

# Canadian Bioinformatics Workshops

[www.bioinformatics.ca](http://www.bioinformatics.ca)

## Creative Commons

This page is available in the following languages:

Afrikaans বাংলা Català Dansk Deutsch Ελληνικά English English (CA) English (GB) English (US) Esperanto  
Español Castellano (AR) Español (CL) Castellano (CO) Español (Ecuador) Castellano (MX) Castellano (PE)  
Euskara Suomi français français (CA) Galego עברית hrvatski Magyar Italiano 日本語 한국어 Macedonian Malayu  
Nederlands Norsk Sesotho sa Leboa polski Português română slovenski jezik српски (latinica) Sotho svenska  
中文 華語 (台灣) isiZulu



### Attribution-Share Alike 2.5 Canada

#### You are free:



**to Share** — to copy, distribute and transmit the work



**to Remix** — to adapt the work



#### Under the following conditions:



**Attribution.** You must attribute the work in the manner specified by the author or licensor (but not in any way that suggests that they endorse you or your use of the work).



**Share Alike.** If you alter, transform, or build upon this work, you may distribute the resulting work only under the same or similar licence to this one.

- For any reuse or distribution, you must make clear to others the licence terms of this work.
- Any of the above conditions can be waived if you get permission from the copyright holder.
- The author's moral rights are retained in this licence.

[Disclaimer](#)

Your fair dealing and other rights are in no way affected by the above.

This is a human-readable summary of the Legal Code (the full licence) available in the following languages:  
[English](#) [French](#)

[Learn how to distribute your work using this licence](#)

# R Review



```
florence — R — 77x44
Last login: Fri May 16 17:29:10 on ttys008
Florence-MacBook-Pro:~ florence$ R

R version 3.1.0 (2014-04-10) -- "Spring Dance"
Copyright (C) 2014 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin10.8.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> a<- c(1:10)
> a
[1] 1 2 3 4 5 6 7 8 9 10
> log2(2)
[1] 1
> log2(a)
[1] 0.000000 1.000000 1.584963 2.000000 2.321928 2.584963 2.807355 3.000000
[9] 3.169925 3.321928
>
```



# Objectives

- To review the basic commands in R
- To review the matrix, data frame and list objects
- To learn more about how to visualize our data
- To become more familiar with R!

# Survey

- What is your experience in R?
  - Never used at all
  - Used for the first time to prepare the workshop
  - Used in my work but very basic
  - Using it rather regularly in my work
- Do you have experience in any other language?
  - Java, C, C++, ...
  - Perl, Python, Ruby, ...



# What is R?

R is a programming language and software environment for statistical computing and graphics

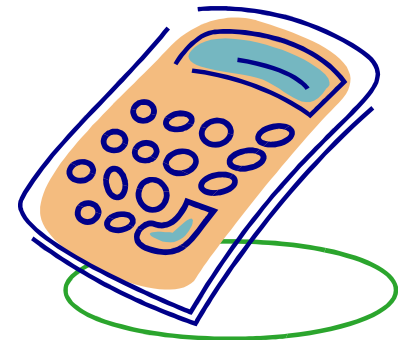
R allows for:

- Data handling and manipulation
- Statistical tests
- Graphics
- Specialized data analysis (i.e. microarray data, Seq data)

# An Overgrown Calculator

- Everything you can do on a calculator you can do in R plus more!

```
> 2+5  
[1] 7  
> 30/10  
[1] 3  
> 20-5  
[1] 15  
> log10(20)  
[1] 1.30103  
> pi  
[1] 3.141593  
> exp(-2)  
[1] 0.1353353  
> sin(0.4)  
[1] 0.3894183
```



# Assignments

- The arrow **<-** is the assignment operator

```
> weight.a <- 10
> weight.a
[1] 10
> weight.b <- 30
> weight.b
[1] 30
> total.weight <- weight.a + weight.b
> total.weight
[1] 40
```

## Tips:

- Avoid single letter names
- Separate words with a period or uppercase letters (i.e. total.weight or totalWeight)



# Code Documentation

```
# Hi there! How are you?  
# This is a comment!
```

- What is it for?
  - Explain what you are going to do with the code
  - Write messages for yourself
- Proper documentation is important!

```
# calculate the sum of 3 numbers  
sum(c(2, 6, 8))
```

# Working Directory

- In which directory are you working?

*getwd()*

```
> getwd()  
[1]  
"/Users/florence/Canadian_Bioinfo_workshop/BiCG_workshop_2014/R_review_2014"
```

- How can you change the working directory?

*setwd()*

```
> setwd("C:/myPATH")  
> setwd("~/myPATH") # on Mac  
> setwd("/Users/florence/myPATH") # on Mac
```

- File list in working directory, and object list in R:

*list.files(); ls()*

# Finding help: within R

- Call help on a function
  - `help(sum)`
  - `?sum`
- Read the documentation
  - See next slide
- Quit the help
  - `q`
- A more general search
  - `help.search("plot")`
  - `??plot`



Name  
of the function

sum

package:base

R Documentation

Sum of Vector Elements

Description:

'sum' returns the sum of all the values present in its arguments.

Usage:

sum(..., na.rm = FALSE)

Arguments:

...: numeric or complex or logical vectors.

na.rm: logical. Should missing values (including 'NaN') be removed?

Details:

This is a generic function: methods can be defined for it directly or via the 'Summary' group generic. For this to work properly, the arguments '...' should be unnamed, and dispatch is on the first argument.

