Introduction to the Command Line (Terminal) and the R Language Syntax

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1) Basics of R

1.1) Basic Steps

- R can be accessed by clicking an icon or entering the command "R" at the system command line, also refered to as Terminal
- This produces a console window or causes R to start up as an interactive program at the current terminal window
- R works fundamentally by a question-and-answer model: enter a line with a command and press Enter
- Then the program does something relevant
- In this course, we will use RStudio and a file format called R Markdown, which allows us to code using not only R, but bash and Python, two other languages we may refer to as the course progresses

1.2) Library ISwR

- This Notebook was inspired in the book Introductory Statistics with R, by Peter Dalgaard
- For the book, R library ISwR (Introductory Statistics with R) can be freely downloaded
- All examples in the book used as reference should run provided that ISwR library is not only installed by also loaded into the current search path
- Library can be installed and loaded by typing the following command into an R chunk

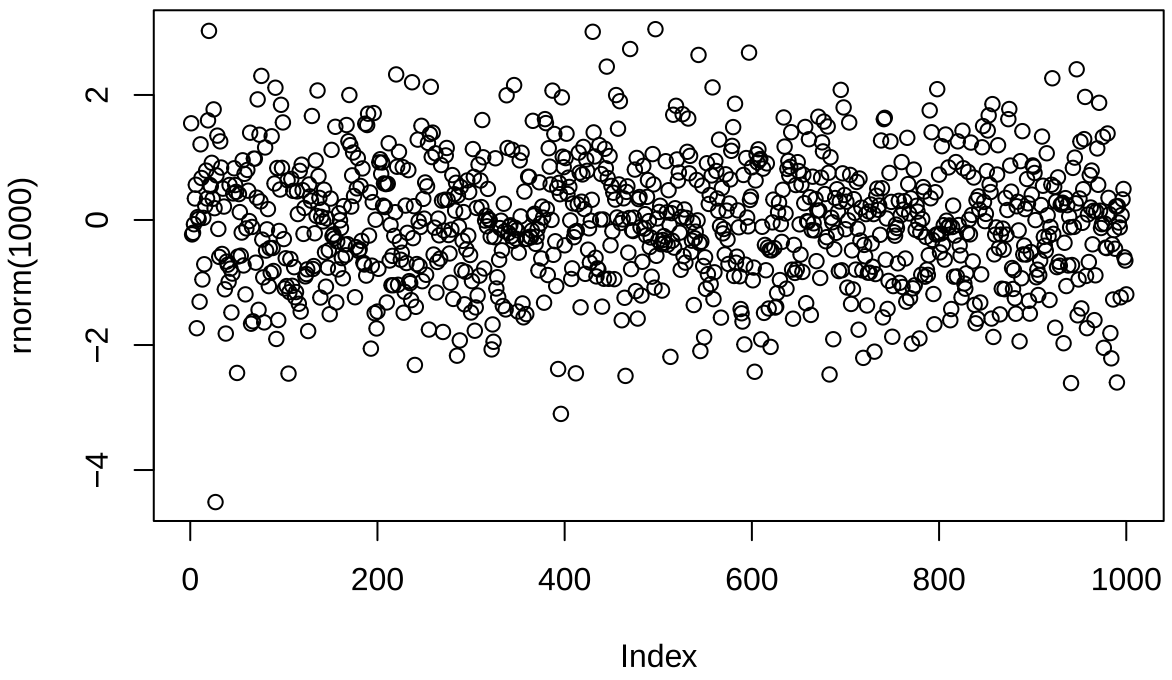
```r
install.packages("ISwR")
library("ISwR")
```

- For a first impression of what R can do, let´s try plotting a graph

1.3) Plot Random Numbers

- Need to insert the R chunk and use the plot function

```r
plot(rnorm(1000))
```



1.4) A Potent Calculator

- R can process simple and complex arithmetic expression and produce a result for the user

```
2 + 2
```

```
## [1] 4
```

- R can also be used to do other standard calculations. Here is how to calculate e to the power of -2

```
exp(-2)
```

```
## [1] 0.1353353
```

- Other than the R chunks, these calculations can be made using the RStudio Console

1.5) Assignments

- Assignments made based on the necessity to store results of calculations and use these results in downstream processing steps in an entire pipeline
- Like other languages, R has symbolic variables: names that can be used to represent values
- To assign value 2 to variable x, one can enter

```
x <- 2
```

- The character <- is called the assignment operator
- There is no immediate visible result, but from now on, x has the value 2 and can be used in subsequent arithmetic operations

1.6) Operations after Variable assignment

- Below, our variable x, is used to perform other calculations

```
x
```

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

```
x + x ## Adition
```

```
## [1] 4
```

```
5*x   ## Multiplication
```

```
## [1] 10
```

```
x^3   ## Potentiation
```

```
## [1] 8
```

1.7) Vectorized Arithmetic

- It is not useful to use one number at a time to run statistics
- One strenght of R is that it can handle entire data vectors as single objects
- A data vector is an array of numbers and a vector variable can be constructed like this

```
weight <- c(60, 72, 57, 90, 95, 72)

## To look at the vector variable, just type its name again
weight
```

```
## [1] 60 72 57 90 95 72
```

- You can do calculations with vectors just like ordinary numbers, so long as they have the same length
- One exception to this rule that we will see will be when we use the mean of weigths of persons (represented by xbar)
- In that case, the mean will be one single number, which will be subtracted from each sample value

1.7) Vectorized Arithmetic

- Suppose the weight vector indicates the weight of men in kilograms
- One simple formula to indicate whether a person is obese or not, is the body mass index (BMI)
- BMI is calculated by dividing the person´s weight by the square of their height, in meters
- Therefore, in R, we need to have a vector with the height values to calculate the bmi vector, containing the body-mass index for the individuals indicated in the weight vector

```
height <- c(1.75, 1.80, 1.65, 1.90, 1.74, 1.91)
bmi <- weight/height^2
bmi
```

```
## [1] 19.59184 22.22222 20.93664 24.93075 31.37799 19.73630
```

1.8) Calculate the Mean of the variable weight

- The mean is calculated by the sum of the observations divided by the total number of observations

$\overline{x} = \sum x_i$ /n

- Let´s calculate the mean of the variable weight

```
sum(weight)
```

```
## [1] 446
```

```
sum(weight)/length(weight)
```

```
## [1] 74.33333
```

1.9) Calculate the Standard-Deviation of the variable weight

- Standard-deviation can be calculated with the following equation

$$SD = \sqrt{(\sum (x_i - \overline{x})^2)/(n-1)}$$

- xbar, the mean of variable weight, can be calculated using the sum and length of variable weight

```
xbar <- sum(weight)/length(weight)
xbar
```

```
## [1] 74.33333
```

