Class_10_visuallization_ggplot2

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2025-01-27

packages

loading required packages

echo is used to hide the section

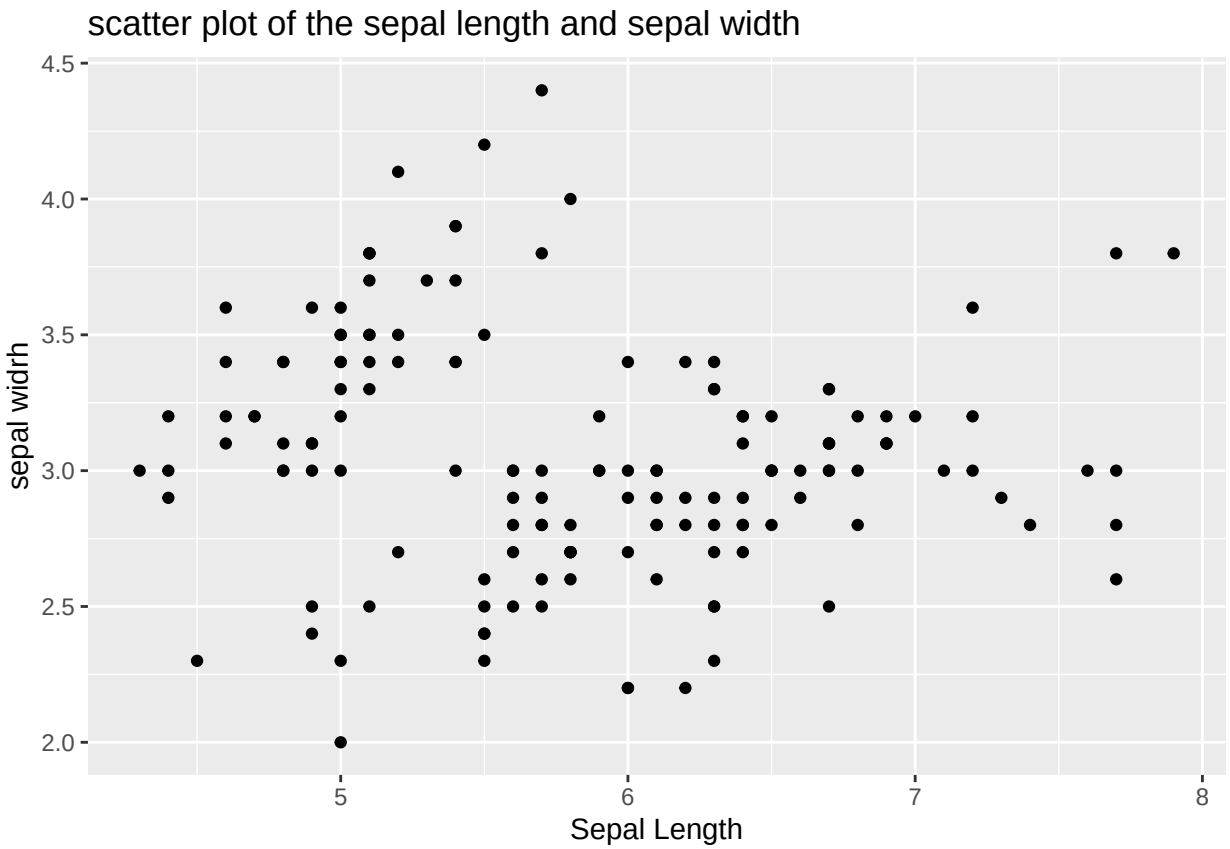
header

Scatter plot

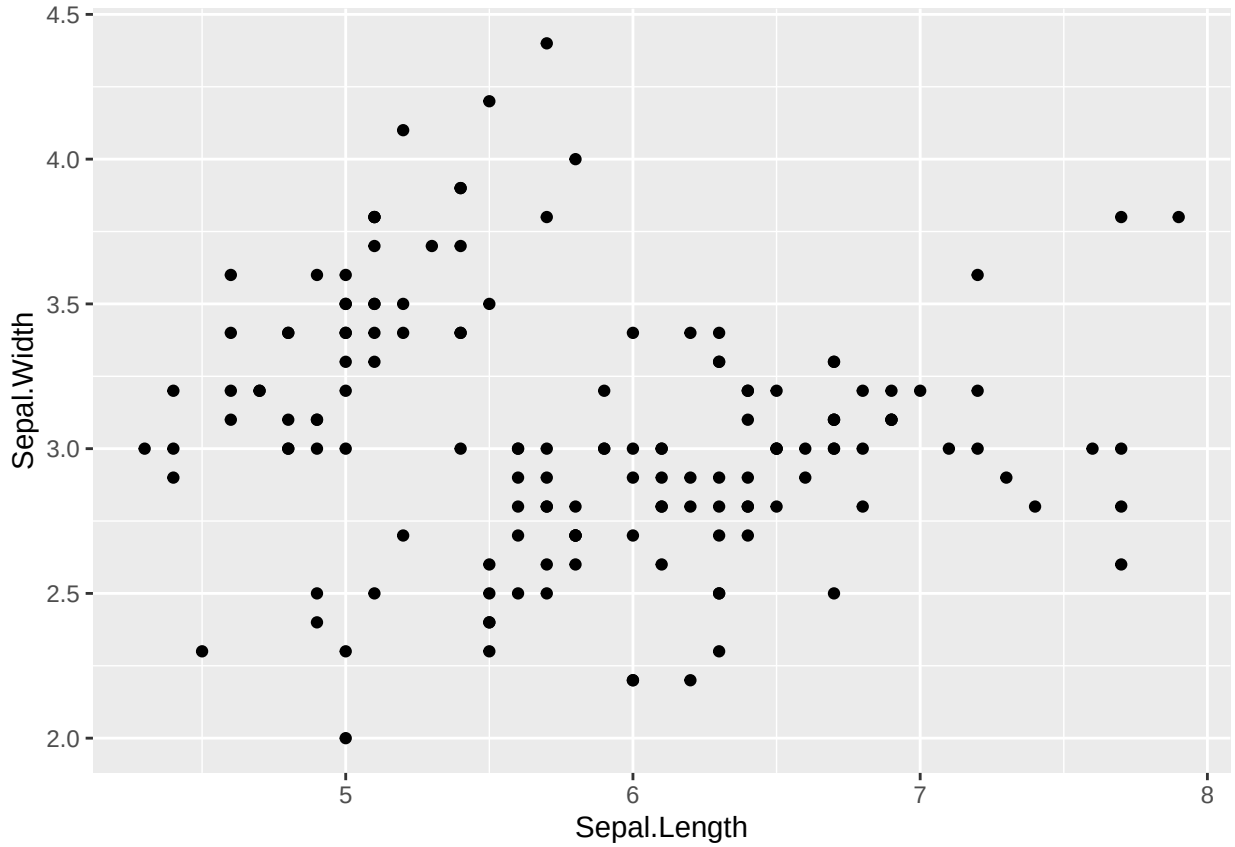
relation between the x and y value

```
data("iris")
```

