2021 Seminar for Final Year Students

Data Analysis and Reporting

Olakunle Joshua (olakunle4impact@yahoo.com (mailto:olakunle4impact@yahoo.com))

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SEMINAR OUTLINE

- Data Analysis Overview
- Introduction to R Studio
- Statistics, Data and Variable
- Analysis and Reporting with R
- Visualization Techniques with R
- Conclusion

Data Analysis Overview

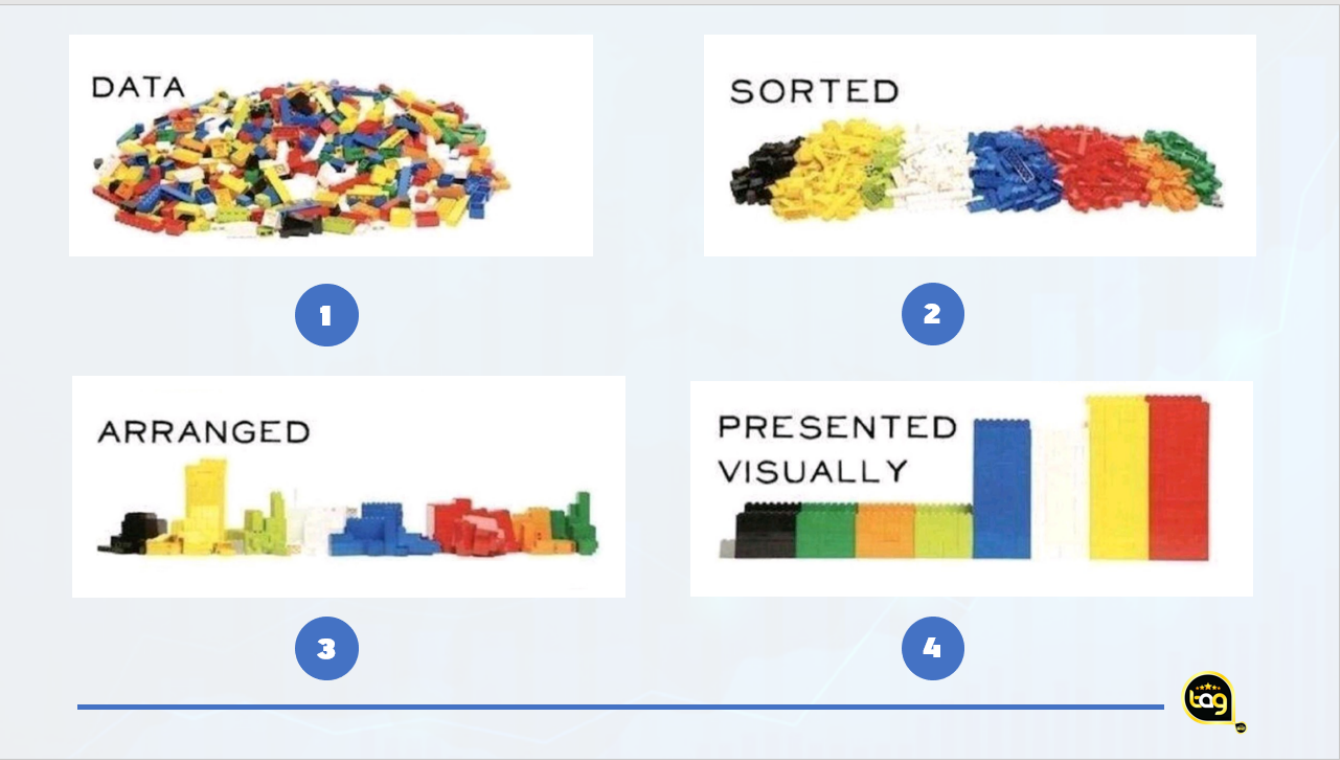


Figure 1: Simple Analogy to describe Data Analysis

The above figure has completely simplified the task we have for today. Looking at the figure very well, we will notice that everything revolves round the very important word that we will first consider in today's seminar. The word **DATA**.

- **Defining a Data**

Data is a common word for every analyst but what exactly does it mean. It is a **collection of facts**, such as numbers, words, measurements, observations or just descriptions of things.

- **Data Collection**

Getting some of these information has become easy in our modern world with the advent of smartphones and computers that has ability to do myriads of things such as gathering data on emails, sales, heartbeat, distance covered, tree heights etc

- **What then is Data Analysis?**

With respect to the figure above, **data analytics** is the analysis of data, whether huge or small, in order to understand it and see how to use the knowledge hidden within it.

Data analysis is a *process* of inspecting, cleansing, transforming, and modeling data with the goal of discovering useful information, informing conclusions, and supporting decision-making.

A simple example I used often in most of my trainings is on recorded information on the depth of a river and the possible knowledge to derive from it for swimmers.

Another example is what happens when we study. Consciously or unconsciously, we feed our system with data, that is the content of any materials or textbooks we are reading at that moment and by default our brain process this information, refine and it gradually begin to guide our actions and decisions.

In the next topic, we will learn more on R Studio, how to generate random data in R and finally, how to import and export data in R. Let's go friends.

Introduction to R Studio

There are many data analysis tools that can be used in analysing data with the aim of deriving useful insight from it. Some of which are: SPSS, Excel, EasyFit, Stata, PSPP, Octave, Matlab, Minitab, Statistica, SAS, Tableau, Python etc.

For the purpose of this seminar, we will be sticking close to the use of R programming software. This is because of the following advantages;

- Flexible, easy to learn and friendly graphical capabilities.
- Effective data storage facilities.
- Large number of free packages available for data analysis. We can also build ours.
- Provides all the capabilities of a programming language.
- Supports getting data from different types of sources.
- Interesting of all, it is **FREE**. Isn't this amazing?

R Studio is an Integrated Development Environment **(IDE)** for the base R. Let us have a look at a typical R Studio environment as shown below;

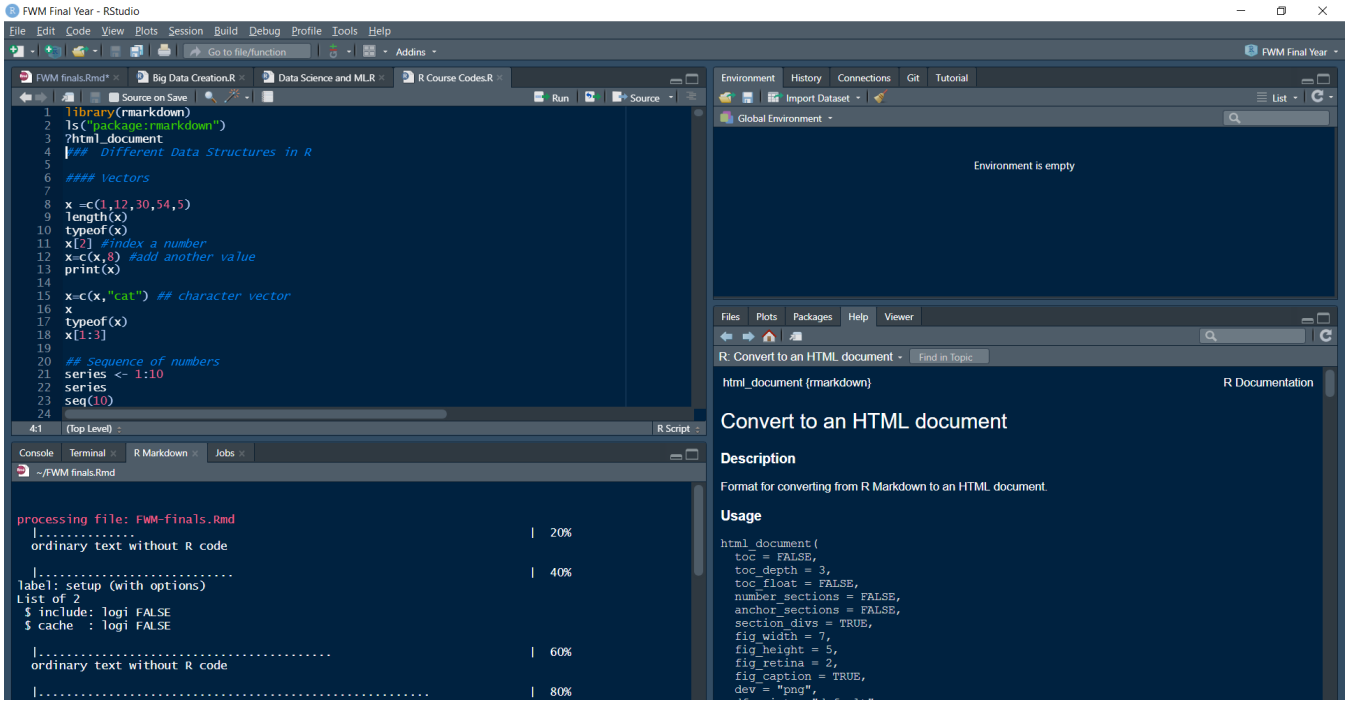


Figure 2: A Typical R Studio Environment

It is very important I talk on the concept of appearance as evident in the background colour I used in Figure 2 which is far different from the default white background colour on your system as a new R User. With some few tricks around the tools, this can be easily changed to your desired colour.

The environment is such a friendly one with a default three (3) panes when the software is first opened. The last pane, most times the editor pane where you write your codes and comments can be created using the file option on the menu bar. We will dwell more on this extensively when we get to session of data analysis with R by God's grace.

Installing R

R is freely available for all the major computing platforms such as macOS, Windows and LINUX.

Base R

- Visit the official R site at https://cran.r-project.org (https://cran.r-project.org)
- Select the operating system of your choice and then click on the download tab
- Run the installer and follow the instructions to successfully install the software.

After you successfully install the software, you should see something like what we have in the figure below;

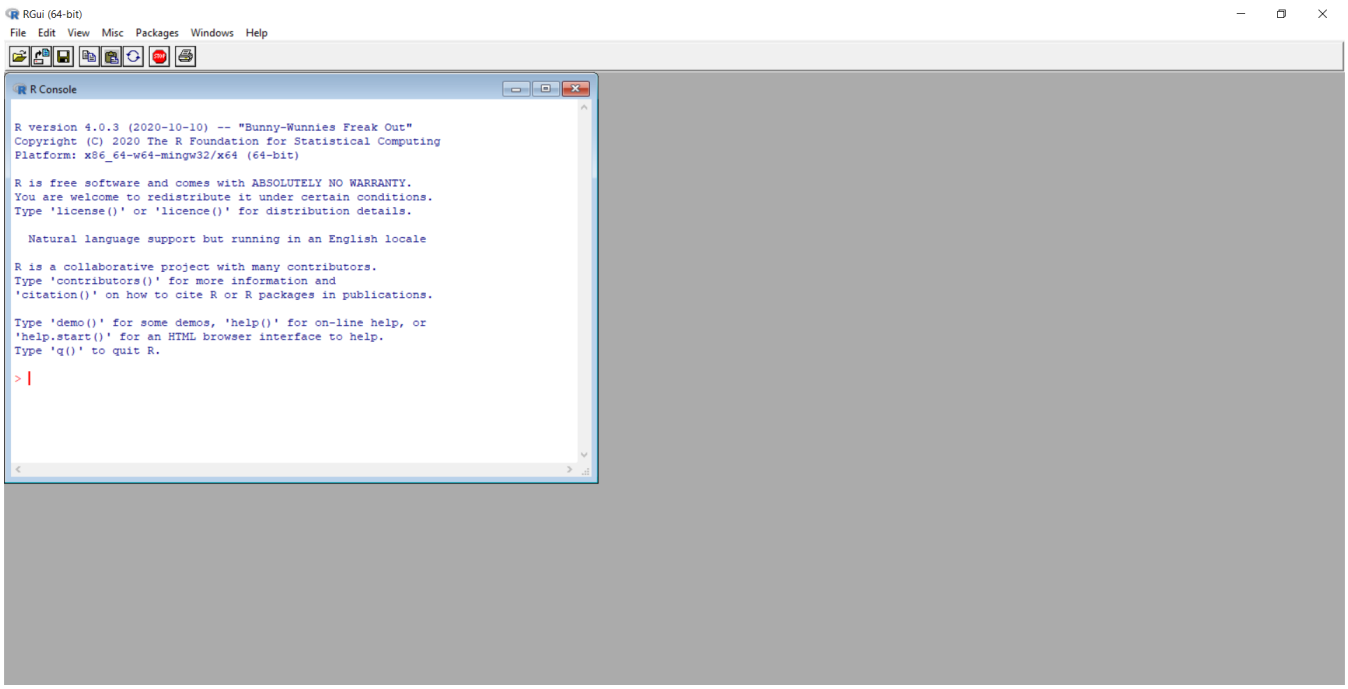


Figure 3: A Typical R Environment

NOTE: The base R is required for R studio to function effectively.

R Studio

- Visit the official R Studio website at https://rstudio.com (https://rstudio.com)
- Click the product option
- Select your server version or desktop version
- Select your OS and click on the download button
- Run the installer and follow the instruction

NOTE: If the base R is not first installed, you might be directed to a website to do this before the R Studio can work effectively.

Statistics, Data and Variable

- **Statistics**

Statistics is the practice of turning data into information to identify trends and understand features of populations. One of the most important keywords from the definition above is **Data** and **Information**.

This can be best seen with the concept of **Input** (raw) and **Output** (refined). The first thing every statistical analyst will always face in the course of performing data analysis is dealing with **raw data** - in other words, the records or observations that make up a sample. These data could be stored in a specialized **R object**.

- **Data**

At this section, we will look more into R Objects.

- **Data Types in R**

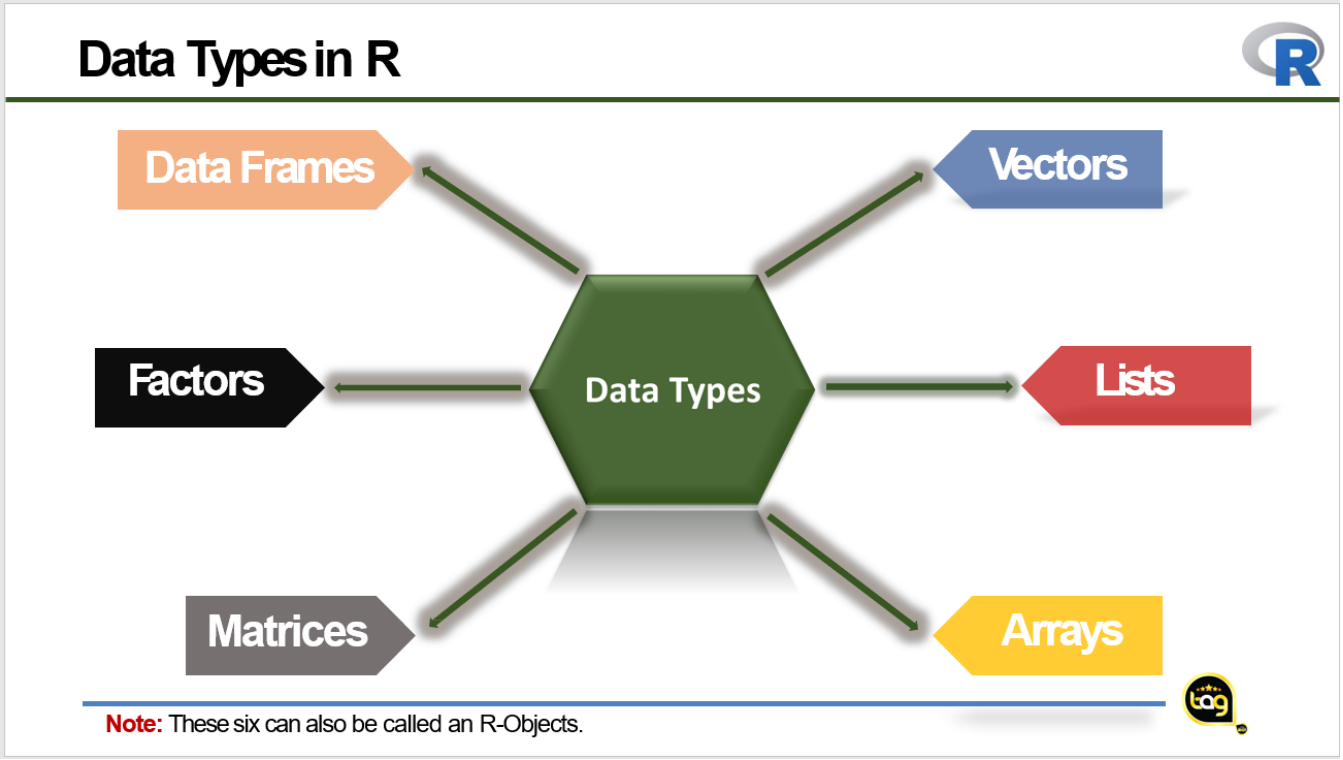


Figure 4: Data Types in R

- **Vector**

A vector is a sequence of data elements of the same basic type. When you want to create vector with more than one element, you should use **c()** function which means to **combine** the elements into a vector.

```
v <- c(1,2,3) # Hit the run button to the line of code or press Ctrl + Enter
print(v)
```

```
[1] 1 2 3
```

```
class(v)
```

```
[1] "numeric"
```

```
ba <- c("FWM","AQFM","WMA")
print(ba)
```

```
[1] "FWM"  "AQFM" "WMA"
```

```
class(ba)
```

```
[1] "character"
```

Basic Interpretation of information on the environment and console panes

```
## The concept of indexing
ba[2]
```

```
[1] "AQFM"
```

```
v[3]
```

```
[1] 3
```

```
## The > sign on the console means R is ready for a new command.
## If it shows a + plus sign, it means the code is incomplete.

## The concept of replacement
ba[2] <- "EMT"
v[3] <- 5

print(ba)
```

```
[1] "FWM" "EMT" "WMA"
```

```
print(v)
```

```
[1] 1 2 5
```

```
## The concept of continuous replacement
v[1:2]
```

```
[1] 1 2
```

```
## Boolean or Logical Masking using comparison operators
v <- c(100,200,300,400)
v[v>200]
```

```
[1] 300 400
```

```
v[v>=200]
```

```
[1] 200 300 400
```

```
v[v<200]
```

```
[1] 100
```

```
v[v<=200]
```

```
[1] 100 200
```

```
my.true <- v>=300
v[my.true] ## It means from v, index out the true values of the object my.true. This is more like filtering
```

```
[1] 300 400
```

```
## The concept of sorting
basal_area <- c(30,25,12,37,40)
sorted_ba <- sort(basal_area)
print(sorted_ba)
```

```
[1] 12 25 30 37 40
```

```
desc_ba <- sort(basal_area, decreasing = TRUE )
print(desc_ba)
```

```
[1] 40 37 30 25 12
```

```
## Adding another value
basal_area <- c(basal_area, c(30,24,30))
print(basal_area)
```

```
[1] 30 25 12 37 40 30 24 30
```

```
## Inbuilt function
length(basal_area)
```

```
[1] 8
```

```
typeof(basal_area)
```

```
[1] "double"
```

```
## The concept of sequencing
bl <- seq(5,7, by = 0.4)
print(bl)
```

```
[1] 5.0 5.4 5.8 6.2 6.6 7.0
```

```
## Coercing a vector into different data types
vt <- c(basal_area, "ba")
print(vt)
```

```
[1] "30" "25" "12" "37" "40" "30" "24" "30" "ba"
```

```
length(vt)
```

```
[1] 9
```

```
class(vt)
```

```
[1] "character"
```

```
vt <- vt[-6]
print(vt)
```

```
[1] "30" "25" "12" "37" "40" "24" "30" "ba"
```

```
class(vt)
```

```
[1] "character"
```

```
vt <- vt[-8]
print(vt)
```

```
[1] "30" "25" "12" "37" "40" "24" "30"
```

```
length(vt)
```

```
[1] 7
```

```
class(vt)
```

```
[1] "character"
```

```
vt <- as.numeric(vt)
length(vt)
```

```
[1] 7
```

```
class(vt)
```

```
[1] "numeric"
```

The simplest of the R-objects is the **vector object** and there are six data types of these atomic vectors, also termed as **six classes of vectors**. The other R-Objects are built upon the atomic vectors.

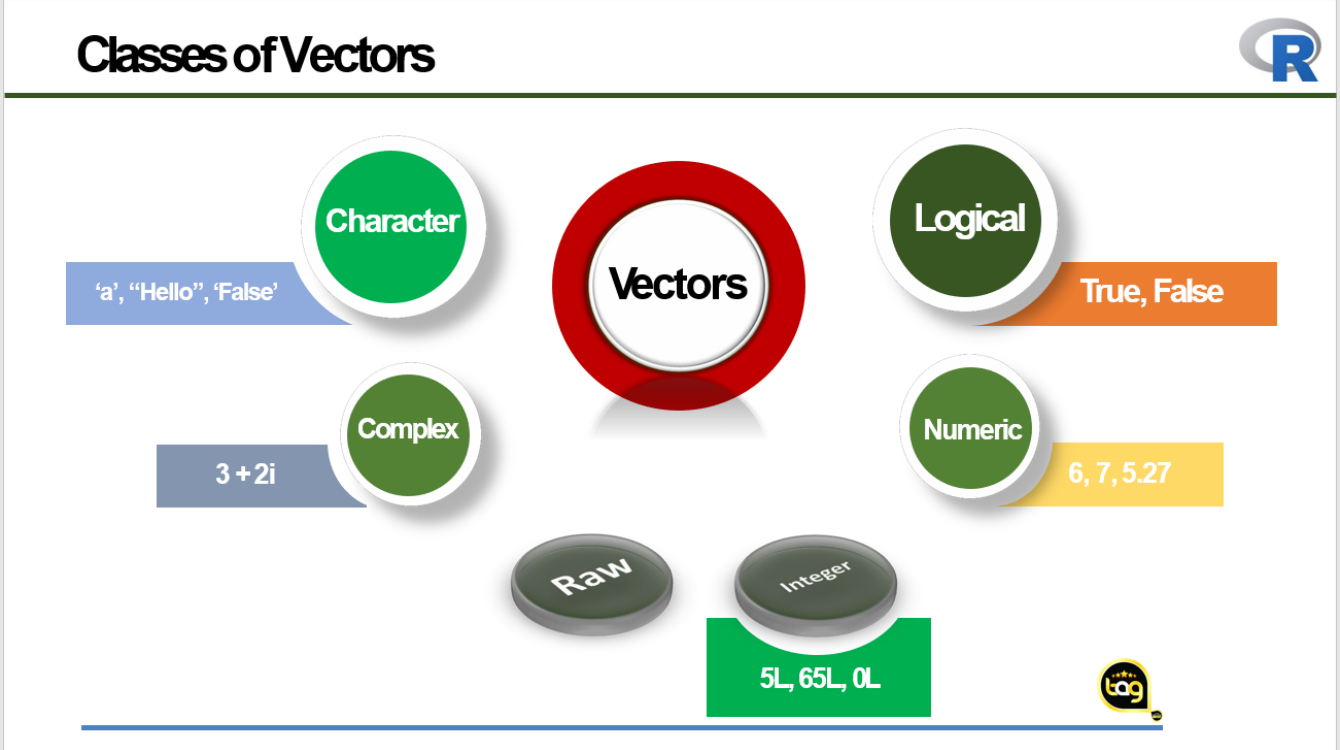


Figure 5: Six classes of vectors

- **List**

A list is an R-object which can contain many different types of elements inside it like vectors, string, numbers, functions and even another list inside it.

```
l <- list(2,"FWM",2+5i,FALSE,5)
print(l)
```

```
[[1]]
[1] 2

[[2]]
[1] "FWM"

[[3]]
[1] 2+5i

[[4]]
[1] FALSE

[[5]]
[1] 5
```

```
class(l)
```

```
[1] "list"
```

```
l2 <- list(1,2,"FUNAAB")
class(l2)
```

```
[1] "list"
```

```
l3 <- c(l,l2)
print(l3)
```

```
[[1]]
[1] 2

[[2]]
[1] "FWM"

[[3]]
[1] 2+5i

[[4]]
[1] FALSE

[[5]]
[1] 5

[[6]]
[1] 1

[[7]]
[1] 2

[[8]]
[1] "FUNAAB"
```

```
class(l3)
```

```
[1] "list"
```

```
l3[4]
```

```
[[1]]
[1] FALSE
```

- **Arrays**

An arrays are the R Data Objects which can store data in more than two dimensions. It takes vectors as input and uses the value in the dim parameter to create an array.

```
a<-array(c(2,3,1),dim=c(2,3,3)) ## Row, column and frequency
print(a)
```

```
, , 1

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 2

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 3

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1
```

Let us modify the code a little as shown below;

```
a<-array(c(2,3,1),dim=c(2,3,3,2))
class(a)
```

```
[1] "array"
```

```
print(a)
```

```
, , 1, 1

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 2, 1

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 3, 1

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 1, 2

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 2, 2

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 3, 2

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1
```

```
## Compare the above with this code below
a<-array(c(2,3,1),dim=c(2,3,6))
print(a)
```

```
, , 1

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 2

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 3

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 4

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 5

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1

, , 6

     [,1] [,2] [,3]
[1,]    2    1    3
[2,]    3    2    1
```

- **Matrices**

They are similar to an array but only store data in two dimensions. Let us take a look at some brief examples.

```
vtr<-c(1,2,3)
vtr1<-c(4,5,6)
mtr<-matrix(c(vtr,vtr1),3,3)
print(mtr)
```

```
     [,1] [,2] [,3]
[1,]    1    4    1
[2,]    2    5    2
[3,]    3    6    3
```

```
volume <- c(12,15,10,11,13,12)
cv <- matrix(volume, 3,2)
class(cv)
```

```
[1] "matrix" "array"
```

```
print(cv)
```

```
     [,1] [,2]
[1,]   12   11
[2,]   15   13
[3,]   10   12
```

cbind and the rbind function

As the names implies, cbind means column binding while rbind means row binding. This approach is used when combing multiple vectors together to form a matrix or an array of two or more dimensions.

```
Girth <- c(1,2,3,4,5)
Height <- c(6,7,8,9,10)
Volume <- Height/2

tree_data <- c(Girth, Height, Volume) ## vectorising
print(tree_data)
```

```
 [1]  1.0  2.0  3.0  4.0  5.0  6.0  7.0  8.0  9.0 10.0  3.0  3.5  4.0  4.5  5.0
```

```
tree_data <- rbind(Girth, Height, Volume)
print(tree_data)
```

```
       [,1] [,2] [,3] [,4] [,5]
Girth     1  2.0    3  4.0    5
Height    6  7.0    8  9.0   10
Volume    3  3.5    4  4.5    5
```

```
## Adding Column Names
locations <- c("loc1","loc2","loc3","loc4","loc5")
colnames(tree_data) <- locations
print(tree_data)
```

```
       loc1 loc2 loc3 loc4 loc5
Girth     1  2.0    3  4.0    5
Height    6  7.0    8  9.0   10
Volume    3  3.5    4  4.5    5
```

```
## Chnaging row names
rownames(tree_data)[1] <- "Basal Area"
print(tree_data)
```

```
           loc1 loc2 loc3 loc4 loc5
Basal Area    1  2.0    3  4.0    5
Height        6  7.0    8  9.0   10
Volume        3  3.5    4  4.5    5
```

```
rownames(tree_data)[3] <- "M Volume"
print(tree_data)
```

```
           loc1 loc2 loc3 loc4 loc5
Basal Area    1  2.0    3  4.0    5
Height        6  7.0    8  9.0   10
M Volume      3  3.5    4  4.5    5
```

```
## Other useful inbuilt functions
colSums(tree_data)
```

```
loc1 loc2 loc3 loc4 loc5
10.0 12.5 15.0 17.5 20.0
```

```
rowSums(tree_data)
```

```
Basal Area     Height   M Volume
        15         40         20
```

```
colMeans(tree_data)
```

```
    loc1     loc2     loc3     loc4     loc5
3.333333 4.166667 5.000000 5.833333 6.666667
```

```
rowMeans(tree_data)
```

```
Basal Area     Height   M Volume
         3          8          4
```

```
nrow(tree_data)
```

```
[1] 3
```

```
ncol(tree_data)
```

```
[1] 5
```

```
## Indexing with matrices
tree_data[2,3]
```

```
[1] 8
```

```
tree_data[1,] ## first role only
```

```
loc1 loc2 loc3 loc4 loc5
   1    2    3    4    5
```

```
tree_data[1:2,] ## first two roles only
```

```
           loc1 loc2 loc3 loc4 loc5
Basal Area    1    2    3    4    5
Height        6    7    8    9   10
```

```
tree_data[,1] ## first column only
```

```
Basal Area     Height   M Volume
         1          6          3
```

```
tree_data[,1:2] ## first two columns only
```

```
           loc1 loc2
Basal Area    1  2.0
Height        6  7.0
M Volume      3  3.5
```

```
## A matrix can easily be coerced to form a data frame.
```

- **Factors**

Factors are the data objects which are used to categorize the data and store it as levels. They are useful in **data analysis for statistical modelling**. Factors are created using the factor() function. The **nlevels** functions gives the count of levels. Let us work around some examples.

```
species <- c("gmelina", "tectona", "gmelina", "azadiracta", "mangifera")
factor(species)
```

```
[1] gmelina    tectona    gmelina    azadiracta mangifera
Levels: azadiracta gmelina mangifera tectona
```

```
nlevels(factor(species))
```

```
[1] 4
```

```
levels(factor(species))
```

```
[1] "azadiracta" "gmelina"    "mangifera"  "tectona"
```

```
### Ordinal categorical variable

temp <- c("cold","hot","med","hot","hot", "cold")
factor(temp)
```

```
[1] cold hot  med  hot  hot  cold
Levels: cold hot med
```

```
temp_R <- factor(temp, ordered = T, levels = c("cold","med","hot"))
temp_R
```

```
[1] cold hot  med  hot  hot  cold
Levels: cold < med < hot
```

```
class(temp_R)
```

```
[1] "ordered" "factor"
```

```
nlevels(temp_R)
```

```
[1] 3
```

```
summary(temp_R)
```

```
cold  med  hot
   2    1    3
```