- Now we can calculate the difference of each replicate in the weight variable and the mean of the weight variable, one by one

```
weight - xbar
```

```
## [1] -14.333333  -2.333333 -17.333333  15.666667  20.666667  -2.333333
```

- Notice how R uses xbar, which has length one, to calculate the new weight - xbar data vector
- xbar is recycled and subracted from every element in the weight variable (weight data vector)

1.10) Calculation of the Standard Deviation

- Calculate the squared deviations

```
(weight - xbar)^2
```

```
## [1] 205.444444   5.444444 300.444444 245.444444 427.111111   5.444444
```

- Calculate the sum of squared deviations

```
sum((weight - xbar)^2)
```

```
## [1] 1189.333
```

- Calculate the standard deviation

```r
sqrt(
  sum(
    (weight - xbar)^2/
      (length(weight)-1)
)
)
```

```
## [1] 15.42293
```

1.11) Standard Statistical Procedures

- It is a standard medical practice to access whether a person is obese or not using validated scientific criteria
- As a simple procedure to show this concept, let's assume that an individual with a normal weight should have a BMI in the range 20-25
- We want to know if our data deviates from the normal range of BMI
- In R, this can be done using a statistical test called t-test
- You do not need to understand what a t-test is, just remember that is is used to evaluate the distribution of sample values compared to the normal distribution
- You can use a one-sample t-test to assess whether the six persons' BMI can be assumed to have mean 22.5 given that they come from a normal distribution
- You can do that using the function t.test

1.11) Standard Statistical Procedures: t-test

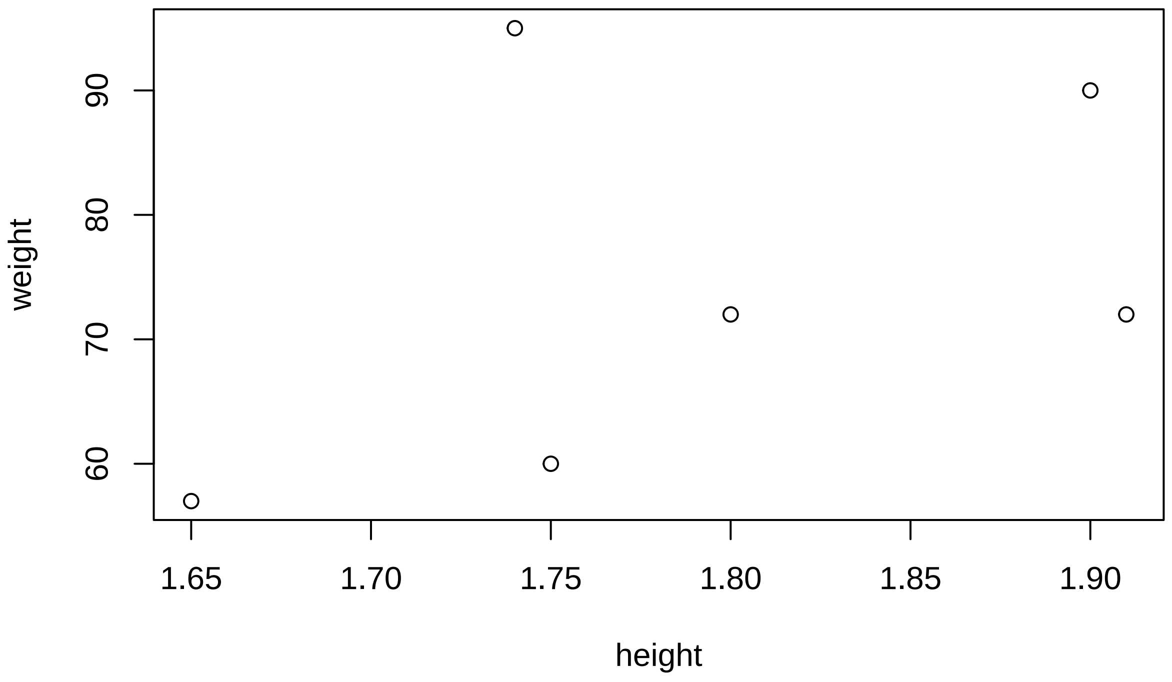
```r
t.test(
  bmi,
  mu = 22.5
)
```

```
##
##  One Sample t-test
##
## data:  bmi
## t = 0.34488, df = 5, p-value = 0.7442
## alternative hypothesis: true mean is not equal to 22.5
## 95 percent confidence interval:
##  18.41734 27.84791
## sample estimates:
## mean of x
##  23.13262
```

1.12) Plot Graphics

- Let's now plot a scatterplot of the height and weight of individuals

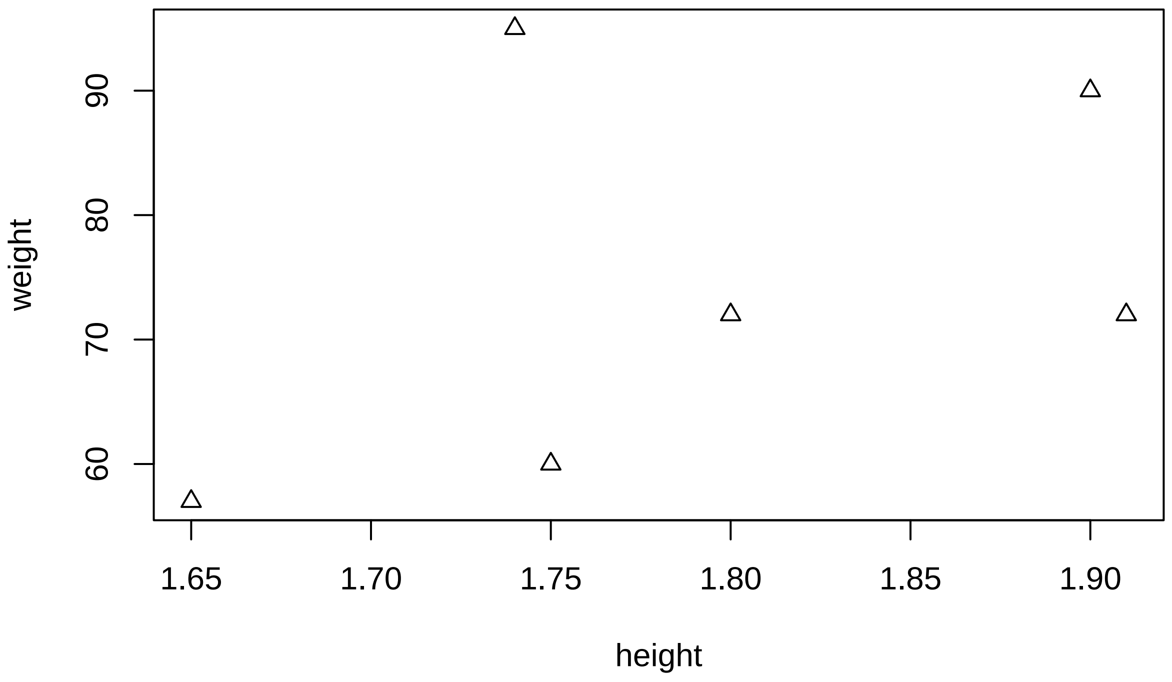
```r
plot(height, weight)
```



1.12) Plot Graphics Modifying the plotting character

- You will frequently want to modify drawing of your graphs in various ways
- One way is usig the parameter "plotting character", pch

```r
plot(height, weight, pch =2)
```