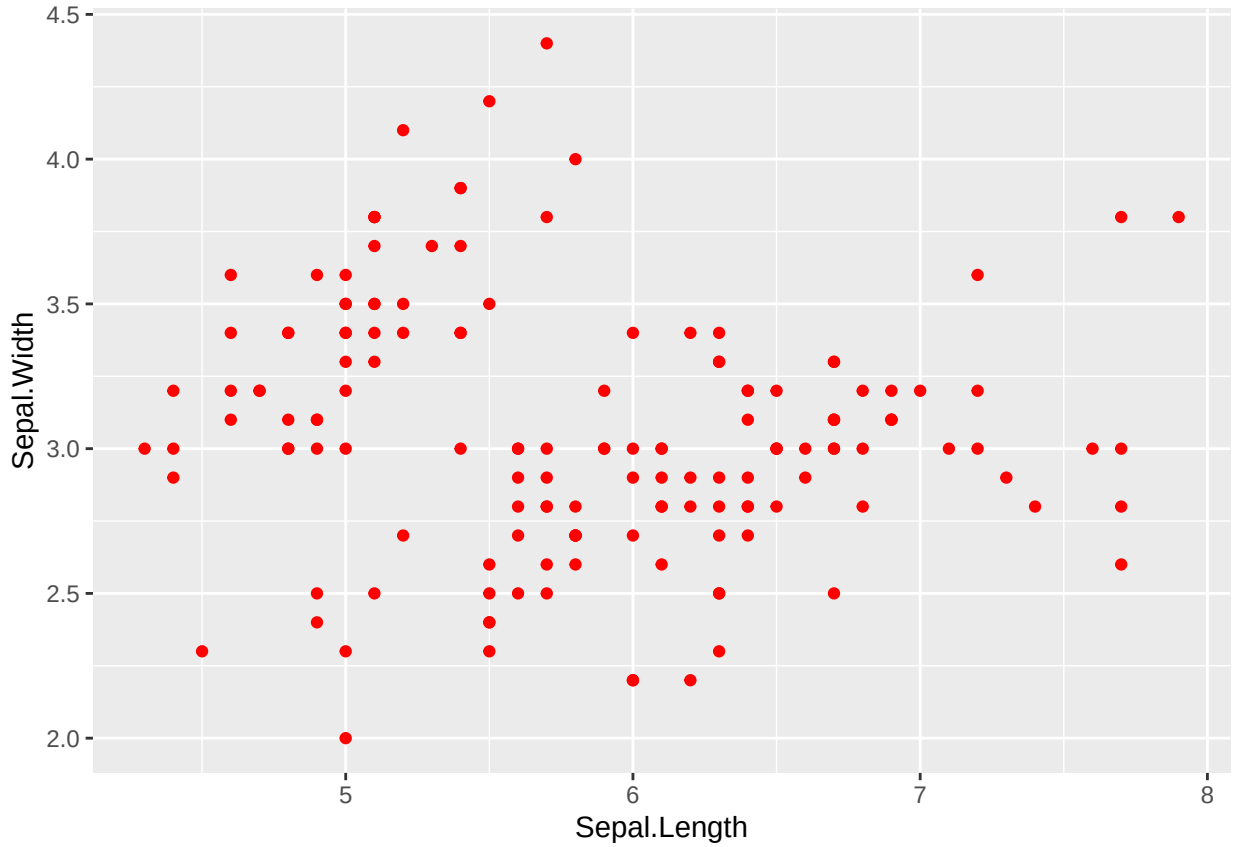
```
ggplot(data = iris) + geom_point(mapping= aes(x = Sepal.Length, y= Sepal.Width))+
  labs(title = "scatter plot of the sepal length and sepal width", x = "Sepal Length", y= "sepal widrh")
```



