AML Hw0: Iris Flowers

Jiwon Jeong

September 2025

1 Iris Flowers Dataset Structure

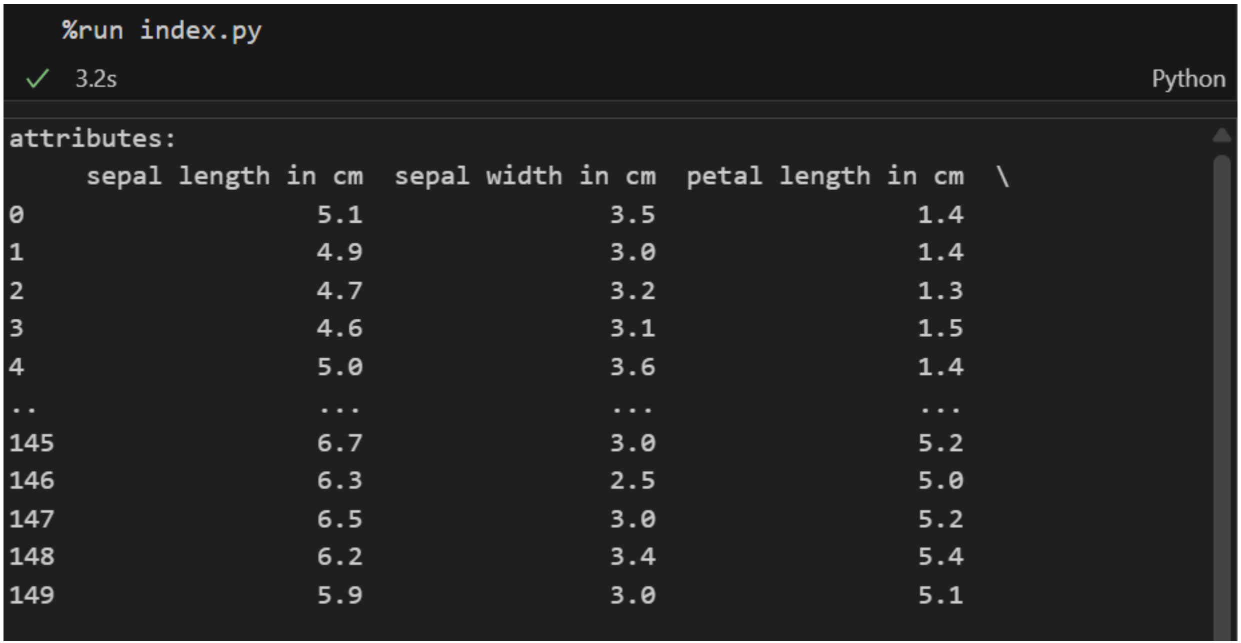
The data set is 3 different iris plant classes of 50 instances each. This means that the data includes 3 different species, and 50 samples for each species.

For each instance, there are 4 attributes. They are numerical measurements to be used for prediction (sepal length, sepal width, petal length, petal width). There is also the label for each sample, being the actual Iris species.

2 Parsing the Dataset

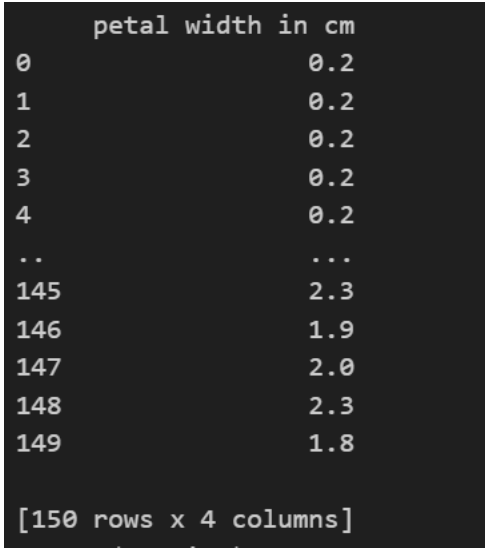
The dataset was parsed for the 4 attributes using pandas, resulting in an $N \times p$ array. Where N is 150, the number of samples, and p is 4, the number of attributes.

```
attributes = pd.read_csv(file_path, usecols=[0,1,2,3],
          header=None, names=[#array of headers names])
```



```
%run index.py
```

```
attributes:
     sepal length in cm  sepal width in cm  petal length in cm  \
0                   5.1                3.5                 1.4   
1                   4.9                3.0                 1.4   
2                   4.7                3.2                 1.3   
3                   4.6                3.1                 1.5   
4                   5.0                3.6                 1.4   
..                  ...                ...                 ...   
145                 6.7                3.0                 5.2   
146                 6.3                2.5                 5.0   
147                 6.5                3.0                 5.2   
148                 6.2                3.4                 5.4   
149                 5.9                3.0                 5.1   
```

