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DU Bioinformatique intégrative

Module 3: « R et statistiques »

Prérequis

A introduction to R

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No conflict of interest to disclose

Un script reprenant l'ensemble du code présenté dans ce diaporama est fourni

Plan des prérequis

- Premiers pas avec R: diapos 1 à 24, 4 vidéos et leur quiz, SWIRL

vidéo1.1
1. ouvrir et quitter R
2. exécution de commandes
3. utilisation d'une fonction built-in de R

vidéo1.2
1. Assigner des objets R
2. Gérer les objets R dans la session R

vidéo1.3
1. Gérer une session R et son répertoire de travail
2. Sauvegarder une session R, les objets et l'historique

vidéo1.4
1. Les lignes de commandes: utiliser un éditeur de texte et lancer un script
2. L'environemment Rstudio

==> tutoriel swirl (diapo 23-24): 5 exercices interactifs

- Les types de variables et d'objets dans R: diapos 25 à 28
- Les vecteurs: diapos 29 à 36 + exercices 1 à 12
- Les matrices: diapos 37 à 47

Premiers pas avec R

R

R – https://www.r-project.org

- Open-source
- statistical programming language available for Windows, Mac, Unix
- Widely used in academia, finance, pharma, social sciences…
- Core language, 'base' and > 3000 contributed packages
- Objectives:
  1. Data manipulation: import, transform, export
  2. Perform statistics
  3. Generate advanced graphics
- Interactive sessions, scripts, packages in the CRAN ("Comprehensive R Archive Network")
- Possible interactions with other languages
- Project started in 1993; 12-12-2019: version R.3.6.2; version 4.0.3 (Bunny-Wunnies Freak Out) on 2020-10-10

- Some useful links or documentation:
  - ✓ R for beginners d'E. Paradis (exists in English and in French)
  - ✓ QuickR: http://www.statmethods.net/index.html
  - ✓ And mostly the help menu: help.start()

Vidéo 1.1. Premiers pas avec R

1. ouvrir et quitter R
2. exécution de commandes
3. utilisation d'une fonction built-in de R

🎬 lien vers la vidéo: https://youtu.be/KebToqxaEts

💻 quizz d'autoévaluation: https://forms.gle/ppYtkBMzJzkXQbYn9

First contact with R

To start

Click on R **in Windows/Mac or tape R in Unix**

prompt '>' at the beginning of your command line

To quit: > q()

-> you may save your current R session by typing q("yes")
or not save your current R session by typing q("no")

Interaction with R:

You write a command and press « Enter »

R executes the command

R waits for another command

trick: use the ↑ and ↓ arrows to move to previous or next commands

Some very simple examples

Enter the commands (here in red)

R answers (here in blue)

Some simple operations:

```
> 2 + 2
[1] 4          # it returns the result
               # an index is shown within '[ ]': if multiple results displayed on different lines, an
               # index at the beginning of each line is given for the first value of the line


> exp(-2)
[1] 0.1353353

> log(100, base = 10)
[1] 2
```

exp() or log() are built-in functions

What is a function?

Functions are a set of pre-programmed commands

A function is characterized by its:

- name
- arguments put within brackets to execute the command

➢ you enter the required parameters within the brackets

➢ to know the parameters of the function and their default settings:

‘?’ followed by the function name

```
>?exp        # a help-window opens
             # equivalent to either one of the following two command lines
> help(exp)
> help.search("exp")
```

The help associated to a function

Several sections:

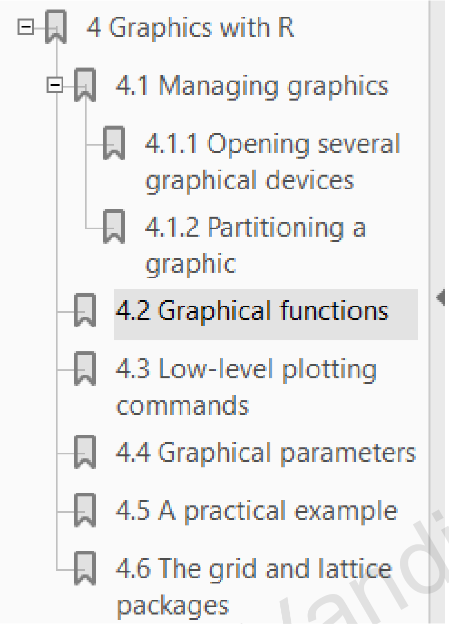
- *Description* -> what is the purpose of the function?
- *Usage* -> how is the function used?
- *Arguments* -> which parameters are used by the function? Defaults values mays be specified
- *Details* -> technical description of the function
- *Value* -> what are the output parameters returned by the function?
- See also -> are there some similar functions in R?
- *Source/ References* -> not always present…
- *Example* -> concrete examples to use the function

