

practical-10

April 17, 2024

1 Data Visualization III

Download the Iris flower dataset or any other dataset into a DataFrame. (e.g., <https://archive.ics.uci.edu/ml/datasets/Iris>). Scan the dataset and give the inference as: 1. List down the features and their types (e.g., numeric, nominal) available in the dataset. 2. Create a histogram for each feature in the dataset to illustrate the feature distributions. 3. Create a boxplot for each feature in the dataset. 4. Compare distributions and identify outliers.

```
[ ]: # import seaborn as sns
      # import matplotlib.pyplot as plt

      # iris = sns.load_dataset('iris')
      # iris

      # iris.info

      # iris.describe()

      # type(iris.sepal_length)

      # iris.sepal_length.dtype

      # iris.sepal_width.dtype

      # iris.petal_length.dtype

      # iris.petal_width.dtype

      # iris.species.dtype

      # fig, axes = plt.subplots(2, 2, figsize = (10, 6))
      # sns.histplot(iris['sepal_length'],ax = axes[0, 0])
      # sns.histplot(iris['sepal_width'],ax = axes[0, 1])
      # sns.histplot(iris['petal_length'],ax = axes[1, 0])
      # sns.histplot(iris['petal_width'],ax = axes[1, 1])
```

```
# # For boxplot
# fig, axes = plt.subplots(2, 2, figsize = (16, 10))
# sns.boxplot(x= 'species', y= 'sepal_length', data= iris, ax= axes[0, 0])
# sns.boxplot(x= 'species', y= 'sepal_width', data= iris, ax= axes[0, 1])
# sns.boxplot(x= 'species', y= 'petal_length', data= iris, ax= axes[1, 0])
# sns.boxplot(x= 'species', y= 'petal_width', data= iris, ax= axes[1, 1])
```

```
[1]: import seaborn as sns
import matplotlib.pyplot as plt
```

```
[2]: iris = sns.load_dataset('iris')
iris
```

```
[2]:      sepal_length  sepal_width  petal_length  petal_width  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
..          ...           ...           ...           ...     ...
145          6.7           3.0           5.2           2.3  virginica
146          6.3           2.5           5.0           1.9  virginica
147          6.5           3.0           5.2           2.0  virginica
148          6.2           3.4           5.4           2.3  virginica
149          5.9           3.0           5.1           1.8  virginica
```

[150 rows x 5 columns]

```
[3]: iris.info
```

```
[3]: <bound method DataFrame.info of      sepal_length  sepal_width  petal_length
petal_width      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
..          ...           ...           ...           ...     ...
145          6.7           3.0           5.2           2.3  virginica
146          6.3           2.5           5.0           1.9  virginica
147          6.5           3.0           5.2           2.0  virginica
148          6.2           3.4           5.4           2.3  virginica
149          5.9           3.0           5.1           1.8  virginica
```

[150 rows x 5 columns]>

```
[4]: iris.describe()
```

```
[4]:      sepal_length  sepal_width  petal_length  petal_width
count      150.000000    150.000000    150.000000    150.000000
mean         5.843333     3.057333     3.758000     1.199333
std          0.828066     0.435866     1.765298     0.762238
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
```

```
[5]: type(iris.sepal_length)
```

```
[5]: pandas.core.series.Series
```

```
[6]: iris.sepal_length.dtype
```

```
[6]: dtype('float64')
```

```
[7]: iris.sepal_width.dtype
```

```
[7]: dtype('float64')
```

```
[8]: iris.petal_length.dtype
```

```
[8]: dtype('float64')
```

```
[9]: iris.petal_width.dtype
```

```
[9]: dtype('float64')
```

```
[10]: iris.species.dtype
```

```
[10]: dtype('O')
```

```
[11]: fig, axes = plt.subplots(2, 2, figsize = (10, 6))
sns.histplot(iris['sepal_length'],ax = axes[0, 0])
sns.histplot(iris['sepal_width'],ax = axes[0, 1])
sns.histplot(iris['petal_length'],ax = axes[1, 0])
sns.histplot(iris['petal_width'],ax = axes[1, 1])
```

F:\Anaconda3\Lib\site-packages\seaborn_oldcore.py:1119: FutureWarning:
use_inf_as_na option is deprecated and will be removed in a future version.
Convert inf values to NaN before operating instead.

