# Iris Flower Classification Project using Machine Learning

Machine learning is almost everywhere nowadays. It's become more and more necessary day by day. From the recommendation of what to buy to recognizing a person, robotics, everywhere is machine learning. So in this project, we'll create the "Hello World" of machine learning which means Iris flower classification.

**Iris flower classification** is a very popular machine learning project. The iris dataset contains three classes of flowers, **Versicolor**, **Setosa**, **Virginica**, and each class contains 4 features, 'Sepal length', 'Sepal width', 'Petal length', 'Petal width'. The aim of the iris flower classification is to predict flowers based on their specific features.

### **Download Iris Flower Classification Project Code**

Please download the source code of iris flower classification with opency: <u>Iris Flower Classification Project Code</u>







# **Steps to Classify Iris Flower:**

- 1. Load the data
- 2. Analyze and visualize the dataset
- 3. Model training.
- 4. Model Evaluation.
- 5. Testing the model.

# Step 1 – Load the data:

# DataFlair Iris Flower Classification

# Import Packages

import numpy as np import matplotlib.pyplot as plt import seaborn as sns import pandas as pd %matplotlib inline

First, we've imported some necessary packages for the project.

- Numpy will be used for any computational operations.
- We'll use Matplotlib and seaborn for data visualization.
- Pandas help to load data from various sources like local storage, database, excel file, CSV file, etc.

columns = ['Sepal length', 'Sepal width', 'Petal length', 'Petal width', 'Class\_labels']

#### # Load the data

df = pd.read\_csv('iris.data', names=columns)

df.head()

- Next, we load the data using pd.read\_csv() and set the column name as per the iris data information.
- Pd.read\_csv reads CSV files. CSV stands for comma separated value.
- df.head() only shows the first 5 rows from the data set table.
- All the numerical values are in centimeters.

| In [7]: | df.head() |              |             |              |             |              |  |  |
|---------|-----------|--------------|-------------|--------------|-------------|--------------|--|--|
| Out[7]: |           | Sepal length | Sepal width | Petal length | Petal width | Class_labels |  |  |
|         | 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  |  |  |

# **Step 2 – Analyze and visualize the dataset:**

Let's see some information about the dataset.

# Some basic statistical analysis about the data df.describe()

In [8]: # Some basic statistical analysis about the data|
df.describe()

Out[8]:

|       | 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    |

From this description, we can see all the descriptions about the data, like average length and width, minimum value, maximum value, the 25%, 50%, and 75% distribution value, etc.

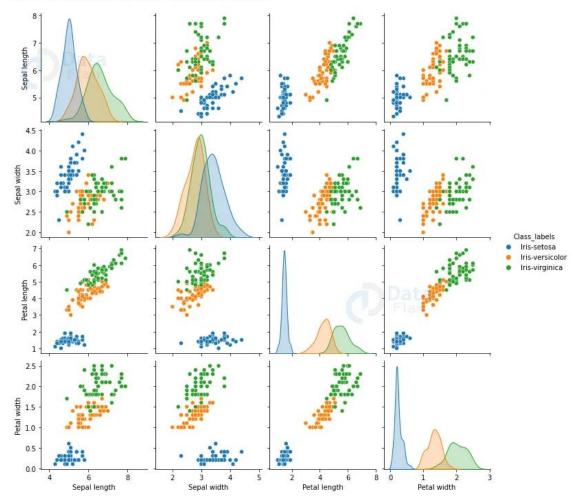
Let's visualize the dataset.

# Visualize the whole dataset

```
sns.pairplot(df, hue='Class_labels')
```

[9]: # Visualize the whole dataset sns.pairplot(df, hue='Class\_labels')

[9]: <seaborn.axisgrid.PairGrid at 0x7f4350a23a90>



- To visualize the whole dataset we used the seaborn pair plot method. It plots the whole dataset's information.
- From this visualization, we can tell that iris-setosa is well separated from the other two flowers.
- And iris virginica is the longest flower and iris setosa is the shortest. Now let's plot the average of each feature of each class.

### # Separate features and target

data = df.values

X = data[:,0:4]

Y = data[:,4]

• Here we separated the features from the target value.

