IRIS FLOWER CLASSIFICATION

In [108…

```
#Importing necessary libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

In [109…

```
#Loading the dataset
df = pd.read_csv("C:/Users/Akash K Shaji/Downloads/Iris.csv")
df.head()
```

Out[109]:

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
0	1	5.1	3.5	1.4	0.2	Iris-setosa
1	2	4.9	3.0	1.4	0.2	Iris-setosa
2	3	4.7	3.2	1.3	0.2	Iris-setosa
3	4	4.6	3.1	1.5	0.2	Iris-setosa
4	5	5.0	3.6	1.4	0.2	Iris-setosa

In [110…

```
#Understanding the structure of the dataset
df.shape
```

Out[110]:

```
(150, 6)
```

The Iris flower classification dataset comprises 150 samples of Iris flowers.

In [111…

```
#Listing columns of the dataset
df.columns.tolist()
```

Out[111]:

```
['Id',
 'SepalLengthCm',
 'SepalWidthCm',
 'PetalLengthCm',
 'PetalWidthCm',
 'Species']
```

The dataset contains 6 variables.

In [112…

```
#Understanding distribution of species
df['Species'].value_counts()
```

Out[112]:

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

The variable contains 3 different iris flower species and there are 50 instances of each species in the column.

Species is the target variable. Since the number of samples for each class is same, the dataset is said to be balanced.

In [113…

```
#Dropping irrelevent column
df = df.drop('Id', axis=1)
df.head()
```

Out[113]:

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	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

In [114…

```
#Checking for null values
df.isnull().sum()
```

Out[114]:

```
SepalLengthCm    0
SepalWidthCm     0
PetalLengthCm    0
PetalWidthCm     0
Species          0
dtype: int64
```

Null values are absent.

In [115…

```
#Checking for duplicate values
num_duplicates = df.duplicated().sum()
print(f"Number of duplicated rows: {num_duplicates}")
```

```
Number of duplicated rows: 3
```

In [116…

```
# removing the duplicated rows
df=df.drop_duplicates()
num_duplicates_rem = df.duplicated().sum()
print(f"Number of duplicated rows after removal: {num_duplicates_rem}")
```

```
Number of duplicated rows after removal: 0
```

In [117…

```
#Summary of the dataframe
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 147 entries, 0 to 149
Data columns (total 5 columns):
 #   Column         Non-Null Count  Dtype  
---  ------         --------------  -----  
 0   SepalLengthCm  147 non-null    float64
 1   SepalWidthCm   147 non-null    float64
 2   PetalLengthCm  147 non-null    float64
 3   PetalWidthCm   147 non-null    float64
 4   Species        147 non-null    object 
dtypes: float64(4), object(1)
memory usage: 6.9+ KB
```

We have 4 numerical variables and 1 categorical variables.

Number of non null values in each column is also obtained.

It also provides an estimate of the memory usage of the DataFrame. Here the memory usage is approximately 6 KB.

In [118…

