```
import pandas as pd
import seaborn as sns
```

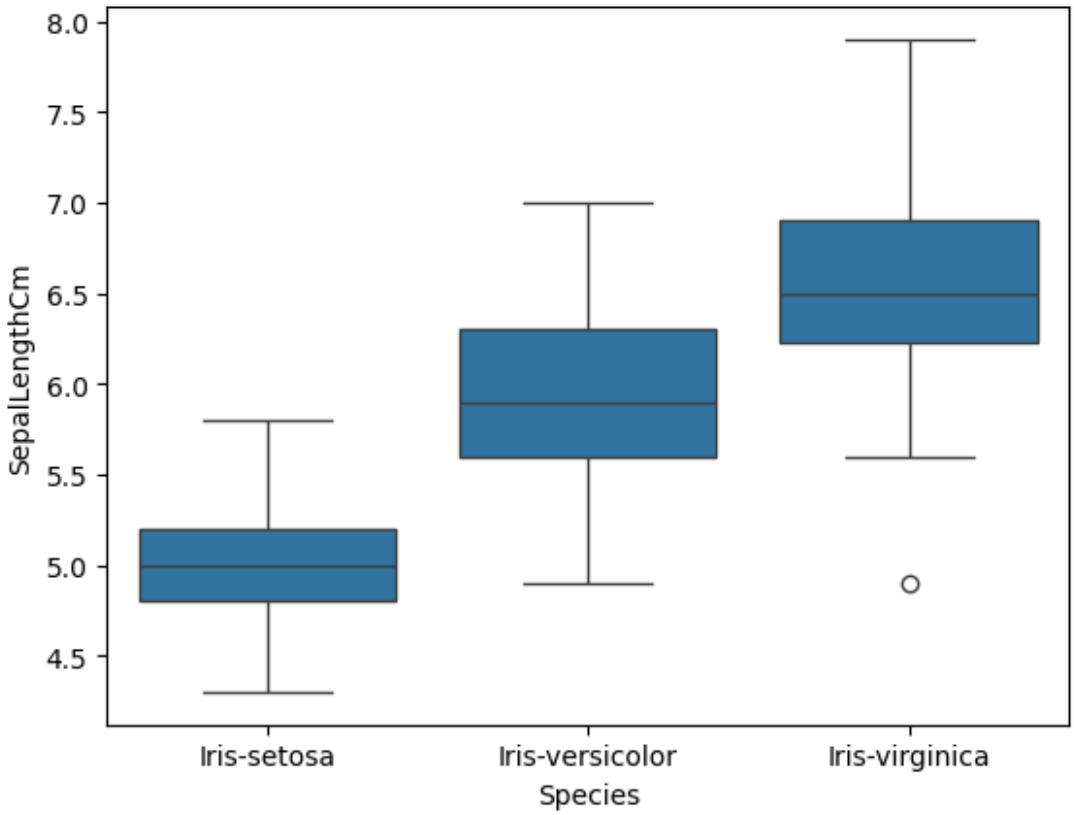
loading the iris dataset using pandas library

```
df = pd.read_csv('iris.csv')

df
```

```
      Id  SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm  \
0      1            5.1           3.5            1.4           0.2
1      2            4.9           3.0            1.4           0.2
2      3            4.7           3.2            1.3           0.2
3      4            4.6           3.1            1.5           0.2
4      5            5.0           3.6            1.4           0.2
..   ...            ...           ...            ...           ...
145  146            6.7           3.0            5.2           2.3
146  147            6.3           2.5            5.0           1.9
147  148            6.5           3.0            5.2           2.0
148  149            6.2           3.4            5.4           2.3
149  150            5.9           3.0            5.1           1.8

            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 6 columns]
```

