Université Paris Dauphine
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Introduction to R

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1 Introduction

R is an interpreted programming language, and a free software environment particularly useful for statistical computing and graphics. Created in the early 1990s by Robert Gentleman and Ross Ihaka, it is a free clone of S-Plus (software sold by MathSoft based on the S programming language).

R is currently developed by the *R Core Development Team*. It provides through libraries a wide range of statistical methods an graphical facilities. All the useful information on R can be found on the *R Core Development Team* website https://www.r-project.org. In particular, the latest versions of R distributions and documentation can be downloaded from the website.

R is also substantially extended by user-created packages, a flexible manner for users to add some functionnalities. Amongst other options, packages are available on The Comprehensive R archive network (CRAN, https://cran.r-project.org/).

The present document is solely a short introduction on the tools we will use throughout the course. For a more comprehensive overview on the use of R , we suggest to read the manual *R for beginners* by Emmanuel Paradis and available at https://cran.r-project.org/doc/contrib/Paradis-rdebuts_en.pdf.

2 How to use R?

2.1 Using a command-line user interface

On Unix systems, R is accessible from a console user interface and does not require a graphical user interface. Once the software installed, it can be run by entering the command R in a Terminal.

When R is opened, the Terminal line starts with the character >. This signals that the console is available for you to type an instruction. When you type an unfinished instruction (for example if you open a parenthesis and do not close it before pressing Enter), the console line starts with the character + instead, indicating that R is waiting for the end of the instruction.

Exercice 1. Starting with R and the command line interface

- Open a Terminal.
- Start the software R by typing R and then press Enter. The Software is now waiting for your command lines.
- Type the simple operation 3 + 5, then press enter.
- To quit the R session, type `q()`, press enter and answer `n`.
- Close the Terminal.

The main drawback on using a command-line interface is that commands are executed on the go. For advanced programming, an alternative is to edit a script, for example script.R , in a text editor and then to call it using the command `source("script.R")`. By default the command `source` simply reads and executes the R code from a file but does not prompt the command line or the output. In order to print the command line before its evaluation, the command `source` has an option `echo` taking logical values `TRUE` or `FALSE`, and in order to print the result of evaluation, it has an option `print.eval` taking logical values `TRUE` or `FALSE`. You can read more on the the command `source` at https://www.rdocumentation.org/packages/base/versions/3.4.1/topics/source.

2.2 Using RStudio

In what follows, we use the integrated development environment (IDE) RStudio (https://www.rstudio.com) which offers an easy-to-use Graphical User Interface available for all the plateform (iOS, Linux and Windows). But other IDE could have been used such as RKward, R Commander or R Tools for Visual Studio (plug-in for Microsoft Visual Studio) to name just a few.

In most IDEs, you will find information stored in several windows which offer a more flexible and efficient manner to use R rather than the simple command line interface. The most important ones are the Console window and the Script or Editor window. Hereafter is the organisation of RStudio interface, see Figure 1.

The Console window (1): by default, it is the bottom left window. It allows to enter command lines after the prompt ">" in the same way as in the Terminal.

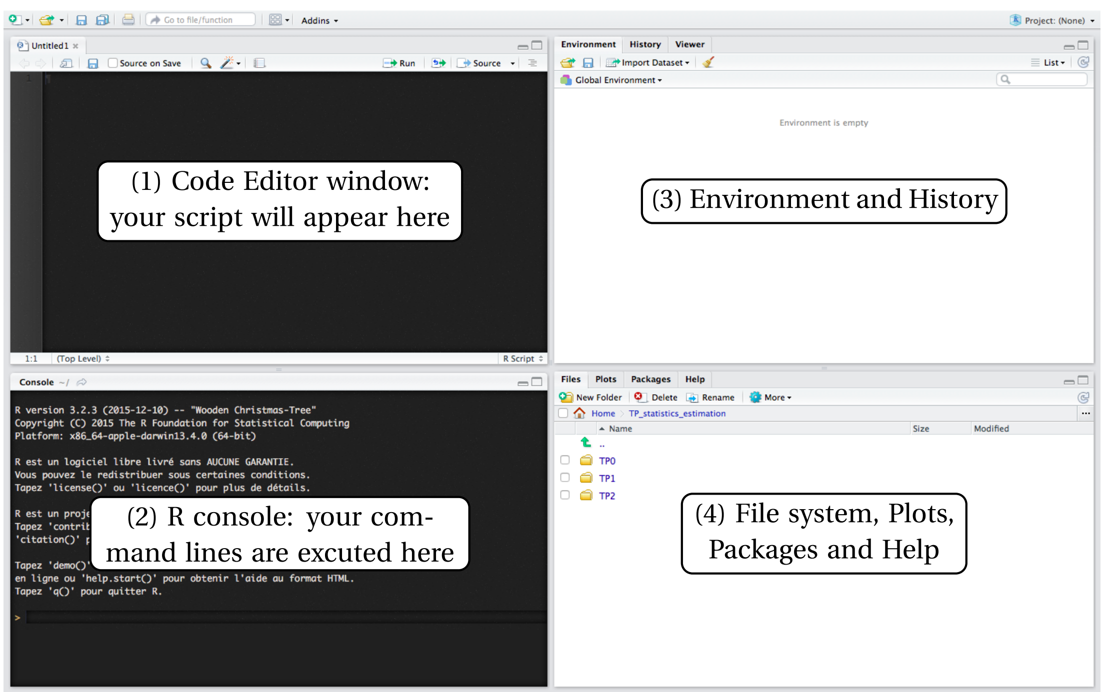


Figure 1: RStudio. Organisation of the different windows by default.