=> the best way to learn how to use the function

Getting help

R for beginners E. Paradis

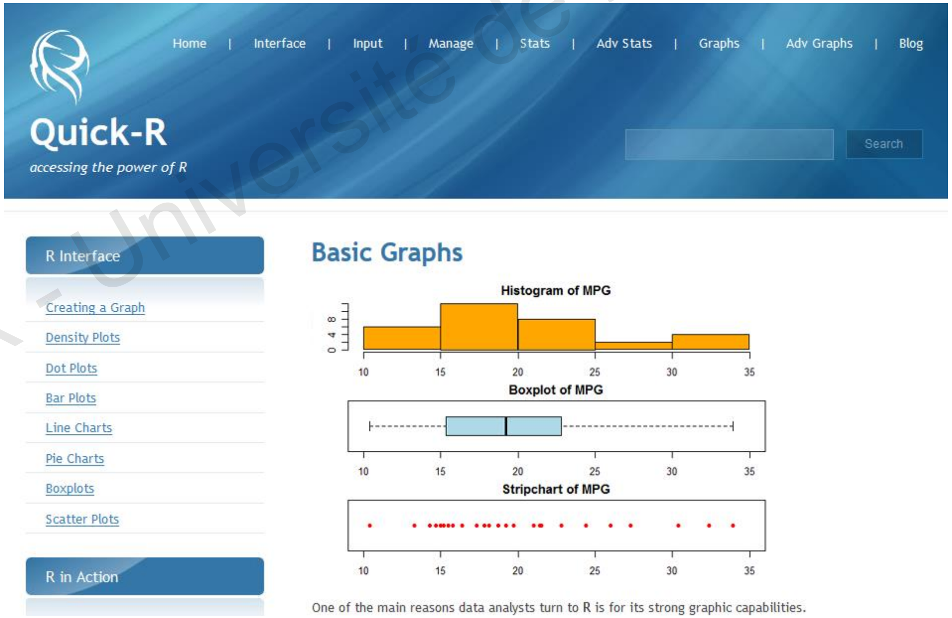
Chapter 4 for graphs quite exhaustive
in moodle in French and English



4 Graphics with R
- 4.1 Managing graphics
  - 4.1.1 Opening several graphical devices
  - 4.1.2 Partitioning a graphic
- 4.2 Graphical functions
- 4.3 Low-level plotting commands
- 4.4 Graphical parameters
- 4.5 A practical example
- 4.6 The grid and lattice packages

QUICK R:

http://www.statmethods.net/
basic and avdanced graphs
with main parameters



Basic Graphs

One of the main reasons data analysts turn to R is for its strong graphic capabilities.

R gallery

http://www.r-graph-gallery.com/all-graphs/
for specific kinds of graphs

And some blogs for specific questions

https://www.stat.ubc.ca/~jenny/STAT545A/block14_colors.html#using-colors-in-r
https://danieljhocking.wordpress.com/2013/03/12/high-resolution-figures-in-r/

Vidéo 1. 2. Premiers pas avec R

1. Assigner des objets R
2. Gérer les objets R dans la session R

🎬 lien vers la vidéo: https://youtu.be/V4Fp0Nmfm3Q

💻 quizz d'autoévaluation: https://forms.gle/vyJ4H7c9bpDAFegr8

Assigning data into R objects, using and reading them

Use ‘<-’ or ‘=‘ to assign values to R objects

```
> x <- 2          # equivalent to x = 2, assigns 2 to the variable x
> y <- x + 3
> s <- " this is a string of characters"
```

Using/reading values

```
> x               # you call the object
[1] 2             # its value is returned….note that an index is written betwen [ ]

> y
[1] 5
> s
[1] "this is a string of characters"

> x + x           # computes the operation knowing the value of x
[1] 4

> x^y             # x to the power y
[1] 32

> x <- 4          # change the value of x
> y
[1] 5             # y not dynamically changed!!!!

> y <- x + 3      # need to reattribute y value to update for the new value x
> y
[1] 7
```

Managing objects in your R session

List all objects present in the memory with the function ls()

```
> ls()
[1] "s" "x"  "y"
```

Delete an object with the function rm()

```
> rm(y) # pour déléter y seulement
> ls()
[1] "s" "x"
 > rm(list=ls()) # pour tout déléter
> ls()
```

Vidéo 1. 3. Premiers pas avec R

1. Gérer une session R et son répertoire de travail
2. Sauvegarder une session R, les objets et l’historique

🎬 lien vers la vidéo: https://youtu.be/7S00g10me5A

💻 quizz d’autoévaluation: https://forms.gle/TL67MHavM3YDzEis8

Managing your session and working directory

Which R version are you using?

```
> sessionInfo() # returns R version as well as the
                  version of loaded packages
```

Getting your working directory

```
> getwd()
```

Setting a working directory

```
> setwd() # indicate the path inside the () and
            flanked by simple ‘ or double quotes”
```

trick: if ignoring the path, slide a text file from the directory where you want to work, there will be an error message but you will see the path of your directory