Description of  
the function

How to use it

Information  
regarding the  
function

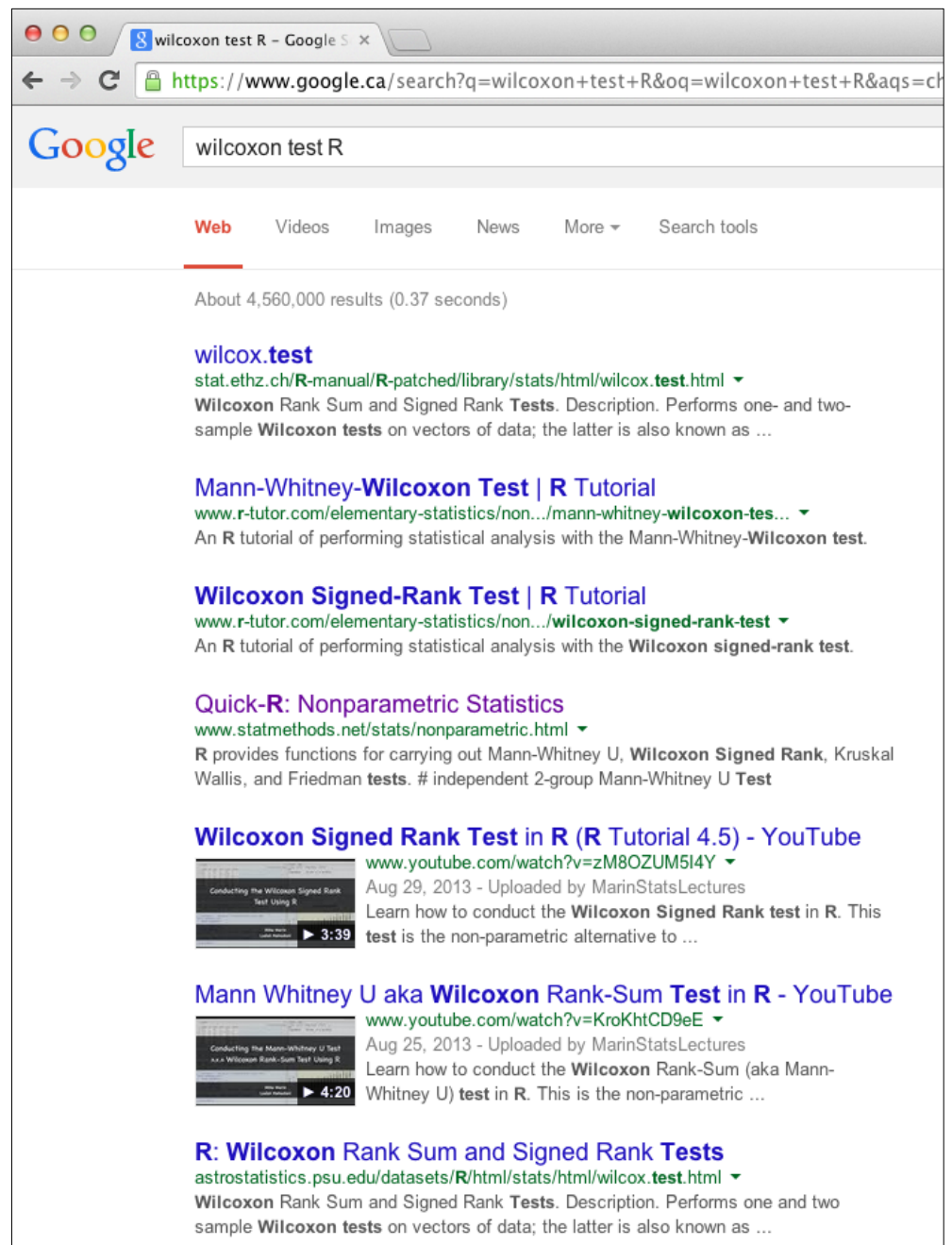
# Finding help: useR

- R website <http://www.r-project.org>
  - Documentation
  - Mailing-list R-help
- Useful links
  - <http://www.rseek.org>
  - <http://www.r-bloggers.com>
  - <http://biostar.stackexchange.com>
- Colleagues
- Local groups
  - GTA useR group

# Finding help: Google & CO

Many blogs, tutorial,  
comments online, ...

=> General web  
search engines are  
useful for that



The screenshot shows a Google search for "wilcoxon test R". The search bar contains the text "wilcoxon test R". Below the search bar, the results are displayed under the "Web" tab. The first result is "wilcoxon.test" from stat.ethz.ch, describing the Wilcoxon Rank Sum and Signed Rank Tests. The second result is "Mann-Whitney-Wilcoxon Test | R Tutorial" from www.r-tutor.com, describing an R tutorial for performing statistical analysis with the Mann-Whitney-Wilcoxon test. The third result is "Wilcoxon Signed-Rank Test | R Tutorial" from www.r-tutor.com, describing an R tutorial for performing statistical analysis with the Wilcoxon signed-rank test. The fourth result is "Quick-R: Nonparametric Statistics" from www.statmethods.net, describing R functions for carrying out Mann-Whitney U, Wilcoxon Signed Rank, Kruskal Wallis, and Friedman tests. The fifth result is "Wilcoxon Signed Rank Test in R (R Tutorial 4.5) - YouTube" from MarinStatsLectures, describing a video on how to conduct the Wilcoxon Signed Rank test in R. The sixth result is "Mann Whitney U aka Wilcoxon Rank-Sum Test in R - YouTube" from MarinStatsLectures, describing a video on how to conduct the Wilcoxon Rank-Sum (aka Mann-Whitney U) test in R. The seventh result is "R: Wilcoxon Rank Sum and Signed Rank Tests" from astrostatistics.psu.edu, describing the Wilcoxon Rank Sum and Signed Rank Tests.

Search results for "wilcoxon test R":

- wilcoxon.test**  
stat.ethz.ch/R-manual/R-patched/library/stats/html/wilcoxon.test.html  
Wilcoxon Rank Sum and Signed Rank Tests. Description. Performs one- and two-sample Wilcoxon tests on vectors of data; the latter is also known as ...
- Mann-Whitney-Wilcoxon Test | R Tutorial**  
www.r-tutor.com/elementary-statistics/non.../mann-whitney-wilcoxon-test...  
An R tutorial of performing statistical analysis with the Mann-Whitney-Wilcoxon test.
- Wilcoxon Signed-Rank Test | R Tutorial**  
www.r-tutor.com/elementary-statistics/non.../wilcoxon-signed-rank-test  
An R tutorial of performing statistical analysis with the Wilcoxon signed-rank test.
- Quick-R: Nonparametric Statistics**  
www.statmethods.net/stats/nonparametric.html  
R provides functions for carrying out Mann-Whitney U, Wilcoxon Signed Rank, Kruskal Wallis, and Friedman tests. # independent 2-group Mann-Whitney U Test
- Wilcoxon Signed Rank Test in R (R Tutorial 4.5) - YouTube**  
www.youtube.com/watch?v=zM8OZUM5I4Y  
Aug 29, 2013 - Uploaded by MarinStatsLectures  
Learn how to conduct the Wilcoxon Signed Rank test in R. This test is the non-parametric alternative to ...
- Mann Whitney U aka Wilcoxon Rank-Sum Test in R - YouTube**  
www.youtube.com/watch?v=KroKhtCD9eE  
Aug 25, 2013 - Uploaded by MarinStatsLectures  
Learn how to conduct the Wilcoxon Rank-Sum (aka Mann-Whitney U) test in R. This is the non-parametric ...
- R: Wilcoxon Rank Sum and Signed Rank Tests**  
astrostatistics.psu.edu/datasets/R/html/stats/html/wilcox.test.html  
Wilcoxon Rank Sum and Signed Rank Tests. Description. Performs one and two sample Wilcoxon tests on vectors of data; the latter is also known as ...

# Vectors



- Vectors are a collection of elements of the same data type

- Numeric

```
> numeric.vector  
[1] 1 2 3 4 5 6 2 1
```

- Character

```
> character.vector  
[1] "Fred" "Barney" "Wilma" "Betty"
```

- Logical

```
> logical.vector  
[1] TRUE TRUE FALSE TRUE
```

# Creating Vectors

- The `c()` function can be used to combine arguments and create vectors; `str()` function can be used to check the

```
structure of the object
```

```
> numeric.vector
```

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

```
> character.vector <- c("Fred", "Barney", "Wilma", "Betty")
```

```
> character.vector
```

```
[1] "Fred"    "Barney"  "Wilma"   "Betty"
```

```
> logical.vector <- c(TRUE, TRUE, FALSE, TRUE)
```

```
> logical.vector
```

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

```
# check the structure of the object:
```

```
> str(logical.vector)
```

```
logi [1:4] TRUE TRUE FALSE TRUE
```



# Vector Indexing

- Use the position in the vector to select value of interest with the operator `[]`

```
> character.vector  
[1] "Fred"    "Barney"  "Wilma"   "Betty"  
  
> character.vector[2]  
[1] "Barney"  
  
> character.vector[2:3]  
[1] "Barney" "Wilma"  
  
> character.vector[c(2,4)]  
[1] "Barney" "Betty"
```

# Factors



- Factors store categorical data (i.e. gender)

```
> gender <- c(1,2,1,1,1,2)
> gender
[1] 1 2 1 1 1 2

> gender.factor <- as.factor(gender)
> gender.factor
[1] 1 2 1 1 1 2
Levels: 1 2

> levels(gender.factor) <- c("male", "female")
> gender.factor
[1] male   female male   male   male   female
Levels: male female
```

# Factor Indexing

- Indexing a factor is the same as indexing a vector

```
> gender.factor
[1] male    female male    male    male    female
Levels: male female

> gender.factor[2]
[1] female
Levels: male female

> gender.factor[2:4]
[1] female male    male
Levels: male female

> gender.factor[c(1,4)]
[1] male male
Levels: male female
```

# Matrix



- Matrices are tables of numbers

```
> ?matrix
##(...)
Usage:
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE,
        dimnames = NULL)

> matrix.example <- matrix(1:12, nrow = 3, ncol=4, byrow = FALSE)
> matrix.example
      [,1] [,2] [,3] [,4]
[1,]    1    4    7   10
[2,]    2    5    8   11
[3,]    3    6    9   12

> matrix.example <- matrix(1:12, nrow = 3, ncol=4, byrow = TRUE)
> matrix.example
      [,1] [,2] [,3] [,4]
[1,]    1    2    3    4
[2,]    5    6    7    8
[3,]    9   10   11   12
```

# Creating Matrices

- The *rbind()* and *cbind()* functions can be used to combine vectors and create matrices. This is equivalent to the *c()* function for vectors

```
> dataset.a <- c(1,22,3,4,5)
> dataset.b <- c(10,11,13,14,15)
> dataset.a
[1] 1 22 3 4 5
> dataset.b
[1] 10 11 13 14 15

> rbind.together <- rbind(dataset.a, dataset.b)
> rbind.together
      [,1] [,2] [,3] [,4] [,5]
dataset.a    1  22   3   4   5
dataset.b   10  11  13  14  15

> cbind.together <- cbind(dataset.a, dataset.b)
```

# Creating Matrices

```
> dataset.a <- c(1,22,3,4,5)
> dataset.b <- c(10,11,13,14,15)
> dataset.a
[1] 1 22 3 4 5
> dataset.b
[1] 10 11 13 14 15

> rbind.together <- rbind(dataset.a, dataset.b)
> rbind.together
      [,1] [,2] [,3] [,4] [,5]
dataset.a    1  22   3   4   5
dataset.b   10  11  13  14  15

> cbind.together <- cbind(dataset.a, dataset.b)
> cbind.together
      dataset.a dataset.b
[1,]         1        10
[2,]        22        11
[3,]         3        13
[4,]         4        14
[5,]         5        15
```

# Matrix Indexing

- Use the row and column positions to select value of interest with the operator `[]`  
i.e `matrixObject[row_id,column_id]`

```
> matrix.example
      [,1] [,2] [,3] [,4]
[1,]    1    2    3    4
[2,]    5    6    7    8
[3,]    9   10   11   12

> matrix.example[2,4]
[1] 8
> matrix.example[2,]
[1] 5 6 7 8
> matrix.example[,4]
[1] 4 8 12
```

# Matrix Indexing

- Re-name rows and columns and select values of interest

```
> colnames(matrix.example) <- c("Sample1", "Sample2", "Sample3", "Sample4")
> rownames(matrix.example) <- paste("gene", 1:3, sep="_")

> matrix.example
      Sample1 Sample2 Sample3 Sample4
gene_1      1      2      3      4
gene_2      5      6      7      8
gene_3      9     10     11     12

> matrix.example[, "Sample2"]
gene_1 gene_2 gene_3
      2      6     10

> matrix.example[1, "Sample2"]
[1] 2

> matrix.example["gene_1", "Sample2"]
[1] 2
```



# Data frames



- Data frames are similar to matrices but each column can be a different data type

```
> people.summary <- data.frame(  
+ age = c(30,29,25,25),  
+ names = c("Fred", "Barney", "Wilma", "Betty"),  
+ gender = c("m", "m", "f", "f")  
+ )
```

```
> people.summary  
  age names gender  
1  30  Fred      m  
2  29 Barney      m  
3  25  Wilma      f  
4  25  Betty      f
```

# Data frame Indexing

- Indexing a data frame can be done the same way you index a matrix  
You can also use the \$ to obtain a column

```
> people.summary  
  age  names gender  
1  30   Fred      m  
2  29 Barney      m  
3  25  Wilma      f  
4  25  Betty      f
```

```
> people.summary[2,1]  
[1] 29
```

```
> people.summary[2,]  
  age  names gender  
2  29 Barney      m
```

```
> people.summary[,1]  
[1] 30 29 25 25
```

```
> people.summary$age  
[1] 30 29 25 25
```



# Lists

- Lists are combinations of data which can vary in data type and length

```
> together.list <- list(  
+ vector.example = dataset.a,  
+ matrix.example = matrix.example,  
+ data.frame.example = people.summary  
+ )  
> together.list  
$vector.example  
[1] 1 22 3 4 5  
  
$matrix.example  
      Sample1 Sample2 Sample3 Sample4  
gene_1      1      2      3      4  
gene_2      5      6      7      8  
gene_3      9     10     11     12  
  
$data.frame.example (to continue)
```



# Lists

```
> together.list <- list(  
+ vector.example = dataset.a,  
+ matrix.example = matrix.example,  
+ data.frame.example = people.summary  
+ )  
> together.list  
$vector.example  
[1] 1 22 3 4 5  
  
$matrix.example  
      Sample1 Sample2 Sample3 Sample4  
gene_1      1      2      3      4  
gene_2      5      6      7      8  
gene_3      9     10     11     12  
  
$data.frame.example  
  age  names gender  
1  30   Fred      m  
2  29 Barney      m  
3  25  Wilma      f  
4  25  Betty      f
```



# List Indexing

- You can index a list by using the \$, [], or [[]]

```
> together.list$matrix.example
      Sample1 Sample2 Sample3 Sample4
gene_1      1      2      3      4
gene_2      5      6      7      8
gene_3      9     10     11     12

> together.list$matrix.example[,3]
gene_1 gene_2 gene_3
      3      7     11
```

```
> together.list["matrix.example"]
$matrix.example
      Sample1 Sample2 Sample3 Sample4
gene_1      1      2      3      4
gene_2      5      6      7      8
gene_3      9     10     11     12

> together.list[["matrix.example"]]
      Sample1 Sample2 Sample3 Sample4
gene_1      1      2      3      4
gene_2      5      6      7      8
gene_3      9     10     11     12

> together.list[["matrix.example"]][,2]
gene_1 gene_2 gene_3
      2      6     10
```

- [ ] allows you to select multiple elements
- \$ and [[]] allows you to select a single element

# Functions

- Functions are a set of commands that work together to perform a given task
- Arguments are parameters you provide to the function for processing

Most functions have reasonable default values

```
> sum(c(1, 2, 3))  
[1] 6  
> log2(10)  
[1] 3.321928  
> sin(0.24)  
[1] 0.2377026  
> mean(c(1, 2, 3, 4, 5))  
[1] 3
```

# Some useful functions such as:


- Length of a vector: *length()*
- Number of rows or columns and dimension of a matrix/data frame: *nrow()*, *ncol()*, *dim()*

```
> character.vector
[1] "Fred"    "Barney"  "Wilma"   "Betty"
> length(character.vector)
[1] 4
> matrix.example
      Sample1 Sample2 Sample3 Sample4
gene_1      1      2      3      4
gene_2      5      6      7      8
gene_3      9     10     11     12
> nrow(matrix.example)
[1] 3
> ncol(matrix.example)
[1] 4
> dim(matrix.example)
[1] 3 4
```

# Some useful functions such as:

- Read a table for text file: *read.table()*
- Write a matrix/data frame in a text file: *write.table()*

```
> ?read.table
read.table("myDataFile.txt", header=TRUE, sep="\t",
stringsAsFactors=FALSE)
> ?write.table
```



```
> write.table(people.summary, file="File_name_people_summary.txt",
quote=FALSE, sep = "\t", row.names = FALSE, col.names = TRUE)
```





# Let's try! (I)

- Use the assignment operator to store three values of your choice
- Calculate and store the sum of the values from above

# Solutions

- Use the assignment operator to store three values on your choice

```
> value.a <- 10  
> value.b <- 3  
> value.c <- 12
```

- Calculate and store the sum of the values from above

```
> sum.values <- value.a + value.b + value.c
```

# Let's try! (II)



We will use the *cars* dataset (included by default in R)

- What data type is the *cars* dataset? and its dimensions?
- Access to the speed values
- Access and store only the *cars* data with speeds greater than 15. How many cars does this affect?
- Reformat the *cars* data into a list
- Access only the *cars* data with speeds greater than 15 from the list you just created. How many cars does this affect? Did you get the same results as above?
- What does *stringsAsFactors* in the `data.frame` function do?

# Solutions

- What data type is the *cars* dataset? and its dimensions?

```
> class(cars)
[1] "data.frame"
> dim(cars)
[1] 50  2
## or
> str(cars)
'data.frame':   50 obs. of  2 variables:
 $ speed: num  4 4 7 7 8 9 10 10 10 11 ...
 $ dist : num  2 10 4 22 16 10 18 26 34 17 ...
```

```
## To look at the object
> head(cars)
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

- Access to the speed values

```
> cars$speed
 [1]  4  4  7  7  8  9 10 10 10 11 11 12 12 12 12 13 13 13 13 14 14 14 14 15 15
[26] 15 16 16 17 17 17 18 18 18 18 19 19 19 20 20 20 20 20 22 23 24 24 24 24 25
```

# Solutions

- Access and store only the *cars* data with speeds greater than 15

How many cars does this affect?

```
> cars.greater.speed <- cars[cars$speed > 15,]  
> nrow(cars.greater.speed)  
[1] 24
```

- Reformat the *cars* data into a list

```
> cars.as.list <- list(SPEED = cars$speed, DISTANCE = cars$dist)  
> cars.as.list  
$SPEED  
 [1]  4  4  7  7  8  9 10 10 10 11 11 12 12 12 12 13 13 13 13 14 14 14 14 15 15  
[26] 15 16 16 17 17 17 18 18 18 18 19 19 19 20 20 20 20 20 22 23 24 24 24 24 25  
  
$DISTANCE  
 [1]  2 10  4 22 16 10 18 26 34 17 28 14 20 24 28 26 34 34 46  
[20] 26 36 60 80 20 26 54 32 40 32 40 50 42 56 76 84 36 46 68  
[39] 32 48 52 56 64 66 54 70 92 93 120 85  
  
> names(cars.as.list)  
[1] "SPEED" "DISTANCE"
```

# Solutions

- Access only the *cars* data with speeds greater than 15 from the list you just created  
How many cars does this affect?  
Did you get the same results as above?

```
> cars.as.list.greater.speed <- cars.as.list$SPEED[cars.as.list$SPEED > 15]

> cars.as.list.greater.speed
[1] 16 16 17 17 17 18 18 18 18 19 19 19 20 20 20 20 20 22 23 24 24 24 24 25

> length(cars.as.list.greater.speed)
[1] 24
```

# Solutions

- What does *stringsAsFactors* in the `data.frame` function do?

```
> ?data.frame
##(...)
logical: should character vectors be converted to factors?
The 'factory-fresh' default is TRUE, but this can be
changed by setting options(stringsAsFactors = FALSE).
```

# Exploratory analysis and plots

- A few tips:
  - Do not show too much information on a plot
  - Think about what message you want to give thanks to the plot
  - Avoid 3D graphics
  - Stay away from Excel (not a statistics package)



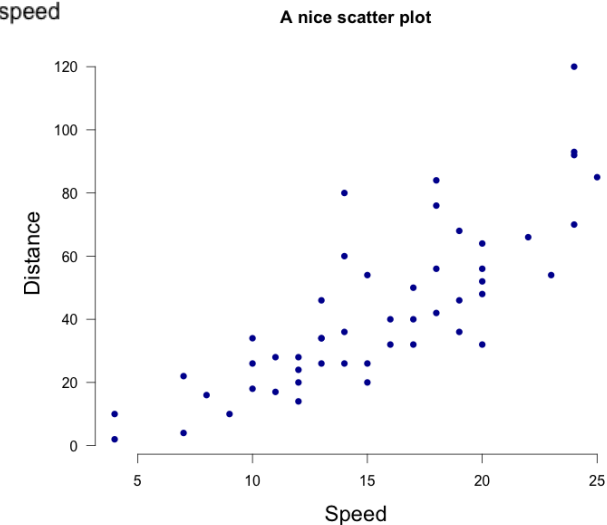
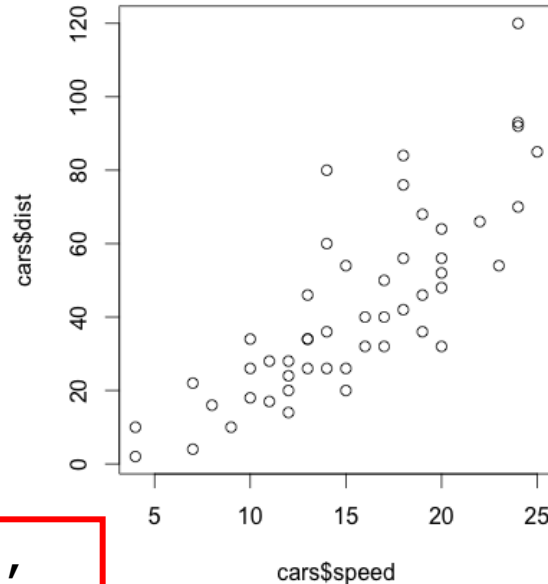
# Let's have a look: simple plot

- Function *plot()*

```
> plot(x=cars$speed,
       y=cars$dist)
```

- Make it nicer

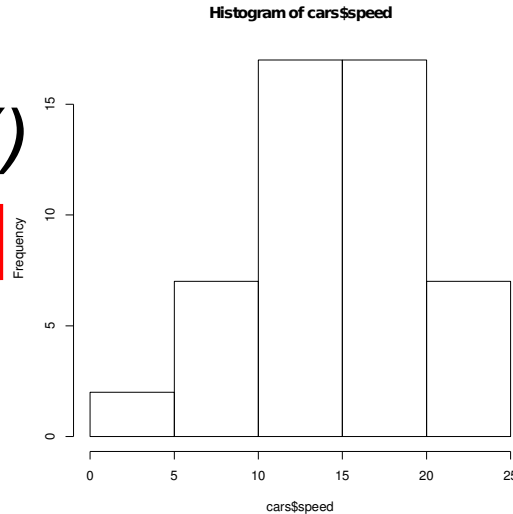
```
> plot(x=cars$speed, y=cars$dist,
       xlab = "Speed",
       ylab = "Distance",
       cex.lab = 1.5,
       main = "A nice scatter plot",
       pch = 16,
       bty = "n",
       col = "dark blue",
       las = 1)
```



# Let's have a look: histogram

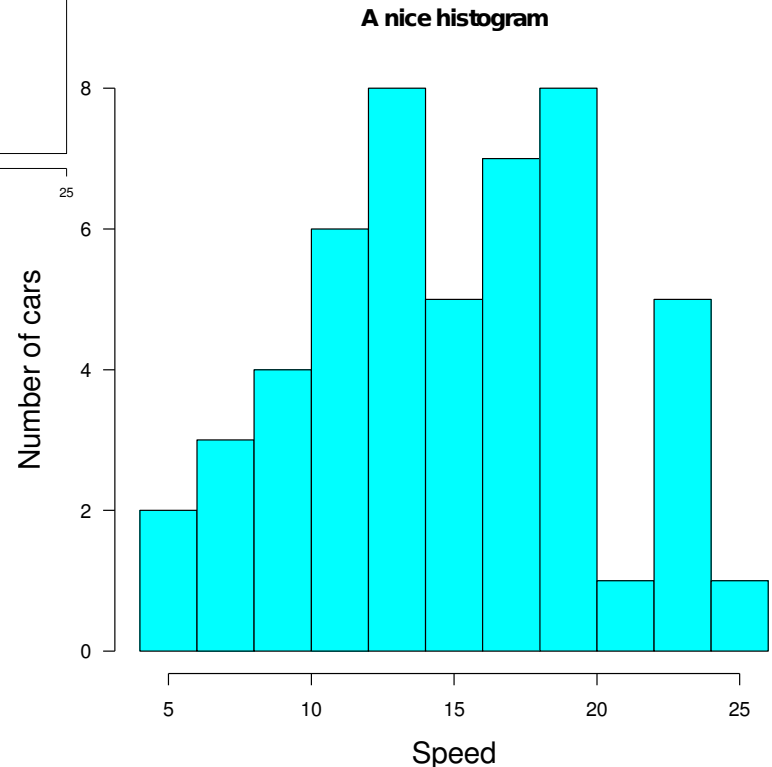
- Function *hist()*

```
> hist(cars$speed)
```



- Make it nicer

```
> hist(cars$speed,  
      xlab = "Speed",  
      ylab = "Number of cars",  
      cex.lab = 1.5,  
      main = "A nice histogram",  
      col = "cyan",  
      breaks = 10,  
      las = 1)
```

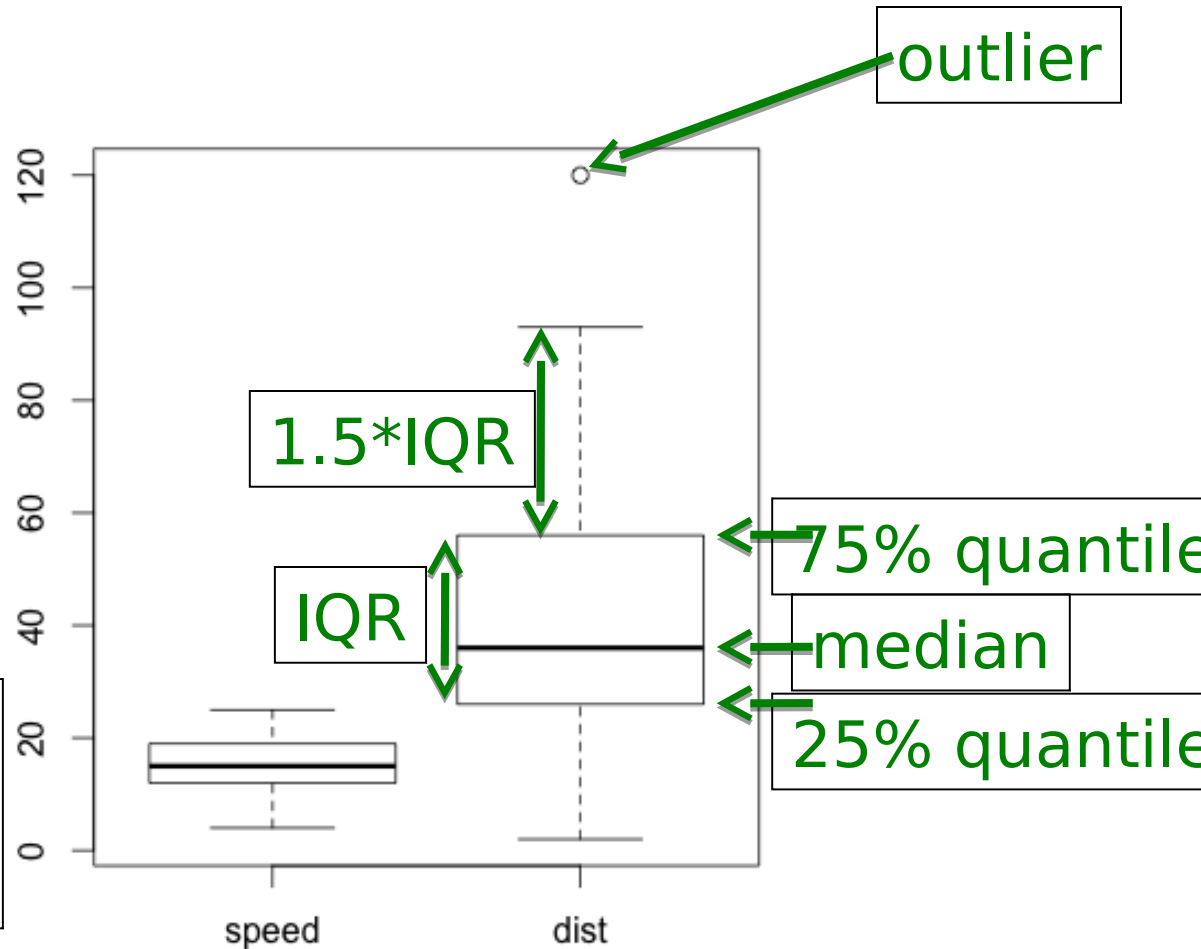


# Let's have a look: boxplot

- Function *boxplot*

