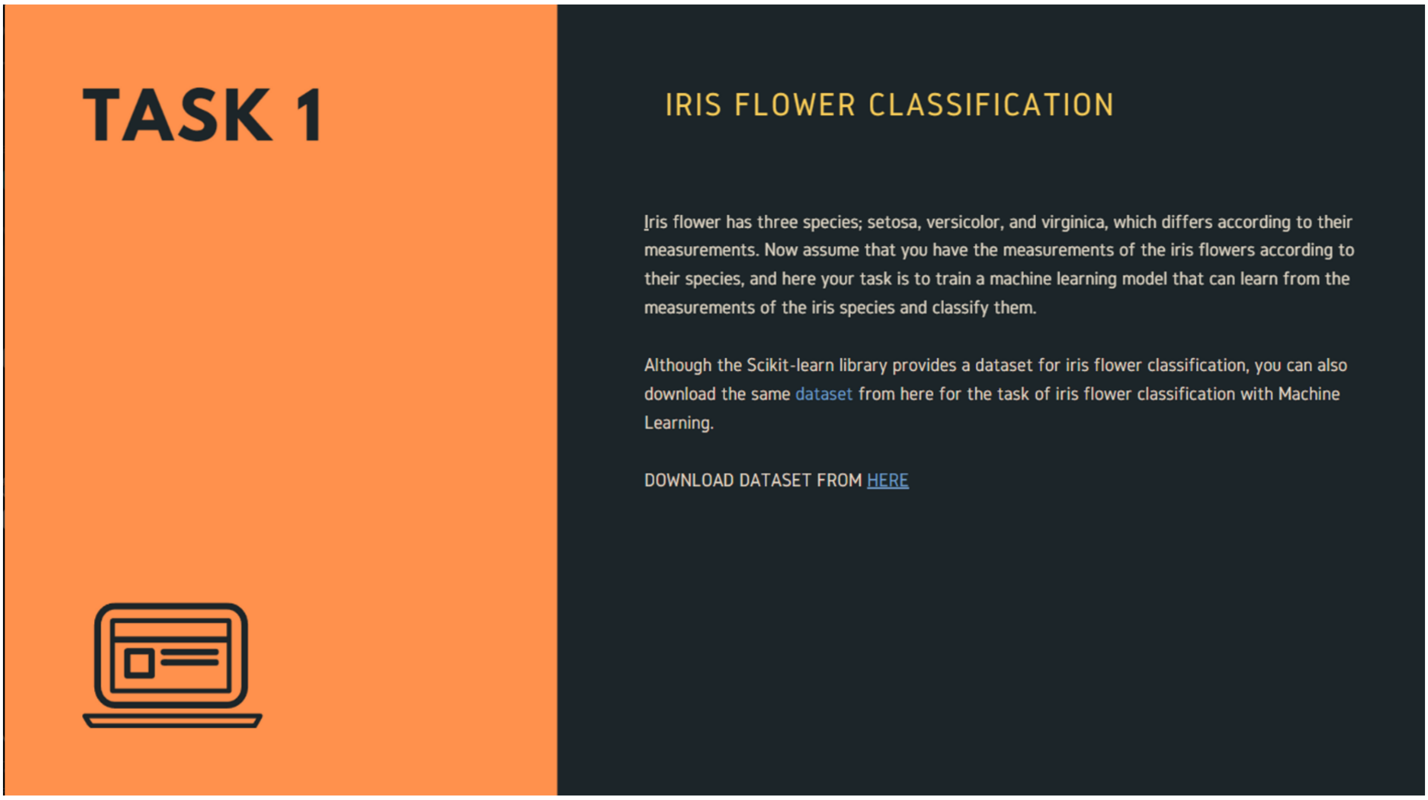


Task 1: Iris Flower Prediction

What is Iris and what are its species?

Iris is a genus of flowering plants that belongs to the **family Iridaceae.

It had a diverse and widespread genus, known for its beautiful and showy flowers.

In this project, I utilized various Python libraries such as NumPy, Matplotlib, Seaborn, and Pandas to load and manipulate the data. The data was visualized using Matplotlib and Seaborn libraries to gain insights and better understand the patterns and characteristics of the Iris flowers.

For the classification task, I trained a Support Vector Machine (SVM) algorithm using the labeled data. The SVM algorithm is known for its effectiveness in handling classification problems. I evaluated the model's performance using appropriate metrics and conducted testing to ensure its accuracy.

