

iris flower classification

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Here we analyze the iris flower data set Load the data set

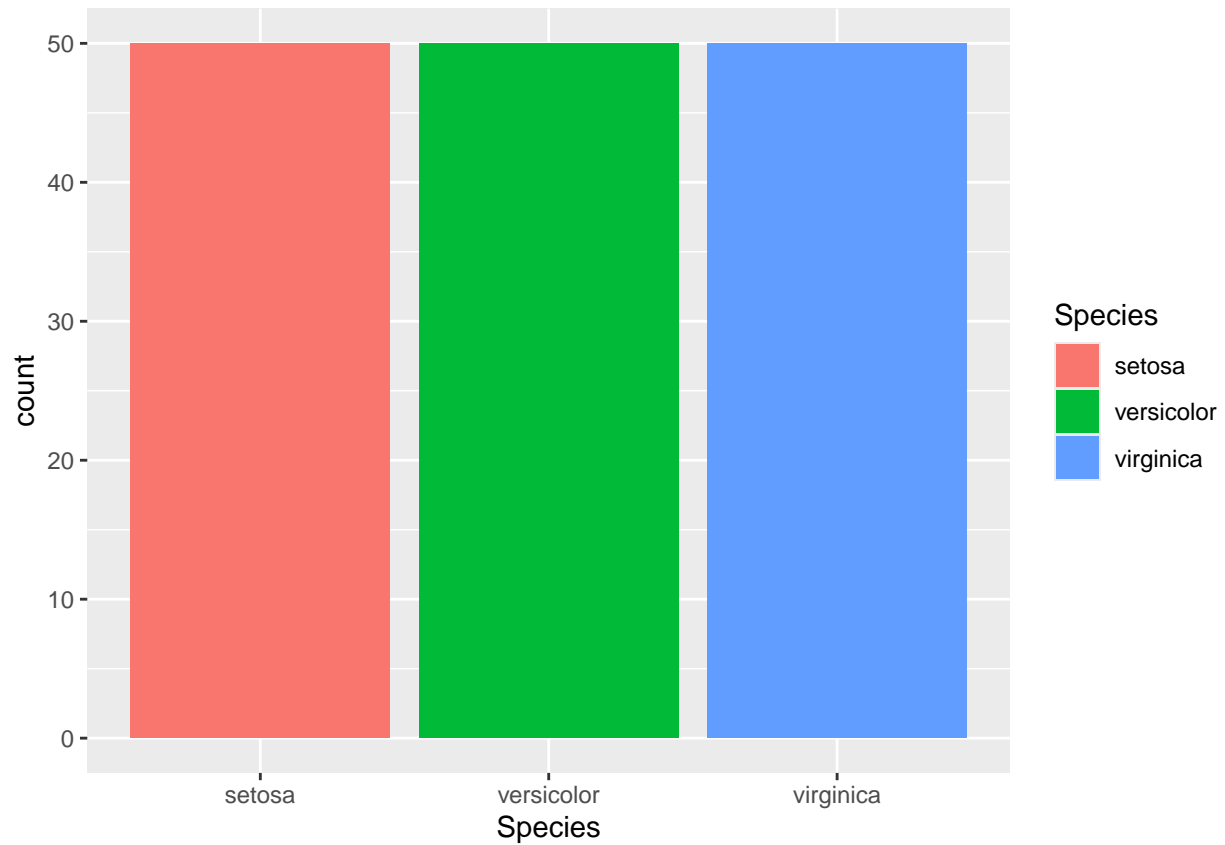
```
data("iris")
data1<- na.omit(iris)
head(data1)
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5.0	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa

Here we predict the flower species by given sepal length, sepal width, petal length and petal width. Thus we find relationship between these 4 parameters and species.