boxplot is use to plot species based on Sepallength also provides outliers

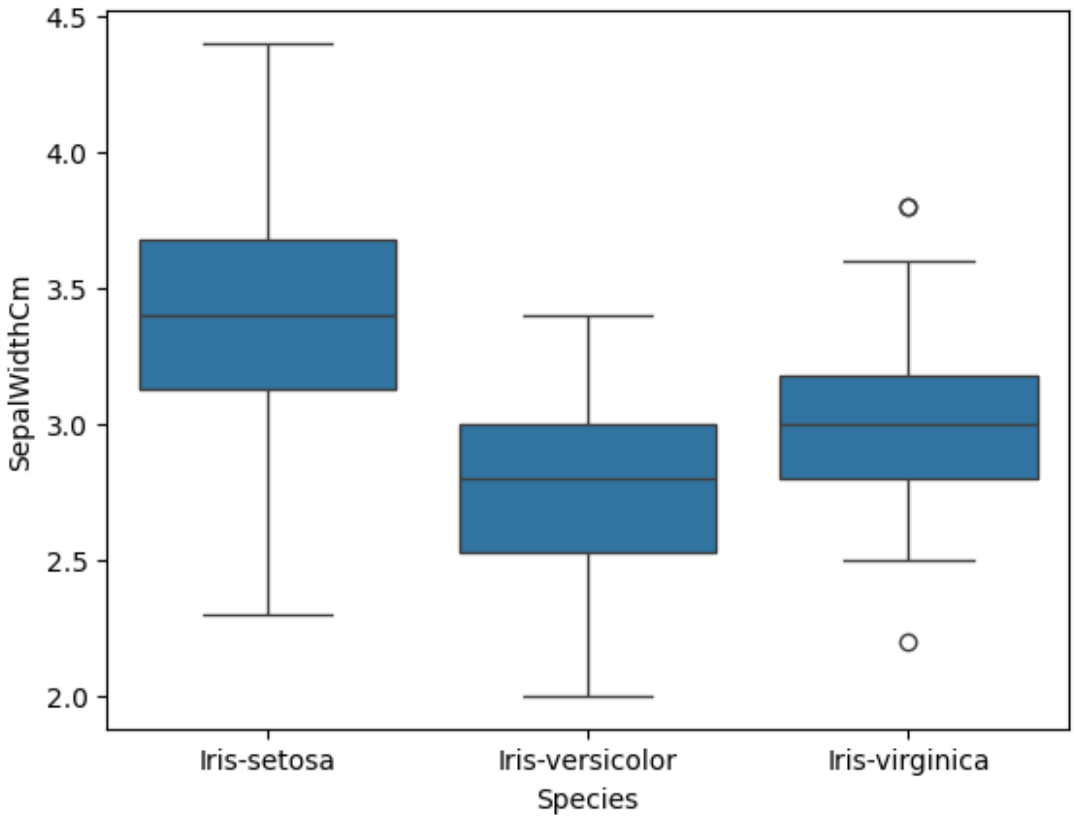
```
sns.boxplot(x= 'Species',y='SepalLengthCm',data=df)

<Axes: xlabel='Species', ylabel='SepalLengthCm'>
```



boxplot is use to plot species based on Sepalwidth also provides outliers

```
sns.boxplot(x= 'Species',y='SepalWidthCm',data=df)
```

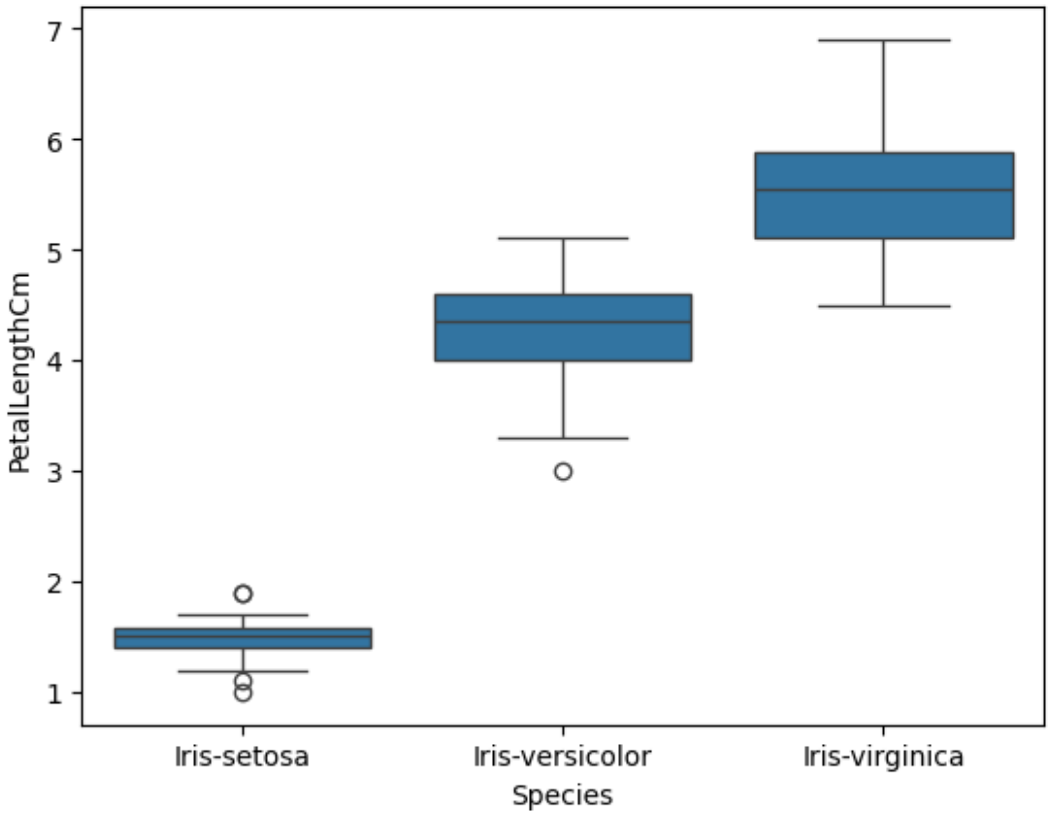
```
<Axes: xlabel='Species', ylabel='SepalWidthCm'>
```