```
#Summary statistics
df.describe().T
```

Out[118]:

	count	mean	std	min	25%	50%	75%	max
SepalLengthCm	147.0	5.856463	0.829100	4.3	5.1	5.8	6.4	7.9
SepalWidthCm	147.0	3.055782	0.437009	2.0	2.8	3.0	3.3	4.4
PetalLengthCm	147.0	3.780272	1.759111	1.0	1.6	4.4	5.1	6.9
PetalWidthCm	147.0	1.208844	0.757874	0.1	0.3	1.3	1.8	2.5

The datapoints are in a certain range therefore numerical instabilities won't be there and there is no need to standardize the data.

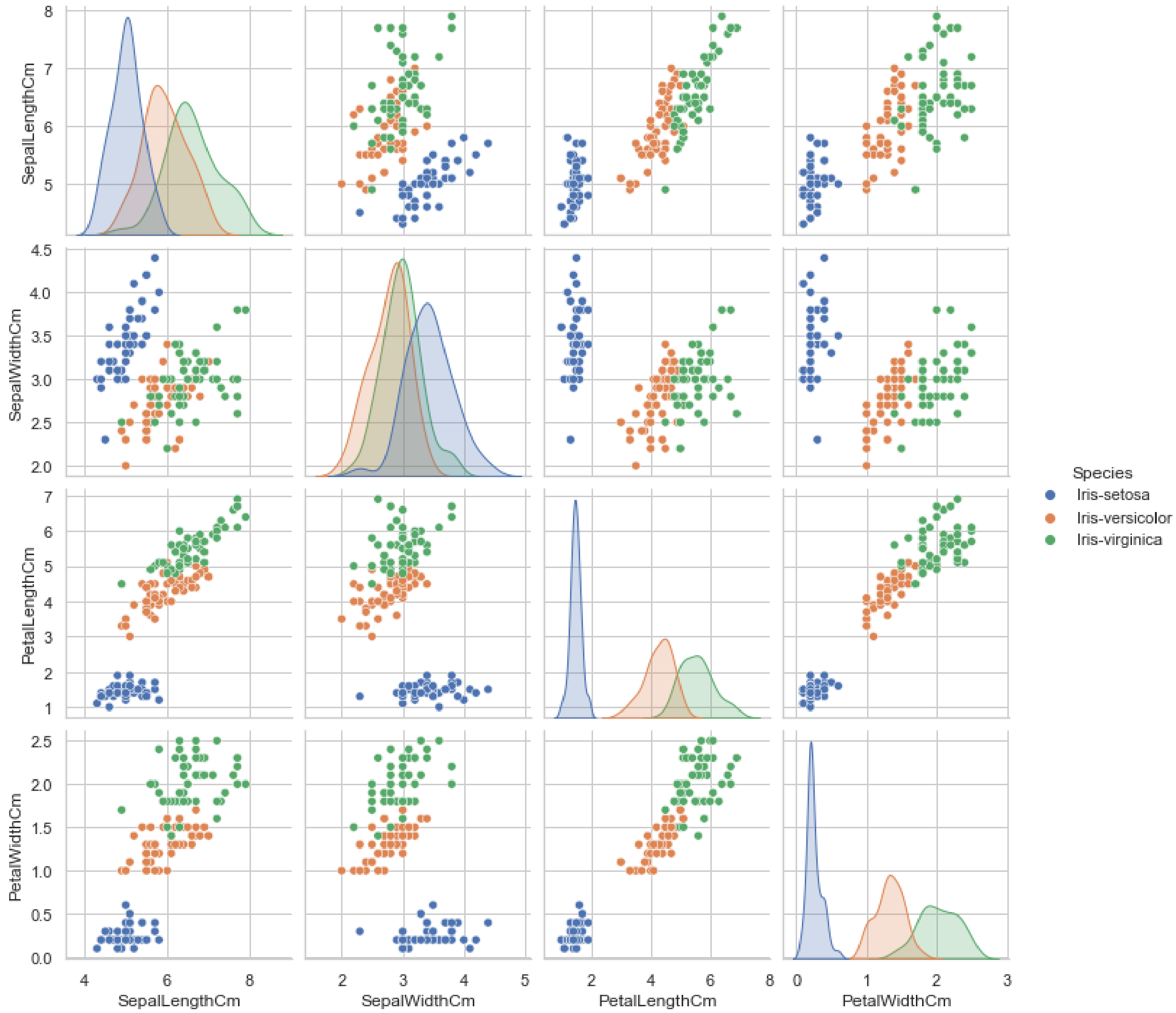
Pairwise Relationships between Features with Species Variation

In [119…

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

Out[119]:

