Solutions to Lafaye de Micheaux, Drouilhet & Liquet's The R Software

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Contents

Solutions to every exercise and every worksheet practical in *The R Software: Fundamentals of Programming and Statistical Analysis* by Pierre Lafaye de Micheaux, Rémy Drouilhet and Benoît Liquet (Springer, Statistics and Computing 40, 2013) — 164 end-of-chapter exercises and 57 worksheet practicals (353 numbered questions) across chapters 3 to 15, worked in R with the book's own data sets, with executed code and committed output throughout. Chapter and exercise numbers follow the published Springer edition; worksheet practicals are labelled `<chapter>.W`, `<chapter>.W.<practical letter>` or `<chapter>.W.<letter>.<study>` (for example `15.W.B.2` is chapter 15, worksheet practical B, second study) so they never collide with exercise numbers. The book is filed at The R Software: Fundamentals of Programming and Statistical Analysis.

1 Basic concepts and data organisation

Contents

1.1 Exercises 3.1–3.7

Problem 3.1. What is the output of this instruction: `1:3^2` ?

Solution. The integers 1 to 9: `^` has higher precedence than `:`, so this is `1:(3^2)`, that is `1:9`.

```
1:3^2
```

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

Problem 3.2. What is the output of this instruction: `(1:5)*2` ?

Solution. The first five even numbers: the product is applied element by element to the vector `1:5`.

```
(1:5)*2
```

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

Problem 3.3. What is the output of these instructions: `var<-3`? `Var*2`?

Solution. The assignment prints nothing and the second instruction is an error, because R is case sensitive: `Var` is not the object `var` (Section 3.1.2).

```
var <- 3
Var*2
```

```
Error: object 'Var' not found
```

Problem 3.4. What is the output of these instructions: `x<-2`? `2x<-2*x`?

Solution. The first line prints nothing; the second is a syntax error, since a variable name may not start with a digit unless it is enclosed in quotes (Section 3.1.2).

```
x <- 2
2x <- 2*x
```

```
Error: unexpected symbol in "2x"
```

Problem 3.5. What is the output of these instructions: `root.of.four <- sqrt(4)`? `root.of.four`?

Solution. `[1] 2`: the dot is a legal character in a variable name, and typing the name displays its value.

```
root.of.four <- sqrt(4)
root.of.four
```

```
[1] 2
```

Problem 3.6. What is the output of these instructions: `x<-1`? `x< -1`?

Solution. `[1] FALSE`: the space turns `x< -1` into the comparison "x less than -1" instead of an assignment, so `x` still equals 1.

```
x<-1
x< -1
```

```
[1] FALSE
```

Problem 3.7. What is the output of this instruction: `An even number <- 16`?

Solution. A syntax error: a variable name may not contain white space unless it is enclosed in quotes (Section 3.1.2).

```
An even number <- 16
```

```
Error: unexpected symbol in "An even"
```

1.2 Exercises 3.8–3.14

Problem 3.8. What is the output of this instruction: `"An even number" <- 16`?

Solution. Nothing is displayed: the quoted name is legal, so the object `An even number` is created with value 16 (it is then accessed with backquotes).

```
"An even number" <- 16
`An even number`
```

```
[1] 16
```

Problem 3.9. What is the output of this instruction: `"2x" <- 14`?

Solution. Nothing is displayed: enclosed in quotes, a name starting with a digit is allowed, and the object `2x` now holds 14.

```
"2x" <- 14
`2x`
```

```
[1] 14
```

Problem 3.10. What is the output of this instruction: `An even number`?

Solution. A syntax error, even after Exercise 3.8 created the object: without quotes (backquotes, `` `An even number` ``) R reads three separate symbols.

```
An even number
```

```
Error: unexpected symbol in "An even"
```

Problem 3.11. Two symbols have been removed from this R output. What are they?

```
> 2
+
[1] 6
```

Solution. An operator at the end of the first line and an operand after the continuation prompt `+`, e.g. `*` and `3` (the incomplete `2*` makes R wait for the rest of the command, Section 3.1.2); `+` and `4` fit equally well.

```
> 2*
+ 3
[1] 6
```

Problem 3.12. What is the output of this instruction: `TRUE + T +FALSE*F + T*FALSE +F` ?

Solution. `[1] 2`: in arithmetic the logicals are converted to numeric (`TRUE`, `T` → 1; `FALSE`, `F` → 0), giving $1 + 1 + 0 + 0 + 0$.

```
TRUE + T +FALSE*F + T*FALSE +F
```

```
[1] 2
```

Problem 3.13. Name the five data types in R.

Solution. `numeric`, `complex`, `logical`, `character` and `raw` (Table 3.1); the missing value `NA` is also listed there, but it is a logical constant rather than a separate type (Section 3.2.1.4).

```
sapply(list(3.27, 3+2i, TRUE, "text", as.raw(28)), class)
```

```
[1] "numeric"   "complex"   "logical"   "character" "raw"
```

Problem 3.14. Give the R instruction which gives the following output:

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

Solution. `X <- matrix(1:12, nrow = 4)`: `matrix()` fills column by column by default.

```
X <- matrix(1:12, nrow = 4)
X
```

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

1.3 Exercise 3.15

Problem 3.15. Name the data structures (classes) available in R.

Solution. Vectors (`c()`), matrices (`matrix()`), multidimensional arrays (`array()`), lists (`list()`), individual×variable tables (`data.frame()`), factors (`factor()`, `ordered()`), dates (`as.Date()`) and time series (`ts()`), as summarised in Table 3.2.

1.4 Worksheet 3.W — Study of Body Mass Index

Problem 3.W. Worksheet 3.W — Worksheet — Study of Body Mass Index
We wish to analyse the characteristics of a sample of children. These children went through a medical examination in their first year of kindergarten in 1996-1997 in schools in Bordeaux (South-West France). The sample below contains information on ten children between the ages of 3 and 4.
The following information is available for each child:

- gender: G for girls and B for boys;
- whether their school is in a ZEP (*zone d'éducation prioritaire*: area targeted for special help in education, recognized as socially deprived): Y for yes and N for no;
- age in years and months (two variables: one for years and one for months);
- weight in kg, rounded to the nearest 100 g;
- height in cm, rounded to the nearest 0.5 cm.

Name	Edward	Cynthia	Eugene	Elizabeth	Patrick	John	Albert	Lawrence	Joseph	Leo
Gender	G	G	B	G	B	B	B	B	B	B
ZEP	Y	Y	Y	Y	N	Y	N	Y	Y	Y
Weight	16	14	13.5	15.4	16.5	16	17	14.8	17	16.7
Years	3	3	3	4	3	4	3	3	4	3
Months	5	10	5	0	8	0	11	9	1	3
Height	100.0	97.0	95.5	101.0	100.0	98.5	103.0	98.0	101.5	100.0

In Statistics, it is of the utmost importance to know the type of the variables under study: qualitative, ordinal or qualitative. These types can be specified in R thanks to the structure functions we introduced earlier in this chapter.

Try the following manipulations under R. Remember to use the work strategy we presented at the beginning of the chapter.

3.1- Choose the best R function to save the data from each variable in vectors which you will call `Individuals`, `Weight`, `Height` and `Gender`.

3.2- Where possible, calculate the mean of the variables.

3.3- Calculate the BMI of the individuals. Group the results in a vector called `BMI` (be careful of the units).

3.4- Group these variables in the R structure which seems most appropriate.

3.5- Use R's online help to get information on the `plot()` function.

3.6- Make a scatter plot of `Weight` as a function of `Height`. Remember to add a title to your graph and to label your axes.

Solution.