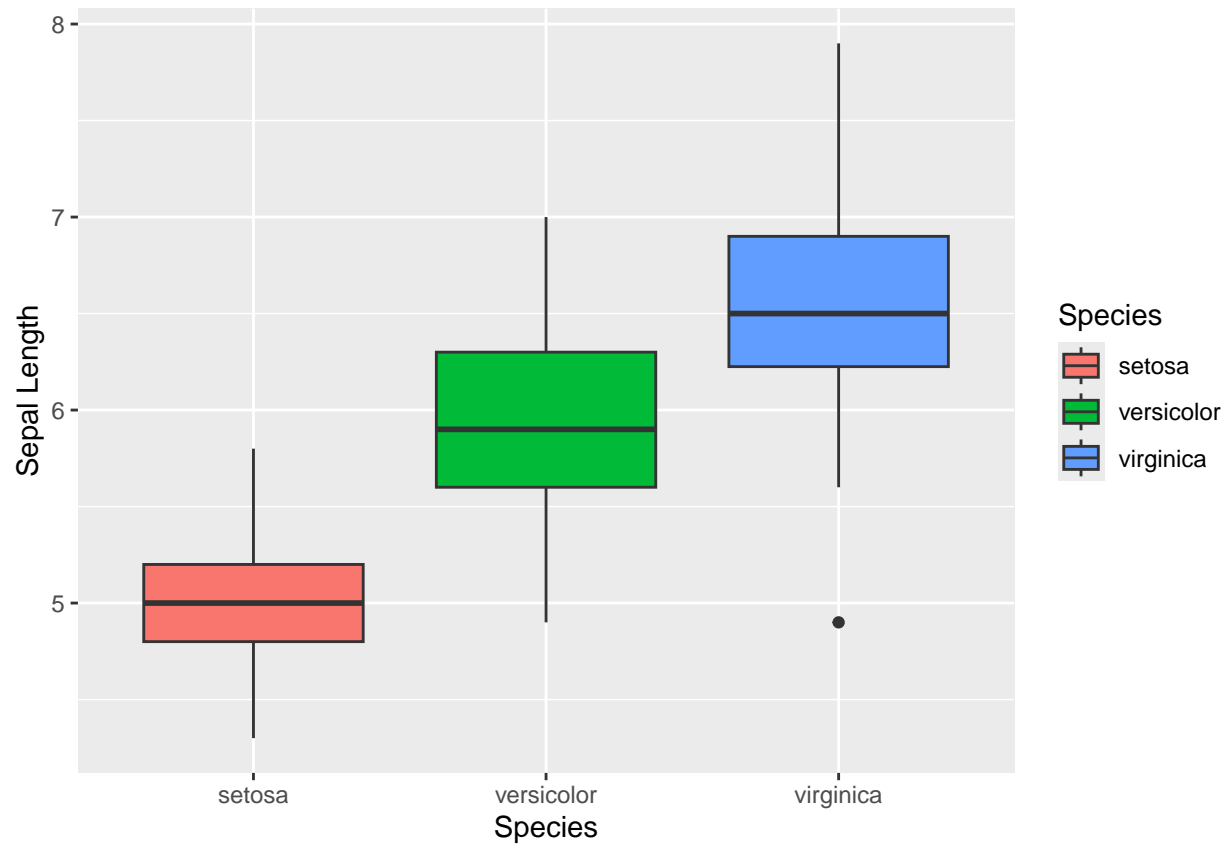
```
library(ggplot2)
```

```
plot1<-ggplot(data1,aes(x=Species,fill=Species))+geom_bar()
plot1
```

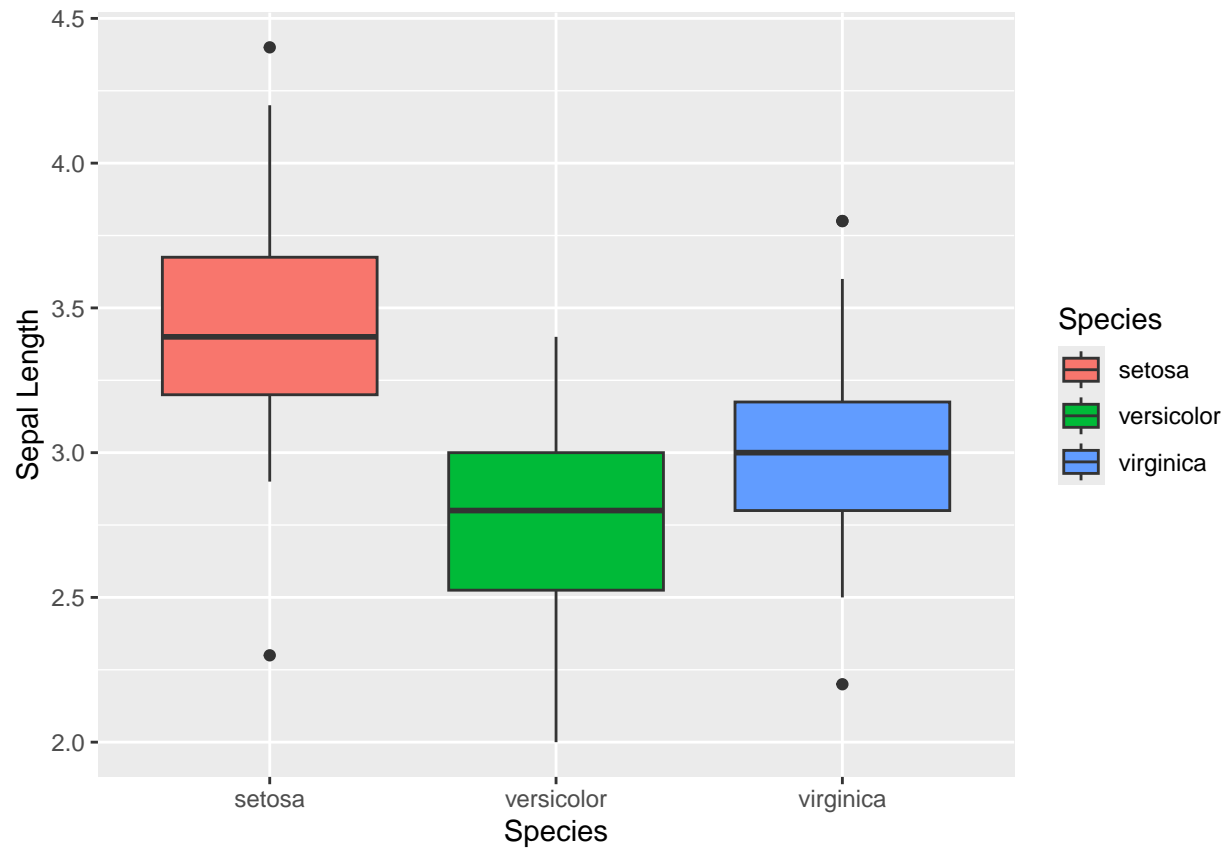


Consider about this plot we can see all the species are present same amount

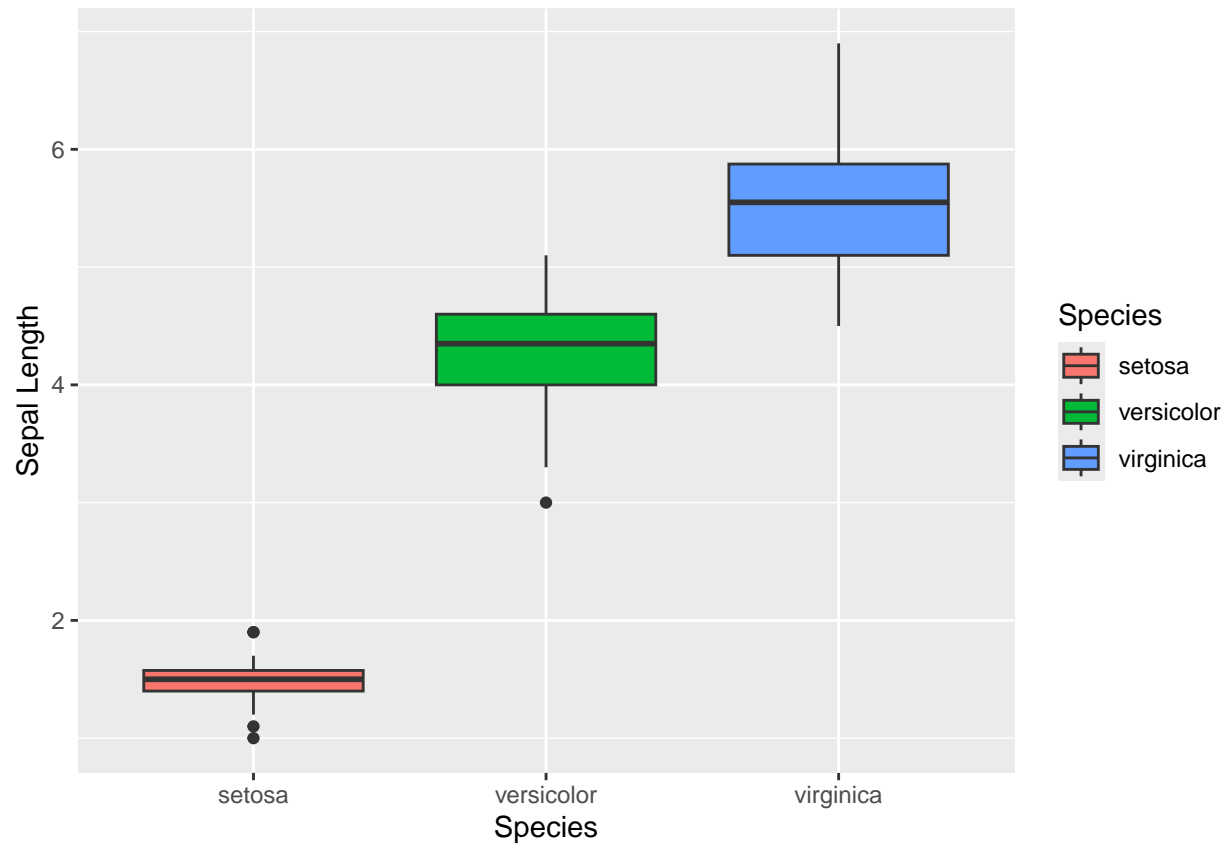
```
plot2<- ggplot(data1,aes(x=Species,y=Sepal.Length,fill=Species))+geom_boxplot()+labs(x="Species",y="Sepal.Length")