boxplot is use to plot species based on petallength also provides outliers

```
sns.boxplot(x= 'Species',y='PetalLengthCm',data=df)
```

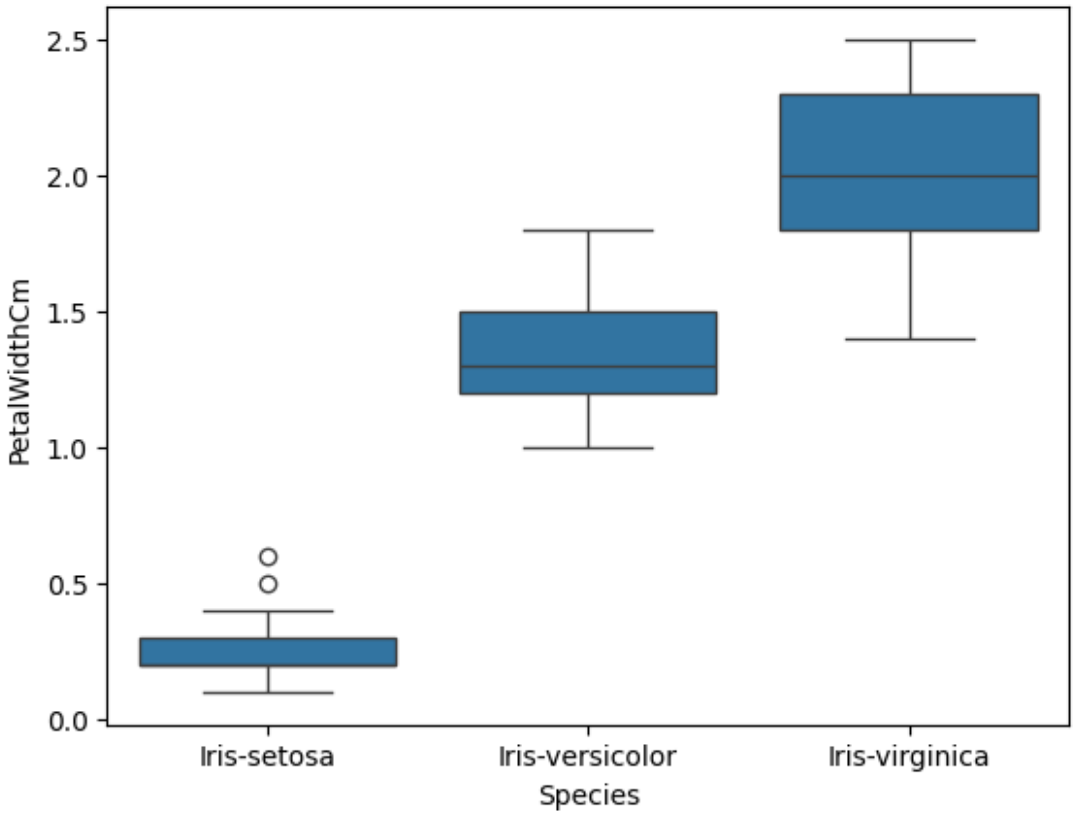
```
<Axes: xlabel='Species', ylabel='PetalLengthCm'>
```



boxplot is use to plot species based on petalwidth also provides outliers for understanding data convergencej

```
sns.boxplot(x= 'Species',y='PetalWidthCm',data=df)
```