3.1- Use `c()` for every variable (Section 3.2.2.1), wrapped in `factor()` for the qualitative ones (`Gender`, `ZEP`, Section 3.2.2.5); names stay a character vector. Following the work strategy of Section 3.1.3, type these lines in a script and send them to the console. (Erratum: the preamble's list of types should read "quantitative, ordinal or qualitative".)

```
Individuals <- c("Edward", "Cynthia", "Eugene", "Elizabeth", "Patrick",
                 "John", "Albert", "Lawrence", "Joseph", "Leo")
Gender <- factor(c("G", "G", "B", "G", "B", "B", "B", "B", "B", "B"))
ZEP    <- factor(c("Y", "Y", "Y", "Y", "N", "Y", "N", "Y", "Y", "Y"))
Weight <- c(16, 14, 13.5, 15.4, 16.5, 16, 17, 14.8, 17, 16.7)
Years  <- c(3, 3, 3, 4, 3, 4, 3, 3, 4, 3)
Months <- c(5, 10, 5, 0, 8, 0, 11, 9, 1, 3)
Height <- c(100, 97, 95.5, 101, 100, 98.5, 103, 98, 101.5, 100)
Gender
```

```
[1] G G B G B B B B B B
Levels: B G
```

3.2- Only the quantitative variables have a mean: 15.69 kg for weight, 99.45 cm for height and 3.73 years for age (years plus months/12); a mean of a factor such as `Gender` is meaningless and R returns `NA`.

```
mean(Weight)
mean(Height)
mean(Years + Months/12)
mean(Gender)
```

```
[1] 15.69
[1] 99.45
[1] 3.733333
[1] NA
Warning message:
In mean.default(Gender) : argument is not numeric or logical: returning NA
```

3.3- BMI is weight in kg divided by the square of height in metres, so the heights must first be divided by 100; the children's BMIs range from 14.8 to 16.7 kg/m^2.

```
BMI <- Weight / (Height/100)^2
round(BMI, 2)
```

```
[1] 16.00 14.88 14.80 15.10 16.50 16.49 16.02 15.41 16.50 16.70
```

3.4- An individual × variable table, i.e. a `data.frame` (Section 3.2.2.4), since it holds columns of different types (character, factors, numerics) with one row per child.

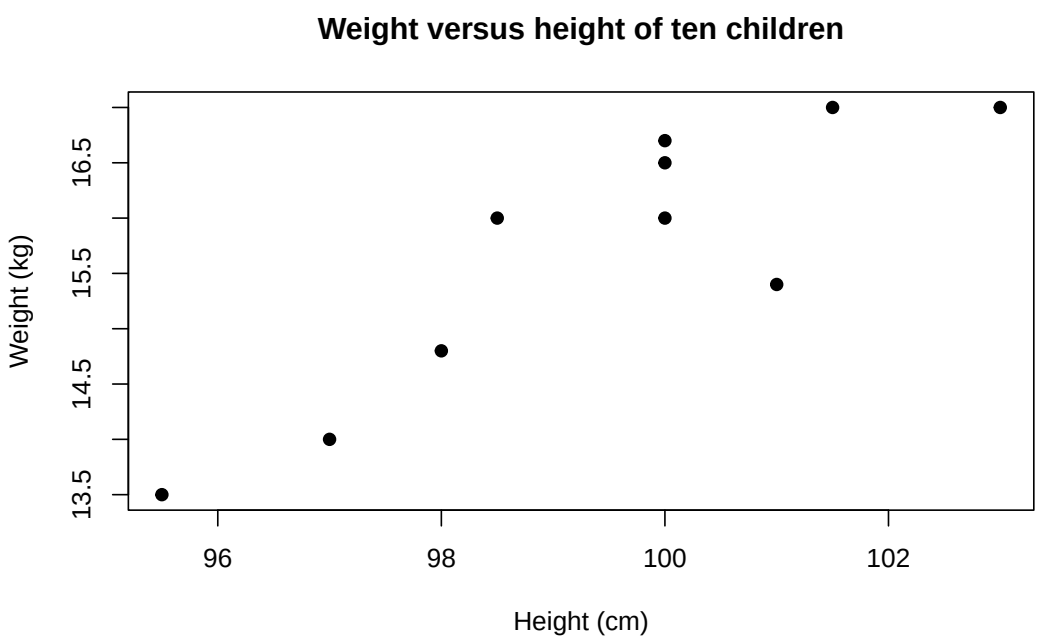
```
Children <- data.frame(Individuals, Gender, ZEP, Weight, Years, Months,
                       Height, BMI)
str(Children)
```

```
'data.frame':        10 obs. of  8 variables:
 $ Individuals: chr  "Edward" "Cynthia" "Eugene" "Elizabeth" ...
 $ Gender     : Factor w/ 2 levels "B","G": 2 2 1 2 1 1 1 1 1 1
 $ ZEP        : Factor w/ 2 levels "N","Y": 2 2 2 2 1 2 1 2 2 2
 $ Weight     : num  16 14 13.5 15.4 16.5 16 17 14.8 17 16.7
 $ Years      : num  3 3 3 4 3 4 3 3 4 3
 $ Months     : num  5 10 5 0 8 0 11 9 1 3
 $ Height     : num  100 97 95.5 101 100 ...
 $ BMI        : num  16 14.9 14.8 15.1 16.5 ...
```