plot2
```



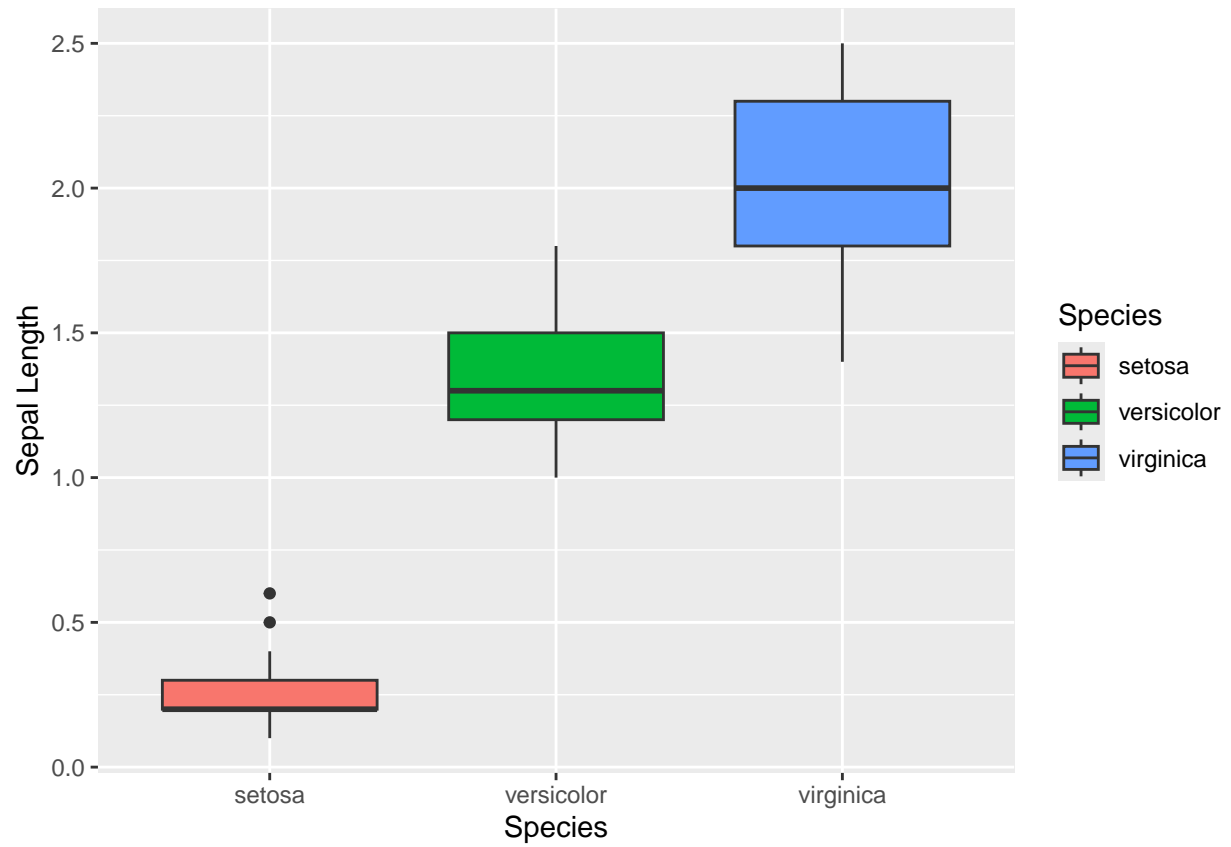
```
plot3<- ggplot(data1,aes(x=Species,y=Sepal.Width,fill=Species))+geom_boxplot()+labs(x="Species",y="Sepal.Width")
plot3
```



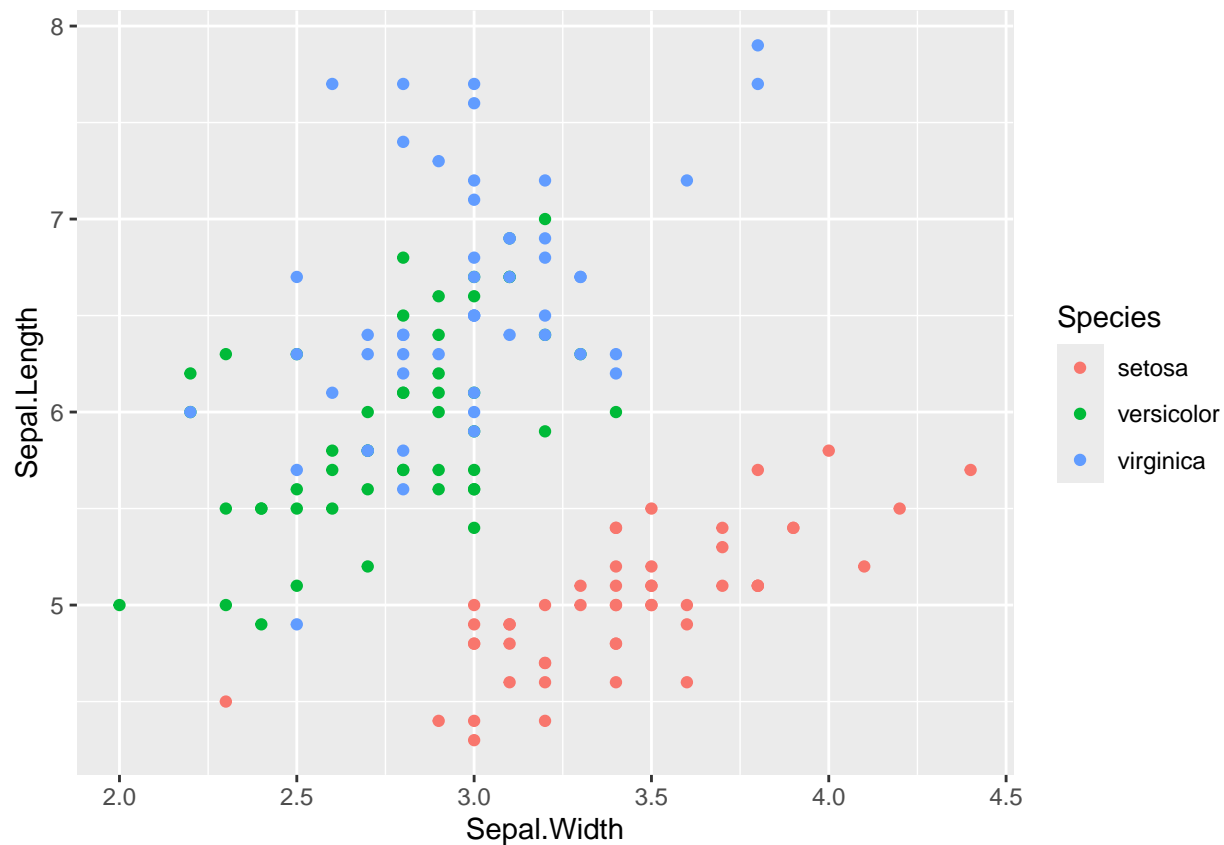
```
plot4<- ggplot(data1,aes(x=Species,y=data1$Petal.Length,fill=Species))+geom_boxplot()+labs(x="Species",  
plot4
```



```
plot5<- ggplot(data1,aes(x=Species,y=Petal.Width,fill=Species))+geom_boxplot()+labs(x="Species",y="Sepal Length")
plot5
```



```
plot6<- ggplot(data1,aes(x=Sepal.Width, y=Sepal.Length,color=Species))+geom_point()  
plot6
```



```
summary(data1)
```

```
##   Sepal.Length   Sepal.Width   Petal.Length   Petal.Width
##   Min.    :4.300   Min.    :2.000   Min.    :1.000   Min.    :0.100
##   1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
##   Median :5.800   Median :3.000   Median :4.350   Median :1.300
##   Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
##   3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
##   Max.    :7.900   Max.    :4.400   Max.    :6.900   Max.    :2.500
##      Species
##   setosa    :50
##   versicolor:50
##   virginica  :50
##
##
##
```