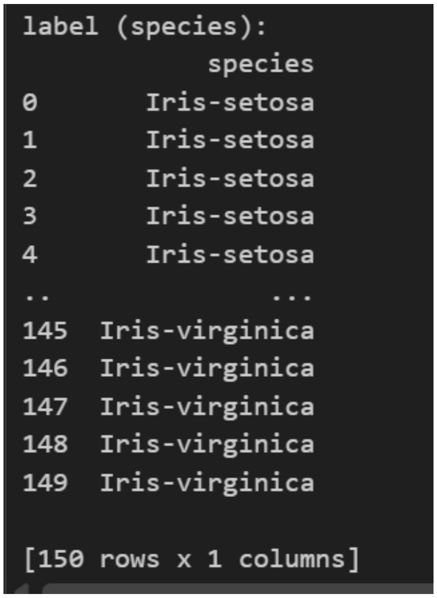


```
     petal width in cm  
0                  0.2  
1                  0.2  
2                  0.2  
3                  0.2  
4                  0.2  
..                 ...  
145                2.3  
146                1.9  
147                2.0  
148                2.3  
149                1.8  

[150 rows x 4 columns]
```

With a similar approach, the same data file was parsed for the N-dimensional label vector.

```
labels = pd.read_csv(file_path, usecols=[4],
         header =None, names=['species'])
```



```
label (species):
           species
0      Iris-setosa
1      Iris-setosa
2      Iris-setosa
3      Iris-setosa
4      Iris-setosa
..             ...
145  Iris-virginica
146  Iris-virginica
147  Iris-virginica
148  Iris-virginica
149  Iris-virginica

[150 rows x 1 columns]
```

3 Visualizing the Dataset

With 4 attributes, but only 2D representations that can show 2 attributes at a time, a series of 2D plots were created. Each plot has the x and y dimensions as two different pairs of attributes. With 12 plots, all possible pairs of two attributes from the 4 attributes were represented.

In code, this was performed by the following nested loop algorithm to create all pairs of different attributes.

```
for x_index in range(4):
 for y_index in range(4):
     if (x_index != y_index):
         axes[x_index,y_index].scatter(attribute_arr[x_index],
              attribute_arr[y_index], c=color_vector)
         # more code to add titles
```