The project focuses on classifying three different species of Iris flowers: Setosa, Versicolor, and Virginia.

Iris has a genus of 300 Species of plants in the family of Iridaceae.

Listed Species of Iris flower are:

1. Setosa: Setosa is often used as a species name in the biological classification of plants and animals. For example, "Iris setosa" is a species of iris, a type of flowering plant.
2. Versicolor: Versicolor is another species name commonly used in biological classification. For instance, "Lobelia versicolor" is a species of flowering plant.
3. Virginia: Virginia is a term that could refer to several things. It is often associated with the U.S. state of Virginia, or it could be a person's name. Additionally, there is a species of opossum called the Virginia opossum (Didelphis virginiana).

I'm delighted to share that the model achieved an accuracy of 100% in classifying the Iris flowers correctly. The repository contains the code implementation, along with detailed documentation, to guide you through the project.

GitHub Repository: https://github.com/sahilkarande/OIBSIP/tree/main/Task1%20-%20Iris%20flower%20Detection

Step 1. Loading the Data

```
# Import Packages

import numpy as np

import matplotlib.pyplot as plt

import seaborn as sns

import pandas as pd
```

- numpy library is used to perform computational operations
- matplotlib and seaborn are used for visualization
- pandas can help us to load data from various sources

```
columns = ['Sepal length', 'Sepal width', 'Petal length', 'Petal width',
'Class_labels'] # As per the iris dataset information
```

- we can load the data using pd.read_csv
- function - `pd.read_csv` is used to reads csv files
- csv: comma separated values

```
# Load the data

df = pd.read_csv('/iris.data', names=columns)
```

Note: All the numerical values will be printed in centimeter unit

```
df.head()
```

	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

- `df.head()` shows first 5 rows of the dataset

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

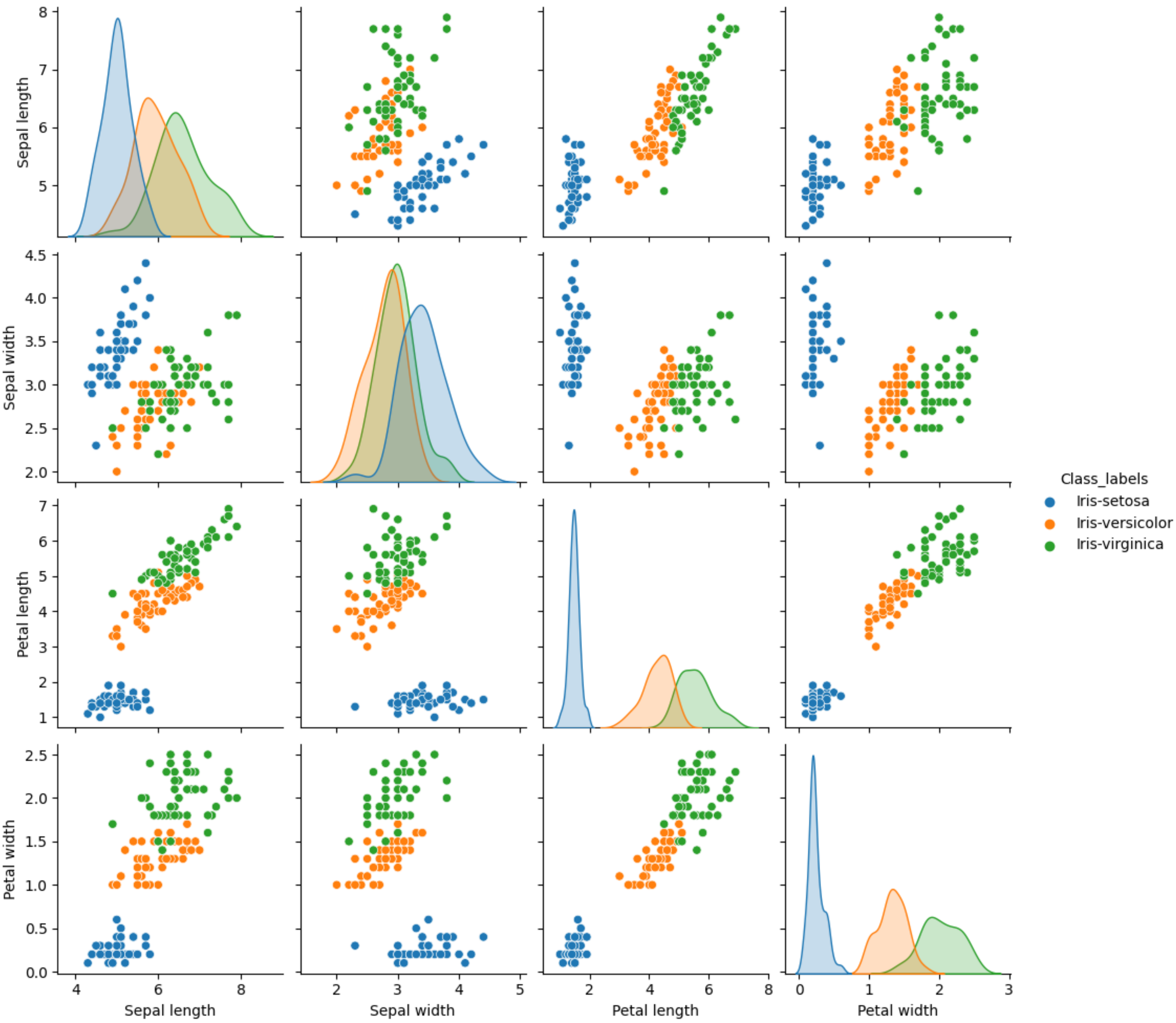
	Sepal length	Sepal width	Petal length	Petal width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000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