- **Data Frames**

Data frames are tabular data objects created with the **data.frame()**. Unlike a matrix in data frame each column can contain different modes of data. It is one of the favourite way of creating tables in R.

```
SN <- c(1:5)
Gender <- c("Male","Male","Female","Male","Female")
Names <- c("Olakunle","Ademola","Tolu","Samson","Lizzy")
Age <- c(24,22,20,28,21)
Class2016 <- data.frame(SN,Gender,Names,Age)
print(Class2016)
```

```
  SN Gender    Names Age
1  1   Male Olakunle  24
2  2   Male  Ademola  22
3  3 Female     Tolu  20
4  4   Male   Samson  28
5  5 Female    Lizzy  21
```

```
## Same way as above
tree <- data.frame(Girth=c(2,5,4), Height=c(10,7,11), Volume=c(0.34,.43,.56))
class(tree)
```

```
[1] "data.frame"
```

```
print(tree)
```

```
  Girth Height Volume
1     2     10   0.34
2     5      7   0.43
3     4     11   0.56
```

```
## Assessing columns of a data frame
tree$Girth ## The girth column alone
```

```
[1] 2 5 4
```

```
tree[1,2] ## first height observation
```

```
[1] 10
```

```
## Getting the names of columns in a data frame
names(tree)
```

```
[1] "Girth"  "Height" "Volume"
```

```
## structure of a data frame
str(tree)
```

```
'data.frame':   3 obs. of  3 variables:
 $ Girth : num  2 5 4
 $ Height: num  10 7 11
 $ Volume: num  0.34 0.43 0.56
```

```
## summary function on a data frame
summary(tree)
```

```
     Girth           Height          Volume     
 Min.   :2.000   Min.   : 7.000   Min.   :0.3400  
 1st Qu.:3.000   1st Qu.: 8.500   1st Qu.:0.3850  
 Median :4.000   Median :10.000   Median :0.4300  
 Mean   :3.667   Mean   : 9.333   Mean   :0.4433  
 3rd Qu.:4.500   3rd Qu.:10.500   3rd Qu.:0.4950  
 Max.   :5.000   Max.   :11.000   Max.   :0.5600  
```

```
## Free R datasets for practice
data()
data(package="datasets")
library(help="datasets")
data("ChickWeight")
str(ChickWeight)
```

```
Classes 'nfnGroupedData', 'nfGroupedData', 'groupedData' and 'data.frame':  578 obs.
of  4 variables:
 $ weight: num  42 51 59 64 76 93 106 125 149 171 ...
 $ Time  : num  0 2 4 6 8 10 12 14 16 18 ...
 $ Chick : Ord.factor w/ 50 levels "18"<"16"<"15"<..: 15 15 15 15 15 15 15 15 15 15
...
 $ Diet  : Factor w/ 4 levels "1","2","3","4": 1 1 1 1 1 1 1 1 1 1 ...
 - attr(*, "formula")=Class 'formula'  language weight ~ Time | Chick
  .. ..- attr(*, ".Environment")=<environment: R_EmptyEnv>
 - attr(*, "outer")=Class 'formula'  language ~Diet
  .. ..- attr(*, ".Environment")=<environment: R_EmptyEnv>
 - attr(*, "labels")=List of 2
  ..$ x: chr "Time"
  ..$ y: chr "Body weight"
 - attr(*, "units")=List of 2
  ..$ x: chr "(days)"
  ..$ y: chr "(gm)"
```

```
summary(ChickWeight)
```

```
     weight           Time           Chick     Diet
 Min.   : 35.0   Min.   : 0.00   13     : 12   1:220
 1st Qu.: 63.0   1st Qu.: 4.00   9      : 12   2:120
 Median :103.0   Median :10.00   20     : 12   3:120
 Mean   :121.8   Mean   :10.72   10     : 12   4:118
 3rd Qu.:163.8   3rd Qu.:16.00   17     : 12
 Max.   :373.0   Max.   :21.00   19     : 12
                                 (Other):506
```

```
head(ChickWeight)
```

```
  weight Time Chick Diet
1     42    0     1    1
2     51    2     1    1
3     59    4     1    1
4     64    6     1    1
5     76    8     1    1
6     93   10     1    1
```

```
tail(ChickWeight)
```

```
    weight Time Chick Diet
573    155   12    50    4
574    175   14    50    4
575    205   16    50    4
576    234   18    50    4
577    264   20    50    4
578    264   21    50    4
```

- **Data Operators in R**

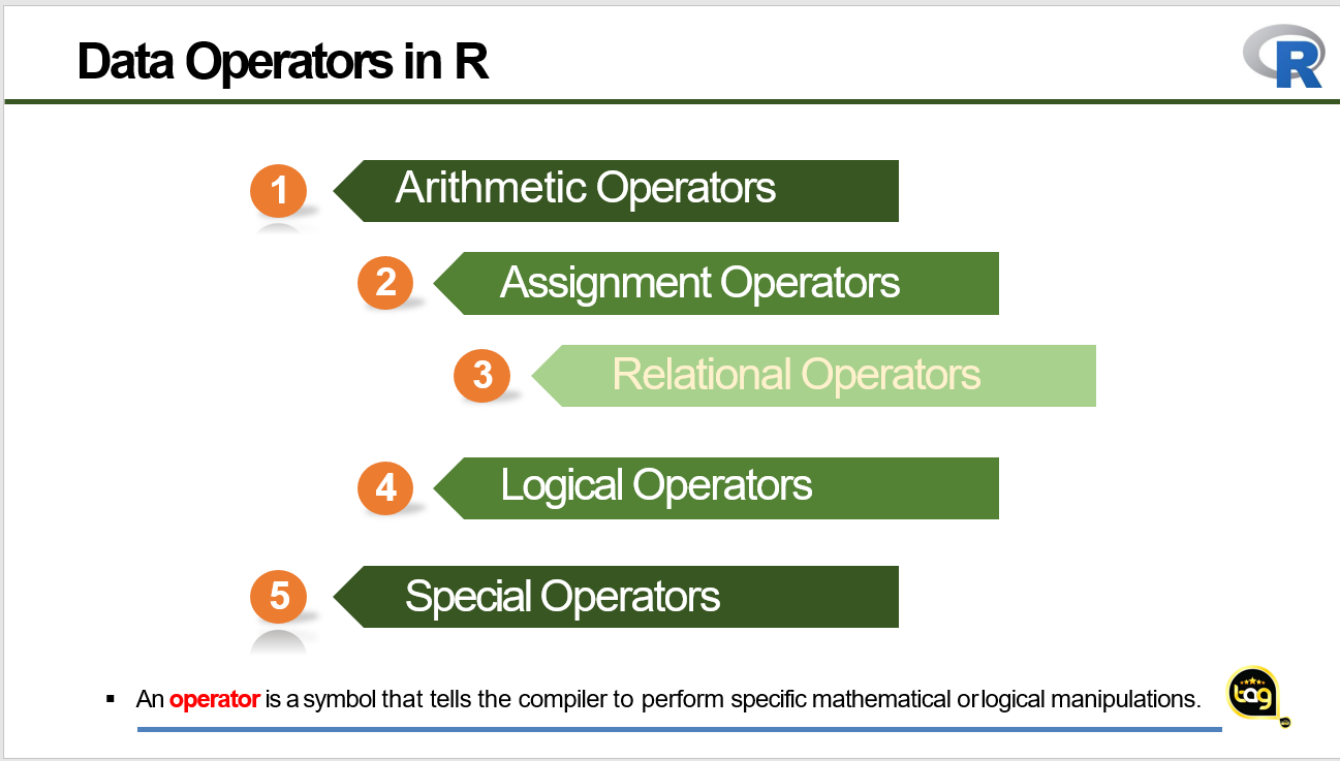


Figure 6: Data Operators in R

- **Arithmetic Operator**

This operator gives us the privilege of using R as a basic calculator. Briefly, we will take some examples performing some basic calculations with this operator.

```
2+5
```

```
[1] 7
```

```
vec1 <- c(1,2,3)
vec2 <- c(4,5,6)

print(vec1 + vec2) ## Addition
```

```
[1] 5 7 9
```

```
print(vec1 - vec2) ## Subtraction
```

```
[1] -3 -3 -3
```

```
print(vec1 * vec2) ## Multiplication
```

```
[1]  4 10 18
```

```
print(vec2 / vec1) ## Division
```

```
[1] 4.0 2.5 2.0
```

```
print(vec2 ^ vec1) ## Power
```

```
[1]   4  25 216
```

```
print(vec2 ** vec1) ## Similarity with python power.
```

```
[1]   4  25 216
```

```
print(vec2 %% vec1) ## Modular division (Remainder)
```

```
[1] 0 1 0
```

```
print(vec2 %/% vec1) ## Flow division (Whole number)
```

```
[1] 4 2 2
```

- **Assignment Operator**

During the section on data types, in one of the examples, we have used the assignment operator to create a variable. Therefore, we will only do little of variable creation using the different types of assignment operators available in R.

```
vec1 <- c(1,2,3) ## Less than assignment operator
vec1 <<- c(1,2,3)
c(4,5,6) -> vec2 ## greater than assignment operator
c(4,5,6) ->> vec2
vec1 = c(1,2,3) ## equal to assignment operator
```

- **Relational Operators**

```
vec1 < vec2
```

```
[1] TRUE TRUE TRUE
```

```
vec1 > vec2
```

```
[1] FALSE FALSE FALSE
```

```
vec1 <= vec2
```

```
[1] TRUE TRUE TRUE
```

```
vec1 >= vec2
```

```
[1] FALSE FALSE FALSE
```

```
vec2 == vec2
```

```
[1] TRUE TRUE TRUE
```

```
vec1 != vec2
```

```
[1] TRUE TRUE TRUE
```

- **Logical Operators**

AND

```
2&3 ## prints TRUE only if both sides are TRUE
```

```
[1] TRUE
```

```
0&1
```

```
[1] FALSE
```

```
TRUE & TRUE
```

```
[1] TRUE
```

```
TRUE & FALSE
```

```
[1] FALSE
```

```
FALSE && FALSE
```

```
[1] FALSE
```

```
TRUE && TRUE
```

```
[1] TRUE
```

```
TRUE && FALSE
```

```
[1] FALSE
```

OR

```
2|3 ## prints TRUE as long one of the sides is TRUE
```

```
[1] TRUE
```

```
0|1
```

```
[1] TRUE
```

```
TRUE | TRUE
```

```
[1] TRUE
```

```
TRUE | FALSE
```

```
[1] TRUE
```

```
FALSE || FALSE
```

```
[1] FALSE
```

```
TRUE || TRUE
```

```
[1] TRUE
```

```
TRUE || FALSE
```

```
[1] TRUE
```

Opposite

```
!0 ## It gives the opposite logical values
```

```
[1] TRUE
```

```
!6
```

```
[1] FALSE
```

```
!TRUE
```

```
[1] FALSE
```

```
!FALSE
```

```
[1] TRUE
```

- **Special Operators**

:

It creates the series of numbers in sequence for a vector.

```
v <- c(1:15)
class(v)
```

```
[1] "integer"
```

%in%

This operator is used to identify if an element belongs to a vector.

```
vec2 %in% v
```

```
[1] TRUE TRUE TRUE
```

%*%

This operator is used to multiply a matrix with its transpose.

```
M = matrix( c(2,6,5,1,10,4),
nrow=2,ncol=3,byrow = TRUE)

t = M %*% t(M)
print(t)
```

```
     [,1] [,2]
[1,]   65   82
[2,]   82  117
```

General View on Variable A variable is a characteristics of an individual in a population, the value of which can differ between entities within that population.

- **Types of Variable**

Numeric Variable: This is one whose observations are naturally recorded as numbers. They are of two types: Continuous and Discreet.

- **Continuous:** They can be recorded as any value in some interval, up to any number of decimal. e.g 15.12mm.
- **Discrete:** It takes only distinct numeric values – and if the range is restricted, then the numbers of possible values is finite. For example, it doesn't make sense to observe 15.245 heads if you are to observe the number of heads in a 20 flip of a coin.

Categorical Variable: Like some discrete variables, categorical variables takes only one of a finite number of possibilities. Unlike discrete variables, however, categorical observations are not always recorded as numeric values.

There are two types of categorical variables. They are:

- **Nominal:** Those that cannot be logically ranked. e.g sex. Sex has two categories. The order of these categories is irrelevant.

```
head(chickwts$feed)
```

```
[1] horsebean horsebean horsebean horsebean horsebean horsebean
Levels: casein horsebean linseed meatmeal soybean sunflower
```

- **Ordinal:** They are variables that can be logically ranked. e.g drug dosage with possible values of low, medium and high. The values can be ordered in either increasing or decreasing amount depending on the nature of the research.
- **Variables in R**

Variables are nothing but reserved memory locations to store values. This means that when you create a variable, you reserve a space in the memory.

- **Finding Variables in R**

To know all the variables currently available in the workspace we use the **ls()** function. Also the **ls()** function can use patterns to match the variable names. Run the command **print(ls())**

- **Removing Variables in R**

print(ls(pattern="var")) this command will produce variables starting with the pattern "var".

Variables can be deleted by using the **rm()** function.

Data Analysis and Reporting with R

In this section, it will be more of practical on the procedure to deriving meaningful insight from your data with R.

Getting and Setting Working Directory

This is an important step we need to take before conducting any kind of analysis with R. What we will be doing here is knowing the exact folder on the system that our software is connected to. It is important we do this because our software will only be able to read in data from that folder and also write out to that same folder when necessary.

There are two ways to doing this. Either **manually** with the help of some inbuilt functions, or through **Session** column on the menu bar.

- **Manually**

```
getwd() ## To get working directory
```

```
[1] "C:/Users/HP Envy X360/OneDrive/Documents/FWM Final Year"
```

```
## setwd(dir= "C:/Users/HP Envy X360/OneDrive/Documents/FWM Final Year/NEW FOLDER")
## The forward slash is used to direct from one folder to the other.
```

Importing and Exporting of Data in R

- **.CSV**

```
dat <- read.csv("StudentsPerformance.csv", header = T)
head(dat[-1]) ## excluding the first column
```

```
  race.ethnicity parental.level.of.education        lunch
1        group B           bachelor's degree     standard
2        group C                some college     standard
3        group B             master's degree     standard
4        group A          associate's degree free/reduced
5        group C                some college     standard
6        group B          associate's degree     standard
  test.preparation.course math.score reading.score writing.score
1                    none         72            72            74
2               completed         69            90            88
3                    none         90            95            93
4                    none         47            57            44
5                    none         76            78            75
6                    none         71            83            78
```

```
str(dat)
```

```
'data.frame':   1000 obs. of  8 variables:
 $ gender                     : chr  "female" "female" "female" "male" ...
 $ race.ethnicity             : chr  "group B" "group C" "group B" "group A" ...
 $ parental.level.of.education: chr  "bachelor's degree" "some college" "master's de
gree" "associate's degree" ...
 $ lunch                      : chr  "standard" "standard" "standard" "free/reduced"
...
 $ test.preparation.course    : chr  "none" "completed" "none" "none" ...
 $ math.score                 : int  72 69 90 47 76 71 88 40 64 38 ...
 $ reading.score              : int  72 90 95 57 78 83 95 43 64 60 ...
 $ writing.score              : int  74 88 93 44 75 78 92 39 67 50 ...
```

- **.txt**

```
## dat1 <- read.table("table.txt", header = T)
```

- **Excel Files**

```
library(readxl)
## example <- read_excel("example.xls")
## head(example)
```

```
## excel_sheets("UnderG data.xlsx") ## To get the name of sheets
## each sheet is more like a data frame.

## read_excel("UnderG data.xlsx", sheet = "Sheet2")
```

NOTE: An easy way to import datasets is via the Global Environment or through the file pane.

- **Using RCurl to read in csv data hosted online or on github**

```
library(RCurl)

 ## dat2 <- read.csv(text = getURL("https://raw.githubusercontent.com/sciruela/Happi
ness-Salaries/ac87cac0e1b440826eaa765e1b2c3e6bc264dad1/data.csv"))

## head(dat2)
```

Indexing and Subsetting Data Frames

```
data(iris)
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
...
```

```
summary(iris)
```

```
 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
```

```
summary(iris$Species)
```

```
    setosa versicolor  virginica
        50         50         50
```

```
head(iris)
```

```
  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
```

```
head(iris,10)
```

```
   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
7           4.6         3.4          1.4         0.3  setosa
8           5.0         3.4          1.5         0.2  setosa
9           4.4         2.9          1.4         0.2  setosa
10          4.9         3.1          1.5         0.1  setosa
```

```
df3 <- iris[1:6,] ## To subset or isolate the first 6 rows.
head(df3)
```

```
  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
```

```
df4 <- iris[,1:2] ## subset the first two columns
head(df4)
```

```
  Sepal.Length Sepal.Width
1          5.1         3.5
2          4.9         3.0
3          4.7         3.2
4          4.6         3.1
5          5.0         3.6
6          5.4         3.9
```

```
y <- iris[, c("Sepal.Length","Sepal.Width")]
head(y)
```

```
  Sepal.Length Sepal.Width
1          5.1         3.5
2          4.9         3.0
3          4.7         3.2
4          4.6         3.1
5          5.0         3.6
6          5.4         3.9
```

Indexing with relational operators

```
head(mtcars[mtcars$cyl==6 & mtcars$am==1,])
```

```
               mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4     21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag 21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Ferrari Dino  19.7   6  145 175 3.62 2.770 15.50  0  1    5    6
```

```
head(mtcars[mtcars$cyl==6 | mtcars$am==1,])
```

```
                mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Mazda RX4      21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag  21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
Datsun 710     22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive 21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
Valiant        18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
Merc 280       19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
```

```
head(mtcars[mtcars$mpg>20 & mtcars$cyl==6 & mtcars$gear==3, ])
```

```
                mpg cyl disp  hp drat    wt  qsec vs am gear carb
Hornet 4 Drive 21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
```

```
head(mtcars[mtcars$mpg>20 | mtcars$cyl==6 | mtcars$gear==3, ])
```

```
                  mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

```
head(mtcars[ (mtcars$mpg>20) & (mtcars$hp>100), c('mpg','cyl')])
```

```
                mpg cyl
Mazda RX4      21.0   6
Mazda RX4 Wag  21.0   6
Hornet 4 Drive 21.4   6
Lotus Europa   30.4   4
Volvo 142E     21.4   4
```

```
vit <- c("Sepal.Length", "Petal.Length", "Species")
df5 <- iris[vit]
head(df5)
```

```
  Sepal.Length Petal.Length Species
1          5.1          1.4  setosa
2          4.9          1.4  setosa
3          4.7          1.3  setosa
4          4.6          1.5  setosa
5          5.0          1.4  setosa
6          5.4          1.7  setosa
```

```
vit1 <- names(iris)%in% c("Species")
vit1
```

```
[1] FALSE FALSE FALSE FALSE  TRUE
```

```
df6 <- iris[!vit1]
head(df6)
```

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

Indexing with the subset function

```
dfset <- subset(iris, iris$Species=="setosa")
head(dfset)
```

```
  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
```

```
head(subset(mtcars, mpg>20 & cyl==6, c("mpg","cyl","disp")))
```

```
                mpg cyl disp
Mazda RX4      21.0   6  160
Mazda RX4 Wag  21.0   6  160
Hornet 4 Drive 21.4   6  258
```

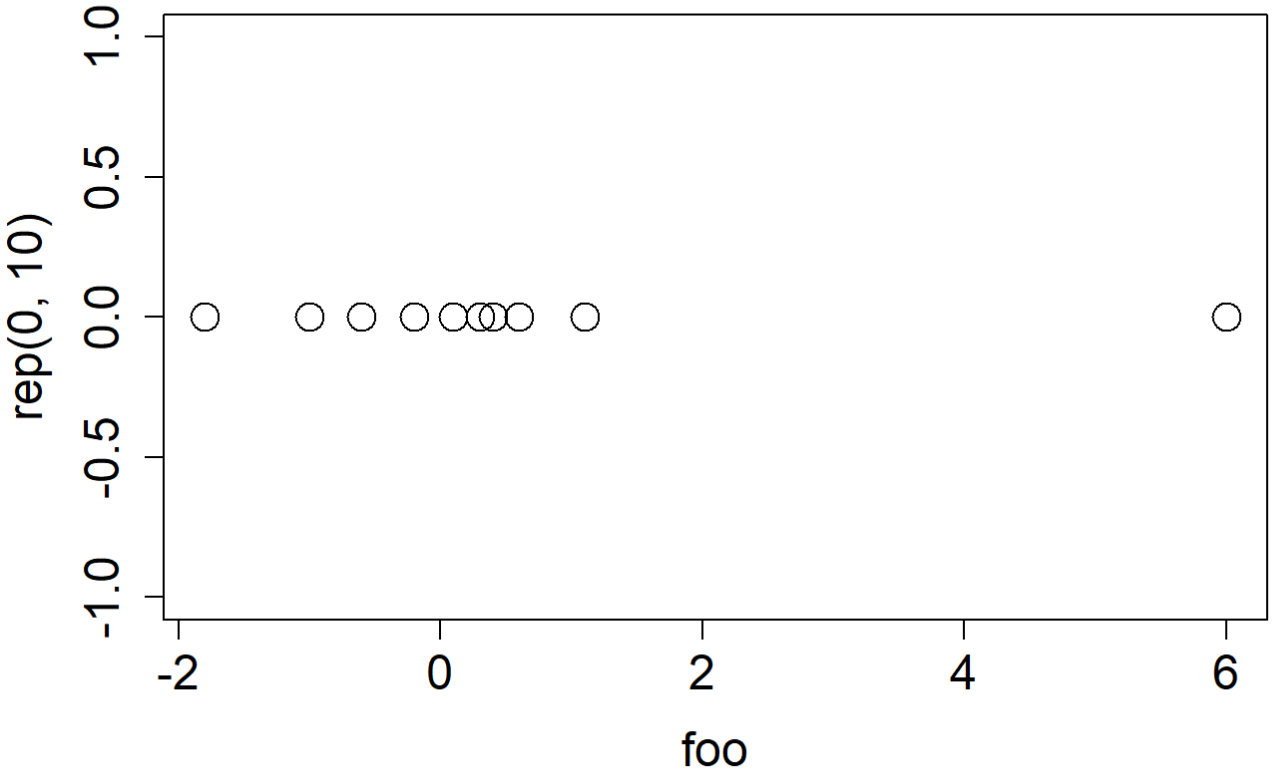
Exploratory Data Analysis (EDA)

Exploratory Data Analysis refers to the critical process of performing initial investigations on data so as to discover patterns, to spot anomalies, to test hypothesis and to check assumptions with the help of summary statistics and graphical representations.

- **Univariate** When discussing or analyzing data related to only one dimension, you are dealing with Univariate Data.

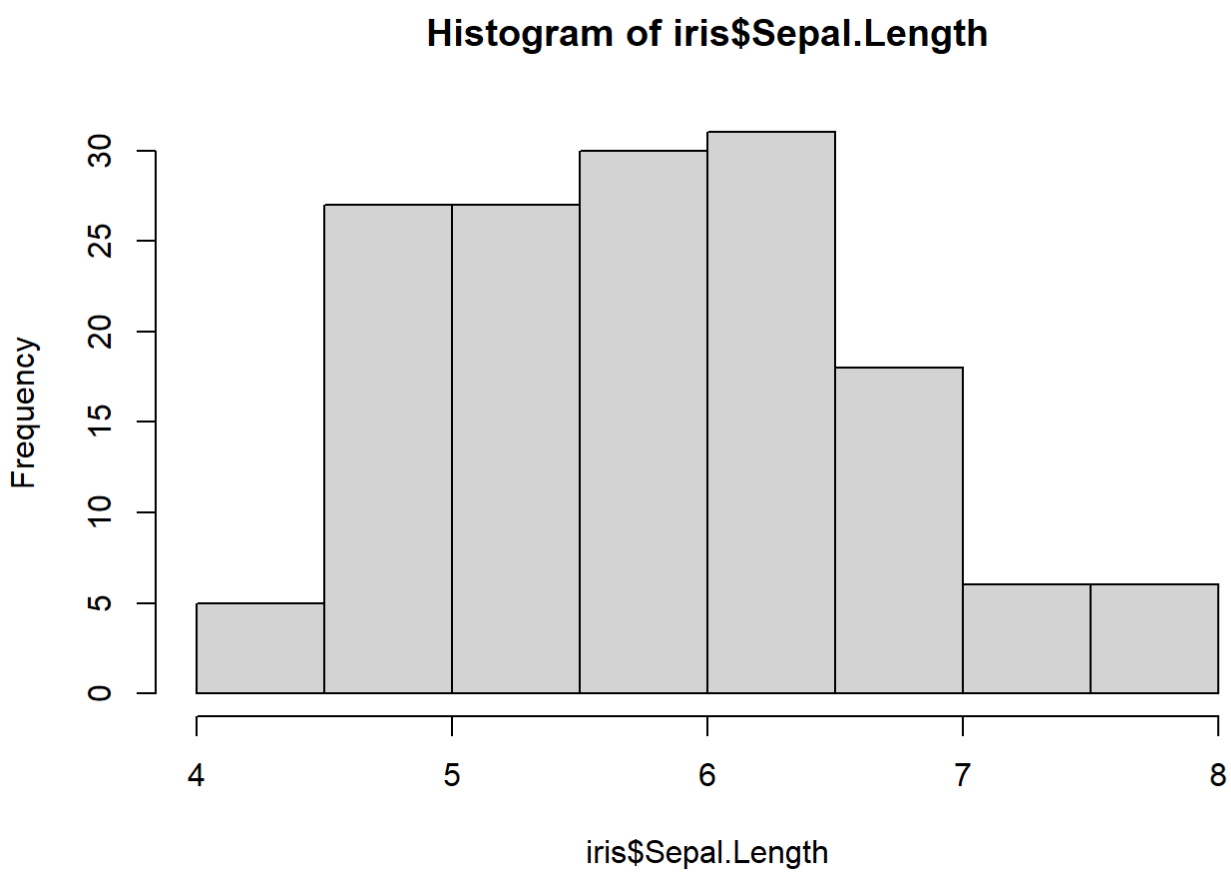
For example, the weight variable in the earlier example **(chickwts)** is univariate since each measurement can be expressed with one component – a single number.

```
foo <- c(0.6,-0.6,0.1,-0.2,-1.0,0.4,0.3,-1.8,1.1,6.0)
plot(foo,rep(0,10),cex=2,cex.axis=1.5,cex.lab=1.5)
```

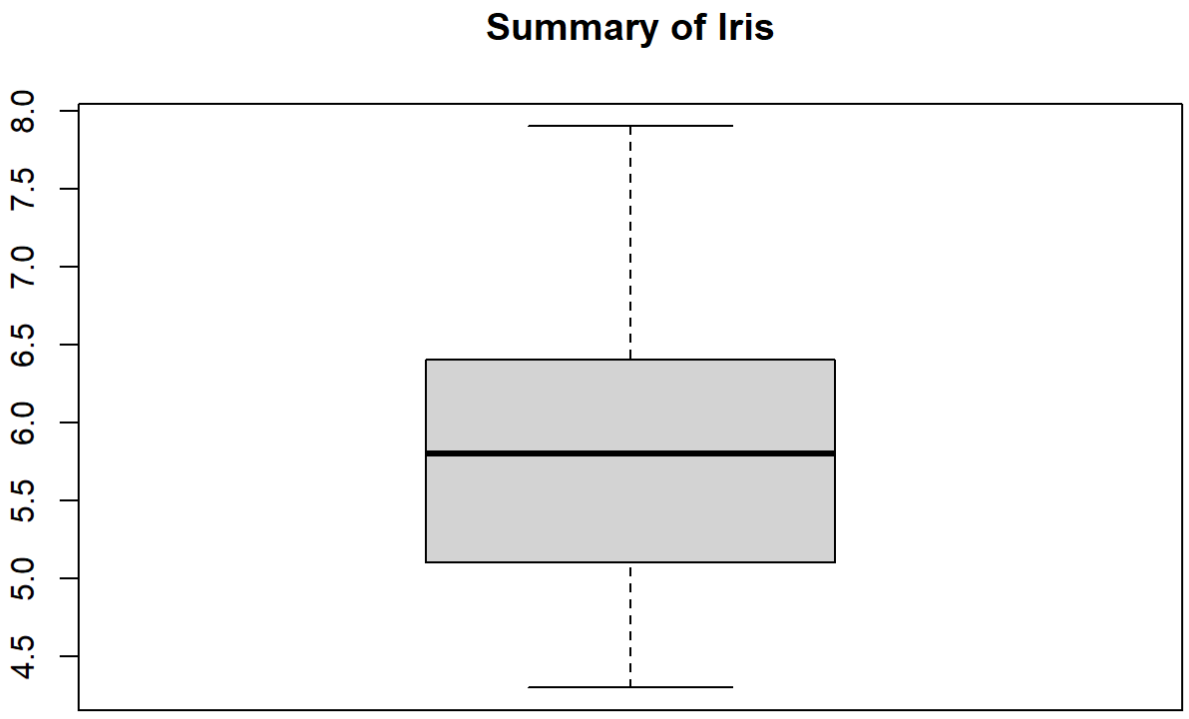


From the above EDA example with a univariate data, we were able to see an abnormal observation in the data popular called an **outlier**.

```
hist(iris$Sepal.Length)
```




```
boxplot(iris$Sepal.Length, main="Summary of Iris", xlab="Sepal Length")
```




```
summary(iris)
```

```
  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
```

```
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
...
```

Multivariate Data

When it is necessary to consider data with respect to variables that exists in more than one dimension (in other words, with more than one component or measurement associated with each observation), your data are considered Multivariate.