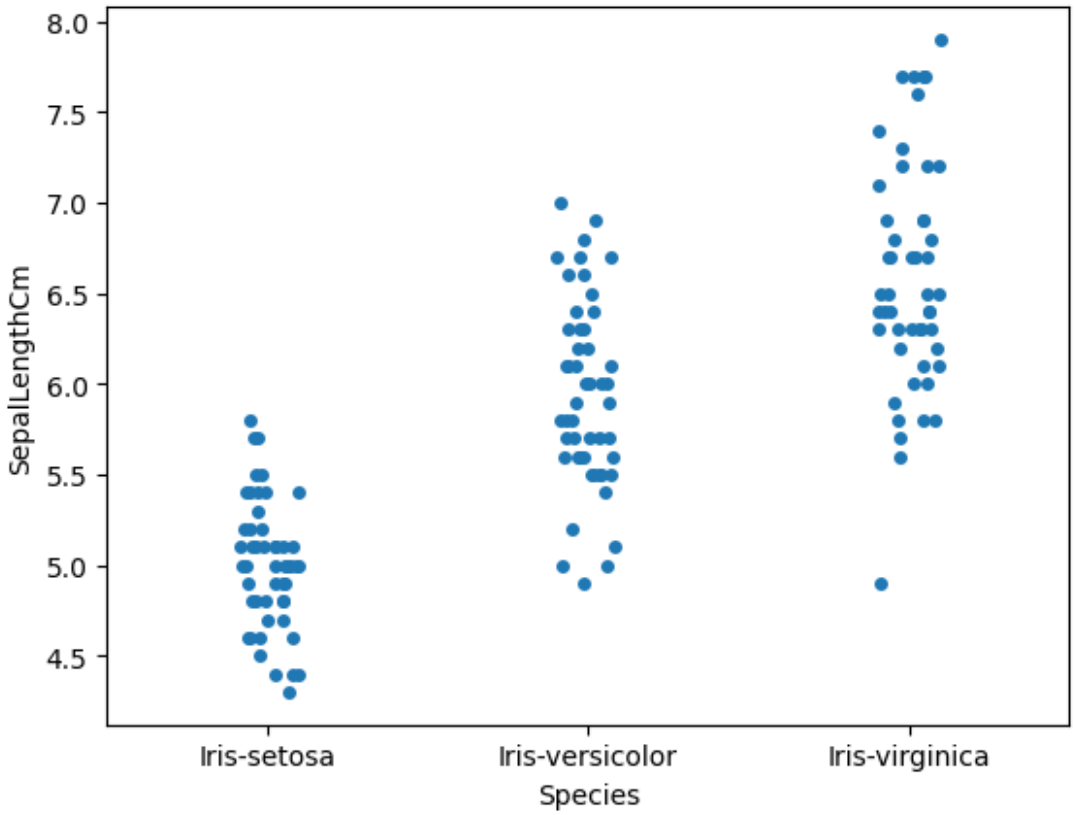
```
<Axes: xlabel='Species', ylabel='PetalWidthCm'>
```



Stripplot is same as boxplot it also used for visulization it givs scattered points

```
sns.stripplot(x='Species', y='SepalLengthCm',data=df)
```