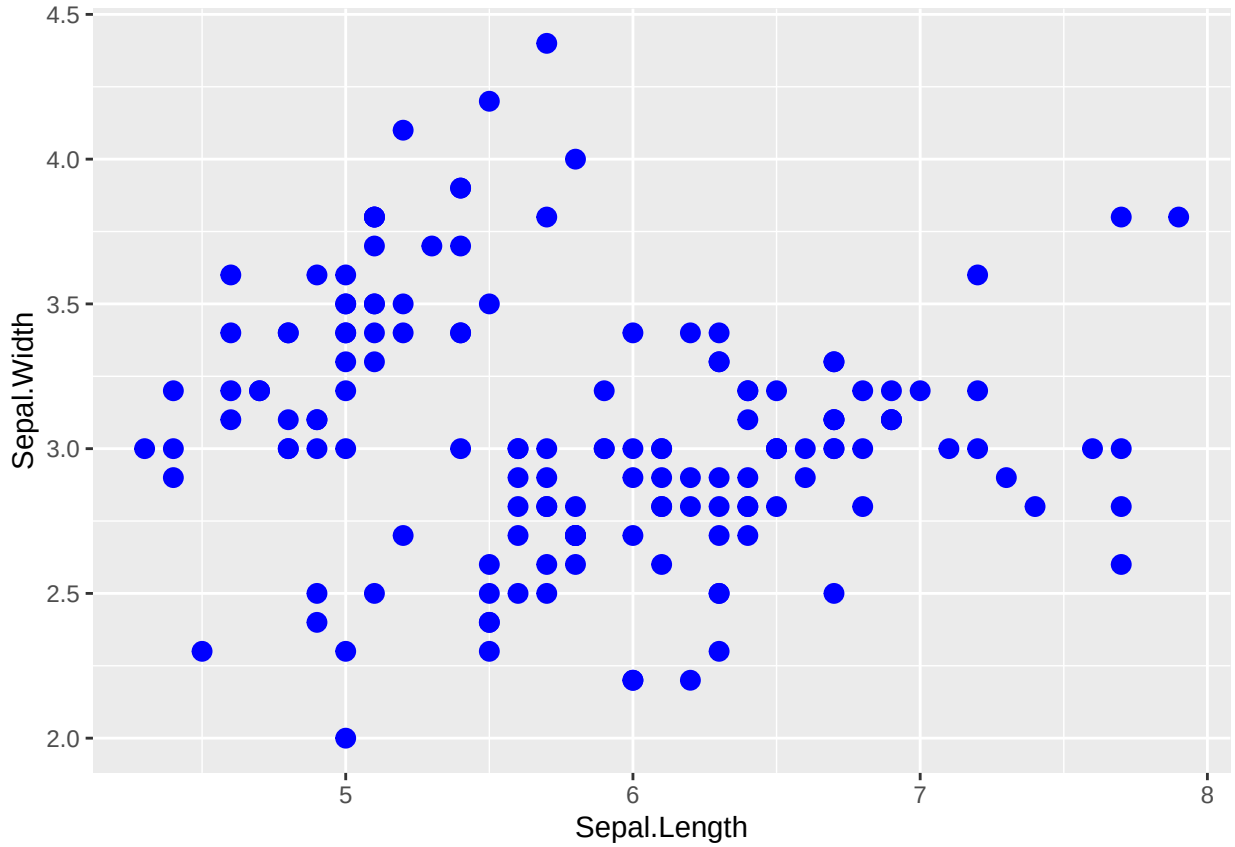

```
ggplot(data = iris)+
  aes(x= Sepal.Length, y= Sepal.Width)+
  geom_point()
```



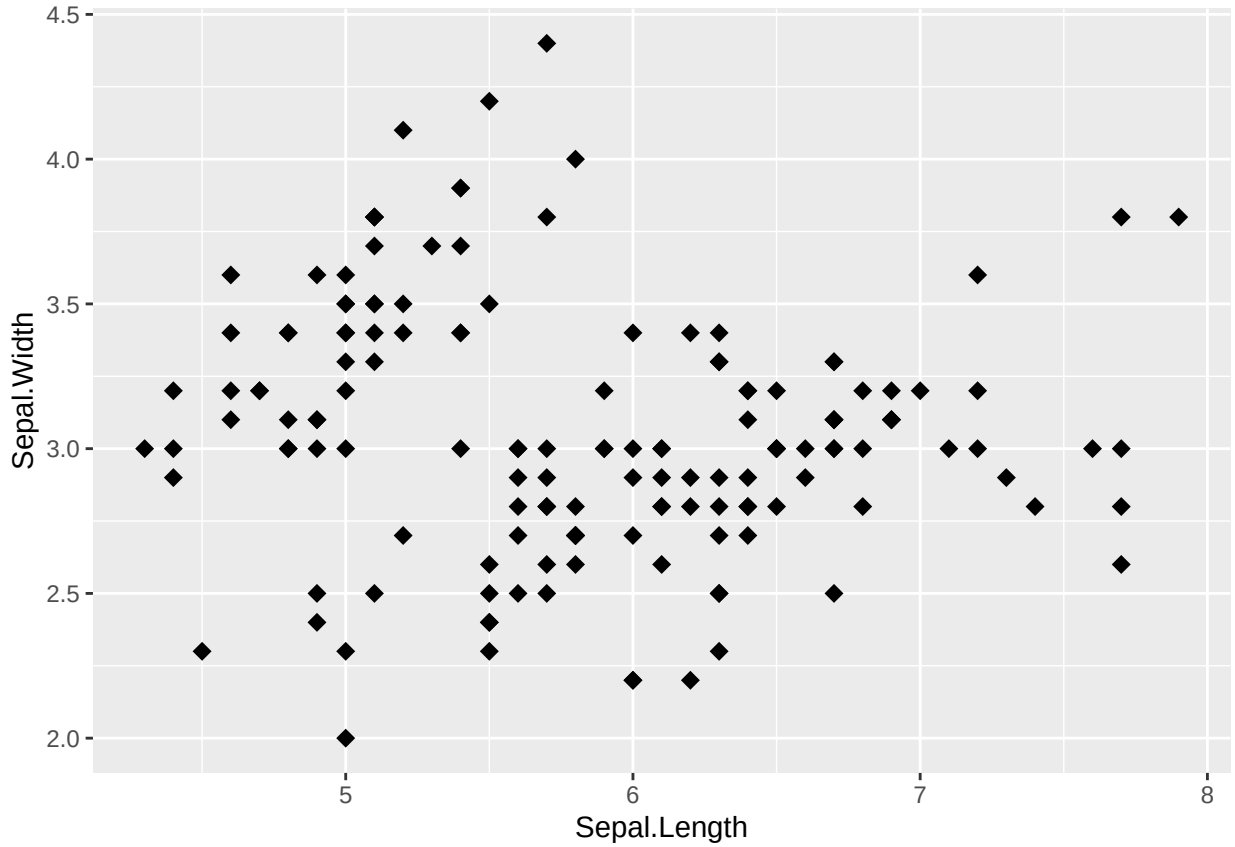

```
ggplot(data = iris, aes(x=Sepal.Length, y=Sepal.Width))+
  geom_point(color = "red")
```



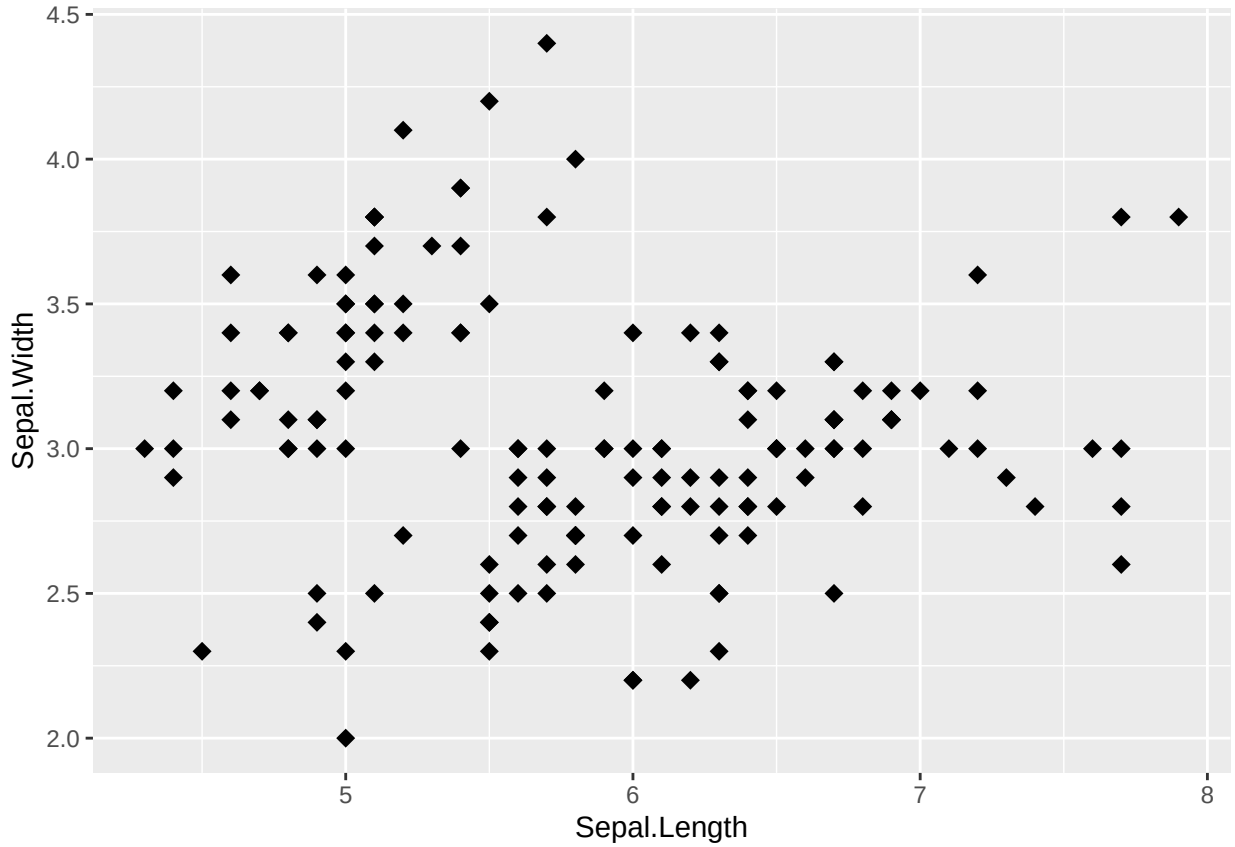

```
ggplot(data = iris, aes(x=Sepal.Length, y=Sepal.Width))+
  geom_point(size= 3, col= "blue")
```



