

IRIS FLOWER CLASSIFICATION

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```
In [1]: import pandas as pd
from sklearn.datasets import load_iris
iris = load_iris()
import warnings
warnings.filterwarnings("ignore")
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, accuracy_score

In [2]: iris = pd.read_csv(r"C:\Users\Siddhi\Desktop\IRIS.csv")
iris

Out[2]:
```

| | 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 |
| ... | ... | ... | ... | ... | ... |
| 145 | 6.7 | 3.0 | 5.2 | 2.3 | Iris-virginica |
| 146 | 6.3 | 2.5 | 5.0 | 1.9 | Iris-virginica |
| 147 | 6.5 | 3.0 | 5.2 | 2.0 | Iris-virginica |
| 148 | 6.2 | 3.4 | 5.4 | 2.3 | Iris-virginica |
| 149 | 5.9 | 3.0 | 5.1 | 1.8 | Iris-virginica |

150 rows x 5 columns

```
In [3]: 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

In [4]: iris.columns

Out[4]: Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_width',
              'species'],
              dtype='object')

In [5]: iris.head()

Out[5]:
```

| | 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 |

In [6]: iris.describe

```
Out[6]:
```

| | <bound method NDFrame.describe of | 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 | |
| ... | ... | ... | ... | ... | ... | |
| 145 | 6.7 | 3.0 | 5.2 | 2.3 | Iris-virginica | |
| 146 | 6.3 | 2.5 | 5.0 | 1.9 | Iris-virginica | |
| 147 | 6.5 | 3.0 | 5.2 | 2.0 | Iris-virginica | |
| 148 | 6.2 | 3.4 | 5.4 | 2.3 | Iris-virginica | |
| 149 | 5.9 | 3.0 | 5.1 | 1.8 | Iris-virginica | |

[150 rows x 5 columns]>

In [7]: iris.shape

```
Out[7]: (150, 5)
```

In [8]: display(iris.head())
display(iris.shape)

```
Out[8]:
```

| | 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 |

(150, 5)

In [9]: iris.isna().sum()

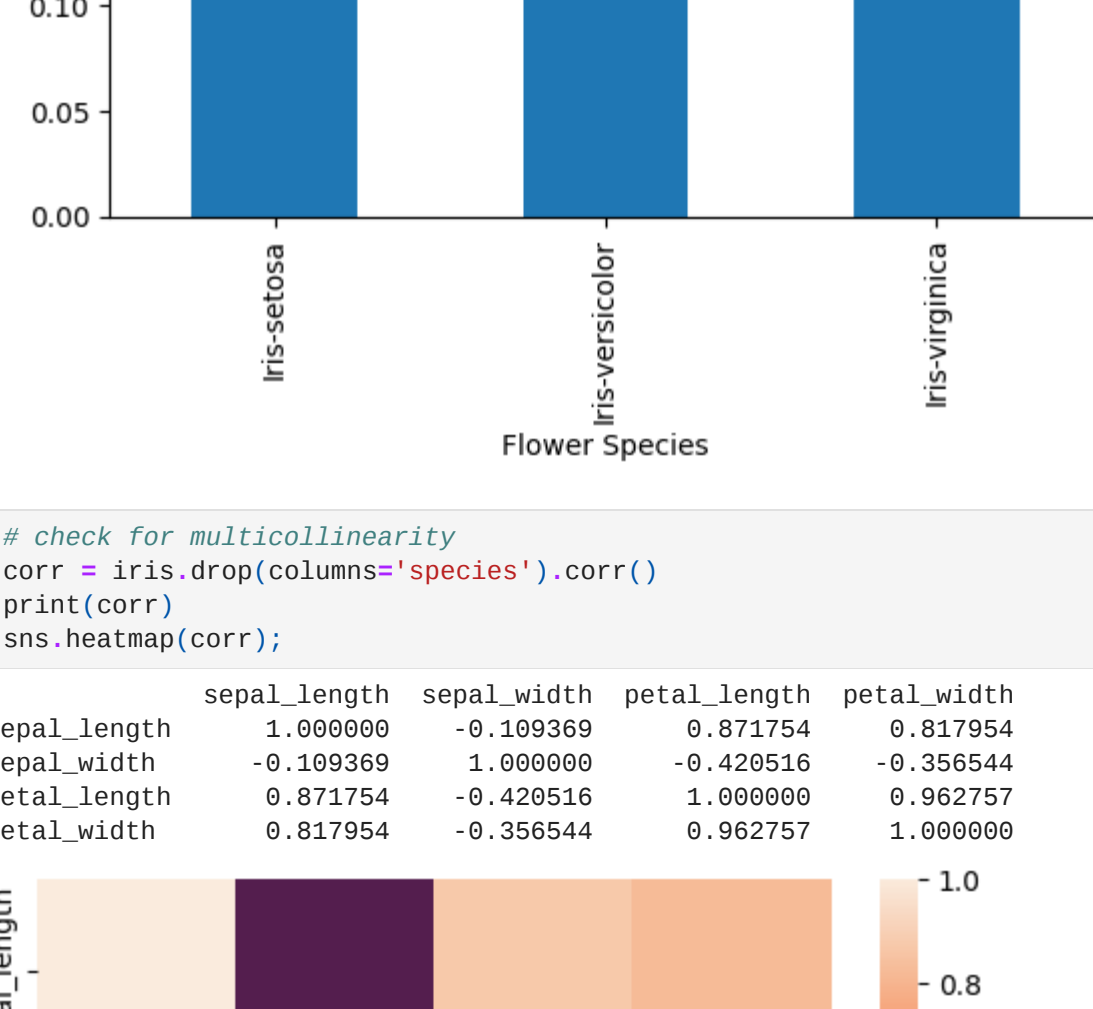
```
Out[9]:
```

| | sepal_length | sepal_width | petal_length | petal_width | species |
|--------------|--------------|-------------|--------------|-------------|---------|
| sepal_length | 0 | | | | |
| sepal_width | 0 | | | | |
| petal_length | 0 | | | | |
| petal_width | 0 | | | | |
| species | 0 | | | | |
| dtype: | int64 | | | | |

Explore

```
In [10]: iris['species'].value_counts(normalize=True).plot(kind='bar')
plt.ylabel('Frequency')
plt.xlabel('Flower Species')
plt.title('Freq of Flowers')
;
```

Out[10]:



```
In [11]: # check for multicollinearity
corr = iris.drop(columns='species').corr()
print(corr)
sns.heatmap(corr);
```

```
Out[11]:
```

| | sepal_length | sepal_width | petal_length | petal_width |
|--------------|--------------|-------------|--------------|-------------|
| sepal_length | 1.000000 | -0.109369 | 0.871754 | 0.817954 |
| sepal_width | -0.109369 | 1.000000 | -0.420516 | -0.356544 |
| petal_length | 0.871754 | -0.420516 | 1.000000 | 0.962757 |
| petal_width | 0.817954 | -0.356544 | 0.962757 | 1.000000 |



In [12]: sns.pairplot(iris, hue='species', diag_kind='hist', corner=True, palette='hls');



Model Building

```
In [13]: # define our features and target
target = 'species'
X = iris.drop(columns=target)
y = iris[target]

In [14]: # convert our target to numerical value
label_encoder = LabelEncoder()
y = label_encoder.fit_transform(y)

In [15]: # split our data to train and test
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=40)
print(X_train.shape)
print(y_train.shape)
print(X_test.shape)
print(y_test.shape)
```

```
Out[15]:
```

(120, 4)
(120, 4)
(30, 4)
(30, 4)

Baseline Model

```
In [16]: # define our baseline model
y_baselinescore = iris['species'].value_counts(normalize=True)[0]
y_baselinescore

Out[16]: 0.3333333333333333

In [17]: # make our model
log = LogisticRegression(max_iter=200)
forest = RandomForestClassifier(random_state=42)
# fit our model
log.fit(X_train, y_train)
forest.fit(X_train, y_train)
```

```
Out[17]:
```

RandomForestClassifier

RandomForestClassifier(random_state=42)

Evaluate

```
In [18]: # get the prediction score for train data
print(f'The accuracy score for Logistic Regression Model = {accuracy_score(y_train, log.predict(X_train))}')
print(f'The accuracy score for Random Forest Classifier = {accuracy_score(y_train, forest.predict(X_train))}')

The accuracy score for logistic Regression Model = 0.9823333333333333
The accuracy score for Random Forest Classifier = 1.0

In [19]: # get the prediction score for test data
print(f'The accuracy score for logistic Regression Model = {accuracy_score(y_test, log.predict(X_test))}')
print(f'The accuracy score for Random Forest Classifier = {accuracy_score(y_test, forest.predict(X_test))}')

The accuracy score for logistic Regression Model = 1.0
The accuracy score for Random Forest Classifier = 1.0

In [20]: # classification report for log model
print(classification_report(y_test, log.predict(X_test)))
```

```
Out[20]:
```

| | precision | recall | f1-score | support |
|--------------|-----------|--------|----------|---------|
| 0 | 1.00 | 1.00 | 1.00 | 8 |
| 1 | 1.00 | 1.00 | 1.00 | 12 |
| 2 | 1.00 | 1.00 | 1.00 | 10 |
| accuracy | | | 1.00 | 30 |
| macro avg | 1.00 | 1.00 | 1.00 | 30 |
| weighted avg | 1.00 | 1.00 | 1.00 | 30 |

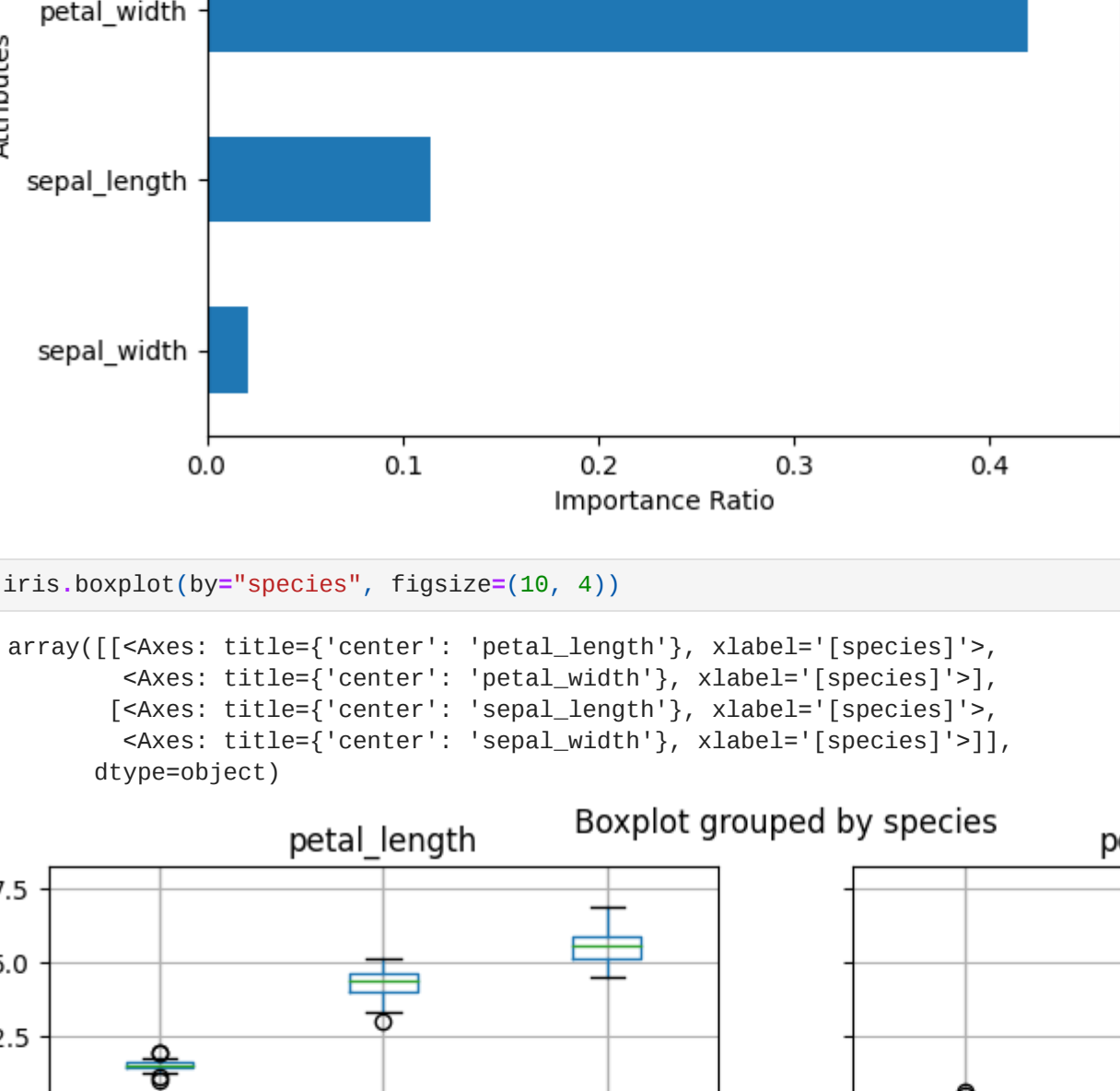
In [21]: # classification report for random forest model
print(classification_report(y_test, forest.predict(X_test)))

```
Out[21]:
```

| | precision | recall | f1-score | support |
|--------------|-----------|--------|----------|---------|
| 0 | 1.00 | 1.00 | 1.00 | 8 |
| 1 | 1.00 | 1.00 | 1.00 | 12 |
| 2 | 1.00 | 1.00 | 1.00 | 10 |
| accuracy | | | 1.00 | 30 |
| macro avg | 1.00 | 1.00 | 1.00 | 30 |
| weighted avg | 1.00 | 1.00 | 1.00 | 30 |

Communicate

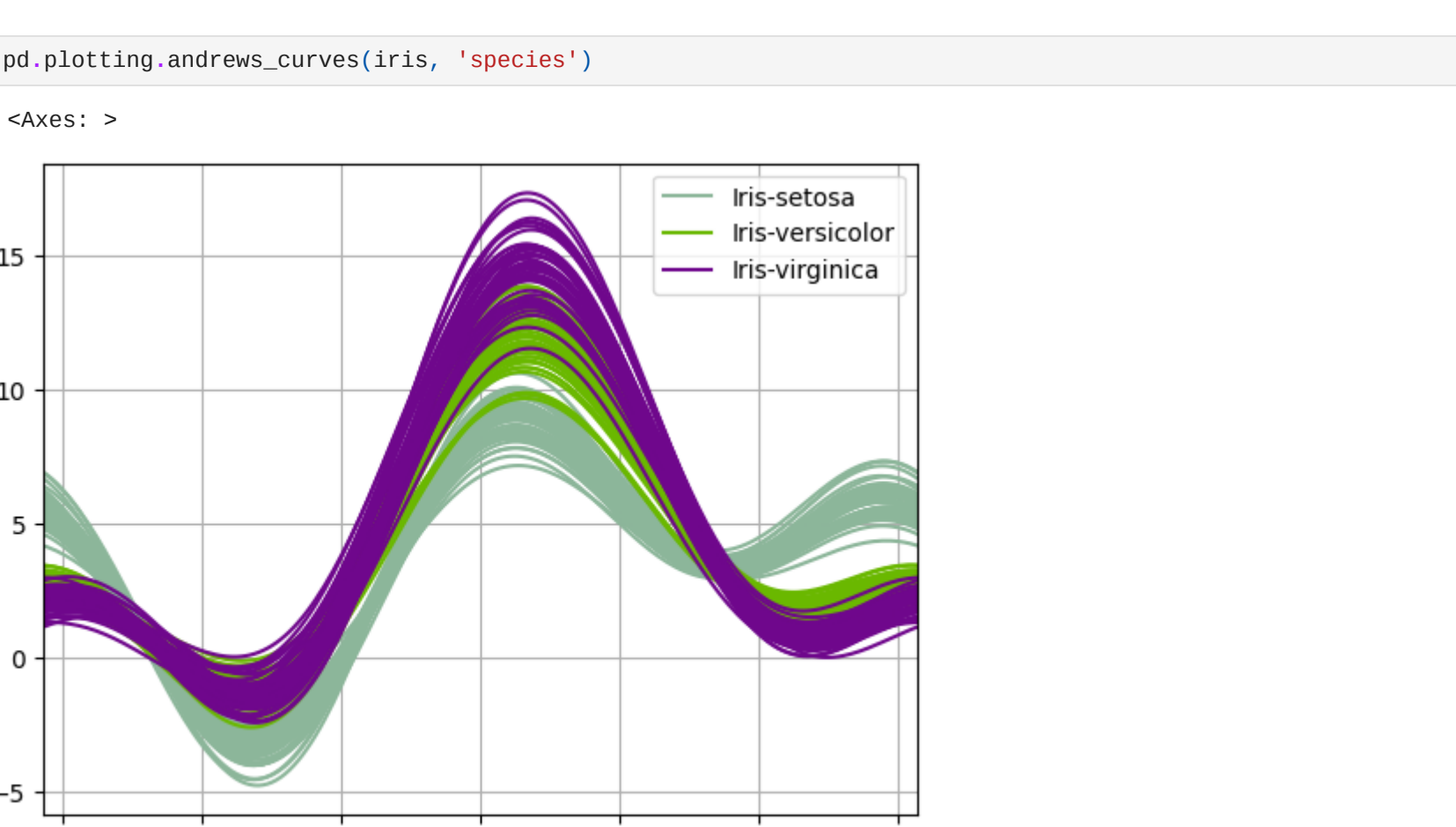
```
In [22]: Features = X_train.columns
# Extract importances from model
Importances = forest.feature_importances_
# Create a series with feature names and importances
feat_imp = pd.Series(Importances, index=Features).sort_values()
# plot 10 most important features
feat_imp.tail().plot(kind='barh')
plt.xlabel('Importance Ratio')
plt.ylabel('Attributes')
plt.title('Features Importances');
```



```
In [23]: iris.boxplot(by='species', figsize=(10, 4))

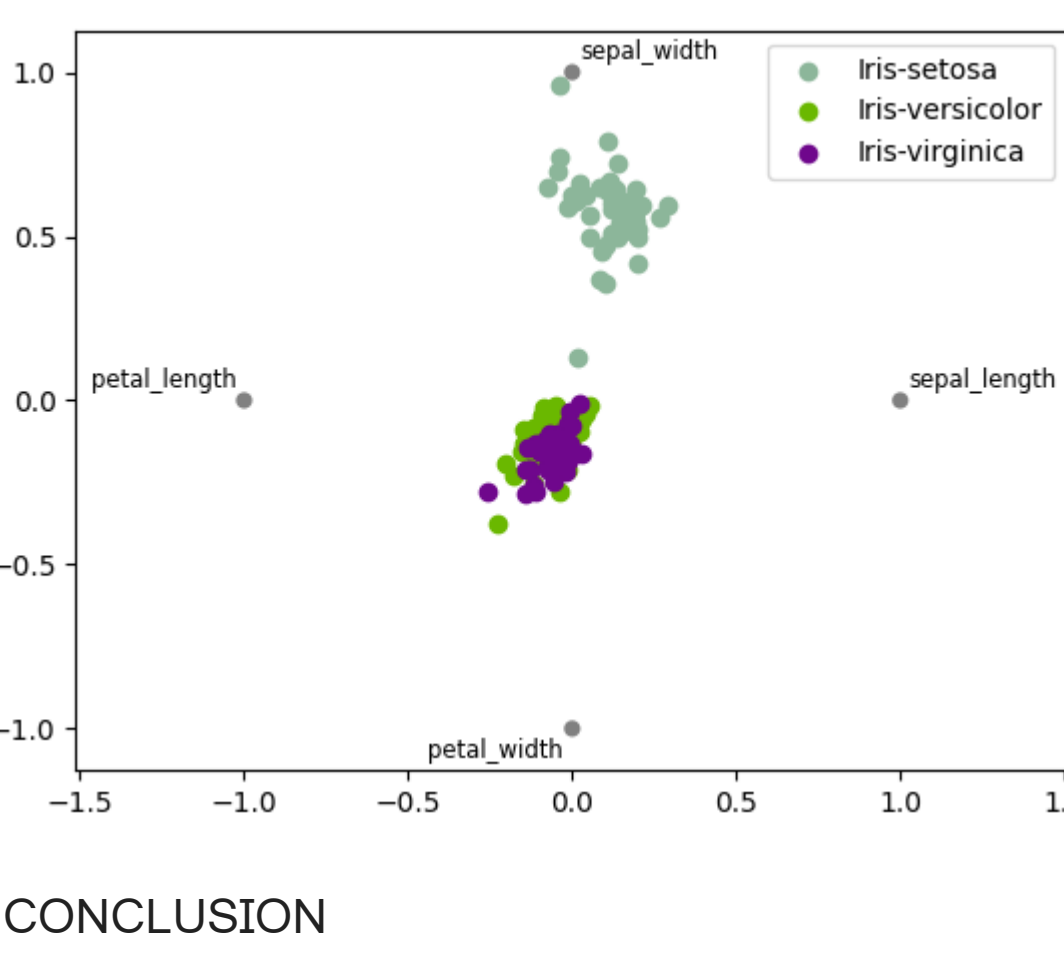
Out[23]:
```

array([[<Axes: title='center': 'petal_length', xlabel='[species]'>,
<Axes: title='center': 'petal_width', xlabel='[species]'>],
[<Axes: title='center': 'sepal_length', xlabel='[species]'>],
<Axes: title='center': 'sepal_width', xlabel='[species]'>]],
dtype=object)



```
In [24]: pd.plotting.andrews_curves(iris, 'species')
```

Out[24]: <Axes: >



pd.plotting.andrews_curves a useful function for visualizing high-dimensional data by representing each observation as a curve. It allows you to color the curves based on a categorical variable using the class_column parameter

```
In [25]: pd.plotting.radviz(iris, 'species')
```

Out[25]: <Axes: >

CONCLUSION

1)Setosa species have lower sepal length but larger width length as compare to virginica and versicolor. 2)Higher sepal length contain virginica species. 3)In order of petal length setosa<versicolor<virginica.

THANK YOU