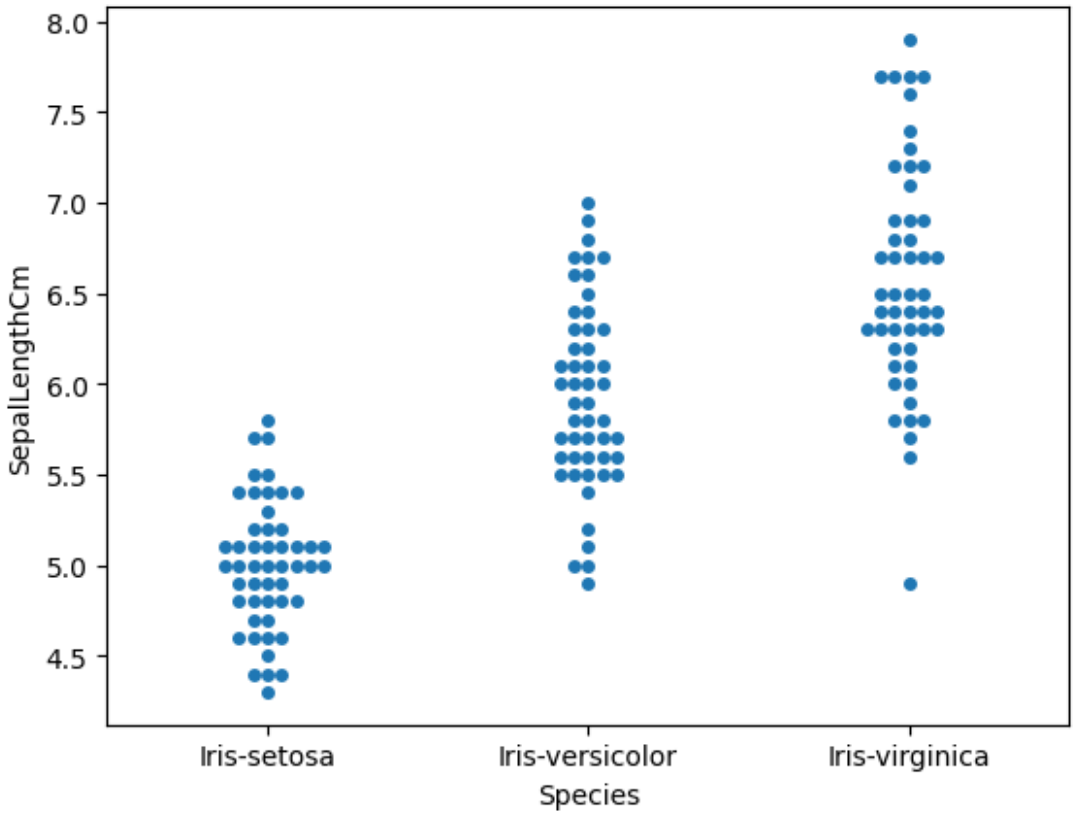
```
<Axes: xlabel='Species', ylabel='SepalLengthCm'>
```



swarmplot is same as boxplot used for visulization

```
sns.swarmplot(x='Species', y='SepalLengthCm',data=df)
```

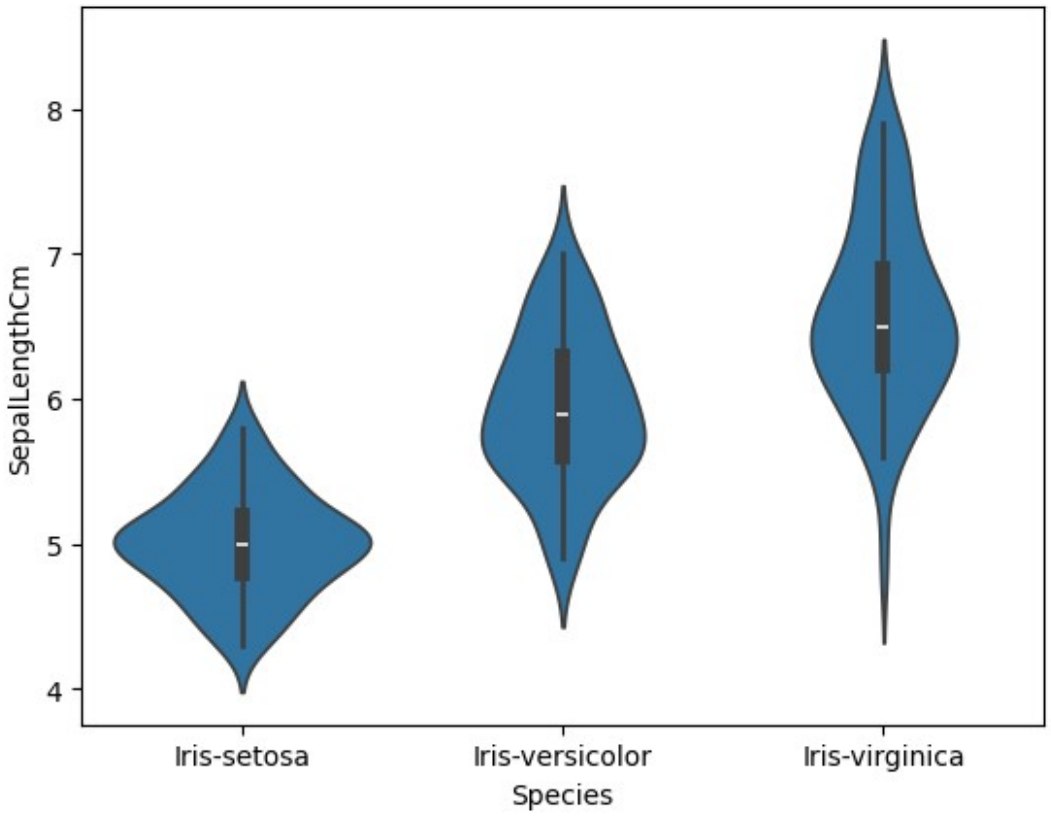
```
<Axes: xlabel='Species', ylabel='SepalLengthCm'>
```



violinplot is same as boxplot used to visulize the data gives violin like structured to understand data convergence

```
sns.violinplot(x='Species', y='SepalLengthCm',data=df)
```

