R for Beginners

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Contents

1 Preamble

The goal of the present document is to give a starting point for people newly interested in R. I chose to emphasize on the understanding of how R works, with the aim of a beginner, rather than expert, use. Given that the possibilities offered by R are vast, it is useful to a beginner to get some notions and concepts in order to progress easily. I tried to simplify the explanations as much as I could to make them understandable by all, while giving useful details, sometimes with tables.

R is a system for statistical analyses and graphics created by Ross Ihaka and Robert Gentleman[1]. R is both a software and a language considered as a dialect of the S language created by the AT&T Bell Laboratories. S is available as the software S-PLUS commercialized by Insightful[2]. There are important differences in the designs of R and of S: those who want to know more on this point can read the paper by Ihaka & Gentleman (1996) or the R-FAQ[3], a copy of which is also distributed with R.

R is freely distributed under the terms of the *GNU General Public Licence*[4]; its development and distribution are carried out by several statisticians known as the *R Development Core Team*.

R is available in several forms: the sources (written mainly in C and some routines in Fortran), essentially for Unix and Linux machines, or some pre-compiled binaries for Windows, Linux, and Macintosh. The files needed to install R, either from the sources or from the pre-compiled binaries, are distributed from the internet site of the *Comprehensive R Archive Network* (CRAN)[5] where the instructions for the installation are also available. Regarding the distributions of Linux (Debian, ...), the binaries are generally available for the most recent versions; look at the CRAN site if necessary.

R has many functions for statistical analyses and graphics; the latter are visualized immediately in their own window and can be saved in various formats (jpg, png, bmp, ps, pdf, emf, pictex, xfig; the available formats may depend on the operating system). The results from a statistical analysis are displayed on the screen, some intermediate results (P-values, regression coefficients, residuals, ...) can be saved, written in a file, or used in subsequent analyses.

The R language allows the user, for instance, to program loops to successively analyse several data sets. It is also possible to combine in a single program different statistical functions to perform more complex analyses. The

[1] Ihaka R. & Gentleman R. 1996. R: a language for data analysis and graphics. *Journal of Computational and Graphical Statistics* 5: 299–314.

[2] See http://www.insightful.com/products/splus/default.asp for more information

[3] http://cran.r-project.org/doc/FAQ/R-FAQ.html

[4] For more information: http://www.gnu.org/

[5] http://cran.r-project.org/

R users may benefit from a large number of programs written for S and available on the internet[6], most of these programs can be used directly with R.

At first, R could seem too complex for a non-specialist. This may not be true actually. In fact, a prominent feature of R is its flexibility. Whereas a classical software displays immediately the results of an analysis, R stores these results in an "object", so that an analysis can be done with no result displayed. The user may be surprised by this, but such a feature is very useful. Indeed, the user can extract only the part of the results which is of interest. For example, if one runs a series of 20 regressions and wants to compare the different regression coefficients, R can display only the estimated coefficients: thus the results may take a single line, whereas a classical software could well open 20 results windows. We will see other examples illustrating the flexibility of a system such as R compared to traditional softwares.

[6]For example: http://stat.cmu.edu/S/

2 A few concepts before starting

Once R is installed on your computer, the software is executed by launching the corresponding executable. The prompt, by default '>', indicates that R is waiting for your commands. Under Windows using the program Rgui.exe, some commands (accessing the on-line help, opening files, ...) can be executed via the pull-down menus. At this stage, a new user is likely to wonder "What do I do now?" It is indeed very useful to have a few ideas on how R works when it is used for the first time, and this is what we will see now.

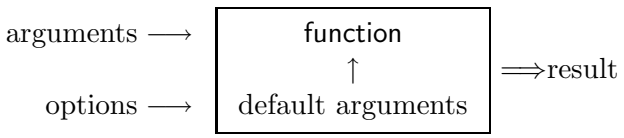
We shall see first briefly how R works. Then, I will describe the "assign" operator which allows creating objects, how to manage objects in memory, and finally how to use the on-line help which is very useful when running R.

2.1 How R works

The fact that R is a language may deter some users who think "I can't program". This should not be the case for two reasons. First, R is an interpreted language, not a compiled one, meaning that all commands typed on the keyboard are directly executed without requiring to build a complete program like in most computer languages (C, Fortran, Pascal, ...).

Second, R's syntax is very simple and intuitive. For instance, a linear regression can be done with the command `lm(y ~ x)` which means "fitting a linear model with y as response and x as predictor". In R, in order to be executed, a function *always* needs to be written with parentheses, even if there is nothing within them (e.g., `ls()`). If one just types the name of a function without parentheses, R will display the content of the function. In this document, the names of the functions are generally written with parentheses in order to distinguish them from other objects, unless the text indicates clearly so.

When R is running, variables, data, functions, results, etc, are stored in the active memory of the computer in the form of *objects* which have a *name*. The user can do actions on these objects with *operators* (arithmetic, logical, comparison, ...) and *functions* (which are themselves objects). The use of operators is relatively intuitive, we will see the details later (p. 25). An R function may be sketched as follows:



The arguments can be objects ("data", formulae, expressions, ...), some

of which could be defined by default in the function; these default values may be modified by the user by specifying options. An R function may require no argument: either all arguments are defined by default (and their values can be modified with the options), or no argument has been defined in the function. We will see later in more details how to use and build functions (p. 67). The present description is sufficient for the moment to understand how R works.

All the actions of R are done on objects stored in the active memory of the computer: no temporary files are used (Fig. 1). The readings and writings of files are used for input and output of data and results (graphics, ...). The user executes the functions via some commands. The results are displayed directly on the screen, stored in an object, or written on the disk (particularly for graphics). Since the results are themselves objects, they can be considered as data and analysed as such. Data files can be read from the local disk or from a remote server through internet.

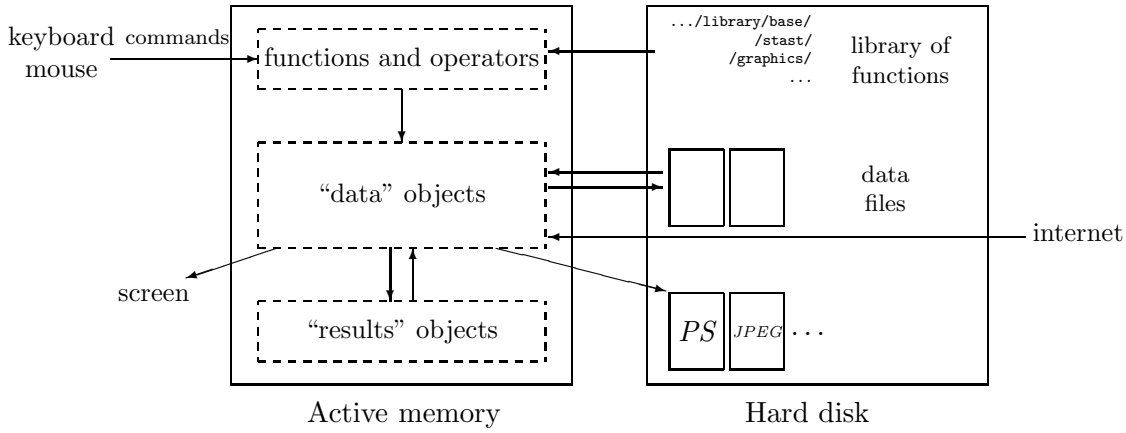


Figure 1: A schematic view of how R works.

The functions available to the user are stored in a library localised on the disk in a directory called R_HOME/library (R_HOME is the directory where R is installed). This directory contains *packages* of functions, which are themselves structured in directories. The package named base is in a way the core of R and contains the basic functions of the language, particularly, for reading and manipulating data. Each package has a directory called R with a file named like the package (for instance, for the package base, this is the file R_HOME/library/base/R/base). This file contains all the functions of the package.

One of the simplest commands is to type the name of an object to display its content. For instance, if an object `n` contents the value 10:

```
> n
[1] 10
```

The digit 1 within brackets indicates that the display starts at the first element of `n`. This command is an implicit use of the function `print` and the above example is similar to `print(n)` (in some situations, the function `print` must be used explicitly, such as within a function or a loop).

The name of an object must start with a letter (A–Z and a–z) and can include letters, digits (0–9), dots (.), and underscores (_). R discriminates between uppercase letters and lowercase ones in the names of the objects, so that `x` and `X` can name two distinct objects (even under Windows).

2.2 Creating, listing and deleting the objects in memory

An object can be created with the "assign" operator which is written as an arrow with a minus sign and a bracket; this symbol can be oriented left-to-right or the reverse:

```
> n <- 15
> n
[1] 15
> 5 -> n
> n
[1] 5
> x <- 1
> X <- 10
> x
[1] 1
> X
[1] 10
```

If the object already exists, its previous value is erased (the modification affects only the objects in the active memory, not the data on the disk). The value assigned this way may be the result of an operation and/or a function:

```
> n <- 10 + 2
> n
[1] 12
> n <- 3 + rnorm(1)
> n
[1] 2.208807
```

The function `rnorm(1)` generates a normal random variate with mean zero and variance unity (p. 17). Note that you can simply type an expression without assigning its value to an object, the result is thus displayed on the screen but is not stored in memory:

```
> (10 + 2) * 5
[1] 60
```

The assignment will be omitted in the examples if not necessary for understanding.

The function `ls` lists simply the objects in memory: only the names of the objects are displayed.

```
> name <- "Carmen"; n1 <- 10; n2 <- 100; m <- 0.5
> ls()
[1] "m"    "n1"   "n2"   "name"
```

Note the use of the semi-colon to separate distinct commands on the same line. If we want to list only the objects which contain a given character in their name, the option `pattern` (which can be abbreviated with `pat`) can be used:

```
> ls(pat = "m")
[1] "m"    "name"
```

To restrict the list of objects whose names start with this character:

```
> ls(pat = "^m")
[1] "m"
```

The function `ls.str` displays some details on the objects in memory:

```
> ls.str()
m :  num 0.5
n1 :  num 10
n2 :  num 100
name :  chr "Carmen"
```

The option `pattern` can be used in the same way as with `ls`. Another useful option of `ls.str` is `max.level` which specifies the level of detail for the display of composite objects. By default, `ls.str` displays the details of all objects in memory, included the columns of data frames, matrices and lists, which can result in a very long display. We can avoid to display all these details with the option `max.level = -1`:

```
> M <- data.frame(n1, n2, m)
> ls.str(pat = "M")
M : 'data.frame':       1 obs. of  3 variables:
 $ n1: num 10
 $ n2: num 100
 $ m : num 0.5
> ls.str(pat="M", max.level=-1)
M : 'data.frame':       1 obs. of  3 variables:
```

To delete objects in memory, we use the function `rm`: `rm(x)` deletes the object `x`, `rm(x,y)` deletes both the objects `x` et `y`, `rm(list=ls())` deletes all the objects in memory; the same options mentioned for the function `ls()` can then be used to delete selectively some objects: `rm(list=ls(pat="^m"))`.

2.3 The on-line help

The on-line help of R gives very useful information on how to use the functions. Help is available directly for a given function, for instance:

```
> ?lm
```

will display, within R, the help page for the function `lm()` (*linear model*). The commands `help(lm)` and `help("lm")` have the same effect. The last one must be used to access help with non-conventional characters:

```
> ?*
Error: syntax error
> help("*")
Arithmetic              package:base              R Documentation

Arithmetic Operators
...
```

Calling help opens a page (this depends on the operating system) with general information on the first line such as the name of the package where is (are) the documented function(s) or operators. Then comes a title followed by sections which give detailed information.

Description: brief description.

Usage: for a function, gives the name with all its arguments and the possible options (with the corresponding default values); for an operator gives the typical use.

Arguments: for a function, details each of its arguments.

Details: detailed description.

Value: if applicable, the type of object returned by the function or the operator.

See Also: other help pages close or similar to the present one.

Examples: some examples which can generally be executed without opening the help with the function `example`.

For beginners, it is good to look at the section **Examples**. Generally, it is useful to read carefully the section **Arguments**. Other sections may be encountered, such as **Note**, **References** or **Author(s)**.

By default, the function `help` only searches in the packages which are loaded in memory. The option `try.all.packages`, which default is `FALSE`, allows to search in all packages if its value is `TRUE`:

```
> help("bs")
No documentation for 'bs' in specified packages and libraries:
you could try 'help.search("bs")'
> help("bs", try.all.packages = TRUE)
Help for topic 'bs' is not in any loaded package but
can be found in the following packages:

  Package               Library
  splines               /usr/lib/R/library
```

Note that in this case the help page of the function `bs` is not displayed. The user can display help pages from a package not loaded in memory using the option `package`:

```
> help("bs", package = "splines")
bs                package:splines                R Documentation

B-Spline Basis for Polynomial Splines

Description:

     Generate the B-spline basis matrix for a polynomial spline.
...
```

The help in html format (read, e.g., with Netscape) is called by typing:

```
> help.start()
```

A search with keywords is possible with this html help. The section **See Also** has here hypertext links to other function help pages. The search with keywords is also possible in R with the function `help.search`. The latter looks for a specified topic, given as a character string, in the help pages of all installed packages. For instance, `help.search("tree")` will display a list of the functions which help pages mention "tree". Note that if some packages have been recently installed, it may be useful to refresh the database used by `help.search` using the option `rebuild` (e.g., `help.search("tree", rebuild = TRUE)`).

The fonction `apropos` finds all functions which name contains the character string given as argument; only the packages loaded in memory are searched:

```
> apropos(help)
[1] "help"         ".helpForCall" "help.search"
[4] "help.start"
```

3 Data with R

3.1 Objects

We have seen that R works with objects which are, of course, characterized by their names and their content, but also by *attributes* which specify the kind of data represented by an object. In order to understand the usefulness of these attributes, consider a variable that takes the value 1, 2, or 3: such a variable could be an integer variable (for instance, the number of eggs in a nest), or the coding of a categorical variable (for instance, sex in some populations of crustaceans: male, female, or hermaphrodite).

It is clear that the statistical analysis of this variable will not be the same in both cases: with R, the attributes of the object give the necessary information. More technically, and more generally, the action of a function on an object depends on the attributes of the latter.

All objects have two *intrinsic* attributes: *mode* and *length*. The mode is the basic type of the elements of the object; there are four main modes: numeric, character, complex[7], and logical (`FALSE` or `TRUE`). Other modes exist but they do not represent data, for instance function or expression. The length is the number of elements of the object. To display the mode and the length of an object, one can use the functions `mode` and `length`, respectively:

```
> x <- 1
> mode(x)
[1] "numeric"
> length(x)
[1] 1
> A <- "Gomphotherium"; compar <- TRUE; z <- 1i
> mode(A); mode(compar); mode(z)
[1] "character"
[1] "logical"
[1] "complex"
```

Whatever the mode, missing data are represented by `NA` (*not available*). A very large numeric value can be specified with an exponential notation:

```
> N <- 2.1e23
> N
[1] 2.1e+23
```

R correctly represents non-finite numeric values, such as $\pm\infty$ with `Inf` and `-Inf`, or values which are not numbers with `NaN` (*not a number*).