```
head(quakes)
```

```
     lat   long depth mag stations
1 -20.42 181.62   562 4.8       41
2 -20.62 181.03   650 4.2       15
3 -26.00 184.10    42 5.4       43
4 -17.97 181.66   626 4.1       19
5 -20.42 181.96   649 4.0       11
6 -19.68 184.31   195 4.0       12
```

```
summary(quakes)
```

```
      lat              long           depth            mag       
 Min.   :-38.59   Min.   :165.7   Min.   : 40.0   Min.   :4.00  
 1st Qu.:-23.47   1st Qu.:179.6   1st Qu.: 99.0   1st Qu.:4.30  
 Median :-20.30   Median :181.4   Median :247.0   Median :4.60  
 Mean   :-20.64   Mean   :179.5   Mean   :311.4   Mean   :4.62  
 3rd Qu.:-17.64   3rd Qu.:183.2   3rd Qu.:543.0   3rd Qu.:4.90  
 Max.   :-10.72   Max.   :188.1   Max.   :680.0   Max.   :6.40  
    stations    
 Min.   : 10.00  
 1st Qu.: 18.00  
 Median : 27.00  
 Mean   : 33.42  
 3rd Qu.: 42.00  
 Max.   :132.00  
```

```
str(quakes)
```

```
'data.frame':   1000 obs. of  5 variables:
 $ lat     : num  -20.4 -20.6 -26 -18 -20.4 ...
 $ long    : num  182 181 184 182 182 ...
 $ depth   : int  562 650 42 626 649 195 82 194 211 622 ...
 $ mag     : num  4.8 4.2 5.4 4.1 4 4 4.8 4.4 4.7 4.3 ...
 $ stations: int  41 15 43 19 11 12 43 15 35 19 ...
```

Decriptive Statistics

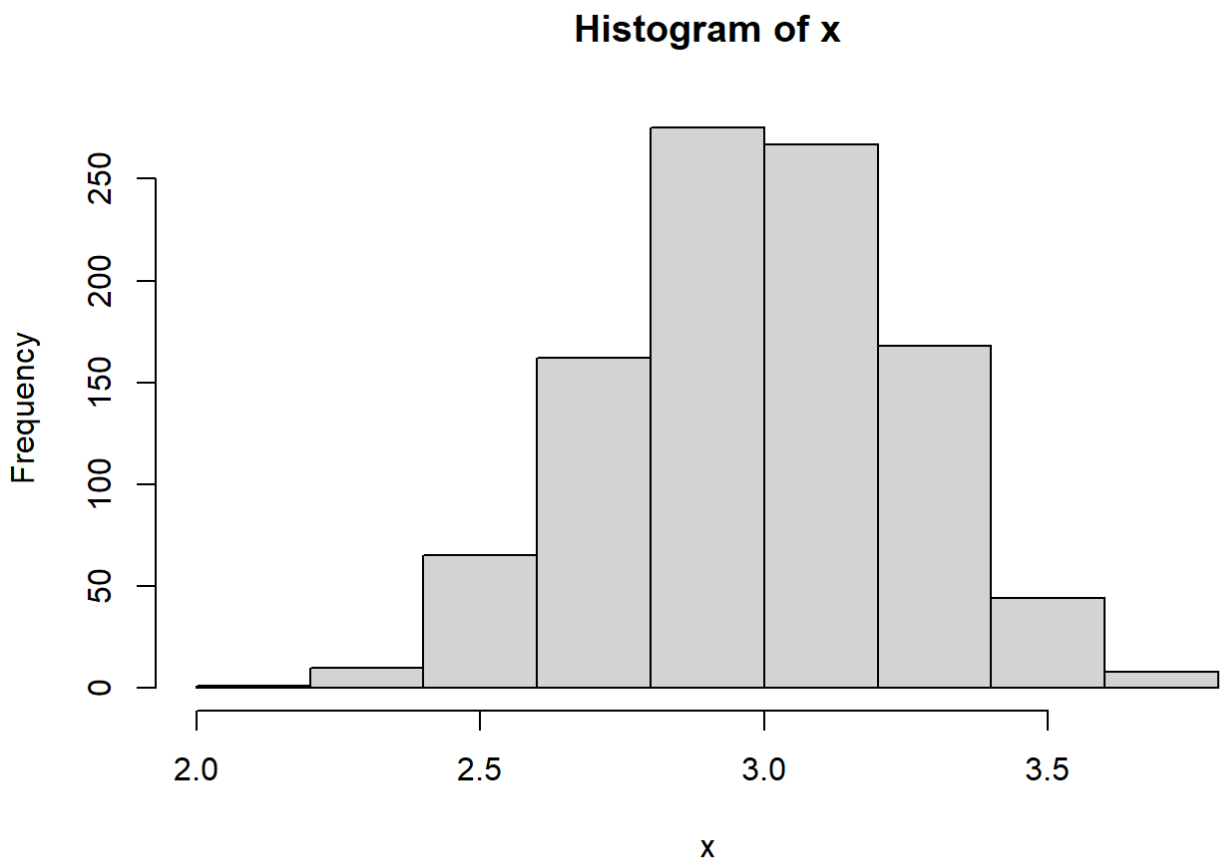
Descriptive statistics is the term given to the analysis of data that helps **describe**, show or summarize data in a meaningful way such that, for example, patterns might emerge from the data.

Descriptive statistics do not, however, allow us to make conclusions beyond the data we have analysed or reach conclusions regarding any hypotheses we might have made. They are simply a way to describe our data.

- **Measures of Central Tendency**

These are ways of describing the central position of a frequency distribution for a group of data.

```
x <- rnorm(1000,3,.25)
hist(x) ## distribution of values of continuous variables
```




```
mean(x)
```

```
[1] 2.988755
```

```
median(x)
```

```
[1] 2.992323
```

```
y <- c(2,5,6,3,7,800,5,3,2,4)
mean(y) ## here, the mean is not a true representative of the salaries, so we report the median
```

```
[1] 83.7
```

```
median(y)
```

```
[1] 4.5
```

```
vab <- table(y) ## To have an idea of the modal value.
vab
```

```
y
  2   3   4   5   6   7 800
  2   2   1   2   1   1   1
```

```
mod <- vab[vab==max(vab)]
mod
```

```
y
2 3 5
2 2 2
```

```
min(y)
```

```
[1] 2
```

```
max(y)
```

```
[1] 800
```

```
range(y)
```

```
[1]   2 800
```

You can get a copy of my book on amazon titled; “Basic Statistics for Undergraduate Studies Using R” (https://www.amazon.com/BASIC-STATISTICS-UNDERGRADUATE-STUDIES-USING/dp/B08C4FTJFT) for more information on simple code to obtain the mode of your distributions.

```
library(moments)
skewness(x)
```

```
[1] -0.1548827
```

```
## Skewness
## Left Skewed: Mean < Median
## Few smaller values reduces the mean

## Right Skewed: Mean > Median
## Few larger values increases the mean
```

- **Measure of Spread**

These are ways of summarizing a group of data by describing how spread out the scores are.

```
#### MEASURE OF VARIATION
std = sd(iris$Sepal.Length)
std
```

```
[1] 0.8280661
```

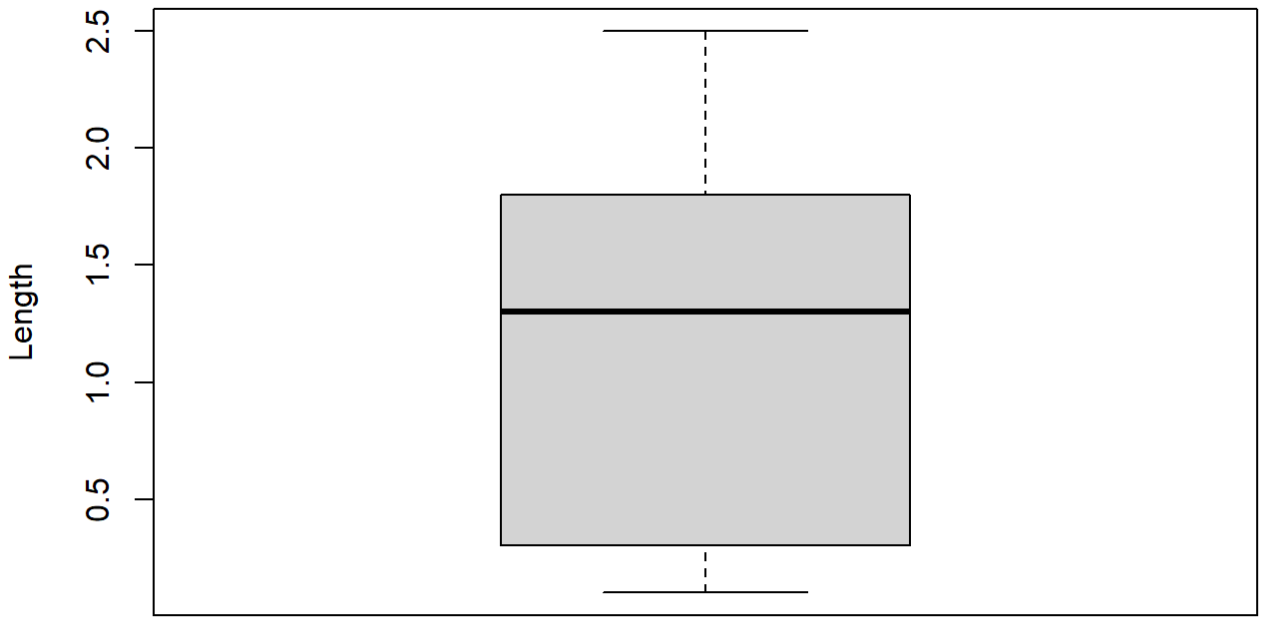
```
var(iris$Sepal.Length)
```

```
[1] 0.6856935
```

```
library(sciplot)
se(iris$Petal.Length)
```

```
[1] 0.144136
```

```
boxplot(iris$Petal.Width, Main = "Petal Length", ylab = "Length") ## 5 point number
 summary.
```




```
IQR(y)
```

```
[1] 2.75
```

Inferential Statistics

Inferential statistics use a random sample of data taken from a population to describe and make inferences about the population.

- **Parameter and Statistics**

We have seen that descriptive statistics provide information about our immediate group of data. Any group of data like this, which includes all the data you are interested in, is called a population. Descriptive statistics are applied to populations, and the properties of populations, like the mean or standard deviation, are called parameters as they represent the whole population (i.e., everybody you are interested in).

Often, however, you do not have access to the whole population you are interested in investigating, but only a limited number of data instead which is called the sample.

Properties of samples, such as the mean or standard deviation, are not called parameters, but statistics. Inferential statistics are techniques that allow us to use these samples to make generalizations about the populations from which the samples were drawn. It is, therefore, important that the sample accurately represents the population. The process of achieving this is called sampling.

The methods of inferential statistics are **(1) the estimation of parameter(s)** and **(2) testing of statistical hypotheses**.

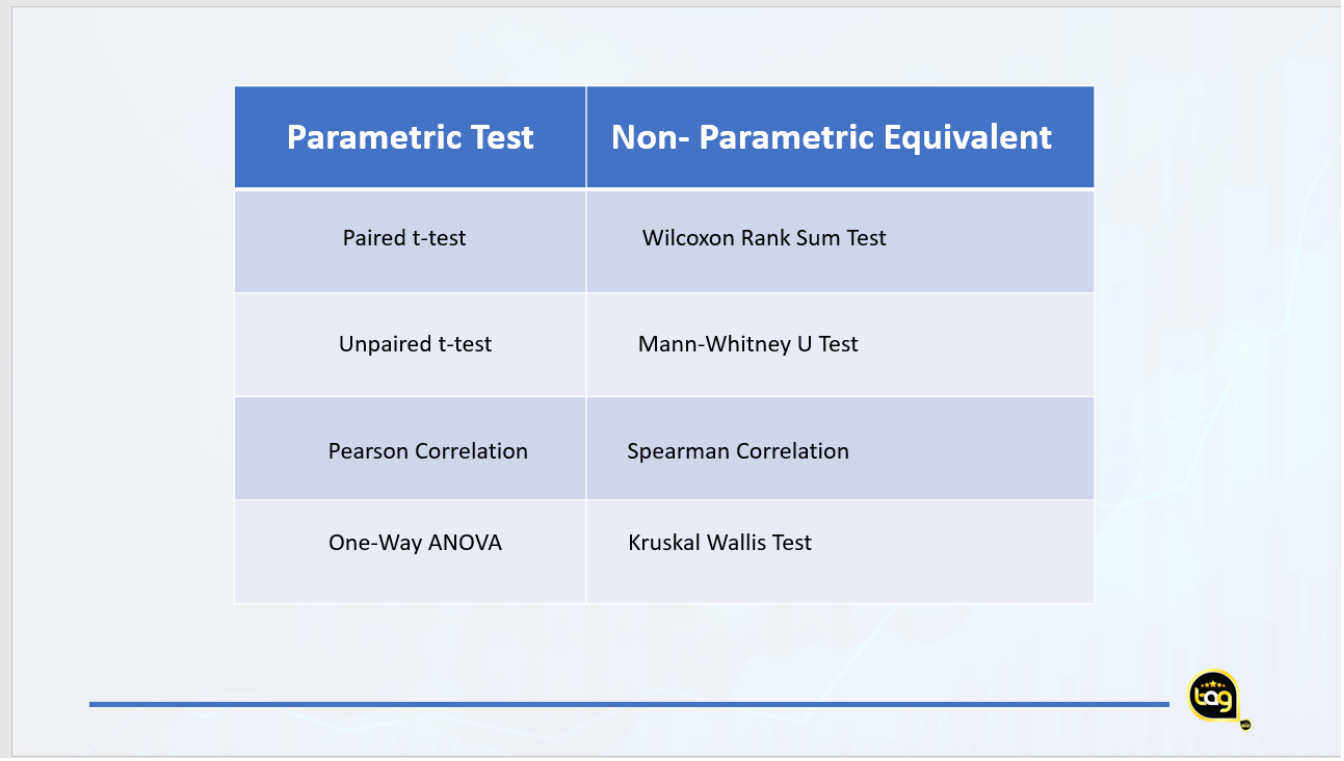
- **Summary:**

The characteristics of that population are referred to as parameters. Estimates from a sample are known as statistics.

Parametric and Non-parametric test

Parametric tests are those that make assumptions about the parameters of the population distribution from which the sample is drawn but nonparametric tests don't require that your data follow the normal distribution. They're also known as distribution-free tests and can provide benefits in certain situations.

Non-parametric tests are valid for both non-Normally distributed data and Normally distributed data, so why not use them all the time? Parametric tests usually have more statistical power than their non-parametric equivalents. In other words, one is more likely to detect significant differences when they truly exist.



Parametric Test	Non- Parametric Equivalent
Paired t-test	Wilcoxon Rank Sum Test
Unpaired t-test	Mann-Whitney U Test
Pearson Correlation	Spearman Correlation
One-Way ANOVA	Kruskal Wallis Test

Figure 7: Parametric and non-parametric tests for comparing two or more groups

- **Hypothesis**

This is defined to be an assumption made with aim of calculating the probability of which the conc(lusion is incorrect. We have two types of it, they are; 1. Null hypothesis 2. Alternate hypothesis

The null hypothesis is the claim that is assumed to be true while the alternate hypothesis is what we are testing for against the null hypothesis.

NOTE

-When H(alt) is define with the less than statement, it is one-sided and can be said to be a lower-tailed test.

-When H(alt) is defined with the greater than statement, it is one-sided and can also be said to be an upper-tailed test.

-When H(alt) is defined with the not equal to sign, it is two-sided and can also be called a two-tailed test.

- **Hypothesis Testing**

After setting up a hypothesis, it is good for us to make some assumptions before carrying out the parametric test. These assumptions are listed below;

- We assume that the samples are taken at random and gives a perfect representation of the population without any element of bias.
- For two or more populations, we assume the equality of variance.
- We assume that the population(s) is normally distributed.

t-Test Application in R

- **One Sample t-test**

Example

Ten individual trees were randomly chosen from a population and their diameters at 1.3m above the ground level were measured in cm. The data is presented below;

25.46,31.51,17.04,30.10,38.40,31.19,37.56,41.70,21.01 and 41.83

In the light of the above dta, could the mean diameter of the population be 28cm?

```
dat <- c(25.46,31.51,17.04,30.10,38.40,31.19,37.56,41.70,21.01,41.83)
dbh_test <- t.test(x=dat, mu=28, alternative = "less")
print(dbh_test)
```

```

    One Sample t-test

data:  dat
t = 1.3294, df = 9, p-value = 0.8918
alternative hypothesis: true mean is less than 28
95 percent confidence interval:
     -Inf 36.51652
sample estimates:
mean of x
    31.58
```

```
names(dbh_test)
```

```
 [1] "statistic"   "parameter"   "p.value"     "conf.int"    "estimate"
 [6] "null.value"  "stderr"      "alternative" "method"      "data.name"
```

```
attributes(dbh_test) ##same as above
```

```
$names
 [1] "statistic"   "parameter"   "p.value"     "conf.int"    "estimate"
 [6] "null.value"  "stderr"      "alternative" "method"      "data.name"

$class
[1] "htest"
```

```
## To get the true C.I, we need to change the alternative argument to two sided.
dbh_test1 <- t.test(x=dat, mu=28, alternative = "two.sided")
names(dbh_test1)
```

```
 [1] "statistic"   "parameter"   "p.value"     "conf.int"    "estimate"
 [6] "null.value"  "stderr"      "alternative" "method"      "data.name"
```

```
dbh_test1$conf.int
```

```
[1] 25.48808 37.67192
attr(,"conf.level")
[1] 0.95
```

- **Exercise**

Suppose a forester sells 16g of a tree seedling. A random sample of 9 seedlings were taken and weighed. 15.5, 16.2, 16.1, 15.8, 15.6, 16.0, 15.8, 15.9, 16.2

Is the average weight at least 16?

Answer

```
seedling <- c(15.5, 16.2, 16.1, 15.8, 15.6, 16.0, 15.8, 15.9, 16.2)
s_test <- t.test(x= seedling, mu= 16, alternative = "less")
print(s_test)
```

```
    One Sample t-test

data:  seedling
t = -1.2, df = 8, p-value = 0.1322
alternative hypothesis: true mean is less than 16
95 percent confidence interval:
     -Inf 16.05496
sample estimates:
mean of x
     15.9
```

- **Unpaired/Independent Samples**

Unpooled Variance: Here, we cannot assume the equality of variances of the two groups.

Example

Suppose the forester in the exercise above selects another 6 random samples of seedling and weighed them. 14.7, 15.2, 16.6, 16.3, 15.4, 16.4

Can we conclude that there is a difference between the mean of the two samples?

```
seedling_samp <- c(14.7, 15.2, 16.6, 16.3, 15.4, 16.4)

testObj <- t.test(x=seedling_samp, y=seedling, alternative = "greater", conf.level = 0.95)
print(testObj)
```

```
    Welch Two Sample t-test

data:  seedling_samp and seedling
t = -0.40942, df = 5.7077, p-value = 0.6514
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
 -0.7720041        Inf
sample estimates:
mean of x mean of y
 15.76667  15.90000
```

Pooled: Here, we can assume equality of variance.

Example

Measurements on tree diameters from two different forest reserves were taken and recorded with the aim of accessing whether there is a difference between the mean diameter values obtained from the forest reserves. Perform a simple test confirming this.

shasha: 102,87,101,96,107,101,91,85,108,67,85,82 Ago-Owu: 73,81,111,109,143,95,92,120,93,89,119,79,90,126,62,92,77,106,105,111

```
shasha <- c(102,87,101,96,107,101,91,85,108,67,85,82)
ago_owu <- c(73,81,111,109,143,95,92,120,93,89,119,79,90,126,62,92,77,106,105,111)
testResult <- t.test(x=shasha, y=ago_owu, alternative = "two.sided", conf.level = 0.
95, var.equal = T)
print(testResult)
```

```

    Two Sample t-test

data:  shasha and ago_owu
t = -0.93758, df = 30, p-value = 0.3559
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -19.016393   7.049727
sample estimates:
mean of x mean of y
 92.66667  98.65000
```

- **Paired/Dependent Samples**

Paired data occur when the measurements forming tow sets of observations are taken from the same individual.

Examples

A forester interested in the rate of growth of his gmelina arborea plantation takes a yearly measurement of the height of his trees and record them. The record for the first and second year are provide below:

height before: 52,66,89,87,89,72,66,65,49,62,70,52,75,63,65,61

height after: 51,66,71,73,70,68,60,51,40,57,65,53,64,56,60,59

```
height_before <- c(52,66,89,87,89,72,66,65,49,62,70,52,75,63,65,61)
height_after <- c(51,66,71,73,70,68,60,51,40,57,65,53,64,56,60,59)

length(height_before); length(height_after)
```

```
[1] 16
```

```
[1] 16
```

```
heightdiff <- height_after - height_before
print(heightdiff)
```

```
 [1]  -1   0 -18 -14 -19  -4  -6 -14  -9  -5  -5   1 -11  -7  -5  -2
```

```
heightdiff_mean <- mean(heightdiff)
heightdiff_sd <- sd(heightdiff)

height_test <- heightdiff_mean / (heightdiff_sd/sqrt(16))
print(height_test)
```

```
[1] -4.801146
```

```
p_val <- pt(height_test, df=15)
print(p_val)
```

```
[1] 0.000116681
```

Doing this with a single line of code as usual.

```
testObject <- t.test(x=height_after, y=height_before, alternative = "less", conf.lev
el = .95, paired = T)
print(testObject)
```

```

    Paired t-test

data:  height_after and height_before
t = -4.8011, df = 15, p-value = 0.0001167
alternative hypothesis: true difference in means is less than 0
95 percent confidence interval:
      -Inf -4.721833
sample estimates:
mean of the differences
               -7.4375
```

You can use the line of code below to get the confidence interval.

```
CI <- heightdiff_mean + c(-1,1) * qt(0.975, df=15) * (heightdiff_sd/sqrt(16))
print(CI)
```

```
[1] -10.739348  -4.135652
```

NOTE:

```
## It can also be used to examine the relationship between a numeric outcome variabl
e y and a categorical explanatory variable with 2 levels. (yes,no)

## boxplot(x~y)
## t.test(y~x, mu=0, alt="two.sided", conf= 0.95, var.eq=F, paired=F)

## t.test(y~x)
## t.test(y[x=="no"], y[x=="yes"])
```

Equality of Variance Test

```
## First with a boxplot
## boxplot(y~x)  ensure both x and y are of the same length.

## var(y); var(x)
## var(y[x=="no]) ; var(y[x=="yes])

## Levene's test

## Null: Population variances are equal.
## library(car)
## leveneTest(y~x)
```

For chi-square analysis with R, please get a copy of my **book** "Basic Statistics for Undergraduate Studies Using R" (https://www.amazon.com/BASIC-STATISTICS-UNDERGRADUATE-STUDIES-USING/dp/B08C4FTJFT).

- **One-way ANOVA**

```
head(chickwts)
```

```
  weight      feed
1    179 horsebean
2    160 horsebean
3    136 horsebean
4    227 horsebean
5    217 horsebean
6    168 horsebean
```

```
levels(chickwts$feed)
```

```
[1] "casein"    "horsebean" "linseed"   "meatmeal"  "soybean"   "sunflower"
```

```
library(dplyr)
chick <- slice(chickwts, c(1:36))
names(chick)
```

```
[1] "weight" "feed"
```

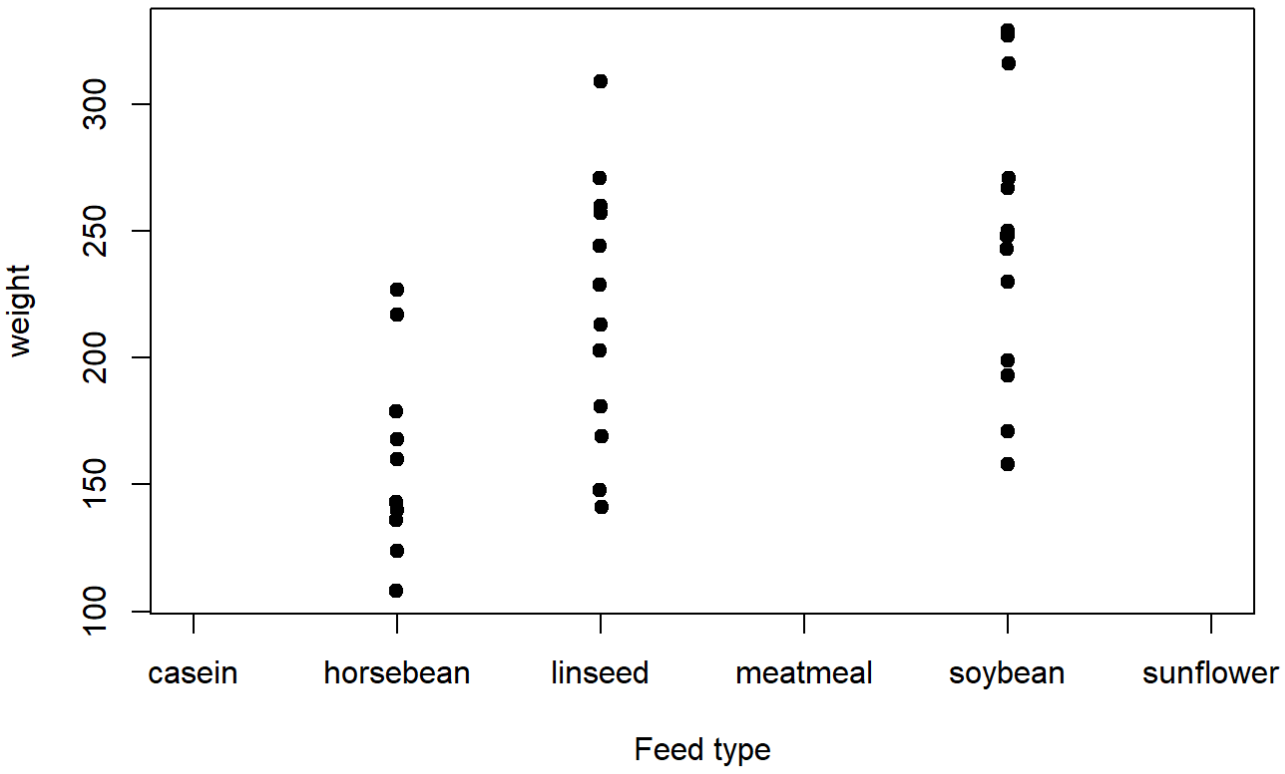
```
str(chick)
```

```
'data.frame':   36 obs. of  2 variables:
 $ weight: num  179 160 136 227 217 168 108 124 143 140 ...
 $ feed  : Factor w/ 6 levels "casein","horsebean",..: 2 2 2 2 2 2 2 2 2 2 ...
```

```
levels(chick$feed)
```

```
[1] "casein"    "horsebean" "linseed"   "meatmeal"  "soybean"   "sunflower"
```

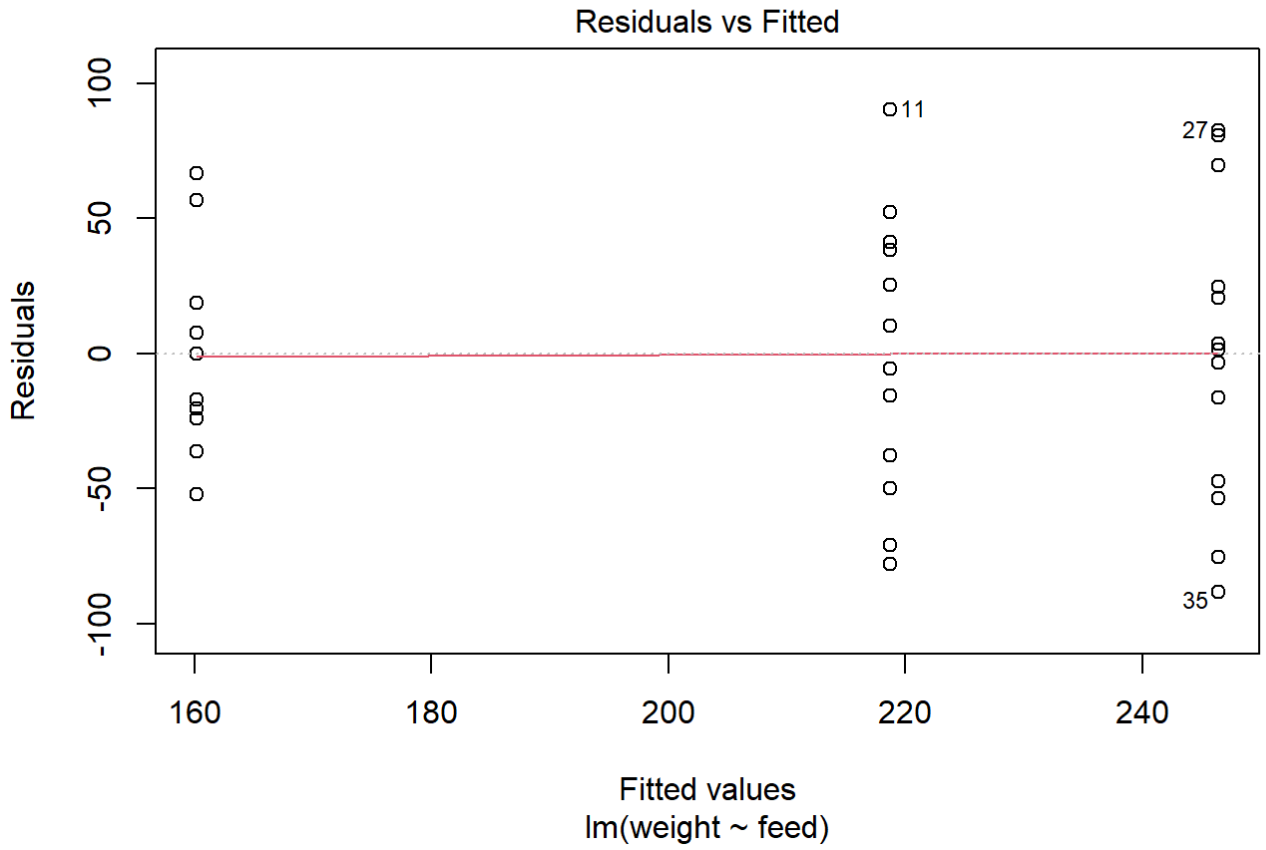
```
stripchart(weight~feed, vertical= T, pch=19, data = chick, xlab="Feed type", method= "jitter", jitter = .004)
```



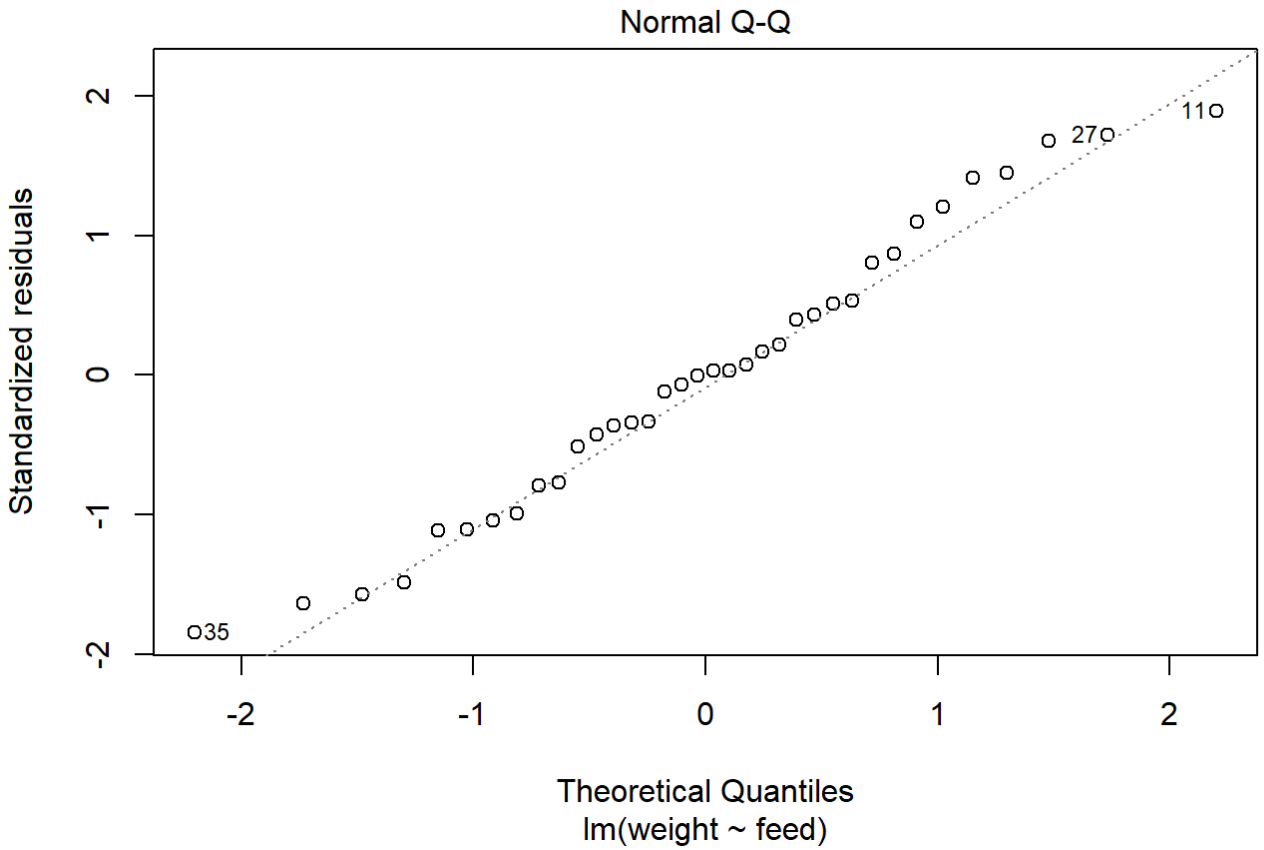
```
result <- lm(weight~feed, data = chick)
anova(result)
```

```
Analysis of Variance Table

Response: weight
          Df Sum Sq Mean Sq F value    Pr(>F)
feed       2  43917 21958.7  8.8879 0.0008169 ***
Residuals 33  81531  2470.6
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

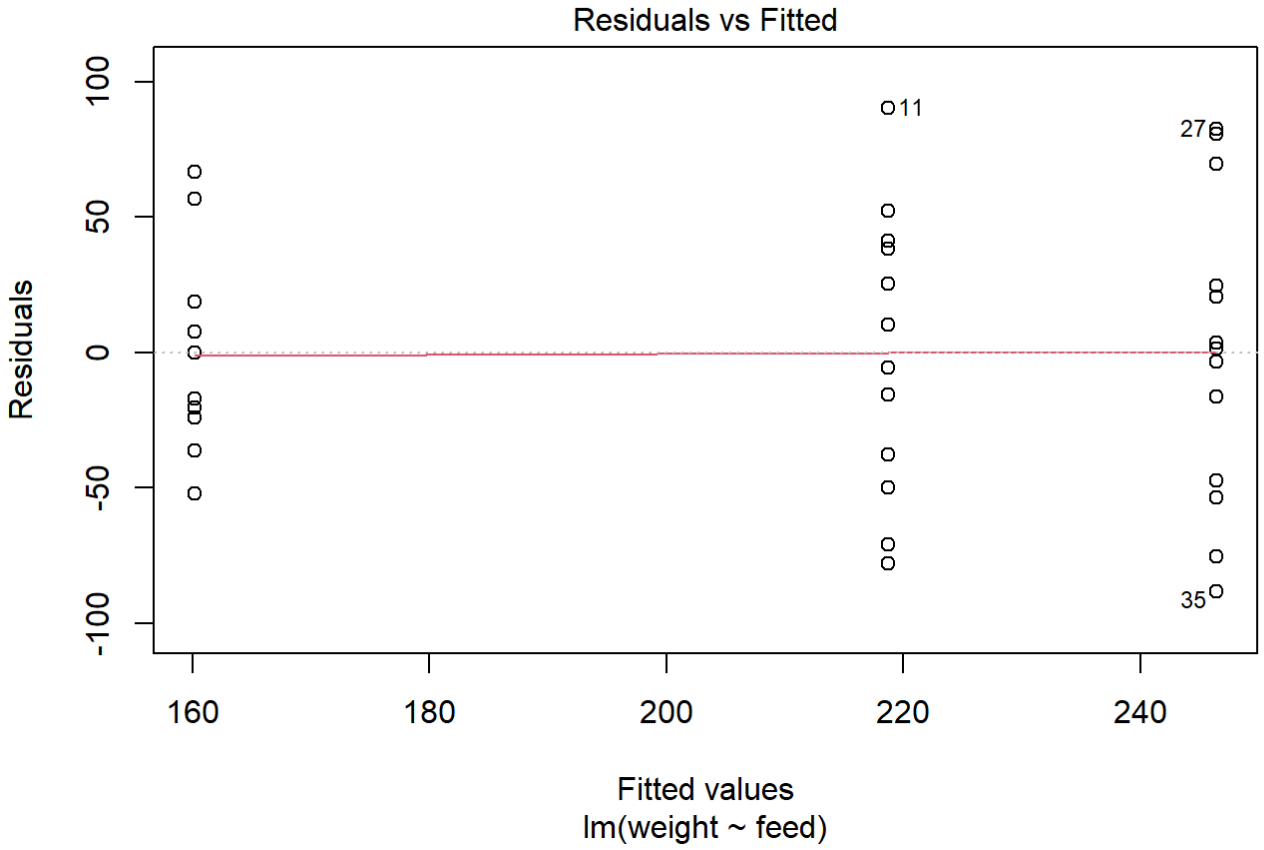
```
plot(result, which = 1)
```

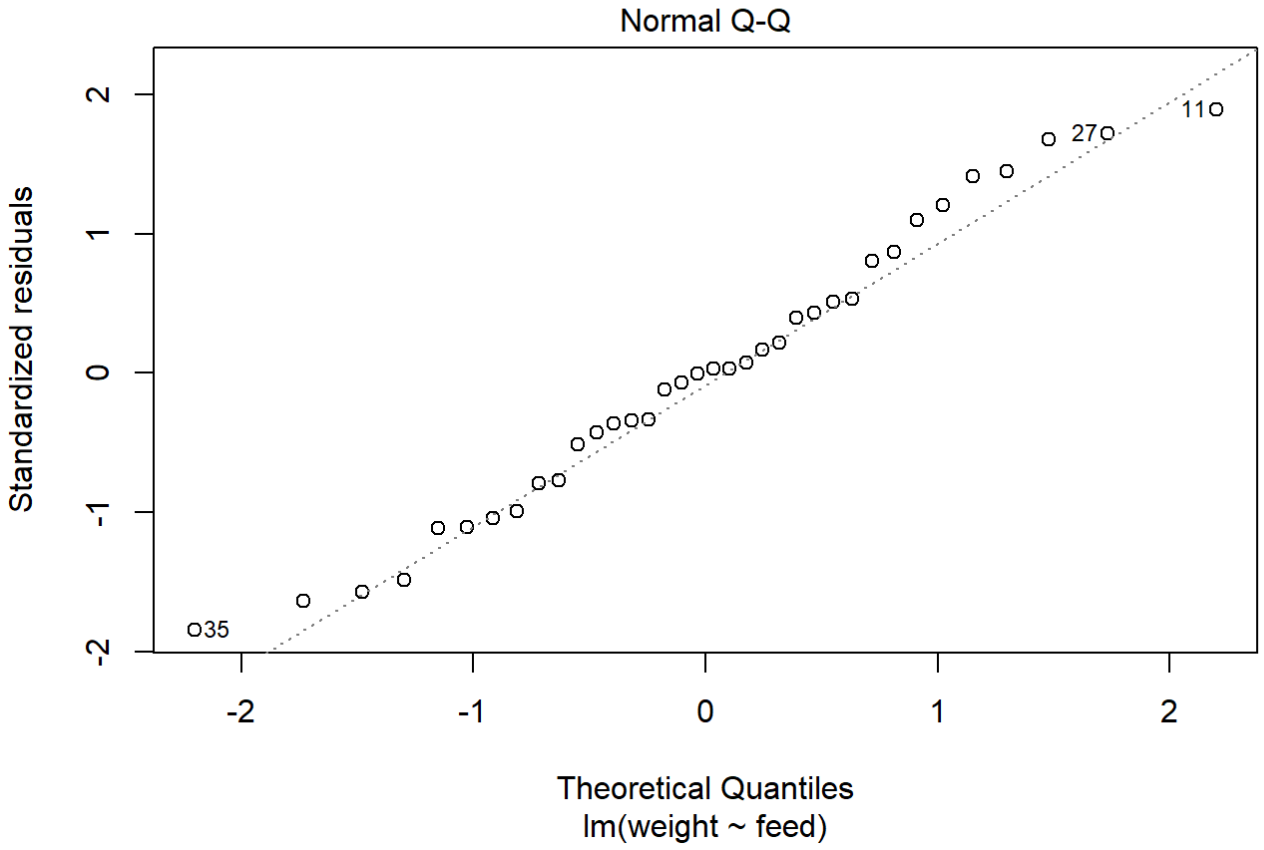


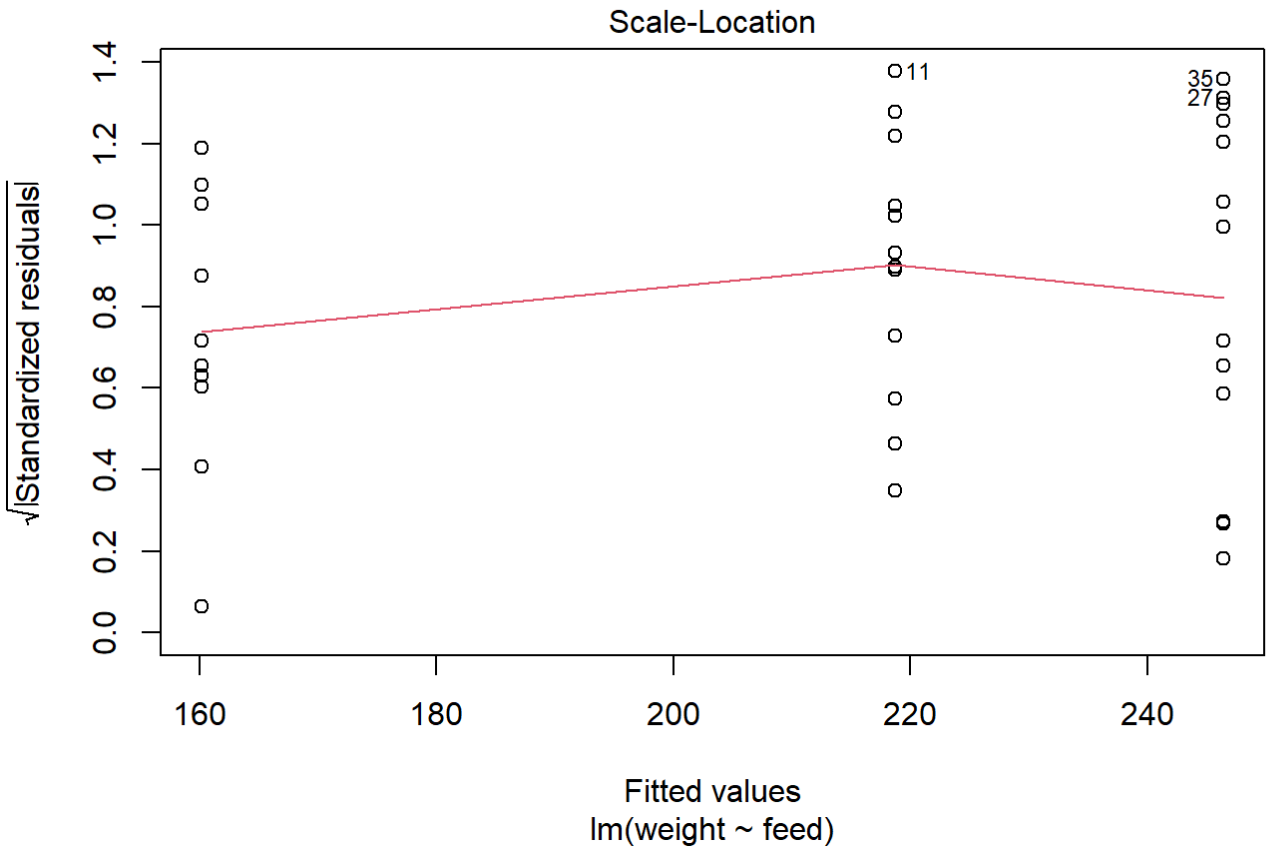

```
## Here we can see that the overall variances are relatively homogenous for all the
 fitted values.

plot(result, which = 2) ## Normality assumptions
```

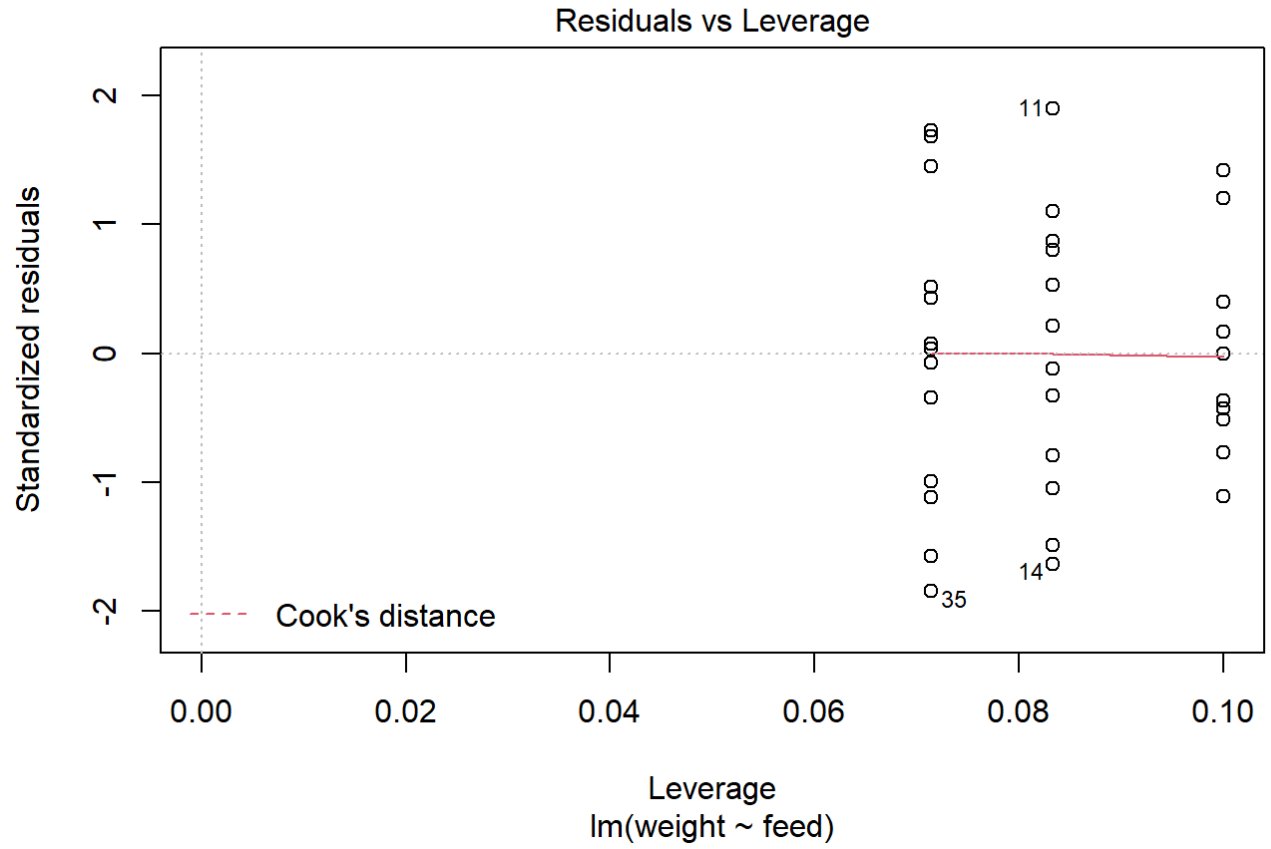



```
## Here we can see it follows the straight line except for a little skewness on top.
plot(result)
```

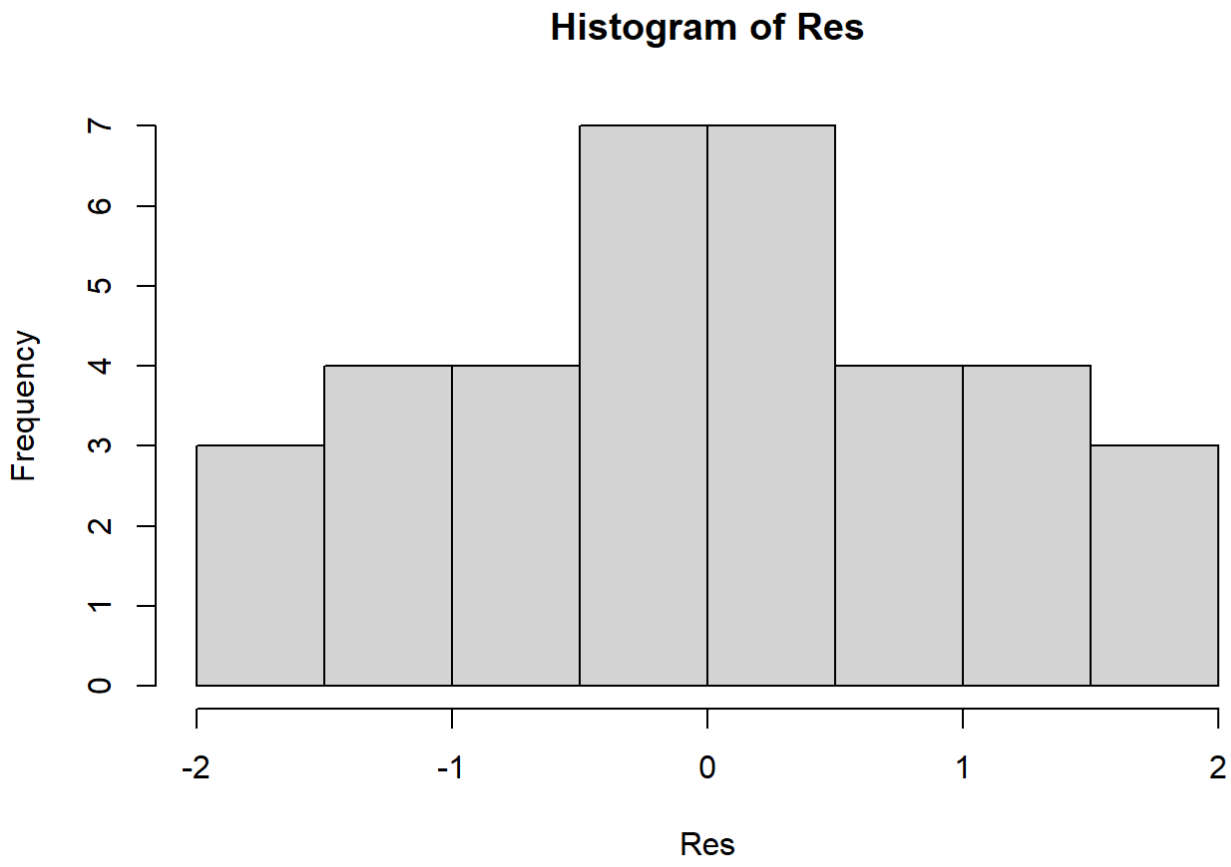

Residuals vs Fitted
Residuals
Fitted values
lm(weight ~ feed)
11
27
35
100
50
0
-50
-100
160
180
200
220
240


Normal Q-Q
Standardized residuals
Theoretical Quantiles
lm(weight ~ feed)
11
27
35
2
1
0
-1
-2


Scale-Location
√|Standardized residuals|
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
11
35
27
160
180
200
220
240
Fitted values
lm(weight ~ feed)


Residuals vs Leverage
Standardized residuals
2
1
0
-1
-2
11
14
35
Cook's distance
0.00
0.02
0.04
0.06
0.08
0.10
Leverage
lm(weight ~ feed)

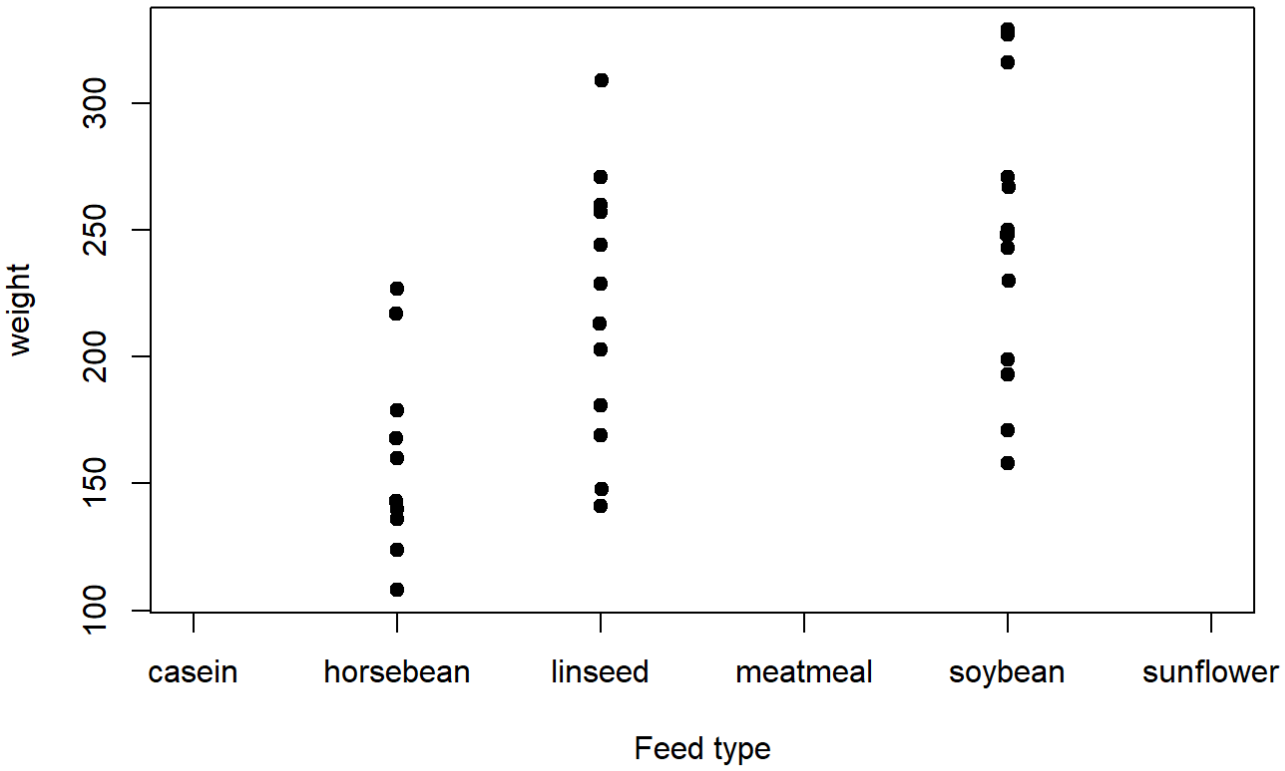
```
Res <- rstandard(result) ## for obtaining standardized residuals
hist(Res)
```




```
TukeyHSD(aov(result))
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = result)

$feed
                      diff       lwr       upr     p adj
linseed-horsebean 58.55000   6.32673 110.77327 0.0252584
soybean-horsebean 86.22857  35.72932 136.72782 0.0005601
soybean-linseed   27.67857 -20.30310  75.66024 0.3447287
```

```
## soybean and horsebean contributes most of the overall significance between the fe
ed type.

 ## Let us visualize this.
stripchart(weight~feed, vertical= T, pch=19, data = chick, xlab="Feed type", method=
"jitter", jitter = .004)

library(agricolae)
```




```
DMRT <- duncan.test(chick$weight, chick$feed, 33, 2470.6)
print(DMRT)
```

```
$statistics
  MSerror Df   Mean       CV
   2470.6 33 213.25 23.30838

$parameters
    test     name.t ntr alpha
  Duncan chick$feed   3  0.05

$duncan
NULL

$means
          chick$weight      std  r Min Max    Q25   Q50    Q75
horsebean     160.2000 38.62584 10 108 227 137.00 151.5 176.25
linseed       218.7500 52.23570 12 141 309 178.00 221.0 257.75
soybean       246.4286 54.12907 14 158 329 206.75 248.0 270.00

$comparison
NULL

$groups
          chick$weight groups
soybean       246.4286      a
linseed       218.7500      a
horsebean     160.2000      b

attr(,"class")
[1] "group"
```

```
LSD <- LSD.test(chick$weight, chick$feed, 33, 2470.6)
print(LSD)
```

```
$statistics
  MSerror Df   Mean       CV
   2470.6 33 213.25 23.30838

$parameters
        test p.ajusted     name.t ntr alpha
  Fisher-LSD      none chick$feed   3  0.05

$means
          chick$weight      std  r      LCL      UCL Min Max    Q25   Q50
horsebean     160.2000 38.62584 10 128.2212 192.1788 108 227 137.00 151.5
linseed       218.7500 52.23570 12 189.5575 247.9425 141 309 178.00 221.0
soybean       246.4286 54.12907 14 219.4016 273.4556 158 329 206.75 248.0
             Q75
horsebean 176.25
linseed   257.75
soybean   270.00

$comparison
NULL

$groups
          chick$weight groups
soybean       246.4286      a
linseed       218.7500      a
horsebean     160.2000      b

attr(,"class")
[1] "group"
```

- **Two-way ANOVA**

This is just an extension of the one-way ANOVA that examines the influence of two different categorical indepenedent variable on one continuous dependent variable.

- denotes interaction and : could be used as well. To add more than one predictor, the plus sign is used.

```
## interaction.plot(c1, c2, response, xlab, ylab, trace.label=)
```

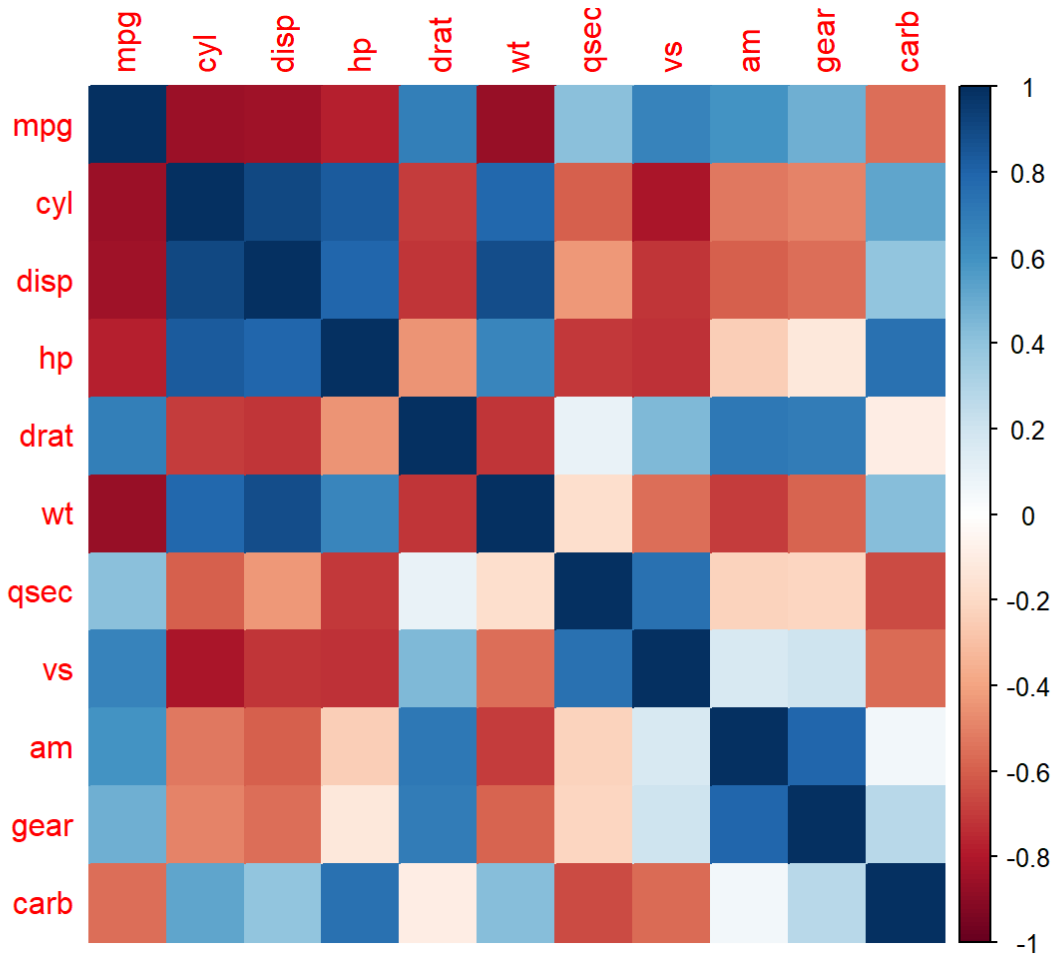
- **Correlation and Regression in R**

```
df = mtcars
num.cols <- sapply(df, is.numeric)
cor.data <- cor(df[, num.cols])
print(cor.data)
```

```
            mpg        cyl       disp         hp        drat         wt
mpg   1.0000000 -0.8521620 -0.8475514 -0.7761684  0.68117191 -0.8676594
cyl  -0.8521620  1.0000000  0.9020329  0.8324475 -0.69993811  0.7824958
disp -0.8475514  0.9020329  1.0000000  0.7909486 -0.71021393  0.8879799
hp   -0.7761684  0.8324475  0.7909486  1.0000000 -0.44875912  0.6587479
drat  0.6811719 -0.6999381 -0.7102139 -0.4487591  1.00000000 -0.7124406
wt   -0.8676594  0.7824958  0.8879799  0.6587479 -0.71244065  1.0000000
qsec  0.4186840 -0.5912421 -0.4336979 -0.7082234  0.09120476 -0.1747159
vs    0.6640389 -0.8108118 -0.7104159 -0.7230967  0.44027846 -0.5549157
am    0.5998324 -0.5226070 -0.5912270 -0.2432043  0.71271113 -0.6924953
gear  0.4802848 -0.4926866 -0.5555692 -0.1257043  0.69961013 -0.5832870
carb -0.5509251  0.5269883  0.3949769  0.7498125 -0.09078980  0.4276059
            qsec         vs          am       gear        carb
mpg   0.41868403  0.6640389  0.59983243  0.4802848 -0.55092507
cyl  -0.59124207 -0.8108118 -0.52260705 -0.4926866  0.52698829
disp -0.43369788 -0.7104159 -0.59122704 -0.5555692  0.39497686
hp   -0.70822339 -0.7230967 -0.24320426 -0.1257043  0.74981247
drat  0.09120476  0.4402785  0.71271113  0.6996101 -0.09078980
wt   -0.17471588 -0.5549157 -0.69249526 -0.5832870  0.42760594
qsec  1.00000000  0.7445354 -0.22986086 -0.2126822 -0.65624923
vs    0.74453544  1.0000000  0.16834512  0.2060233 -0.56960714
am   -0.22986086  0.1683451  1.00000000  0.7940588  0.05753435
gear -0.21268223  0.2060233  0.79405876  1.0000000  0.27407284
carb -0.65624923 -0.5696071  0.05753435  0.2740728  1.00000000
```

```
## library(DT)
## datatable(cor.data, extensions = "buttons", options = list(
##  dom = "Bfrtip",
##  buttons = c("copy","csv","excel","pdf","print")
## ))

## Just for making a nice datatable with copy options.
```

```
library(corrgram)
library(corrplot)

print(corrplot(cor.data, method = "color"))
```


mpg
cyl
disp
hp
drat
wt
qsec
vs
am
gear
carb
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1