1.13) Plot an expected Line for BMI

```
hh <- 22.5*(height)^2
```

1.14) Vectors

- The weight and height vectors are called numeric vectors
- Besides numeric vectors, there are numeric and character vectors

2) Using other libraries

2.1) The iris data-frame

- Now we have a better understanding of what R can give us, let us use another library more commonly used datasets
- At times, it is possible that you will need to figure out different ways to install a library to use it

```
library(datasets)
```

- In the next chunk, we access the iris data, and look at a summary of the dataset

```
data(iris)
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  
##                 
##                 
## 
```

2.1) The iris data-frame

- Another form to look at the iris data-frame is typing its name

```
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
## 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
## 11            5.4         3.7          1.5         0.2     setosa
## 12            4.8         3.4          1.6         0.2     setosa
## 13            4.8         3.0          1.4         0.1     setosa
## 14            4.3         3.0          1.1         0.1     setosa
## 15            5.8         4.0          1.2         0.2     setosa
## 16            5.7         4.4          1.5         0.4     setosa
## 17            5.4         3.9          1.3         0.4     setosa
## 18            5.1         3.5          1.4         0.3     setosa
## 19            5.7         3.8          1.7         0.3     setosa
## 20            5.1         3.8          1.5         0.3     setosa
## 21            5.4         3.4          1.7         0.2     setosa
## 22            5.1         3.7          1.5         0.4     setosa
## 23            4.6         3.6          1.0         0.2     setosa
## 24            5.1         3.3          1.7         0.5     setosa
## 25            4.8         3.4          1.9         0.2     setosa
## 26            5.0         3.0          1.6         0.2     setosa
## 27            5.0         3.4          1.6         0.4     setosa
## 28            5.2         3.5          1.5         0.2     setosa
## 29            5.2         3.4          1.4         0.2     setosa
## 30            4.7         3.2          1.6         0.2     setosa
## 31            4.8         3.1          1.6         0.2     setosa
## 32            5.4         3.4          1.5         0.4     setosa
## 33            5.2         4.1          1.5         0.1     setosa
## 34            5.5         4.2          1.4         0.2     setosa
## 35            4.9         3.1          1.5         0.2     setosa
## 36            5.0         3.2          1.2         0.2     setosa
## 37            5.5         3.5          1.3         0.2     setosa
## 38            4.9         3.6          1.4         0.1     setosa
## 39            4.4         3.0          1.3         0.2     setosa
## 40            5.1         3.4          1.5         0.2     setosa
## 41            5.0         3.5          1.3         0.3     setosa
## 42            4.5         2.3          1.3         0.3     setosa
## 43            4.4         3.2          1.3         0.2     setosa
## 44            5.0         3.5          1.6         0.6     setosa
## 45            5.1         3.8          1.9         0.4     setosa
## 46            4.8         3.0          1.4         0.3     setosa
## 47            5.1         3.8          1.6         0.2     setosa
## 48            4.6         3.2          1.4         0.2     setosa
## 49            5.3         3.7          1.5         0.2     setosa
## 50            5.0         3.3          1.4         0.2     setosa
## 51            7.0         3.2          4.7         1.4 versicolor
## 52            6.4         3.2          4.5         1.5 versicolor
## 53            6.9         3.1          4.9         1.5 versicolor
## 54            5.5         2.3          4.0         1.3 versicolor
## 55            6.5         2.8          4.6         1.5 versicolor
## 56            5.7         2.8          4.5         1.3 versicolor
## 57            6.3         3.3          4.7         1.6 versicolor
## 58           4.9         2.4          3.3         1.0 versicolor
## 59           6.6         2.9          4.6         1.3 versicolor
## 60           5.2         2.7          3.9         1.4 versicolor
## 61           5.0         2.0          3.5         1.0 versicolor
## 62           5.9         3.0          4.2         1.5 versicolor
## 63           6.0         2.2          4.0         1.0 versicolor
## 64           6.1         2.9          4.7         1.4 versicolor
## 65           5.6         2.9          3.6         1.3 versicolor
## 66           6.7         3.1          4.4         1.4 versicolor
## 67           5.6         3.0          4.5         1.5 versicolor
## 68           5.8         2.7          4.1         1.0 versicolor
## 69           6.2         2.2          4.5         1.5 versicolor
## 70           5.6         2.5          3.9         1.1 versicolor
## 71           5.9         3.2          4.8         1.8 versicolor
## 72           6.1         2.8          4.0         1.3 versicolor
## 73           6.3         2.5          4.9         1.5 