[7] The mode complex will not be discussed in this document.

```
> x <- 5/0
> x
[1] Inf
> exp(x)
[1] Inf
> exp(-x)
[1] 0
> x - x
[1] NaN
```

A value of mode character is input with double quotes ". It is possible to include this latter character in the value if it follows a backslash \. The two charaters altogether \" will be treated in a specific way by some functions such as `cat` for display on screen, or `write.table` to write on the disk (p. 14, the option `qmethod` of this function).

```
> x <- "Double quotes \" delimitate R's strings."
> x
[1] "Double quotes \" delimitate R's strings."
> cat(x)
Double quotes " delimitate R's strings.
```

Alternatively, variables of mode character can be delimited with single quotes (’); in this case it is not necessary to escape double quotes with backslashes (but single quotes must be!):

```
> x <- 'Double quotes " delimitate R\'s strings.'
> x
[1] "Double quotes \" delimitate R's strings."
```

The following table gives an overview of the type of objects representing data.

object	**modes**	**several modes possible in the same object?**
vector	numeric, character, complex *or* logical	No
factor	numeric *or* character	No
array	numeric, character, complex *or* logical	No
matrix	numeric, character, complex *or* logical	No
data frame	numeric, character, complex *or* logical	Yes
ts	numeric, character, complex *or* logical	No
list	numeric, character, complex, logical, function, expression, ...	Yes

A vector is a variable in the commonly admitted meaning. A factor is a categorical variable. An array is a table with k dimensions, a matrix being a particular case of array with $k = 2$. Note that the elements of an array or of a matrix are all of the same mode. A data frame is a table composed with one or several vectors and/or factors all of the same length but possibly of different modes. A 'ts' is a time series data set and so contains additional attributes such as frequency and dates. Finally, a list can contain any type of object, included lists!

For a vector, its mode and length are sufficient to describe the data. For other objects, other information is necessary and it is given by *non-intrinsic* attributes. Among these attributes, we can cite *dim* which corresponds to the dimensions of an object. For example, a matrix with 2 lines and 2 columns has for `dim` the pair of values [2, 2], but its length is 4.

3.2 Reading data in a file

For reading and writing in files, R uses the working directory. To find this directory, the command `getwd()` (*get working directory*) can be used, and the working directory can be changed with `setwd("C:/data")` or `setwd("/home/-paradis/R")`. It is necessary to give the path to a file if it is not in the working directory.[8]

R can read data stored in text (ASCII) files with the following functions: `read.table` (which has several variants, see below), `scan` and `read.fwf`. R can also read files in other formats (Excel, SAS, SPSS, ...), and access SQL-type databases, but the functions needed for this are not in the package `base`. These functionalities are very useful for a more advanced use of R, but we will restrict here to reading files in ASCII format.

The function `read.table` has for effect to create a data frame, and so is the main way to read data in tabular form. For instance, if one has a file named data.dat, the command:

```
> mydata <- read.table("data.dat")
```

will create a data frame named `mydata`, and each variable will be named, by default, `V1`, `V2`, ... and can be accessed individually by `mydata$V1`, `mydata$V2`, ..., or by `mydata["V1"]`, `mydata["V2"]`, ..., or, still another solution, by `mydata[, 1]`, `mydata[,2 ]`, ...[9] There are several options whose default values (i.e. those used by R if they are omitted by the user) are detailed in the following table:

```
read.table(file, header = FALSE, sep = "", quote = "\"'", dec = ".",
```

[8] Under Windows, it is useful to create a short-cut of Rgui.exe then edit its properties and change the directory in the field "Start in:" under the tab "Short-cut": this directory will then be the working directory if R is started from this short-cut.

[9] There is a difference: `mydata$V1` and `mydata[, 1]` are vectors whereas `mydata["V1"]` is a data frame. We will see later (p. 18) some details on manipulating objects.

```
row.names, col.names, as.is = FALSE, na.strings = "NA",
colClasses = NA, nrows = -1,
skip = 0, check.names = TRUE, fill = !blank.lines.skip,
strip.white = FALSE, blank.lines.skip = TRUE,
comment.char = "#")
```

`file`	the name of the file (within `""` or a variable of mode character), possibly with its path (the symbol \ is not allowed and must be replaced by /, even under Windows), or a remote access to a file of type URL (http://...)
`header`	a logical (`FALSE` or `TRUE`) indicating if the file contains the names of the variables on its first line
`sep`	the field separator used in the file, for instance `sep="\t"` if it is a tabulation
`quote`	the characters used to cite the variables of mode character
`dec`	the character used for the decimal point
`row.names`	a vector with the names of the lines which can be either a vector of mode character, or the number (or the name) of a variable of the file (by default: `1`, `2`, `3`, ...)
`col.names`	a vector with the names of the variables (by default: `V1`, `V2`, `V3`, ...)
`as.is`	controls the conversion of character variables as factors (if `FALSE`) or keeps them as characters (`TRUE`); `as.is` can be a logical, numeric or character vector specifying the variables to be kept as character
`na.strings`	the value given to missing data (converted as `NA`)
`colClasses`	a vector of mode character giving the classes to attribute to the columns
`nrows`	the maximum number of lines to read (negative values are ignored)
`skip`	the number of lines to be skipped before reading the data
`check.names`	if `TRUE`, checks that the variable names are valid for R
`fill`	if `TRUE` and all lines do not have the same number of variables, "blanks" are added
`strip.white`	(conditional to `sep`) if `TRUE`, deletes extra spaces before and after the character variables
`blank.lines.skip`	if `TRUE`, ignores "blank" lines
`comment.char`	a character defining comments in the data file, the rest of the line after this character is ignored (to disable this argument, use `comment.char = ""`)

The variants of `read.table` are useful since they have different default values:

```
read.csv(file, header = TRUE, sep = ",", quote="\"", dec=".",
         fill = TRUE, ...)
read.csv2(file, header = TRUE, sep = ";", quote="\"", dec=",",
          fill = TRUE, ...)
read.delim(file, header = TRUE, sep = "\t", quote="\"", dec=".",
           fill = TRUE, ...)
read.delim2(file, header = TRUE, sep = "\t", quote="\"", dec=",",
            fill = TRUE, ...)
```

The function `scan` is more flexible than `read.table`. A difference is that it is possible to specify the mode of the variables, for example:

```
> mydata <- scan("data.dat", what = list("", 0, 0))
```

reads in the file data.dat three variables, the first is of mode character and the next two are of mode numeric. Another important distinction is that `scan()` can be used to create different objects, vectors, matrices, data frames, lists, ... In the above example, `mydata` is a list of three vectors. By default, that is if `what` is omitted, `scan()` creates a numeric vector. If the data read do not correspond to the mode(s) expected (either by default, or specified by `what`), an error message is returned. The options are the followings.

```
scan(file = "", what = double(0), nmax = -1, n = -1, sep = "",
     quote = if (sep=="\n") "" else "'\"", dec = ".",
     skip = 0, nlines = 0, na.strings = "NA",
     flush = FALSE, fill = FALSE, strip.white = FALSE, quiet = FALSE,
     blank.lines.skip = TRUE, multi.line = TRUE, comment.char = "",
     allowEscapes = TRUE)
```

`file`	the name of the file (within `""`), possibly with its path (the symbol \ is not allowed and must be replaced by /, even under Windows), or a remote access to a file of type URL (http://...); if `file=""`, the data are entered with the keyboard (the entree is terminated by a blank line)
`what`	specifies the mode(s) of the data (numeric by default)
`nmax`	the number of data to read, or, if `what` is a list, the number of lines to read (by default, `scan` reads the data up to the end of file)
`n`	the number of data to read (by default, no limit)
`sep`	the field separator used in the file
`quote`	the characters used to cite the variables of mode character
`dec`	the character used for the decimal point
`skip`	the number of lines to be skipped before reading the data
`nlines`	the number of lines to read
`na.string`	the value given to missing data (converted as `NA`)
`flush`	a logical, if `TRUE`, `scan` goes to the next line once the number of columns has been reached (allows the user to add comments in the data file)
`fill`	if `TRUE` and all lines do not have the same number of variables, "blanks" are added
`strip.white`	(conditional to `sep`) if `TRUE`, deletes extra spaces before and after the character variables
`quiet`	a logical, if `FALSE`, `scan` displays a line showing which fields have been read
`blank.lines.skip`	if `TRUE`, ignores blank lines
`multi.line`	if `what` is a list, specifies if the variables of the same individual are on a single line in the file (`FALSE`)
`comment.char`	a character defining comments in the data file, the rest of the line after this character is ignored (the default is to have this disabled)
`allowEscapes`	specifies whether C-style escapes (e.g., '\t') be processed (the default) or read as verbatim

The function `read.fwf` can be used to read in a file some data in *fixed width format*:

```
read.fwf(file, widths, header = FALSE, sep = "\t",
         as.is = FALSE, skip = 0, row.names, col.names,
         n = -1, buffersize = 2000, ...)
```

The options are the same than for `read.table()` except `widths` which specifies the width of the fields (`buffersize` is the maximum number of lines read simultaneously). For example, if a file named data.txt has the data indicated on the right, one can read the data with the following command:

```
A1.501.2
A1.551.3
B1.601.4
B1.651.5
C1.701.6
C1.751.7
```

```
> mydata <- read.fwf("data.txt", widths=c(1, 4, 3))
> mydata
  V1   V2  V3
1  A 1.50 1.2
2  A 1.55 1.3
3  B 1.60 1.4
4  B 1.65 1.5
5  C 1.70 1.6
6  C 1.75 1.7
```

3.3 Saving data

The function `write.table` writes in a file an object, typically a data frame but this could well be another kind of object (vector, matrix, ...). The arguments and options are:

```
write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ",
            eol = "\n", na = "NA", dec = ".", row.names = TRUE,
            col.names = TRUE, qmethod = c("escape", "double"))
```

`x`	the name of the object to be written
`file`	the name of the file (by default the object is displayed on the screen)
`append`	if `TRUE` adds the data without erasing those possibly existing in the file
`quote`	a logical or a numeric vector: if `TRUE` the variables of mode character and the factors are written within `""`, otherwise the numeric vector indicates the numbers of the variables to write within `""` (in both cases the names of the variables are written within `""` but not if `quote = FALSE`)
`sep`	the field separator used in the file
`eol`	the character to be used at the end of each line (`"\n"` is a carriage-return)
`na`	the character to be used for missing data
`dec`	the character used for the decimal point
`row.names`	a logical indicating whether the names of the lines are written in the file
`col.names`	id. for the names of the columns
`qmethod`	specifies, if `quote=TRUE`, how double quotes `"` included in variables of mode character are treated: if `"escape"` (or `"e"`, the default) each `"` is replaced by `\"`, if `"d"` each `"` is replaced by `""`

To write in a simpler way an object in a file, the command `write(x, file="data.txt")` can be used, where `x` is the name of the object (which can be a vector, a matrix, or an array). There are two options: `nc` (or `ncol`) which defines the number of columns in the file (by default `nc=1` if `x` is of mode character, `nc=5` for the other modes), and `append` (a logical) to add the data without deleting those possibly already in the file (`TRUE`) or deleting them if the file already exists (`FALSE`, the default).

To record a group of objects of any type, we can use the command `save(x, y, z, file= "xyz.RData")`. To ease the transfert of data between different machines, the option `ascii = TRUE` can be used. The data (which are now called a *workspace* in R's jargon) can be loaded later in memory with `load("xyz.RData")`. The function `save.image()` is a short-cut for `save(list =ls(all=TRUE), file=".RData")`.

3.4 Generating data

3.4.1 Regular sequences

A regular sequence of integers, for example from 1 to 30, can be generated with:

```
> x <- 1:30
```

The resulting vector `x` has 30 elements. The operator '`:`' has priority on the arithmetic operators within an expression:

```
> 1:10-1
 [1] 0 1 2 3 4 5 6 7 8 9
> 1:(10-1)
[1] 1 2 3 4 5 6 7 8 9
```

The function `seq` can generate sequences of real numbers as follows:

```
> seq(1, 5, 0.5)
[1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
```

where the first number indicates the beginning of the sequence, the second one the end, and the third one the increment to be used to generate the sequence. One can use also:

```
> seq(length=9, from=1, to=5)
[1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
```

One can also type directly the values using the function `c`:

```
> c(1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5)
[1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
```

It is also possible, if one wants to enter some data on the keyboard, to use the function `scan` with simply the default options:

```
> z <- scan()
1: 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
10:
Read 9 items
> z
[1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
```

The function `rep` creates a vector with all its elements identical:

```
> rep(1, 30)
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

The function `sequence` creates a series of sequences of integers each ending by the numbers given as arguments:

```
> sequence(4:5)
[1] 1 2 3 4 1 2 3 4 5
> sequence(c(10,5))
 [1]  1  2  3  4  5  6  7  8  9 10  1  2  3  4  5
```

The function `gl` (*generate levels*) is very useful because it generates regular series of factors. The usage of this fonction is `gl(k, n)` where `k` is the number of levels (or classes), and `n` is the number of replications in each level. Two options may be used: `length` to specify the number of data produced, and `labels` to specify the names of the levels of the factor. Examples:

```
> gl(3, 5)
 [1] 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3
Levels:  1 2 3
> gl(3, 5, length=30)
 [1] 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3
Levels:  1 2 3
> gl(2, 6, label=c("Male", "Female"))
 [1] Male   Male   Male   Male   Male   Male
 [7] Female Female Female Female Female Female
Levels:  Male Female
> gl(2, 10)
 [1] 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2
Levels:  1 2
> gl(2, 1, length=20)
 [1] 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2
Levels:  1 2
> gl(2, 2, length=20)
 [1] 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2
Levels:  1 2
```

Finally, `expand.grid()` creates a data frame with all combinations of vectors or factors given as arguments:

```
> expand.grid(h=c(60,80), w=c(100, 300), sex=c("Male", "Female"))
   h   w    sex
1 60 100   Male
2 80 100   Male
3 60 300   Male
4 80 300   Male
5 60 100 Female
6 80 100 Female
7 60 300 Female
8 80 300 Female
```

3.4.2 Random sequences

law	**function**
Gaussian (normal)	`rnorm(n, mean=0, sd=1)`
exponential	`rexp(n, rate=1)`
gamma	`rgamma(n, shape, scale=1)`
Poisson	`rpois(n, lambda)`
Weibull	`rweibull(n, shape, scale=1)`
Cauchy	`rcauchy(n, location=0, scale=1)`
beta	`rbeta(n, shape1, shape2)`
'Student' (t)	`rt(n, df)`
Fisher–Snedecor (F)	`rf(n, df1, df2)`
Pearson (χ^2)	`rchisq(n, df)`
binomial	`rbinom(n, size, prob)`
multinomial	`rmultinom(n, size, prob)`
geometric	`rgeom(n, prob)`
hypergeometric	`rhyper(nn, m, n, k)`
logistic	`rlogis(n, location=0, scale=1)`
lognormal	`rlnorm(n, meanlog=0, sdlog=1)`
negative binomial	`rnbinom(n, size, prob)`
uniform	`runif(n, min=0, max=1)`
Wilcoxon's statistics	`rwilcox(nn, m, n)`, `rsignrank(nn, n)`

It is useful in statistics to be able to generate random data, and R can do it for a large number of probability density functions. These functions are of the form `rfunc(n, p1, p2, ...)`, where *`func`* indicates the probability distribution, `n` the number of data generated, and `p1`, `p2`, ... are the values of the parameters of the distribution. The above table gives the details for each distribution, and the possible default values (if none default value is indicated, this means that the parameter must be specified by the user).

Most of these functions have counterparts obtained by replacing the letter `r` with `d`, `p` or `q` to get, respectively, the probability density (`dfunc(x, ...)`),

the cumulative probability density (`pfunc(x, ...)`), and the value of quantile (`qfunc(p, ...)`, with $0 <$ `p` < 1). The last two series of functions can be used to find critical values or P-values of statistical tests. For instance, the critical values for a two-tailed test following a normal distribution at the 5% threshold are:

```
> qnorm(0.025)
[1] -1.959964
> qnorm(0.975)
[1] 1.959964
```

For the one-tailed version of the same test, either `qnorm(0.05)` or `1 - qnorm(0.95)` will be used depending on the form of the alternative hypothesis.

The P-value of a test, say $\chi^2 = 3.84$ with $df = 1$, is:

```
> 1 - pchisq(3.84, 1)
[1] 0.05004352
```

3.5 Manipulating objects

3.5.1 Creating objects

We have seen previously different ways to create objects using the assign operator; the mode and the type of objects so created are generally determined implicitly. It is possible to create an object and specifying its mode, length, type, etc. This approach is interesting in the perspective of manipulating objects. One can, for instance, create an 'empty' object and then modify its elements successively which is more efficient than putting all its elements together with `c()`. The indexing system could be used here, as we will see later (p. 26).

It can also be very convenient to create objects from others. For example, if one wants to fit a series of models, it is simple to put the formulae in a list, and then to extract the elements successively to insert them in the function `lm`.

At this stage of our learning of R, the interest in learning the following functionalities is not only practical but also didactic. The explicit construction of objects gives a better understanding of their structure, and allows us to go further in some notions previously mentioned.

Vector. The function `vector`, which has two arguments `mode` and `length`, creates a vector which elements have a value depending on the mode specified as argument: 0 if numeric, `FALSE` if logical, or `""` if character. The following functions have exactly the same effect and have for single argument the length of the vector: `numeric()`, `logical()`, and `character()`.

Factor. A factor includes not only the values of the corresponding categorical variable, but also the different possible levels of that variable (even if they are not present in the data). The function `factor` creates a factor with the following options:

```
factor(x, levels = sort(unique(x), na.last = TRUE),
       labels = levels, exclude = NA, ordered = is.ordered(x))
```

`levels` specifies the possible levels of the factor (by default the unique values of the vector `x`), `labels` defines the names of the levels, `exclude` the values of `x` to exclude from the levels, and `ordered` is a logical argument specifying whether the levels of the factor are ordered. Recall that `x` is of mode numeric or character. Some examples follow.

