

PRACTICAL NO : 10

DATA VISUALIZATION 3

CODE :

```
import seaborn as sns  
dataset = sns.load_dataset('iris')  
dataset.head()
```

```
import matplotlib.pyplot as plt  
#fig, axes = plt.subplots(2,2, figsize = (16,9))  
sns.histplot(dataset['sepal_length'])  
sns.histplot(dataset['sepal_width'])  
sns.histplot(dataset['petal_length'])  
sns.histplot(dataset['petal_width'])
```

```
import matplotlib.pyplot as plt  
#fig, axes = plt.subplots(2,2, figsize = (16,9))  
sns.boxplot(y='petal_length',x='species', data = dataset)  
sns.boxplot(y='petal_width',x='species', data = dataset)  
sns.boxplot(y='sepal_length',x='species', data = dataset)  
sns.boxplot(y='sepal_width',x='species', data = dataset)
```

OUTPUT :

```
Console 1/A X

In [1]: runfile('E:/DSBDA/dsbdapr10.py', wdir='E:/DSBDA')

In [2]: dataset.head()
Out[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

In [3]: sns.histplot(dataset['sepal_length'])
Out[3]: <Axes: xlabel='sepal_length', ylabel='Count'>
```

Important
Figures are displayed in the Plots pane by default. To make them also appear inline in the console, you need to uncheck "Mute inline plotting" under the options menu of Plots.

```
In [4]: sns.histplot(dataset['sepal_width'])
Out[4]: <Axes: xlabel='sepal_width', ylabel='Count'>

In [5]: sns.histplot(dataset['petal_length'])
Out[5]: <Axes: xlabel='petal_length', ylabel='Count'>

In [6]: sns.histplot(dataset['petal_width'])
Out[6]: <Axes: xlabel='petal_width', ylabel='Count'>

In [7]: sns.boxplot(y='petal_length',x='species', data = dataset)
Out[7]: <Axes: xlabel='species', ylabel='petal_length'>
```

IPython Console History