versicolor
## 74           6.1         2.8          4.7         1.2 versicolor
## 75           6.4         2.9          4.3         1.3 versicolor
## 76           6.6         3.0          4.4         1.4 versicolor
## 77           6.8         2.8          4.8         1.4 versicolor
## 78           6.7         3.0          5.0         1.7 versicolor
## 79           6.0         2.9          4.5         1.5 versicolor
## 80           5.7         2.6          3.5         1.0 versicolor
## 81           5.5         2.4          3.8         1.1 versicolor
## 82           5.5         2.4          3.7         1.0 versicolor
## 83           5.8         2.7          3.9         1.2 versicolor
## 84           6.0         2.7          5.1         1.6 versicolor
## 85           5.4         3.0          4.5         1.5 versicolor
## 86           6.0         3.4          4.5         1.6 versicolor
## 87           6.7         3.1          4.7         1.5 versicolor
## 88           6.3         2.3          4.4         1.3 versicolor
## 89           5.6         3.0          4.1         1.3 versicolor
## 90           5.5         2.5          4.0         1.3 versicolor
## 91           5.5         2.6          4.4         1.2 versicolor
## 92           6.1         3.0          4.6         1.4 versicolor
## 93           5.8         2.6          4.0         1.2 versicolor
## 94           5.0         2.3          3.3         1.0 versicolor
## 95           5.6         2.7          4.2         1.3 versicolor
## 96           5.7         3.0          4.2         1.2 versicolor
## 97           5.7         2.9          4.2         1.3 versicolor
## 98           6.2         2.9          4.3         1.3 versicolor
## 99           5.1         2.5          3.0         1.1 versicolor
## 100          5.7         2.8          4.1         1.3 versicolor
## 101          6.3         3.3          6.0         2.5  virginica
## 102          5.8         2.7          5.1         1.9  virginica
## 103          7.1         3.0          5.9         2.1  virginica
## 104          6.3         2.9          5.6         1.8  virginica
## 105          6.5         3.0          5.8         2.2  virginica
## 106          7.6         3.0          6.6         2.1  virginica
## 107          4.9         2.5          4.5         1.7  virginica
## 108          7.3         2.9          6.3         1.8  virginica
## 109          6.7         2.5          5.8         1.8  virginica
## 110          7.2         3.6          6.1         2.5  virginica
## 111          6.5         3.2          5.1         2.0  virginica
## 112          6.4         2.7          5.3         1.9  virginica
## 113          6.8         3.0          5.5         2.1  virginica
## 114          5.7         2.5          5.0         2.0  virginica
## 115          5.8         2.8          5.1         2.4  virginica
## 116          6.4         3.2          5.3         2.3  virginica
## 117          6.5         3.0          5.5         1.8  virginica
## 118          7.7         3.8          6.7         2.2  virginica
## 119          7.7         2.6          6.9         2.3  virginica
## 120          6.0         2.2          5.0         1.5  virginica
## 121          6.9         3.2          5.7         2.3  virginica
## 122          5.6         2.8          4.9         2.0  virginica
## 123          7.7         2.8          6.7         2.0  virginica
## 124          6.3         2.7          4.9         1.8  virginica
## 125          6.7         3.3          5.7         2.1  virginica
## 126          7.2         3.2          6.0         1.8  virginica
## 127          6.2         2.8          4.8         1.8  virginica
## 128          6.1         3.0          4.9         1.8  virginica
## 129          6.4         2.8          5.6         2.1  virginica
## 130          7.2         3.0          5.8         1.6  virginica
## 131          7.4         2.8          6.1         1.9  virginica
## 132          7.9         3.8          6.4         2.0  virginica
## 133          6.4         2.8          5.6         2.2  virginica
## 134          6.3         2.8          5.1         1.5  virginica
## 135          6.1         2.6          5.6         1.4  virginica
## 136          7.7         3.0          6.1         2.3  virginica
## 137          6.3         3.4          5.6         2.4  virginica
## 138          6.4         3.1          5.5         1.8  virginica
## 139          6.0         3.0          4.8         1.8  virginica
## 140          6.9         3.1          5.4         2.1  virginica
## 141          6.7         3.1          5.6         2.4  virginica
## 142          6.9         3.1          5.1         2.3  virginica
## 143          5.8         2.7          5.1         1.9  virginica
## 144          6.8         3.2          5.9         2.3  virginica
## 145          6.7         3.3          5.7         2.5  virginica
## 146          6.7         3.0          5.2         2.3  virginica
## 147          6.3         2.5          5.0         1.9  virginica
## 148          6.5         3.0          5.2         2.0  virginica
## 149          6.2         3.4          5.4         2.3  virginica
## 150          5.9         3.0          5.1         1.8  virginica
```

3.1) More Visualization of the iris dataset

We need to cover these basic R functions:

- dim()
- head()
- View()
- class()
- str()

```
dim(iris)
```

```
## [1] 150   5
```

```r
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
```

```r
View(iris)
class(iris)
```

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

```r
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 ...
```

3.2) Visualize iris dataset with basic R functions

- head

```r
head(iris, n = 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
```

- number of columns and rows

```r
dim(iris)
```

```
## [1] 150   5
```

- the class() function

```r
class(iris)
```

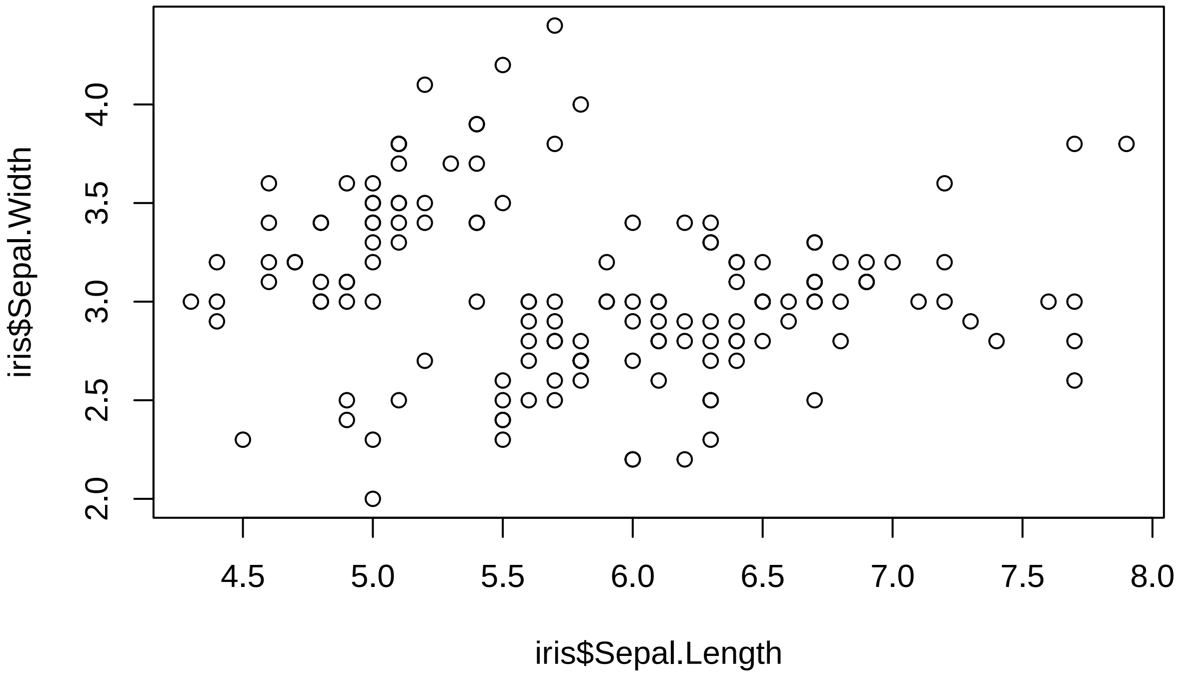
```
## [1] "data.frame"
```

4) More Visualization

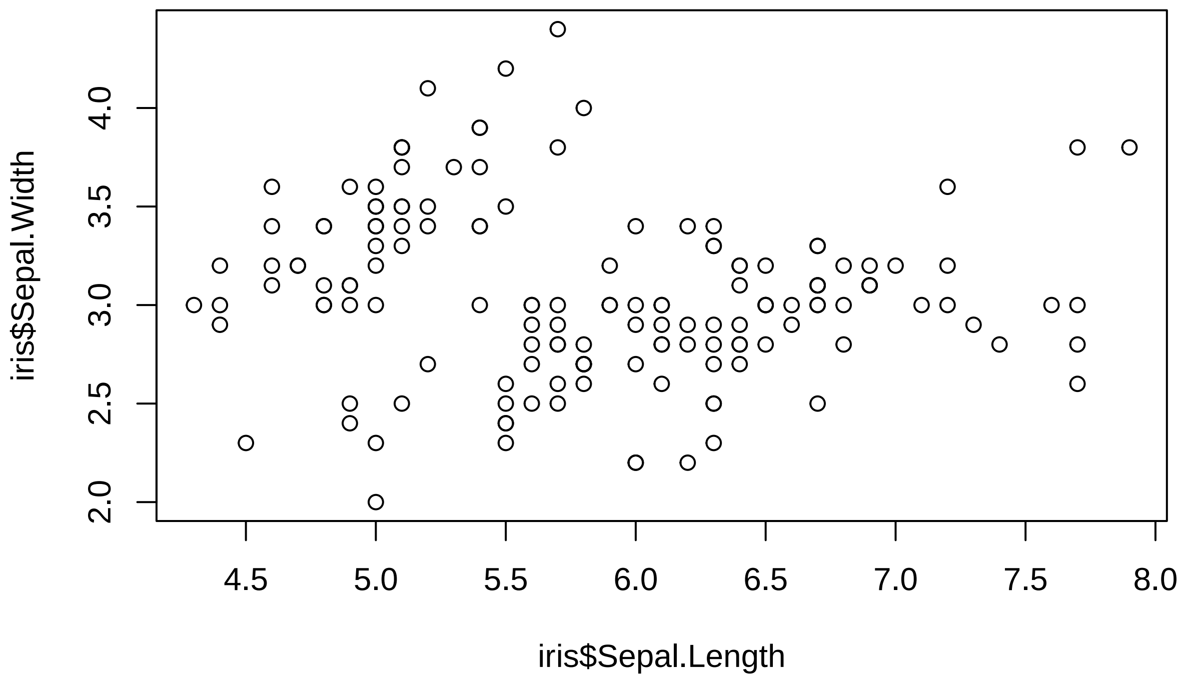
4.1) Scatterplot

```
plot(data=iris, iris$Sepal.Length, iris$Sepal.Width) ## R will complain about this command
```

```
## Warning in plot.window(...): "data" is not a graphical parameter

## Warning in plot.xy(xy, type, ...): "data" is not a graphical parameter

## Warning in axis(side = side, at = at, labels = labels, ...): "data" is not a
## graphical parameter

## Warning in axis(side = side, at = at, labels = labels, ...): "data" is not a
## graphical parameter

## Warning in box(...): "data" is not a graphical parameter

## Warning in title(...): "data" is not a graphical parameter
```

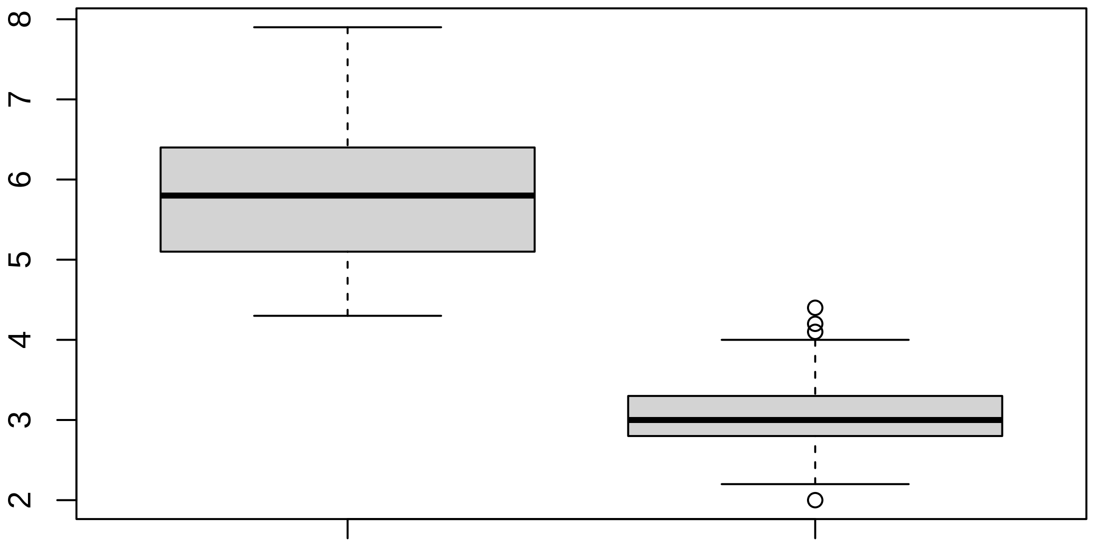


```
plot(iris$Sepal.Length, iris$Sepal.Width) ## According to the error, this was plotted using a different
```



