Iris Flower Classification

Steps to Classiffy Iris Flowers:

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

Load the data:

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

```
columns = ['Sepal_length', 'Sepal_width', 'Petal_length', 'Petal_width', 'species']
iris = pd.read_csv("/content/drive/MyDrive/IRIS.csv")
```

```
print(iris.head())
```

```
   sepal_length  sepal_width  petal_length  petal_width      species
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
```

```
iris.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
 #   Column        Non-Null Count  Dtype  
---  ------        --------------  -----  
 0   sepal_length  150 non-null    float64
 1   sepal_width   150 non-null    float64
 2   petal_length  150 non-null    float64
 3   petal_width   150 non-null    float64
 4   species       150 non-null    object 
dtypes: float64(4), object(1)
memory usage: 6.0+ KB
```

```
#checking for null values
iris.isnull().sum()
```

```
sepal_length    0
sepal_width     0
petal_length    0
petal_width     0
species         0
dtype: int64
```

- **We can see that all values are 0, it means that there are no null values over the entire data frame**

Analyze and visualize the dataset:

```
iris.describe()
```

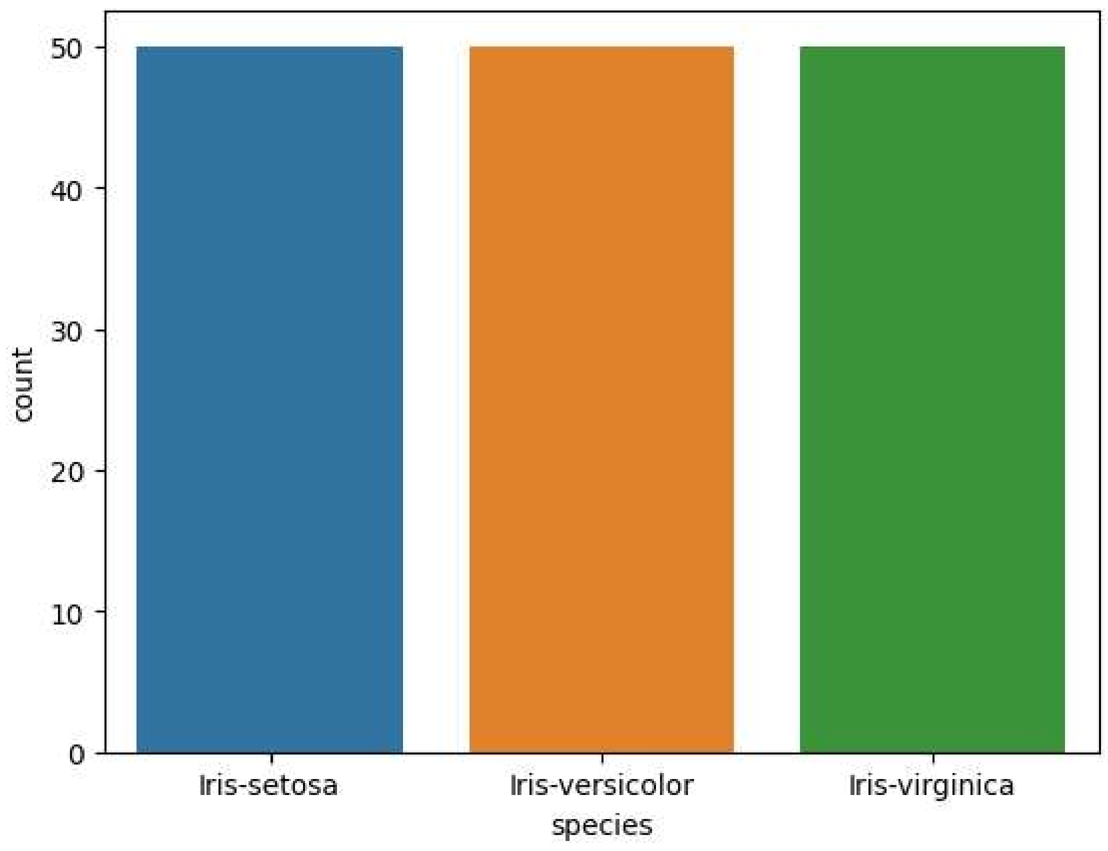
	sepal_length	sepal_width	petal_length	petal_width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000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