```
> boxplot(cars)
```

IQR:  
Inter Quantile Range  
25%-75% quantile



# Other useful functions related to figures

- Function *par()*
  - Allow to set many graphical parameters such as *mfrow*, *bg*, *col*,...
  - See *?par*
- Function *pdf()* then *dev.off()*
  - To save your plot as a .pdf figure

```
?pdf
```

```
##(...)
```

```
Description:
```

```
‘pdf’ starts the graphics device driver for producing PDF  
graphics.
```

# Missing values

- R deals with missing values in a object using the *NA* value
- We can detect NA values with the *is.na()* function

```
> val <- c(1,3,5,NA,3,6)
> val
[1] 1 3 5 NA 3 6

> is.na(val)
[1] FALSE FALSE FALSE TRUE FALSE FALSE

> which(is.na(val))
[1] 4
```

# Let's try! (IV)



```
val <- c(1,3,5,NA,3,6)
```

- Compute the sum of *val* removing missing values
- I want the average of *val*, and I do `mean(val)`  
I am not happy with the result. What can I do?

# Solutions

- Compute the sum of x removing missing values

```
> val <- c(1,3,5,NA,3,6)
> sum(val, na.rm = TRUE)
[1] 18
```

- I want the average of x, and I do mean(x)  
I am not happy with the result  
What can I do?

```
> mean(val)
[1] NA
> mean(val, na.rm = TRUE)
[1] 3.6
```

# How to save and reload your data?

- Use the functions `save()` or `save.image()` and `load()`

```
> ?save
```

```
##(...)
```

Description:

'save' writes an external representation of R objects to the specified file. The objects can be read back from the file at a later date by using the function 'load' (or 'data' in some cases).

'save.image()' is just a short-cut for 'save my current workspace', i.e., 'save(list = ls(all = TRUE), file = ".RData")'. It is also what happens with 'q("yes")'.

```
> save(cars.as.list, file="my_cars_as_list.RData")
```

```
> load(file="my_cars_as_list.RData") #if the file is present in the working  
directory, if not, indicate the path of the .RData file
```

```
> save(cars.as.list, numeric.vector, rbind.together,  
file="my_Objects_Rreview_May2014.RData")
```

```
> load(file="my_Objects_Rreview_May2014.RData")
```

```
## To save all the objects in the R session
```

```
> save.image(file="Rreview_2014.RData")
```

```
## after closing you R session for example, load the data with:
```

```
> load(file="Rreview_2014.RData")
```



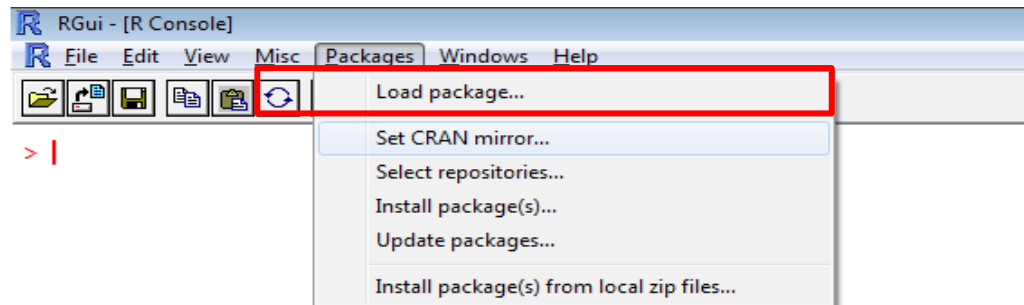
# A few words about packages

- <http://cran.r-project.org/>
- "Currently, the CRAN package repository features 5563 available packages"
- To install a package: *install.packages()*

```
## install.packages("PackageName")  
> install.packages("heatmap.plus")
```

- How to set your CRAN?

```
> chooseCRANmirror()
```



# A few words on Bioconductor

- Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data.
- Site: <http://bioconductor.org/>
- Contains method, dataset and annotation packages
- May 2014: 824 software packages !
- To install a Bioconductor package:

```
> source("http://bioconductor.org/biocLite.R")  
## biocLite("PackageName")  
> biocLite("DESeq2")  
> library("DESeq2")
```

Any questions?

Try and test by yourself! □

# Extra slides



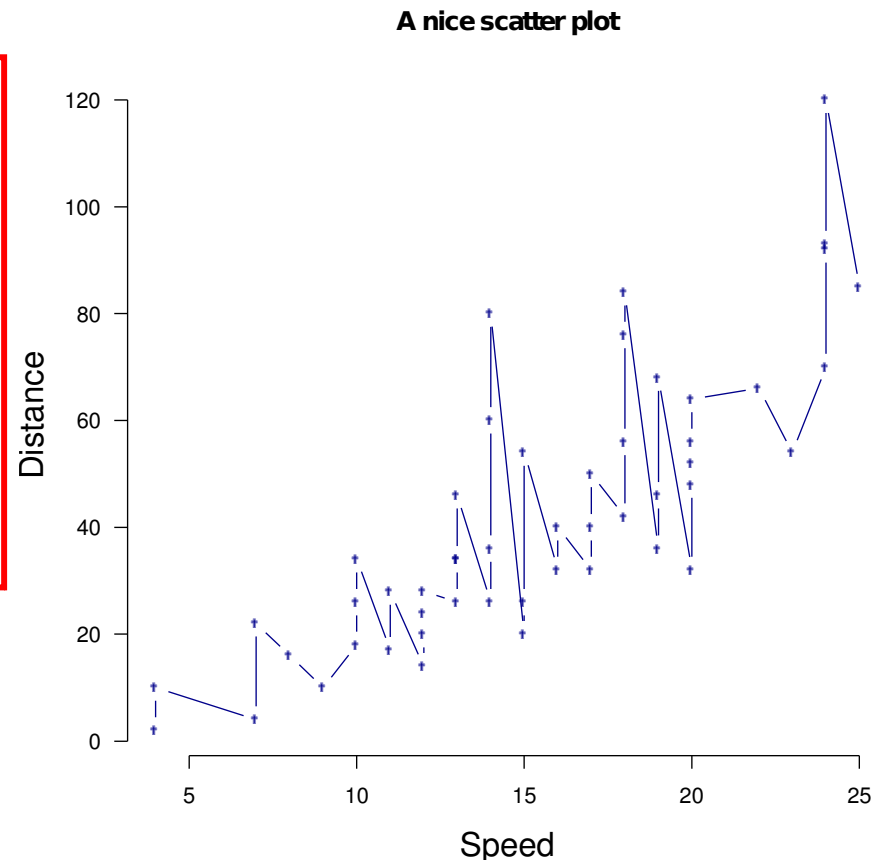
## Let's try plotting! (III)

- Do a scatter plot with connected dots
- Make your customized version of the boxplot
- How can you change the  $1.5 \times \text{IQR}$  parameter?
- Print the scatter plot and the boxplot on top of each other and save the figure in a pdf file

# Solutions

- Do a scatter plot with connected dots

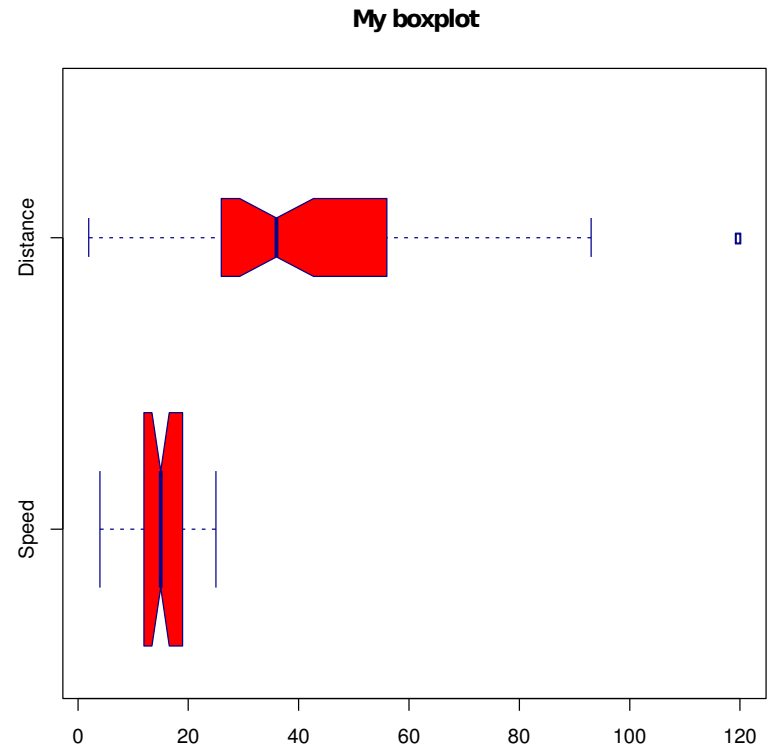
```
> plot(cars$speed, cars$dist,  
       xlab = "Speed",  
       ylab = "Distance",  
       cex.lab = 1.5,  
       main = "A nice scatter plot",  
       pch = 16,  
       bty = "n",  
       col = "dark blue",  
       type = "b",  
       las = 1)
```



# Solutions

- Make your customized version of the boxplot

