main

September 9, 2025

[1]:
```python
# 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
```

[2]:
```python
columns = ['Sepal length', 'Sepal width', 'Petal length', 'Petal width',␣
 ↪'Class_labels']
# Load the data
df = pd.read_csv('iris.data', names=columns)
df.head()
```

[2]:

	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

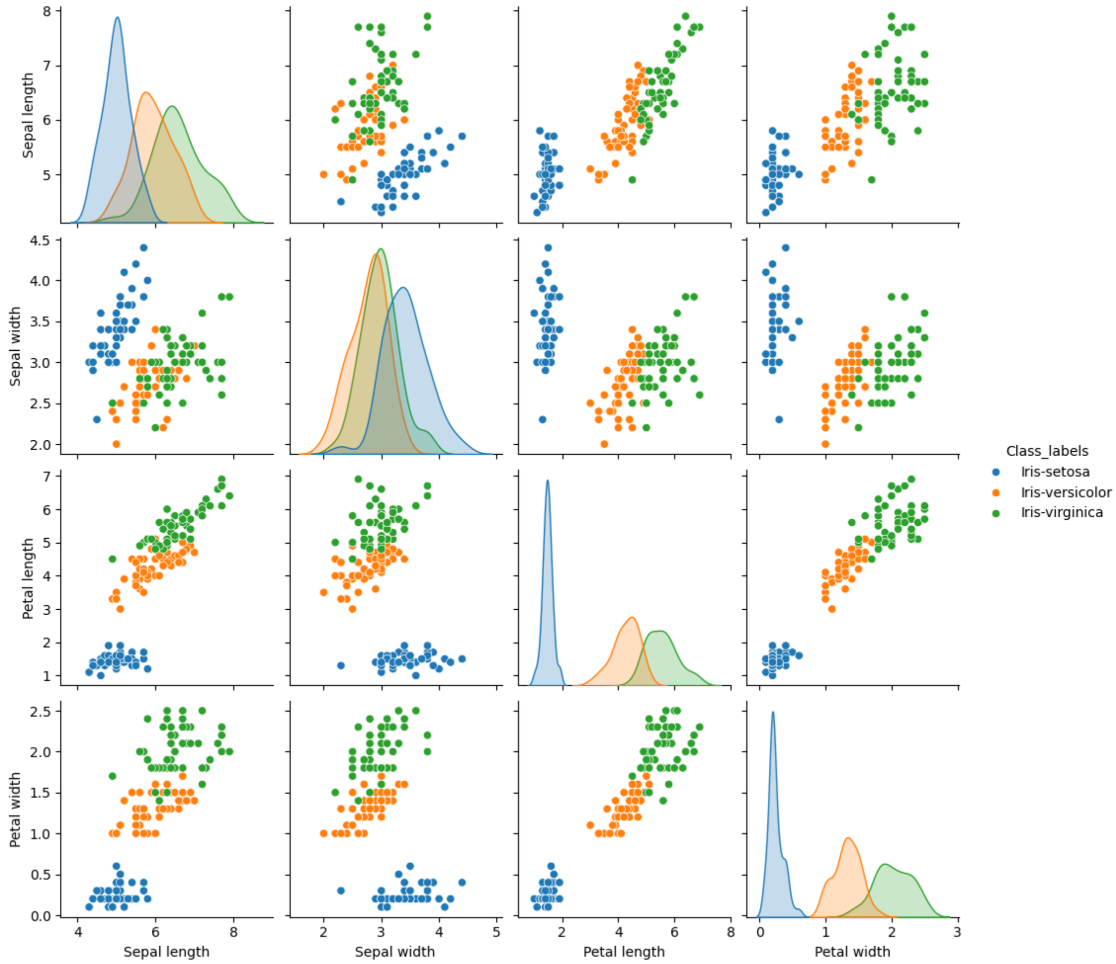
[3]:
```python
# Some basic statistical analysis about the data
df.describe()
```

[3]:

	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

[4]:
```python
# Visualize the whole dataset
sns.pairplot(df, hue='Class_labels')
```

