



UNIVERSITÄT  
LEIPZIG

**Data Visualisation**  
BIOSTATISTICS FOR BEGINNERS  
-  
BASIC STATISTICS FOR BIOLOGISTS

**Erik Kusch**  
*PhD Student*  
Aarhus University  
Department of Bioscience  
Section for Ecoinformatics & Biodiversity  
Center for Biodiversity and Dynamics in a Changing World (BIOCHANGE)  
Ny Munkegade 116, Building 1540  
8000 Aarhus  
Denmark  
email: erik@i-solution.de

## Summary:

These are the solutions to the exercises contained within the handout to “Data Visualisation” which walks you through the basics of data visualisation in R using `ggplot2`. The plots presented here are using data from the `iris` data set supplied through the `datasets` package.

Keep in mind that there is probably a myriad of other ways to reach the same conclusions as presented in these solutions.

## Contents

1	Packages	2
2	Loading R-internal data sets ( <code>iris</code> )	2
3	Inspect the data set	2
4	Boxplot of <code>Petal.Length</code> by Species	3
5	Scatterplot of <code>Petal.Length</code> and <code>Petal.Width</code>	4
6	Scatterplot of <code>Petal.Length</code> and <code>Petal.Width</code> grouped by Species	4
7	Relationship of <code>Sepal.Length</code> and <code>Sepal.Width</code>	5
8	Relationship of <code>Sepal.Length</code> and <code>Sepal.Width</code> (grouped by Species)	5

# 1. Packages

Recall the exercise that went along with the last seminar (Descriptive Statistics) where we learnt the difference between a basic and advanced preamble for package loading in R. Here (and in future exercises) I will only supply you with the advanced version of the preamble.

Now let's load the `ggplot2` package into our R session so we'll be able to use its functionality for data visualisation as well as the `datasets` package to get the `iris` data set.

```
# function to load packages and install them if they haven't been installed yet
install.load.package <- function(x) {
  if (!require(x, character.only = TRUE))
    install.packages(x)
  require(x, character.only = TRUE)
}
# packages to load/install if necessary
package_vec <- c("ggplot2", "datasets")
# applying function install.load.package to all packages specified in package_vec
sapply(package_vec, install.load.package)

## ggplot2 datasets
##      TRUE      TRUE
```

## 2. Loading R-internal data sets (iris)

The `iris` data set is included in the `datasets` package in R. An R-internal data set is loaded through the command `data()`. Take note that you do not have to assign this command's output to a new object (via `<-`). Instead, the dataset is loaded to your current environment by its name (`iris`, in this case). Keep in mind that this **can override** objects of the same name that are already present in your current session of R.

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

## 3. Inspect the data set

Since we know that `iris` is a dataset, we can be reasonably sure that this object will be complex enough to warrant using the `str()` function for inspection:

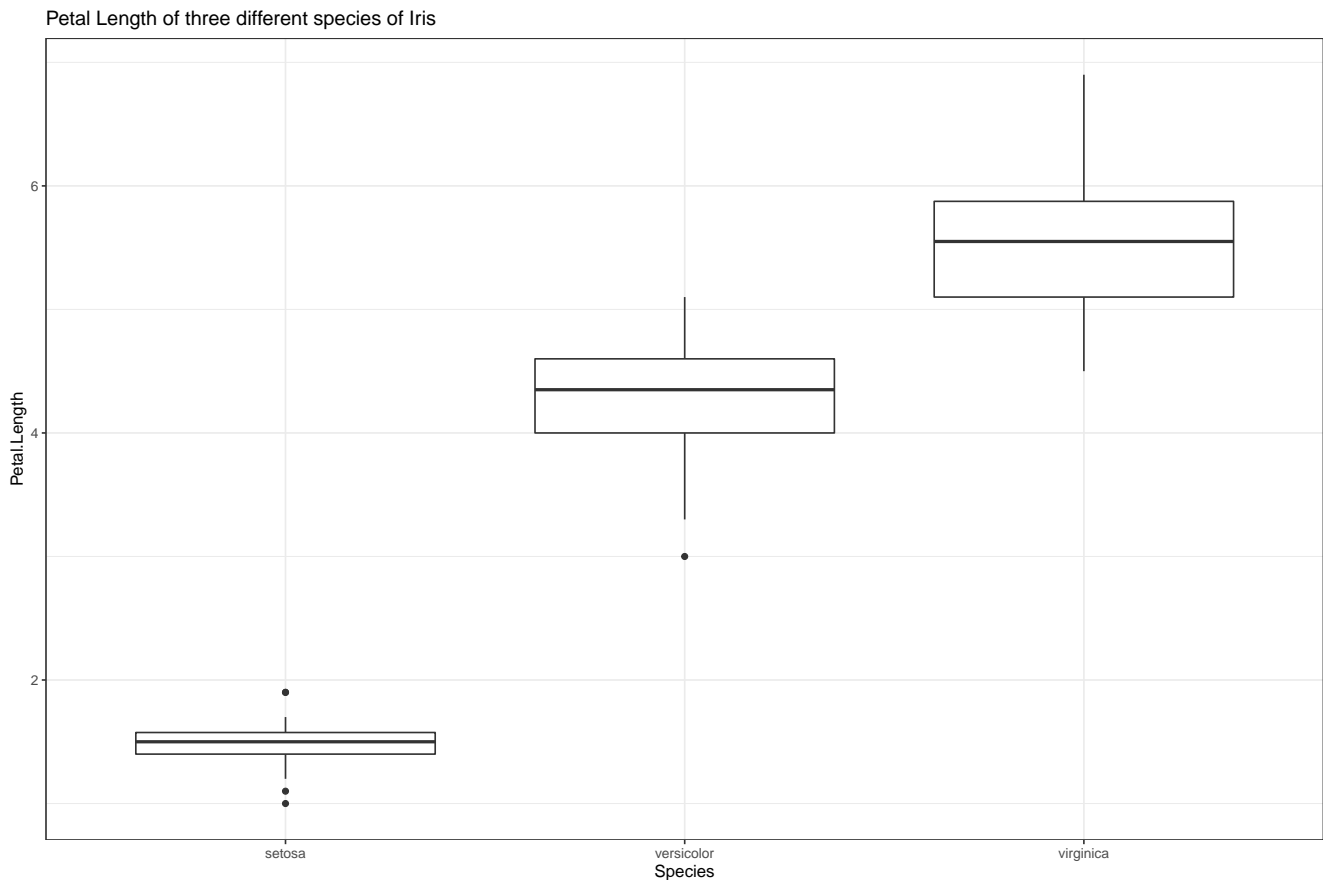
```
str(iris)

## '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 ...
```