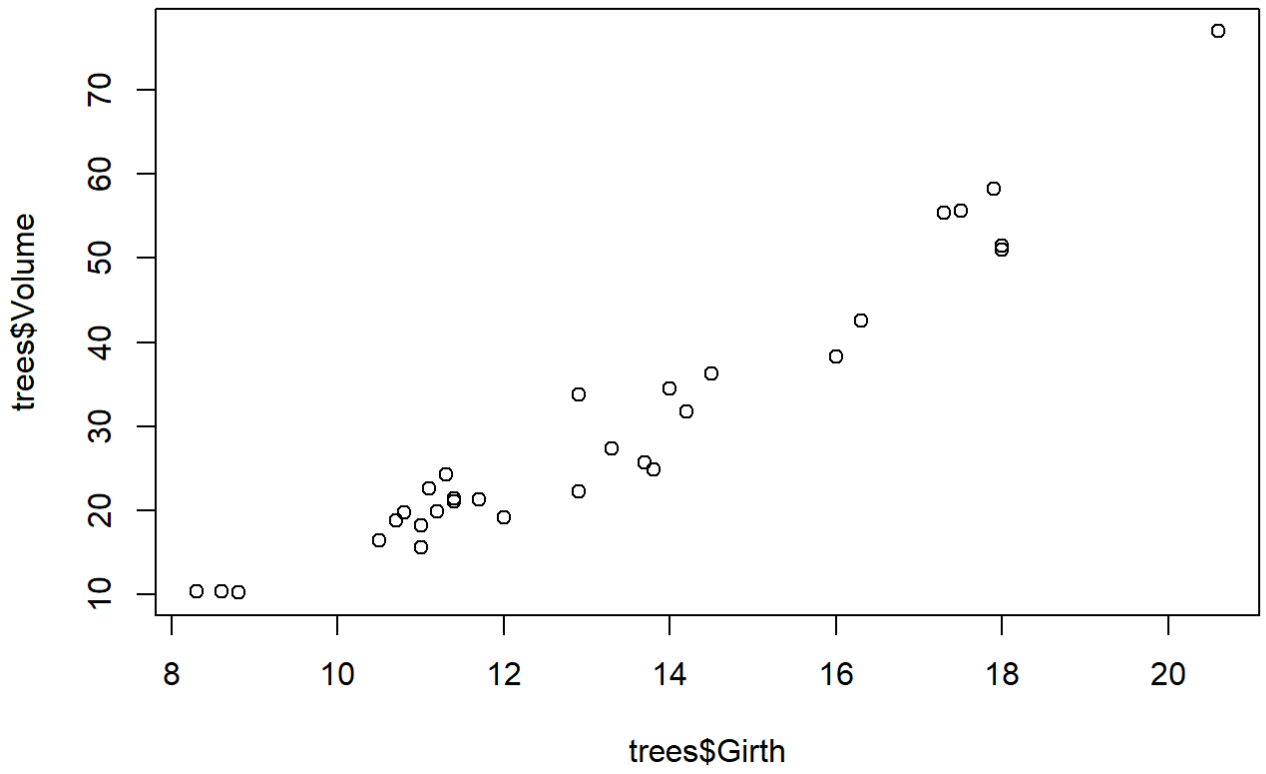
```
            mpg        cyl       disp         hp        drat         wt
mpg   1.0000000 -0.8521620 -0.8475514 -0.7761684  0.68117191 -0.8676594
cyl  -0.8521620  1.0000000  0.9020329  0.8324475 -0.69993811  0.7824958
disp -0.8475514  0.9020329  1.0000000  0.7909486 -0.71021393  0.8879799
hp   -0.7761684  0.8324475  0.7909486  1.0000000 -0.44875912  0.6587479
drat  0.6811719 -0.6999381 -0.7102139 -0.4487591  1.00000000 -0.7124406
wt   -0.8676594  0.7824958  0.8879799  0.6587479 -0.71244065  1.0000000
qsec  0.4186840 -0.5912421 -0.4336979 -0.7082234  0.09120476 -0.1747159
vs    0.6640389 -0.8108118 -0.7104159 -0.7230967  0.44027846 -0.5549157
am    0.5998324 -0.5226070 -0.5912270 -0.2432043  0.71271113 -0.6924953
gear  0.4802848 -0.4926866 -0.5555692 -0.1257043  0.69961013 -0.5832870
carb -0.5509251  0.5269883  0.3949769  0.7498125 -0.09078980  0.4276059
            qsec         vs          am       gear        carb
mpg   0.41868403  0.6640389  0.59983243  0.4802848 -0.55092507
cyl  -0.59124207 -0.8108118 -0.52260705 -0.4926866  0.52698829
disp -0.43369788 -0.7104159 -0.59122704 -0.5555692  0.39497686
hp   -0.70822339 -0.7230967 -0.24320426 -0.1257043  0.74981247
drat  0.09120476  0.4402785  0.71271113  0.6996101 -0.09078980
wt   -0.17471588 -0.5549157 -0.69249526 -0.5832870  0.42760594
qsec  1.00000000  0.7445354 -0.22986086 -0.2126822 -0.65624923
vs    0.74453544  1.0000000  0.16834512  0.2060233 -0.56960714
am   -0.22986086  0.1683451  1.00000000  0.7940588  0.05753435
gear -0.21268223  0.2060233  0.79405876  1.0000000  0.27407284
carb -0.65624923 -0.5696071  0.05753435  0.2740728  1.00000000
```

Visualization Techniques with R

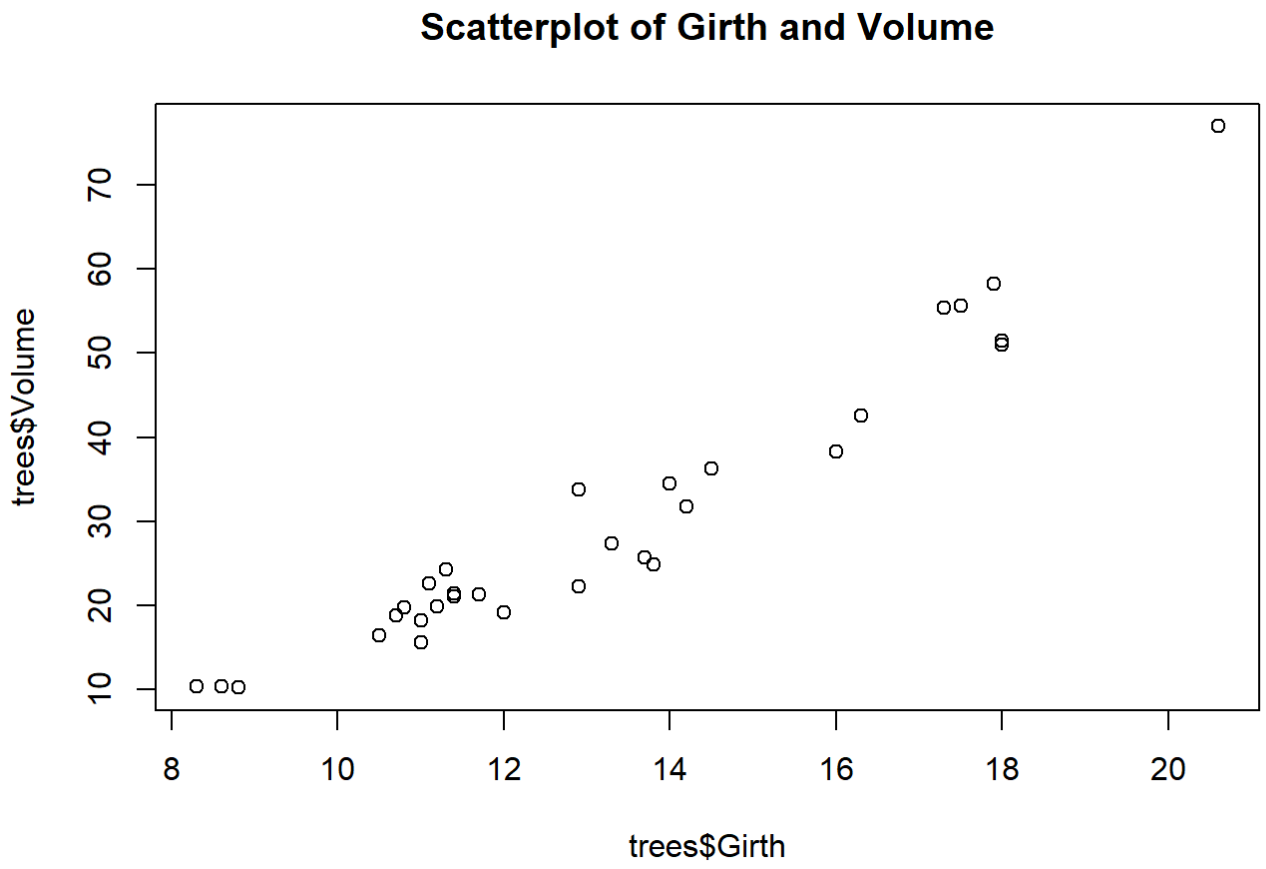
- **The Plot Function**

For visualizing simple scatreplots. You can make reference to my new book for more examples of other plot functions.

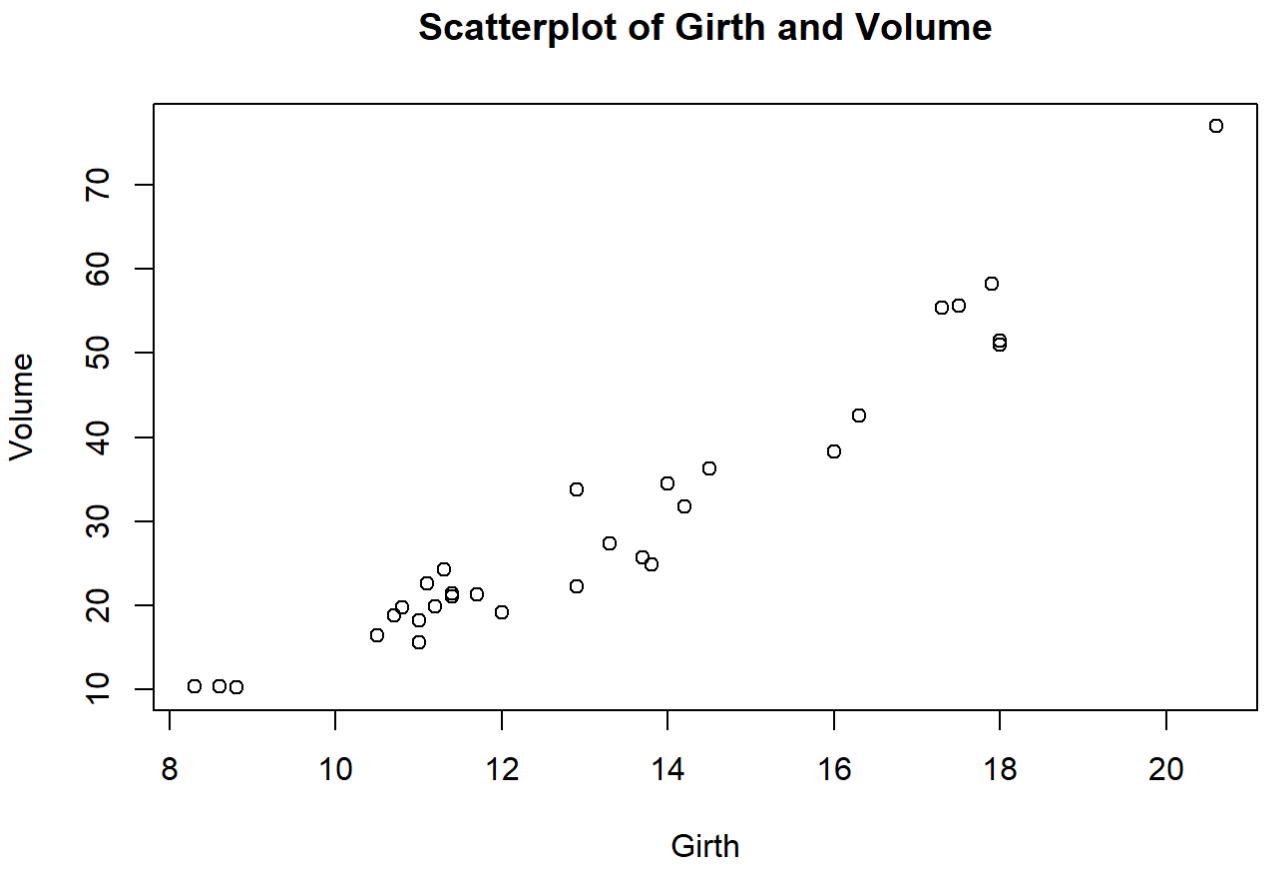
```
plot(trees$Girth,trees$Volume)
```




```
## To add title
plot(trees$Girth,trees$Volume, main = "Scatterplot of Girth and Volume")
```




```
## To add labels
plot(trees$Girth,trees$Volume, main = "Scatterplot of Girth and Volume",
     xlab = "Girth", ylab = "Volume")
```



- **ggplot2**

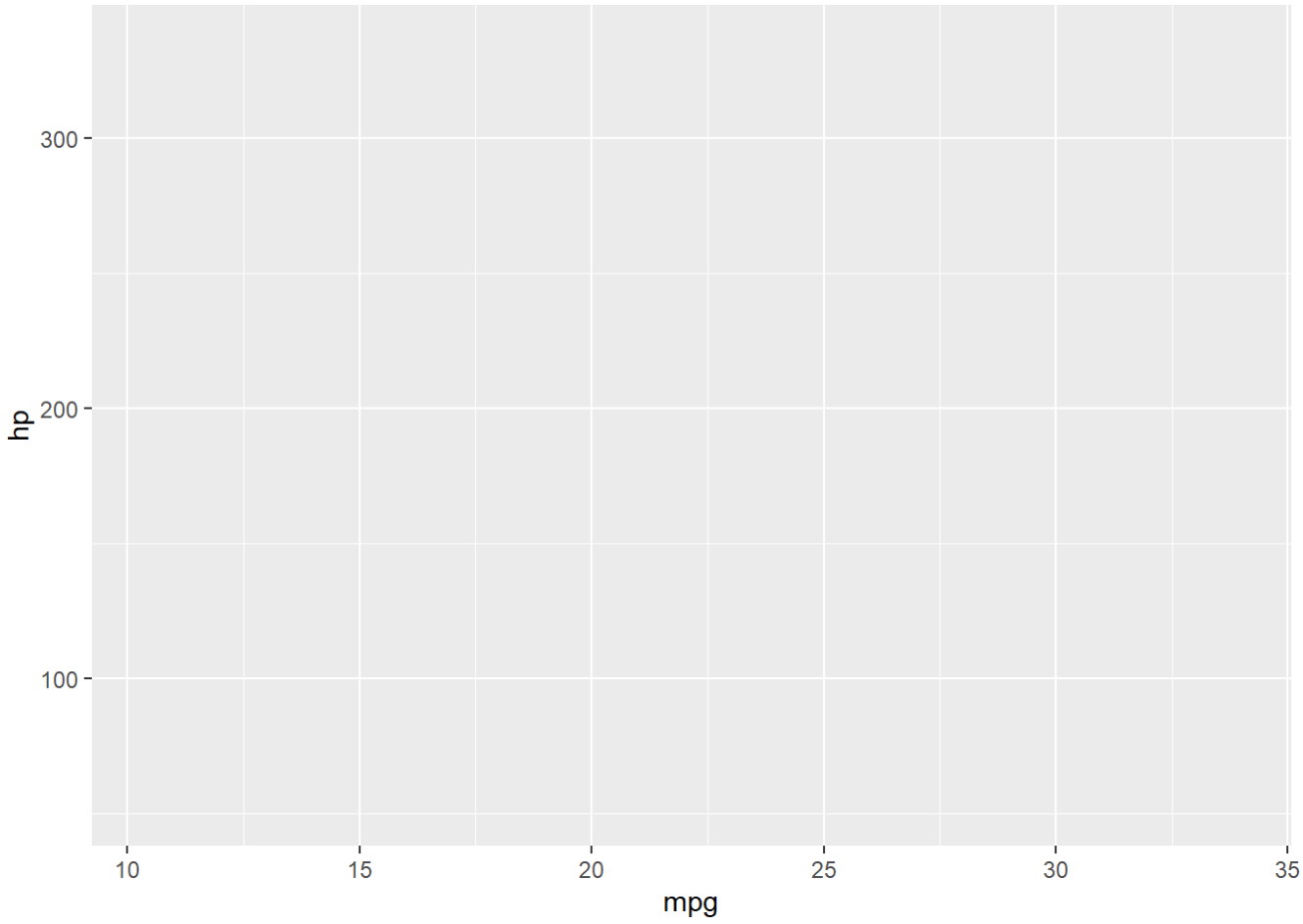
This is one of the most popular data visualization package for R created by Hadley Wickham. It follows a distict pattern of graphics and it builds on the ideas of adding layers.

ggplot2 layers

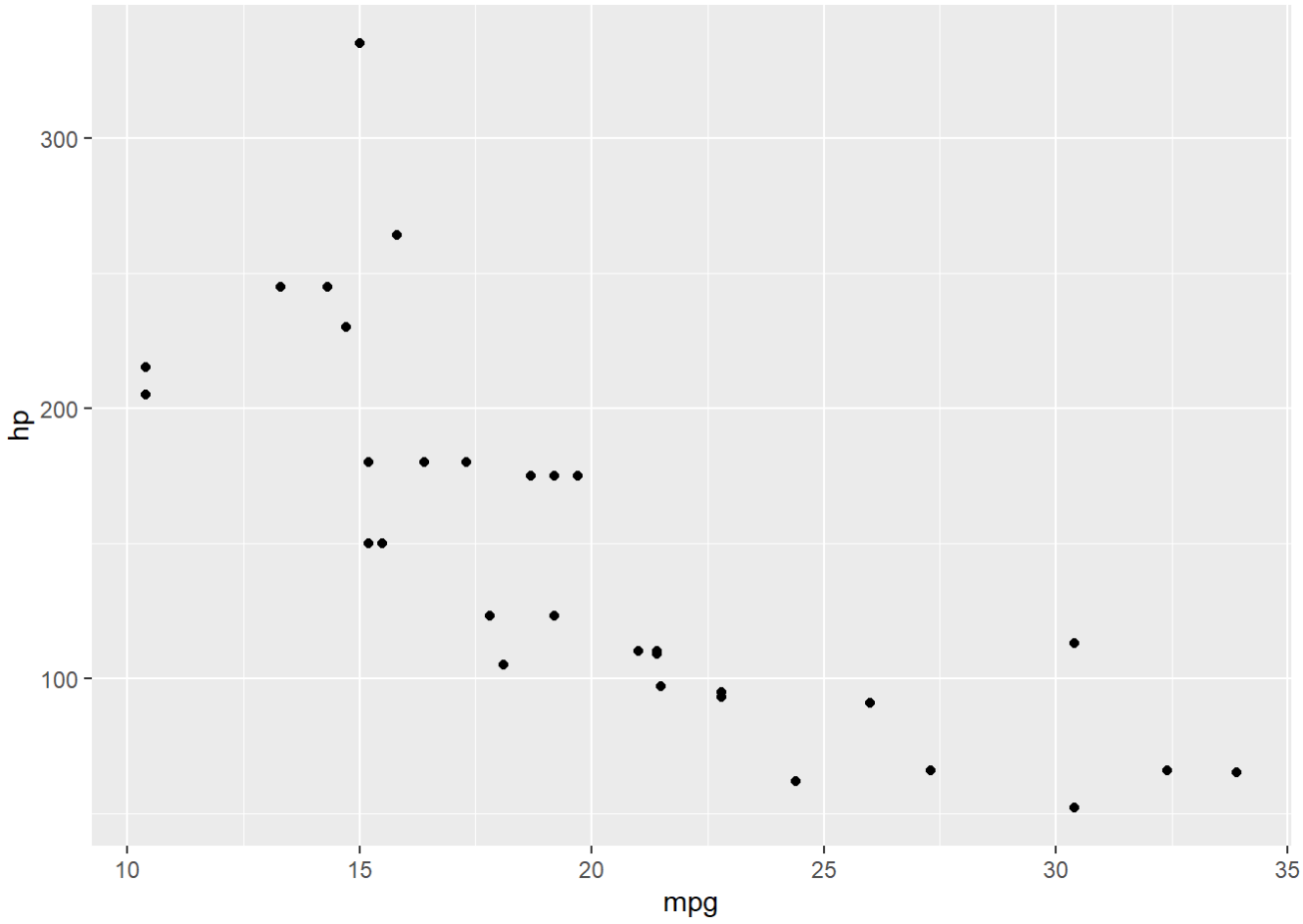
1. Data
2. Aesthetics
3. Geometry

```
## Ensure ggplot2 package is installed on your software
library(ggplot2)
ggplot(data = mtcars) ## with this nothing will show up.
```

```
ggplot(data = mtcars, aes(x=mpg, y=hp)) ## data + aesthetics
```

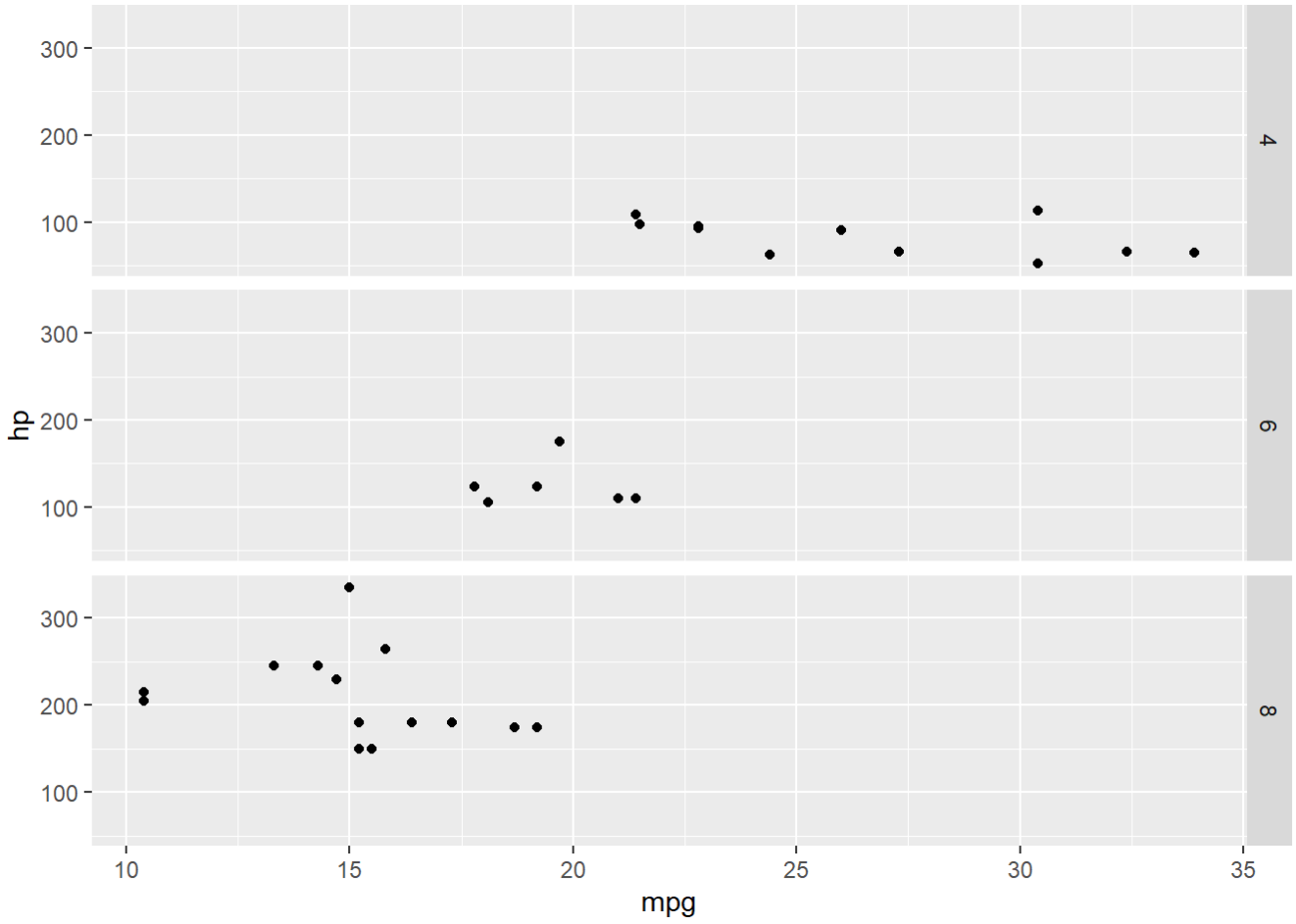



```
pl <- ggplot(data = mtcars, aes(x=mpg, y=hp))
pl + geom_point() ## point for scatterplot geometry.
```

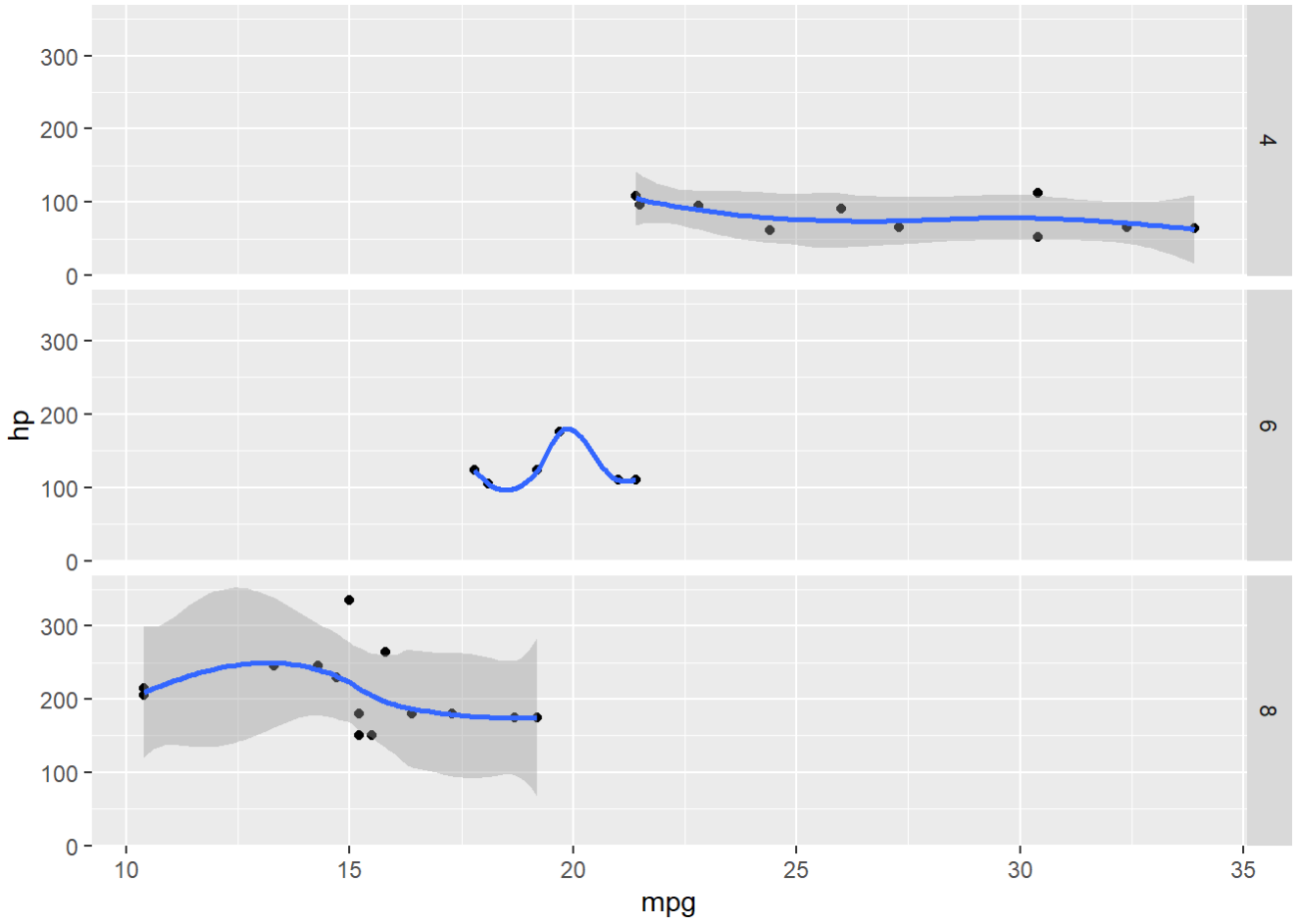


4. Facets
5. Statistics
6. Coordinates
7. Themes

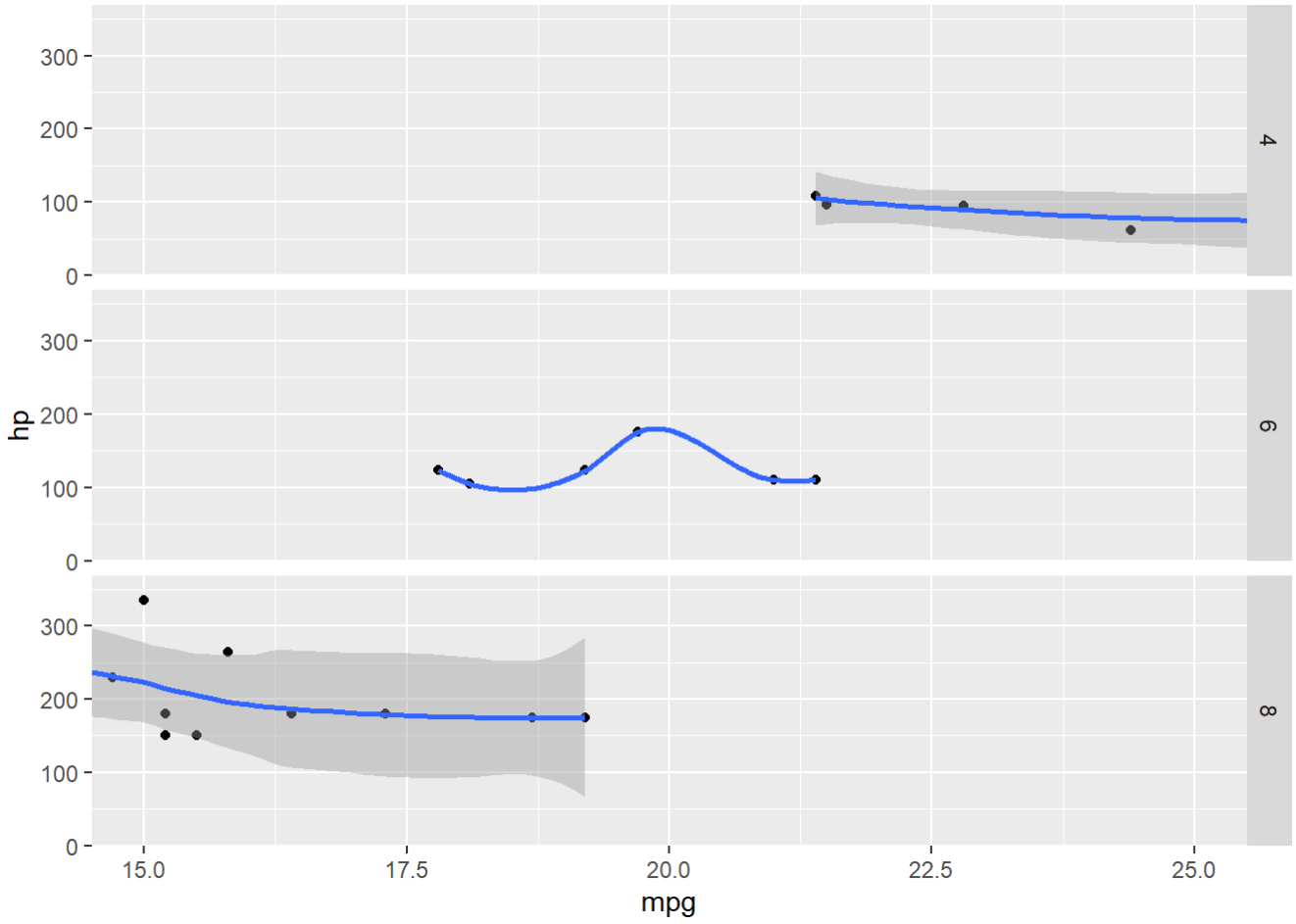
```
pl <- pl + geom_point()
pl + facet_grid(cyl~.) ## Multiple plots of mpg vs hp seperated by cyl levels
```