Creating a folder in your working directory

Listing all files and folders in your working directory

```
> list.files ()      # returns all files and folders within the working directory
                        add pattern= ".txt" uf you want to list only the .txt files
                        like ls in Unix
```

Creating a new folder

```
> dir.create (“myfolder”)      # creates a folder named “myfolder” in my working directory
                                # like mkdir in Unix
> list.files (“myfolder”)
[1] "myfolder"
> ls ()                         # but it is not in my R session !!!!!
 character(0)
```

Connecting to a new file in your working directory (wd)

Opening a connection to a new file to write in

```
> zz <- file(“mynewfile.txt”, open=“wt”) # opens a new file to write in my working directory
> list.files ()
[1] "myfolder“ “mynewfile.txt”
> close(zz)
```

↳ diverting R console outputs with sink()

```
> sink(“myRoutputs.Rout”) # diverts the console outputs to myRoutputs.Rout within the wd
> 1+1
> is.numeric(x)
> sink()     #to close ->  open myRoutputs.Rout in a text editor to see how it looks like
```

or using file() before:

```
> zz <- file(“myRoutputs2.Rout”, open=“wt”)
> sink(zz)               # diverts the console outputs to myRoutputs2.Rout within the wd
> is.numeric(x)
> 1:10
> sink()
> close(zz) #to close ->  open myRoutputs2.Rout in a text editor to see how it looks like
```

Saving your session, data and history

Saving one object from your session

```
> save(x, file=“x.RData”)
```

Saving all objects

```
> save.image(file=“AllMyData.RData”)
```

Saving your history

```
> savehistory(file=“MyHistory.Rhistory”) # save all your commands in a text file
```

After closing R and restarting it, load your data in a new session

```
> load(“x.RData”)              # load only x

> load(“AllMyData.RData”)      # load all objects saved from the session
```

Vidéo 1. 4. Premiers pas avec R

1. Les lignes de commandes: utiliser un éditeur de texte et lancer un script
2. L’environnement Rstudio

🎬 lien vers la vidéo: https://youtu.be/V-zO-hoi_WM

💻 quizz d’autoévaluation: https://forms.gle/WVfik1kJWMyFHap17

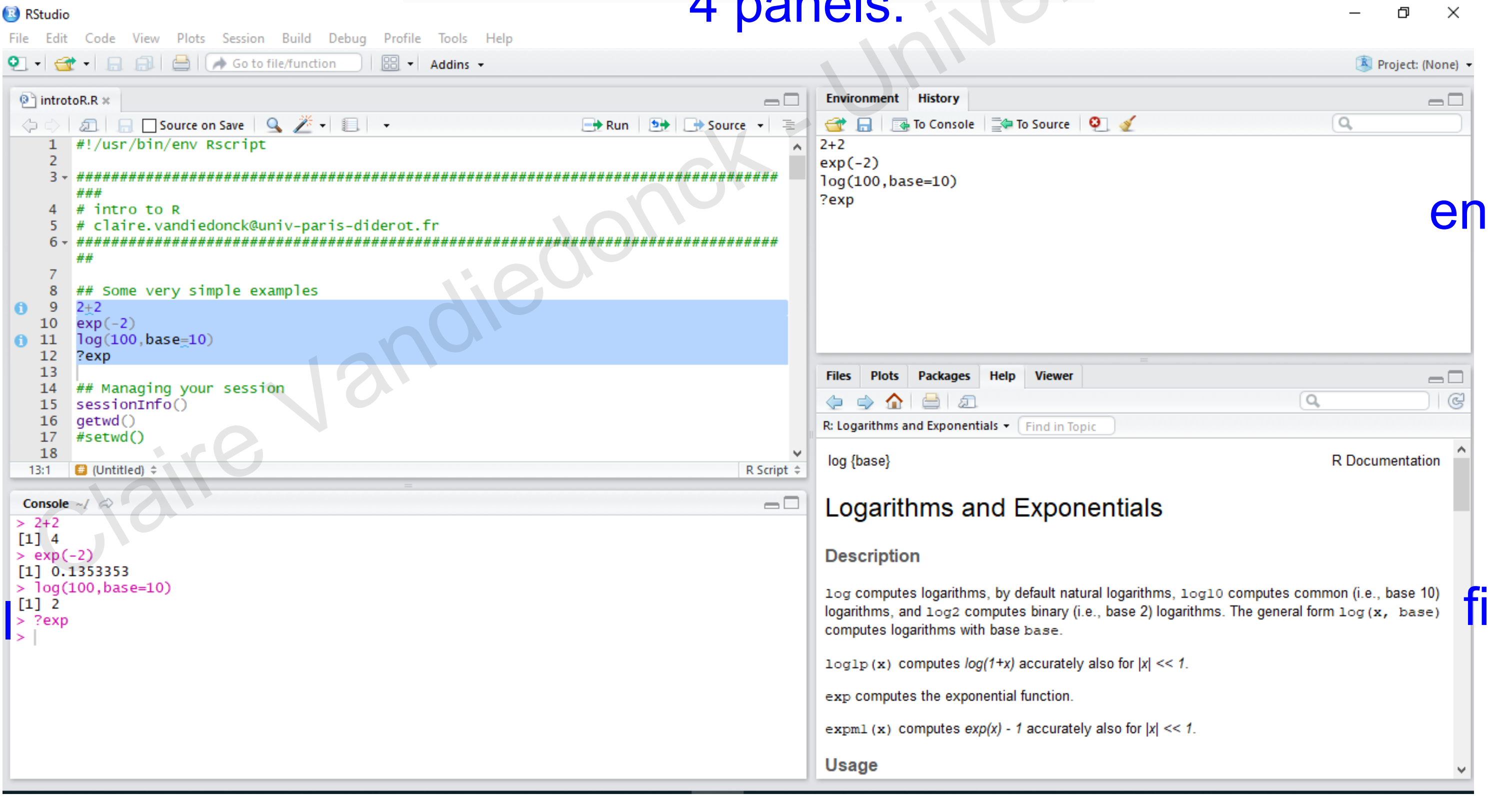
Saving your command lines in a text editor