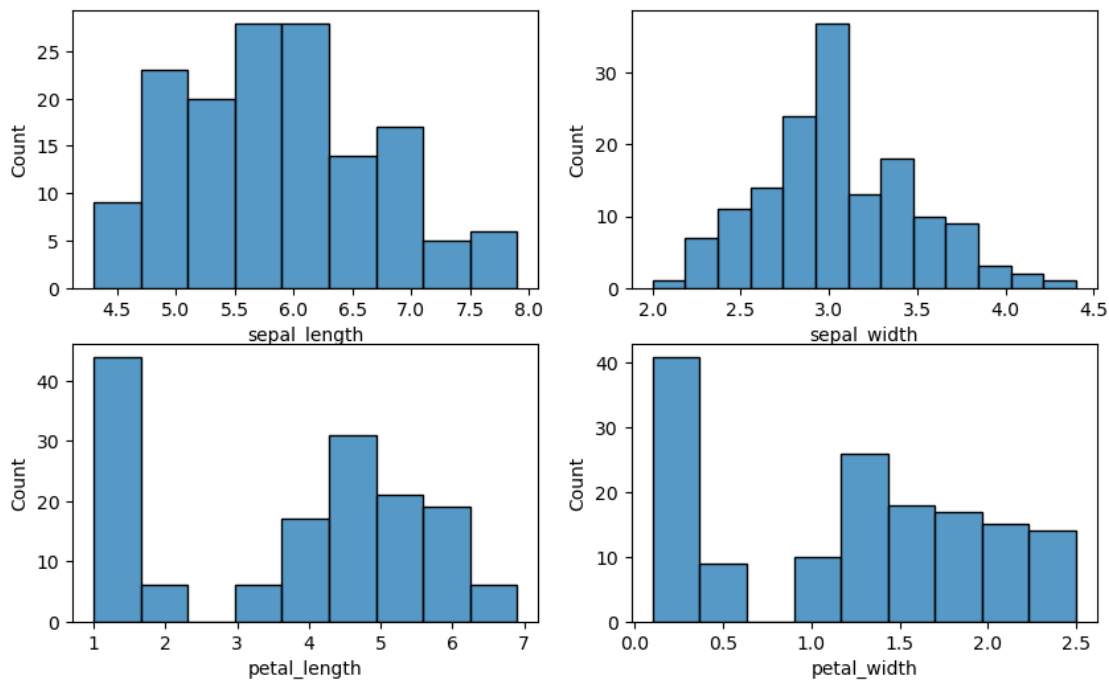
with pd.option_context('mode.use_inf_as_na', True):

F:\Anaconda3\Lib\site-packages\seaborn_oldcore.py:1119: FutureWarning:
use_inf_as_na option is deprecated and will be removed in a future version.

Convert inf values to NaN before operating instead.

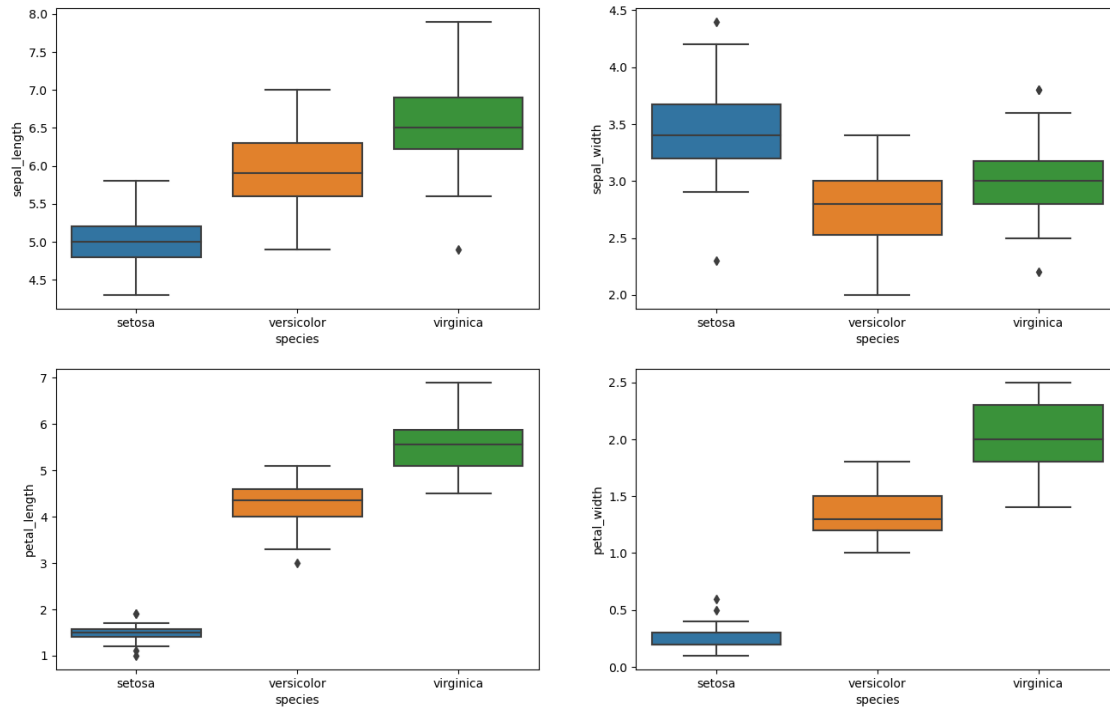
```
with pd.option_context('mode.use_inf_as_na', True):  
F:\Anaconda3\Lib\site-packages\seaborn\_oldcore.py:1119: FutureWarning:  
use_inf_as_na option is deprecated and will be removed in a future version.  
Convert inf values to NaN before operating instead.  
with pd.option_context('mode.use_inf_as_na', True):  
F:\Anaconda3\Lib\site-packages\seaborn\_oldcore.py:1119: FutureWarning:  
use_inf_as_na option is deprecated and will be removed in a future version.  
Convert inf values to NaN before operating instead.  
with pd.option_context('mode.use_inf_as_na', True):
```

[11]: <Axes: xlabel='petal_width', ylabel='Count'>



```
[12]: # For boxplot  
fig, axes = plt.subplots(2, 2, figsize = (16, 10))  
sns.boxplot(x= 'species', y= 'sepal_length', data= iris, ax= axes[0, 0])  
sns.boxplot(x= 'species', y= 'sepal_width', data= iris, ax= axes[0, 1])  
sns.boxplot(x= 'species', y= 'petal_length', data= iris, ax= axes[1, 0])  
sns.boxplot(x= 'species', y= 'petal_width', data= iris, ax= axes[1, 1])
```

[12]: <Axes: xlabel='species', ylabel='petal_width'>



[]: