

## Creating Scatterplots and Boxplots in R

This tutorial will use the common Iris dataset that is included in R. We'll learn how to open the dataset, view the structure, view a summary of the data, and create visuals to understand the data.

### Step 1: Load the Iris Dataset

Iris is included in base R so there is no need to download it from another source.

```
3 #Step 1: Load the Iris dataset
4 data(iris)
```

The `'data()'` function will open the dataset in your workspace.

### Step 2: View the Iris Dataset

Examine the structure of the Iris dataset.

```
6 #Step 2: View the structure of the Iris dataset
7 str(iris)
```

The `'str()'` function will display information about the variables and their types. This is what will appear when you run the line:

```
> #Step 2: View the structure of the Iris dataset
> str(iris)
'data.frame': 150 obs. of 5 variables:
 $ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species : Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 1 1 1 1 1 ...
```

### Step 3: Summarize the Iris Dataset

Load the summary statistics for each variable of the dataset.

```
9 #Step 3: Display the summary statistics of the Iris dataset
10 summary(iris)
```

The `'summary()'` function will display the summary statistics of your variables. This includes information such as minimum and maximum, median, and mean. This is what will appear when you run the line:

```
> #Step 3: Display the summary statistics of the Iris dataset
> summary(iris)
```

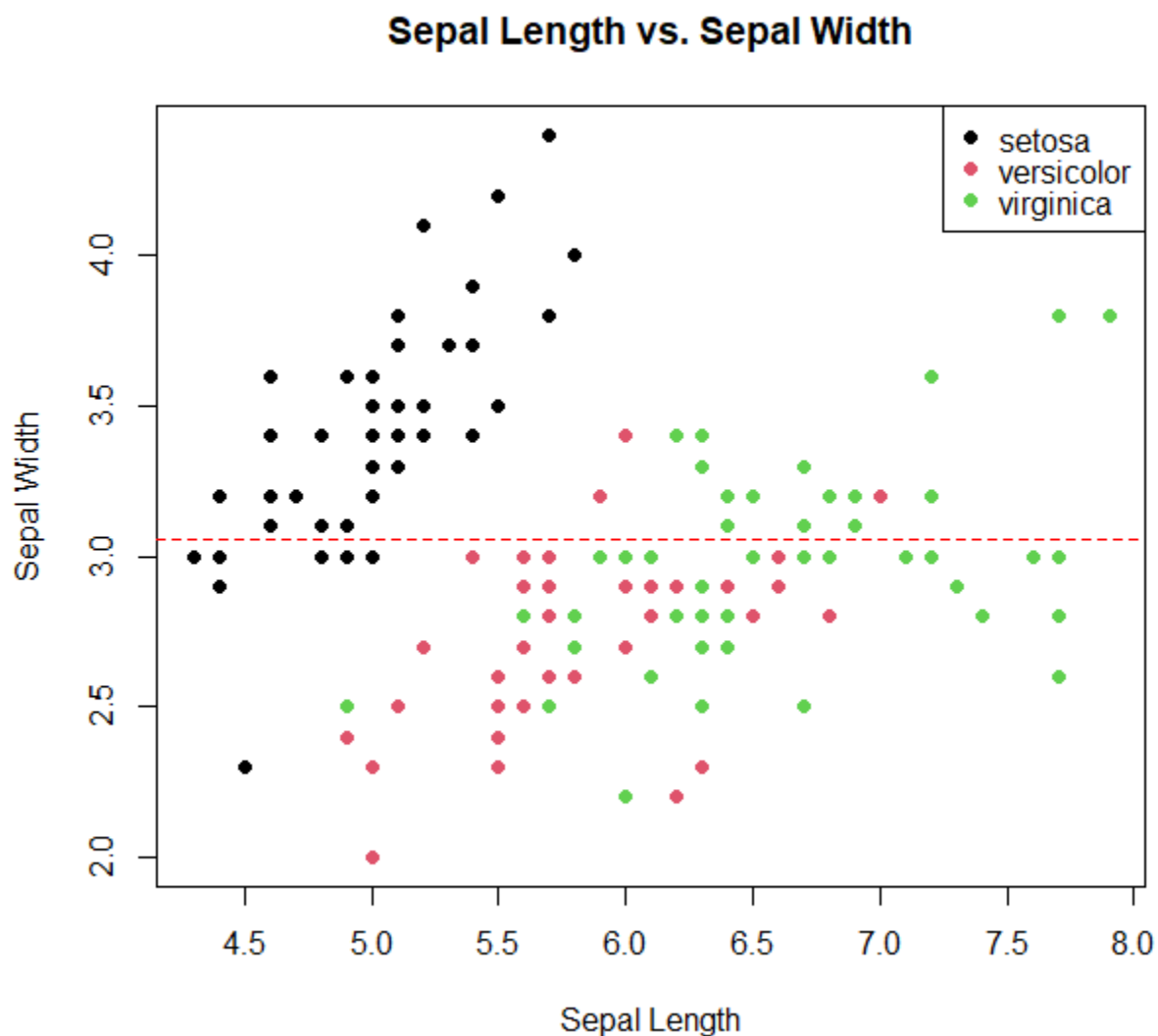
Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
Min. :4.300	Min. :2.000	Min. :1.000	Min. :0.100	setosa :50
1st Qu.:5.100	1st Qu.:2.800	1st Qu.:1.600	1st Qu.:0.300	versicolor:50
Median :5.800	Median :3.000	Median :4.350	Median :1.300	virginica :50
Mean :5.843	Mean :3.057	Mean :3.758	Mean :1.199	
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	