- On windows:
  R studio
  Notepad++ with NppToR
  EMACS
  vi
  Tinn-R

- On Mac:
  R studio
  EMACS
  Komodo edit

- On linux:
  Rstudio
  Gedit
  Geany
  vi
  Emacs

4 panels:



```
#!/usr/bin/env Rscript
###################################################################################
###
# intro to R
# claire.vandiedonck@univ-paris-diderot.fr
###################################################################################
##

## Some very simple examples
2+2
exp(-2)
log(100,base=10)
?exp

## Managing your session
sessionInfo()
getwd()
#setwd()
```

```
2+2
exp(-2)
log(100,base=10)
?exp
```

```
> 2+2
[1] 4
> exp(-2)
[1] 0.1353353
> log(100,base=10)
[1] 2
> ?exp
> 
```

log {base}   R Documentation

Logarithms and Exponentials

Description

`log` computes logarithms, by default natural logarithms, `log10` computes common (i.e., base 10) logarithms, and `log2` computes binary (i.e., base 2) logarithms. The general form `log(x, base)` computes logarithms with base `base`.

`log1p(x)` computes *log(1+x)* accurately also for |x| << 1.

`exp` computes the exponential function.

`expm1(x)` computes *exp(x) - 1* accurately also for |x| << 1.

Usage

script

environment

terminal

figures,

file browser,

help…

R style and language rules

MUST READ:

https://google.github.io/styleguide/Rguide.xml

- Avoid any accent, space, special characters

- Comments

# Any line starting with "#" will not be read by R
# you may report some results as comments
# you are highly advised to comment your command lines for your and other's usage

- To name your variables, do not use reservded letters or reserved words already used by R (names of functions or of data class):
  eg. c, t, table, data, pi, TRUE, FALSE, T, F, letters, mean, var, …
  => A good text editor higlight them

Running a set of command lines

Save your commands in a text file: « myscript.R » in your working directory

In R, run automatically all the command lines:

```
> source ("myscript.R")
```

Interactive tutorials

Let's use the « swirl » library {swirl} https://swirlstats.com/students.html

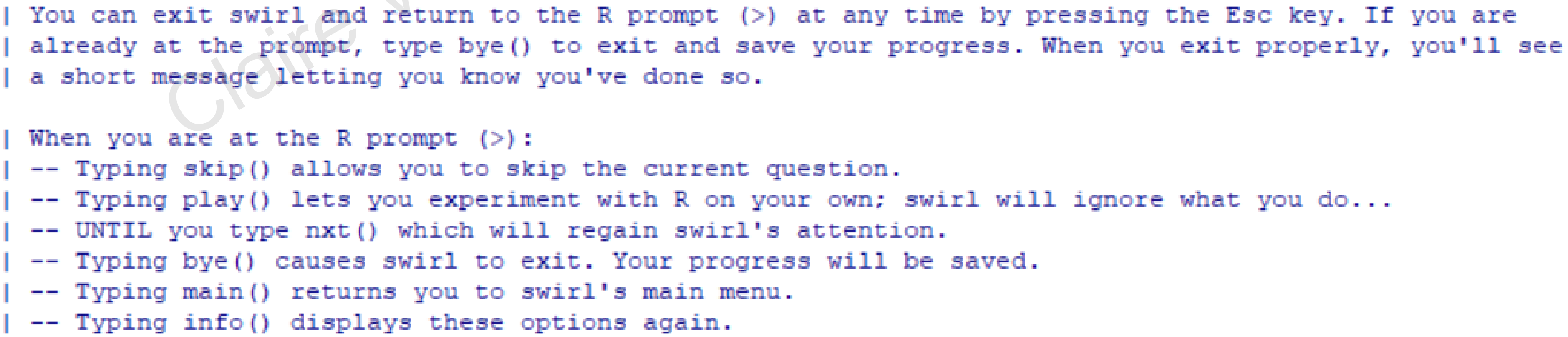
```
> install.packages(”swirl”) # this command has to be done only once

> library(swirl) # this command has to be performed at each R session in which you
                 # want to use swirl

> swirl()        # to start swirl
```