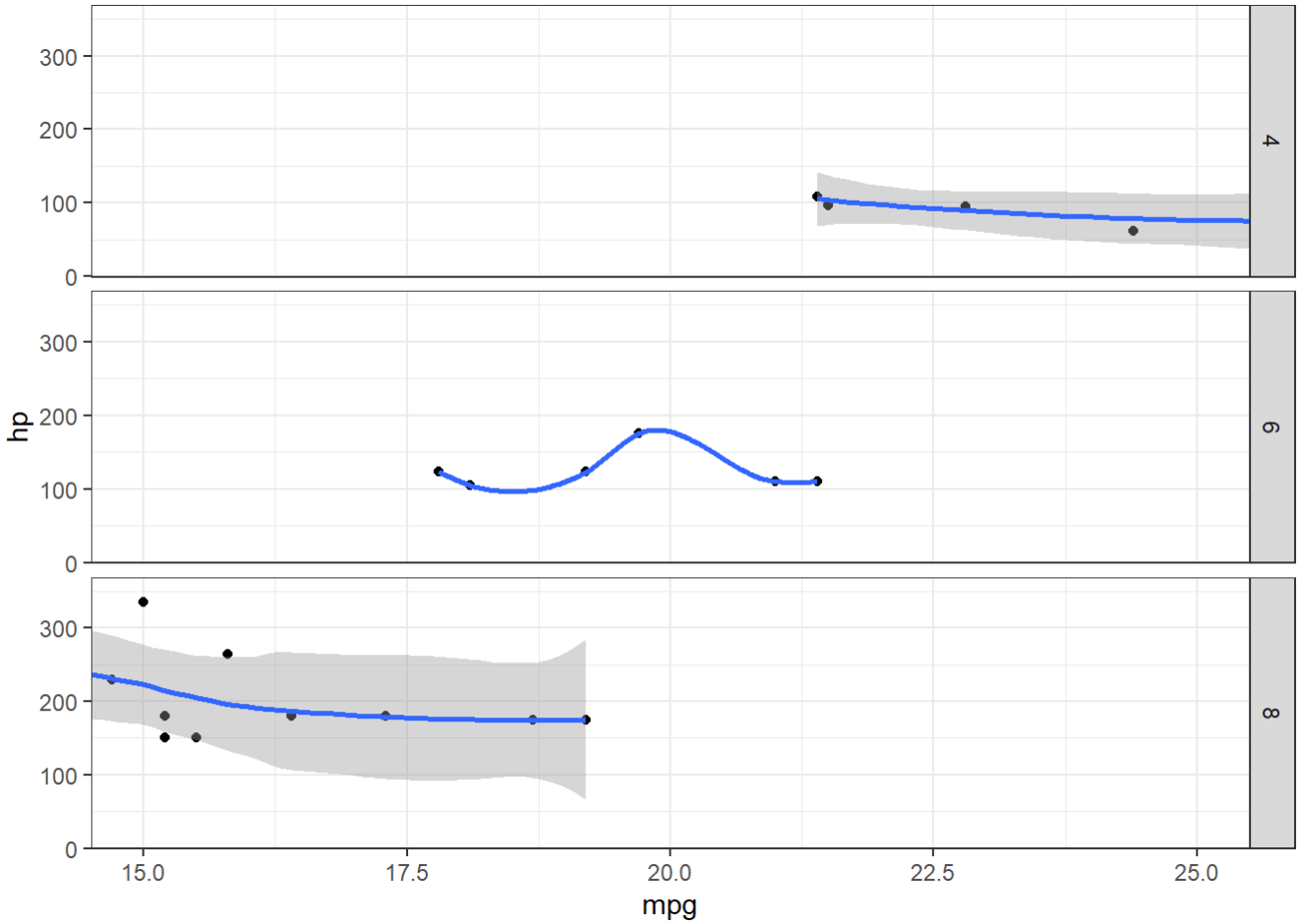

```
## Adding a smoot fit
pl + facet_grid(cyl~.) + stat_smooth() ## provides an error measure
```




```
## manipulating coordinates
pl2 <- pl + facet_grid(cyl~.) + stat_smooth()
pl2 + coord_cartesian(xlim = c(15,25)) ## For bringing in and out of the axes
```

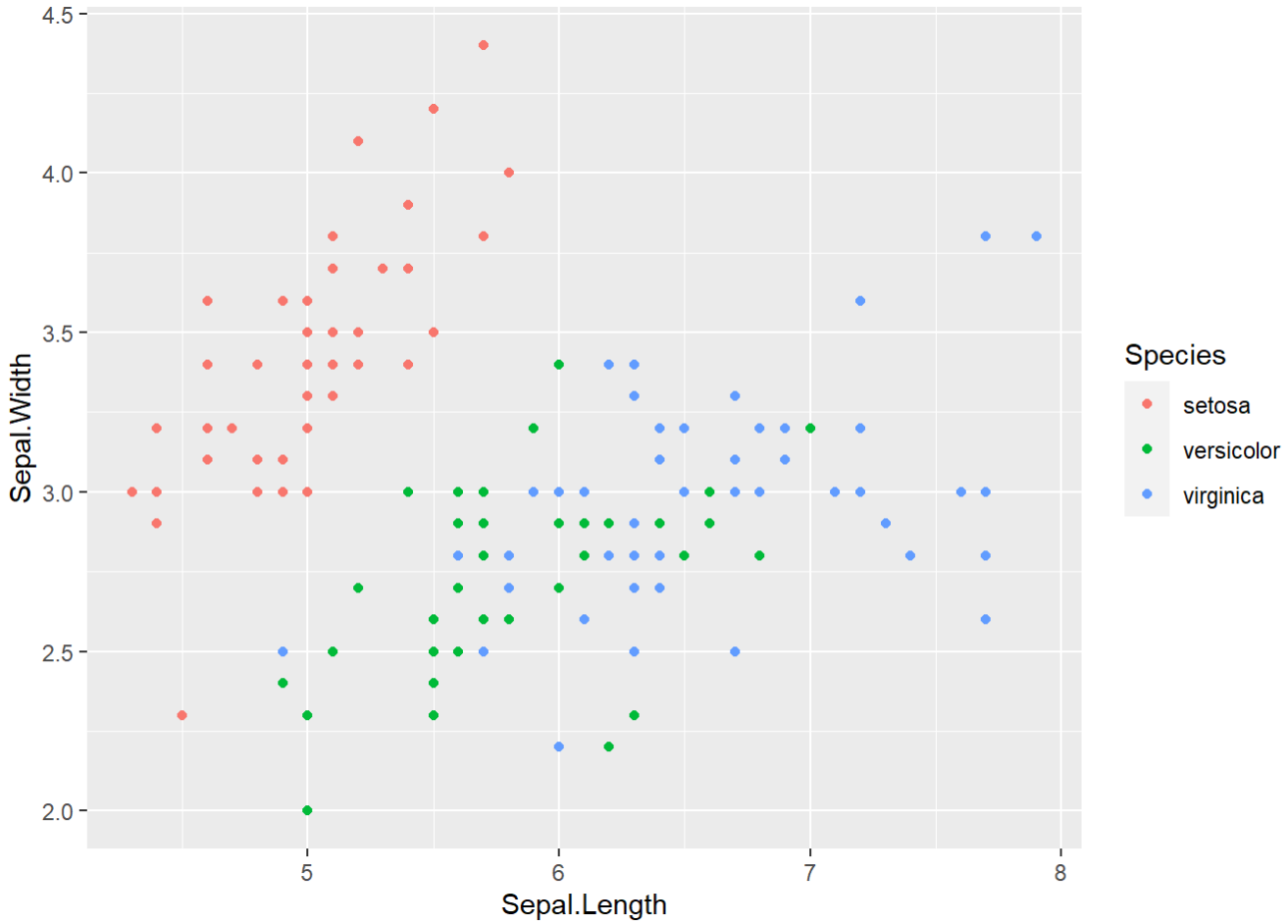



```
## Themes
pl2 + coord_cartesian(xlim = c(15,25)) + theme_bw()
```

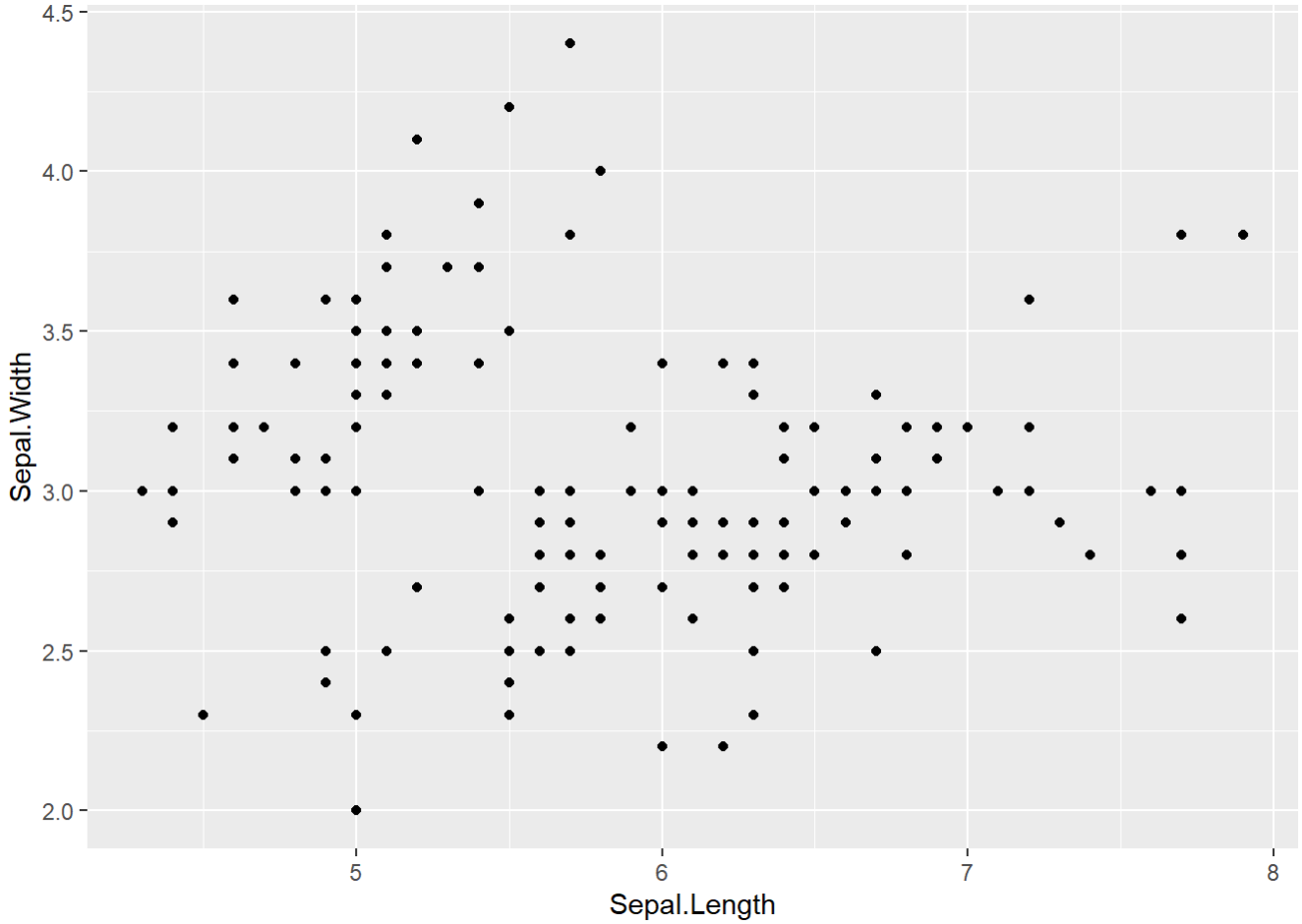


- **qplot**

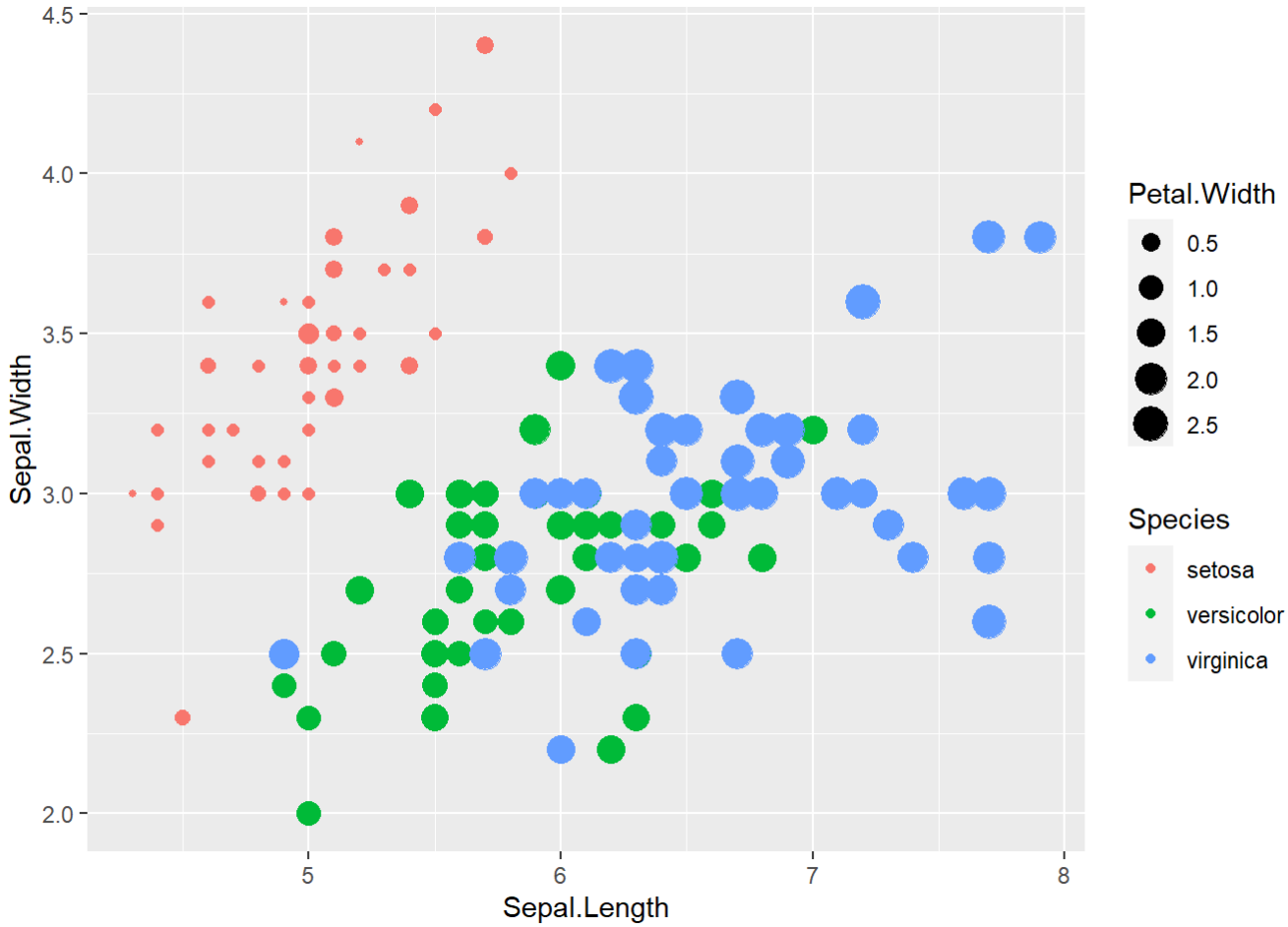
```
qplot(Sepal.Length, Sepal.Width, data=iris, color = Species)
```



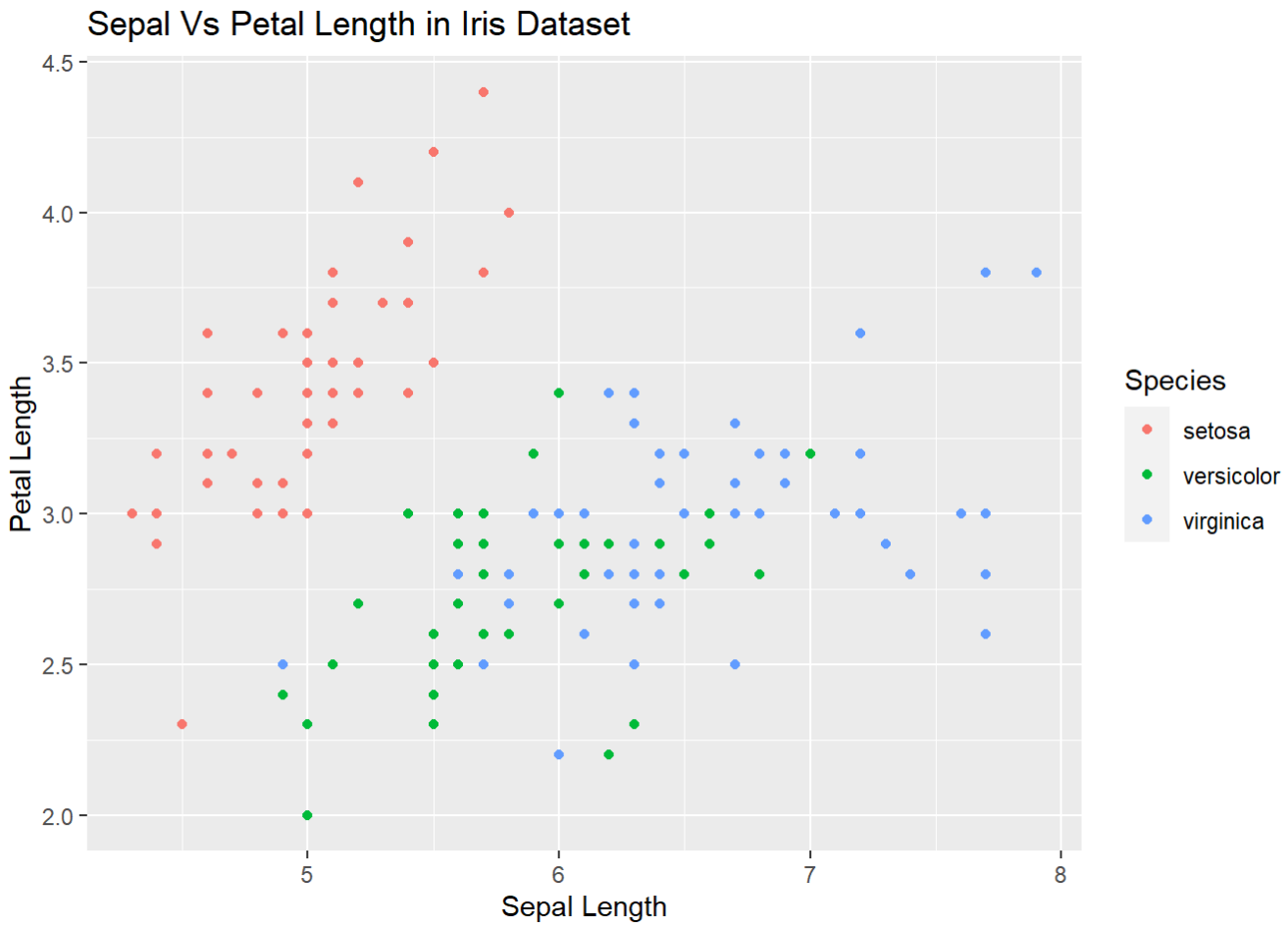

```
## Graph shwoing the relationship btw length and width of 3 different species

qplot(Sepal.Length, Sepal.Width, data=iris)
```



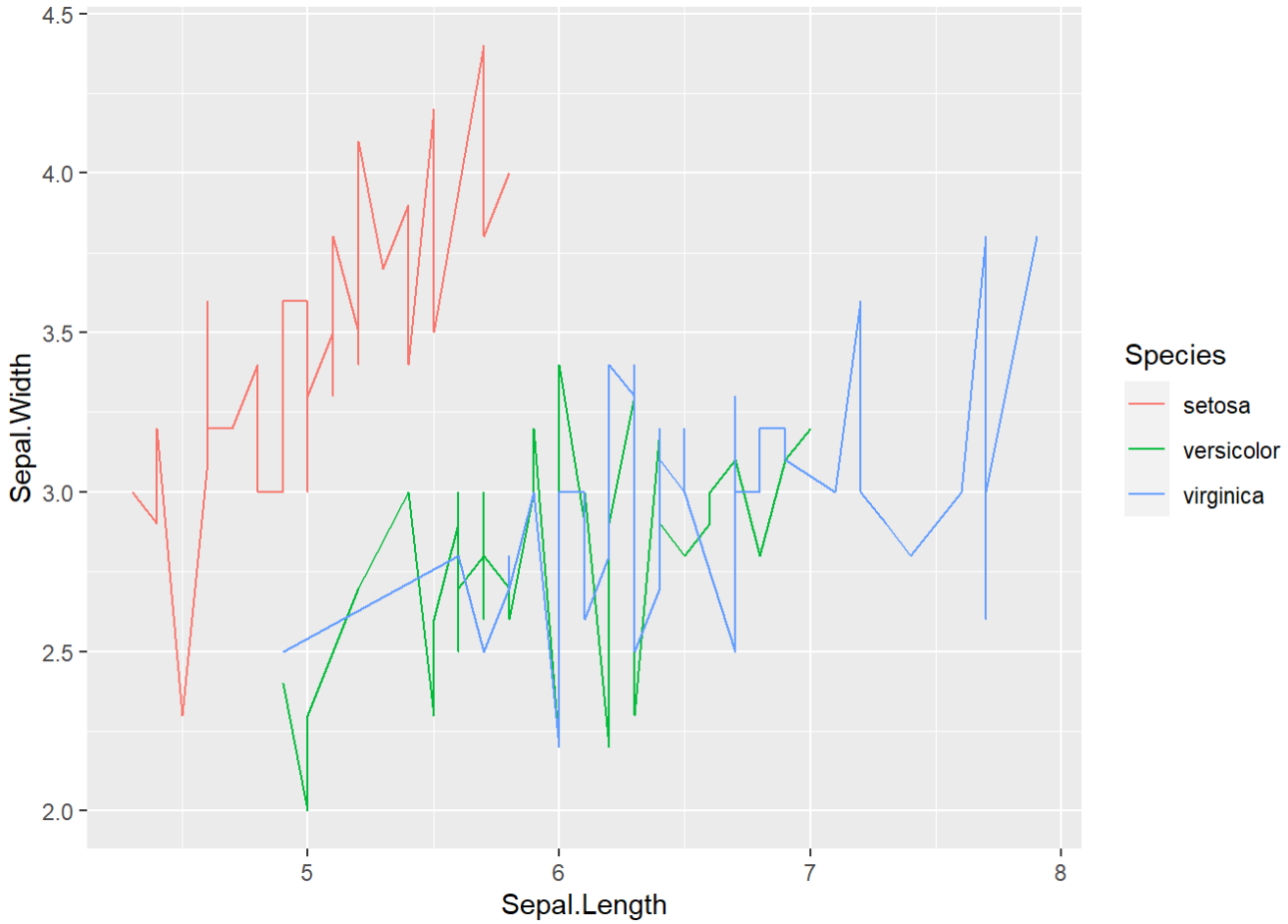

```
qplot(Sepal.Length, Sepal.Width, data=iris, color = Species, size = Petal.Width)
```



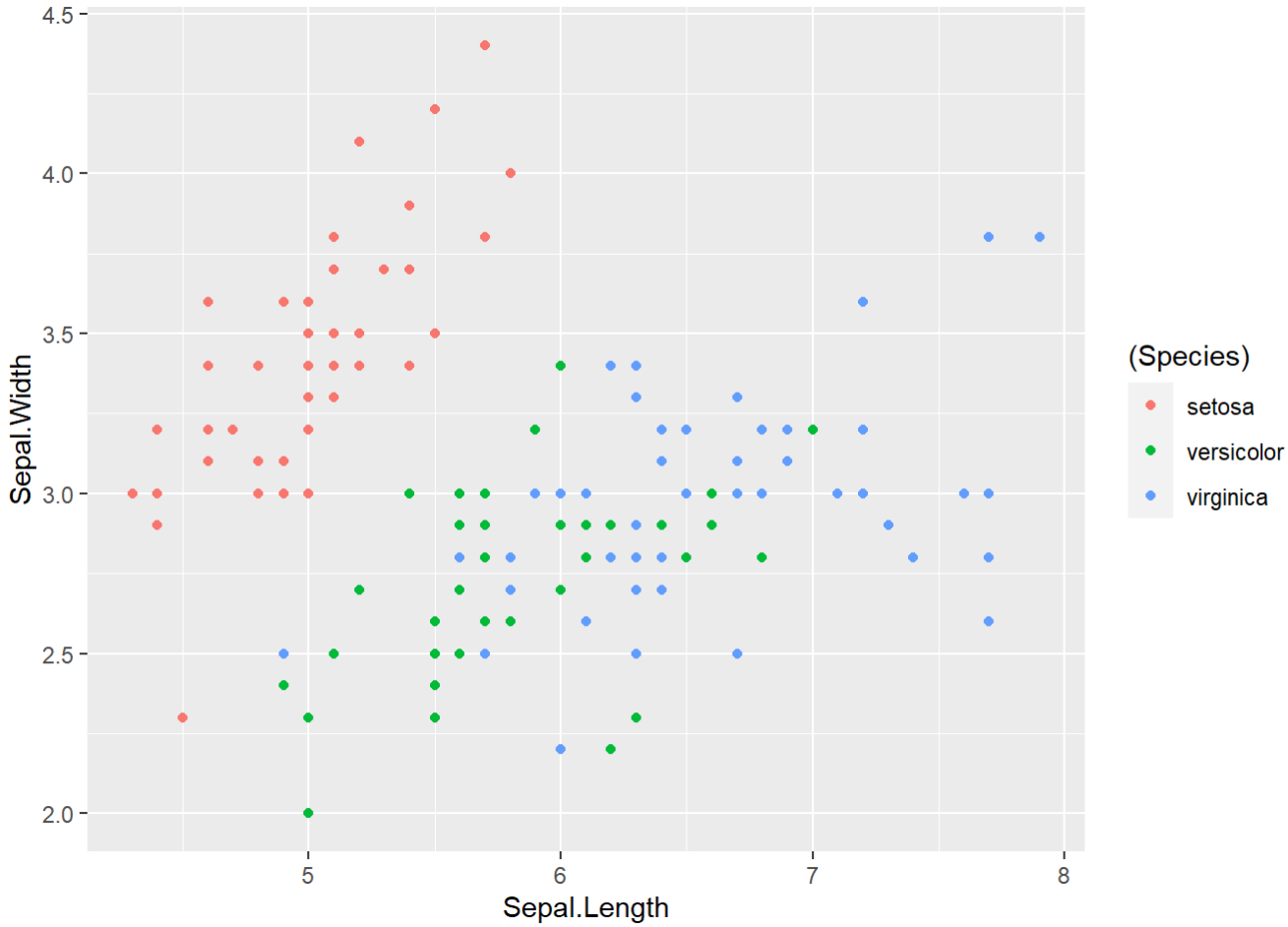

```
## The bases for size is Petal width. So, Setosa have the smallest.

##Adding labels to the plot
qplot(Sepal.Length, Sepal.Width, data=iris, color = Species,
      xlab = "Sepal Length", ylab = "Petal Length",
      main = "Sepal Vs Petal Length in Iris Dataset")
```



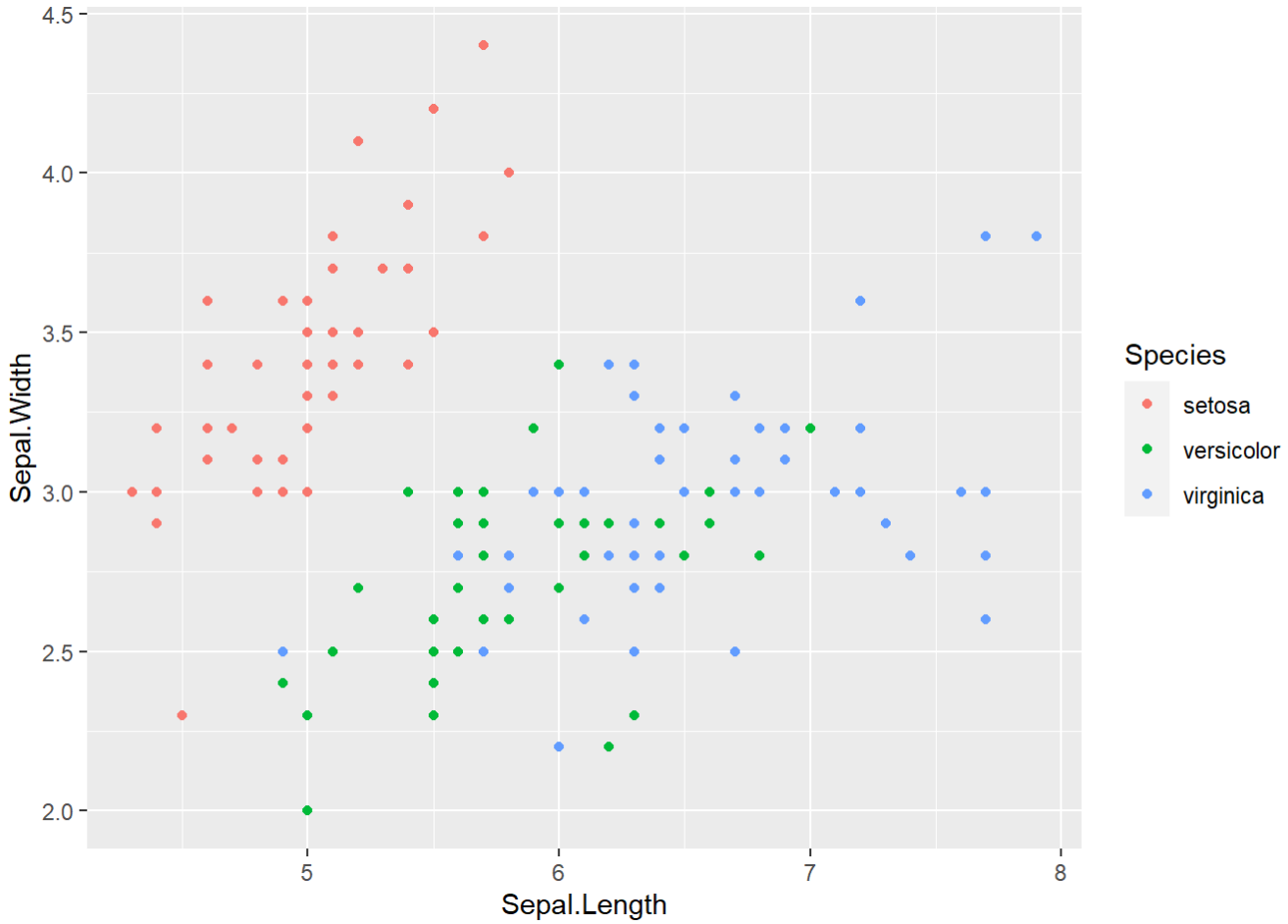

```
qplot(Sepal.Length, Sepal.Width, data=iris, geom = "line", color = Species)
```



