iris_flower_classification

March 31, 2025

[81]:
```
# Import necessary libraries
import pandas as pd  # Data manipulation
import seaborn as sns  # Data visualization
import matplotlib.pyplot as plt  # Plotting
from sklearn.model_selection import train_test_split  # Splitting data
from sklearn.preprocessing import StandardScaler  # Feature scaling
from sklearn.ensemble import RandomForestClassifier # Initialize the Random␣
↪Forest model
from sklearn.metrics import accuracy_score, classification_report,␣
↪confusion_matrix # Evaluate model performance using accuracy Model evaluation
from sklearn.inspection import permutation_importance
```

[58]:
```
# Load the Iris dataset
df = pd.read_csv('IRIS.csv')
```

0.1 Exploratoty Data Analysis

[59]:
```
# Display basic information
df.head()
```

[59]:

	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

[60]:
```
# check the summary
df.describe()
```

[60]:

	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
```

0.1.1 Insights

we have here a data set with 150 observations of 3 species of Iris flower (setosa,virginica and versicolor) observed on four covariates, the sepal and petal length and width. in this summary we see the mean of each observed covariates (sl: 5.84, sw:3.05, pl:3.75, pw:1.2) by the standar deviation we can say that the covariate with much variance in the values is the petal_length with std = 1.76 and the covariate with less variance is the sepal_with with std = 0.4

[61]:
```python
# type information of each column
df.info()
```

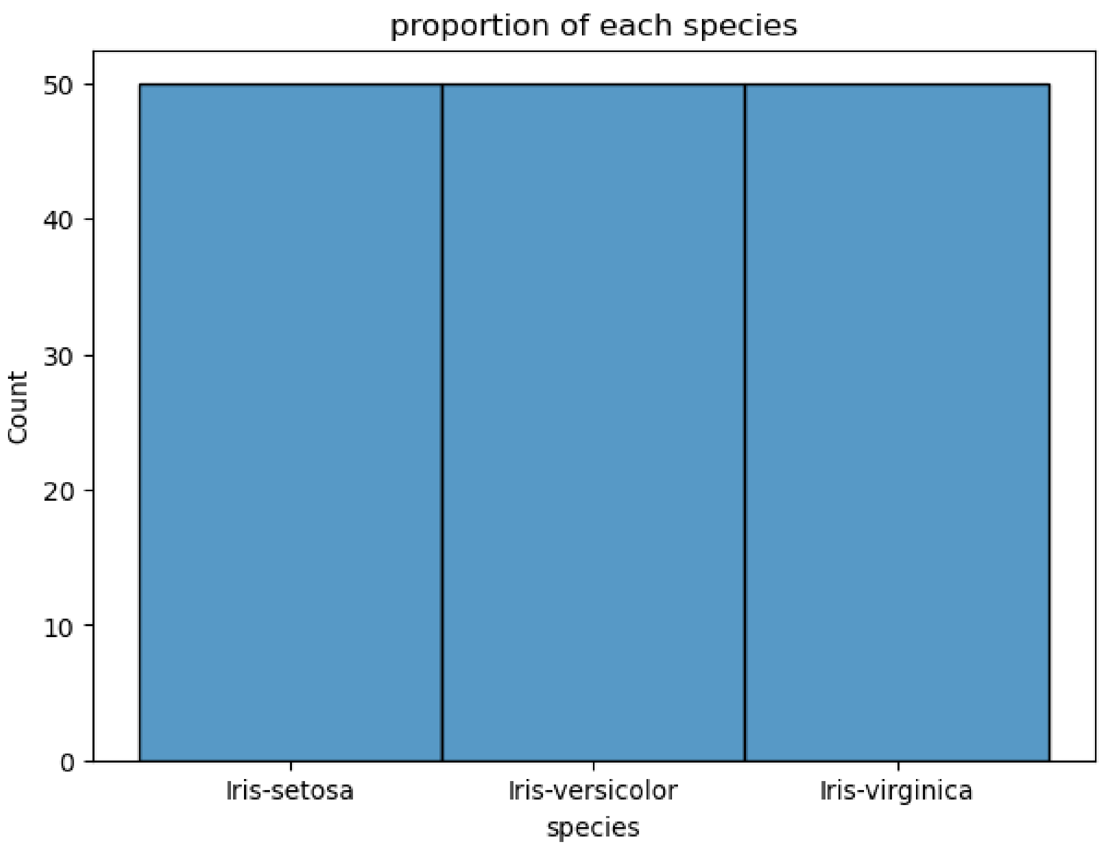
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   sepal_length  150 non-null    float64
 1   sepal_width   150 non-null    float64
 2   petal_length  150 non-null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

[62]:
```python
# Check for missing values
print("Missing values:\n", df.isnull().sum())
```

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

[63]:
```python
# proportion of each species in the dataset
plt.figure(figsize=(7,5))
sns.histplot(data=df,x="species",palette={'Iris-setosa': 'blue',␣
 ↪'Iris-versicolor': 'orange','Iris-virginica': 'green'})
plt.title("proportion of each species")
plt.show()
```