```
> factor(1:3)
[1] 1 2 3
Levels:  1 2 3
> factor(1:3, levels=1:5)
[1] 1 2 3
Levels:  1 2 3 4 5
> factor(1:3, labels=c("A", "B", "C"))
[1] A B C
Levels:  A B C
> factor(1:5, exclude=4)
[1] 1  2  3  NA 5
Levels:  1 2 3 5
```

The function `levels` extracts the possible levels of a factor:

```
> ff <- factor(c(2, 4), levels=2:5)
> ff
[1] 2 4
Levels:  2 3 4 5
> levels(ff)
[1] "2" "3" "4" "5"
```

Matrix. A matrix is actually a vector with an additional attribute (dim) which is itself a numeric vector with length 2, and defines the numbers of rows and columns of the matrix. A matrix can be created with the function `matrix`:

```
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE,
       dimnames = NULL)
```

The option `byrow` indicates whether the values given by `data` must fill successively the columns (the default) or the rows (if `TRUE`). The option `dimnames` allows to give names to the rows and columns.

```
> matrix(data=5, nr=2, nc=2)
     [,1] [,2]
[1,]    5    5
[2,]    5    5
> matrix(1:6, 2, 3)
     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6
> matrix(1:6, 2, 3, byrow=TRUE)
     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    4    5    6
```

Another way to create a matrix is to give the appropriate values to the dim attribute (which is initially `NULL`):

```
> x <- 1:15
> x
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15
> dim(x)
NULL
> dim(x) <- c(5, 3)
> x
     [,1] [,2] [,3]
[1,]    1    6   11
[2,]    2    7   12
[3,]    3    8   13
[4,]    4    9   14
[5,]    5   10   15
```

Data frame. We have seen that a data frame is created implicitly by the function `read.table`; it is also possible to create a data frame with the function `data.frame`. The vectors so included in the data frame must be of the same length, or if one of the them is shorter, it is "recycled" a whole number of times:

```
> x <- 1:4; n <- 10; M <- c(10, 35); y <- 2:4
> data.frame(x, n)
  x  n
1 1 10
2 2 10
```

```
3 3 10
4 4 10
> data.frame(x, M)
  x  M
1 1 10
2 2 35
3 3 10
4 4 35
> data.frame(x, y)
Error in data.frame(x, y) :
    arguments imply differing number of rows: 4, 3
```

If a factor is included in a data frame, it must be of the same length than the vector(s). It is possible to change the names of the columns with, for instance, `data.frame(A1=x, A2=n)`. One can also give names to the rows with the option `row.names` which must be, of course, a vector of mode character and of length equal to the number of lines of the data frame. Finally, note that data frames have an attribute dim similarly to matrices.

List. A list is created in a way similar to data frames with the function `list`. There is no constraint on the objects that can be included. In contrast to `data.frame()`, the names of the objects are not taken by default; taking the vectors `x` and `y` of the previous example:

```
> L1 <- list(x, y); L2 <- list(A=x, B=y)
> L1
[[1]]
[1] 1 2 3 4

[[2]]
[1] 2 3 4

> L2
$A
[1] 1 2 3 4

$B
[1] 2 3 4

> names(L1)
NULL
> names(L2)
[1] "A" "B"
```

Time-series. The function `ts` creates an object of class `"ts"` from a vector (single time-series) or a matrix (multivariate time-series), and some op-

tions which characterize the series. The options, with the default values, are:

```
ts(data = NA, start = 1, end = numeric(0), frequency = 1,
   deltat = 1, ts.eps = getOption("ts.eps"), class, names)
```

`data`	a vector or a matrix
`start`	the time of the first observation, either a number, or a vector of two integers (see the examples below)
`end`	the time of the last observation specified in the same way than `start`
`frequency`	the number of observations per time unit
`deltat`	the fraction of the sampling period between successive observations (ex. `1/12` for monthly data); only one of `frequency` or `deltat` must be given
`ts.eps`	tolerance for the comparison of series. The frequencies are considered equal if their difference is less than `ts.eps`
`class`	class to give to the object; the default is `"ts"` for a single series, and `c("mts", "ts")` for a multivariate series
`names`	a vector of mode character with the names of the individual series in the case of a multivariate series; by default the names of the columns of `data`, or `Series 1`, `Series 2`, ...

A few examples of time-series created with `ts`:

```
> ts(1:10, start = 1959)
Time Series:
Start = 1959
End = 1968
Frequency = 1
 [1]  1  2  3  4  5  6  7  8  9 10
> ts(1:47, frequency = 12, start = c(1959, 2))
     Jan Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec
1959       1   2   3   4   5   6   7   8   9  10  11
1960  12  13  14  15  16  17  18  19  20  21  22  23
1961  24  25  26  27  28  29  30  31  32  33  34  35
1962  36  37  38  39  40  41  42  43  44  45  46  47
> ts(1:10, frequency = 4, start = c(1959, 2))
     Qtr1 Qtr2 Qtr3 Qtr4
1959         1    2    3
1960    4    5    6    7
1961    8    9   10
> ts(matrix(rpois(36, 5), 12, 3), start=c(1961, 1), frequency=12)
         Series 1 Series 2 Series 3
```

```
Jan 1961        8        5        4
Feb 1961        6        6        9
Mar 1961        2        3        3
Apr 1961        8        5        4
May 1961        4        9        3
Jun 1961        4        6       13
Jul 1961        4        2        6
Aug 1961       11        6        4
Sep 1961        6        5        7
Oct 1961        6        5        7
Nov 1961        5        5        7
Dec 1961        8        5        2
```

Expression. The objects of mode expression have a fundamental role in R. An expression is a series of characters which makes sense for R. All valid commands are expressions. When a command is typed directly on the keyboard, it is then *evaluated* by R and executed if it is valid. In many circumstances, it is useful to construct an expression without evaluating it: this is what the function `expression` is made for. It is, of course, possible to evaluate the expression subsequently with `eval()`.

```
> x <- 3; y <- 2.5; z <- 1
> exp1 <- expression(x / (y + exp(z)))
> exp1
expression(x/(y + exp(z)))
> eval(exp1)
[1] 0.5749019
```

Expressions can be used, among other things, to include equations in graphs (p. 42). An expression can be created from a variable of mode character. Some functions take expressions as arguments, for example `D` which returns partial derivatives:

```
> D(exp1, "x")
1/(y + exp(z))
> D(exp1, "y")
-x/(y + exp(z))^2
> D(exp1, "z")
-x * exp(z)/(y + exp(z))^2
```

3.5.2 Converting objects

The reader has surely realized that the differences between some types of objects are small; it is thus logical that it is possible to convert an object from a type to another by changing some of its attributes. Such a conversion will be done with a function of the type `as.`*`something`*. R (version 2.1.0) has, in the

packages base and utils, 98 of such functions, so we will not go in the deepest details here.

The result of a conversion depends obviously of the attributes of the converted object. Genrally, conversion follows intuitive rules. For the conversion of modes, the following table summarizes the situation.

Conversion to	Function	Rules
numeric	`as.numeric`	`FALSE` → 0
		`TRUE` → 1
		`"1"`, `"2"`, ... → 1, 2, ...
		`"A"`, ... → `NA`
logical	`as.logical`	0 → `FALSE`
		other numbers → `TRUE`
		`"FALSE"`, `"F"` → `FALSE`
		`"TRUE"`, `"T"` → `TRUE`
		other characters → `NA`
character	`as.character`	1, 2, ... → `"1"`, `"2"`, ...
		`FALSE` → `"FALSE"`
		`TRUE` → `"TRUE"`

There are functions to convert the types of objects (`as.matrix`, `as.ts`, `as.data.frame`, `as.expression`, ...). These functions will affect attributes other than the modes during the conversion. The results are, again, generally intuitive. A situation frequently encountered is the conversion of factors into numeric values. In this case, R does the conversion with the numeric coding of the levels of the factor:

```
> fac <- factor(c(1, 10))
> fac
[1] 1 10
Levels:  1 10
> as.numeric(fac)
[1] 1 2
```

This makes sense when considering a factor of mode character:

```
> fac2 <- factor(c("Male", "Female"))
> fac2
[1] Male   Female
Levels: Female Male
> as.numeric(fac2)
[1] 2 1
```

Note that the result is not `NA` as may have been expected from the table above.

To convert a factor of mode numeric into a numeric vector but keeping the levels as they are originally specified, one must first convert into character, then into numeric.

```
> as.numeric(as.character(fac))
[1] 1 10
```

This procedure is very useful if in a file a numeric variable has also non-numeric values. We have seen that `read.table()` in such a situation will, by default, read this column as a factor.

3.5.3 Operators

We have seen previously that there are three main types of operators in R[10]. Here is the list.

Operators					
Arithmetic		Comparison		Logical	
`+`	addition	`<`	lesser than	`! x`	logical NOT
`-`	subtraction	`>`	greater than	`x & y`	logical AND
`*`	multiplication	`<=`	lesser than or equal to	`x && y`	id.
`/`	division	`>=`	greater than or equal to	`x | y`	logical OR
`^`	power	`==`	equal	`x || y`	id.
`%%`	modulo	`!=`	different	`xor(x, y)`	exclusive OR
`%/%`	integer division				

The arithmetic and comparison operators act on two elements (`x + y`, `a < b`). The arithmetic operators act not only on variables of mode numeric or complex, but also on logical variables; in this latter case, the logical values are coerced into numeric. The comparison operators may be applied to any mode: they return one or several logical values.

The logical operators are applied to one (`!`) or two objects of mode logical, and return one (or several) logical values. The operators "AND" and "OR" exist in two forms: the single one operates on each elements of the objects and returns as many logical values as comparisons done; the double one operates on the first element of the objects.

It is necessary to use the operator "AND" to specify an inequality of the type $0 < x < 1$ which will be coded with: `0 < x & x < 1`. The expression `0 < x < 1` is valid, but will not return the expected result: since both operators are the same, they are executed successively from left to right. The comparison `0 < x` is first done and returns a logical value which is then compared to 1 (`TRUE` or `FALSE < 1`): in this situation, the logical value is implicitly coerced into numeric (`1` or `0 < 1`).

[10] The following characters are also operators for R: `$`, `@`, `[`, `[[`, `:`, `?`, `<-`, `<<-`, `=`, `::`. A table of operators describing precedence rules can be found with `?Syntax`.

```
> x <- 0.5
> 0 < x < 1
[1] FALSE
```

The comparison operators operate on *each* element of the two objects being compared (recycling the values of the shortest one if necessary), and thus returns an object of the same size. To compare 'wholly' two objects, two functions are available: `identical` and `all.equal`.

```
> x <- 1:3; y <- 1:3
> x == y
[1] TRUE TRUE TRUE
> identical(x, y)
[1] TRUE
> all.equal(x, y)
[1] TRUE
```

`identical` compares the internal representation of the data and returns `TRUE` if the objects are strictly identical, and `FALSE` otherwise. `all.equal` compares the "near equality" of two objects, and returns `TRUE` or display a summary of the differences. The latter function takes the approximation of the computing process into account when comparing numeric values. The comparison of numeric values on a computer is sometimes surprising!

```
> 0.9 == (1 - 0.1)
[1] TRUE
> identical(0.9, 1 - 0.1)
[1] TRUE
> all.equal(0.9, 1 - 0.1)
[1] TRUE
> 0.9 == (1.1 - 0.2)
[1] FALSE
> identical(0.9, 1.1 - 0.2)
[1] FALSE
> all.equal(0.9, 1.1 - 0.2)
[1] TRUE
> all.equal(0.9, 1.1 - 0.2, tolerance = 1e-16)
[1] "Mean relative  difference: 1.233581e-16"
```

3.5.4 Accessing the values of an object: the indexing system

The indexing system is an efficient and flexible way to access selectively the elements of an object; it can be either *numeric* or *logical*. To access, for example, the third value of a vector `x`, we just type `x[3]` which can be used either to extract or to change this value:

```
> x <- 1:5
```

```
> x[3]
[1] 3
> x[3] <- 20
> x
[1]  1  2 20  4  5
```

The index itself can be a vector of mode numeric:

```
> i <- c(1, 3)
> x[i]
[1]  1 20
```

If `x` is a matrix or a data frame, the value of the ith line and jth column is accessed with `x[i, j]`. To access all values of a given row or column, one has simply to omit the appropriate index (without forgetting the comma!):

```
> x <- matrix(1:6, 2, 3)
> x
     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6
> x[, 3] <- 21:22
> x
     [,1] [,2] [,3]
[1,]    1    3   21
[2,]    2    4   22
> x[, 3]
[1] 21 22
```

You have certainly noticed that the last result is a vector and not a matrix. The default behaviour of R is to return an object of the lowest dimension possible. This can be altered with the option `drop` which default is `TRUE`:

```
> x[, 3, drop = FALSE]
     [,1]
[1,]   21
[2,]   22
```

This indexing system is easily generalized to arrays, with as many indices as the number of dimensions of the array (for example, a three dimensional array: `x[i, j, k]`, `x[, , 3]`, `x[, , 3, drop = FALSE]`, and so on). It may be useful to keep in mind that indexing is made with square brackets, while parentheses are used for the arguments of a function:

```
> x(1)
Error: couldn't find function "x"
```

Indexing can also be used to suppress one or several rows or columns using negative values. For example, `x[-1, ]` will suppress the first row, while `x[-c(1, 15), ]` will do the same for the 1st and 15th rows. Using the matrix defined above:

```
> x[, -1]
     [,1] [,2]
[1,]    3   21
[2,]    4   22
> x[, -(1:2)]
[1] 21 22
> x[, -(1:2), drop = FALSE]
     [,1]
[1,]   21
[2,]   22
```

For vectors, matrices and arrays, it is possible to access the values of an element with a comparison expression as the index:

```
> x <- 1:10
> x[x >= 5] <- 20
> x
 [1]  1  2  3  4 20 20 20 20 20 20
> x[x == 1] <- 25
> x
 [1] 25  2  3  4 20 20 20 20 20 20
```

A practical use of the logical indexing is, for instance, the possibility to select the even elements of an integer variable:

```
> x <- rpois(40, lambda=5)
> x
 [1]  5  9  4  7  7  6  4  5 11  3  5  7  1  5  3  9  2  2  5  2
[21]  4  6  6  5  4  5  3  4  3  3  3  7  7  3  8  1  4  2  1  4
> x[x %% 2 == 0]
 [1] 4 6 4 2 2 2 4 6 6 4 4 8 4 2 4
```

Thus, this indexing system uses the logical values returned, in the above examples, by comparison operators. These logical values can be computed beforehand, they then will be recycled if necessary:

```
> x <- 1:40
> s <- c(FALSE, TRUE)
> x[s]
 [1]  2  4  6  8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40
```

Logical indexing can also be used with data frames, but with caution since different columns of the data drame may be of different modes.

For lists, accessing the different elements (which can be any kind of object) is done either with single or with double square brackets: the difference is that with single brackets a list is returned, whereas double brackets *extract* the object from the list. The result can then be itself indexed as previously seen for vectors, matrices, etc. For instance, if the third object of a list is a vector, its ith value can be accessed using `my.list[[3]][i]`, if it is a three dimensional array using `my.list[[3]][i, j, k]`, and so on. Another difference is that `my.list[1:2]` will return a list with the first and second elements of the original list, whereas `my.list[[1:2]]` will no not give the expected result.

3.5.5 Accessing the values of an object with names

The *names* are labels of the elements of an object, and thus of mode character. They are generally optional attributes. There are several kinds of names (*names*, *colnames*, *rownames*, *dimnames*).

The *names* of a vector are stored in a vector of the same length of the object, and can be accessed with the function `names`.