The Script or Editor window (2): by default, it is the top left window. Each pane corresponds to a file with extension `.R` (called script) made of `R` command lines (and eventually comments indicated by a line starting with symbol #). A script is particularly useful because it allows to save the command lines in a file but also allows to implement more complex codes. To run the code in the Console window, the user can:

(i) use the button "Run". The current line or the selected lines will be sent to the Console.

(ii) press "ctrl+enter". The current line or the selected lines will be sent to the Console.

(iii) use the button "Source". The whole code is sent to the Console. If you wish to print the command line and their evaluations, use the button "Source with Echo" instead.

When working on a script, you should very regularly save your file with extension .R.

The Workspace or Environment window (3): by default, the top right window contains 2 or 3 panes. The first one called "Environment" lists all the data and objects stored in the current `R` session memory. The second one called "History" shows the historic of all the command lines you typed or loaded into the Console. You can save your console history as a file with extension .Rhistory. The last one called "Viewer" allows to view local web content.

Files, Plots, Packages, Help (4): by default, the bottom right window contains 4 panes. The pane "Files" corresponds to the file system. The various graphics produced by `R` are displayed in the pane "Plots". A list of installed packages (you can pick the one you want to load or not) is available in the pane "Packages". Finally, the pane "Help" contains the help documentation.

Exercice 2. Starting with RStudio

- Open RStudio
- Type the simple operation 3 + 5 in the Console, then press enter.
- Create a script: from the toolbar go to "File > New File > R Script" (an untitled file appears in the Editor window).
- Type the operation 3 + 5 in the Editor window and execute it.
- Quit RStudio either using "File > Quit Session" from the toolbar or by typing `q()` in the Console.

2.3 Getting help

If internet provides a wide help documentation (the website https://www.rdocumentation.org is a perfect example), you can get the documentation on any function or object *JohnDoe* and its uses from the command line interface by using the command `help(JohnDoe)` or its highly helpful shortcut `?JohnDoe`. In RStudio, you can also get help from the pane Help (by default in the bottom right window, see Figure 1). It is also possible to get help in HTML format using the command `help.start()`.

Exercice 3. Getting help on Source

1. In a Terminal:
   - try `help(source)` and `?source`. To quit the documentation press q.
2. In RStudio:
   - try `help(source)` and `?source` in the Console and Editor windows.
   - search for the documentation in the "Help" pane.

2.4 Working directory

The working directory is the location in the file system where `R` writes and reads information by default. The command `getwd()` provides the current working directory. In order to select another working directory, three options are available:

(i) the command line `setwd("`*`path_to_directory`*`")` allows to specify the path to the working directory;

(ii) in the pane "Files" from the bottom right window, navigate in the file system till you are at the desired location, then click on menu "More" and select "Set As Working Directory";

(iii) in the menu "Session" from the toolbar (for some version of RStudio in the menu "Tools" from the toolbar), go to "Set Working Directory > Choose Directory..." and select the desired location.

2.5 Libraries

`R` provides numerous tools to run statistical analysis. The various functions as well as some datasets are stored in libraries which should be loaded in order to have access to their contents. A library can be loaded:

(i) either with the command line `library(`*`library_to_load`*`)`,

(ii) or by ticking the library in the pane "Packages" from RStudio,

and it can be unloaded:

(i) either with the command line `detach(package:`*`library_to_unload`*`)`,

(ii) or by unticking the library in the pane "Packages" from RStudio.

A huge range on libraries can be found on internet. Most of them are available on the CRAN and can be installed using:

(i) either with the command line `install.packages(`*`library_to_install`*`)`.

(ii) or by clicking on the Install button in the pane "Packages" from RStudio and then by selecting the desired package in the list.

Exercice 4. Working directory and libraries

- Create a new folder "statistics_estimation" and a subfolder "TP0".
- Download in "TP0" the file "script_example.R" from `https://sites.google.com/site/statistics1estimation/`.
- Fill line 8 in "script_example.R" to add the MASS library and line 32 to unload the Mass library.

1. In a Terminal:
   - start `R` and find the current working directory.
   - Set the working directory to the folder "TP0".
   - Type the command `source("script_example.R")`, then press enter. What is happening?
   - Type the command `source("script_example.R", echo = TRUE)`, then press enter. What is the option `"echo"` doing?
   - Type the command `source("script_example.R", print.eval = TRUE)`, then press enter. . What is the option `"print.eval"` doing?
   - Why does the previous command `source("script_example.R", echo = TRUE)` print functions evaluation?
2. In RStudio:
   - find the current working directory.
   - Set the working directory to the folder "TP0" either using the pane "Files" or using "Session" from the toolbar.
   - Open "script_example.R" using the pane "Files" or "File" from the toolbar and add a command line at the top of the document to set the working directory to the folder "TP0".
   - Execute the script. The histogram appears in the pane "Plots".
   - Load and unload the library MASS using the pane "Packages".

3 `R` Objects

The basic elements of `R` are organised in a data structure which includes vectors, matrices, arrays, data frames and lists. But it contains some more complex and extensible objects such as regression models and time-series to name but a few. Note that there is no structure corresponding to scalar in `R` . A scalar is represented by a single-element vector. `R` is not limited to the those programming features and also allows to define functions (see Section 7).

A R object is defined by its class which describes data's structure and by its type which describes the contents. Whithout being exhaustive, the main types are:

- null (empty object),
- logical,
- integer,
- numeric,
- complex,
- character.

A logical value is encoded using the strings `TRUE` and `False`, or altenatively using their abbreviations `T` and `F`. Decimal numbers must be encoded with a decimal point while character strings must be in between double quotes `" "`. Finally, missing values are encoded by the character string `NA`. The following table shows some possible types for a given class:

Structure	Type
Vector Matrix Array Time-serie	Homogeneous: can contain only one type among null, logical, integer, numeric, complex or character
Data frame List	heterogeneous: can contain elements of different types among null, logical, integer, numeric, complex or character

When creating an object in R , it is possible to assign it. For assignement it is possible to use either = or <-, but we advocate in favor of the back arrow in this course for the sake of clarity and readibility.