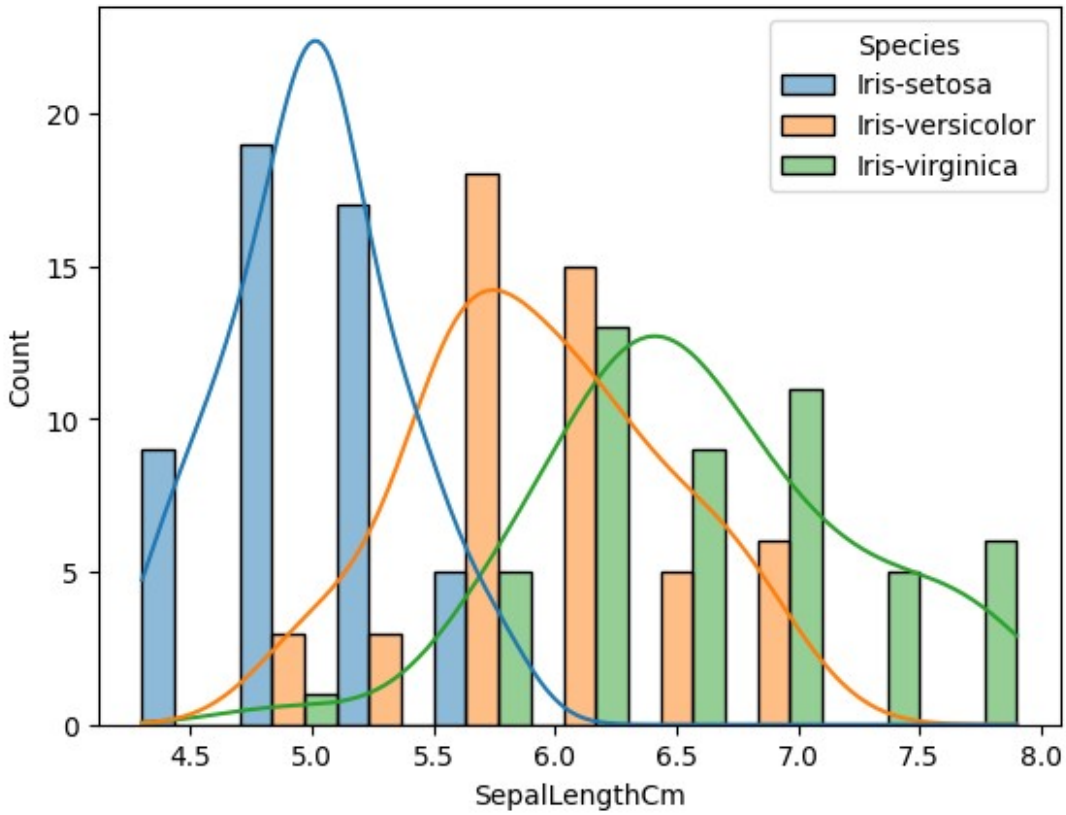
```
<Axes: xlabel='Species', ylabel='SepalLengthCm'>
```



histogram use to visulize sepallength feature of dataset on the basis of species

```
sns.histplot(x='SepalLengthCm',hue='Species',multiple='dodge',kde=True
,data=df)
```