The `iris` dataset contains four measurements (`Sepal.Length`, `Sepal.Width`, `Petal.Length`, `Petal.Width`) for 150 flowers representing three species of iris (*Iris setosa*, *versicolor* and *virginica*).

## 4. Boxplot of Petal.Length by Species

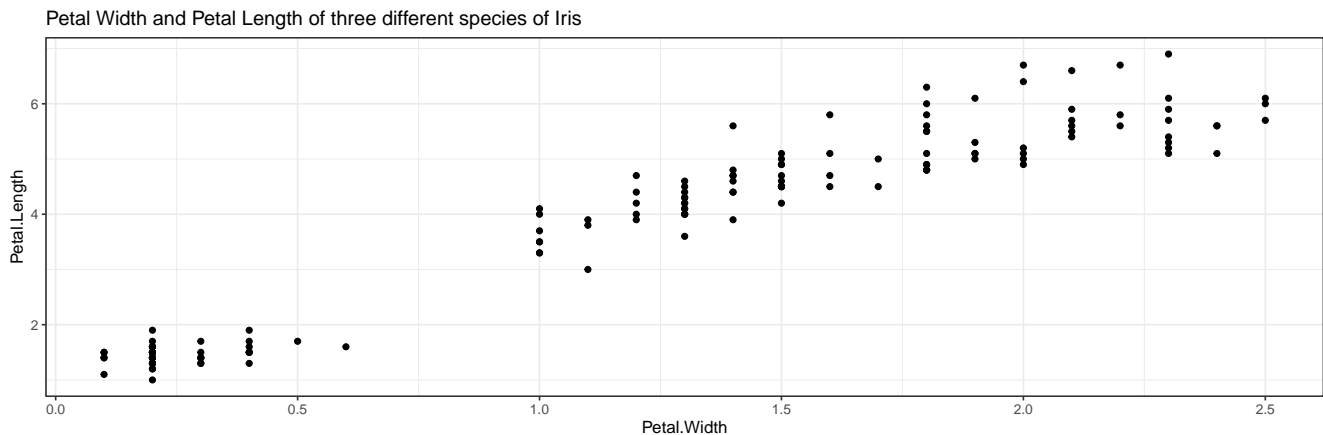
```
ggplot(iris, # the data set
  aes(x=Species, y=Petal.Length) # aesthetics
) + geom_boxplot() + # this is the end of the bare minimum plot
theme_bw() + labs(title="Petal Length of three different species of Iris")
```



This boxplot shows us exactly how the distributions of petal length measurements of our three species of Iris are differing from one another. Despite the obvious trend in the data, **be sure not to report results through figures alone!** We will find out how to test whether the pattern we can observe here holds up to scrutiny at a later point in time of our seminars.

