

DATA EXPLORATION USING SEABORN

Import the iris dataset:

```
from sklearn.datasets import load_iris
iris = load_iris()
data = pd.DataFrame(iris.data, columns=iris.feature_names)
label = pd.DataFrame(list(map(lambda x : iris.target_names[x], iris.target)), columns=['Species'])
iris = pd.concat([data, label], axis=1)
print(iris.head())
```

Expected output after this stage is shown below. You do NOT have to execute the following 2 lines. They are given as reference for expected output only.

In [3]: `from IPython.display import Image
Image(filename='iris.png')`

Out[3]:

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)	Species
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa

Execute the following steps:

- 1) Use the `distplot()` to see the distribution of the `SepalLengthCm`, `SepalWidthCm`, `PetalLengthCm`, `PetalWidthCm` features. Plot them as subplots in a single image.
- 2) Do a boxplot of all features except 'Species'.
- 3) Do a countplot for the feature 'Species'.
- 4) Do a pairplot on the features 'SepalLengthCm', 'SepalWidthCm', 'PetalLengthCm', 'PetalWidthCm', 'Species'.
- 5) Do an `lplot` on the following `SepalLengthCm`, `PetalLengthCm`. Using `hue`, display the different species in different colors.
- 6) Do a barplot of 'Species' vs 'SepalLengthCm'.
- 7) Using `heatmap`, plot the correlation matrix.