```
<seaborn.axisgrid.PairGrid at 0x1f755565d90>
```



The diagonal of the pair plot displays histograms (or kernel density estimations) of each feature for each species. These plots show the distribution of each feature within each species.

The off-diagonal plots show scatter plots of pairs of features. Iris-Setosa usually forms distinct clusters and is often well-separated from the other two species.

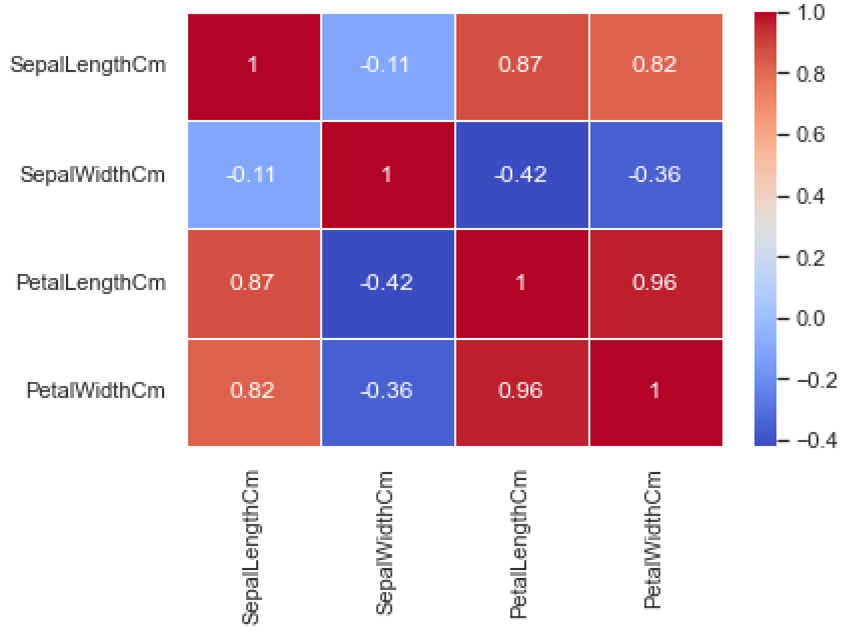
Versicolor and Virginica might overlap in some feature combinations, making it challenging to distinguish them solely based on these features.

In [120…