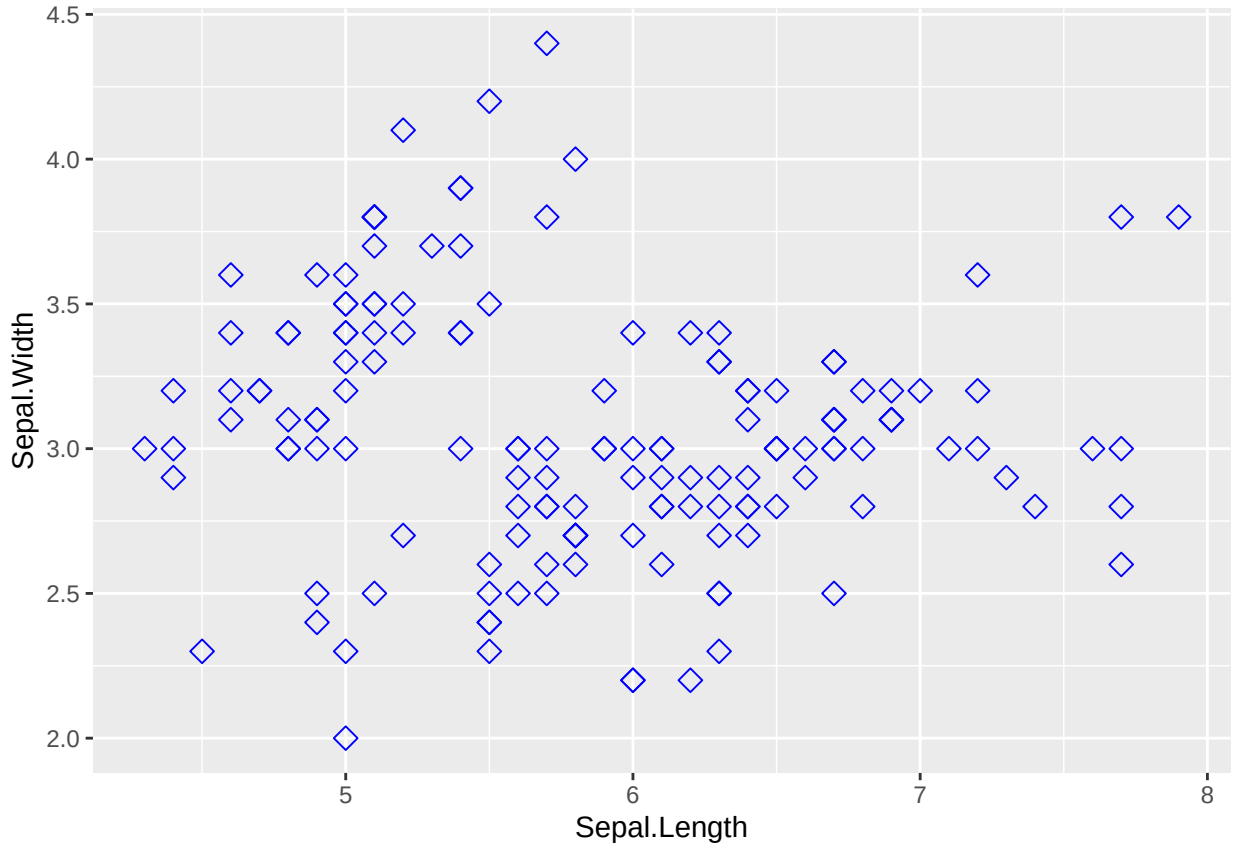

```
ggplot(data = iris, aes(x=Sepal.Length, y=Sepal.Width))+
  geom_point(size= 3, shape=18)
```




```
ggplot(data = iris, aes(x=Sepal.Length, y=Sepal.Width))+
  geom_point(size= 3, shape=18)
```

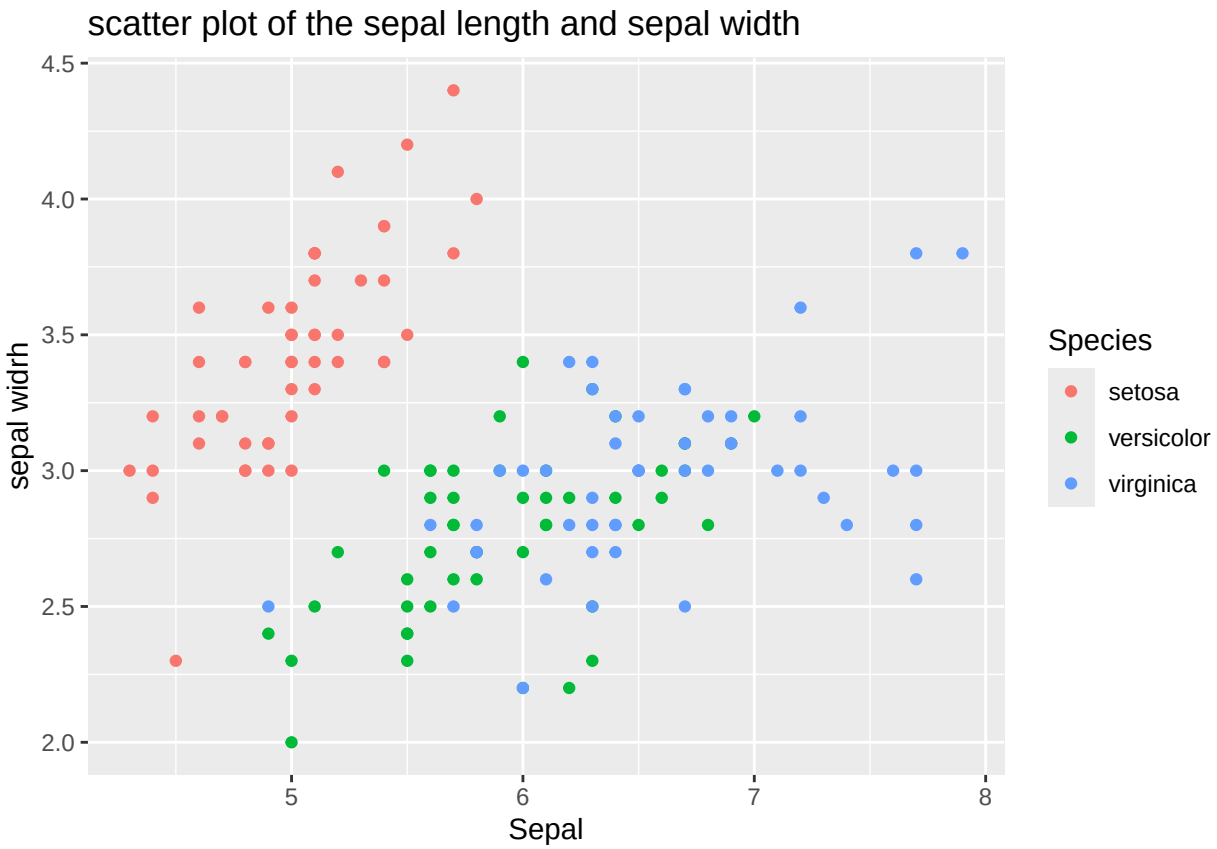



```
ggplot(data = iris, aes(x=Sepal.Length, y=Sepal.Width))+
  geom_point(size= 3, shape="diamond filled", col= "blue")
```