4.2) Boxplot

```r
boxplot(data=iris, iris$Sepal.Length, iris$Sepal.Width)
```

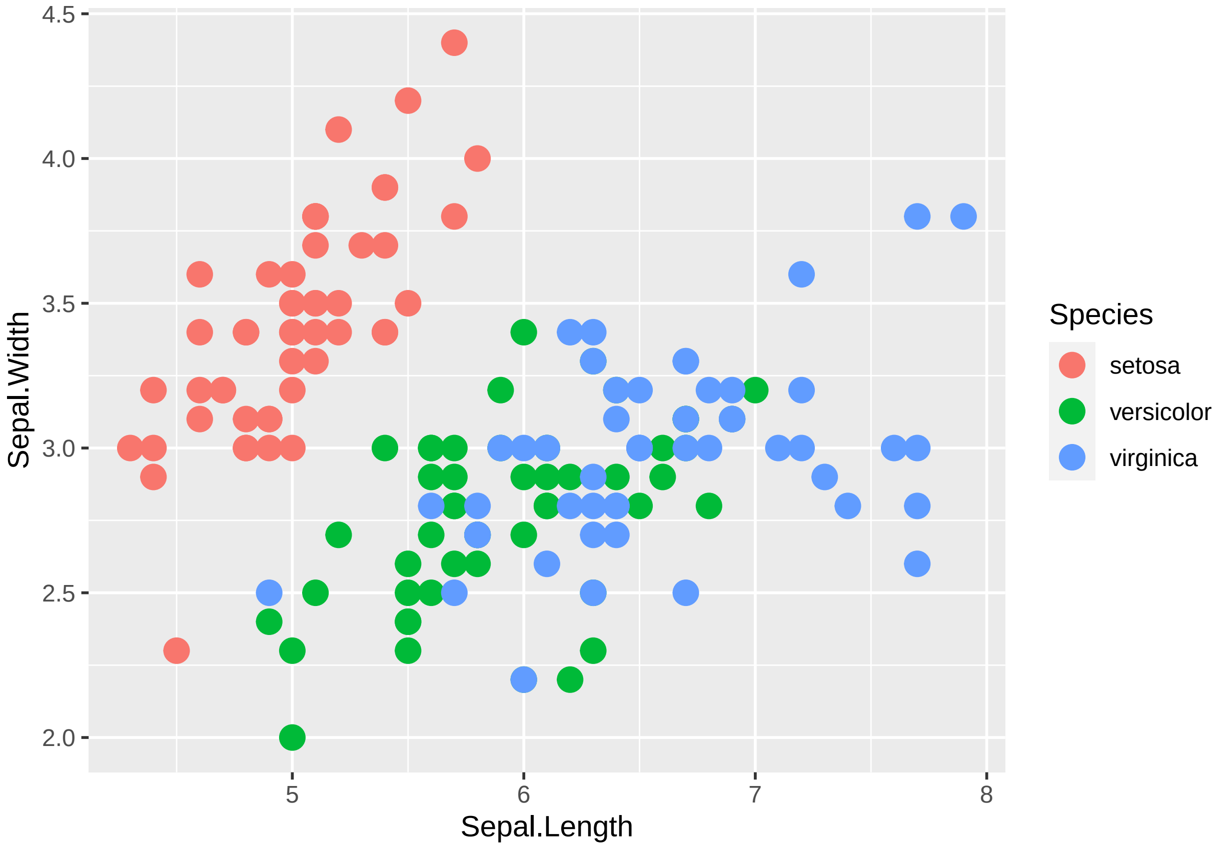


5) Data Visualization with specialized libraries

- In R, there are packages designed with the purpose of making good-looking graphics. This is the case with the ggplot2. The chunk below installs the ggplot2 library, loads the library into the R environment and then plots the data present in the iris data-frame.
- You can uncomment the installation line if you need to install it

5.1) Ggplot2

```
#install.packages("ggplot2")
library(ggplot2)
ggplot(data=iris, aes(x=Sepal.Length, y=Sepal.Width, color=Species)) + geom_point(size=4)
```



In our activities to visualize human genomic data, we will use a library called qqman, to visualize the biological association, through a plot known as the Manhattan plot.

5.2) Visualizing GWAS

The simplest definition of a GWAS is the statistical or significant association between a phenotype (trait) and a genotype. This association can be called biological association.

5.3.1) Package installation

- We need to install and load package qqman

```
## install.packages("qqman")
library(qqman)
```

```
##
## For example usage please run: vignette('qqman')
```

```
##
## Citation appreciated but not required:
## Turner, (2018). qqman: an R package for visualizing GWAS results using Q-Q and manhattan plots. Jour
##
```

- After, we load data-frame to be visualized
- Exact location of text file in your system needs to be determined

```
GWAS_TABLE <- read.table("~/Desktop/Arquivos/chr4.txt",
                         sep = " ",
                         header = T)
```

5.3.3) Get information about object with head()

- Use head() function to inspect the data-frame just loaded

```
head(GWAS_TABLE, n = 10)
```

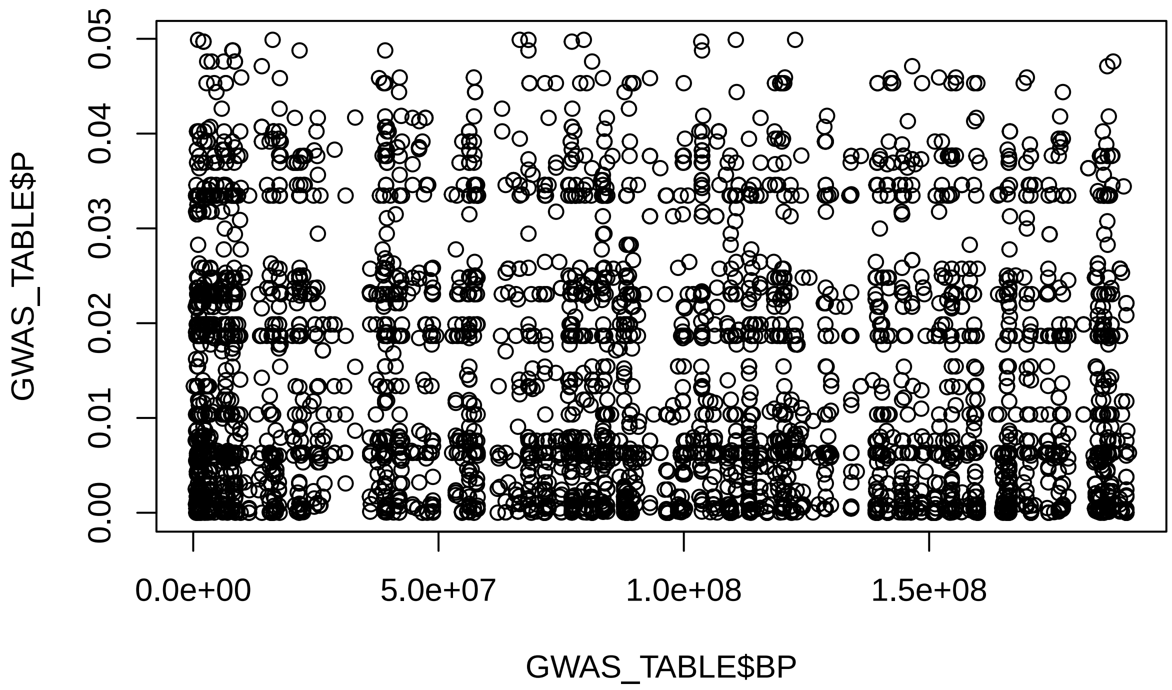
```
##    CHR         SNP     BP         P
## 1    4 chr4:128096 128096 0.0133500
## 2    4 chr4:516586 516586 0.0076260
## 3    4 chr4:523979 523979 0.0024960
## 4    4 chr4:527217 527217 0.0217400
## 5    4 chr4:566177 566177 0.0008988
## 6    4 chr4:578679 578679 0.0162100
## 7    4 chr4:578790 578790 0.0103700
## 8    4 chr4:579307 579307 0.0334600
## 9    4 chr4:580259 580259 0.0190400
## 10   4 chr4:585318 585318 0.0317600
```

5.3.4) Plotting GWAS data-frame

- In this section we use functions plot() and boxplot() to visualize data-frame
- In the y access, we see genomic coordinates and in the x access, p-valoues of the biological association
- Note that depending on the synthax used for plotting, R may complain