- this gives the description of the data we have provided
- it provides the description like percentile, mean, std, etc. of a data frame or a series of numeric values.

Step 2. Analyzing & Visualization

```
# Visualize the whole dataset

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

```
<seaborn.axisgrid.PairGrid at 0x7f12edf157e0>
```



- now let us visualize the data based on the numerical values we provided and along with the sepal length, sepal width, petal length, and petal height
- the visualization is done by using the seaborn pair plot method
- it plots the information of the whole dataset

```
# Seperate features and target
```

```
data = df.values

X = data[:,0:4]

Y = data[:,4]
```

-`df` refers to a DataFrame object which contains the dataset. The `.values` attribute retrieves the underlying NumPy array representation of the DataFrame.

- `X = data[:, 0:4]`: This line extracts the features from the `data` array. It uses NumPy array indexing to select all rows (`:`) and the columns from index 0 to 3 (0-based indexing). This means that the features are stored in the data array's first four columns and assigned to the variable `X`.

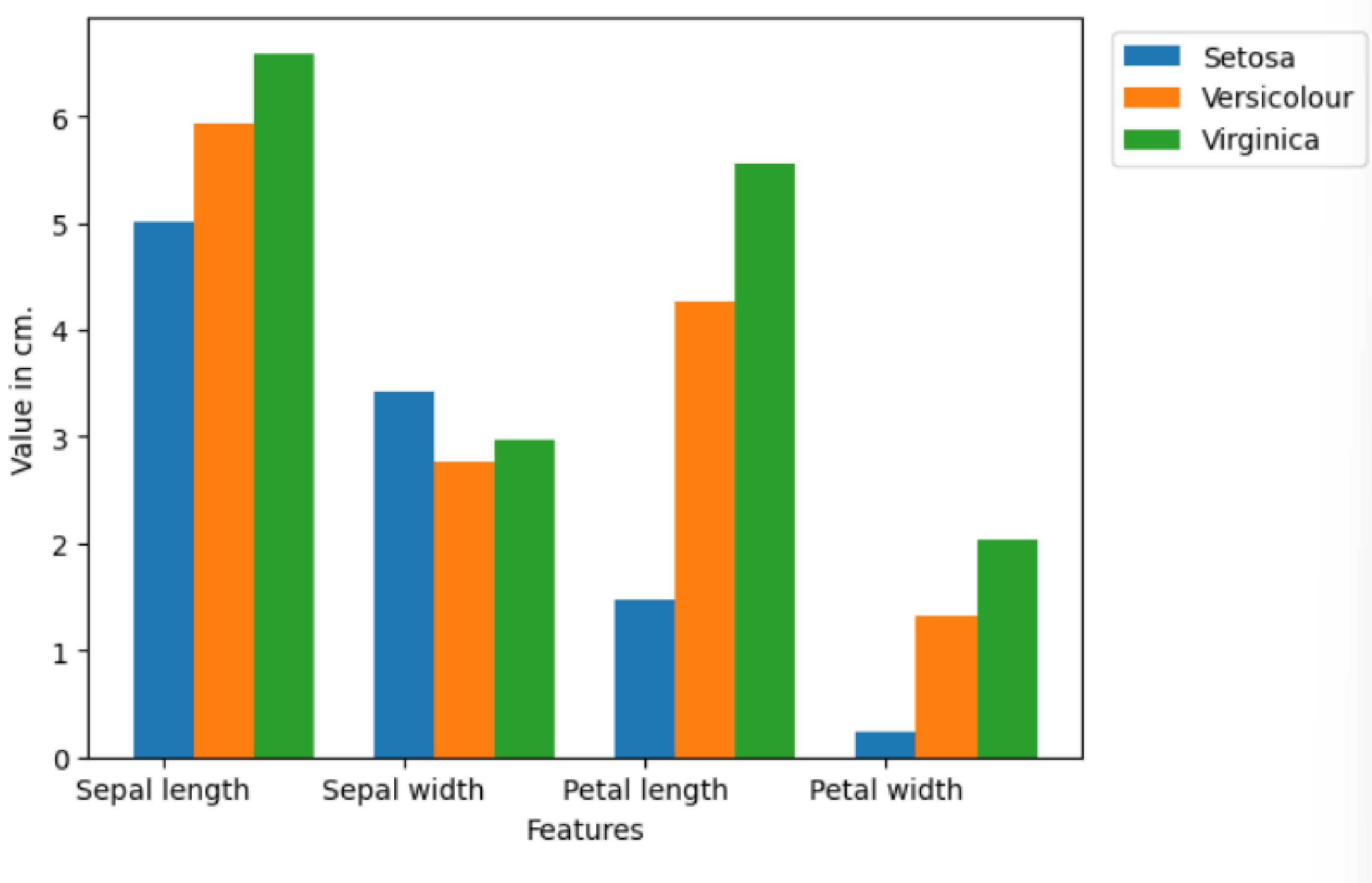
- `Y = data[:, 4]`: This line extracts the target variable from the `data` array. It uses NumPy array indexing similar to the previous line but only selects the column with index 4. This means that the target variable is stored in the fifth column of the `data` array and is assigned to the variable `Y`.

```
# Calculate avarage of each feature 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, it helps to iterate over the features and classes.
- The code reshapes the `Y_Data` array from a 1D array to a 2D array with a (4, 3) shape. but we have 4 features for every 3 classes. So we reshaped Y_Data to a (4, 3) shaped array.
- 4 features and 3 classes, so we want to organize the average values accordingly.
- Then we change the axis of the reshaped matrix.
- After reshaping, the code swaps the axes of the reshaped array using `np.swapaxes()`. This is done to make it easier to plot the data later on.