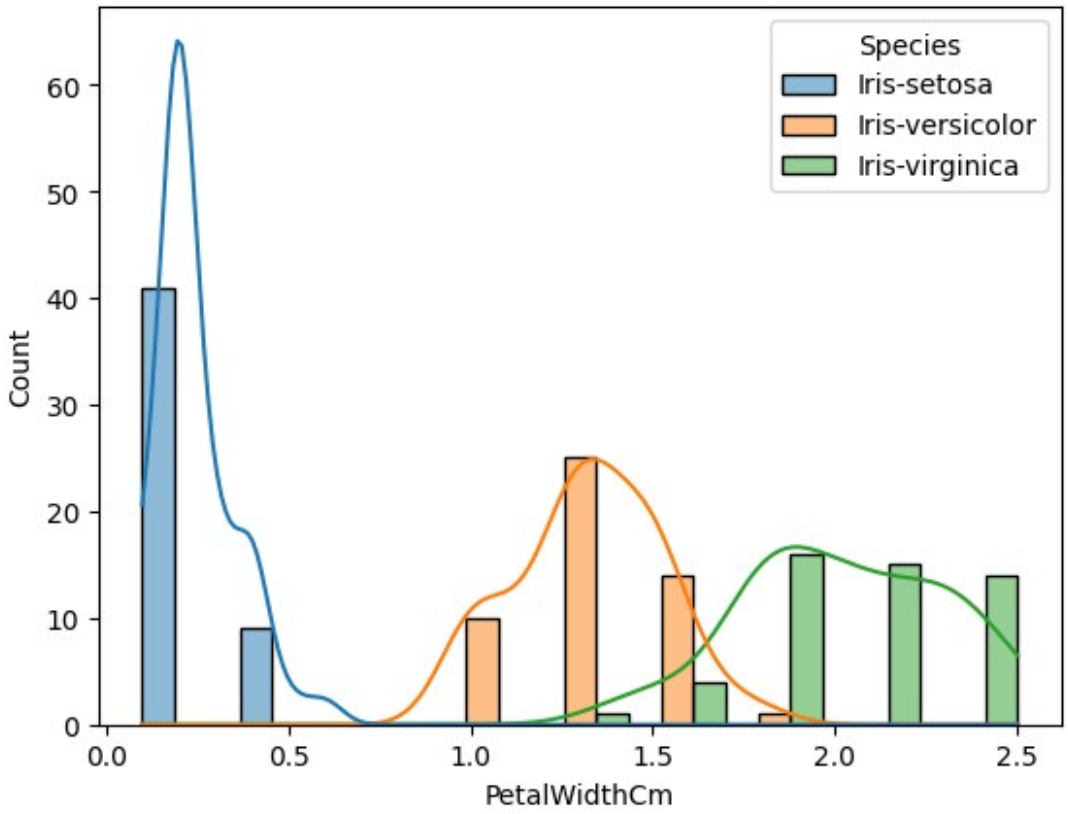
```
<Axes: xlabel='SepalLengthCm', ylabel='Count'>
```



histogram use to visulize petalwidth feature of dataset on the basis of species

```
sns.histplot(x='PetalWidthCm',hue='Species',multiple='dodge',kde=True,
data=df)
```

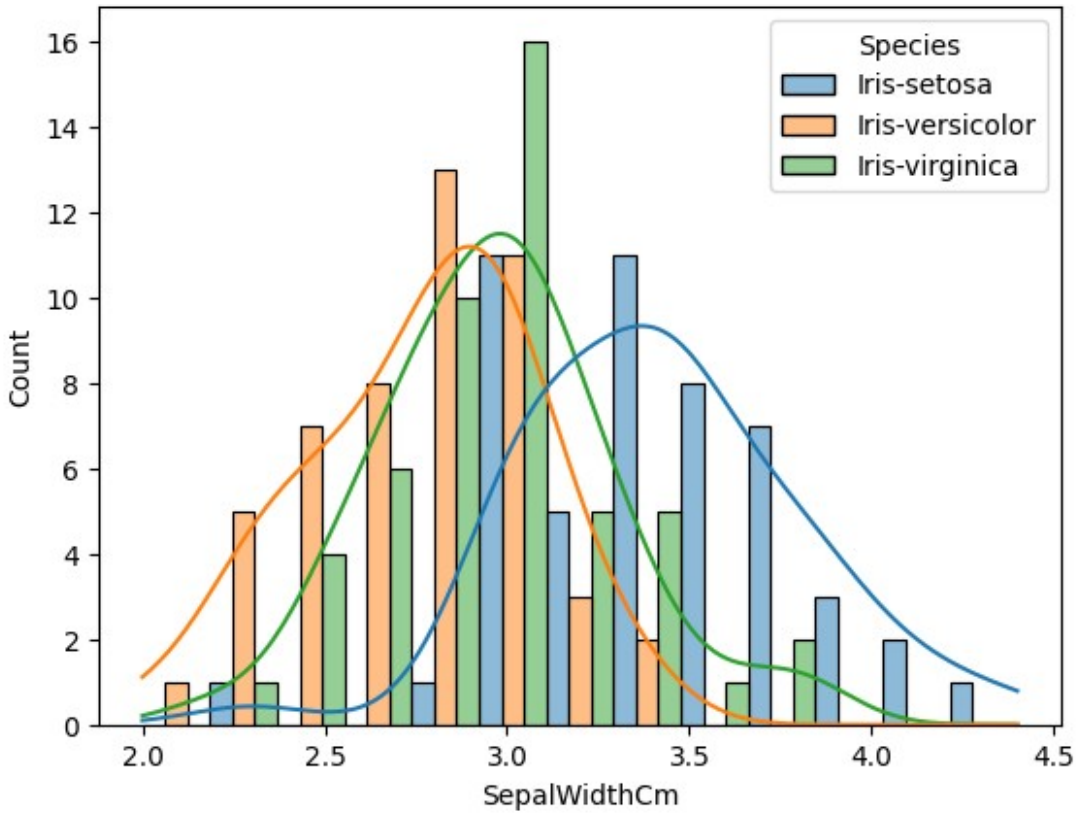
```
<Axes: xlabel='PetalWidthCm', ylabel='Count'>
```