```
> boxplot(cars,  
  width = c(3,1),  
  col = "red",  
  border = "dark blue",  
  names = c("Speed", "Distance"),  
  main = "My boxplot",  
  notch = TRUE,  
  horizontal = TRUE)
```



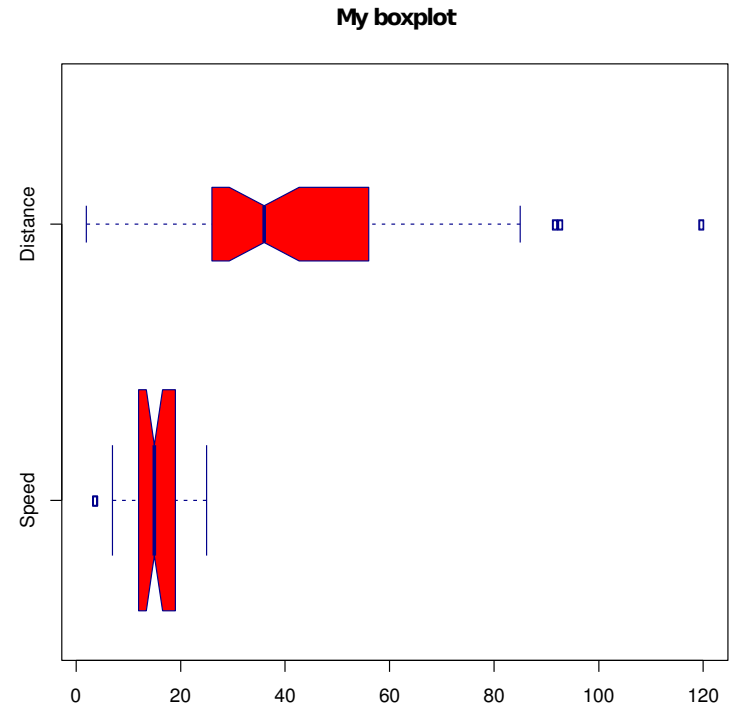


# Solutions

- How can you change the  $1.5 \times \text{IQR}$  parameter?

```
> boxplot(cars,  
  width = c(3,1),  
  col = "red",  
  border = "dark blue",  
  names = c("Speed", "Distance"),  
  main = "My boxplot",  
  range = 1,  
  notch = TRUE,  
  horizontal = TRUE)
```

range, default  
= 1.5



# Solutions

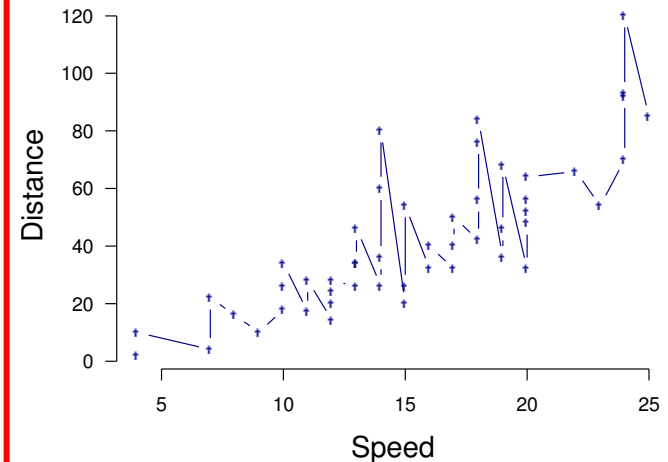
- Print the scatter plot and the boxplot on top of each other and save the figure in a pdf file

```
> pdf("myfigure.pdf", height=18, width=8)
> par(mfrow=c(2,1))

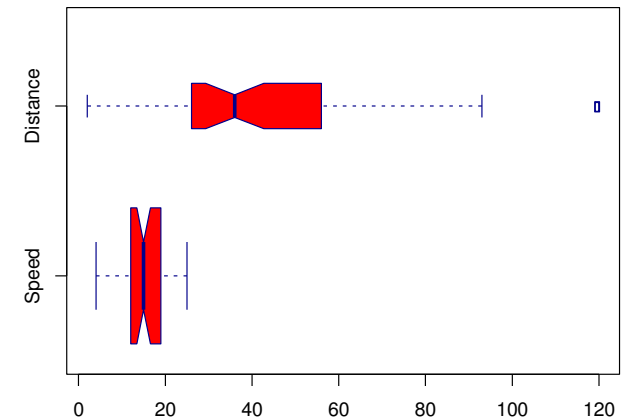
> plot(cars$speed, cars$dist,
       xlab = "Speed", ylab = "Distance",
       cex.lab = 1.5,
       main = "A nice scatter plot",
       pch = 16,
       bty = "n",
       col = "dark blue",
       type = "b",
       las = 1)

> boxplot(cars,
          width = c(3,1),
          col = "red",
          border = "dark blue",
          names = c("Speed", "Distance"),
          main = "My boxplot",
          notch = TRUE,
          horizontal = TRUE)
> dev.off()
```

A nice scatter plot



My boxplot



# Statement control: If

- If/else