```
#Correlation Plot
sns.heatmap(df.corr(), annot=True, cmap='coolwarm', linewidths=0.5)
```

Out[120]:

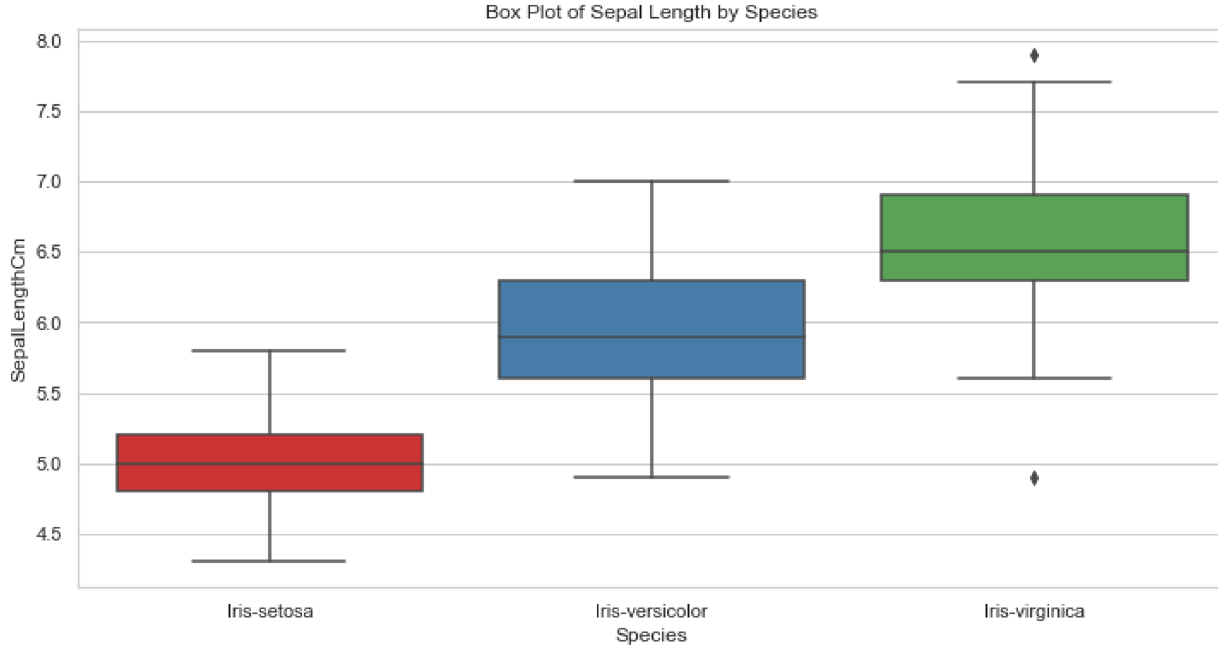
```
<AxesSubplot:>
```

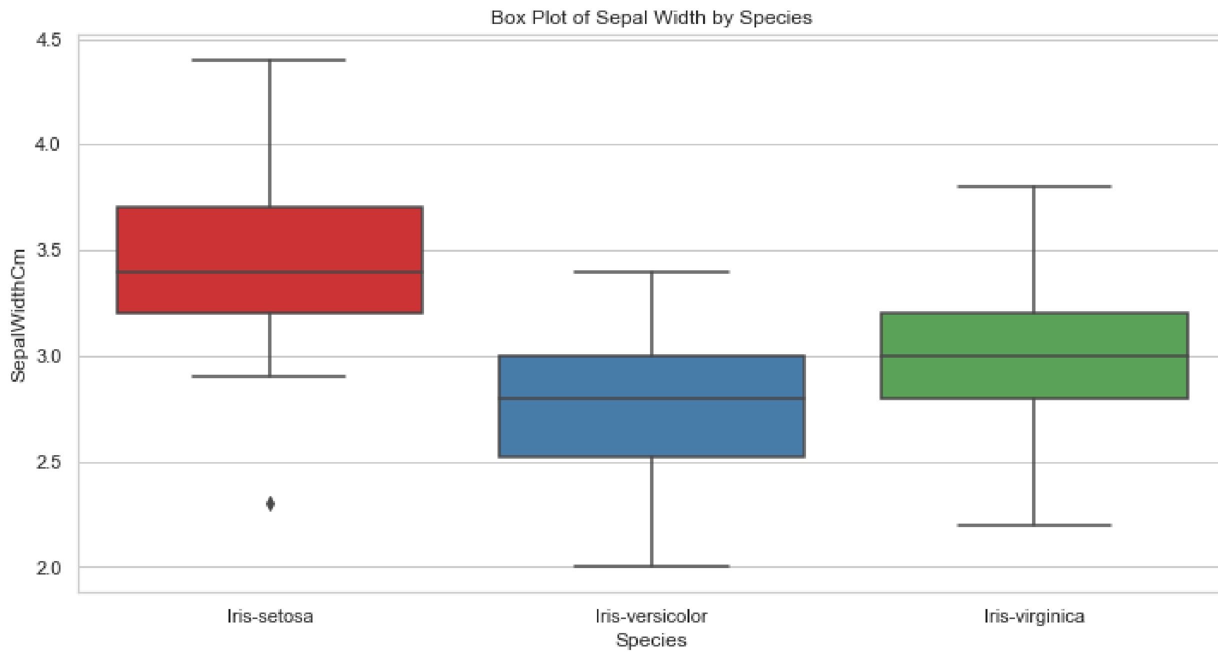


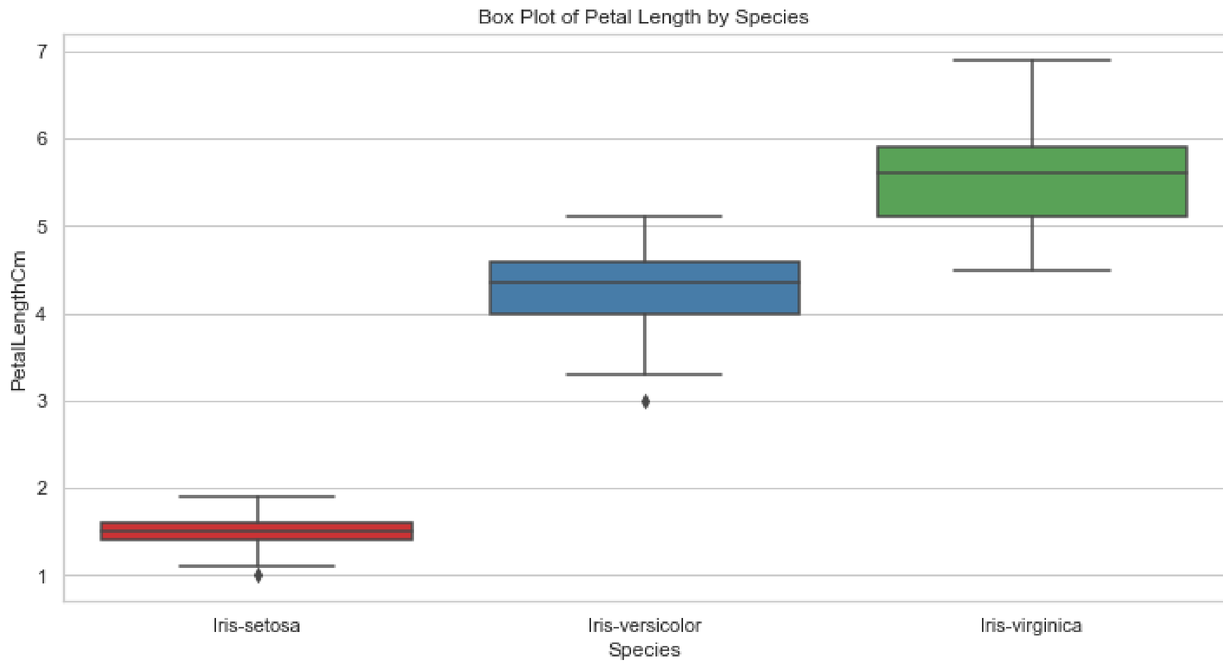
There is strong positive correlation between some variables are observed. eg: PetalWidth and PetalLength is showing strong positive correlation.

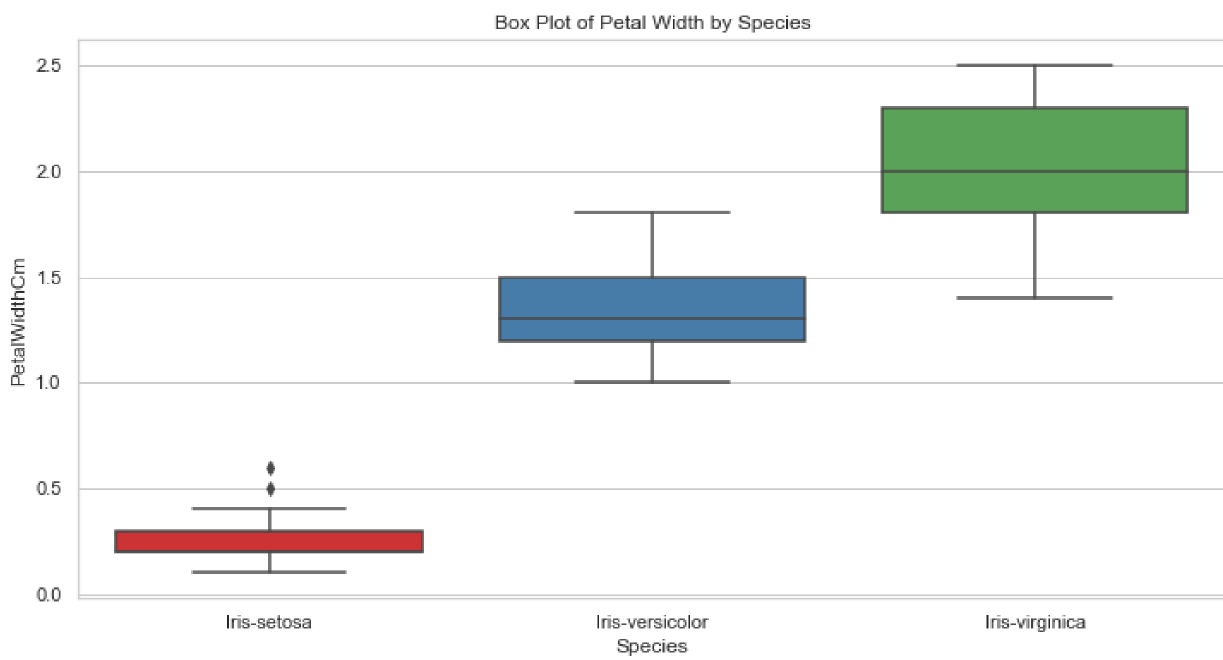
In [121…