#### Step 4: Visualize the Data with a Scatterplot

This scatterplot will create a visualization of the relationship between sepal length and sepal width for the three species in the dataset.

```
12 #Step 4: Create a scatterplot comparing Sepal Width and Length
13 plot(iris$Sepal.Length, iris$Sepal.Width, pch = 19, col = iris$Species,
14      main = "Sepal Length vs. Sepal Width", xlab = "Sepal Length", ylab = "Sepal width")
15 legend("topright", legend = levels(iris$Species), col = 1:3, pch = 19)
16 abline(h = mean(iris$Sepal.Width), col = "red", lty = 2)
```

The `plot()` function creates a scatter plot using Sepal Length and Sepal Width variables. `pch = 19` sets the point character and `col` will differentiate the points by species. The `legend()` function will add a legend to the plot. `abline()` can be used to add a horizontal line at the mean of Sepal Width. This is how the plot should look:



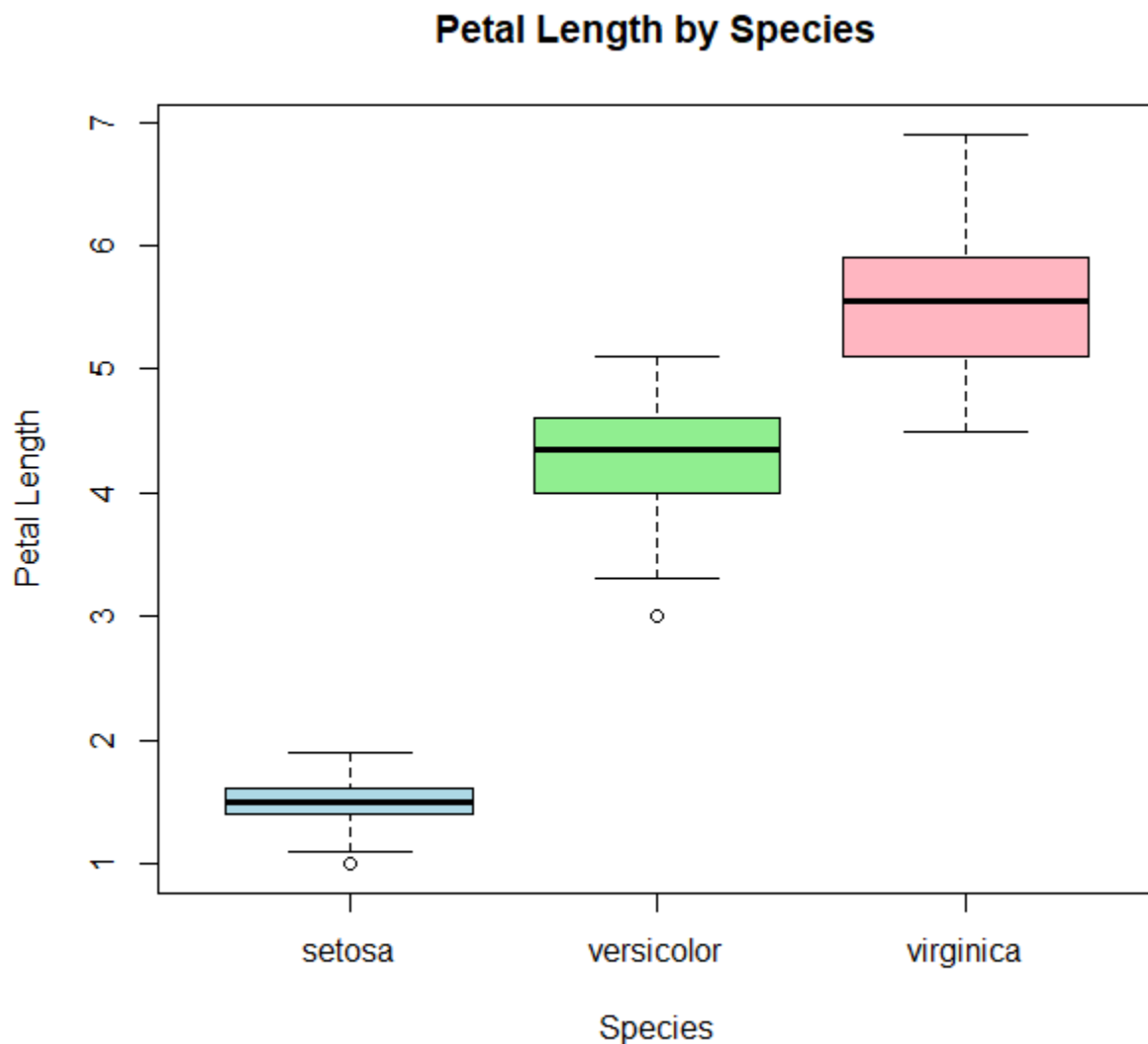
## Step 5: Visualize the Data with a Boxplot

This boxplot will create a visual distribution of the petal lengths for each species.

```
18 #Step 5: Create a boxplot to compare Petal Lengths
19 boxplot(Petal.Length ~ Species, data = iris,
20         main = "Petal Length by Species",
21         xlab = "Species", ylab = "Petal Length",
22         col = c("lightblue", "light green", "light pink"))
```

The `'boxplot()'` function generates a boxplot using the provided variables.

`'iris$Petal.Length ~ iris$Species'` specifies that the variable being plotted against species will be petal length. `'main'`, `'xlab'`, and `'ylab'` specify the titles and axis labels for the graph. `'col'` selects a color for the box plot of each species. Here is how the graph will look:



**References:**

- Example Tutorial: [http://betsymccall.net/edu/CDSE/coding/R/bar\\_graphs.pdf](http://betsymccall.net/edu/CDSE/coding/R/bar_graphs.pdf)
- RDocumentation: <https://www.rdocumentation.org/>