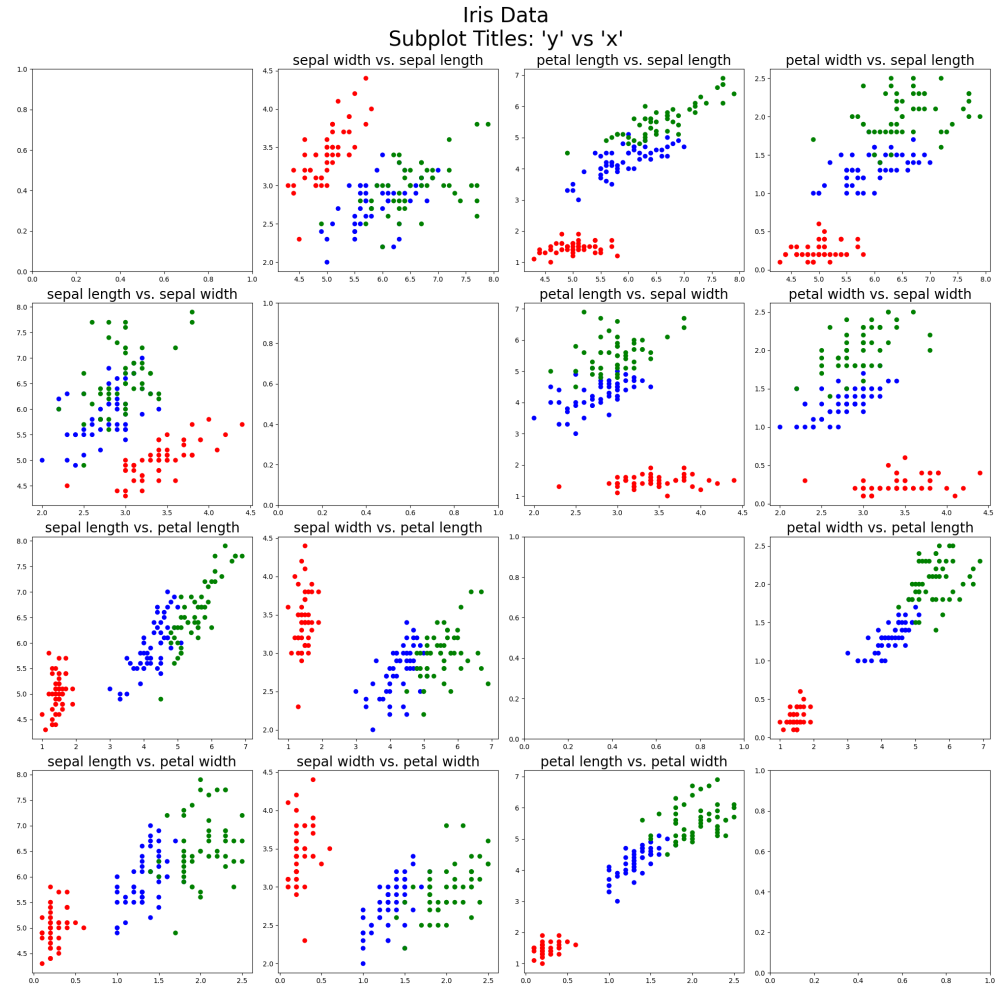
In the above code, axes[x_index, y_index] is responsible for creating a subplot on the position of (x_index, y_index). And the variable attribute_arr is an p×N array (constructed transpose of the parsed attributes data array), where the n-th element of attribute_arr will give the nth attribute's N-dimension vector. Lastly, color_vector is an N-dimension vector of assigned colors for each sample based on the label (species). The code for this is shown below.

```
 # get each attribute vector
attributes_matrix = attributes.to_numpy()
sepal_length = attributes_matrix[:,0:1]
sepal_width = attributes_matrix[:,1:2]
```

```
petal_length = attributes_matrix[:,2:3]
petal_width = attributes_matrix[:,3:4]

# create a graph using 2 attribute vector
# (for non-same attributes) for all possible pairs
# red is Iris-setosa, green is Iris-virginica, blue is Iris-versicolor
color_map = {
    'Iris-setosa': 'red',
    'Iris-virginica': 'green',
    'Iris-versicolor': 'blue'
}
labels_array = labels.to_numpy().tolist()
color_vector = [color_map[species[0]] for species in labels_array]
attribute_arr = [sepal_length, sepal_width, petal_length, petal_width]
attribute_category_strings = ["sepal length", "sepal width",
            "petal length", "petal width"]
```

The final result is shown below. Red is Iris-setosa, green is Iris-virginica, and blue is Iris-versicolor.



As seen, the Iris dataset was properly visualized. Based on visuals, it seems that Iris-setosa is the distinguishable species from the other two species (separated well on most dimensions). And Iris-virginica and Iris-versicolor are poorly distinguiable (not well separated on most dimensions). This aligns with the description of the dataset by R.A. Fischer in the UC Irvine Machine Learning.

4 Source Code

The source code can be found at https://github.com/JiwonJJeong/CT-applied-machine-learningGitHub in the /hw-0 directory.