Example 1.

```
> # The following line is interpreted as the sum of two vectors
> # of size one and will return a vector of size one.
> 3 + 5

[1] 8

> # The following line assigns the value of the sum to the
> # variable a
> a <- 3 + 5
```

Given an object `x`, it is possible to test for its structure/type (variable information) or to convert its structure/type (variable conversion).

Variable information: R contains methods whose prefix is `is.`, such as:

- is.null(x),
- is.logical(x),
- is.numeric(x),
- is.complex(x),
- is.character(x),
- is.vector(x),
- is.matrix(x),
- is.data.frame(x),
- is.list(x).

Variable conversion: R provides methods whose prefix is `as`, like:

- as.logical(x),
- as.numeric(x),
- as.complex(x),
- as.character(x),
- as.vector(x),
- as.matrix(x),
- as.data.frame(x),
- as.list(x).

3.1 Vectors

Vectors are the most basic object in `R`. A vector is made of an ordered collection of elements of same nature which, as already mentionned, can be numerical, logical or alphanumerical. A vector can be manually built using the command `c(item1, item2,...)`.

Exercice 5. Type the following commands in a console.

1. Creating a vector

`a <- c(3, 5.6, 1, 4, -7)`	Assign a numerical vector of length 5 with values 3, 5.6, 1, 4, - 7 to variable `a`
`a`	Display vector `a`
`bool <- a == 4`	Assign boolean vector of the length of `a` and whose values are `TRUE` if the corresponding component of `a` is equal to 4 and `FALSE` otherwise
`text <- c("big","small")`	Assign a character vector of length 2 with values `big` and `small` to variable `text`

2. Accessing or extracting elements

`a[1]`	Return the first value of vector `a`
`a[-2]`	Return all but the second element of vector `a`
`a[1:3]`	Return first 3 elements of vector `a`
`a[-(1:3)]`	Return elements from 4 to the end of vector `a`
`a[2:4]`	Return elements from 2 to 4 of vector `a`
`a[-(2:4)]`	Return all but elements from 2 to 4 of vector `a`
`a[1,4,2]`	Return an error message

`a[c(1,4,2)]`	Return specific elements 1, 4 and 2 (in that order) of `a`
`a[a > 2]`	Return all elements greater than 2 in vector `a`
`a[a > 2 & a < 4]`	Return all elements between 2 and 4 in vector `a`
`text[text %in% c("b", "medium", "small")]`	Return elements of `text` that are in the given set `{b, medium, small}`

3. Useful functions for a vector

`is.vector(text)`	Function `is.vector()` returns the logical value `TRUE` if its argument is a vector and `FALSE` otherwise.
`length(a)`	Return the number of elements of `a`
`sum(a)`	Return the sum of all elements of `a`
`t(a)`	Return the transpose vector. The result is a row vector

4. Operations with a scalar

`2*a`	Product by a scalar

`b <- a-4`	Subtraction of a scalar: create a vector with the length of `a` and whose values are equal to those of `a` minus 4, then assign it to `b`

5. Operations between vectors

`d <- a[c(1,3,5)]`	
`e <- 3/d`	Create a vector `e` with the same length than `d` and whose elements i is equal to 3/d[i]
`d+e`	Summation of vectors `d` and `e`
`d-e`	Difference of vectors `d` and `e`
`d <- d+e`	Replace `d` by the vector resulting from adding `d` and `e`
`d*e`	Element-wise multiplication of vectors `d` and `e`
`e/d`	Element-wise division of vector `e` by vector `d`
`t(d)%*%e`	Scalar product of row vector `t(d)` and column vector `e`

6. Generating replicated vectors

`x <- 1:5`	Create a vector `x` of integers between 1 and 5
`rep(x, 2)`	Replicate vector `x` two times
`rep(x, each = 2)`	Replicate each element of `x` two times
`?rep`	Access the help page of function `rep()`

7. Generating a sequence

`seq(0, 1, length = 11)`	Return a sequence of 11 equaly spaced elements between 0 and 1
`seq(1.575, 5.125, by=0.05)`	Return a sequence between `1.575` and `5.125` with increment `0.05`
`?seq`	Access the help page of function `seq()`

8. Generating random samples

`sample(c(0,1), 10, replace = T)`	Sampling from {0,1} 10 times with replacement
`sample(c(1,2,3),3)`	Random permutation: sampling from {1,2,3} without replacement
`letters[2]`	Return the second letter (lower case) of the alphabet
`LETTERS[2]`	Return the second letter (capital) of the alphabet
`sample(letters[1:9], 5)`	Sample 5 letters among the first 9 without replacement
`?sample`	Access the help page of function `sample()`

9. Transforming a vector

`sort(a)`	Sort vector `a` into ascending (by default) or descending order

`order(a)`	Return the permutation to rearrange elements of a in ascending (by default) or descending order
`?order`	Access the help page of function `order()`
`abs(d)`	Return the absolute values of elements of `d`
`exp(d)`	Return the exponential values of elements of `d`
`log(abs(d))`	Return the log values of elements `abs(d)`

3.2 Matrices

Like vectors, matrices can be of any type, but cannot contain elements of different types. The syntax to create a $n \times p$ matrix is: `matrix(vec, nrow = n, ncol = p)` where `vec` is a vector containing the elements of the matrix which will be filled by column unless the option `byrow = T` is included. The elements of `vec` are recycled, *i.e.*, reused till the matrix is full. Note:

- if `vec` is a single-element vector, the matrix generated with the aforementionned command will be filled with the value of `vec`;
- if `vec` is a non single-element vector, it is not mandatory to specify both `nrow` and `ncol`. Only one dimension is required, for example `nrow`, the second dimension, for example `ncol`, being the number of element in `vec` divided by `ncol`;
- if both `nrow` and `ncol` are specified and the number of elements in `vec` is not a multiple or a divider of $n \times p$ a warning message will be printed since some elements will be omitted.