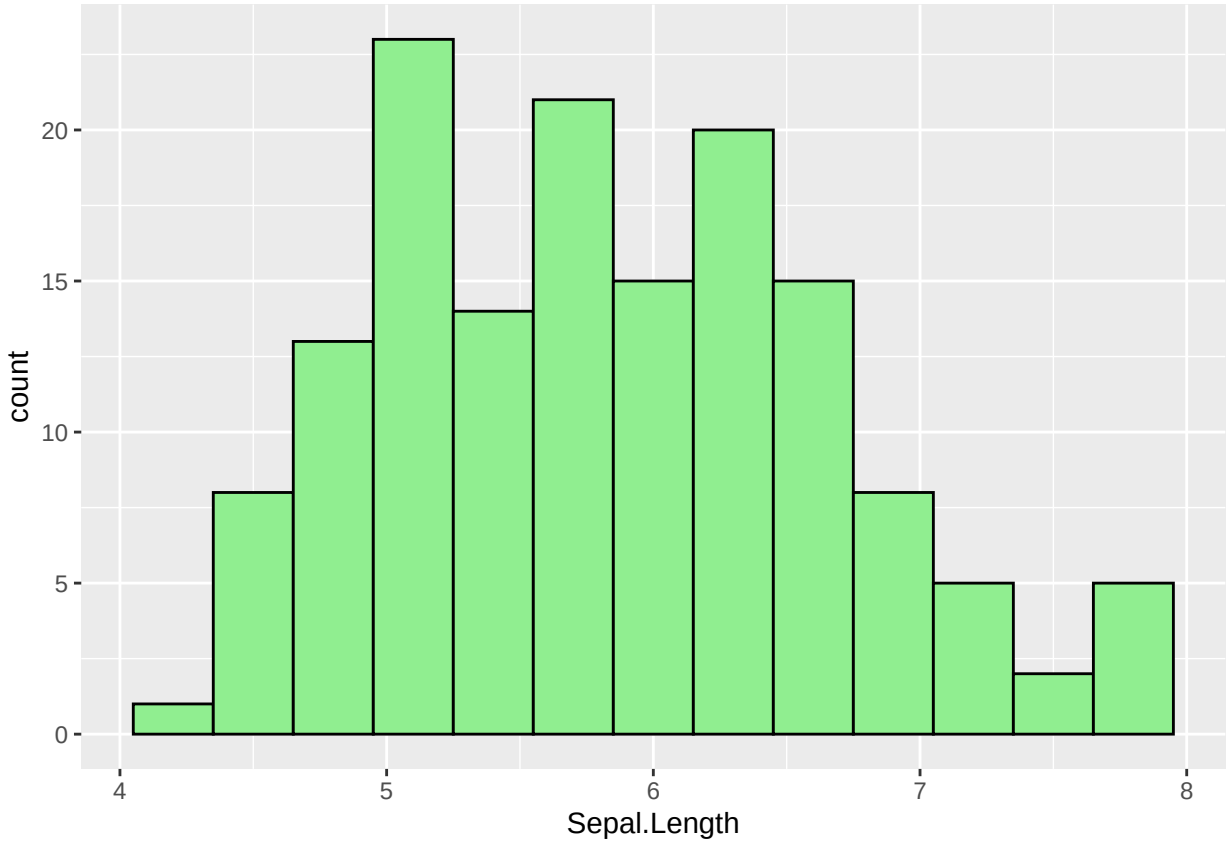

```
ggplot(data = iris, aes(x=Sepal.Length, y=Sepal.Width,col= Species))+
  geom_point()
```

```
ggplot(data = iris, aes(x=Sepal.Length, y=Sepal.Width,col= Species))+
  geom_point()+
  labs(title = "scatter plot of the sepal length and sepal width", x = "Sepal", y= "sepal widrh")
```