```
/tmp/ipykernel_55034/283284621.py:3: UserWarning: Ignoring `palette` because no
`hue` variable has been assigned.
  sns.histplot(data=df,x="species",palette={'Iris-setosa': 'blue', 'Iris-
versicolor': 'orange','Iris-virginica': 'green'})
```

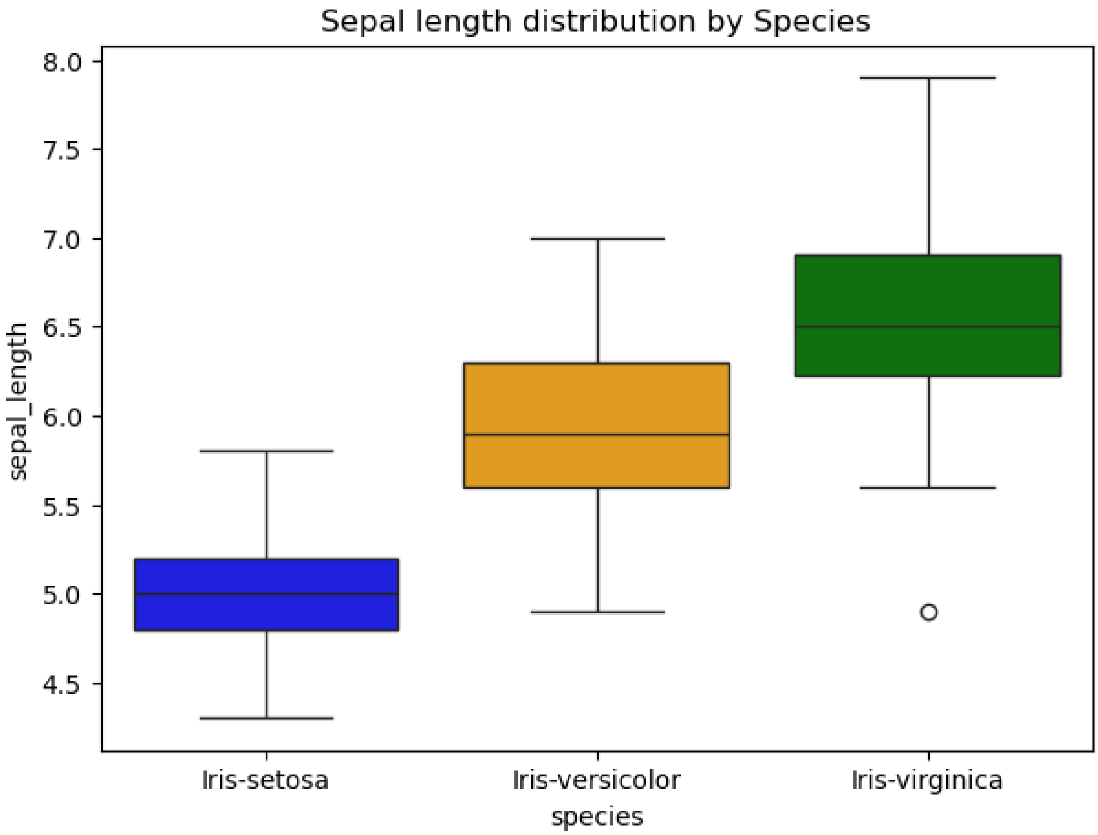


0.1.2 Insigth

Here we can see that the species are equaly represented in the dataset so the data are not imbalance.

[64]:
```
# Boxplot to analyze distribution
plt.figure(figsize=(7, 5))
sns.boxplot(data=df, x='species', y='sepal_length',palette={'Iris-setosa':␣
↪'blue', 'Iris-versicolor': 'orange','Iris-virginica': 'green'})
plt.title('Sepal length distribution by Species')
plt.show()
```

```
/tmp/ipykernel_55034/2545745143.py:3: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same
effect.