Exercice 6. Type the following commands in a console.

1. Creating a matrix

```
a <- 1:20
b <- sample(1:10, 20, replace = T)
```

`M <- matrix(a, nrow = 5)`	Create a numerical matrix `M` from `a` with 5 rows and `length(a)/5` = 4 columns by filling it by columns
`N <- matrix(a, nrow = 5, byrow = T)`	Create a numerical matrix `N` from `a` with 5 rows and `length(a)/5` = 4 columns by filling it by rows
`O <- matrix(b, ncol = 10)`	Create a numerical matrix `O` from `b` with 10 columns and `length`(b)/2 = 2 rows by filling it by columns
`P <- matrix(NA, 2, 5)`	Create a 2×5 matrix `P` filled with NA
`M; N; O; P`	Display consecutively matrices `M`, `N` `O` and `P`

2. Accessing or extracting elements

`M[3,2]`	Return element on the 3rd row and 2nd column of `M`

`M[5,]`	Return 5th row of `M`
`M[,2]`	Return 2nd column of `M`
`M[c(1,3,4),]`	Return 1st, 3rd and 4th rows of `M`
`M[,c(1,4)]`	Return 1st and 4th columns of `M`
`M[-2,]`	Remove 2nd row of `M`
`M[,-3]`	Remove 3rd column of `M`
`M[-c(1,3),]`	Remove 1st and 3rd rows of `M`
`M[,-c(2,4)]`	Remove 2nd and 4th columns of `M`
`O>5`	Display a matrix of booleans where element `[i,j]` is `TRUE` if `a[i,j]>5`
`O[O<5] <- 0`	Set to 0 all elements of `a` lower than 5
`diag(M)`	Return the diagonal, *i.e.*, all the elements `M[i,i]`, of `M`
`diag(M) <- 1`	Set to 1 the diagonal, *i.e.*, all the elements `M[i,i]`, of `M`

3. Useful functions for a matrix

`dim(M)`	Return the dimensions of matrix `M`
`nrow(M)`	Return the number of rows of `M`
`ncol(M)`	Return the number of columns of `M`
`Q <- t(N)`	Transpose matrix `N`
`apply(M, 2, sum)`	Return the sum of `M` column-wise (deprecated)
`colSums(M)`	Faster version of `apply(M,2,sum)`
`apply(M, 1, sum)`	Return the sum of `M` row-wise (deprecated)
`rowSums(M)`	Faster version of `apply(M,2,sum)`

4. Operations with a scalar

`3*O`	Product by a scalar: each component of `O` is multiplied by 3
`Q-4`	Subtraction of a scalar: substract 4 to each element of `Q`

5. Operations between matrices: `R` controls dimension adequacy!

`M*N`	Element-wise multiplication between `M` and `N`
`M%*%Q`	Matrix product between `M` and `Q`
`M*Q`	Print an error message due to incompatible dimension for element-wise product
`M%*%N`	Print an error message due to incompatible dimension for matrix product
`rbind(M, N)`	Vertical concatenation of matrices `M` and `N`
`cbind(M, N)`	Horizontal concatenation of matrices `M` and `N`

3.3 Arrays

The object `array` is aimed for matrices with more than two dimensions. The data creation relies on the command `array(vec, c(n,p,q...))` where `vec` is a vector giving data used to fill the array by column, and the argument `c(n,p,q...)` gives the dimensions: `n` is the number of rows, `p` the number of columns, `q` the number of matrices...

Exercice 7. Type the following commands in a console.

1. Creating an array

`x <- array(1:50, c(2,5,5))`	Create an array `x` with 5 matrices of dimension 2×5 from vector 1:50
`x`	Display x

2. Accessing or extracting elements

`x[1, 2, 3]`	Return the element on the 1st row, 2nd column in the 3nd matrix

3. Useful functions for an array

`dim(x)`	Return the dimensions of the array x
`aperm(x)`	Generalized transpose of `x`: `x[i,j,k]` becomes `x[k,j,i]`

3.4 Lists

A list is an ordered collection of objects which can be of different types. The elements of a list can thus be any objects defined in R. This property is used by some functions to return complex results as a single object.

Creating a list of named or unnamed arguments is done using the command `list(name1 = item1, name2 = item2, ...)` where the names are optional. Each element of a list can be accessed either with its index or name in double square brackets: *name_of_list* `[[`*index_of_argument*`]]` or with its name preceded by the symbol $: *name_of_list* `$`*name_of_argument*.

Exercice 8. Type the following commands in a console.

1. Creating a list

`L <- list(num = 1:5, letters[1:3], bool = T)`	Create a list `L` with 1st and 3rd arguments named and 2nd argument unnamed
`L`	

2. Accessing or extracting elements

`L$num`	Return the element named `num` in `L`
`L[["num"]]`	Return the element named `num` in `L`
`L$a`	Return `NULL`: no element named `a` in `L`
`L[[1]]`	Return the 1st element of `L`
`L[[2]]`	Return the 2nd element of `L`

3.5 Data Frames

In R, a data frame is similar to a matrix but the columns can be of various types. Data frames constitute a special class of lists devoted to storing data for analysis. Each component of the list is the equivalent of a column or variable, and the elements of these components correspond to rows or individuals. Specific methods for statistical analysis are associated with this class.