Then follow the instructions and practice with tutorials n°1 and 3 to 6 of the “R Programming” course (choice n°1 = “R programming: the basics of R programming” and “1: R programming”).

To quit swirl: choose 0 several times or enter bye(). At any time during a lesson, the instructions are:



```
| You can exit swirl and return to the R prompt (>) at any time by pressing the Esc key. If you are
| already at the prompt, type bye() to exit and save your progress. When you exit properly, you'll see
| a short message letting you know you've done so.

| When you are at the R prompt (>):
| -- Typing skip() allows you to skip the current question.
| -- Typing play() lets you experiment with R on your own; swirl will ignore what you do...
| -- UNTIL you type nxt() which will regain swirl's attention.
| -- Typing bye() causes swirl to exit. Your progress will be saved.
| -- Typing main() returns you to swirl's main menu.
| -- Typing info() displays these options again.
```

If it fails finding the "1: R programming" course

1. you may try to install the course with the following command:

```
> swirl::install_course("R_Programming")
```

2. The swirl website may also be temporary down and the "1: R programming" not accessible. If it happens, you can install the " R_Programming.swc " course manually from an archive repository: https://web.archive.org/web/20200219034901/http://swirlstats.com/scn/R_Programming.swc size (127 Ko)
Then, in R or Rstudio, install the course with this command:

```
> swirl::install_course()
```

and with Rstudio, select the "R_Programming.swc" file. If in R without Rstudio, enter the file name with its path.

You are now ready to start swirl and the R programming course (cf. previous slide)

Les types de variables et d'objets

Classes of R Objects

Main variable types

numeric / integer
character
logical (FALSE / TRUE / NA)
complex
time, time series
factors

- mode() or typeof() returns the type of the object
- class() returns the class of the object
- is.logical() tells us if the object is a logical type. There is also is.character(), is.numeric(), is.integer(), is.null(), is.na()
- as.character(), as.numeric()…to coerce objects from one type to another

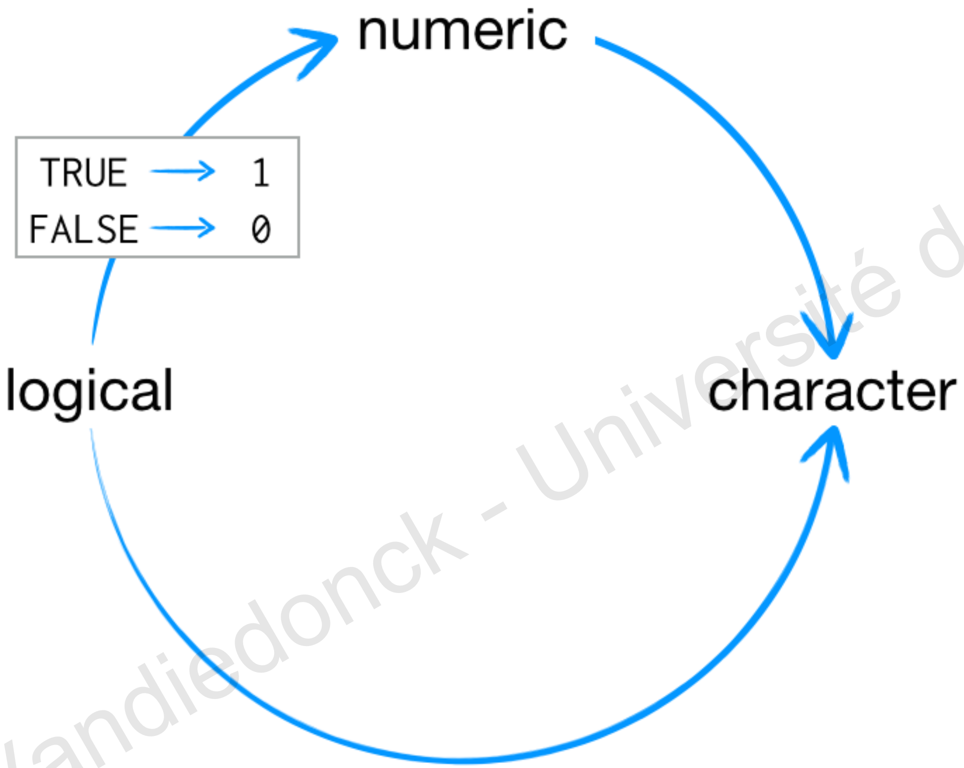
```
> x <- c(3,7,1,2)
> x<2
[1] FALSE FALSE  TRUE FALSE
> x==2
[1] FALSE FALSE FALSE  TRUE

> mode(x) # idem as class(x)
[1] "numeric“
> mode(s) # idem as class(s)
[1] "character“

> as.numeric( x < 2 )
[1] 0 0 1 0
```