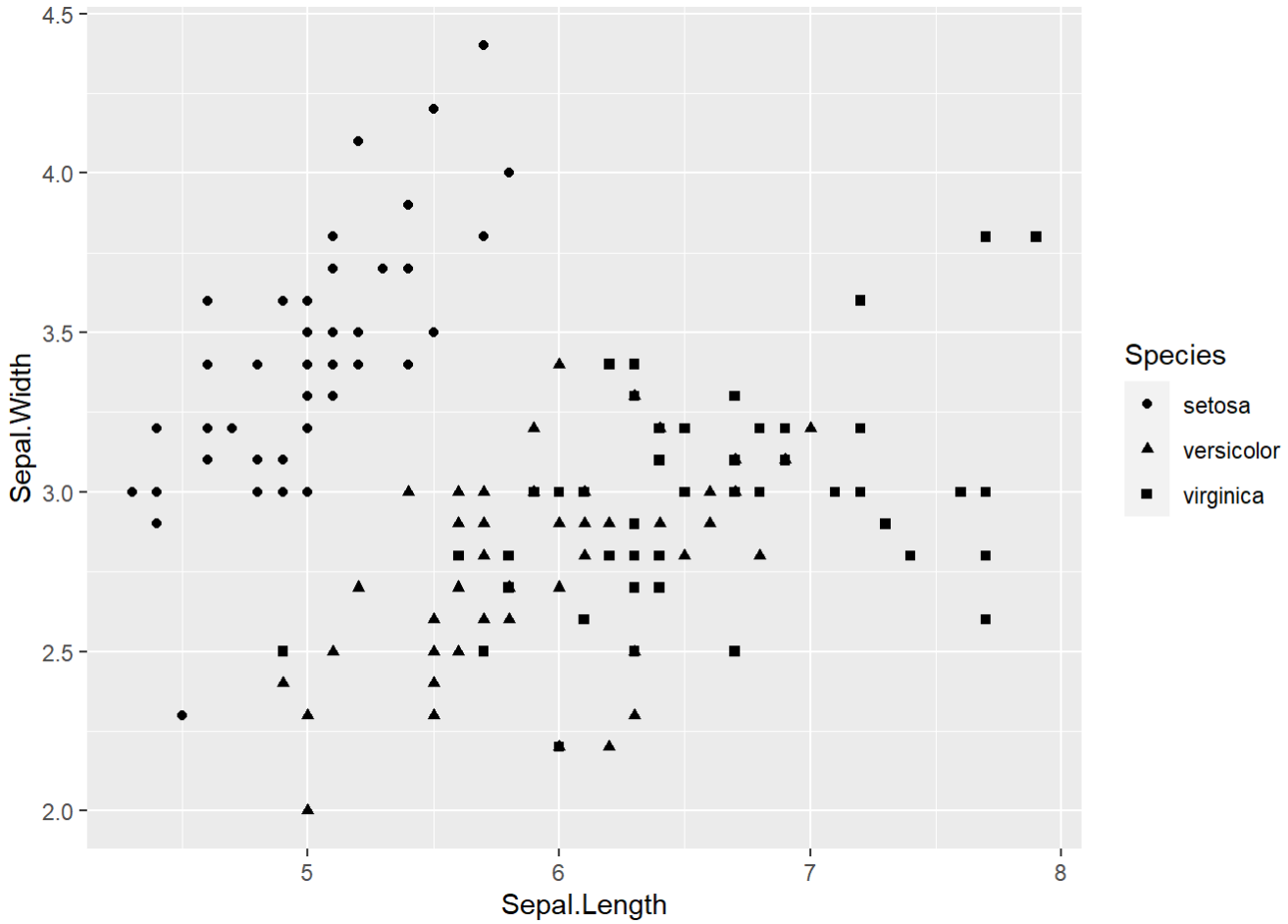

```
## Distinguish between species using color scheme
ggplot(data = iris, aes(Sepal.Length, Sepal.Width)) + geom_point(aes(color = (Specie
s)))
```



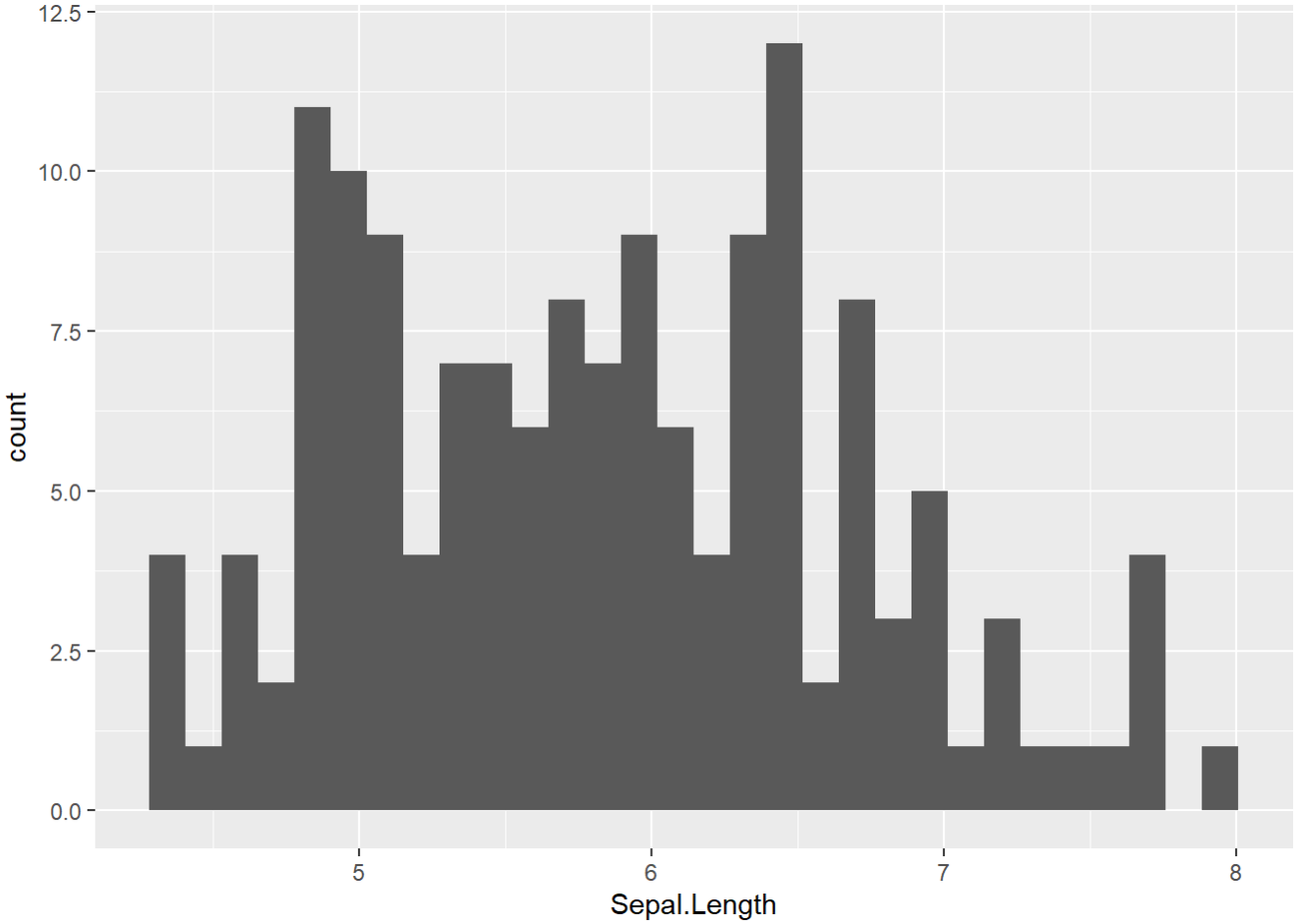

```
# OR
ggplot(data = iris, aes(Sepal.Length, Sepal.Width, colour = Species)) + geom_point()
```



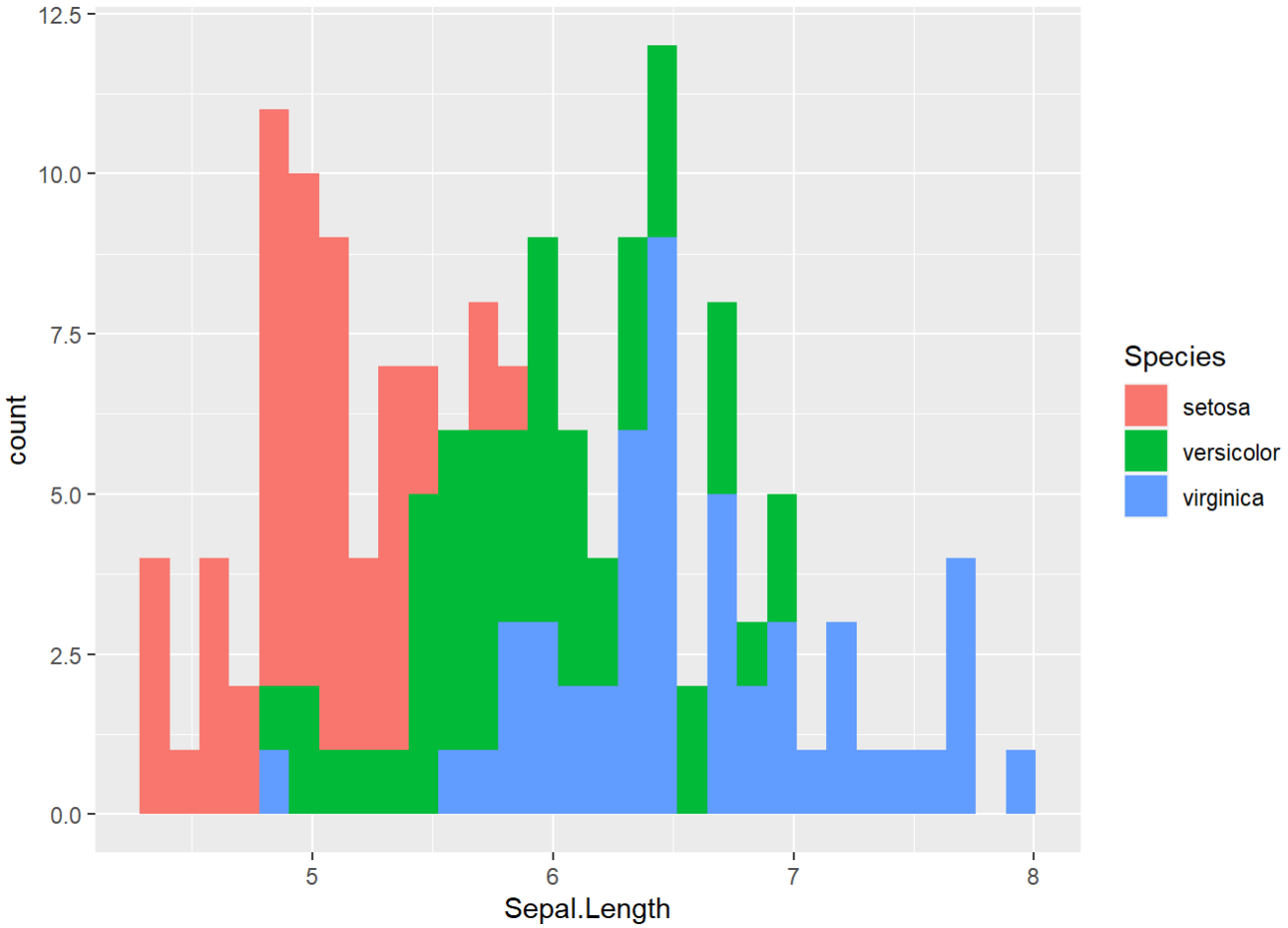

```
ggplot(data = iris, aes(Sepal.Length, Sepal.Width, shape = Species)) + geom_point()
```



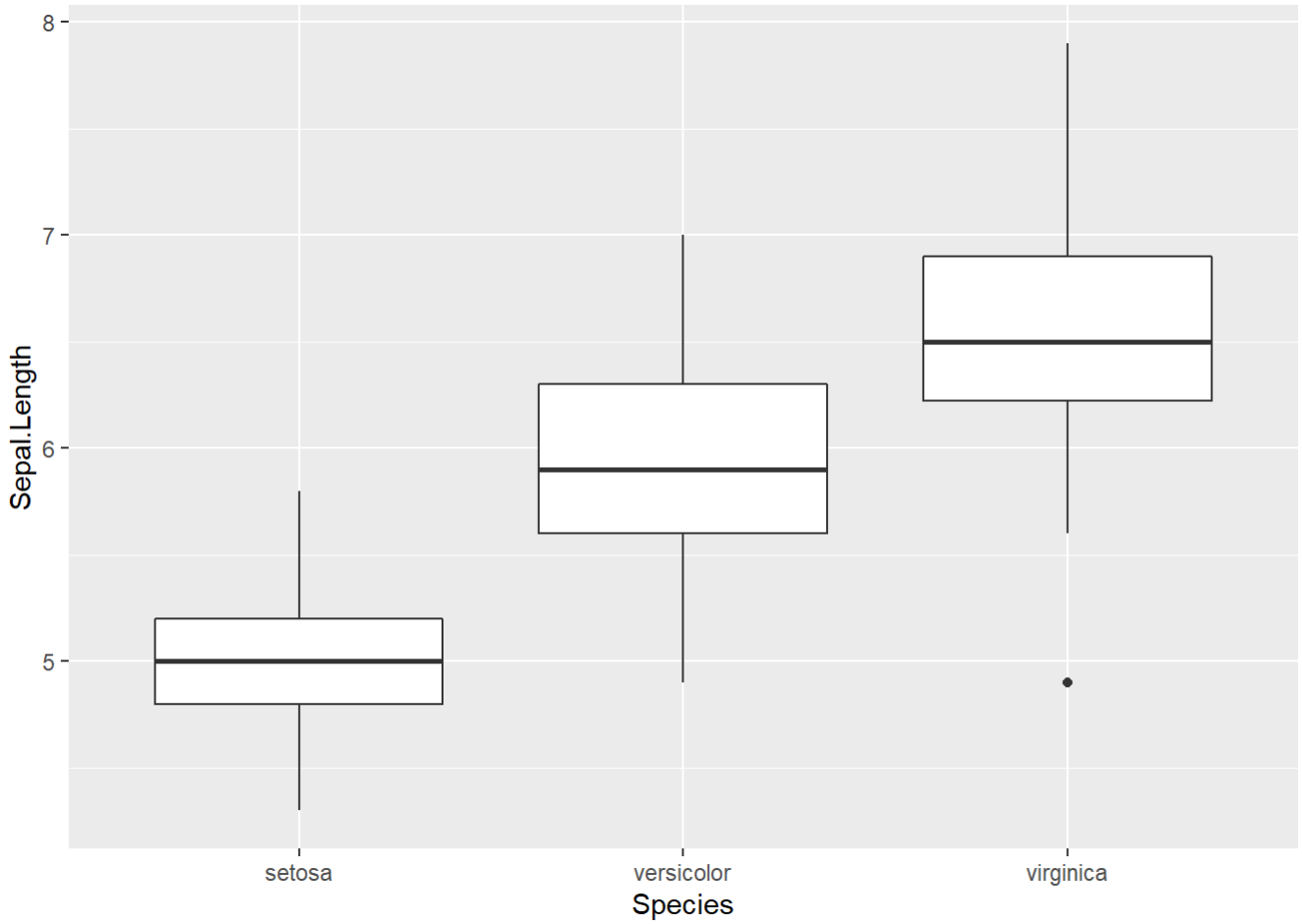

```
## Histogram
ggplot(iris, aes(x= Sepal.Length)) +geom_histogram()
```



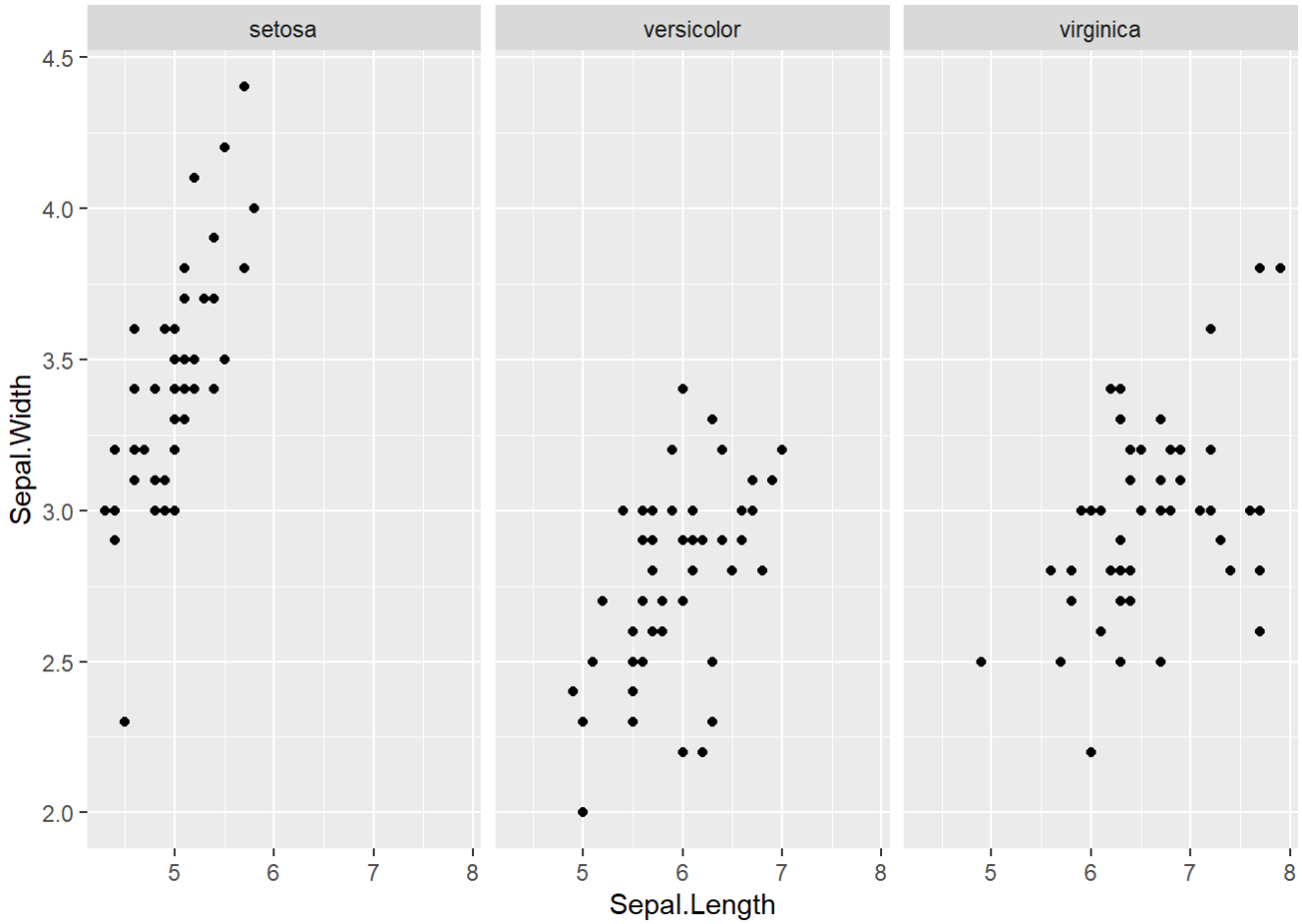

```
ggplot(iris, aes(x= Sepal.Length, fill = Species)) +geom_histogram()
```



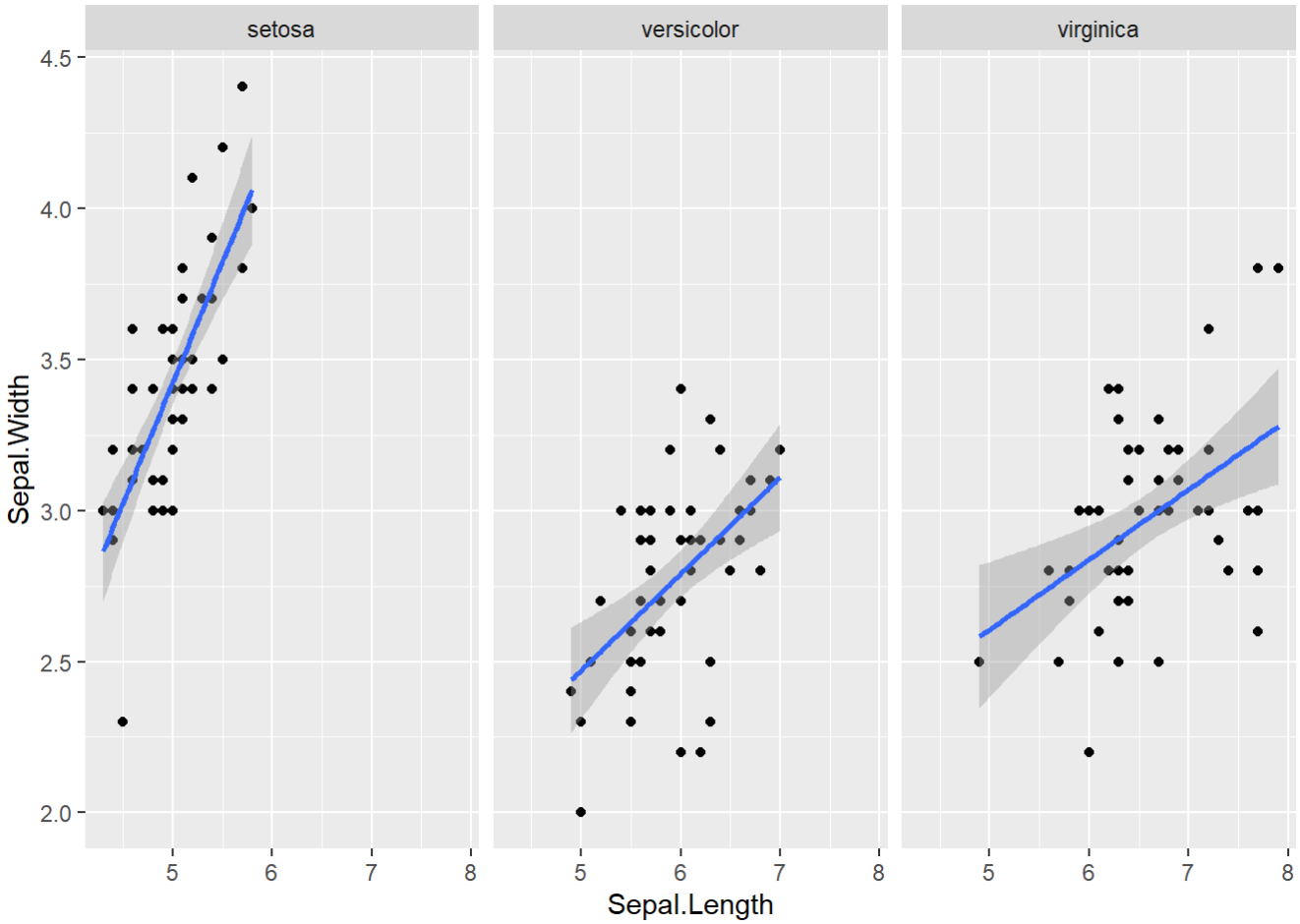

```
## Boxplot
ggplot(iris, aes(x= Species, y= Sepal.Length)) + geom_boxplot()
```




```
## Visualizing relationship between variables for the 3 species
ggplot(data = iris, aes(Sepal.Length, Sepal.Width)) + geom_point() + facet_grid(. ~
 Species)
```



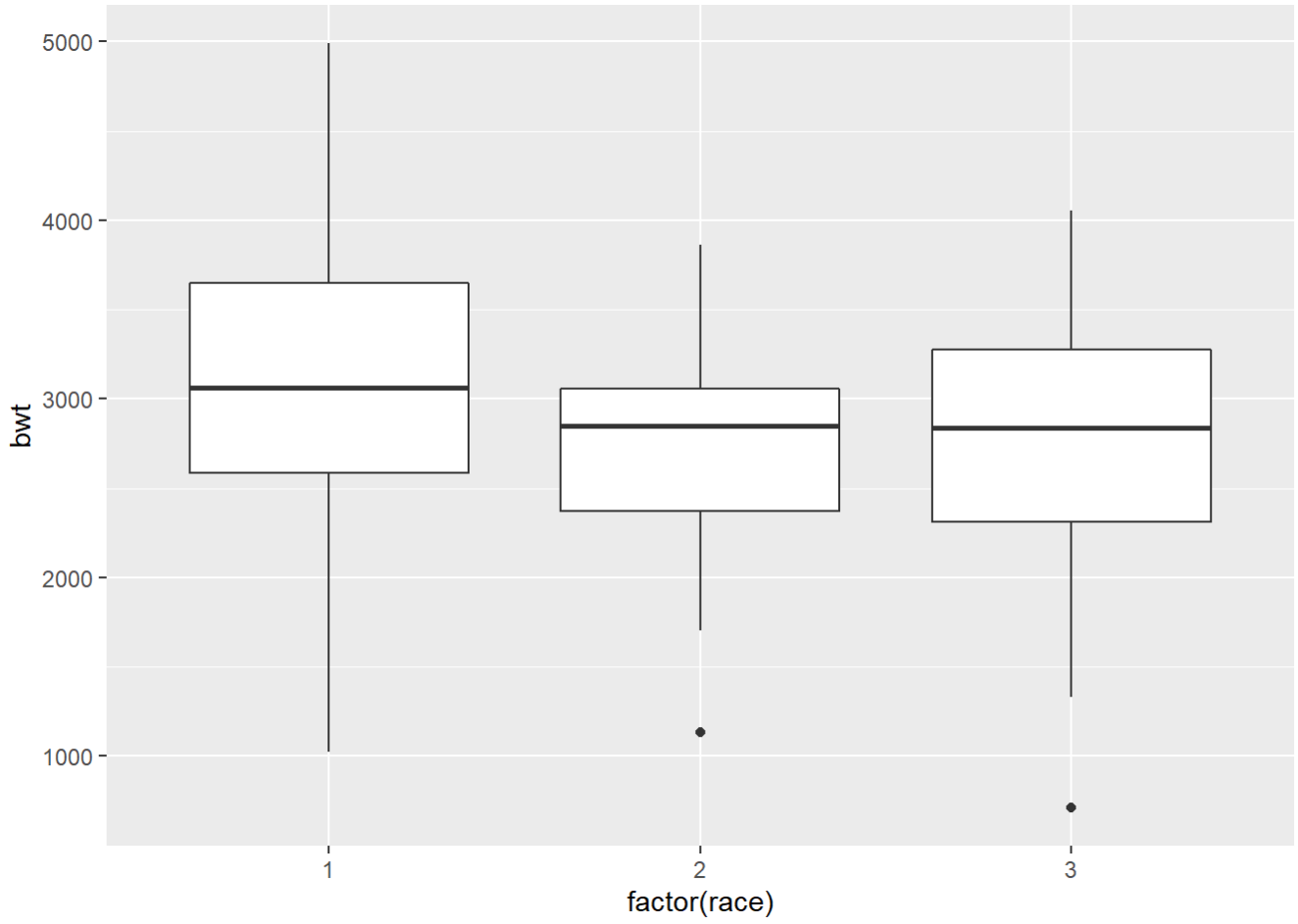

```
ggplot(data = iris, aes(Sepal.Length, Sepal.Width)) + geom_point() + facet_grid(. ~ Species) + geom_smooth(method = "lm")
```