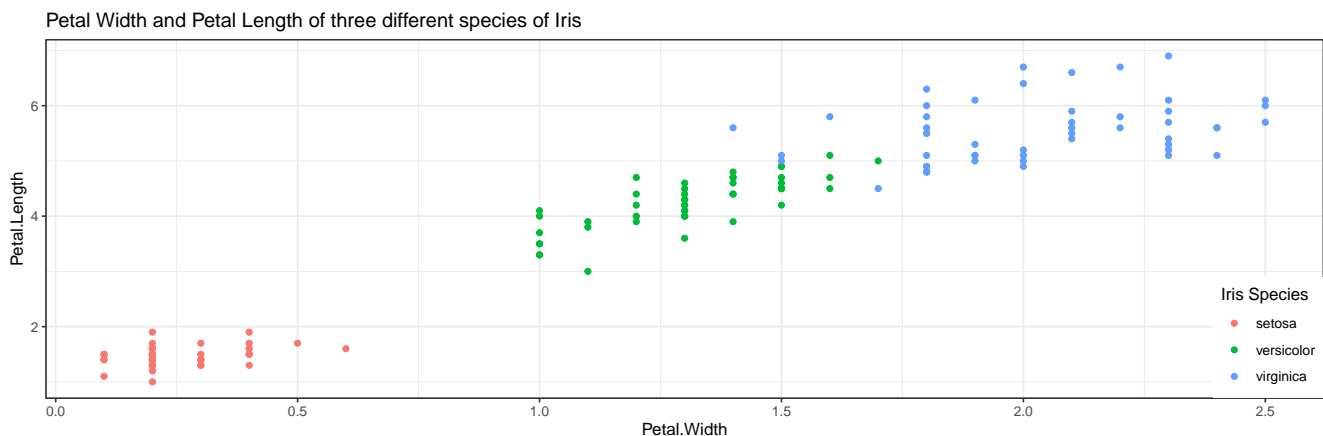
## 5. Scatterplot of Petal.Length and Petal.Width

```
ggplot(iris, # the data set
      aes(x=Petal.Width, y=Petal.Length) # aesthetics
    ) + geom_point() + # this is the end of the bare minimum plot
    theme_bw() + labs(title="Petal Width and Petal Length of three different species of Iris")
```



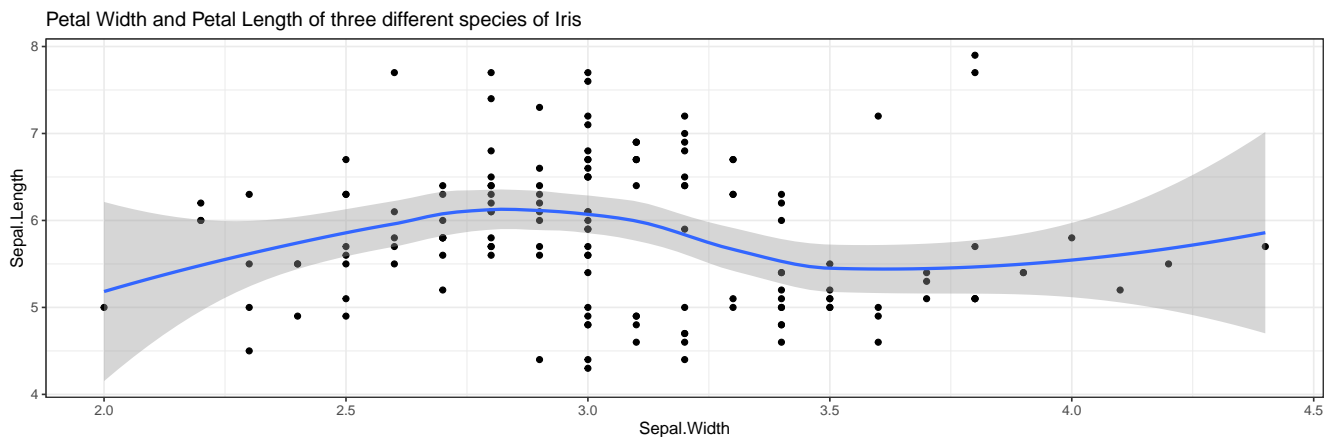
## 6. Scatterplot of Petal.Length and Petal.Width grouped by Species

```
ggplot(iris, # the data set
      aes(x=Petal.Width, y=Petal.Length, colour = Species) # aesthetics
    ) + geom_point() + # this is the end of the bare minimum plot
    theme_bw() + labs(title="Petal Width and Petal Length of three different species of Iris") +
    theme(legend.justification=c(1,0), legend.position=c(1,0)) + # legend inside
    scale_color_discrete(name="Iris Species") # Change legend title
```



## 7. Relationship of Sepal.Length and Sepal.Width

```
ggplot(iris, # the data set
  aes(x=Sepal.Width, y=Sepal.Length) # aesthetics
) + geom_point() + geom_smooth() + # this is the end of the bare minimum plot
theme_bw() + labs(title="Petal Width and Petal Length of three different species of Iris")
```



## 8. Relationship of Sepal.Length and Sepal.Width (grouped by Species)

```
ggplot(iris, # the data set
  aes(x=Sepal.Width, y=Sepal.Length, colour = Species) # aesthetics
) + geom_point() + geom_smooth() + # this is the end of the bare minimum plot
theme_bw() + labs(title="Petal Width and Petal Length of three different species of Iris") +
theme(legend.justification=c(1,0), legend.position=c(1,0)) + # legend inside
scale_color_discrete(name="Iris Species") # Change legend title
```