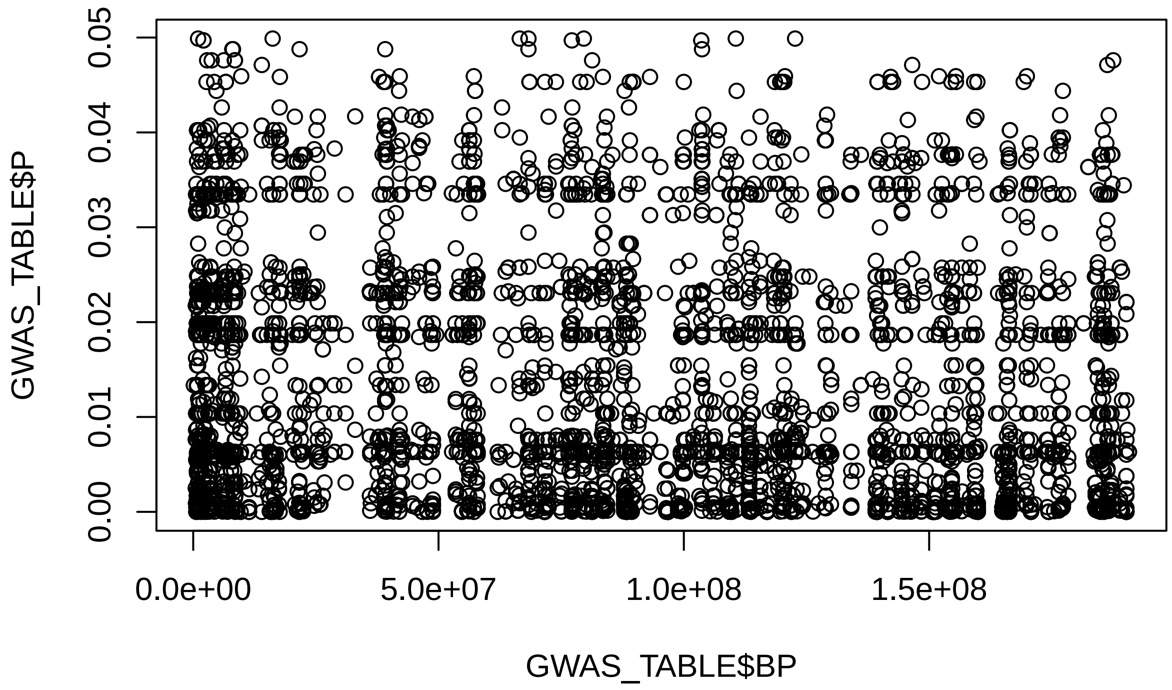
```
plot(data=GWAS_TABLE, GWAS_TABLE$BP, GWAS_TABLE$P) ## R complains
```

```
## Warning in plot.window(...): "data" is not a graphical parameter

## Warning in plot.xy(xy, type, ...): "data" is not a graphical parameter

## Warning in axis(side = side, at = at, labels = labels, ...): "data" is not a
## graphical parameter

## Warning in axis(side = side, at = at, labels = labels, ...): "data" is not a
## graphical parameter

## Warning in box(...): "data" is not a graphical parameter

## Warning in title(...): "data" is not a graphical parameter
```



5.3.4) Plotting GWAS data-frame

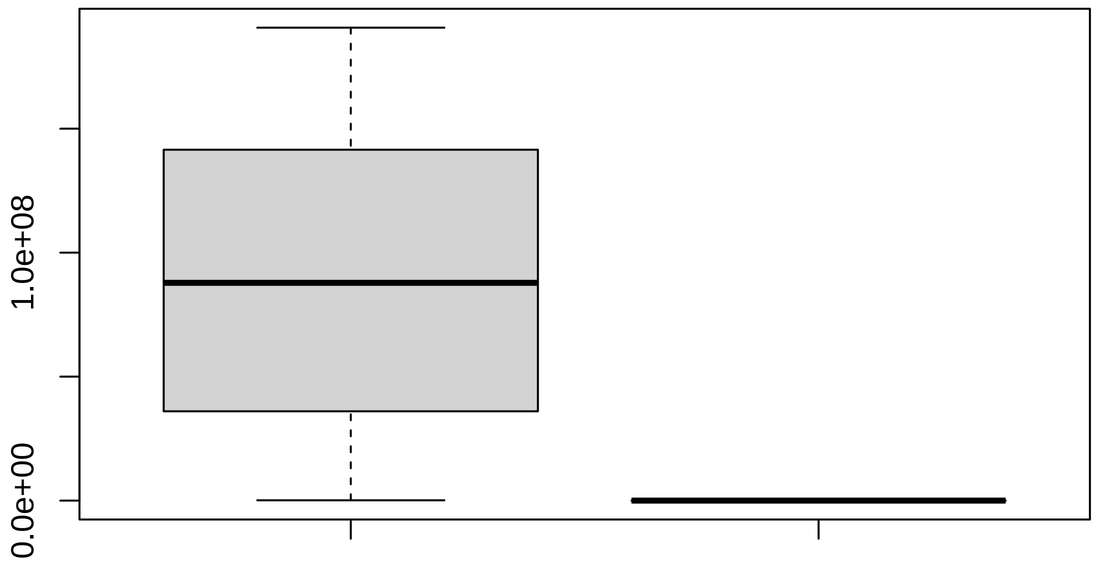
```
plot(GWAS_TABLE$BP, GWAS_TABLE$P) ## R does not complain
```



5.4) Boxplot

- Boxplot

```r
boxplot(data=GWAS_TABLE, GWAS_TABLE$BP, GWAS_TABLE$P)
```



5.5) Boxplot

- Compare the chromosomal coordinates and the values of the p-values in the boxplot above
- The chunk below allows one to ommit NA values in data-frame

```r
GWAS_TABLE_Ommit <- na.omit(GWAS_TABLE)
```

A seguir, criamos uma variável que armazena as posições das SNPs a serem realçadas em verde no Manhattan plot. Estas SNPs são mutações biológica e estatisticamente associadas à Doença de Huntington no gene de uma sortilina, localizada em proximidade física ao gene da proteína huntingtina mutada, a qual é a causadora medeliana (segue as leis de segregação genética de Mendel) da Doença de Huntington.