3.5- Type `help(plot)` or `?plot` (Section 3.1.3); the page documents the generic `plot(x, y, ...)`, lists under `...` the common arguments `type`, `main`, `sub`, `xlab`, `ylab` and `asp`, points to `?par` for graphical parameters, and `example(plot)` runs its examples.

3.6- Pass `Height` as `x` and `Weight` as `y`, with `main`, `xlab` and `ylab` for the title and axis labels; the plot shows weight rising roughly with height.

```
plot(Height, Weight, pch = 19, main = "Weight versus height of ten children",
     xlab = "Height (cm)", ylab = "Weight (kg)")
```



2 Importing, exporting and producing data

Contents

2.1 Exercises 4.1–4.7

Problem 4.1. Name the three main R functions to import data from an ASCII text file.

Solution. `read.table()` (rectangular data tables), `read.ftable()` (contingency tables) and `scan()` (the flexible, low-level reader for every other layout); see Table 4.1.

Problem 4.2. One of the usual data reading functions takes the following arguments: `header`, `sep`, `dec`, `row.names`, `skip`, `nrows`. Explain their purpose. Give an example of a value each argument can take.

Solution. The function is `read.table()` (Table 4.2):

Argument	Purpose	Example
`header`	whether the first line holds the variable names	`TRUE`
`sep`	field separator on each line	`"\t"`, `" "`
`dec`	decimal mark of the numbers	`","`
`row.names`	column (number or name) giving the individuals' names	`1`
`skip`	number of lines to skip at the top of the file before reading	`5`
`nrows`	maximum number of rows (individuals) to read	`100`

For instance, the first three individuals of the book's file (decimal comma, space separator):

```
x <- read.table("http://www.biostatisticien.eu/springeR/Intima_Media_Thickness.txt",
                header = TRUE, sep = " ", dec = ",", skip = 0, nrows = 3)
x
```

```
  GENDER AGE height weight tobacco packyear SPORT measure alcohol
1      1  33    170     70       1        1     0    0.52       1
2      2  33    177     67       2       20     0    0.42       1
3      2  53    164     63       1       30     0    0.65       0
```

Problem 4.3. What is the purpose of the function `readLines()`?

Solution. `readLines()` reads a file line by line as raw character strings, so its first few lines (argument `n`) show how the file is laid out and hence which `read.table()` arguments are needed (Section 4.1.1):

```
readLines("http://www.biostatisticien.eu/springeR/Intima_Media_Thickness.txt", n = 3)
```

```
[1] "GENDER AGE height weight tobacco packyear SPORT measure alcohol"
[2] "1 33 170 70 1 1 0 0,52 1"
[3] "2 33 177 67 2 20 0 0,42 1"
```

Here the header line, the space separator and the decimal comma are visible at once.

Problem 4.4. What is the purpose of the function `fix()`?

Solution. `fix(X)` opens the data.frame or matrix `X` in R's mini spreadsheet so its values (and variable names) can be viewed and edited by hand; the modified object is saved back under the same name when the window is closed (Sections 4.1.2 and 4.3.3). Unlike `View()`, it allows editing, and unlike `edit()`, it needs no reassignment.

Problem 4.5. Give the specificities of the functions `read.csv()`, `read.csv2()`, `read.delim()` and `read.delim2()`.