```
x <- 2
if (x>0) {
  cat("Positive value:",x,"\n")
} else if (x<0) {
  cat("Negative value:",x,"\n")
}
```

Positive value: 2

"\n" is to go to the next line

- If/else if/else

```
x <- -3
if (x>0) {
  cat("Positive value:",x,"\n")
} else if (x==0) {
  cat("Zero:",x,"\n")
} else {
  cat("Negative value:",x,"\n")
}
```

Negative value: -3

# Loop, loop, loop: For

- Indexes

```
for (i in 1:5) {  
  cat(i)  
}
```

```
12345>
```

- Vectors

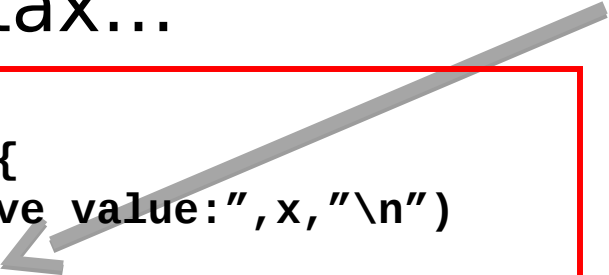
```
values <- c(2,1,3,6,5)  
for (value in values) {  
  ## cat(value)  
  print(value)  
}
```

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

# Loop, loop, loop: While

- Easy syntax...

```
x <- 4
while (x>0) {
  cat("positive value:",x,"\n")
  x <- x-1
}
```




Make sure something changes in each loop

```
positive value: 4
positive value: 3
positive value: 2
positive value: 1
```

- And easy mistakes...

```
x <- 4
while (x>0) {
  cat("positive value:",x,"\n")
  x <- x+1
}
```



Oops.. we have a problem here...  
Infinite loop

Make sure that the end criteria will happen



# Let's try! (V)

- Print all numbers from 1 to 10
- Print all even numbers from 1 to 10
- Print the speed of the first 8 cars using *while*
- Print the first 8 cars that have a speed more than 9
- How many cars have a speed greater than 10?  
What is their mean distance?

# One way to do it with what we learned

- Print all numbers from 1 to 10

```
# create "sample" to browse
sample <- 1:10
for (n in sample) {
  # print each number in "sample"
  print (n)
}
```

```
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
[1] 7
[1] 8
[1] 9
[1] 10
```

- Print all even numbers from 1 to 10

```
# create the sample to browse
sample <- 1:10
for (n in sample) {
  # test the rest of the division by 2 (see if even)
  if (n %% 2 == 0) {
    print (n)
  }
  # no need for a else here (and it is not required)
}
```

```
[1] 2
[1] 4
[1] 6
[1] 8
[1] 10
```

# One way to do it with what we learned

- Print the speed of the first 8 cars using *while*

```
# we initialize the index to track how many cars were printed
# 1 to start at the first car
index <- 1
# we continue until the index is 8
while (index <= 8) {
  # to access the speed of the car
  speed <- cars[index, "speed"]
  # we print with \n to go to the next line
  cat("Car #", index, "speed:", speed, "\n")
  # every iteration we go to the next car
  index <- index + 1
}
```

```
Car # 1 speed: 4
Car # 2 speed: 4
Car # 3 speed: 7
Car # 4 speed: 7
Car # 5 speed: 8
Car # 6 speed: 9
Car # 7 speed: 10
Car # 8 speed: 10
```



# One way to do it with what we learned

- Print the first 8 cars that have a speed more than 9

```
# we initialize the variables so that they can be used in the loop
# 0 on the counter to add up
counter <- 0
# each time we find an appropriate car, 1 on the index to start at the first car
index <- 1
while (counter < 8) {
  # to access the speed of the car
  speed <- cars[index, "speed"]
  # if it is more than 9
  if (speed > 9) {
    # we print the car found, with \n to go to the next line
    cat("Car #", index, "speed:", speed, "\n")
    # and track that we have printed one more car
    counter <- counter + 1
  }
  # every time we go to the next car
  index <- index + 1
}
```

```
Car # 7 speed: 10
Car # 8 speed: 10
Car # 9 speed: 10
Car # 10 speed: 11
Car # 11 speed: 11
Car # 12 speed: 12
Car # 13 speed: 12
Car # 14 speed: 12
```

# One way to do it with what we learned

- How many cars have a speed greater than 10?  
What is their mean distance?

```
# we put 0 to add up the values we have while browsing the cars
count      <- 0
distance <- 0
# we browse all cars by their index
for (i in 1:nrow(cars)) {
  # test if the speed of the car exceeds 10
  if (cars[i, "speed"] > 10) {
    # here we add it to the group of cars considered
    count      <- count + 1
    # we add its distance to compute the mean afterwards
    distance <- distance + cars[i, "dist"]
  }
}
# we compute the distance with the global sum of all distances and the number
of # cars used to get that global sum
distanceMean <- distance / count
# print the results, "\n" is used to go to the next line
cat(count, "cars, mean distance", distanceMean, "\n")
```

```
41 cars, mean distance 48.95122
```

# Creating functions

To create a function you need to:

- State you want to create a function with *function()*
- Include required arguments in brackets ()
- Contain the commands in the curly brackets {}
- State your return object, using *return()*

```
> function.example <- function(vector.of.values){  
+ sum.exponent.value <- sum(vector.of.values)^2  
+ return(sum.exponent.value)  
+ }
```

```
> dataset.a  
[1] 1 22 3 4 5  
> function.example(dataset.a)  
[1] 1225
```

# Creating functions continued...

- You can add in default values to arguments

```
> function.example <- function(vector.of.values, exponent.value = 2){  
+   sum.exponent.value <- sum(vector.of.values)^exponent.value  
+   return(sum.exponent.value)  
+ }  
  
> dataset.a  
[1] 1 22 3 4 5  
> function.example(dataset.a)  
[1] 1225  
> function.example(dataset.a, exponent.value = 10)  
[1] 2.758547e+15
```



## et's try! (VI)

- Create a function that takes in a vector and returns its mean
- Create a function that takes in a numeric vector and minimum cutoff value. Return the mean, median and variance for the numbers in the vector that are greater than the minimum cutoff. Use all positive values if the user does not input a minimum cutoff value

# Possible Solutions

- Create a function that takes in a vector and returns its mean

```
> calculate.mean <- function(x){  
+   to.return <- mean(x)  
+   return(to.return)  
+ }  
  
> dataset.a  
[1] 1 22 3 4 5  
> calculate.mean(dataset.a)  
[1] 7
```

# Possible Solutions

- Create a function that takes in a numeric vector and minimum cutoff value. Return the mean, median and variance for the numbers in the vector that are greater than the minimum cutoff. Use all positive values if the user does not input a minimum cutoff value

```
> summary.selection <- function(vector.of.values, cutoff.value = 0){  
+   selected <- vector.of.values[vector.of.values > cutoff.value]  
+   mean.value <- mean(selected)  
+   median.value <- median(selected)  
+   var.value <- var(selected)  
+   to.return <- list( mean = mean.value, median = median.value, var =  
var.value)  
+   return(to.return)  
+ }
```

```
> summary.selection(dataset.a)  
$mean  
[1] 7  
$median  
[1] 4  
$var  
[1] 72.5
```