The command `data.frame(name1 = var1, name2 = var2, ...)` creates a data frame of named or unnamed variables. If the group of variables did not share the same length, shorter vectors are recycled to the length of the longest. A data frame can also be created from an external file using the command `read.table(...)`.

Data frames are a structure where data conversion is quite useful. Indeed, it is possible to transform a matrix `M` into a data frame with the command `as.data.frame(M)`. The reverse transformation is also possible with the command `as.matrix` but is somewhat more delicate. If the data frame is homogenous and contains only numerical values, the command will return a numerical matrix. Althought in the most common case of heterogeneous data, the matrix will be of character type.

Exercice 9. Type the following commands in a console.

1. Creating a data frame

`v1 <- sample(1:12, 30, replace = T)`	
`v2 <- sample(LETTERS[1:10], 30, replace = T)`	
`v3 <- runif(10)`	10 independent realisations of the uniform distribution over [0,1] (see Section 4)
`v4 <- rnorm(15)`	15 independent realisations of the normal distribution with mean 0 and variance 1 (see Section 4)
`v1;v2;v3;v4`	
`df <- data.frame(v1, v2, v3, v4)`	Create a data frame with 30 observations of 4 variables. Observations of `v3` and `v4` are replicated to the length of `v1`
`df`	

2. Accessing or extracting elements: the command to access matrices elements are also available for data frames.

`df$v2`	Return the observations of variable named `v2`
`df[["v1"]]`	Return the observations of variable named `v1`

3. Data conversion

`M <- matrix(1:15, nrow = 3)`	
`M <- as.data.frame(M)`	Convert `M` into a data frame
`is.data.frame(M)`	Test if `M` is a data frame

`N <- as.matrix(df)`	Convert `df` into a matrix (type character) and assign it to `N`

4. Dealing with data

`data()`	Open a window listing all data framesavailable in R
`data(women)`	Load data frame `women`
`names(women)`	Display variable names of data frame `women`
`height`	Return an error message
`attach(women)`	Database `women` attache to R: objects in the database can be accessed by simply giving their names
`height`	Return `women$height` (because `women` is now attached to R)

4 Usual distributions

`R` provides usual probability distributions listed below:

Distribution	**Name**	**Parameters**	**Default values**
Beta	`beta`	`shape1, shape2`	
Binomial	`binom`	`size, prob`	
Cauchy	`cauchy`	`location, scale`	`location = 0, scale = 1`
Chi-Squared	`chisq`	`df`	
Exponential	`exp`	`rate (= 1/mean)`	`rate = 1`
Fisher	`f`	`df1, df2`	
Gamma	`gamma`	`shape, rate (= 1/scale)`	`rate = 1`
Geometric	`geom`	`prob`	
Hypergeometric	`hyper`	`m, n, k`	
Log-Normal	`lnorm`	`mean, sd`	`mean = 0, sd = 1`
Logistic	`logis`	`location, scale`	`location = 0, scale = 1`
Normal	`norm`	`mean, sd`	`mean = 0, sd = 1`
Poisson	`pois`	`lambda`	
Student	`t`	`df`	
Uniform	`unif`	`min, max`	`min = 0, max = 1`
Weibull	`weibull`	`shape`	

For each distribution available, there are four commands prefixed by letters `d, p, q` and `r`, and followed by the name of the distribution. For instance, `dnorm, pnorm, qnorm` and `rnorm` are the commands corresponding to the normal distribution, and `dweibull, pweibull, qweibull` and `rweibull` the ones corresponding to the Weibull distribution.

- `dname` denotes either the probability density function for a continuous variable or the probability mass function, *i.e.*, $\mathbb{P}(X = k)$, for a discrete variable.
- `pname` denotes the cumulative distribution function, *i.e.*, $\mathbb{P}(X \leq x)$.
- `qname` denotes the quantile function, in other words the value at which the cumulative distribution function reaches a certain probability. In the continuous case, if `pname(x) = p` then `qname(p) = x`. In the discrete case, it returns the smallest integer u such that $\mathbb{P}(X \leq u) \geq p$.
- `rname` generates independent random realisations from the distribution.

Exercice 10. Comment the following commands line

```
qnorm(0.975)
pnorm(1.96)
rnorm(5)
dnorm(0)
x <- seq(-1,1,0.25)
dnorm(x)
rnorm(3, 5, 0.5)
dunif(x)
runif(3)
rt(5,10)
```

5 Some useful functions for exploratory statistics

The current section is the opportunity to list some of the most useful functions to sumarize data.

Function	Brief description
`summary`	Compute summaries of observed data contained in a vector (of type `numeric`, `factor`, ...) or in a data frame, column by column
	For a vector of observations of a quantitative variable
`mean`	Empirical mean
`sd`	Empirical standard deviation
`var`	Empirical variance: unbiased estimator (the denominator is $n-1$)
`median`	Empirical median
`quantile`	Empirical quantiles
`cor`	Empirical linear correlation coefficient between two variables
	For a vector of observations of a qualitative variable
`table(v2)`	Summary of qualitative variable

Exercice 11. Comment the following commands line

```
data(women); names(women)
attach(women)
mean(height); var(height); sd(height); median(height); quantile(height)
summary(weight)
summary(women)
```

6 Plots in R

Plots are useful to visualize your results and a major tool to check that you have obtained what was required. It is important to use the correct options when plotting an object as the default values can sometimes lead to wrong plots! Hereafter are listed some of the major graphical tools you will use.

Function	Brief description
`plot`	Generic function for plotting an abject (point clouds, curves, barplot, ...)
`hist`	Draw histogram in frequencies or probability densities
`truehist`	Alternative to draw histogram from the library MASS
`boxplot`	Draw one or many boxplot in parallel
`pie`	Draw a pie chart

`plot` and `hist` are described in more detail below and we refer to the R documentation for more details on the other graphical tools.