```
> x <- 1:3
> names(x)
NULL
> names(x) <- c("a", "b", "c")
> x
a b c
1 2 3
> names(x)
[1] "a" "b" "c"
> names(x) <- NULL
> x
[1] 1 2 3
```

For matrices and data frames, *colnames* and *rownames* are labels of the columns and rows, respectively. They can be accessed either with their respective functions, or with `dimnames` which returns a list with both vectors.

```
> X <- matrix(1:4, 2)
> rownames(X) <- c("a", "b")
> colnames(X) <- c("c", "d")
> X
  c d
a 1 3
b 2 4
> dimnames(X)
[[1]]
[1] "a" "b"
```

```
[[2]]
[1] "c" "d"
```

For arrays, the names of the dimensions can be accessed with `dimnames`:

```
> A <- array(1:8, dim = c(2, 2, 2))
> A
, , 1

     [,1] [,2]
[1,]    1    3
[2,]    2    4

, , 2

     [,1] [,2]
[1,]    5    7
[2,]    6    8

> dimnames(A) <- list(c("a", "b"), c("c", "d"), c("e", "f"))
> A
, , e

  c d
a 1 3
b 2 4

, , f

  c d
a 5 7
b 6 8
```

If the elements of an object have names, they can be extracted by using them as indices. Actually, this should be termed 'subsetting' rather than 'extraction' since the attributes of the original object are kept. For instance, if a data frame `DF` contains the variables `x`, `y`, and `z`, the command `DF["x"]` will return a data frame with just `x`; `DF[c("x", "y")]` will return a data frame with both variables. This works with lists as well if the elements in the list have names.

As the reader surely realizes, the index used here is a vector of mode character. Like the numeric or logical vectors seen above, this vector can be defined beforehand and then used for the extraction.

To extract a vector or a factor from a data frame, on can use the operator `$` (e.g., `DF$x`). This also works with lists.

3.5.6 The data editor

It is possible to use a graphical spreadsheet-like editor to edit a "data" object. For example, if `X` is a matrix, the command `data.entry(X)` will open a graphic editor and one will be able to modify some values by clicking on the appropriate cells, or to add new columns or rows.

The function `data.entry` modifies directly the object given as argument without needing to assign its result. On the other hand, the function `de` returns a list with the objects given as arguments and possibly modified. This result is displayed on the screen by default, but, as for most functions, can be assigned to an object.

The details of using the data editor depend on the operating system.

3.5.7 Arithmetics and simple functions

There are numerous functions in R to manipulate data. We have already seen the simplest one, `c` which concatenates the objects listed in parentheses. For example:

```
> c(1:5, seq(10, 11, 0.2))
 [1]  1.0  2.0  3.0  4.0  5.0 10.0 10.2 10.4 10.6 10.8 11.0
```

Vectors can be manipulated with classical arithmetic expressions:

```
> x <- 1:4
> y <- rep(1, 4)
> z <- x + y
> z
[1] 2 3 4 5
```

Vectors of different lengths can be added; in this case, the shortest vector is recycled. Examples:

```
> x <- 1:4
> y <- 1:2
> z <- x + y
> z
[1] 2 4 4 6
> x <- 1:3
> y <- 1:2
> z <- x + y
Warning message:
longer object length
 is not a multiple of shorter object length in: x + y
> z
[1] 2 4 4
```

Note that R returned a warning message and not an error message, thus the operation has been performed. If we want to add (or multiply) the same value to all the elements of a vector:

```
> x <- 1:4
> a <- 10
> z <- a * x
> z
[1] 10 20 30 40
```

The functions available in R for manipulating data are too many to be listed here. One can find all the basic mathematical functions (`log`, `exp`, `log10`, `log2`, `sin`, `cos`, `tan`, `asin`, `acos`, `atan`, `abs`, `sqrt`, ...), special functions (`gamma`, `digamma`, `beta`, `besselI`, ...), as well as diverse functions useful in statistics. Some of these functions are listed in the following table.

`sum(x)`	sum of the elements of `x`
`prod(x)`	product of the elements of `x`
`max(x)`	maximum of the elements of `x`
`min(x)`	minimum of the elements of `x`
`which.max(x)`	returns the index of the greatest element of `x`
`which.min(x)`	returns the index of the smallest element of `x`
`range(x)`	id. than `c(min(x), max(x))`
`length(x)`	number of elements in `x`
`mean(x)`	mean of the elements of `x`
`median(x)`	median of the elements of `x`
`var(x)` or `cov(x)`	variance of the elements of `x` (calculated on $n - 1$); if `x` is a matrix or a data frame, the variance-covariance matrix is calculated
`cor(x)`	correlation matrix of `x` if it is a matrix or a data frame (1 if `x` is a vector)
`var(x, y)` or `cov(x, y)`	covariance between `x` and `y`, or between the columns of `x` and those of `y` if they are matrices or data frames
`cor(x, y)`	linear correlation between `x` and `y`, or correlation matrix if they are matrices or data frames

These functions return a single value (thus a vector of length one), except `range` which returns a vector of length two, and `var`, `cov`, and `cor` which may return a matrix. The following functions return more complex results.

`round(x, n)`	rounds the elements of `x` to `n` decimals
`rev(x)`	reverses the elements of `x`
`sort(x)`	sorts the elements of `x` in increasing order; to sort in decreasing order: `rev(sort(x))`
`rank(x)`	ranks of the elements of `x`

`log(x, base)`	computes the logarithm of `x` with base `base`
`scale(x)`	if `x` is a matrix, centers and reduces the data; to center only use the option `center=FALSE`, to reduce only `scale=FALSE` (by default `center=TRUE, scale=TRUE`)
`pmin(x,y,...)`	a vector which ith element is the minimum of `x[i]`, `y[i]`, ...
`pmax(x,y,...)`	id. for the maximum
`cumsum(x)`	a vector which ith element is the sum from `x[1]` to `x[i]`
`cumprod(x)`	id. for the product
`cummin(x)`	id. for the minimum
`cummax(x)`	id. for the maximum
`match(x, y)`	returns a vector of the same length than `x` with the elements of `x` which are in `y` (`NA` otherwise)
`which(x == a)`	returns a vector of the indices of `x` if the comparison operation is true (`TRUE`), in this example the values of `i` for which `x[i] == a` (the argument of this function must be a variable of mode logical)
`choose(n, k)`	computes the combinations of k events among n repetitions $= n!/[(n-k)!k!]$
`na.omit(x)`	suppresses the observations with missing data (`NA`) (suppresses the corresponding line if `x` is a matrix or a data frame)
`na.fail(x)`	returns an error message if `x` contains at least one `NA`
`unique(x)`	if `x` is a vector or a data frame, returns a similar object but with the duplicate elements suppressed
`table(x)`	returns a table with the numbers of the differents values of `x` (typically for integers or factors)
`table(x, y)`	contingency table of `x` and `y`
`subset(x, ...)`	returns a selection of `x` with respect to criteria (`...`, typically comparisons: `x$V1 < 10`); if `x` is a data frame, the option `select` gives the variables to be kept (or dropped using a minus sign)
`sample(x, size)`	resample randomly and without replacement `size` elements in the vector `x`, the option `replace = TRUE` allows to resample with replacement

3.5.8 Matrix computation

R has facilities for matrix computation and manipulation. The functions `rbind` and `cbind` bind matrices with respect to the lines or the columns, respectively:

```
> m1 <- matrix(1, nr = 2, nc = 2)
> m2 <- matrix(2, nr = 2, nc = 2)
> rbind(m1, m2)
     [,1] [,2]
[1,]    1    1
[2,]    1    1
[3,]    2    2
[4,]    2    2
> cbind(m1, m2)
     [,1] [,2] [,3] [,4]
```

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

The operator for the product of two matrices is '`%*%`'. For example, considering the two matrices `m1` and `m2` above:

```
> rbind(m1, m2) %*% cbind(m1, m2)
     [,1] [,2] [,3] [,4]
[1,]    2    2    4    4
[2,]    2    2    4    4
[3,]    4    4    8    8
[4,]    4    4    8    8
> cbind(m1, m2) %*% rbind(m1, m2)
     [,1] [,2]
[1,]   10   10
[2,]   10   10
```

The transposition of a matrix is done with the function `t`; this function works also with a data frame.

The function `diag` can be used to extract or modify the diagonal of a matrix, or to build a diagonal matrix.

```
> diag(m1)
[1] 1 1
> diag(rbind(m1, m2) %*% cbind(m1, m2))
[1] 2 2 8 8
> diag(m1) <- 10
> m1
     [,1] [,2]
[1,]   10    1
[2,]    1   10
> diag(3)
     [,1] [,2] [,3]
[1,]    1    0    0
[2,]    0    1    0
[3,]    0    0    1
> v <- c(10, 20, 30)
> diag(v)
     [,1] [,2] [,3]
[1,]   10    0    0
[2,]    0   20    0
[3,]    0    0   30
> diag(2.1, nr = 3, nc = 5)
     [,1] [,2] [,3] [,4] [,5]
[1,]  2.1  0.0  0.0    0    0
[2,]  0.0  2.1  0.0    0    0
[3,]  0.0  0.0  2.1    0    0
```

R has also some special functions for matrix computation. We can cite here `solve` for inverting a matrix, `qr` for decomposition, `eigen` for computing eigenvalues and eigenvectors, and `svd` for singular value decomposition.

4 Graphics with R

R offers a remarkable variety of graphics. To get an idea, one can type `demo(graphics)` or `demo(persp)`. It is not possible to detail here the possibilities of R in terms of graphics, particularly since each graphical function has a large number of options making the production of graphics very flexible.

The way graphical functions work deviates substantially from the scheme sketched at the beginning of this document. Particularly, the result of a graphical function cannot be assigned to an object[11] but is sent to a *graphical device*. A graphical device is a graphical window or a file.

There are two kinds of graphical functions: the *high-level plotting functions* which create a new graph, and the *low-level plotting functions* which add elements to an existing graph. The graphs are produced with respect to *graphical parameters* which are defined by default and can be modified with the function `par`.

We will see in a first time how to manage graphics and graphical devices; we will then somehow detail the graphical functions and parameters. We will see a practical example of the use of these functionalities in producing graphs. Finally, we will see the packages grid and lattice whose functioning is different from the one summarized above.

4.1 Managing graphics

4.1.1 Opening several graphical devices

When a graphical function is executed, if no graphical device is open, R opens a graphical window and displays the graph. A graphical device may be open with an appropriate function. The list of available graphical devices depends on the operating system. The graphical windows are called `X11` under Unix/Linux and `windows` under Windows. In all cases, one can open a graphical window with the command `x11()` which also works under Windows because of an alias towards the command `windows()`. A graphical device which is a file will be open with a function depending on the format: `postscript()`, `pdf()`, `png()`, ... The list of available graphical devices can be found with `?device`.

The last open device becomes the active graphical device on which all subsequent graphs are displayed. The function `dev.list()` displays the list of open devices:

```
> x11(); x11(); pdf()
> dev.list()
```

[11] There are a few remarkable exceptions: `hist()` and `barplot()` produce also numeric results as lists or matrices.

```
X11 X11 pdf
  2   3   4
```

The figures displayed are the device numbers which must be used to change the active device. To know what is the active device:

```
> dev.cur()
pdf
  4
```

and to change the active device:

```
> dev.set(3)
X11
  3
```

The function `dev.off()` closes a device: by default the active device is closed, otherwise this is the one which number is given as argument to the function. R then displays the number of the new active device:

```
> dev.off(2)
X11
  3
> dev.off()
pdf
  4
```

Two specific features of the Windows version of R are worth mentioning: a Windows Metafile device can be open with the function `win.metafile`, and a menu "History" displayed when the graphical window is selected allowing recording of all graphs drawn during a session (by default, the recording system is off, the user switches it on by clicking on "Recording" in this menu).

4.1.2 Partitioning a graphic

The function `split.screen` partitions the active graphical device. For example:

```
> split.screen(c(1, 2))
```

divides the device into two parts which can be selected with `screen(1)` or `screen(2)`; `erase.screen()` deletes the last drawn graph. A part of the device can itself be divided with `split.screen()` leading to the possibility to make complex arrangements.

These functions are incompatible with others (such as `layout` or `coplot`) and must not be used with multiple graphical devices. Their use should be limited, for instance, to graphical exploration of data.

The function `layout` partitions the active graphic window in several parts where the graphs will be displayed successively. Its main argument is a matrix with integer numbers indicating the numbers of the "sub-windows". For example, to divide the device into four equal parts:

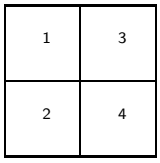
```
> layout(matrix(1:4, 2, 2))
```

It is of course possible to create this matrix previously allowing to better visualize how the device is divided:

```
> mat <- matrix(1:4, 2, 2)
> mat
     [,1] [,2]
[1,]    1    3
[2,]    2    4
> layout(mat)
```

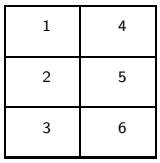
To actually visualize the partition created, one can use the function `layout.show` with the number of sub-windows as argument (here 4). In this example, we will have:

```
> layout.show(4)
```

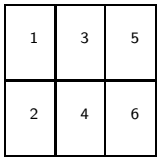


The following examples show some of the possibilities offered by `layout()`.

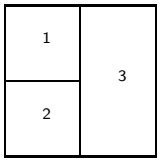
```
> layout(matrix(1:6, 3, 2))
> layout.show(6)
```




```
> layout(matrix(1:6, 2, 3))
> layout.show(6)
```




```
> m <- matrix(c(1:3, 3), 2, 2)
> layout(m)
> layout.show(3)
```

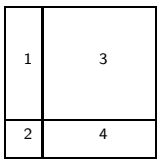


In all these examples, we have not used the option `byrow` of `matrix()`, the sub-windows are thus numbered column-wise; one can just specify `matrix(..., byrow=TRUE)` so that the sub-windows are numbered row-wise. The numbers

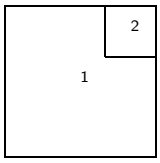
in the matrix may also be given in any order, for example, `matrix(c(2, 1, 4, 3), 2, 2)`.

By default, `layout()` partitions the device with regular heights and widths: this can be modified with the options `widths` and `heights`. These dimensions are given relatively[12]. Examples:

```
> m <- matrix(1:4, 2, 2)
> layout(m, widths=c(1, 3),
          heights=c(3, 1))
> layout.show(4)
```

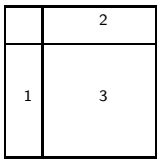



```
> m <- matrix(c(1,1,2,1),2,2)
> layout(m, widths=c(2, 1),
          heights=c(1, 2))
> layout.show(2)
```

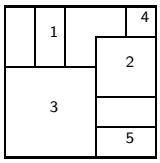


Finally, the numbers in the matrix can include zeros giving the possibility to make complex (or even esoterical) partitions.