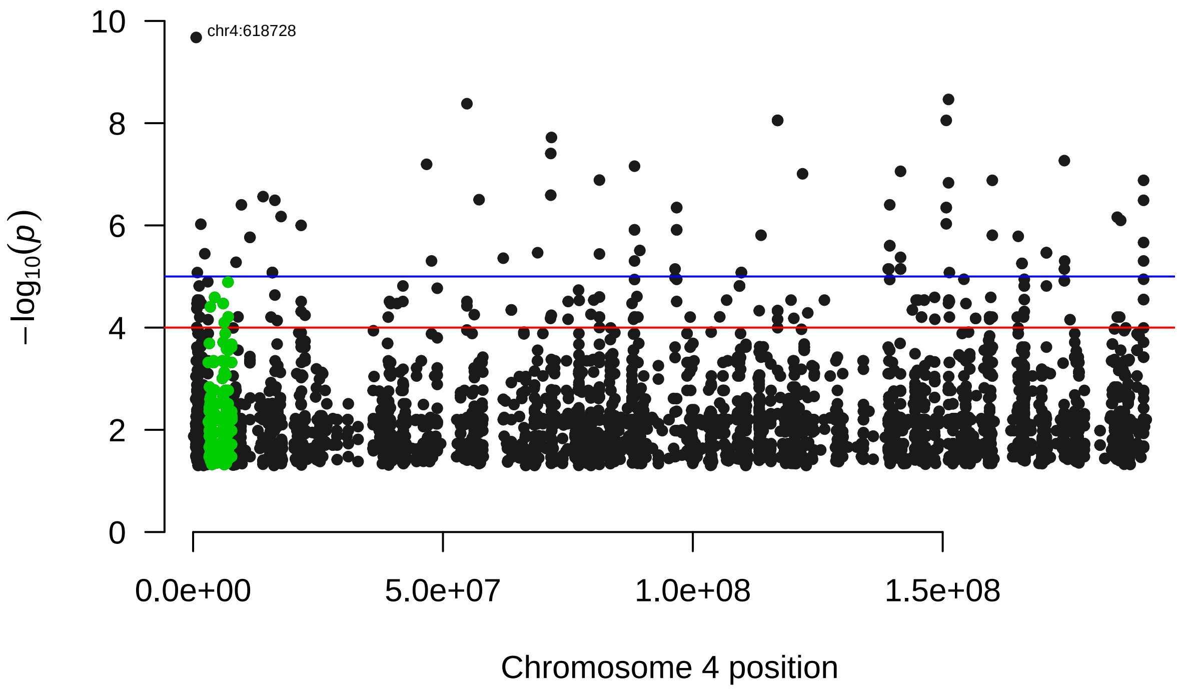
5.6) Create vector to highlight genome coordinates in Manhattan plot

```r
SNP_HIGHLIGHT <- c("chr4:3043512","chr4:3043513","chr4:3048207","chr4:3224216",
                   "chr4:3231772","chr4:3233844","chr4:3235081","chr4:3235084",
                   "chr4:3236881","chr4:3236883","chr4:3241845","chr4:3243804",
                   "chr4:3263138","chr4:3265130","chr4:3265710","chr4:3314646",
                   "chr4:3380088","chr4:3409359","chr4:3411110","chr4:3415336",
                   "chr4:3415378","chr4:3438643","chr4:3446091","chr4:3449886",
                   "chr4:3473066","chr4:3476809","chr4:3480439","chr4:3487151",
                   "chr4:3496058","chr4:3496110","chr4:3506933","chr4:3508752",
                   "chr4:3510957","chr4:3512690","chr4:3517746","chr4:3518190",
                   "chr4:3529671","chr4:3532327","chr4:3533066","chr4:3746133",
                   "chr4:3747842","chr4:3748134","chr4:3765305","chr4:3765336",
                   "chr4:3944253","chr4:3944752","chr4:3944888","chr4:3946166",
                   "chr4:3946175","chr4:3969218","chr4:4051294","chr4:4076788",
                   "chr4:4103104","chr4:4103105","chr4:4109198","chr4:4109210",
                   "chr4:4240627","chr4:4242705","chr4:4243668","chr4:4245210",
                   "chr4:4245510","chr4:4245513","chr4:4245591","chr4:4245926",
                   "chr4:4245929","chr4:4246109","chr4:4246433","chr4:4246453",
                   "chr4:4246457","chr4:4246497","chr4:4249414","chr4:4249415",
                   "chr4:4249484","chr4:4271623","chr4:4275306","chr4:4304749",
                   "chr4:4318931","chr4:4318970","chr4:4319564","chr4:4319728",
                   "chr4:4319750","chr4:4322078","chr4:4709657","chr4:4732282",
                   "chr4:4789635","chr4:4822960","chr4:4824890","chr4:4825092",
                   "chr4:4825180","chr4:4865316","chr4:4865321","chr4:5018702",
                   "chr4:5812778","chr4:5814082","chr4:5833660","chr4:5833899",
                   "chr4:5835541","chr4:5851205","chr4:5862752","chr4:5862938",
                   "chr4:5862943","chr4:5901873","chr4:5905499","chr4:5906287",
                   "chr4:6018891","chr4:6019046","chr4:6020190","chr4:6020367",
                   "chr4:6025638","chr4:6025656","chr4:6025766","chr4:6026058",
                   "chr4:6083488","chr4:6204935","chr4:6235553","chr4:6237142",
                   "chr4:6238466","chr4:6239906","chr4:6240929","chr4:6245022",
                   "chr4:6245618","chr4:6245732","chr4:6245915","chr4:6246075",
                   "chr4:6246373","chr4:6246959","chr4:6290594","chr4:6292020",
                   "chr4:6294095","chr4:6298375","chr4:6316092","chr4:6321396",
                   "chr4:6324647","chr4:6324785","chr4:6327669","chr4:6328354",
                   "chr4:6328507","chr4:6333130","chr4:6333559","chr4:6333669",
                   "chr4:6335966","chr4:6435341","chr4:6435486","chr4:6435926",
                   "chr4:6437191","chr4:6437197","chr4:6457121","chr4:6457131",
                   "chr4:6457132","chr4:6568390","chr4:6570032","chr4:6570768",
                   "chr4:6596360","chr4:6613252","chr4:6613462","chr4:6620991",
                   "chr4:6624771","chr4:6626154","chr4:6641969","chr4:6642090",
                   "chr4:6644466","chr4:6644467","chr4:6644468","chr4:6647889",
                   "chr4:6648300","chr4:6662665","chr4:6663319","chr4:6663715",
                   "chr4:6674554","chr4:6678553","chr4:6678599","chr4:6690535",
                   "chr4:6698664","chr4:6698667","chr4:6698706","chr4:6720572",
                   "chr4:6911679","chr4:6985889","chr4:6987394","chr4:7002344",
                   "chr4:7004495","chr4:7004506","chr4:7005196","chr4:7005199",
                   "chr4:7024077","chr4:7024398","chr4:7029430","chr4:7031064",
                   "chr4:7044357","chr4:7044380","chr4:7048842","chr4:7052115",
                   "chr4:7055253","chr4:7064243","chr4:7067765","chr4:7073187",
                   "chr4:7074027","chr4:7677967","chr4:7701947","chr4:7702795",
                   "chr4:7703505","chr4:7703807","chr4:7704795","chr4:7704818",
                   "chr4:7709703","chr4:7712150","chr4:7714490","chr4:7733843",
                   "chr4:7735162","chr4:7735164","chr4:7736103","chr4:7736112")
```

5.7) Plot Manhattan plot

- Finally, we plot the Manhattanh plot graph

```
manhattan(GWAS_TABLE_Ommit,
          highlight = SNP_HIGHLIGHT,
          annotateTop = T,
          annotatePval = 0.20,
          genomewideline = -log10(0.0001))
```



chr4:618728
10
8
6
4
2
0
$-\log_{10}(p)$
0.0e+00
5.0e+07
1.0e+08
1.5e+08
Chromosome 4 position