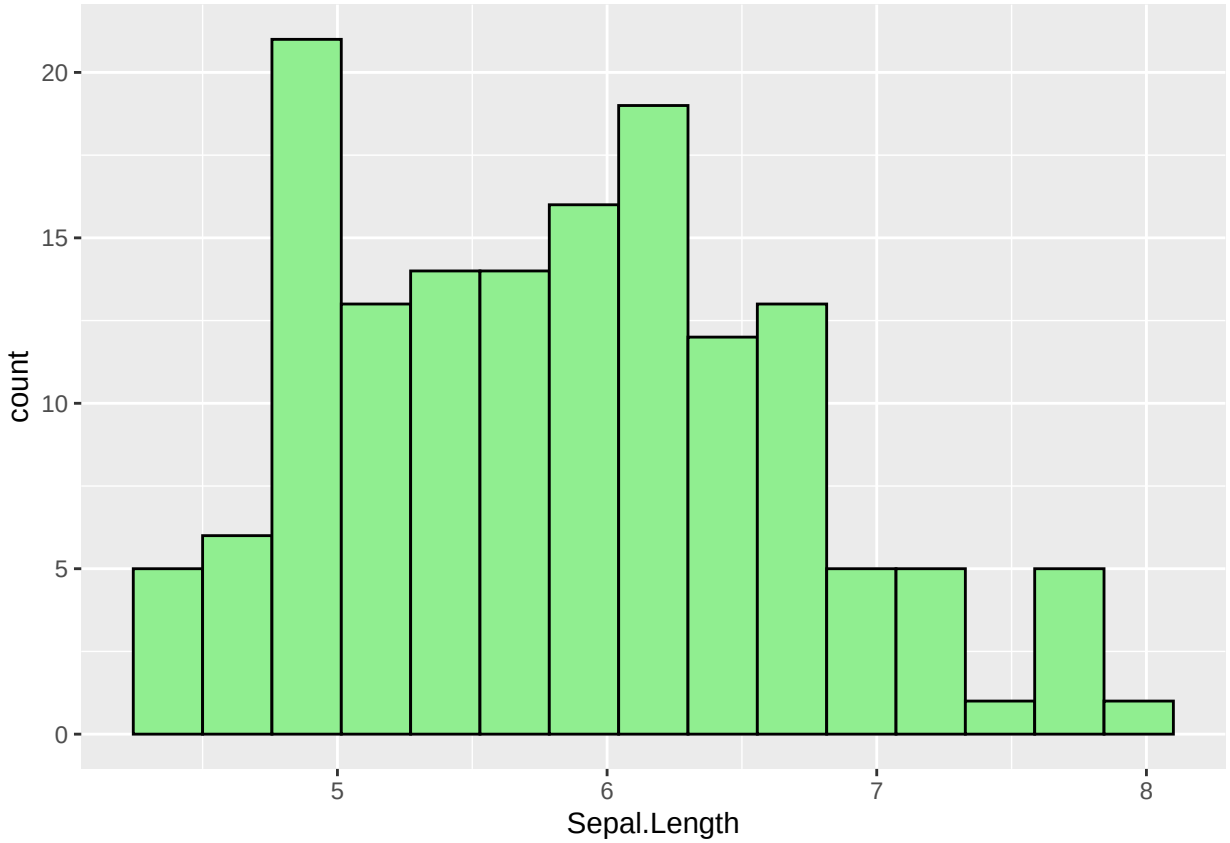


#Histogram

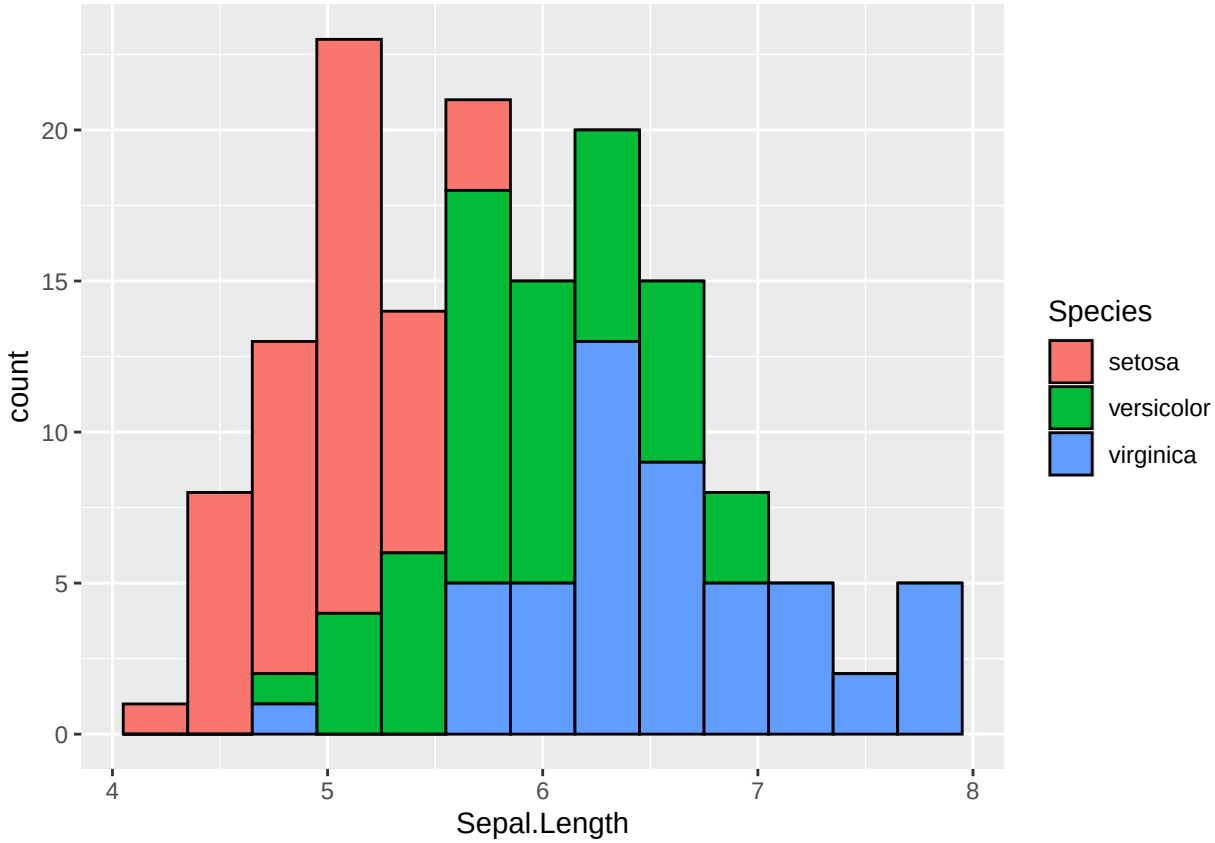
```
ggplot(data = iris, aes(x= Sepal.Length))+
  geom_histogram(binwidth =.3, fill= "lightgreen", col="black")
```