```
> m <- matrix(0:3, 2, 2)
> layout(m, c(1, 3), c(1, 3))
> layout.show(3)
```




```
> m <- matrix(scan(), 5, 5)
1:  0 0 3 3 3 1 1 3 3 3
11:  0 0 3 3 3 0 2 2 0 5
21:  4 2 2 0 5
26:
Read 25 items
> layout(m)
> layout.show(5)
```



[12] They can be given in centimetres, see `?layout`.

4.2 Graphical functions

Here is an overview of the high-level graphical functions in R.

`plot(x)`	plot of the values of `x` (on the y-axis) ordered on the x-axis
`plot(x, y)`	bivariate plot of `x` (on the x-axis) and `y` (on the y-axis)
`sunflowerplot(x, y)`	id. but the points with similar coordinates are drawn as a flower which petal number represents the number of points
`pie(x)`	circular pie-chart
`boxplot(x)`	"box-and-whiskers" plot
`stripchart(x)`	plot of the values of `x` on a line (an alternative to `boxplot()` for small sample sizes)
`coplot(x~y | z)`	bivariate plot of `x` and `y` for each value (or interval of values) of `z`
`interaction.plot (f1, f2, y)`	if `f1` and `f2` are factors, plots the means of `y` (on the y-axis) with respect to the values of `f1` (on the x-axis) and of `f2` (different curves); the option `fun` allows to choose the summary statistic of `y` (by default `fun=mean`)
`matplot(x,y)`	bivariate plot of the first column of `x` *vs.* the first one of `y`, the second one of `x` *vs.* the second one of `y`, etc.
`dotchart(x)`	if `x` is a data frame, plots a Cleveland dot plot (stacked plots line-by-line and column-by-column)
`fourfoldplot(x)`	visualizes, with quarters of circles, the association between two dichotomous variables for different populations (`x` must be an array with `dim=c(2, 2, k)`, or a matrix with `dim=c(2, 2)` if $k = 1$)
`assocplot(x)`	Cohen–Friendly graph showing the deviations from independence of rows and columns in a two dimensional contingency table
`mosaicplot(x)`	'mosaic' graph of the residuals from a log-linear regression of a contingency table
`pairs(x)`	if `x` is a matrix or a data frame, draws all possible bivariate plots between the columns of `x`
`plot.ts(x)`	if `x` is an object of class `"ts"`, plot of `x` with respect to time, `x` may be multivariate but the series must have the same frequency and dates
`ts.plot(x)`	id. but if `x` is multivariate the series may have different dates and must have the same frequency
`hist(x)`	histogram of the frequencies of `x`
`barplot(x)`	histogram of the values of `x`
`qqnorm(x)`	quantiles of `x` with respect to the values expected under a normal law
`qqplot(x, y)`	quantiles of `y` with respect to the quantiles of `x`
`contour(x, y, z)`	contour plot (data are interpolated to draw the curves), `x` and `y` must be vectors and `z` must be a matrix so that `dim(z)=c(length(x), length(y))` (`x` and `y` may be omitted)
`filled.contour (x, y, z)`	id. but the areas between the contours are coloured, and a legend of the colours is drawn as well
`image(x, y, z)`	id. but the actual data are represented with colours
`persp(x, y, z)`	id. but in perspective
`stars(x)`	if `x` is a matrix or a data frame, draws a graph with segments or a star where each row of `x` is represented by a star and the columns are the lengths of the segments

`symbols(x, y, ...)`	draws, at the coordinates given by `x` and `y`, symbols (circles, squares, rectangles, stars, thermometres or "boxplots") which sizes, colours, etc, are specified by supplementary arguments
`termplot(mod.obj)`	plot of the (partial) effects of a regression model (`mod.obj`)

For each function, the options may be found with the on-line help in R. Some of these options are identical for several graphical functions; here are the main ones (with their possible default values):

`add=FALSE`	if `TRUE` superposes the plot on the previous one (if it exists)
`axes=TRUE`	if `FALSE` does not draw the axes and the box
`type="p"`	specifies the type of plot, `"p"`: points, `"l"`: lines, `"b"`: points connected by lines, `"o"`: id. but the lines are over the points, `"h"`: vertical lines, `"s"`: steps, the data are represented by the top of the vertical lines, `"S"`: id. but the data are represented by the bottom of the vertical lines
`xlim=, ylim=`	specifies the lower and upper limits of the axes, for example with `xlim=c(1, 10)` or `xlim=range(x)`
`xlab=, ylab=`	annotates the axes, must be variables of mode character
`main=`	main title, must be a variable of mode character
`sub=`	sub-title (written in a smaller font)

4.3 Low-level plotting commands

R has a set of graphical functions which affect an already existing graph: they are called *low-level plotting commands*. Here are the main ones:

`points(x, y)`	adds points (the option `type=` can be used)
`lines(x, y)`	id. but with lines
`text(x, y, labels, ...)`	adds text given by `labels` at coordinates (`x`,`y`); a typical use is: `plot(x, y, type="n"); text(x, y, names)`
`mtext(text, side=3, line=0, ...)`	adds text given by `text` in the margin specified by `side` (see `axis()` below); `line` specifies the line from the plotting area
`segments(x0, y0, x1, y1)`	draws lines from points (`x0`,`y0`) to points (`x1`,`y1`)
`arrows(x0, y0, x1, y1, angle= 30, code=2)`	id. with arrows at points (`x0`,`y0`) if `code=2`, at points (`x1`,`y1`) if `code=1`, or both if `code=3`; `angle` controls the angle from the shaft of the arrow to the edge of the arrow head
`abline(a,b)`	draws a line of slope `b` and intercept `a`
`abline(h=y)`	draws a horizontal line at ordinate `y`
`abline(v=x)`	draws a vertical line at abcissa `x`
`abline(lm.obj)`	draws the regression line given by `lm.obj` (see section 5)

`rect(x1, y1, x2, y2)`	draws a rectangle which left, right, bottom, and top limits are `x1`, `x2`, `y1`, and `y2`, respectively
`polygon(x, y)`	draws a polygon linking the points with coordinates given by `x` and `y`
`legend(x, y, legend)`	adds the legend at the point (`x`,`y`) with the symbols given by `legend`
`title()`	adds a title and optionally a sub-title
`axis(side, vect)`	adds an axis at the bottom (`side=1`), on the left (`2`), at the top (`3`), or on the right (`4`); `vect` (optional) gives the abcissa (or ordinates) where tick-marks are drawn
`box()`	adds a box around the current plot
`rug(x)`	draws the data `x` on the x-axis as small vertical lines
`locator(n, type="n", ...)`	returns the coordinates (x, y) after the user has clicked `n` times on the plot with the mouse; also draws symbols (`type="p"`) or lines (`type="l"`) with respect to optional graphic parameters (`...`); by default nothing is drawn (`type="n"`)

Note the possibility to add mathematical expressions on a plot with `text(x, y, expression(...))`, where the function `expression` transforms its argument in a mathematical equation. For example,

```
> text(x, y, expression(p == over(1, 1+e^-(beta*x+alpha))))
```

will display, on the plot, the following equation at the point of coordinates (x, y):

$$\mathrm{p} = \frac{1}{1 + \mathrm{e}^{-(\beta \mathrm{x} + \alpha)}}$$

To include in an expression a variable we can use the functions `substitute` and `as.expression`; for example to include a value of R^2 (previously computed and stored in an object named `Rsquared`):

```
> text(x, y, as.expression(substitute(R^2==r, list(r=Rsquared))))
```

will display on the plot at the point of coordinates (x, y):

$$\mathrm{R}^2 = 0.9856298$$

To display only three decimals, we can modify the code as follows:

```
> text(x, y, as.expression(substitute(R^2==r,
+                           list(r=round(Rsquared, 3)))))
```

will display:

$$\mathrm{R}^2 = 0.986$$

Finally, to write the R in italics:

```
> text(x, y, as.expression(substitute(italic(R)^2==r,
+                           list(r=round(Rsquared, 3)))))
```

$$R^2 = 0.986$$

4.4 Graphical parameters

In addition to low-level plotting commands, the presentation of graphics can be improved with graphical parameters. They can be used either as options of graphic functions (but it does not work for all), or with the function `par` to change permanently the graphical parameters, i.e. the subsequent plots will be drawn with respect to the parameters specified by the user. For instance, the following command:

```
> par(bg="yellow")
```

will result in all subsequent plots drawn with a yellow background. There are 73 graphical parameters, some of them have very similar functions. The exhaustive list of these parameters can be read with `?par`; I will limit the following table to the most usual ones.

`adj`	controls text justification with respect to the left border of the text so that `0` is left-justified, `0.5` is centred, `1` is right-justified, values > 1 move the text further to the left, and negative values further to the right; if two values are given (e.g., `c(0, 0)`) the second one controls vertical justification with respect to the text baseline
`bg`	specifies the colour of the background (e.g., `bg="red"`, `bg="blue"`; the list of the 657 available colours is displayed with `colors()`)
`bty`	controls the type of box drawn around the plot, allowed values are: `"o"`, `"l"`, `"7"`, `"c"`, `"u"` ou `"]"` (the box looks like the corresponding character); if `bty="n"` the box is not drawn
`cex`	a value controlling the size of texts and symbols with respect to the default; the following parameters have the same control for numbers on the axes, `cex.axis`, the axis labels, `cex.lab`, the title, `cex.main`, and the sub-title, `cex.sub`
`col`	controls the colour of symbols; as for `cex` there are: `col.axis`, `col.lab`, `col.main`, `col.sub`
`font`	an integer which controls the style of text (`1`: normal, `2`: italics, `3`: bold, `4`: bold italics); as for `cex` there are: `font.axis`, `font.lab`, `font.main`, `font.sub`
`las`	an integer which controls the orientation of the axis labels (`0`: parallel to the axes, `1`: horizontal, `2`: perpendicular to the axes, `3`: vertical)
`lty`	controls the type of lines, can be an integer (`1`: solid, `2`: dashed, `3`: dotted, `4`: dotdash, `5`: longdash, `6`: twodash), or a string of up to eight characters (between `"0"` and `"9"`) which specifies alternatively the length, in points or pixels, of the drawn elements and the blanks, for example `lty="44"` will have the same effet than `lty=2`
`lwd`	a numeric which controls the width of lines
`mar`	a vector of 4 numeric values which control the space between the axes and the border of the graph of the form `c(bottom, left, top, right)`, the default values are `c(5.1, 4.1, 4.1, 2.1)`
`mfcol`	a vector of the form `c(nr,nc)` which partitions the graphic window as a matrix of `nr` lines and `nc` columns, the plots are then drawn in columns (see section 4.1.2)
`mfrow`	id. but the plots are then drawn in line (see section 4.1.2)
`pch`	controls the type of symbol, either an integer between 1 and 25, or any single character within `""` (Fig. 2)
`ps`	an integer which controls the size in points of texts and symbols

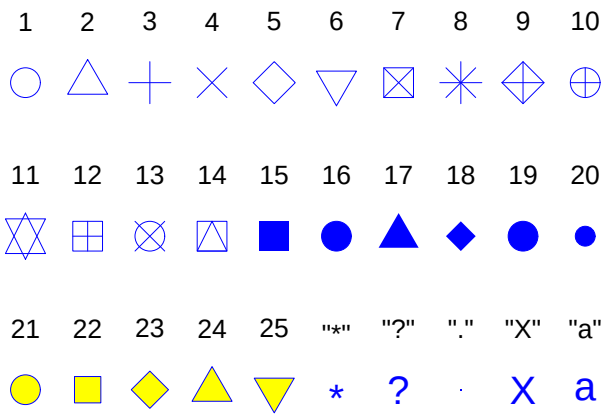


Figure 2: The plotting symbols in R (`pch=1:25`). The colours were obtained with the options `col="blue", bg="yellow"`, the second option has an effect only for the symbols 21–25. Any character can be used (`pch="*"`, `"?"`, `"."`, ...).

`pty`	a character which specifies the type of the plotting region, `"s"`: square, `"m"`: maximal
`tck`	a value which specifies the length of tick-marks on the axes as a fraction of the smallest of the width or height of the plot; if `tck=1` a grid is drawn
`tcl`	id. but as a fraction of the height of a line of text (by default `tcl=-0.5`)
`xaxt`	if `xaxt="n"` the x-axis is set but not drawn (useful in conjunction with `axis(side=1, ...)`)
`yaxt`	if `yaxt="n"` the y-axis is set but not drawn (useful in conjunction with `axis(side=2, ...)`)

4.5 A practical example

In order to illustrate R's graphical functionalities, let us consider a simple example of a bivariate graph of 10 pairs of random variates. These values were generated with:

```
> x <- rnorm(10)
> y <- rnorm(10)
```

The wanted graph will be obtained with `plot()`; one will type the command:

```
> plot(x, y)
```

and the graph will be plotted on the active graphical device. The result is shown on Fig. 3. By default, R makes graphs in an "intelligent" way:

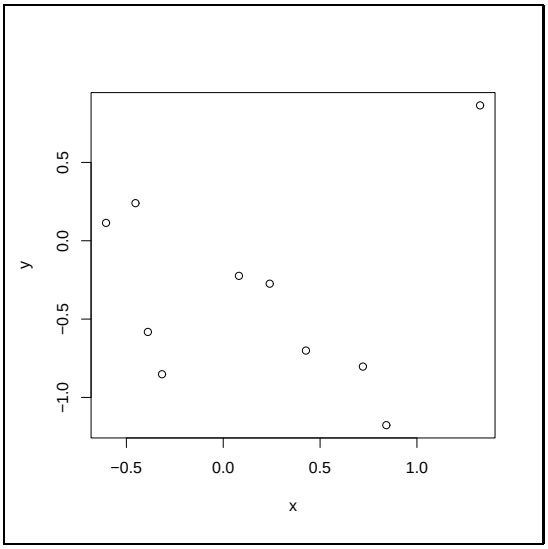


Figure 3: The function `plot` used without options.

the spaces between tick-marks on the axes, the placement of labels, etc, are calculated so that the resulting graph is as intelligible as possible.

The user may, nevertheless, change the way a graph is presented, for instance, to conform to a pre-defined editorial style, or to give it a personal touch for a talk. The simplest way to change the presentation of a graph is to add options which will modify the default arguments. In our example, we can modify significantly the figure in the following way:

```
plot(x, y, xlab="Ten random values", ylab="Ten other values",
     xlim=c(-2, 2), ylim=c(-2, 2), pch=22, col="red",
     bg="yellow", bty="l", tcl=0.4,
     main="How to customize a plot with R", las=1, cex=1.5)
```

The result is on Fig. 4. Let us detail each of the used options. First, `xlab` and `ylab` change the axis labels which, by default, were the names of the variables. Then, `xlim` and `ylim` allow us to define the limits on both axes[13]. The graphical parameter `pch` is used here as an option: `pch=22` specifies a square which contour and background colours may be different and are given by, respectively, `col` and `bg`. The table of graphical parameters gives the meaning of the modifications done by `bty`, `tcl`, `las` and `cex`. Finally, a title is added with the option `main`.

The graphical parameters and the low-level plotting functions allow us to go further in the presentation of a graph. As we have seen previously, some graphical parameters cannot be passed as arguments to a function like `plot`.

[13]By default, R adds 4% on each side of the axis limit. This behaviour may be altered by setting the graphical parameters `xaxs="i"` and `yaxs="i"` (they can be passed as options to `plot()`).

Figure 4: The function `plot` used with options.

We will now modify some of these parameters with `par()`, it is thus necessary to type several commands. When the graphical parameters are changed, it is useful to save their initial values beforehand to be able to restore them afterwards. Here are the commands used to obtain Fig. 5.