histogram use to visulize sepalwidth feature of dataset on the basis of species

```
sns.histplot(x='SepalWidthCm',hue='Species',multiple='dodge',kde=True,
data=df)
```

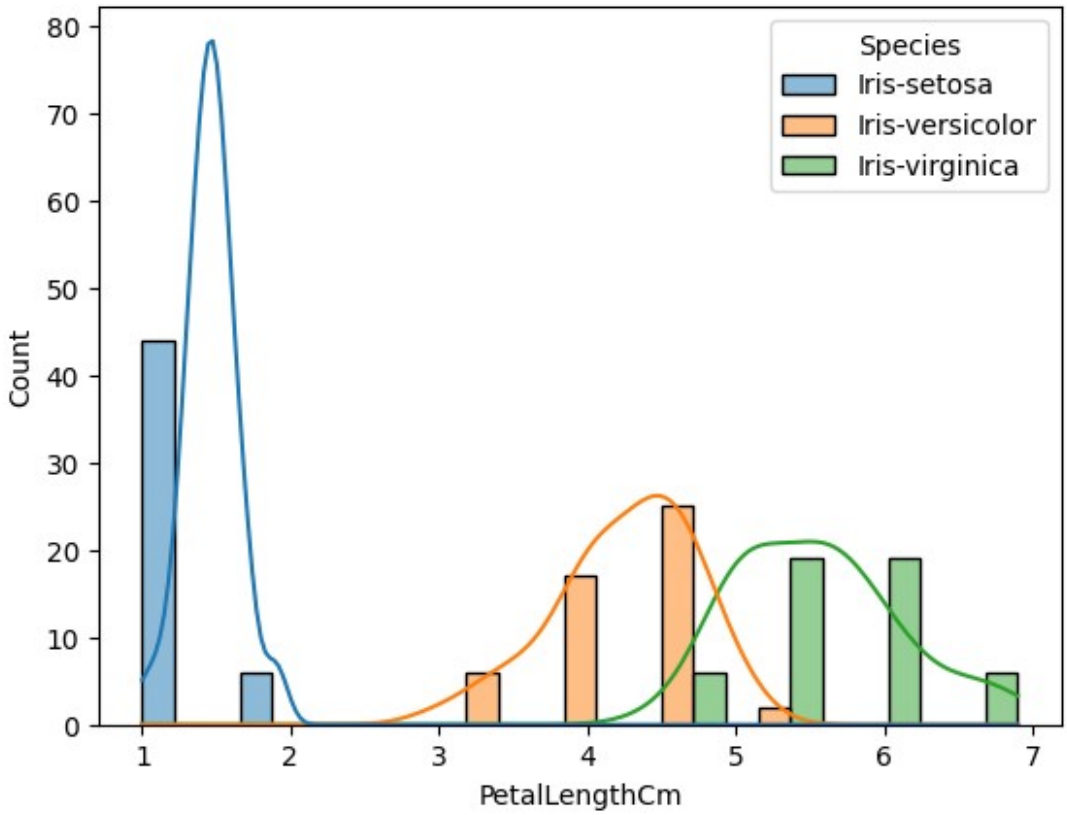
```
<Axes: xlabel='SepalWidthCm', ylabel='Count'>
```



histogram use to visulize petallength feature of dataset on the basis of species

```
sns.histplot(x='PetalLengthCm',hue='Species',multiple='dodge',kde=True
,data=df)
```

```
<Axes: xlabel='PetalLengthCm', ylabel='Count'>
```


Species
Iris-setosa
Iris-versicolor
Iris-virginica
Count
PetalLengthCm
0
10
20
30
40
50
60
70
80
1
2
3
4
5
6
7