  sns.boxplot(data=df, x='species', y='sepal_length',palette={'Iris-setosa':
'blue', 'Iris-versicolor': 'orange','Iris-virginica': 'green'})
```

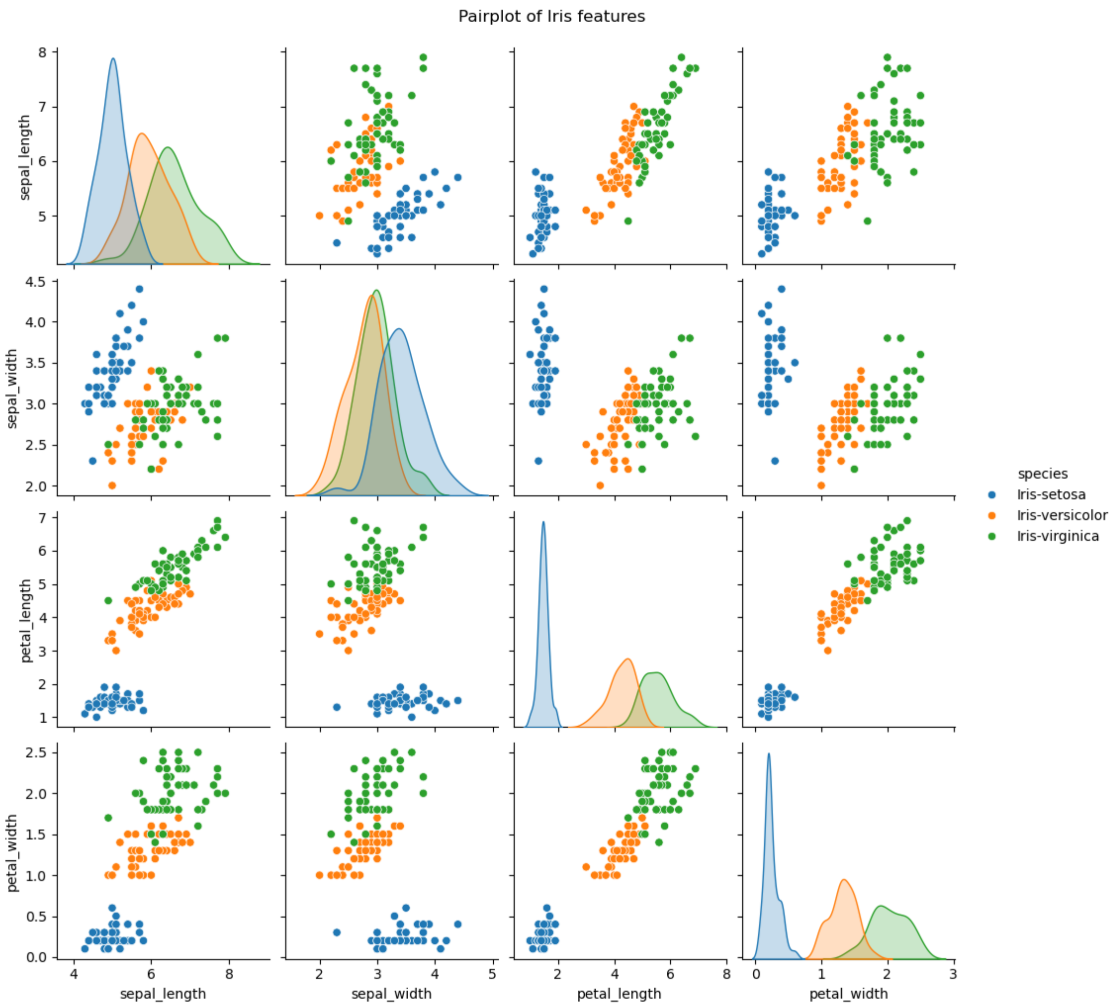


0.1.3 Insights

Here we can see that the distrinution of the scpecies in terms of sepal_length are centerarround the mean value. Also we can see that the sepal_length in each species are not the same with a the the value of sepal_length of versicolor in average gretter than the setosa one and less in average than the virginica one.

[65]:
```
# Data visualization
plt.figure(figsize=(7, 5))
sns.pairplot(df, hue='species')
plt.suptitle('Pairplot of Iris features', y=1.02)
plt.show()
```

```
<Figure size 700x500 with 0 Axes>
```



0.1.4 Insights

In this figure we can see the different relations betwen the covariate where there is a positive correlation between the petal_length and the petal_with, the sepal_legnth and the petal_width and the petal_length and the sepal_length. since the increase of one of them is follow by the increase nthe other values we can also say that the petal length and the the petal width are good covariates to distinguish the setosa species from the other.

[66]:
```
# Select only numeric columns for correlation analysis
numeric_df = df.select_dtypes(include=['float64', 'int64'])

# Generate correlation heatmap
plt.figure(figsize=(8, 5))
sns.heatmap(numeric_df.corr(), annot=True, cmap='coolwarm', fmt='.2f')
plt.title('Feature Correlation Heatmap')
plt.show()
```

0.1.5 Insigths

This corelation matrix come to confirm us our interpretation of the plots in the pair plot here we can see the highly positive correlation between sepal_length,petal_length and petal_width and the negative correlation betwen sepal_width and the three other covariates.

0.2 Classification part

[67]:
```
# Preparing data for model training

# remove the target column on the data that we want to train our model on.
X = df.drop(columns=['species'])
# keep the target aside for the prediction
y = df['species']
```

[68]:
```
# Splitting data into training and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42, stratify=y) # Split dataset into training and testing sets
```

[69]:
```
print(f"Dimension of the train set: {X_train.shape}")
print(f"Dimension of the test set: {X_test.shape}")
```

```
Dimension of the train set: (120, 4)
Dimension of the test set: (30, 4)
```

[70]:
```
# look at some observation before standardise
X_train.head(5)
```

[70]:

	sepal_length	sepal_width	petal_length	petal_width
8	4.4	2.9	1.4	0.2
106	4.9	2.5	4.5	1.7
76	6.8	2.8	4.8	1.4
9	4.9	3.1	1.5	0.1
89	5.5	2.5	4.0	1.3

[71]:
```
# Standardizing the data to keep the values of each covariate in a same range␣
↪to avoid
# the model to
scaler = StandardScaler() # Standardize the features
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

[72]:
```
# look at some observation after standardisation
X_train[0:5]
```

[72]:
```
array([[-1.72156775, -0.32483982, -1.34703555, -1.32016847],
       [-1.12449223, -1.22612948,  0.41429037,  0.65186742],
       [ 1.14439475, -0.55016223,  0.58474127,  0.25746024],
       [-1.12449223,  0.12580502, -1.29021859, -1.45163753],
       [-0.40800161, -1.22612948,  0.13020555,  0.12599118]])
```

0.3 Recall

we want to epmhase the fact that wheter random forest classifier are scale invarant it is always a good practice to standardasie the data in the same range of values.

[73]:
```
# Model training using a random forest model "RandomForestClassifier"
model = RandomForestClassifier(n_estimators=100, random_state=42)

# Train the model
model.fit(X_train, y_train)
```

[73]:
```
RandomForestClassifier(random_state=42)
```

[74]:
```
# Model evaluation
y_pred = model.predict(X_test)
accuracy = accuracy_score(y_test, y_pred)# Evaluate model performance using␣
↪accuracy
```

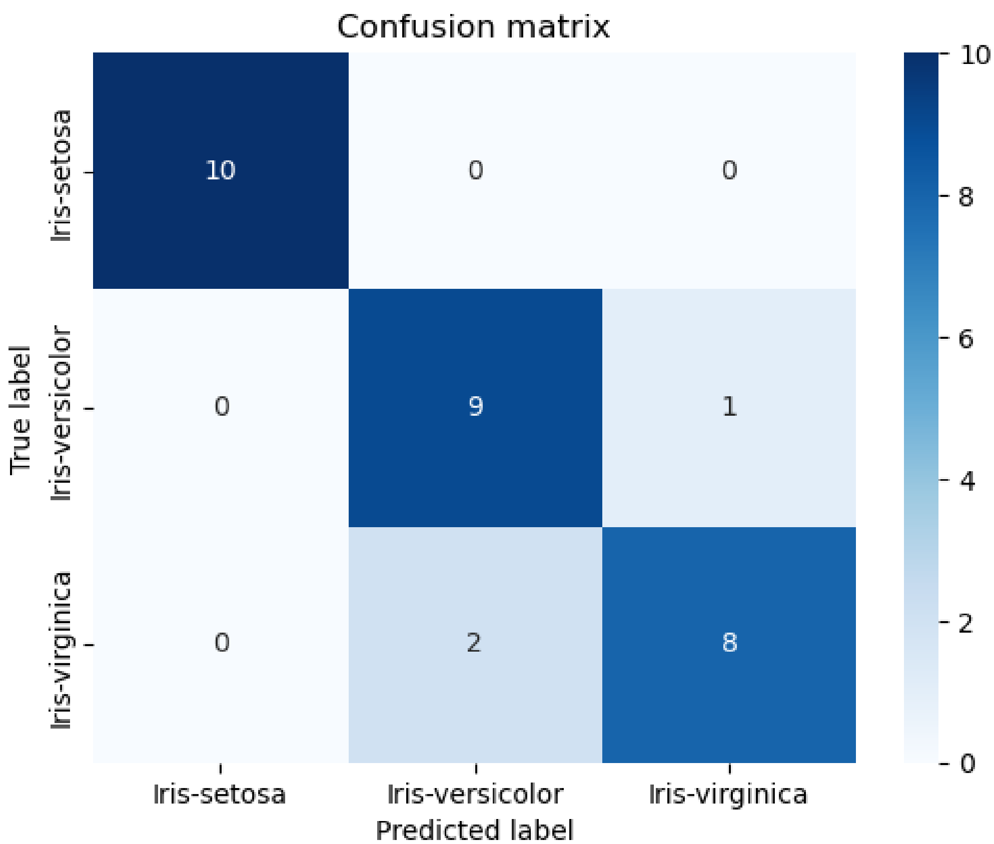
[75]:
```
print(f'\nModel Accuracy: {accuracy:.2f}')
print('\nClassification Report:\n', classification_report(y_test, y_pred))
```

```
Model Accuracy: 0.90

Classification Report:
                  precision    recall  f1-score   support

    Iris-setosa       1.00      1.00      1.00        10
Iris-versicolor       0.82      0.90      0.86        10
 Iris-virginica       0.89      0.80      0.84        10

       accuracy                           0.90        30
      macro avg       0.90      0.90      0.90        30
   weighted avg       0.90      0.90      0.90        30
```

0.4 Interpratation

The model get an accuracy of 90% with a high precision (100%) in the setosa species. : - Iris-setosa (Perfect Classification) - Iris-versicolor (Good Performance, Slightly Lower Precision) - Iris-virginica (Lower Recall)

[78]:
```
# Compute the confusion matrix
cm = confusion_matrix(y_test, y_pred)
# Create a heatmap for better visualization
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=model.classes_,␣
 ↪yticklabels=model.classes_)
# Labels
plt.xlabel("Predicted label")
plt.ylabel("True label")
plt.title("Confusion matrix")
plt.show()
```



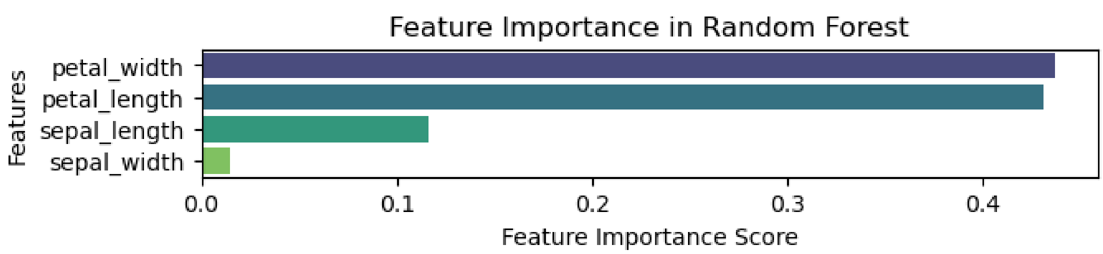
0.4.1 Insigths

Here we can see that the model classsify verry well the setosa class with 100% well classify on the 10 examples in the test But also the model strugle a little bit with the two other classes.

[92]:
```
## Assess for the important covariates in our model

# Get feature importance scores
feature_importances = model.feature_importances_
# construct a dataframe for a later visualisation
feature_importance_df = pd.DataFrame({
    'Feature': df.drop(columns=['species']).columns,
    'Importance': feature_importances
})
# Sort features by importance (highest to lowest)
feature_importance_df = feature_importance_df.sort_values(by='Importance',␣
 ↪ascending=False)

# Plot feature importance
plt.figure(figsize=(7, 1))
```

```
sns.barplot(x=feature_importance_df['Importance'],␣
 ↪y=feature_importance_df['Feature'], palette="viridis")
plt.xlabel("Feature Importance Score")
plt.ylabel("Features")
plt.title("Feature Importance in Random Forest")
plt.show()
```

```
/tmp/ipykernel_55034/311918143.py:15: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in
v0.14.0. Assign the `y` variable to `hue` and set `legend=False` for the same
effect.

  sns.barplot(x=feature_importance_df['Importance'],
y=feature_importance_df['Feature'], palette="viridis")
```



0.4.2 Insigth

As we said earlier the most important feature for the model to well caracterise each class are the petal_width and the petal_length.