```
opar <- par()
par(bg="lightyellow", col.axis="blue", mar=c(4, 4, 2.5, 0.25))
plot(x, y, xlab="Ten random values", ylab="Ten other values",
     xlim=c(-2, 2), ylim=c(-2, 2), pch=22, col="red", bg="yellow",
     bty="l", tcl=-.25, las=1, cex=1.5)
title("How to customize a plot with R (bis)", font.main=3, adj=1)
par(opar)
```

Let us detail the actions resulting from these commands. First, the default graphical parameters are copied in a list called here `opar`. Three parameters will be then modified: `bg` for the colour of the background, `col.axis` for the colour of the numbers on the axes, and `mar` for the sizes of the margins around the plotting region. The graph is drawn in a nearly similar way to Fig. 4. The modifications of the margins allowed to use the space around the plotting area. The title here is added with the low-level plotting function `title` which allows to give some parameters as arguments without altering the rest of the graph. Finally, the initial graphical parameters are restored with the last command.

Now, total control! On Fig. 5, R still determines a few things such as the number of tick marks on the axes, or the space between the title and the plotting area. We will see now how to totally control the presentation of the graph. The approach used here is to plot a "blank" graph with `plot(..., type="n")`, then to add points, axes, labels, etc, with low-level plotting func-

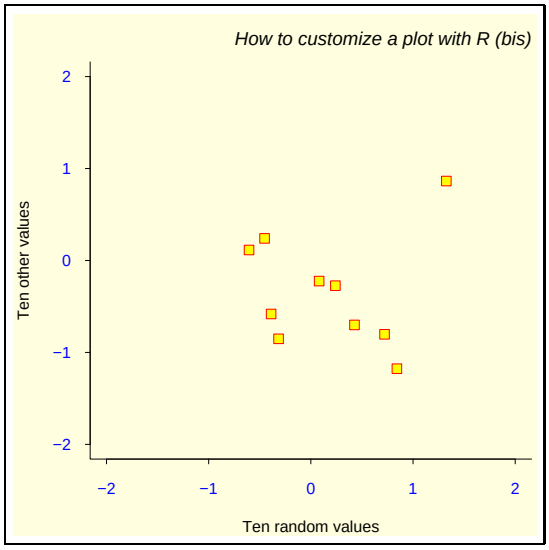


Figure 5: The functions `par`, `plot` and `title`.

tions. We will fancy a few arrangements such as changing the colour of the plotting area. The commands follow, and the resulting graph is on Fig. 6.

```
opar <- par()
par(bg="lightgray", mar=c(2.5, 1.5, 2.5, 0.25))
plot(x, y, type="n", xlab="", ylab="", xlim=c(-2, 2),
     ylim=c(-2, 2), xaxt="n", yaxt="n")
rect(-3, -3, 3, 3, col="cornsilk")
points(x, y, pch=10, col="red", cex=2)
axis(side=1, c(-2, 0, 2), tcl=-0.2, labels=FALSE)
axis(side=2, -1:1, tcl=-0.2, labels=FALSE)
title("How to customize a plot with R (ter)",
      font.main=4, adj=1, cex.main=1)
mtext("Ten random values", side=1, line=1, at=1, cex=0.9, font=3)
mtext("Ten other values", line=0.5, at=-1.8, cex=0.9, font=3)
mtext(c(-2, 0, 2), side=1, las=1, at=c(-2, 0, 2), line=0.3,
      col="blue", cex=0.9)
mtext(-1:1, side=2, las=1, at=-1:1, line=0.2, col="blue", cex=0.9)
par(opar)
```

Like before, the default graphical parameters are saved, and the colour of the background and the margins are modified. The graph is then drawn with `type="n"` to not plot the points, `xlab="", ylab=""` to not write the axis labels, and `xaxt="n", yaxt="n"` to not draw the axes. This results in drawing only the box around the plotting area, and defining the axes with respect to `xlim` et `ylim`. Note that we could have used the option `axes=FALSE` but in this case neither the axes, nor the box would have been drawn.

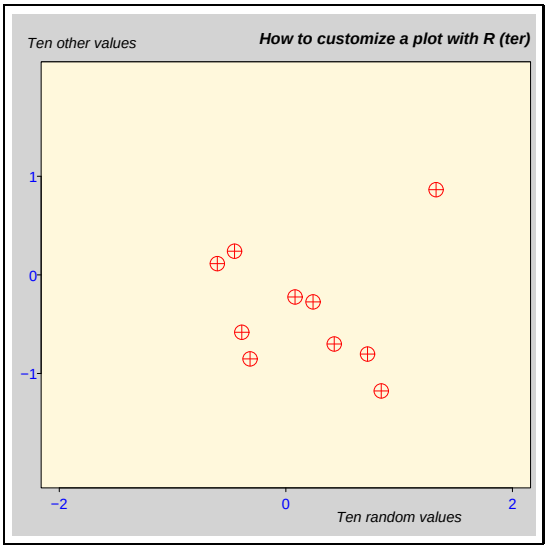


Figure 6: A "hand-made" graph.

The elements are then added in the plotting region so defined with some low-level plotting functions. Before adding the points, the colour inside the plotting area is changed with `rect()`: the size of the rectangle are chosen so that it is substantially larger than the plotting area.

The points are plotted with `points()`; a new symbol was used. The axes are added with `axis()`: the vector given as second argument specifies the coordinates of the tick-marks. The option `labels=FALSE` specifies that no annotation must be written with the tick-marks. This option also accepts a vector of mode character, for example `labels=c("A", "B", "C")`.

The title is added with `title()`, but the font is slightly changed. The annotations on the axes are written with `mtext()` (*marginal text*). The first argument of this function is a vector of mode character giving the text to be written. The option `line` indicates the distance from the plotting area (by default `line=0`), and `at` the coordinnate. The second call to `mtext()` uses the default value of `side` (3). The two other calls to `mtext()` pass a numeric vector as first argument: this will be converted into character.

4.6 The grid and lattice packages

The packages grid and lattice implement the grid and lattice systems. Grid is a new graphical mode with its own system of graphical parameters which are distinct from those seen above. The two main distinctions of grid compared to the base graphics are:

- a more flexible way to split graphical devices using *viewports* which could be overpalling (graphical objects may even be shared among distinct viewports, e.g., arrows);

- graphical objects (*grob*) may be modified or removed from a graph without requiring the re-draw all the graph (as must be done with base graphics).

Grid graphics cannot usually be combined or mixed with base graphics (the gridBase package must be used to do this). However, it is possible to use both graphical modes in the same session on the same graphical device.

Lattice is essentially the implementation in R of the Trellis graphics of S-PLUS. Trellis is an approach for visualizing multivariate data which is particularly appropriate for the exploration of relations or interactions among variables[14]. The main idea behind lattice (and Trellis as well) is that of conditional multiple graphs: a bivariate graph will be split in several graphs with respect to the values of a third variable. The function `coplot` uses a similar approach, but lattice offers much wider functionalities. Lattice uses the grid graphical mode.

Most functions in lattice take a formula as their main argument[15], for example `y ~ x`. The formula `y ~ x | z` means that the graph of `y` with respect to `x` will be plotted as several graphs with respect to the values of `z`.

The following table gives the main functions in lattice. The formula given as argument is the typical necessary formula, but all these functions accept a conditional formula (`y ~ x | z`) as main argument; in the latter case, a multiple graph, with respect to the values of `z`, is plotted as will be seen in the examples below.

`barchart(y ~ x)`	histogram of the values of `y` with respect to those of `x`
`bwplot(y ~ x)`	"box-and-whiskers" plot
`densityplot(~ x)`	density functions plot
`dotplot(y ~ x)`	Cleveland dot plot (stacked plots line-by-line and column-by-column)
`histogram(~ x)`	histogram of the frequencies of `x`
`qqmath(~ x)`	quantiles of `x` with respect to the values expected under a theoretical distribution
`stripplot(y ~ x)`	single dimension plot, `x` must be numeric, `y` may be a factor
`qq(y ~ x)`	quantiles to compare two distributions, `x` must be numeric, `y` may be numeric, character, or factor but must have two 'levels'
`xyplot(y ~ x)`	bivariate plots (with many functionalities)
`levelplot(z ~ x*y)` `contourplot(z ~ x*y)`	coloured plot of the values of `z` at the coordinates given by `x` and `y` (`x`, `y` and `z` are all of the same length)
`cloud(z ~ x*y)`	3-D perspective plot (points)
`wireframe(z ~ x*y)`	id. (surface)
`splom(~ x)`	matrix of bivariate plots
`parallel(~ x)`	parallel coordinates plot

Let us see now some examples in order to illustrate a few aspects of lattice. The package must be loaded in memory with the command `library(lattice)`

[14] http://cm.bell-labs.com/cm/ms/departments/sia/project/trellis/index.html

[15] `plot()` also accepts a formula as its main argument: if `x` and `y` are two vectors of the same length, `plot(y ~ x)` and `plot(x, y)` will give identical graphs.

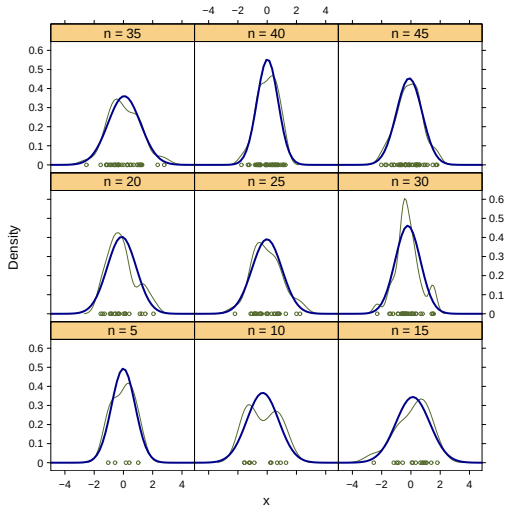


Figure 7: The function `densityplot`.

so that the functions can be accessed.

Let us start with the graphs of density functions. Such graphs can be done simply with `densityplot(~ x)` which will plot a curve of the empirical density function with the points corresponding to the observations on the x-axis (similarly to `rug()`). Our example will be slightly more complicated with the superposition, on each plot, of the curves of empirical density and those predicted from a normal law. It is necessary to use the argument `panel` which defines what is drawn on each plot. The commands are:

```
n <- seq(5, 45, 5)
x <- rnorm(sum(n))
y <- factor(rep(n, n), labels=paste("n =", n))
densityplot(~ x | y,
            panel = function(x, ...) {
                panel.densityplot(x, col="DarkOliveGreen", ...)
                panel.mathdensity(dmath=dnorm,
                                  args=list(mean=mean(x), sd=sd(x)),
                                  col="darkblue")
            })
```

The first three lines of command generate a random sample of independent normal variates which is split in sub-samples of size equal to 5, 10, 15, ..., and 45. Then comes the call to `densityplot` producing a plot for each sub-sample. `panel` takes as argument a function. In our example, we have defined a function which calls two functions pre-defined in lattice: `panel.densityplot` to draw the empirical density function, and `panel.mathdensity` to draw the density function predicted from a normal law. The function `panel.densityplot` is called by default if no argument is given to `panel`: the command `densityplot`

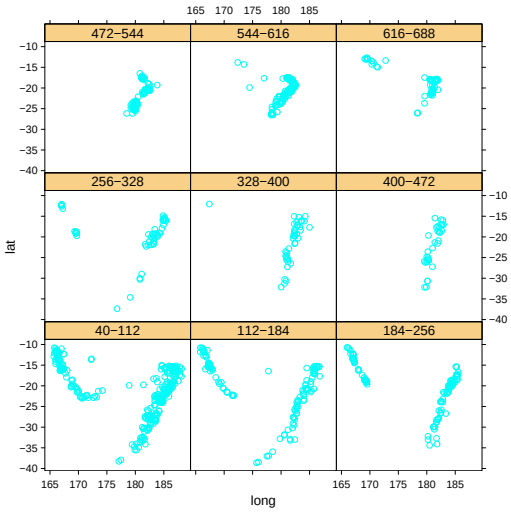


Figure 8: The function `xyplot` with the data "quakes".

`(~ x | y)` would have resulted in the same graph than Fig. 7 but without the blue curves.

The next examples are taken, more or less modified, from the help pages of lattice, and use some data sets available in R: the locations of 1000 seismic events near the Fiji Islands, and some flower measurements made on three species of iris.

Fig. 8 shows the geographic locations of the seismic events with respect to depth. The commands necessary for this graph are:

```
data(quakes)
mini <- min(quakes$depth)
maxi <- max(quakes$depth)
int <- ceiling((maxi - mini)/9)
inf <- seq(mini, maxi, int)
quakes$depth.cat <- factor(floor(((quakes$depth - mini) / int)),
                      labels=paste(inf, inf + int, sep="-"))
xyplot(lat ~ long | depth.cat, data = quakes)
```

The first command loads the data `quakes` in memory. The five next commands create a factor by dividing the depth (variable `depth`) in nine equally-ranged intervals: the levels of this factor are labelled with the lower and upper bounds of these intervals. It then suffices to call the function `xyplot` with the appropriate formula and an argument `data` indicating where `xyplot` must look for the variables[16].

With the data `iris`, the overlap among the different species is sufficiently small so they can be plotted on the figure (Fig. 9). The commands are:

[16] `plot()` cannot take an argument `data`, the location of the variables must be given explicitly, for example `plot(quakes$long ~ quakes$lat)`.

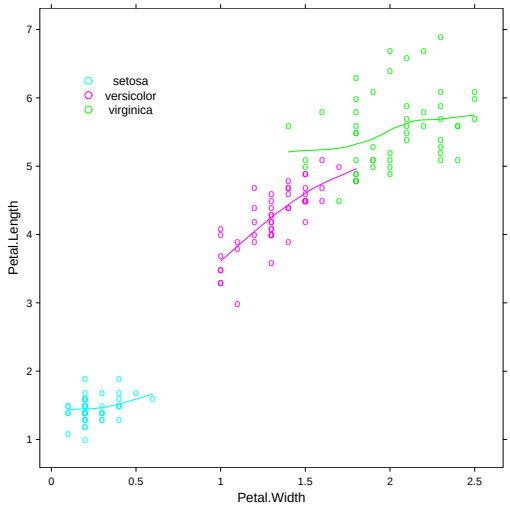


Figure 9: The function `xyplot` with the data "iris".

```
data(iris)
xyplot(
  Petal.Length ~ Petal.Width, data = iris, groups=Species,
  panel = panel.superpose,
  type = c("p", "smooth"), span=.75,
  auto.key = list(x = 0.15, y = 0.85)
)
```

The call to the function `xyplot` is here a bit more complex than in the previous example and uses several options that we will detail. The option `groups`, as suggested by its name, defines groups that will be used by the other options. We have already seen the option `panel` which defines how the different groups will be represented on the graph: we use here a pre-defined function `panel.superpose` in order to superpose the groups on the same plot. No option is passed to `panel.superpose`, the default colours will be used to distinguish the groups. The option `type`, like in `plot()`, specifies how the data are represented, but here we can give several arguments as a vector: `"p"` to draw points and `"smooth"` to draw a smooth curve which degree of smoothness is specified by `span`. The option `auto.key` adds a legend to the graph: it is only necessary to give, as a list, the coordinates where the legend is to be plotted. Note that here these coordinates are relative to the size of the plot (i.e. in [0, 1]).

We will see now the function `splom` with the same data on iris. The following commands were used to produce Fig. 10:

```
splom(
  ~iris[1:4], groups = Species, data = iris, xlab = "",
  panel = panel.superpose,
```

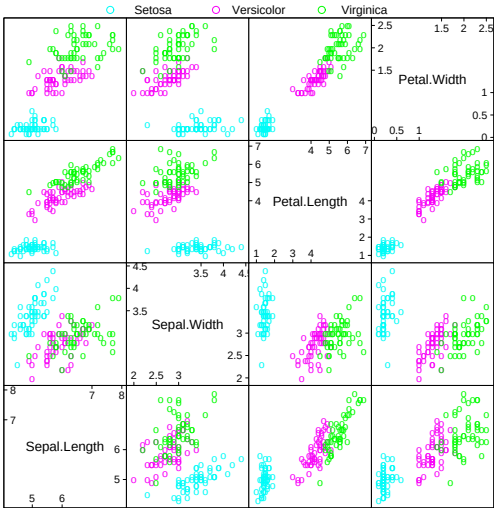


Figure 10: The function `splom` with the data "iris" (1).