Solution. All four are `read.table()` with `header = TRUE` and preset separator and decimal mark (Section 4.1.1):

Function	sep	dec
`read.csv()`	`","`	`"."`
`read.csv2()`	`";"`	`","`
`read.delim()`	`"\t"` (tab)	`"."`
`read.delim2()`	`"\t"` (tab)	`","`

Problem 4.6. What is the purpose of the function `read.ftable()`?

Solution. `read.ftable()` reads a contingency table stored as a "flat" table in a text file (when only counts, not the individual data, are available) and returns an object of class `ftable` (Section 4.1.1):

```
tab <- read.ftable(url("http://www.biostatisticien.eu/springeR/Intima_ftable-en.txt"))
tab
```

```
                    alcohol nondrinker occasional drinker regular drinker
GENDER tobacco
M      non-smoker                    6                19               7
       former smoker                 0                 9               0
       smoker                        1                 6               5
F      non-smoker                   12                26               2
       former smoker                 3                 5               1
       smoker                        1                 6               1
```

Under R 4.5 the bare URL string makes `read.ftable()` fail when closing the connection, hence the `url()` wrapper.

Problem 4.7. What is the difference between the functions `scan()` and `read.table()`?

Solution. `read.table()` reads a rectangular file into a data.frame (one column per variable, with names, separators and types handled for you), whereas `scan()` reads the file as a stream of values into a vector (or a list, via `what`), ignoring the table structure; it is lower-level, faster and more flexible (`what`, `skip`, `nlines`, `sep`), so it handles irregular files that `read.table()` cannot (Table 4.1):

```
cat("a b\n1 2\n3 4\n", file = f <- tempfile())
scan(f, skip = 1)
read.table(f, header = TRUE)
```

```
Read 4 items
[1] 1 2 3 4
  a b
1 1 2
2 3 4
```

2.2 Exercises 4.8–4.14

Problem 4.8. Explain how you would import data from an Excel spreadsheet. Give details.

Solution. Three routes (Section 4.1.2):

1. Copy-paste: select the data range in Excel, copy it (CTRL+C / COMMAND+C), then read the clipboard with `x <- read.table(file("clipboard"), sep = "\t", header = TRUE, dec = ",")` (Excel puts tab-separated text on the clipboard; on macOS use `pipe("pbpaste")` instead of `file("clipboard")`). If the range holds formulae or hidden characters, first paste-special the values into a new sheet.
2. Intermediate ASCII file: in Excel, File / Save as … with type "Text (tab-separated) (*.txt)", then use `read.delim()` (or `read.delim2()` for a decimal comma).
3. A dedicated package reading `.xls` / `.xlsx` directly: `read_excel()` from `readxl`, which needs no external software but reads local files only. The authors' companion solution uses `read.xls()` from `gdata` (Section 4.1.2.3), but that Perl-based function was removed in `gdata` 3.0.

```
library(readxl)
```

```r
f <- tempfile(fileext = ".xls")
download.file("http://www.biostatisticien.eu/springeR/Intima_Media_Thickness.xls",
              f, mode = "wb", quiet = TRUE)
d <- as.data.frame(read_excel(f))    # sheet = 1 by default
head(d, 3)
```

```
  GENDER AGE height weight tobacco packyear SPORT measure alcohol
1      1  33    170     70       1        1     0    0.52       1
2      2  33    177     67       2       20     0    0.42       1
3      2  53    164     63       1       30     0    0.65       0
```

Problem 4.9. Which package includes several functions to import data from commercial statistical software?

Solution. `foreign`: `read.spss()` (SPSS, `.sav`), `read.mtp()` (Minitab, `.mtp`), `read.xport()` (SAS XPORT, `.xpt`), among others (Table 4.3; Matlab files need `readMat()` from `R.matlab`):

```r
library(foreign)
b <- read.spss("http://www.biostatisticien.eu/springeR/bmichild.sav", to.data.frame = TRUE)
head(b, 3)
```

```
  SEXE zep poids an mois taille
1    F   0  16.0  3    5  100.0
2    F   0  14.0  3   10   97.0
3    G   0  13.5  3    5   95.5
```

Problem 4.10. When reading a large data file, which argument to the function `read.table()` can speed up the reading?