- **From the above table, we can see all the description about the data, like average length, minimum value, maximum value, the 25%, 50% and 75% discription value,etc**

```
iris['species'].value_counts()
```

```
Iris-setosa        50
Iris-versicolor    50
Iris-virginica     50
Name: species, dtype: int64
```

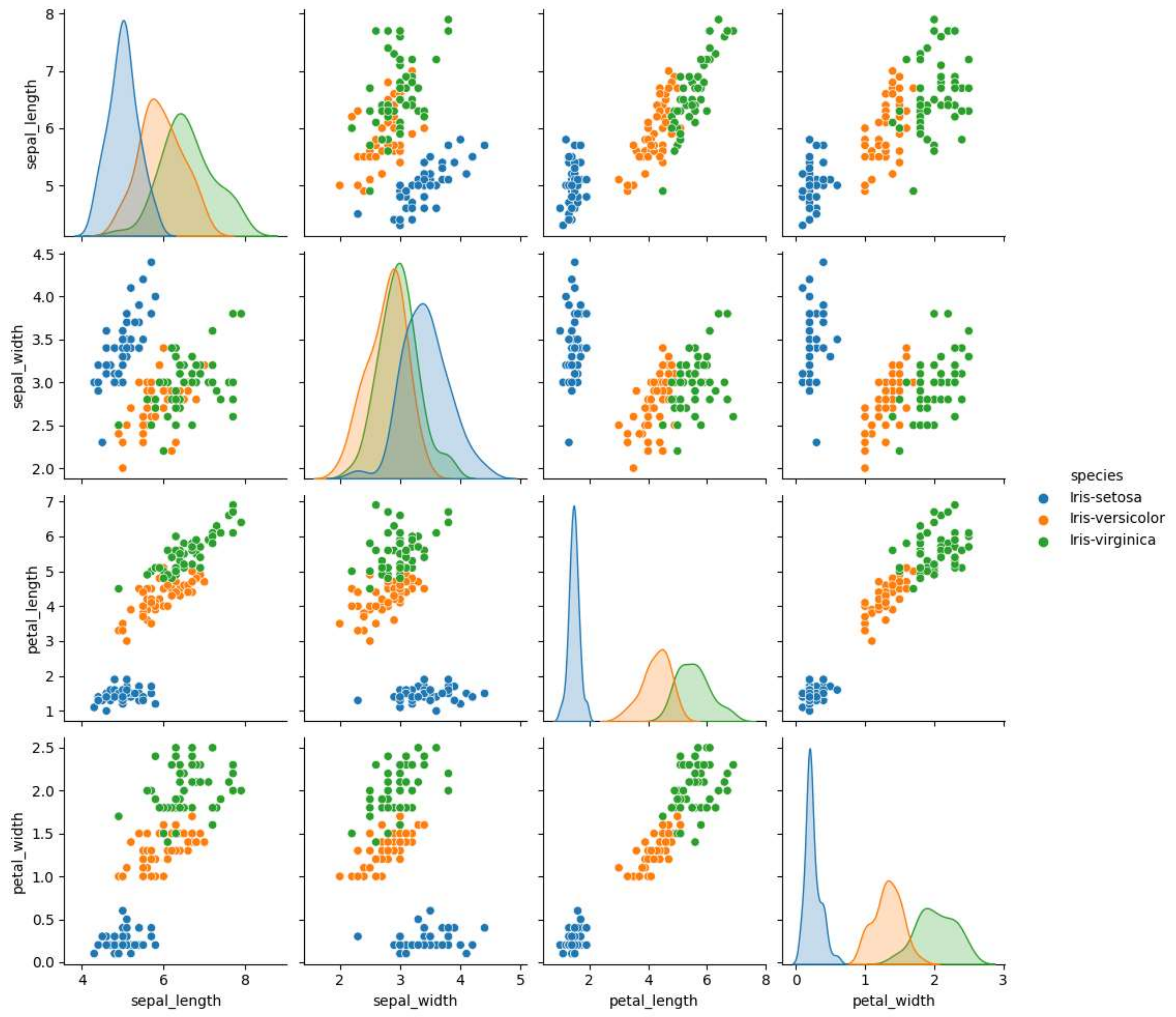
```
sns.countplot(data=iris, x='species');
```



- **We have 150 rows in which 50 belongs to Iris-setosa, 50 belongs to Iris-versicolor, and the remaining 50 belong to Iris-virginica**

```
#Visualize the whole dataset
sns.pairplot(iris, hue='species')
```

```
<seaborn.axisgrid.PairGrid at 0x7a21fefe1e70>
```