```
  auto.key = list(columns = 3)
)
```

The main argument is this time a matrix (the four first columns of `iris`). The result is the set of possible bivariate plots among the columns of the matrix, like the standard function `pairs`. By default, `splom` adds the text "Scatter Plot Matrix" under the x-axis: to avoid this, the option `xlab=""` was used. The other options are similar to the previous example, except that `columns = 3` for `auto.key` was specified so the legend is displayed in three columns.

Fig. 10 could have been done with `pairs()`, but this latter function cannot make conditional graphs like on Fig. 11. The code used is relatively simple:

```
splom(~iris[1:3] | Species, data = iris, pscales = 0,
      varnames = c("Sepal\nLength", "Sepal\nWidth", "Petal\nLength"))
```

The sub-graphs being relatively small, we added two options to improve the legibility of the figure: `pscales = 0` removes the tick-marks on the axes (all sub-graphs are drawn on the same scales), and the names of the variables were re-defined to display them on two lines (`"\n"` codes for a line break in a character string).

The last example uses the method of parallel coordinates for the exploratory analysis of multivariate data. The variables are arranged on an axis (e.g., the y-axis), and the observed values are plotted on the other axis (the variables are scaled similarly, e.g., by standardizing them). The different values of the same individual are joined by a line. With the data `iris`, Fig. 12 is obtained with the following code:

```
parallel(~iris[, 1:4] | Species, data = iris, layout = c(3, 1))
```

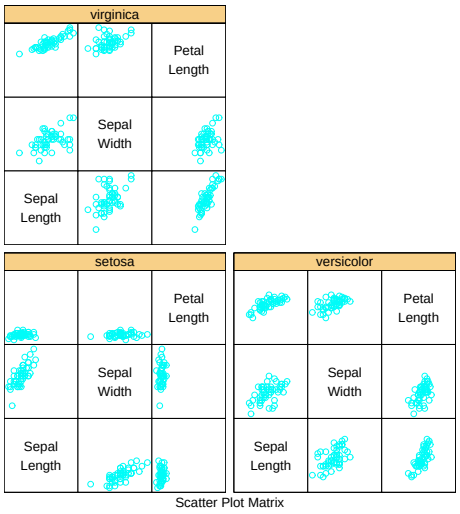


Figure 11: The function `splom` with the data "iris" (2).

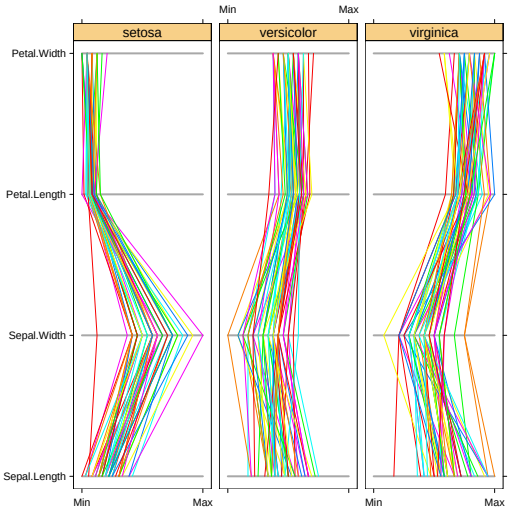


Figure 12: The function `parallel` with the data "iris".

5 Statistical analyses with R

Even more than for graphics, it is impossible here to go in the details of the possibilities offered by R with respect to statistical analyses. My goal here is to give some landmarks with the aim to have an idea of the features of R to perform data analyses.

The package stats contains functions for a wide range of basic statistical analyses: classical tests, linear models (including least-squares regression, generalized linear models, and analysis of variance), distributions, summary statistics, hierarchical clustering, time-series analysis, nonlinear least squares, and multivariate analysis. Other statistical methods are available in a large number of packages. Some of them are distributed with a base installation of R and are labelled *recommanded*, and many other packages are *contributed* and must be installed by the user.

We will start with a simple example which requires no other package than stats in order to introduce the general approach to data analysis in R. Then, we will detail some notions, *formulae* and *generic functions*, which are useful whatever the type of analysis performed. We will conclude with an overview on packages.

5.1 A simple example of analysis of variance

The function for the analysis of variance in stats is `aov`. In order to try it, let us take a data set distributed with R: `InsectSprays`. Six insecticides were tested in field conditions, the observed response was the number of insects. Each insecticide was tested 12 times, thus there are 72 observations. We will not consider here the graphical exploration of the data, but will focus on a simple analysis of variance of the response with respect to the insecticide. After loading the data in memory with the function `data`, the analysis is performed after a square-root transformation of the response:

```
> data(InsectSprays)
> aov.spray <- aov(sqrt(count) ~ spray, data = InsectSprays)
```

The main (and mandatory) argument of `aov` is a formula which specifies the response on the left-hand side of the tilde symbol `~` and the predictor on the right-hand side. The option `data = InsectSprays` specifies that the variables must be found in the data frame `InsectSprays`. This syntax is equivalent to:

```
> aov.spray <- aov(sqrt(InsectSprays$count) ~ InsectSprays$spray)
```

or still (if we know the column numbers of the variables):

```
> aov.spray <- aov(sqrt(InsectSprays[, 1]) ~ InsectSprays[, 2])
```

The first syntax is to be preferred since it is clearer.

The results are not displayed since they are assigned to an object called `aov.spray`. We will then used some functions to extract the results, for example `print` to display a brief summary of the analysis (mostly the estimated parameters) and `summary` to display more details (included the statistical tests):

```
> aov.spray
Call:
   aov(formula = sqrt(count) ~ spray, data = InsectSprays)

Terms:
                    spray Residuals
Sum of Squares  88.43787  26.05798
Deg. of Freedom        5        66

Residual standard error: 0.6283453
Estimated effects may be unbalanced
> summary(aov.spray)
            Df Sum Sq Mean Sq F value    Pr(>F)
spray        5 88.438  17.688  44.799 < 2.2e-16 ***
Residuals   66 26.058   0.395
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

We may remind that typing the name of the object as a command is similar to the command `print(aov.spray)`. A graphical representation of the results can be done with `plot()` or `termplot()`. Before typing `plot(aov.spray)` we will divide the graphics into four parts so that the four diagnostics plots will be done on the same graph. The commands are:

```
> opar <- par()
> par(mfcol = c(2, 2))
> plot(aov.spray)
> par(opar)
> termplot(aov.spray, se=TRUE, partial.resid=TRUE, rug=TRUE)
```

and the resulting graphics are on Figs. 13 and 14.

5.2 Formulae

Formulae are a key element in statistical analyses with R: the notation used is the same for (almost) all functions. A formula is typically of the form `y ~ model` where `y` is the analysed response and *`model`* is a set of terms for which some parameters are to be estimated. These terms are separated with arithmetic symbols but they have here a particular meaning.

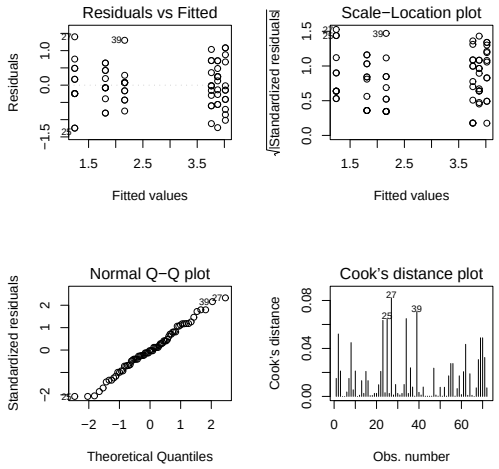


Figure 13: Graphical representation of the results from the function `aov` with `plot()`.

`a+b`	additive effects of `a` and of `b`
`X`	if `X` is a matrix, this specifies an additive effect of each of its columns, i.e. `X[,1]+X[,2]+...+X[,ncol(X)]`; some of the columns may be selected with numeric indices (e.g., `X[,2:4]`)
`a:b`	interactive effect between `a` and `b`
`a*b`	additive and interactive effects (identical to `a+b+a:b`)
`poly(a, n)`	polynomials of `a` up to degree n
`^n`	includes all interactions up to level n, i.e. `(a+b+c)^2` is identical to `a+b+c+a:b+a:c+b:c`
`b %in% a`	the effects of `b` are nested in `a` (identical to `a+a:b`, or `a/b`)
`-b`	removes the effect of `b`, for example: `(a+b+c)^2-a:b` is identical to `a+b+c+a:c+b:c`
`-1`	`y~x-1` is a regression through the origin (id. for `y~x+0` or `0+y~x`)
`1`	`y~1` fits a model with no effects (only the intercept)
`offset(...)`	adds an effect to the model without estimating any parameter (e.g., `offset(3*x)`)

We see that the arithmetic operators of R have in a formula a different meaning than they have in expressions. For example, the formula `y~x1+x2` defines the model $y = \beta_1 x_1 + \beta_2 x_2 + \alpha$, and not (if the operator `+` would have its usual meaning) $y = \beta(x_1 + x_2) + \alpha$. To include arithmetic operations in a formula, we can use the function `I`: the formula `y~I(x1+x2)` defines the model $y = \beta(x_1 + x_2) + \alpha$. Similarly, to define the model $y = \beta_1 x + \beta_2 x^2 + \alpha$, we will use the formula `y ~ poly(x, 2)` (and not `y ~ x + x^2`). However, it is

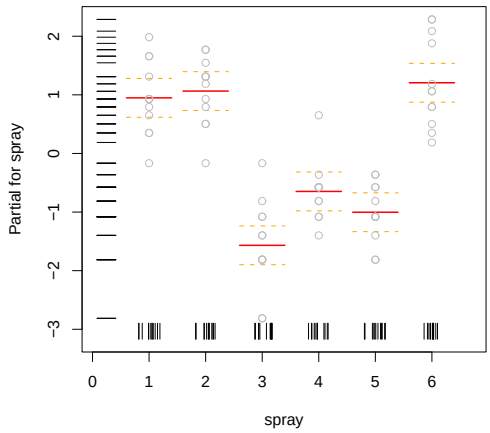


Figure 14: Graphical representation of the results from the function `aov` with `termplot()`.

possible to include a function in a formula in order to transform a variable as seen above with the insect sprays analysis of variance.

For analyses of variance, `aov()` accepts a particular syntax to define random effects. For instance, `y ~ a + Error(b)` means the additive effects of the fixed term `a` and the random one `b`.

5.3 Generic functions

We remember that R's functions act with respect to the attributes of the objects possibly passed as arguments. The *class* is an attribute deserving some attention here. It is very common that the R statistical functions return an object of class with the same name (e.g., `aov` returns an object of class `"aov"`, `lm` returns one of class `"lm"`). The functions that we can use subsequently to extract the results will act specifically with respect to the class of the object. These functions are called *generic*.

For instance, the function which is most often used to extract results from analyses is `summary` which displays detailed results. Whether the object given as argument is of class `"lm"` (linear model) or `"aov"` (analysis of variance), it sounds obvious that the information to display will not be the same. The advantage of generic functions is that the syntax is the same in all cases.

An object containing the results of an analysis is generally a list, and the way it is displayed is determined by its class. We have already seen this notion that the action of a function depends on the kind of object given as argument. It is a general feature of R[17]. The following table gives the main generic func-

[17] There are more than 100 generic functions in R.

tions which can be used to extract information from objects resulting from an analysis. The typical usage of these functions is:

```
> mod <- lm(y ~ x)
> df.residual(mod)
[1] 8
```

`print`	returns a brief summary
`summary`	returns a detailed summary
`df.residual`	returns the number of residual degrees of freedom
`coef`	returns the estimated coefficients (sometimes with their standard-errors)
`residuals`	returns the residuals
`deviance`	returns the deviance
`fitted`	returns the fitted values
`logLik`	computes the logarithm of the likelihood and the number of parameters
`AIC`	computes the Akaike information criterion or AIC (depends on `logLik()`)

A function like `aov` or `lm` returns a list with its different elements corresponding to the results of the analysis. If we take our example of an analysis of variance with the data `InsectSprays`, we can look at the structure of the object returned by `aov`:

```
> str(aov.spray, max.level = -1)
List of 13
 - attr(*, "class")= chr [1:2] "aov" "lm"
```

Another way to look at this structure is to display the names of the object:

```
> names(aov.spray)
 [1] "coefficients"  "residuals"     "effects"
 [4] "rank"          "fitted.values" "assign"
 [7] "qr"            "df.residual"   "contrasts"
[10] "xlevels"       "call"          "terms"
[13] "model"
```

The elements can then be extracted as we have already seen:

```
> aov.spray$coefficients
(Intercept)      sprayB      sprayC      sprayD
  3.7606784   0.1159530  -2.5158217  -1.5963245
     sprayE      sprayF
 -1.9512174   0.2579388
```

`summary()` also creates a list which, in the case of `aov()`, is simply a table of tests:

```
> str(summary(aov.spray))
List of 1
 $ :Classes anova  and 'data.frame':    2 obs. of  5 variables:
  ..$ Df     : num [1:2] 5 66
  ..$ Sum Sq : num [1:2] 88.4 26.1
  ..$ Mean Sq: num [1:2] 17.688  0.395
  ..$ F value: num [1:2] 44.8   NA
  ..$ Pr(>F) : num [1:2] 0 NA
 - attr(*, "class")= chr [1:2] "summary.aov" "listof"
> names(summary(aov.spray))
NULL
```

Generic functions do not generally perform any action on objects: they call the appropriate function with respect to the class of the argument. A function called by a generic is a *method* in R's jargon. Schematically, a method is constructed as *`generic.cls`*, where *`cls`* is the class of the object. For instance, in the case of `summary`, we can display the corresponding methods:

```
> apropos("^summary")
 [1] "summary"               "summary.aov"
 [3] "summary.aovlist"       "summary.connection"
 [5] "summary.data.frame"    "summary.default"
 [7] "summary.factor"        "summary.glm"
 [9] "summary.glm.null"      "summary.infl"
[11] "summary.lm"            "summary.lm.null"
[13] "summary.manova"        "summary.matrix"
[15] "summary.mlm"           "summary.packageStatus"
[17] "summary.POSIXct"       "summary.POSIXlt"
[19] "summary.table"
```

We can see the difference for this generic in the case of a linear regression, compared to an analysis of variance, with a small simulated example:

```
> x <- y <- rnorm(5)
> lm.spray <- lm(y ~ x)
> names(lm.spray)
 [1] "coefficients"  "residuals"     "effects"
 [4] "rank"          "fitted.values" "assign"
 [7] "qr"            "df.residual"   "xlevels"
[10] "call"          "terms"         "model"
> names(summary(lm.spray))
 [1] "call"          "terms"         "residuals"
 [4] "coefficients"  "sigma"         "df"
 [7] "r.squared"     "adj.r.squared" "fstatistic"
[10] "cov.unscaled"
```

The following table shows some generic functions that do supplementary analyses from an object resulting from an analysis, the main argument being

this latter object, but in some cases a further argument is necessary like for `predict` or `update`.

`add1`	tests successively all the terms that can be added to a model
`drop1`	tests successively all the terms that can be removed from a model
`step`	selects a model with AIC (calls `add1` and `drop1`)
`anova`	computes a table of analysis of variance or deviance for one or several models
`predict`	computes the predicted values for new data from a fitted model
`update`	re-fits a model with a new formula or new data

There are also various utilities functions that extract information from a model object or a formula, such as `alias` which finds the linearly dependent terms in a linear model specified by a formula.