The graphical possibilities in R are not limited to the aforementionned. For example, the libraries `ggplot2` has encountered a growing success and offers flexible tools to produce high quality plots. However its use will not be addressed in this course. Visit the webpage http://ggplot2.org for more details on `ggplot2`.

Preliminary remarks

A useful webpage to read concerning graphics is http://www.statmethods.net/graphs/creating.html

Graphical parameters. The command `par` is useful to set some graphical parameters. For instance `par(mfrow = c(nrow, ncol))` allows to display several plots side by side on `nrow` rows and `ncol` columns. It is also possible to modify the margin of the graphical window with the command `par(mai = c(..., ..., ..., ...))`. Many other graphical options are available: see `?par`. See for example http://www.statmethods.net/advgraphs/parameters.html.

Navigating betwenn plots. When drawing many plots on different windows, it is possible in RStudio to naviagte between plots using the blue arrows from the "Plots" pane. When using a command line interface, viewing several plots at a time may sometimes be problematic since a new plot will overwrite the previous one. But solution exists as shown at http://www.statmethods.net/graphs/creating.html.

Saving a plot. In RStudio, once a plot has been drawn, it can be saved in various format using the button "Export" from the "Plots" pane. It is also possible to save a plot as .eps or .pdf file using the command line `dev.copy2eps(file = "plotname.eps")` or `dev.copy2pdf(file = "plotname.pdf")`: see for example `?dev.copy2eps` and `?dev.copy2pdf`. For some alternatives, see http://www.statmethods.net/graphs/creating.html.

6.1 Histograms

Histograms are mostly used to visualize a distribution. The syntax to draw a histogram is `hist(x, list of options)`, where `x` is the dataset. The following options are useful:

- `breaks = N` to specify the number `N` of classes (of "bars");
- `freq = F` to display a histogram in probability (total area of one), rather than in counts (which is the default). Alternatively you can use the option `probability = T`.

Exercice 12. Observe the difference between the two following histograms

```
data(women); attach(women)
hist(height, breaks = 15)
hist(height, breaks = 15, freq = F)
```

6.2 Scatter plots

Scatter plots are useful to visualize the link between two variables. The syntax to draw such a plot is `plot(x, y, list of options)`. Note that `plot(x, options)` puts the variable `x` on the y-axis and the indices on the x-axis.

By default, the command plots a point cloud which correspond to the option `type = "p"`. The properties of the points can be edited using:

- `pch = ...` change the symbol for points. For example `pch = 19` to have solid circle or `pch = 15` to have filled square;
- `cex = ...` change the size of points.

It is possible to have lines between points too:

- `type = "l"` option to have lines between points;
- `type = "b"` option to have both points and lines.

Exercice 13. Draw the following scatter plots

```
x <- seq(0, 1, 0.1); plot(x, x - x * x + 2)
plot(x, x - x * x + 2, type = "l")
plot(x, x - x * x + 2, type = "b", pch = 19)
```

6.3 Options common to histograms and scatter plots

Hereafter some helpful options to customize a plot are listed especiallyto add titles and captions.

Function	Brief description
`col = ...`	To change the color. For example `col = "blue"` (quotation marks are important). A useful guide of color is available at http://www.stat.columbia.edu/~tzheng/files/Rcolor.pdf
`lty = ...`	To change the line type. For example `lty = 1` for solid line or `lty = 2` for dashed line
`lwd = ...`	To change the line width
`main = "myTitle"`	To add a title displayed above the plot
`xlim = c(xmin, xmax)`	To choose the range of the x-axis
`ylim = c(ymin, ymax)`	Same than `xlim` but for the y-axis
`xlab = ("x caption")`	To change the caption on the x-axis
`ylab = ("y caption")`	Same than `xlab` but for the y-axis
`cex.main = ...`	To change the size of main title
`cex.axis = ...`	To change the size of axis annotation
`cex.lab = ...`	To change the size of axis labels

6.4 Additions to an existing plot

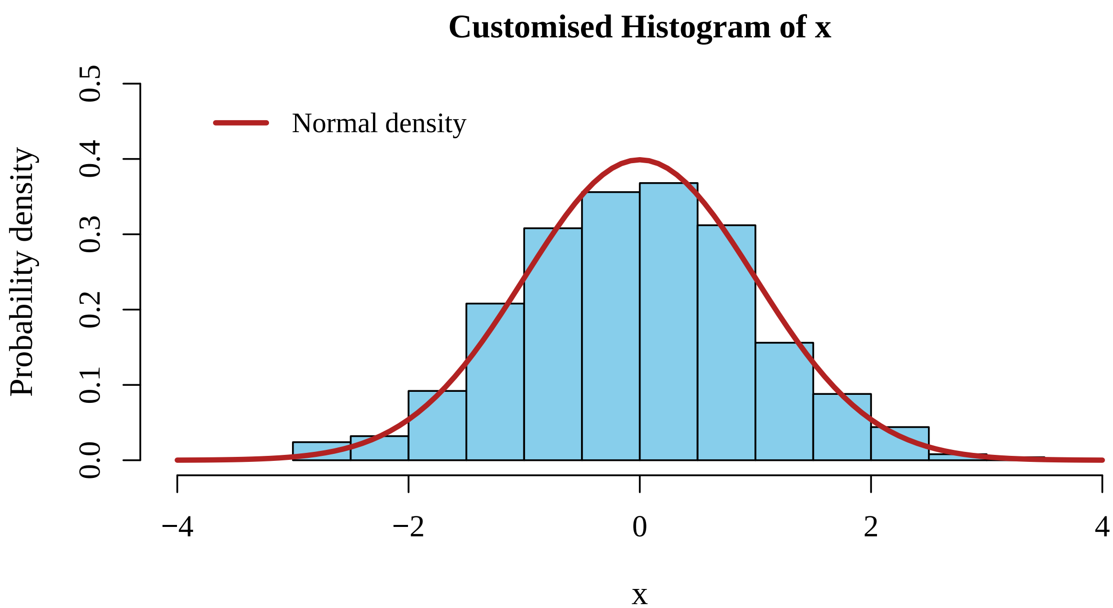
The following functions allow to add graphical element to an existing plot. The various graphical options are available for those functions as well.

Function	Brief description
`points(x, y)`	Add a point cloud using the same principle as `plot(x, y, type = "p")`
`lines(x, y)`	Add lines between the coordinates of `x` and `y` using the same principle as `plot(x, y, type = "l")`
`abline(v = a)`	Add a vertical line of equation $x = a$
`abline(h = b)`	Add a horizontal line of equation $y = b$
`curve(fonction, add = T)`	Add a curve to an existing plot. Note that without `add = T`, a new plot is created

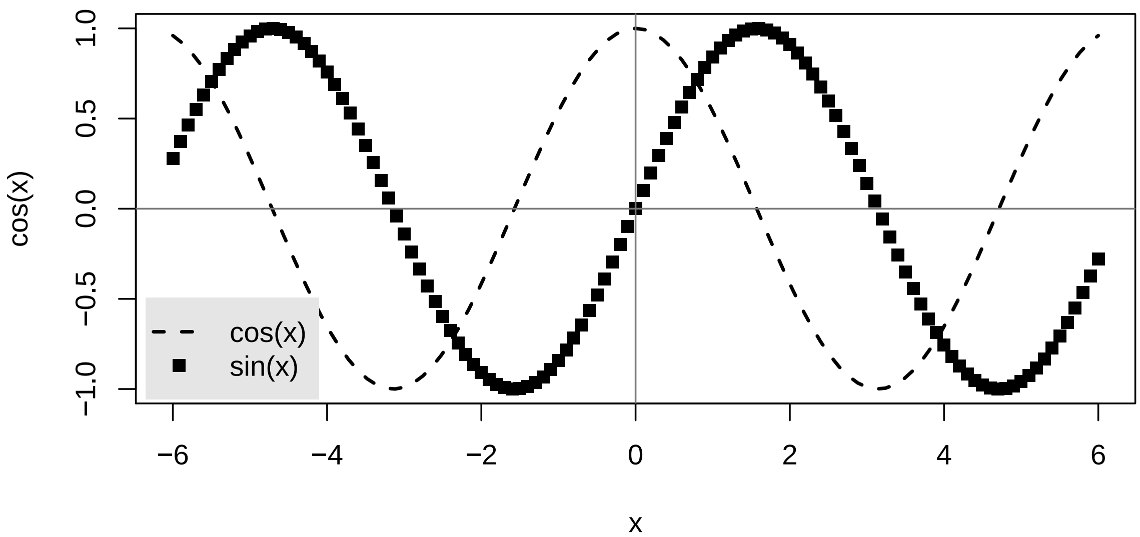
When adding elements to an existing plot, it is recommanded to add a legend for the readibility of the graph. This can be achieve using the function `legend`.

6.5 Example

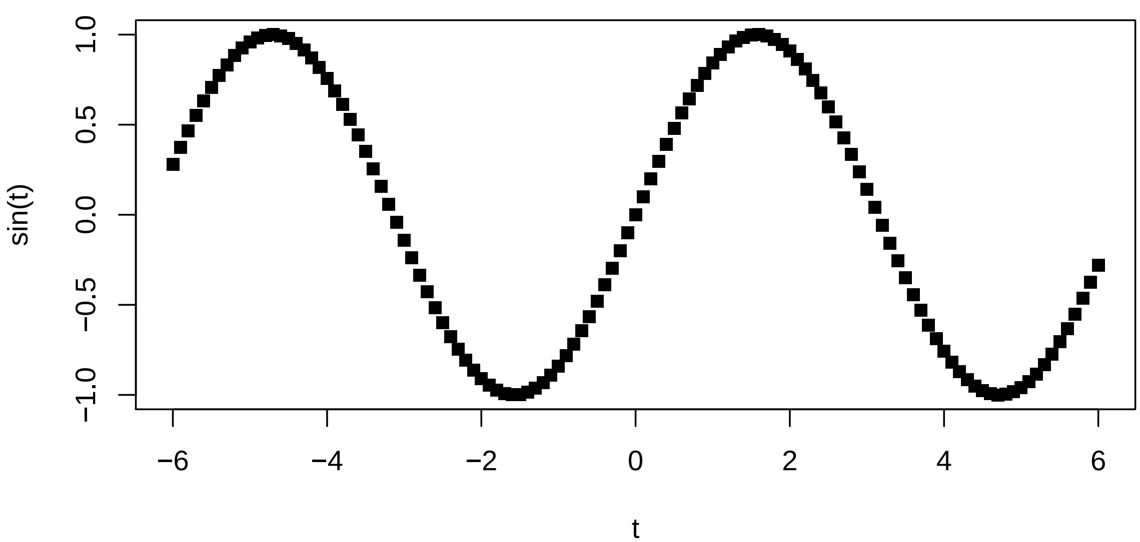
```
# Some custom graphical parameters
par(mai = c(0.9,0.9,0.5,0.2), family="serif")
# A sample from the standard normal distribution
x <- rnorm(500)
hist(x, breaks = 20, freq = F, col = "skyblue",
     cex.lab = 1.2, cex.axis = 1.1, xlim = c(-4, 4), ylim = c(0, 0.5),
     main = "Customised Histogram of x", ylab = "Probability density")
curve(dnorm(x), add = TRUE, col = "firebrick", lwd = 3)
legend("topleft", c("Normal density"), box.lty = 0,
       col = c("firebrick"), lty = c(1), lwd = c(3), inset = 0.05)
```




```
# Some custom graphical parameters
par(mai = c(0.9,0.9,0.2,0.2))
# The cosinus curve between -6 and 6
curve(cos(x), xlim = c(-6, 6), lty = 2, lwd = 2)
# Adding the sinus curve between -6 and 6
t <- seq(-6, 6, by = 0.1)
points(t, sin(t), pch = 15)
abline(h = 0, col = "gray47")
abline(v = 0, col = "gray47")
legend("bottomleft", c("cos(x)", "sin(x)"), box.lty = 0, bg = "gray90",
       lty = c(2,1), pch = c(NA,15), lwd = c(2, NA), inset = 0.01)
```




```
plot(t, sin(t), pch = 15)
```




```
dev.off() # reset par to default values and delete plots

null device
          1
```

7 Building a new function

R supports procedural programming and users can define their own functions. To that end it is better to use the Editor window from RStudio, or a text editor if you use R with a command interface.

Generally speaking, a new function is defined using the following expression:

```
function_name <- function(arg1, arg2, ...) {
  block of instructions
  return(...)
}
```

The function takes a list of arguments as input. Some of the arguments, for example `arg2`, can take default values. In that case, the user indicates it in the function definition by adding the default value in the arguments list, *i.e.*, `arg2 = default2`.

The function definition (source code) is given between braces: R will excute line by line those instructions. It is highly recommended to add comments inside the code of the functions by using the hash symbol #. Upon execution, R returns the value given in the statement `return()`. If this statement was omitted, it returns the output of the last evaluation made in the source code.

All values assigned are local in scope, that is variables created in the core of function definition do not exist outside of the braces. Upon execution, a copy of the arguments is sent to the function so that they can be modified but the original values are unchanged.

Example 2.

```
> y <- 1
> square <- function(x) {
      y <- x * x  # Create a local variable y containing x squared
      return(y)  # Return the value stored in y
  }
> square(3)

[1] 9

> y  # y has not been modified

[1] 1
```

To conlude, the command `fix(square)` will open a window to edit the function `square`. Have a try.

8 Few notions of programming: conditional constructs and loops

Conditional constructs `if-then-else` and looping commands `while` and `for` are common in most programming langage. The commands `if-then-else` and `while` rely on conditions that is a boolean expression (logical variable or a binary expression). The relational operators are:

- < (lower),
- > (greater),
- <= (lower or equal),
- >= (greater or equal),
- == (equal),
- != (different),

and the main logical operators

- `!` (logical negation),
- `&` (and),
- `|` (or).

To test a given boolean expression `bool`:

- `if(bool == T)` is equivalent to `if(bool)`,
- `if(bool == F)` is equivalent to `if(!bool)`,
- `while(bool == T)` is equivalent to `while(bool)`,
- `while(bool == F)` is equivalent to `while(!bool)`.

The conditional constructs `if-then-else` allows to run conditional instructions.

Example 3. Conditional constructs

```
> i <- sample(1:10, 1)
> i

[1] 7

> if (i < 5) { # If i is lower than 5 do
    i <- 4 * i
  } else if (i < 8){ # If i is greater than 5 and lower than 8 do
    i <- 2 * i - 7
  } else { # Otherwise do
    i <- -3 * i + 5
  }
> i

[1] 7
```

Another major aspect of programming language is the use of loops. The command `while` allows to repeat instructions till a stopping condition is met. The command `for` allows to repeat instructions a fixed number of time according to a sequence of indices.

Example 4. `while` and `for` loops

```
> bool <- T
> i <- 0
> while (bool) {
      # While the value of bool is true, do the following
      # instructions
      i <- i + 1  # Increment i
      if (i > 10) {
          # Stopping condition
          bool <- F
      }
  }
```

```
> i

[1] 11

> s <- 0
> x <- rnorm(10000)
> for (i in 1:length(x)) {
      # For i from 1 to length(x) = 10000 do
      s <- s + x[i]
  }
> s

[1] 38.93002

> # We can get the same result using scalar product on vectors
> u <- rep(1, length(x))
> t(u) %*% x

         [,1]
[1,] 38.93002
```

R can encounter memory issues if you call a very high number of loop iterations, even if they contain very simple instructions. Indeed, as shown in Example 5, loops are costly in processing time. As far as possible, loops should be avoided and replaced by matrix operations which are much faster (the matrix operators in R use loops written in C).

Example 5. Consumming loops

```
> s <- 0; x <- rnorm(20000); u <- rep(1, length(x))
> # Time elapsed when using a loop
> system.time(for (i in 1:length(x)) {s <- s + x[i]})[3]

elapsed
  0.011

> # Time elapsed when using matrix operation
> system.time(t(u) %*% x)[3]

elapsed
  0.001
```

9 Handling created objects

A list all objects created during a session is available using the command `ls()` or in the Environment window of RStudio. An object can be removed using the command `rm(object_to_remove)`. In RStudio, all the objects can be deleted using the brush button from the Environment window.

Exercice 14. Listing and deleting objects

`rm(list = ls())`	Delete all existing variables
`ls()`	Empty workspace
`a <- 1:10`	
`b <- list(10, "foo", a)`	
`f <- function(x){return(x/3)}`	
`ls()`	List of variables created
`rm("f")`	Remove the function `f`
`ls()`	The function `f` does not exist anymore
`f(3)`	Print an error message

Note that upon exit, `R` offers to save your objects as a .RData file.