- The code then creates an array called `X_axis` which will be used as the x-axis for the plot. It is initialized with values ranging from 0 to the number of features minus 1.

```
# Plot the avarage
```

```
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 can clearly see the Virginica is the longest and setosa is the shortest flower.

Step 3 – Model training:

```
# Split the data to train and test the 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 - Evaluating the Model

```
# Predict from the test dataset

predictions = svn.predict(X_test)
```

- 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.
- The classification report gives a detailed report of the prediction.

```
# Calculate the accuracy

from sklearn.metrics import accuracy_score

accuracy_score(y_test, predictions)
```

1.0

When we execute accuracy_score(y_test, predictions), it returns a value of 1.0. This means that the accuracy of the model on the given test dataset is 100% or perfect.

```
# 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        11
Iris-versicolor       1.00      1.00      1.00        12
 Iris-virginica       1.00      1.00      1.00         7

       accuracy                           1.00        30
      macro avg       1.00      1.00      1.00        30
   weighted avg       1.00      1.00      1.00        30
```

Step 5 - Model Testing

```
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))
```

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

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

```
# 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)
```

- 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.

```
model.predict(X_new)
```

```
array(['Iris-setosa', 'Iris-versicolor', 'Iris-virginica'], dtype=object)
```

In this project, we gained hands-on experience in training a supervised machine learning model using the Iris Flower Classification Project with Machine Learning. Throughout this project, we obtained knowledge and skills related to machine learning, data analysis, data visualization, and model development, among other aspects.