67%
```

5 Discussion

By tuning our hyperparameters, we have a significant decrease in training accuracy but a larger increase in test accuracy. This means that our model is able to generalize better and has prevented overfitting. Performing well in test data means performing well on unseen data and thus, our model has better performance due to hyperparameter tuning.

6 Conclusion

Our model achieved considerably high accuracy on the Iris Dataset. The Iris dataset is however a relatively small dataset, and most models can perform well on this dataset. That being said 96.67% accuracy is still high and taking ensembles of many such models might give us 100% accuracy in the test dataset. For larger datasets, we might need more complex kernel functions or might rely on larger models like deep neural networks.

7 References

[1] https://archive.ics.uci.edu/ml/datasets/iris

[2] Cortes, Corinna; Vapnik, Vladimir (1995). "Support-vector networks" (PDF). Machine Learning. 20 (3): 273–297. CiteSeerX 10.1.1.15.9362. doi:10.1007/BF00994018. S2CID 206787478.