# Calculate average of each features for all classes

```
Y_Data = np.array([np.average(X[:, i][Y==j].astype('float32')) for i in range (X.shape[1]) for j in (np.unique(Y))])

Y_Data_reshaped = Y_Data.reshape(4, 3)

Y_Data_reshaped = np.swapaxes(Y_Data_reshaped, 0, 1)

X_axis = np.arange(len(columns)-1)

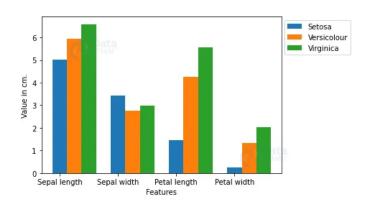
width = 0.25
```

- Np.average calculates the average from an array.
- Here we used two for loops inside a list. This is known as list comprehension.
- List comprehension helps to reduce the number of lines of code.
- The Y\_Data is a 1D array, but we have 4 features for every 3 classes. So we reshaped Y\_Data to a (4, 3) shaped array.
- Then we change the axis of the reshaped matrix.

#### # Plot the average

```
plt.bar(X_axis, Y_Data_reshaped[0], width, label = 'Setosa')
plt.bar(X_axis+width, Y_Data_reshaped[1], width, label = 'Versicolour')
plt.bar(X_axis+width*2, Y_Data_reshaped[2], width, label = 'Virginica')
plt.xticks(X_axis, columns[:4])
plt.xlabel("Features")
plt.ylabel("Value in cm.")
plt.legend(bbox_to_anchor=(1.3,1))
plt.show()
```

We used matplotlib to show the averages in a bar plot.



### **Step 3 – Model training:**

# Split the data to train and test dataset.

from sklearn.model\_selection import train\_test\_split

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, Y, test\_size=0.2)

• Using train\_test\_split we split the whole data into training and testing datasets. Later we'll use the testing dataset to check the accuracy of the model.

# Support vector machine algorithm

from sklearn.svm import SVC

```
svn = SVC()
```

svn.fit(X\_train, y\_train)

- Here we imported a support vector classifier from the scikit-learn support vector machine.
- Then, we created an object and named it svn.
- After that, we feed the training dataset into the algorithm by using the svn.fit() method.

### **Step 4 – Model Evaluation:**

# Predict from the test dataset

predictions = svn.predict(X\_test)

# Calculate the accuracy

from sklearn.metrics import accuracy\_score

accuracy\_score(y\_test, predictions)

- Now we predict the classes from the test dataset using our trained model.
- Then we check the accuracy score of the predicted classes.
- accuracy\_score() takes true values and predicted values and returns the percentage of accuracy.

#### **Output:**

0.966666666666666

The accuracy is above 96%.

Now let's see the detailed classification report based on the test dataset.

#### # A detailed classification report

from sklearn.metrics import classification\_report

print(classification\_report(y\_test, predictions))

precision recall f1-score support

Iris-setosa 1.00 1.00 1.00 9

Iris-versicolor 1.00 0.83 0.91 12

```
Iris-virginica 0.82 1.00 0.90 9
accuracy 0.93 30
macro avg 0.94 0.94 0.94 30
weighted avg 0.95 0.93 0.93 30
```

- The classification report gives a detailed report of the prediction.
- Precision defines the ratio of true positives to the sum of true positive and false positives.
- Recall defines the ratio of true positive to the sum of true positive and false negative.
- F1-score is the mean of precision and recall value.
- Support is the number of actual occurrences of the class in the specified dataset.

# **Step 5 – Testing the model:**

```
X_{new} = np.array([[3, 2, 1, 0.2], [4.9, 2.2, 3.8, 1.1], [5.3, 2.5, 4.6, 1.9]])
```

#Prediction of the species from the input vector

```
prediction = svn.predict(X_new)
print("Prediction of Species: {}".format(prediction))
```

Here we take some random values based on the average plot to see if the model can predict accurately.

### **Output:**

Prediction of Species: ['Iris-setosa' 'Iris-versicolor' 'Iris-virginica']

It looks like the model is predicting correctly because the setosa is shortest and virginica is the longest and versicolor is in between these two.

```
# Save the model
import pickle
with open('SVM.pickle', 'wb') as f:
pickle.dump(svn, f)
# Load the model
with open('SVM.pickle', 'rb') as f:
```

model = pickle.load(f)

model.predict(X\_new)

- We can save the model using pickle format.
- And again we can load the model in any other program using pickle and use it using model.predict to predict the iris data.

### **Summary:**

In this project, we learned to train our own supervised machine learning model using Iris Flower Classification Project with Machine Learning. Through this project, we learned about machine learning, data analysis, data visualization, model creation, etc.