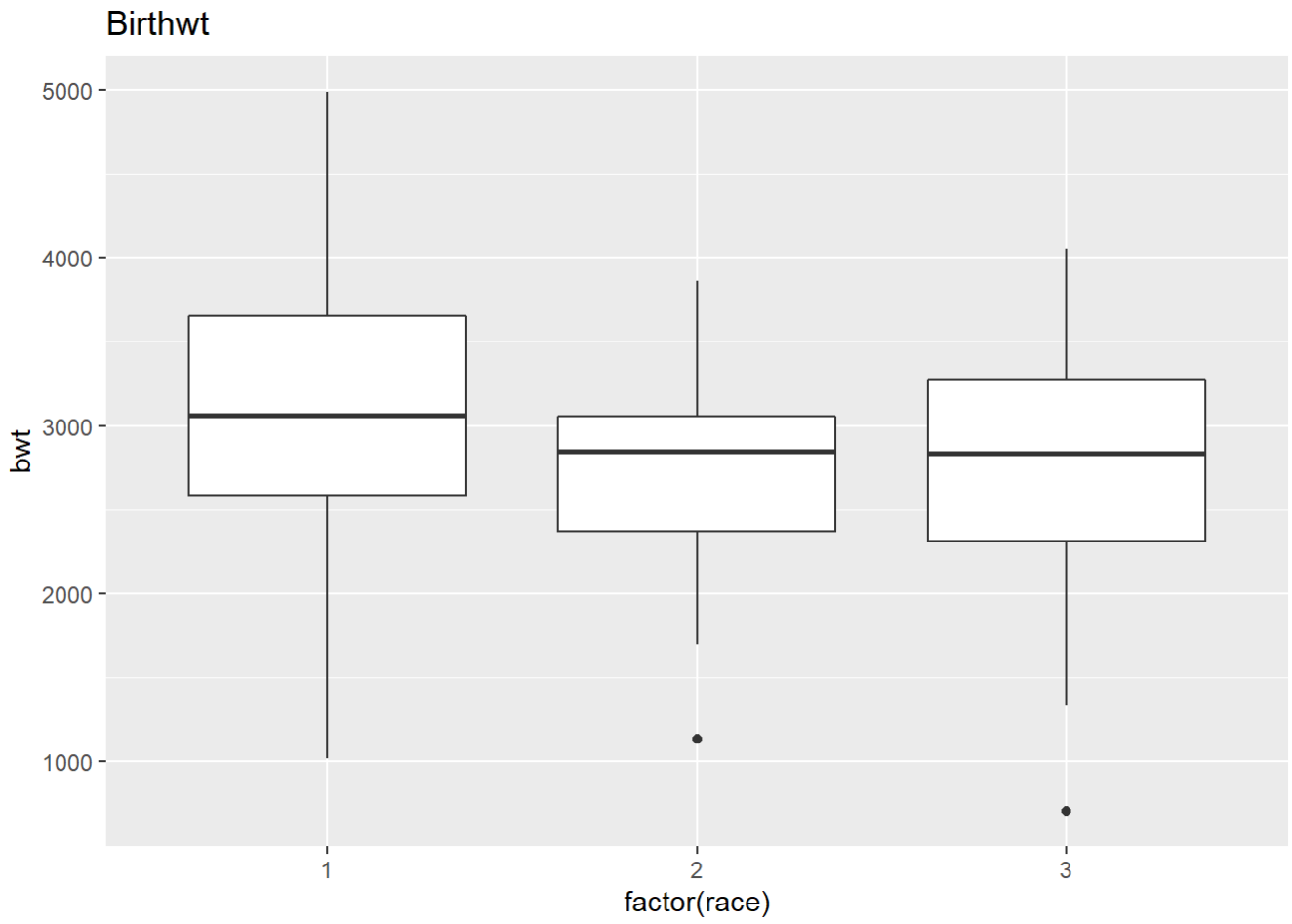

```
library(MASS)
head(birthwt)
```

```
   low age lwt race smoke ptl ht ui ftv  bwt
85   0  19 182    2     0   0  0  1   0 2523
86   0  33 155    3     0   0  0  0   3 2551
87   0  20 105    1     1   0  0  0   1 2557
88   0  21 108    1     1   0  0  1   2 2594
89   0  18 107    1     1   0  0  1   0 2600
91   0  21 124    3     0   0  0  0   0 2622
```

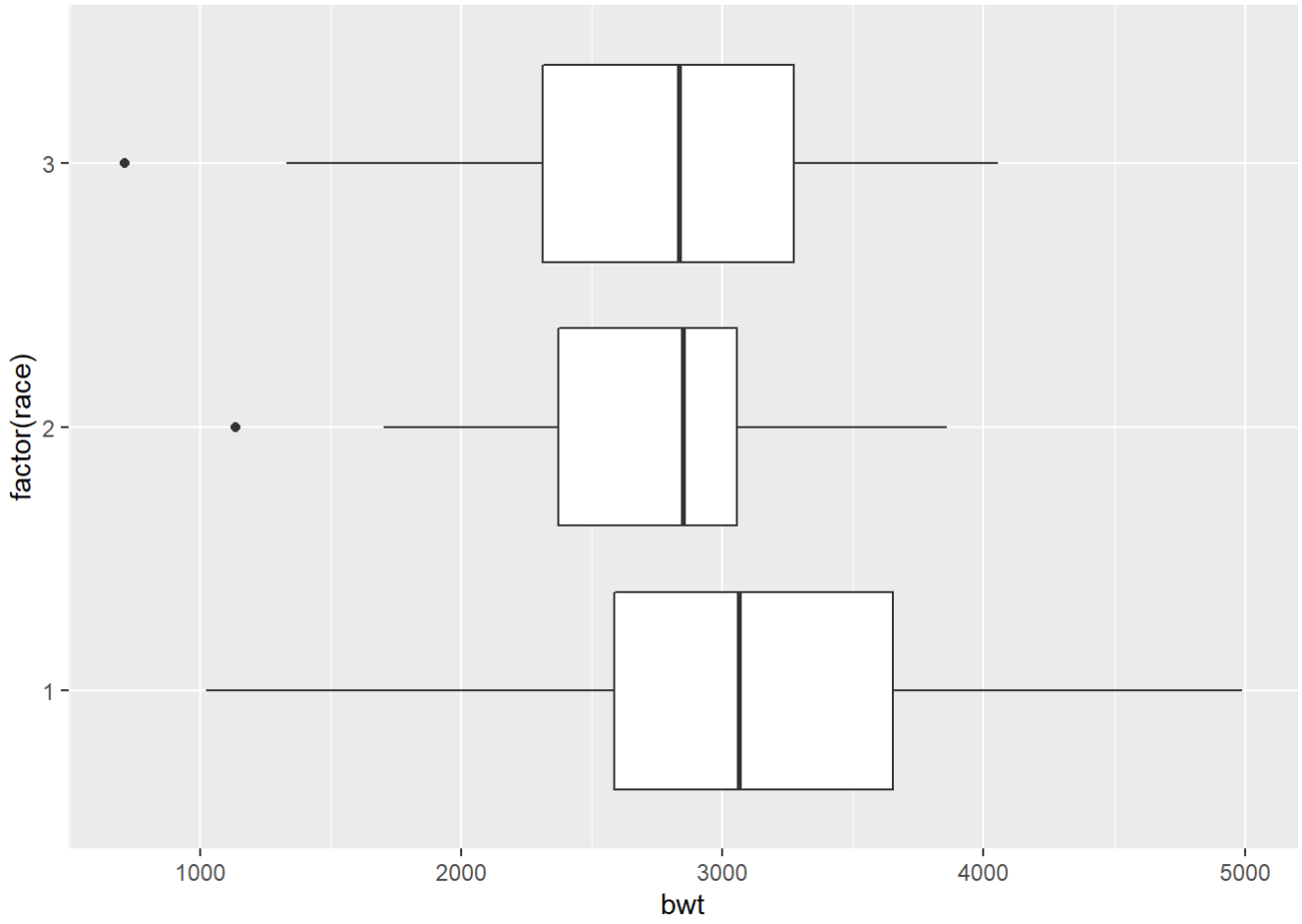
```
## compare numerical variables across all categories
ggplot(birthwt, aes(x= factor(race), y= bwt)) +geom_boxplot()
```




```
## Do you notice the presence of an outlier?
ggplot(birthwt, aes(x= factor(race), y= bwt)) +geom_boxplot() +ggtitle("Birthwt")
```



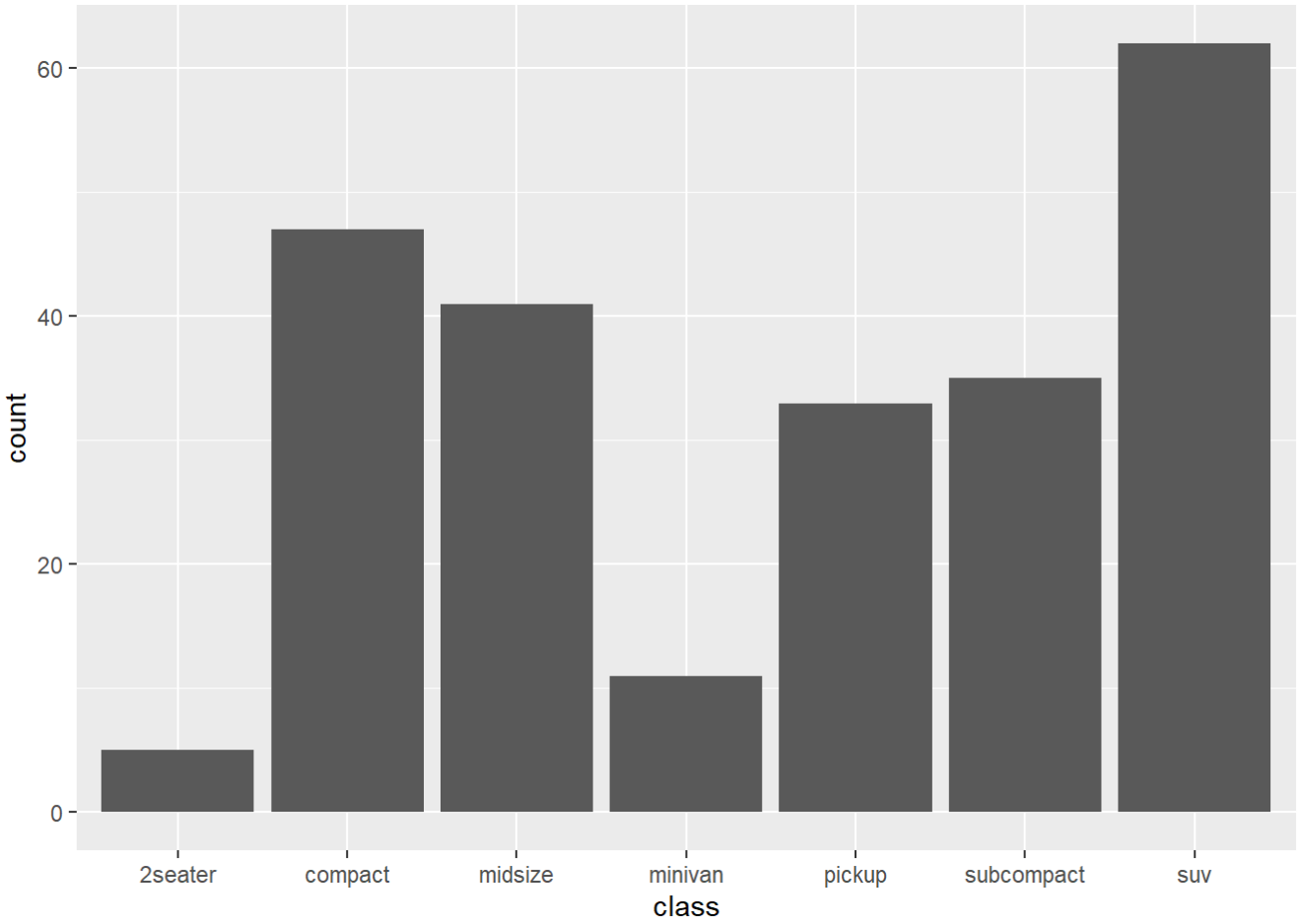

```
ggplot(birthwt, aes(x= factor(race), y= bwt)) +geom_boxplot() + coord_flip()
```



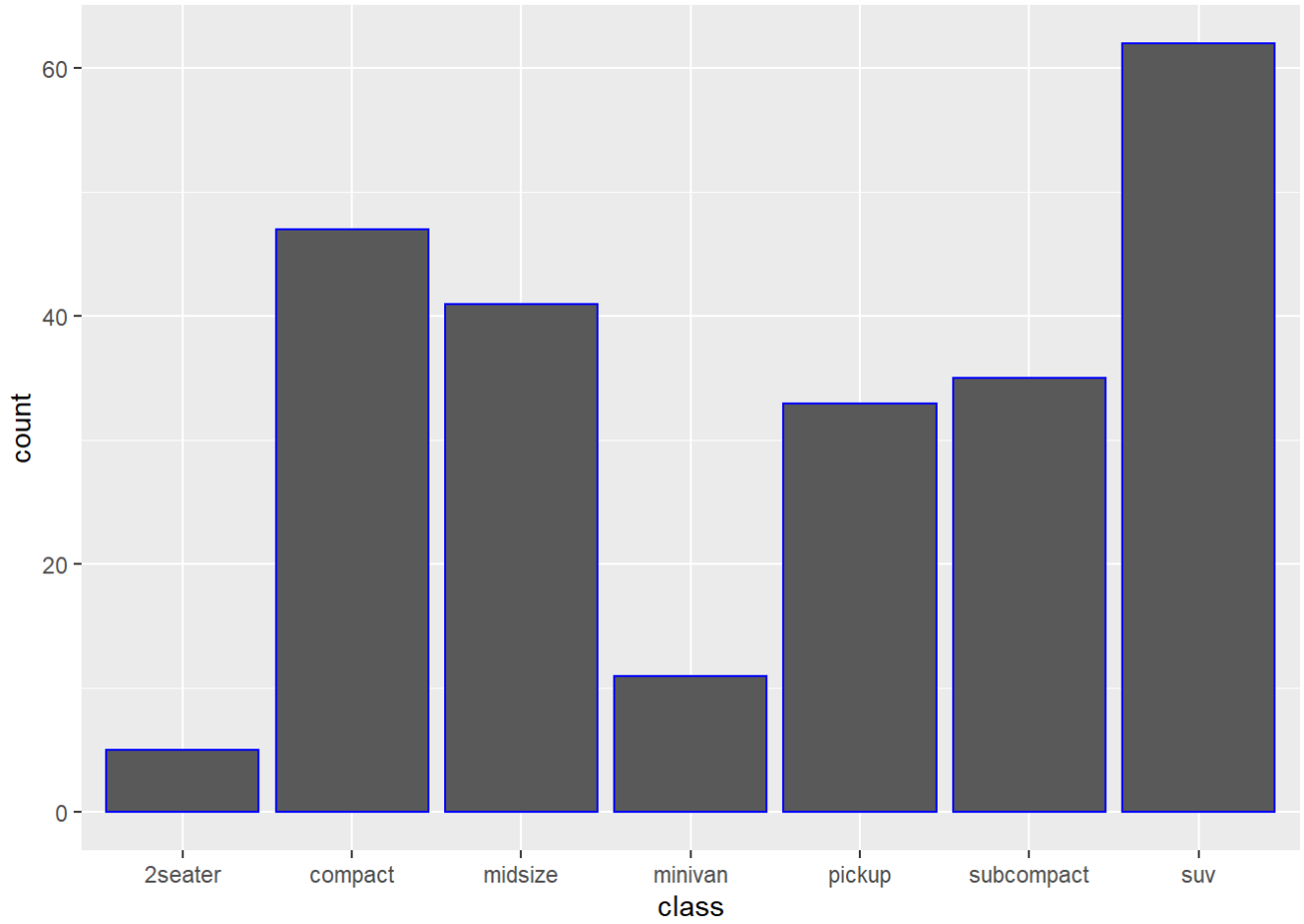

```
### BARPLOT
library(ggplot2)
df <- mpg
head(df)
```

```
# A tibble: 6 x 11
  manufacturer model displ  year   cyl trans      drv     cty   hwy fl    class
  <chr>        <chr> <dbl> <int> <int> <chr>      <chr> <int> <int> <chr> <chr>
1 audi         a4      1.8  1999     4 auto(l5)   f        18    29 p     compa~
2 audi         a4      1.8  1999     4 manual(m5) f        21    29 p     compa~
3 audi         a4      2    2008     4 manual(m6) f        20    31 p     compa~
4 audi         a4      2    2008     4 auto(av)   f        21    30 p     compa~
5 audi         a4      2.8  1999     6 auto(l5)   f        16    26 p     compa~
6 audi         a4      2.8  1999     6 manual(m5) f        18    26 p     compa~
```

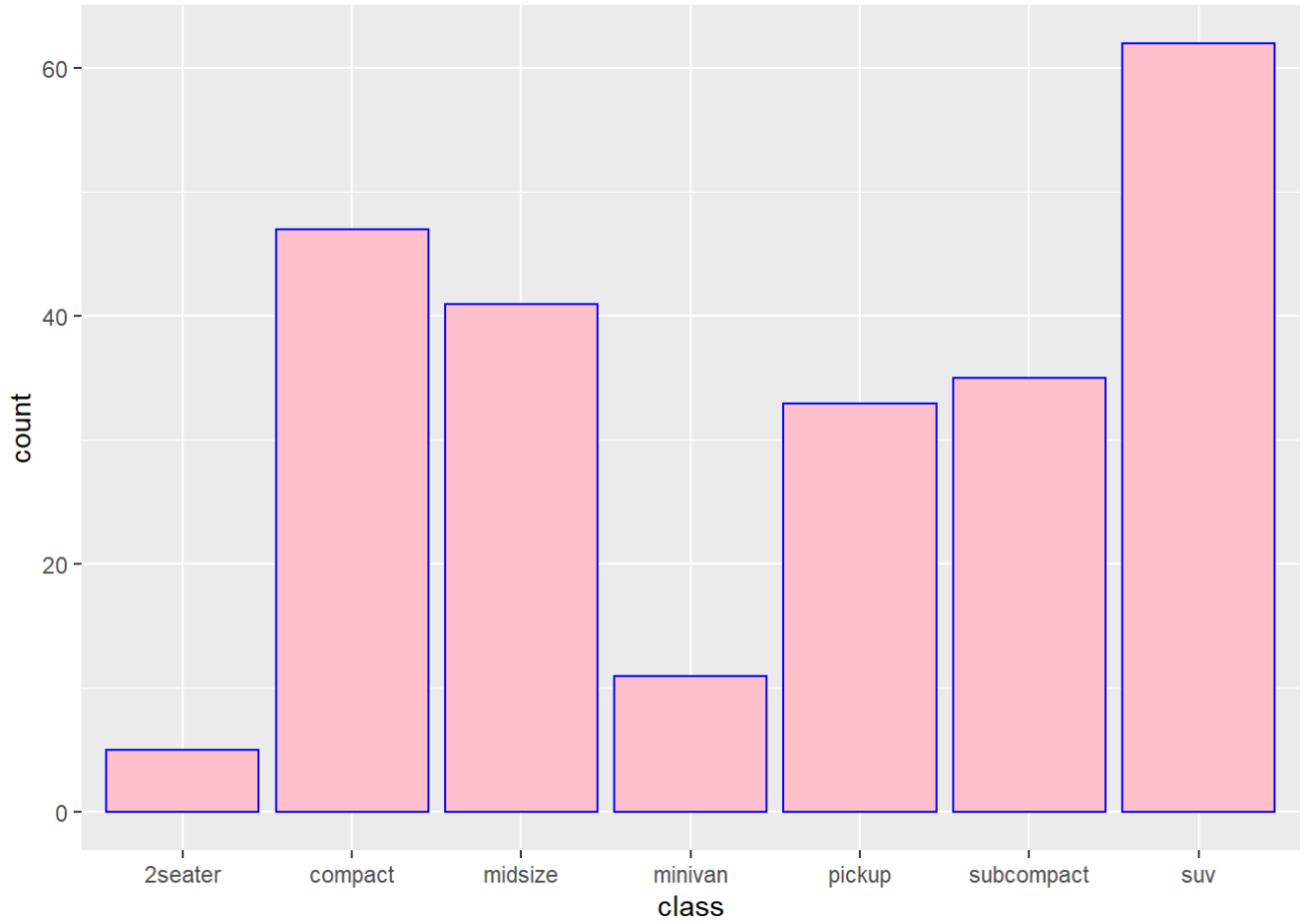
```
## Scatterplot have continuous data on the x but barplot have a categorical data.

## They both have counts on their y axis
pl <- ggplot(df, aes(x=class))
print(pl + geom_bar())
```



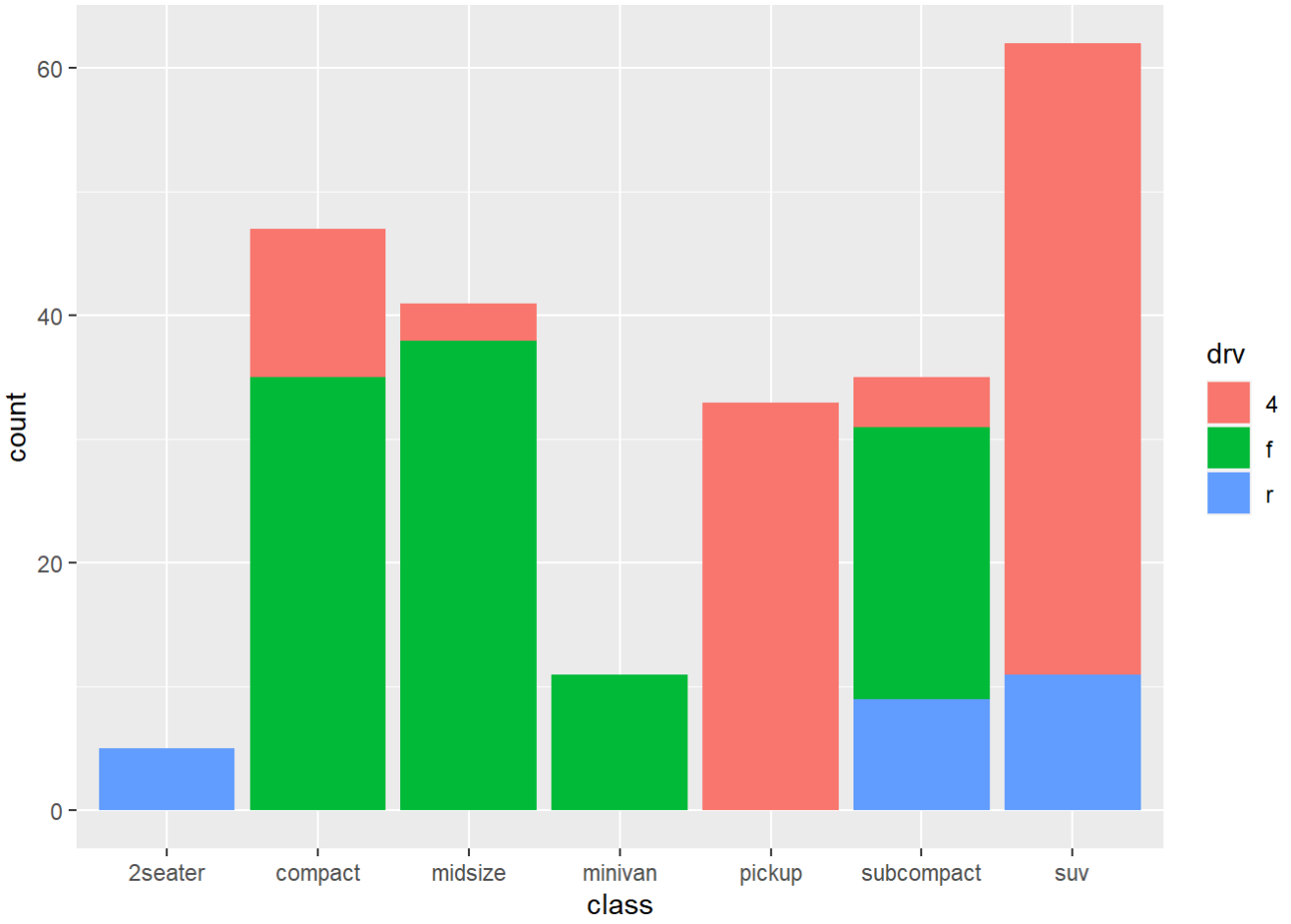

```
print(pl + geom_bar(color="blue")) ## for outline colour
```



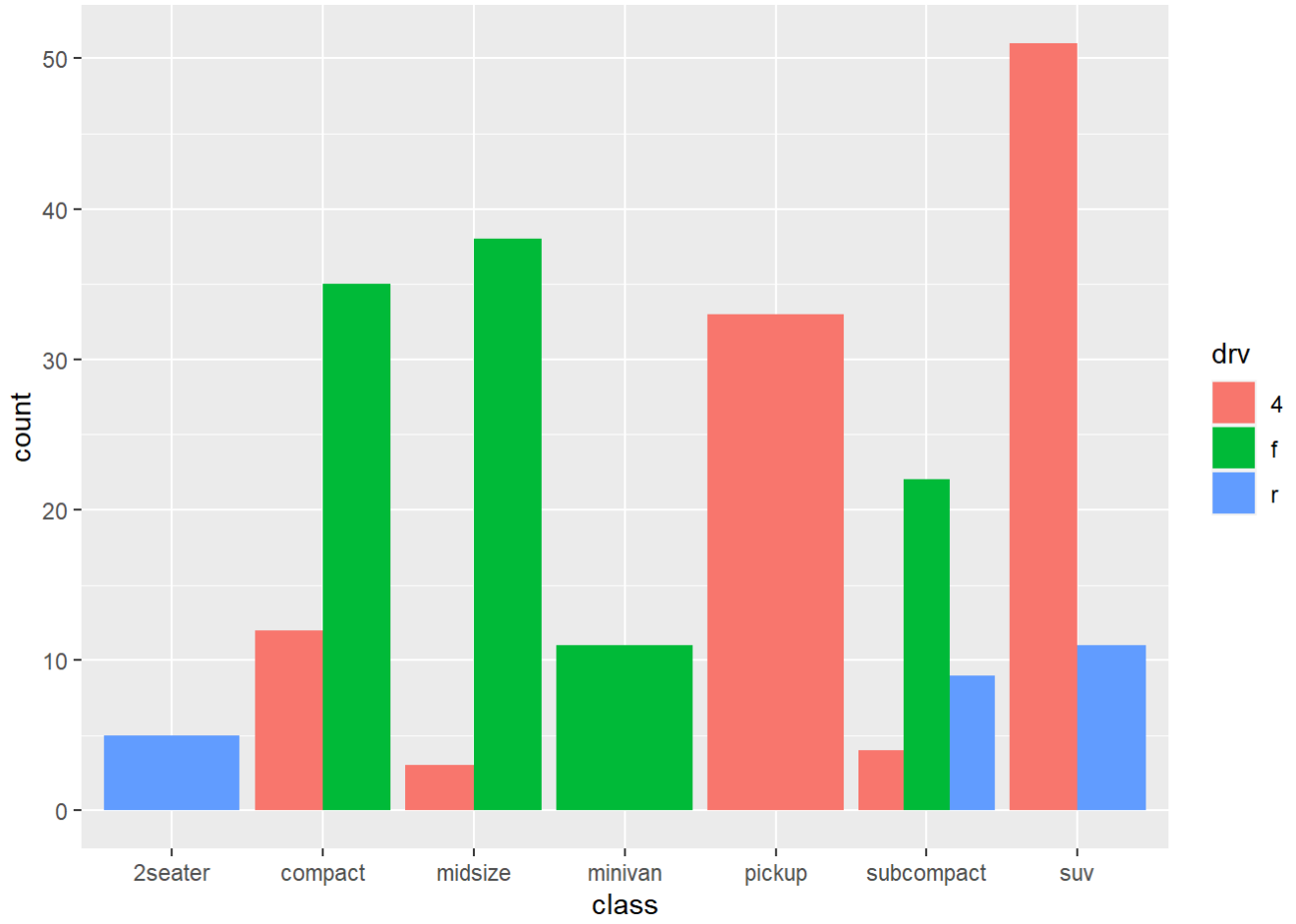

```
print(pl + geom_bar(color="blue", fill="pink"))
```



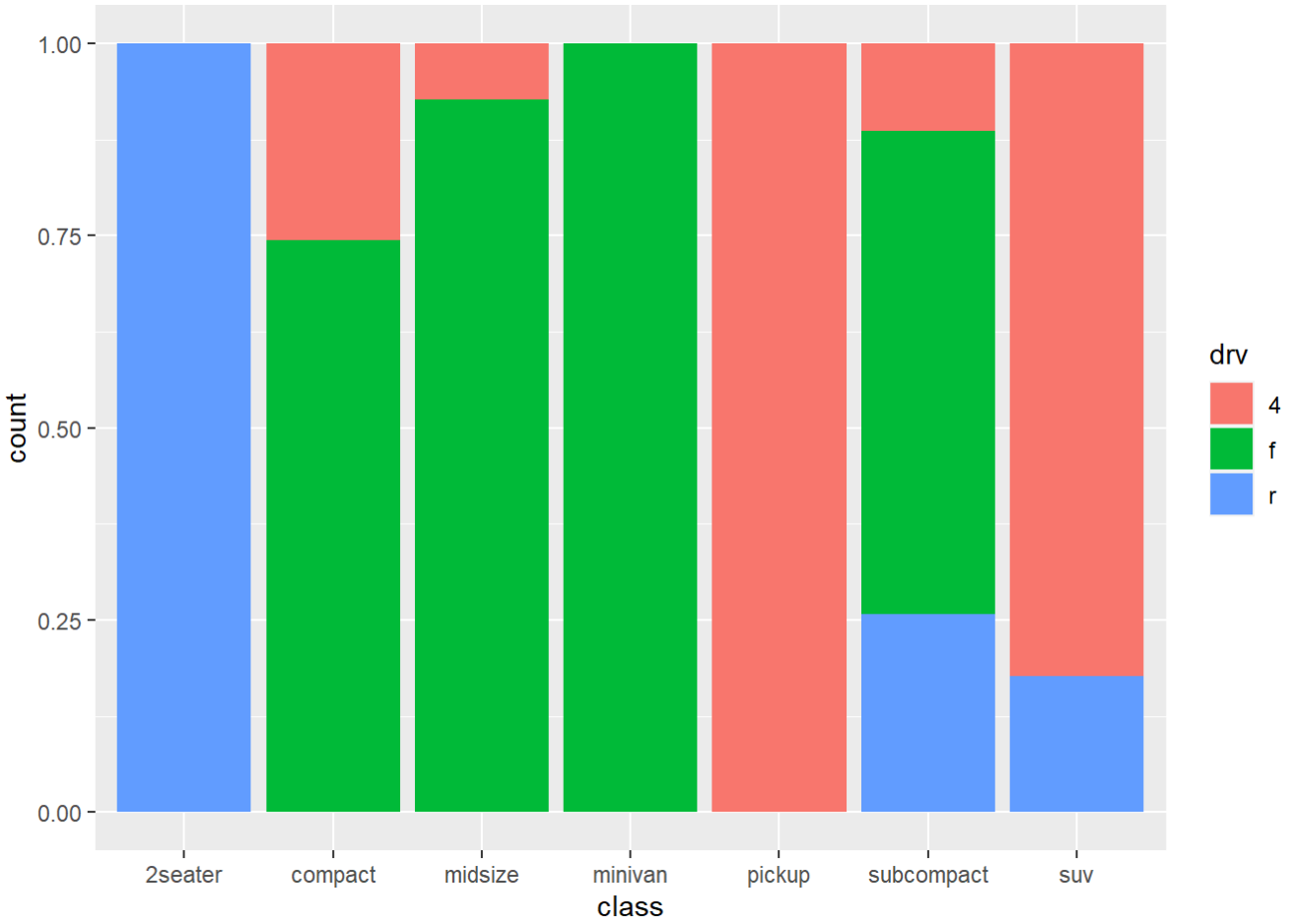

```
## We can also define our fill with another factor column in the data frame. To do t
his, we will introduce the aes(inside the geom)
print(pl + geom_bar(aes(fill=drv))) ## This will automatically create a stacked bar
 for us.
```




```
print(pl + geom_bar(aes(fill=drv ), position = "dodge")) ## This helps in comparing
```




```
print(pl + geom_bar(aes(fill=drv ), position = "fill")) ## This shows the percentage instead of count
```



Conclusion

R is such an interesting programming language for statistical analysis, amazing visualization and reporting possibilities. To learn more, you need to read more and practice more.

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It's a great privilege.

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