Finally, there are, of course, graphical functions such as `plot` which displays various diagnostics, or `termplot` (see the above example), though this latter function is not generic but calls `predict`.

5.4 Packages

The following table lists the *standard* packages which are distributed with a base installation of R. Some of them are loaded in memory when R starts; this can be displayed with the function `search`:

```
> search()
[1] ".GlobalEnv"        "package:methods"
[3] "package:stats"     "package:graphics"
[5] "package:grDevices" "package:utils"
[7] "package:datasets"  "Autoloads"
[9] "package:base"
```

The other packages may be used after being loaded:

```
> library(grid)
```

The list of the functions in a package can be displayed with:

```
> library(help = grid)
```

or by browsing the help in html format. The information relative to each function can be accessed as previously seen (p. 7).

Package	Description
base	base R functions
datasets	base R datasets
grDevices	graphics devices for base and grid graphics
graphics	base graphics
grid	grid graphics
methods	definition of methods and classes for R objects and programming tools
splines	regression spline functions and classes
stats	statistical functions
stats4	statistical functions using S4 classes
tcltk	functions to interface R with Tcl/Tk graphical user interface elements
tools	tools for package development and administration
utils	R utility functions

Many *contributed* packages add to the list of statistical methods available in R. They are distributed separately, and must be installed and loaded in R. A complete list of the contributed packages, with descriptions, is on the CRAN Web site[18]. Several of these packages are *recommanded* since they cover statistical methods often used in data analysis. The recommended packages are often distributed with a base installation of R. They are briefly described in the following table.

Package	Description
boot	resampling and bootstraping methods
class	classification methods
cluster	clustering methods
foreign	functions for reading data stored in various formats (S3, Stata, SAS, Minitab, SPSS, Epi Info)
KernSmooth	methods for kernel smoothing and density estimation (including bivariate kernels)
lattice	Lattice (Trellis) graphics
MASS	contains many functions, tools and data sets from the libraries of "Modern Applied Statistics with S" by Venables & Ripley
mgcv	generalized additive models
nlme	linear and non-linear mixed-effects models
nnet	neural networks and multinomial log-linear models
rpart	recursive partitioning
spatial	spatial analyses ("kriging", spatial covariance, ...)
survival	survival analyses

[18] http://cran.r-project.org/src/contrib/PACKAGES.html

There are two other main repositories of R packages: the Omegahat Project for Statistical Computing[19] which focuses on web-based applications and interfaces between softwares and languages, and the Bioconductor Project[20] specialized in bioinformatic applications (particularly for the analysis of microarray data).

The procedure to install a package depends on the operating system and whether R was installed from the sources or pre-compiled binaries. In the latter situation, it is recommended to use the pre-compiled packages available on CRAN's site. Under Windows, the binary Rgui.exe has a menu "Packages" allowing to install packages via internet from the CRAN Web site, or from zipped files on the local disk.

If R was compiled, a package can be installed from its sources which are distributed as a '.tar.gz' file. For instance, if we want to install the package `gee`, we will first download the file gee_4.13-6.tar.gz (the number 4.13-6 indicates the version of the package; generally only one version is available on CRAN). We will then type from the system (and not in R) the command:

```
R CMD INSTALL gee_4.13-6.tar.gz
```

There are several useful functions to manage packages such as `installed.packages`, `CRAN.packages`, or `download.packages`. It is also useful to type regularly the command:

```
> update.packages()
```

which checks the versions of the packages installed against those available on CRAN (this command can be called from the menu "Packages" under Windows). The user can then update the packages with more recent versions than those installed on the computer.

[19] http://www.omegahat.org/R/
[20] http://www.bioconductor.org/

6 Programming with R in pratice

Now that we have done an overview of R's functionalities, let us return to the language and programming. We will see a few simple ideas likely to be used in practice.

6.1 Loops and vectorization

An advantage of R compared to softwares with pull-down menus is the possibility to program simply a series of analyses which will be executed successively. This is common to any computer language, but R has some particular features which make programming easier for non-specialists.

Like other languages, R has some *control structures* which are not dissimilar to those of the C language. Suppose we have a vector `x`, and for each element of `x` with the value `b`, we want to give the value 0 to another variable `y`, otherwise 1. We first create a vector `y` of the same length than `x`:

```
y <- numeric(length(x))
for (i in 1:length(x)) if (x[i] == b) y[i] <- 0 else y[i] <- 1
```

Several instructions can be executed if they are placed within braces:

```
for (i in 1:length(x)) {
    y[i] <- 0
    ...
}

if (x[i] == b) {
    y[i] <- 0
    ...
}
```

Another possible situation is to execute an instruction as long as a condition is true:

```
while (myfun > minimum) {
    ...
}
```

However, loops and control structures can be avoided in most situations thanks to a feature of R: *vectorization*. Vectorization makes loops implicit in expression, and we have seen many cases. Let us consider the addition of two vectors:

```
> z <- x + y
```

This addition could be written with a loop, as this is done in most languages:

```
> z <- numeric(length(x))
> for (i in 1:length(z)) z[i] <- x[i] + y[i]
```

In this case, it is necessary to create the vector `z` beforehand because of the use of the indexing system. We realize that this explicit loop will work only if `x` and `y` are of the same length: it must be changed if this is not true, whereas the first expression will work in all situations.

The conditional executions (`if ... else`) can be avoided with the use of the logical indexing; coming back to the above example:

```
> y[x == b] <- 0
> y[x != b] <- 1
```

In addition to being simpler, vectorized expressions are computationally more efficient, particularly with large quantities of data.

There are also several functions of the type 'apply' which avoids writing loops. `apply` acts on the rows and/or columns of a matrix, its syntax is `apply(X, MARGIN, FUN, ...)`, where `X` is a matrix, `MARGIN` indicates whether to consider the rows (`1`), the columns (`2`), or both (`c(1, 2)`), `FUN` is a function (or an operator, but in this case it must be specified within brackets) to apply, and `...` are possible optional arguments for `FUN`. A simple example follows.

```
> x <- rnorm(10, -5, 0.1)
> y <- rnorm(10, 5, 2)
> X <- cbind(x, y)  # the columns of X keep the names "x" and "y"
> apply(X, 2, mean)
        x         y
-4.975132  4.932979
> apply(X, 2, sd)
        x         y
0.0755153 2.1388071
```

`lapply()` acts on a list: its syntax is similar to `apply` and it returns a list.

```
> forms <- list(y ~ x, y ~ poly(x, 2))
> lapply(forms, lm)
[[1]]

Call:
FUN(formula = X[[1]])

Coefficients:
```

```
(Intercept)            x
     31.683        5.377


[[2]]

Call:
FUN(formula = X[[2]])

Coefficients:
(Intercept)  poly(x, 2)1  poly(x, 2)2
     4.9330       1.2181      -0.6037
```

`sapply()` is a flexible variant of `lapply()` which can take a vector or a matrix as main argument, and returns its results in a more user-friendly form, generally as a table.

6.2 Writing a program in R

Typically, an R program is written in a file saved in ASCII format and named with the extension '.R'. A typical situation where a program is useful is when one wants to do the same tasks several times. In our first example, we want to do the same plot for three different species of birds, the data being in three distinct files. We will proceed step by step, and see different ways to program this very simple problem.

First, let us make our program in the most intuitive way by executing successively the needed commands, taking care to partition the graphical device beforehand.

```
layout(matrix(1:3, 3, 1))              # partition the graphics
data <- read.table("Swal.dat")         # read the data
plot(data$V1, data$V2, type="l")
title("swallow")                       # add a title
data <- read.table("Wren.dat")
plot(data$V1, data$V2, type="l")
title("wren")
data <- read.table("Dunn.dat")
plot(data$V1, data$V2, type="l")
title("dunnock")
```

The character '#' is used to add comments in a program: R then goes to the next line.

The problem of this first program is that it may become quite long if we want to add other species. Moreover, some commands are executed several times, thus they can be grouped together and executed after changing some arguments. The strategy used here is to put these arguments in vectors of mode character, and then use the indexing to access these different values.

```
layout(matrix(1:3, 3, 1))                # partition the graphics
species <- c("swallow", "wren", "dunnock")
file <- c("Swal.dat" , "Wren.dat", "Dunn.dat")
for(i in 1:length(species)) {
    data <- read.table(file[i])          # read the data
    plot(data$V1, data$V2, type="l")
    title(species[i])                    # add a title
}
```

Note that there are no double quotes around `file[i]` in `read.table()` since this argument is of mode character.

Our program is now more compact. It is easier to add other species since the vectors containing the species and file names are at the beginning of the program.

The above programs will work correctly if the data files '.dat' are located in the working directory of R, otherwise the user must either change the working directory, or specifiy the path in the program (for example: `file <- "/home/paradis/data/Swal.dat"`). If the program is written in the file Mybirds.R, it will be called by typing:

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

Like for any input from a file, it is necessary to give the path to access the file if it is not in the working directory.

6.3 Writing your own functions

We have seen that most of R's work is done with functions which arguments are given within parentheses. Users can write their own functions, and these will have exactly the same properties than other functions in R.

Writing your own functions allows an efficient, flexible, and rational use of R. Let us come back to our example of reading some data followed by plotting a graph. If we want to do this operation in different situations, it may be a good idea to write a function:

```
myfun <- function(S, F)
{
    data <- read.table(F)
    plot(data$V1, data$V2, type="l")
    title(S)
}
```

To be executed, this function must be loaded in memory, and this can be done in several ways. The lines of the function can be typed directly on the keyboard, like any other command, or copied and pasted from an editor. If the function has been saved in a text file, it can be loaded with `source()`

like another program. If the user wants some functions to be loaded each time when R starts, they can be saved in a workspace `.RData` which will be loaded in memory if it is in the working directory. Another possibility is to configure the file '.Rprofile' or 'Rprofile' (see `?Startup` for details). Finally, it is possible to create a package, but this will not be discussed here (see the manual "Writing R Extensions").

Once the function is loaded, we will be able with a single command to read the data and plot the graph, for instance with `myfun("swallow", "Swal.dat")`. Thus, we have now a third version of our program:

```
layout(matrix(1:3, 3, 1))
myfun("swallow", "Swal.dat")
myfun("wren", "Wrenn.dat")
myfun("dunnock", "Dunn.dat")
```

We may also use `sapply()` leading to a fourth version of our program:

```
layout(matrix(1:3, 3, 1))
species <- c("swallow", "wren", "dunnock")
file <- c("Swal.dat" , "Wren.dat", "Dunn.dat")
sapply(species, myfun, file)
```

In R, it is not necessary to declare the variables used within a function. When a function is executed, R uses a rule called *lexical scoping* to decide whether an object is local to the function, or global. To understand this mechanism, let us consider the very simple function below:

```
> foo <- function() print(x)
> x <- 1
> foo()
[1] 1
```

The name `x` is not used to create an object within `foo()`, so R will seek in the *enclosing* environment if there is an object called `x`, and will print its value (otherwise, a message error is displayed, and the execution is halted).

If `x` is used as the name of an object within our function, the value of `x` in the global environment is not used.

```
> x <- 1
> foo2 <- function() { x <- 2; print(x) }
> foo2()
[1] 2
> x
[1] 1
```

This time `print()` uses the object `x` that is defined within its environment, that is the environment of `foo2`.

The word "*enclosing*" above is important. In our two example functions, there are *two* environments: the global one, and the one of the function `foo` or `foo2`. If there are three or more nested environments, the search for the objects is made progressively from a given environment to the enclosing one, and so on, up to the global one.

There are two ways to specify arguments to a function: by their positions or by their names (also called *tagged arguments*). For example, let us consider a function with three arguments:

```
foo <- function(arg1, arg2, arg3) {...}
```

`foo()` can be executed without using the names `arg1`, ..., if the corresponding objects are placed in the correct position, for instance: `foo(x, y, z)`. However, the position has no importance if the names of the arguments are used, e.g. `foo(arg3 = z, arg2 = y, arg1 = x)`. Another feature of R's functions is the possibility to use default values in their definition. For instance:

```
foo <- function(arg1, arg2 = 5, arg3 = FALSE) {...}
```

The commands `foo(x)`, `foo(x, 5, FALSE)`, and `foo(x, arg3 = FALSE)` will have exactly the same result. The use of default values in a function definition is very useful, particularly when used with tagged arguments (i.e. to change only one default value such as `foo(x, arg3 = TRUE)`.

To conclude this section, let us see another example which is not purely statistical, but it illustrates the flexibility of R. Consider we wish to study the behaviour of a non-linear model: Ricker's model defined by:

$$N_{t+1} = N_t \exp\left[r\left(1 - \frac{N_t}{K}\right)\right]$$

This model is widely used in population dynamics, particularly of fish. We want, using a function, to simulate this model with respect to the growth rate r and the initial number in the population N_0 (the carrying capacity K is often taken equal to 1 and this value will be taken as default); the results will be displayed as a plot of numbers with respect to time. We will add an option to allow the user to display only the numbers in the last few time steps (by default all results will be plotted). The function below can do this numerical analysis of Ricker's model.

```
ricker <- function(nzero, r, K=1, time=100, from=0, to=time)
{
    N <- numeric(time+1)
    N[1] <- nzero
    for (i in 1:time) N[i+1] <- N[i]*exp(r*(1 - N[i]/K))
    Time <- 0:time
    plot(Time, N, type="l", xlim=c(from, to))
}
```

Try it yourself with:

```
> layout(matrix(1:3, 3, 1))
> ricker(0.1, 1); title("r = 1")
> ricker(0.1, 2); title("r = 2")
> ricker(0.1, 3); title("r = 3")
```

7 Literature on R

Manuals. Several manuals are distributed with R in R_HOME/doc/manual/:

- *An Introduction to R* [R-intro.pdf],
- *R Installation and Administration* [R-admin.pdf],
- *R Data Import/Export* [R-data.pdf],
- *Writing R Extensions* [R-exts.pdf],
- *R Language Definition* [R-lang.pdf].

The files may be in different formats (pdf, html, texi, ...) depending on the type of installation.

FAQ. R is also distributed with an FAQ (*Frequently Asked Questions*) localized in the directory R_HOME/doc/html/. A version of the R-FAQ is regularly updated on CRAN's Web site:

http://cran.r-project.org/doc/FAQ/R-FAQ.html

On-line resources. The CRAN Web site hosts several documents, bibliographic resources, and links to other sites. There are also a list of publications (books and articles) about R or statistical methods[21] and some documents and tutorials written by R's users[22].

Mailing lists. There are four discussion lists on R; to subscribe, send a message, or read the archives see: http://www.R-project.org/mail.html.

The general discussion list 'r-help' is an interesting source of information for the users of R (the three other lists are dedicated to annoucements of new versions, and for developers). Many users have sent to 'r-help' functions or programs which can be found in the archives. If a problem is encountered with R, it is thus important to proceed in the following order before sending a message to 'r-help':

1. read carefully the on-line help (possibly using the search engine);
2. read the R-FAQ;
3. search the archives of 'r-help' at the above address, or by using one of the search engines developed on some Web sites[23];
4. read the "posting guide"[24] before sending your question(s).

[21] http://www.R-project.org/doc/bib/R-publications.html
[22] http://cran.r-project.org/other-docs.html
[23] The addresses of these sites are listed at http://cran.r-project.org/search.html
[24] http://www.r-project.org/posting-guide.html

R News. The electronic journal *R News* aims to fill the gap between the electronic discussion lists and traditional scientific publications. The first issue was published on January 2001[25].

Citing R in a publication. Finally, if you mention R in a publication, you must cite the following reference:

> R Development Core Team (2005). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL: http://www.R-project.org.

[25] http://cran.r-project.org/doc/Rnews/