```
#Boxplot for each feature grouped by species
sns.set(style="whitegrid")

plt.figure(figsize=(12, 6))  # Set the figure size
sns.boxplot(x="Species", y="SepalLengthCm", data=df, palette="Set1")
plt.title("Box Plot of Sepal Length by Species")
plt.show()

plt.figure(figsize=(12, 6))
sns.boxplot(x="Species", y="SepalWidthCm", data=df, palette="Set1")
plt.title("Box Plot of Sepal Width by Species")
plt.show()

plt.figure(figsize=(12, 6))
sns.boxplot(x="Species", y="PetalLengthCm", data=df, palette="Set1")
plt.title("Box Plot of Petal Length by Species")
plt.show()

plt.figure(figsize=(12, 6))
sns.boxplot(x="Species", y="PetalWidthCm", data=df, palette="Set1")
plt.title("Box Plot of Petal Width by Species")
plt.show()
```


Box Plot of Sepal Length by Species
8.0
7.5
7.0
6.5
6.0
5.5
5.0
4.5
SepalLengthCm
Iris-setosa
Iris-versicolor
Iris-virginica
Species


Box Plot of Sepal Width by Species
4.5
4.0
3.5
3.0
2.5
2.0
SepalWidthCm
Iris-setosa
Iris-versicolor
Iris-virginica
Species





Label Encoding

In [122…

```
from sklearn.preprocessing import LabelEncoder
cols=['Species']
le=LabelEncoder()
df[cols]=df[cols].apply(le.fit_transform)
df.head()
```

Out[122]:

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
0	5.1	3.5	1.4	0.2	0
1	4.9	3.0	1.4	0.2	0
2	4.7	3.2	1.3	0.2	0
3	4.6	3.1	1.5	0.2	0
4	5.0	3.6	1.4	0.2	0

Iris-setosa is encoded as 0

Iris-versicolor is encoded as 1

Iris-virginica is encoded as 2

Determining target variable and feature variable

In [123…

```
# X is the fature variable
X = df.drop('Species', axis = 1)
X
```

Out[123]:

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2
...	...	...	...	...
145	6.7	3.0	5.2	2.3
146	6.3	2.5	5.0	1.9
147	6.5	3.0	5.2	2.0
148	6.2	3.4	5.4	2.3
149	5.9	3.0	5.1	1.8

147 rows × 4 columns

In [124…

```
# y is the target variable
y = df['Species']
y
```

Out[124]:
```
0      0
1      0
2      0
3      0
4      0
      ..
145    2
146    2
147    2
148    2
149    2
Name: Species, Length: 147, dtype: int32
```

Splitting the dataset into training and testing sets

In [125…
```
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, random_state=
```

Logistic Regression

In [126…
```
from sklearn.linear_model import LogisticRegression
LR = LogisticRegression(multi_class='multinomial', solver='lbfgs')
LR.fit(X_train, y_train)
LR_pred = LR.predict(X_test)
```

In [127…
```
from sklearn.metrics import confusion_matrix,accuracy_score
confusion_matrix(y_test,LR_pred)
```

Out[127]:
```
array([[11,  0,  0],
       [ 0,  9,  1],
       [ 0,  1,  8]], dtype=int64)
```

In [128…
```
accuracy_score(y_test,LR_pred)
```

Out[128]:
```
0.9333333333333333
```

In [129…
```
from sklearn.metrics import precision_score, recall_score
precision = precision_score(y_test, LR_pred, average='weighted')
recall = recall_score(y_test, LR_pred, average='weighted')
print("Precision:", precision)
print("Recall:", recall)
```