[4]: <seaborn.axisgrid.PairGrid at 0x74f449d21a90>



[5]:
```
# Separate features and target
data = df.values
X = data[:,0:4]
Y = data[:,4]
```

[6]:
```
# 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
```

[7]:
```
# 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')
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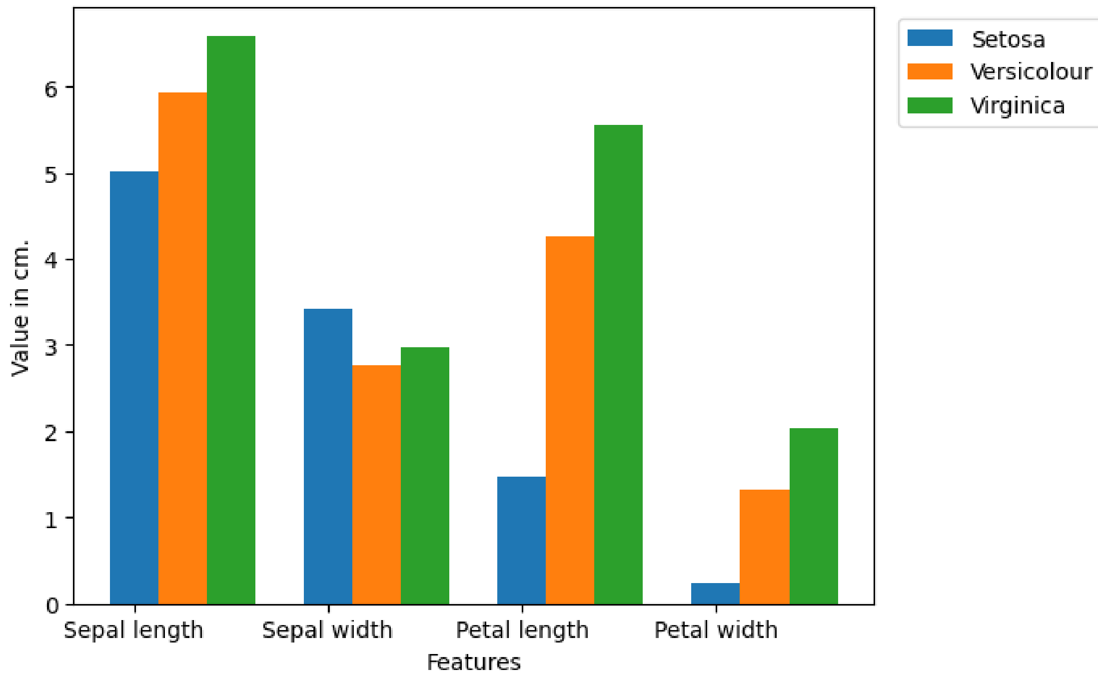
```python
plt.bar(X_axis+width*2, Y_Data_reshaped[2], width, label = 'Virginica')
plt.xticks(X_axis, columns[:4])
plt.xlabel("Features")
plt.ylabel("Value in cm.")
plt.legend(bbox_to_anchor=(1.3,1))
plt.show()
```



[8]:
```python
# 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)
```

[9]:
```python
# Support vector machine algorithm
from sklearn.svm import SVC
svn = SVC()
svn.fit(X_train, y_train)
```

[9]: SVC()

[11]:
```python
# Predict from the test dataset
predictions = svn.predict(X_test)

# Calculate the accuracy
from sklearn.metrics import accuracy_score
accuracy_score(y_test, predictions)
```

[11]: 0.9333333333333333

[14]:
```
# 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        12
Iris-versicolor       0.80      1.00      0.89         8
 Iris-virginica       1.00      0.80      0.89        10

       accuracy                           0.93        30
      macro avg       0.93      0.93      0.93        30
   weighted avg       0.95      0.93      0.93        30
```

[15]:
```
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-versicolor']
```

[16]:
```
# 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)
```

[16]: array(['Iris-setosa', 'Iris-versicolor', 'Iris-versicolor'], dtype=object)

[ ]: