1) Iris Flowers Classification ML Project :

Steps to Classify Iris Flower:

- 1. Loading of the dataset
- 2. Analyzing and visualizing the dataset
- 3. Model training
- 4. Model Evaluation
- 5. Testing the model

```
In [1]: # First we have to import some packages
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
%matplotlib inline
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.metrics import classification_report
```

Step 1 - Load the data:

```
In [2]: df = pd.read_csv("C:\\Users\\User\\Downloads\\Iris.csv")
    df.head()
```

Out[2]:

	ld	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
-) 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
	1 5	5.0	3.6	1.4	0.2	Iris-setosa

Step 2 – Analyze and visualize the dataset:

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

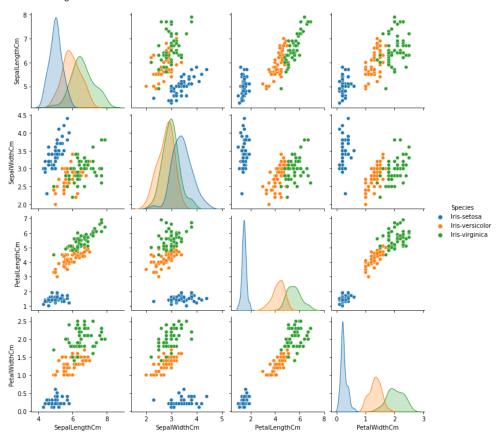
Out[3]:

	ld	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
count	150.000000	150.000000	150.000000	150.000000	150.000000
mean	75.500000	5.843333	3.054000	3.758667	1.198667
std	43.445368	0.828066	0.433594	1.764420	0.763161
min	1.000000	4.300000	2.000000	1.000000	0.100000
25%	38.250000	5.100000	2.800000	1.600000	0.300000
50%	75.500000	5.800000	3.000000	4.350000	1.300000
75%	112.750000	6.400000	3.300000	5.100000	1.800000
max	150.000000	7.900000	4.400000	6.900000	2.500000

```
In [4]: #Drop unwanted columns
df=df.drop(columns="Id")
```

```
In [5]: # Visualize the whole dataset
sns.pairplot(df, hue='Species')
```

Out[5]: <seaborn.axisgrid.PairGrid at 0x18f79d697f0>



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.

Step 3 – Model training:

```
In [6]: # Split the data to train and test dataset.
    train, test = train_test_split(df, test_size = 0.3) # in this our main data is split into train and test

# the attribute test_size=0.3 splits the data into 70% and 30% ratio. train=70% and test=30%

print(train.shape)

print(test.shape)

(105, 5)
(45, 5)

In [7]: train_X = train[['SepalLengthCm', 'SepalWidthCm', 'PetalLengthCm', 'PetalWidthCm']]# taking the training data features
    train_y=train.Species # output of our training data
    test_X= test[['SepalLengthCm', 'SepalWidthCm', 'PetalLengthCm', 'PetalWidthCm']] # taking test data features
    test_y = test.Species # output value of test data
```

```
In [8]: train_X.head(2)
Out[8]:
                SepalLengthCm SepalWidthCm PetalLengthCm PetalWidthCm
           138
                          6.0
                                        3.0
                                                       4.8
                                                                    1.8
           134
                          6.1
                                        2.6
                                                       5.6
                                                                    1.4
 In [9]: test_X.head(2)
Out[9]:
                SepalLengthCm \>\>\> SepalWidthCm \>\>\>\> PetalLengthCm \>\>\>\>\> PetalWidthCm
           116
                          6.5
                                        3.0
                                                                    1.8
           122
                          7.7
                                        2.8
                                                                    2.0
                                                       6.7
In [10]: train_y.head() ##output of the training data
Out[10]: 138
                   Iris-virginica
                   Iris-virginica
          134
          93
                  Iris-versicolor
                      Iris-setosa
          41
                      Iris-setosa
          Name: Species, dtype: object
In [11]: # Support vector machine algorithm
          from sklearn.svm import SVC
          svn = SVC()
          svn.fit(train_X, train_y)
Out[11]: SVC()
          Step 4 – Model Evaluation:
In [12]: # Predict from the test dataset
predictions = svn.predict(test_X)
          # Calculate the accuracy
          accuracy_score(test_y, predictions)
Out[12]: 1.0
In [13]: # A detailed classification report
          print(classification_report(test_y, predictions))
                                          recall f1-score
                             precision
                                                                support
              Iris-setosa
                                  1.00
                                             1.00
                                                        1.00
          Iris-versicolor
                                  1.00
                                             1.00
                                                        1.00
                                                                      18
           Iris-virginica
                                  1.00
                                                        1.00
                                                                      16
                  accuracy
                                                        1.00
                                                                      45
                                  1.00
                                             1.00
                                                        1.00
                                                                      45
                 macro avg
             weighted avg
                                  1.00
          Step 5 – Testing the model:
In [14]: 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']
In [15]: # Save the model
```

import pickle

In []:

Load the model

model.predict(X_new)

with open('SVM.pickle', 'wb') as f:
 pickle.dump(svn, f)

with open('SVM.pickle', 'rb') as f:
 model = pickle.load(f)

Out[15]: array(['Iris-setosa', 'Iris-versicolor', 'Iris-virginica'], dtype=object)