- **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**

```
data = iris.values
X = data[:,0:4]
Y = data[:,4]
```

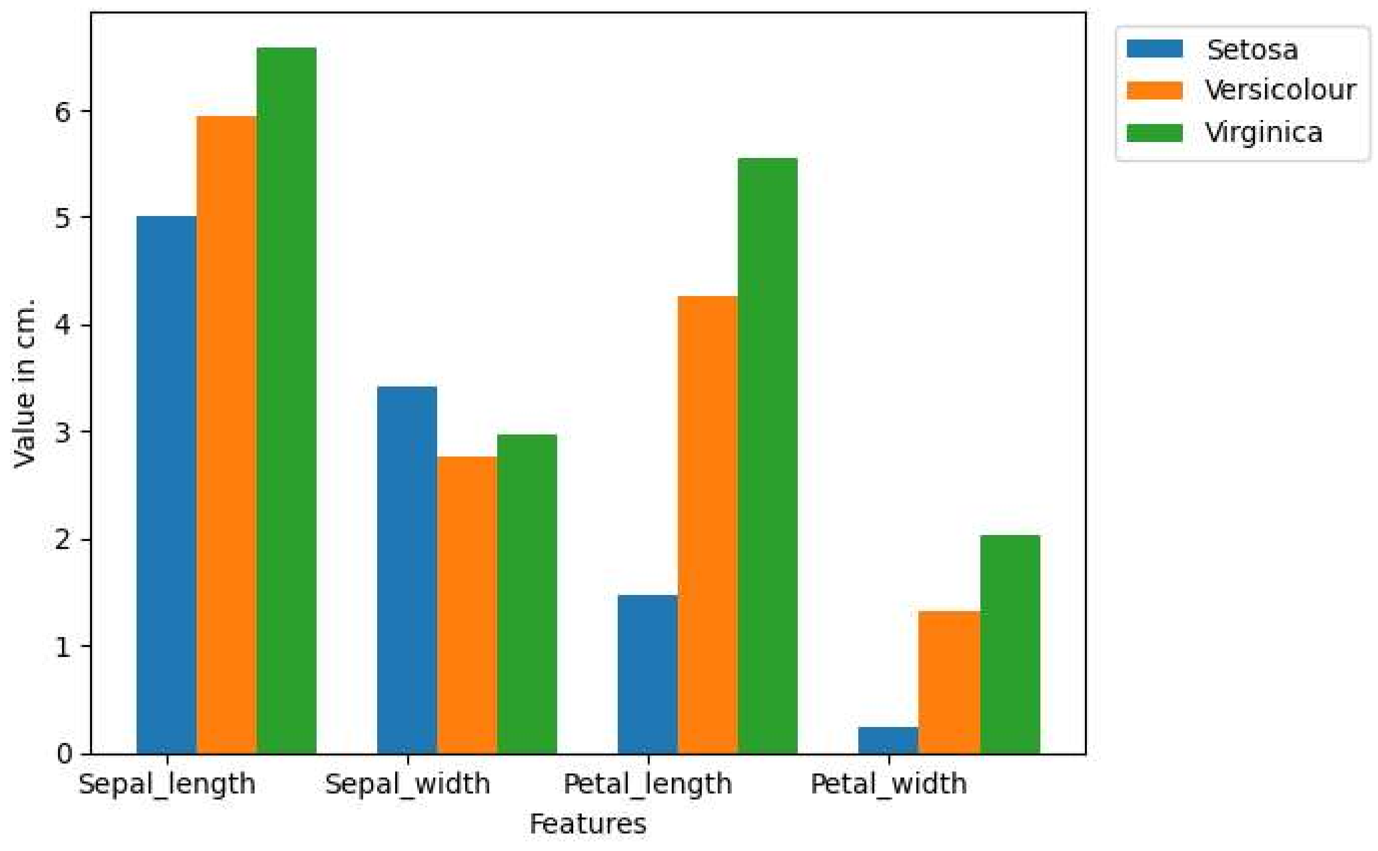
- Here we separated the features from the target value.

```
# 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()
```



- **Here we can clearly see the verginica is the longest and setosa is the shortest flower**

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)
```

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)
```

```
1.0
```

- The accuracy is 100%

```
# 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        10
Iris-versicolor       1.00      1.00      1.00        12
 Iris-virginica       1.00      1.00      1.00         8

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

The classification report gives 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.

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))
```

```
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)
```

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