```
Precision: 0.9333333333333333
Recall: 0.9333333333333333
```

In [130…
```
from sklearn.metrics import f1_score
f1_score = f1_score(y_test, LR_pred, average='weighted')
print("F1 Score:", f1_score)
```

```
F1 Score: 0.9333333333333333
```

In [131…
```
from sklearn.metrics import classification_report
report = classification_report(y_test, LR_pred)
print("Classification Report:\n", report)
```

```
Classification Report:
               precision    recall  f1-score   support

           0       1.00      1.00      1.00        11
           1       0.90      0.90      0.90        10
           2       0.89      0.89      0.89         9

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

Decision tree classifier

In [132…

```
from sklearn.tree import DecisionTreeClassifier
DT=DecisionTreeClassifier()
DT.fit(X_train,y_train)
DT_pred = DT.predict(X_test)
```

In [133…

```
confusion_matrix(y_test,DT_pred)
```

Out[133]:

```
array([[11,  0,  0],
       [ 0,  9,  1],
       [ 0,  0,  9]], dtype=int64)
```

In [134…

```
accuracy_score(y_test,DT_pred)
```

Out[134]:

```
0.9666666666666667
```

In [135…

```
report = classification_report(y_test, DT_pred)
print("Classification Report:\n", report)
```

```
Classification Report:
               precision    recall  f1-score   support

           0       1.00      1.00      1.00        11
           1       1.00      0.90      0.95        10
           2       0.90      1.00      0.95         9

    accuracy                           0.97        30
   macro avg       0.97      0.97      0.96        30
weighted avg       0.97      0.97      0.97        30
```

Random forest

In [136…

```
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier()
rfc.fit(X_train,y_train)
rfc_pred = rfc.predict(X_test)
```

In [137…

```
# model evaluation
confusion_matrix(y_test,rfc_pred)
```

Out[137]:

```
array([[11,  0,  0],
       [ 0,  9,  1],
       [ 0,  1,  8]], dtype=int64)
```

In [138…
```
accuracy_score(y_test, rfc_pred)
```
Out[138]:
```
0.9333333333333333
```

In [139…
```
report = classification_report(y_test, rfc_pred)
print("Classification Report:\n", report)
```
```
Classification Report:
               precision    recall  f1-score   support

           0       1.00      1.00      1.00        11
           1       0.90      0.90      0.90        10
           2       0.89      0.89      0.89         9

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

K-nearest neighbour

In [140…
```
from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors=2)
knn.fit(X_train,y_train)
knn_pred = knn.predict(X_test)
```

In [141…
```
confusion_matrix(y_test,knn_pred)
```
Out[141]:
```
array([[11,  0,  0],
       [ 0,  9,  1],
       [ 0,  1,  8]], dtype=int64)
```

In [142…
```
accuracy_score(y_test,knn_pred)
```
Out[142]:
```
0.9333333333333333
```

In [143…
```
report = classification_report(y_test, knn_pred)
print("Classification Report:\n", report)
```
```
Classification Report:
               precision    recall  f1-score   support

           0       1.00      1.00      1.00        11
           1       0.90      0.90      0.90        10
           2       0.89      0.89      0.89         9

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

In a classification problem, there are several model evaluation measures that help you assess the performance of your classifier. Here we used confusion matrix, accuracy score and classification report to evaluate the model.

For each model we got the same accuracy score of 0.933 indicates approximately 93.33% of the predictions made by the model match the actual true labels in the test set.

We have a 3x3 confusion matrix since we are evaluating a multiclass classification model. Each row in the matrix represents the true class, and each column represents the predicted class.

Classification report provides a comprehensive summary of the performance of a classification model by presenting various evaluation metrics such as precision, recall, F-1 score and support.