Special values :	*NA*	*Not Available = missing data*
	NaN	*Not a Number = computation is not possible*
	-Inf/Inf	*positive and negative infinites*
	NULL	*the value does not exist (rather than being unknown)*

Coercion rules



- if character strings are present, everything will be coerced to a character string.
- otherwise logical values are coerced to numbers: TRUE is converted to 1, FLASE to 0
- values are converted to the simplest type required to represent all information
- object attributes are dropped
- the ordering is roughly:

  logical < integer < numeric < complex < character < list

Classes of R Objects

Main data structures

object	Heterogeneous = several types may coexist
vector	no
matrix	no
dataframe	yes
list	yes

Les vecteurs

Vector

The most elementary R object

Some functions to create vectors: c(), seq(), x:y, rep(), append()…

```
> a <- c()        # creates an empty vector that can be further filled
> a
NULL

> weight <- c(60, 72, 57, 90, 95, 72) #c() stands for concatenate
> weight
[1] 60 72 57 90 95 72

> 4:10
[1]  4  5  6  7  8  9 10

> seq(4,10)       # returns all numeric values from 4 to 10 (with an increment of 1 =default)
[1]  4  5  6  7  8  9 10

> seq(2,10,2)     # returns all numeric values from 1 to 10 with an increment of 2
[1]  2  4  6  8 10

> rep(4, 2)       # repeats 4 twice
[1] 4 4
```

Vector

You may combine functions which are read from inside to the outside:

```
> rep(seq(4,10),2)
[1]  4  5  6  7  8  9 10  4  5  6  7  8  9 10
> c(rep(1,4), rep(2,4))
[1] 1 1 1 1 2 2 2 2
```

A vector is homogeneous

```
> c(5,s)
[1] "5"    " this is a string of characters“         #5 is not read as an integer
> mode(c(5,s))                                 # it is converted/coerced into a character with “ “
[1] "character“
> class(c55,s))
[1] "character“
```

To get its size and data type, use fonctions length() and str() (for structure)

```
> length(1:10)                                      # the vector is of size 10
[1] 10
> length(weight)                                    # the vector is of size 6
[1] 6
> str(weight)                                       # the vector is of size 6 with numeric values
 num [1:6] 60 72 57 90 95 72
```

Vector

You may apply arithmetic operators on numeric values in vectors:

+	to add
-	to substract
*	to multiply
/	to divide
^	to raise to the power (or **)
%%	to estimate the remainder of a division (modulo)

```
>size <- c(1.75, 1.8, 1.65, 1.9, 1.74, 1.91)
>size^2
[1] 3.0625 3.2400 2.7225 3.6100 3.0276 3.6481

>bmi <- weight/size^2 # creates a vector with the computed body mass index
>bmi
[1] 19.59184 22.22222 20.93664 24.93075 31.37799 19.73630
```

Vector

You may apply pre-computed functions, in particular some descriptive stat functions

```
> size
[1] 1.75 1.80 1.65 1.90 1.74 1.91
> sort(size)                          # sorts the data
[1] 1.65 1.74 1.75 1.80 1.90 1.91
> mean(size)
[1] 1.791667
> sd(size)                            # returns the standard deviation
[1] 0.1002829
> median(size)
[1] 1.775
> min(size)
[1] 1.65
> max(size)
[1] 1.91
> range(size)
[1] 1.65 1.91
> summary(size)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.650   1.742   1.775   1.792   1.875   1.910
```

Vector

Retrieving a value within a vector using its index (**R is 1-based**)

```
> size
[1] 1.75 1.80 1.65 1.90 1.74 1.91

> size[1]             # returns the 1st value within vector “size”
[1] 1.75
> size[2]             # returns the 2nd value within vector “size”
[1] 1.8
> size[6]             # returns the 6th value within vector “size”
[1] 1.91

> size[c(2,6)]        # returns the 2nd and the 6th value within vector “size”
[1] 1.80 1.91

> size[c(6,2)]        # returns the 6th and the 2nd value within vector “size”
[1] 1.91 1.80

> min(size[c(6,2)]) # returns the min between the 6th and the 2nd value
[1] 1.80
```

Vector

Attributing names to values of a vector after or at the creation of the vector

```
> names(size)
[1] NULL            # there are currently no names

> names(size) <- c(“Fabien”, “Pierre”, “Sandrine”, “Claire”, “Bruno”, “Delphine”)
                    # names the values of the vector “size”
> size
Fabien   Pierre Sandrine   Claire    Bruno Delphine
    1.75     1.80     1.65     1.90     1.74     1.91
> str(size)
Named num [1:6] 1.75 1.8 1.65 1.9 1.74 1.91
 - attr(*, "names")= chr [1:6] "Fabien" "Pierre" "Sandrine" "Claire" ...

> my_vector <- c("one"=1, "two"=2, "three"=3) # or giving the names at the vector creation
> my_vector
  one   two three
    1     2     3
> str(my_vector)
 Named num [1:3] 1 2 3
 - attr(*, "names")= chr [1:3] "one" "two" "three"
```

Summary on vectors

Format	one-dimension
Datatype	homogeneous: only one type of character, numeric, logical, factor.. -> ceorcion if heterogeneous - check with class() or mode() - checking type with is.num() , is.charachter() , … - conversion with as.num() , as.charachter() , …
Creation	c() , : , seq() , rep() , sample() , rnorm() , …
Adding new items	c()
Size	length()
Slicing	my_vector[i]
Filling	my_vector[i] <- "toto"
Naming	names()

Les matrices

Matrix

Matrix: 2-dimension object (rows x columns)
contains only one kind of variables (eg. numeric) = homogeneous

↳ fonctions to create a matrix

matrix()
rbind() to append rows
cbind() to bind columns

```
> myData <- matrix(c(1,2,3, 11,12,13), nrow = 2, ncol = 3, byrow = TRUE)
> myData
     [,1] [,2] [,3]      # returns a matrix of 2 rows and 3 columns
[1,]    1    2    3      # it is filled by rows with the data provided in vector c(1,2,3, 11,12,13)
[2,]   11   12   13
> myData <- matrix(c(1,2,3, 11,12,13), nrow = 2, ncol = 3, byrow = FALSE)
> myData
     [,1] [,2] [,3]      # same but filling the matrix by columns = the default
[1,]    1    3   12
[2,]    2   11   13
> length(myData)         # total number of elements (like a vector, elements read by columns)
[1] 6
> myData[4]              # returns the 4th element read by columns
[1] 11
```

Matrix indexes

Indexes and dimensions:

```
> myData
 [,1] [,2] [,3]
[1,]    1    3   12
[2,]    2   11   13
Dim(myData)
[1] 2 3
```

☞Note the indexes separated by a comma:

[i,] indicates the ith row

[,j] indicates the jth column

Subsetting matrices into vectors:

```
> myData[1,2]        # returns the value of the 1st row and 2nd column
[1] 3
> myData[2,1]        # returns the value of the 2nd row and 1st column
[1] 2
> myData[,1]          # returns the values of the vector corresponding to the 1st column
[1] 1 2
> myData[2,]          # returns the values of the vector corresponding to the 2nd row
[1]  2 11 13
> myData[,2:3]       # subsets the initial matrix returning a sub-matrix
      [,1] [,2]      # with all rows of the 2nd and 3rd columns from the initial matrix
[1,]    3   12       # the generated matrix has 2 rows and 2 columns
[2,]   11   13
> dim(myData[,2:3]) # the generated matrix has 2 rows and 2 columns
[1] 2 2
```

Matrix structure and dimension

Getting dimension and structure of a matrix:

```
> dim(myData)
[1] 2 3
> mode(myData) # returns the type of data
[1] “numeric“
> class(myData) # returns the kind of object
[1] "matrix“
> class(myData[,1]) # reminder for vectors, class returns the type of data and not vector itself
[1] "numeric"
> str(myData)
 num [1:2, 1:3] 1 2 3 11 12 13 # data type and dimensions
```

Or look at the length of the rows and of the columns

```
> nrow(myData)
[1] 2
> ncol(myData)
[1] 3
> length(myData[1,])                    # length of the first row = hence number of columns
[1] 3
> length(myData[,1])                     # length of the first column = hence number of rows
[1] 2
> dim(myData)[1]                         # the first dimension = hence number of columns
[1] 2
```

Creating an empty matrix

```
> newmatrix <- matrix(NA, 2,3) # or matrix(, 2,3) with NA by default
> newmatrix
     [,1] [,2] [,3]
[1,]   NA   NA   NA
[2,]   NA   NA   NA
> dim(newmatrix)
[1] 2 3

> is.na(newmatrix)
     [,1] [,2] [,3]
[1,] TRUE TRUE TRUE
[2,] TRUE TRUE TRUE

> mode(newmatrix)
[1] "logical"
> class(newmatrix)
[1] matrix
> str(newmatrix)
logi [1:2, 1:3] NA NA NA NA NA NA
```

Filling a matrix

```
> newmatrix[2,3] <- "toto"          # filling the 2nd row and 3rd column value
> newmatrix
[,1] [,2] [,3]
[1,] NA   NA   NA
[2,] NA   NA   "toto"
> newmatrix[,1] <- "tutu"            # filling the 1st column with same values
> newmatrix
     [,1]   [,2] [,3]
[1,] "tutu" NA   NA
[2,] "tutu" NA   "toto"
> newmatrix[,2] <- c("titi" ,"tata")   # filling the 2nd column with different values
> newmatrix
     [,1]   [,2]   [,3]
[1,] "tutu" "titi" NA
[2,] "tutu" "tata" "toto"
> is.na(newmatrix)              #testing whether the values in the matrix are missing values
[,1]  [,2]  [,3]
[1,] FALSE FALSE  TRUE          #only the 3 values in first row was NA
[2,] FALSE FALSE FALSE
```

Creating a matrix with cbind/rbind

- with cbind(): binding vectors by columns

```
> myData2 <- cbind(weight, size, bmi) # creates another matrix binding vectors as columns
>row.names(myData2)
[1] "Fabien"   "Pierre"   "Sandrine" "Claire"   "Bruno"    "Delphine"
> myData2
           weight size bmi
Fabien       60 1.75 19.59184
Pierre       72 1.80 22.22222
Sandrine     57 1.65 20.93664
Claire       90 1.90 24.93075
Bruno        95 1.74 31.37799
Delphine     72 1.91 19.73630
```

- with rbind(): binding vectors by rows

```
> myData3 <- rbind(weight, size, bmi)
> myData3
         Fabien   Pierre Sandrine   Claire    Bruno Delphine
weight 60.00000 72.00000 57.00000 90.00000 95.00000  72.0000
size    1.75000  1.80000  1.65000  1.90000  1.74000   1.9100
bmi    19.59184 22.22222 20.93664 24.93075 31.37799  19.7363

> t(myData2) # transpose myData2 -> we obtain the same matrix as myData3!
```

Note: t() is a function, so do not call an R object t!
Use a color-case text editor for R to know reserved words

Row/column names of matrices

Names of rows and columns are stored in a vector :

```
> rownames(myData2)                # returns the vector of the names of the rows
[1] "Fabien"   "Pierre"   "Sandrine" "Claire"   "Bruno"    "Delphine"
> colnames(myData2)                # returns the vector of the names of the column
[1] "weight" "size"   "bmi"
> rownames(myData)                 # the vector is empty for this other object
NULL
> colnames(myData)                 # the vector is empty for this other object
NULL
```

Giving names to rows and columns :

```
> colnames(myData) <- c("one", "two", "three") # gives names to columns
> rownames(myData) <- c("A", "B")              # gives names to rows
> myData
  one two three
A   1   3    12
B   2  11    13
```

Subsetting matrices using row/column names :

```
> myData["B",]          # gets row called "B"
one   two three
  2    11    13
> myData[,"two"]        # gets column called "two"
 A  B
 3 11
```

Functions on matrices

As expected, operators work on numeric matrices:

```
> myData2*2
         weight size      bmi
Fabien      120 3.50 39.18367
Pierre      144 3.60 44.44444
Sandrine    114 3.30 41.87328
Claire      180 3.80 49.86150
Bruno       190 3.48 62.75598
Delphine    144 3.82 39.47260
```

All columns of a matrix can be explored at once with some functions

```
> summary(myData2)
     weight              size             bmi
 Min.   :57.00   Min.   :1.650   Min.   :19.59
 1st Qu.:63.00   1st Qu.:1.742   1st Qu.:20.04
 Median :72.00   Median :1.775   Median :21.58
 Mean   :74.33   Mean   :1.792   Mean   :23.13
 3rd Qu.:85.50   3rd Qu.:1.875   3rd Qu.:24.25
 Max.   :95.00   Max.   :1.910   Max.   :31.38
```

But most functions need to specify the vector corresponding to the column of interest

```
 > mean(myData2)
[1] 33.08587                           # mean of all data
 > mean(myData2[,1])                   # mean of the vector corresponding to
 [1] 74.33333                          # the first column only
```

Summary on matrices

Format	two-dimensions
Datatype	class() to check it is a matrix homogeneous: only one type of character, numeric, logical, factor -> ceorcion if heterogeneous -> check with mode()
Creation	matrix() , cbind() , rbind()
Adding new items	cbind() , rbind()
Size	length() -> nb of items
Dim	dim(), str()
Slicing	my_vector[i,j]
Filling	my_vector[i,j] <- "toto"
Naming	colnames() , rownames()

Saving data…

I can save the whole data in a single .Rdata object:

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

Or I can save only some anthropometric data (weigth, size and bmi) :

```
> save(weight,size,bmi,file=" anthropo.Rdata")
```

I can load them in a new R session with the following command:

```
> load("anthropo.Rdata")
> ls()
[1] "bmi"    "size"   "weight"
```