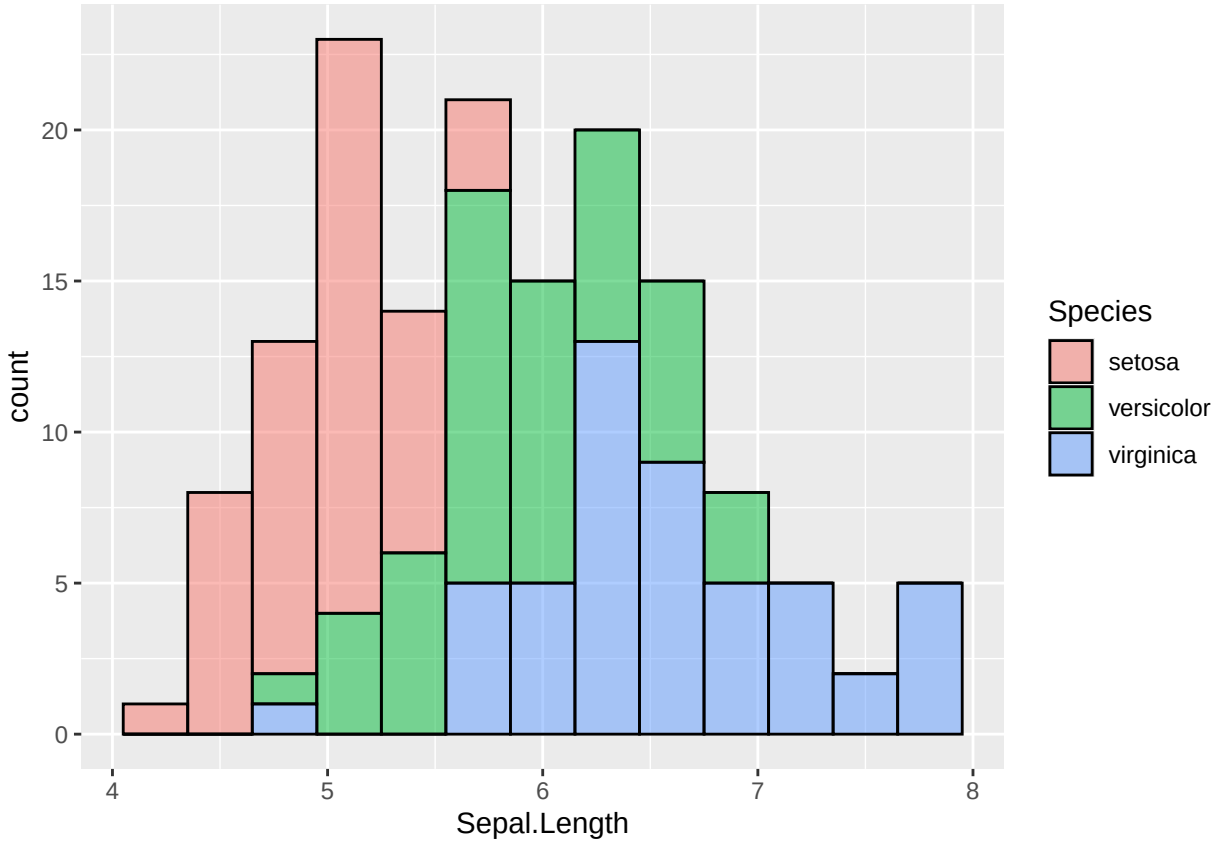

```
ggplot(data = iris, aes(x= Sepal.Length))+
  geom_histogram(bins =15, fill= "lightgreen", col="black")
```




```
ggplot(data = iris, aes(x= Sepal.Length,fill= Species))+
  geom_histogram(binwidth =.3,  col="black")
```




```
ggplot(data = iris, aes(x= Sepal.Length,fill= Species))+
  geom_histogram(binwidth =.3,  col="black", alpha= .5)
```


count
20
15
10
5
0
4
5
6
7
8
Sepal.Length
Species
setosa
versicolor
virginica