Solution. `colClasses`, which declares the type of each column (e.g. `colClasses = rep("character", 3)`) so that R does not have to scan the whole file to infer them; in Section 4.1.4 this cuts the reading of `dbsnp123.dat` from about 5 minutes to 14 seconds. Giving `nrows` (even a mild over-estimate) also helps memory allocation.

Problem 4.11. Which R function should be used to write to a file a data set contained in a data.frame? Which other function do you know?

Solution. `write.table()` (Section 4.2.1); the other one is `write()`, meant for vectors and matrices (argument `ncolumns`, and it writes the transpose of a matrix). The wrappers `write.csv()` / `write.csv2()` are `write.table()` with CSV presets.

```r
X <- data.frame(Weight = c(80, 90, 75), Height = c(182, 190, 160))
f <- tempfile(fileext = ".txt")
write.table(X, file = f, sep = "\t", row.names = FALSE)
readLines(f)
```

```
[1] "\"Weight\"\t\"Height\"" "80\t182"                "90\t190"
[4] "75\t160"
```

Problem 4.12. Name the four basic functions to create a vector.

Solution. `c()`, `seq()`, `":"()` and `rep()` (Section 4.3.1).

Problem 4.13. Explain how the function `seq()` can be used to get the following vector:

```
[1] 1.0 1.1 1.2 1.3 1.4 1.5 1.6 1.7 1.8 1.9 2.0
```

Solution. Give the endpoints and either the step `by` or the number of values `length`:

```r
seq(from = 1, to = 2, by = 0.1)
```

```r
seq(1, 2, length = 11)
```

```
[1] 1.0 1.1 1.2 1.3 1.4 1.5 1.6 1.7 1.8 1.9 2.0
[1] 1.0 1.1 1.2 1.3 1.4 1.5 1.6 1.7 1.8 1.9 2.0
```

Problem 4.14. Give the shortest R instruction which outputs the following vector:
`1 1 2 2 3 3`

Solution. `rep(1:3, e = 2)`, i.e. `rep(1:3, each = 2)` with the argument name partially matched:

```r
rep(1:3, e = 2)
```

```
[1] 1 1 2 2 3 3
```

2.3 Exercises 4.15–4.16

Problem 4.15. Give the shortest R instruction which outputs the following vector:
`1 2 3 1 2 3`

Solution. `rep(1:3, 2)`, since the second argument `times` repeats the whole vector:

```r
rep(1:3, 2)
```

```
[1] 1 2 3 1 2 3
```

Problem 4.16. Name two R functions which can be used to enter data by hand in a mini spreadsheet.

Solution. `data.entry()` (variables of possibly different lengths, created directly in the workspace) and `de()` (e.g. `X <- as.data.frame(de(""))` for an individuals × variables table); see Section 4.3.3. `fix()` then edits an existing data.frame in the same spreadsheet. These open an interactive window, so they cannot be run in a script.

2.4 Worksheet 4.W.A.1 — Fever blisters (entering data from a hard copy)

Problem 4.W.A.1. Worksheet 4.W.A.1 — Entering data from a hard copy — Fever blisters
Fever blisters: Thirty patients have been randomly assigned to one of five treatments against fever blisters, including one placebo (there are six patients in each treatment group). For each patient, the number of days between the apparition of the first blisters and complete healing has been recorded.

trt1 (placebo)	trt2	trt3	trt4	trt5
5	4	6	7	9
8	6	4	4	3
7	6	4	6	5
7	3	5	6	7
10	5	4	3	7
8	6	3	5	6

We would like to know whether there is a difference between the treatments, by comparing the mean healing time in each independent random sample (treatment group). The relevant statistical method is called ANOVA; we shall present it in Chapter 15. In this practical, we shall simply see how to enter these data in R to compute the sample mean for each treatment.
4.1- Enter the data in R directly, using the function `de()`.
4.2- Use the function `attach()`, then the function `mean()` to compute the mean for each treatment.
4.3- Compute the means of all treatments simultaneously thanks to the function `colMeans()`.
4.4- Use the function `write.table()` to save your data.frame in a file called blisters.txt.
4.5- Open your file in a text editor and check that there was no problem.
4.6- Use the function `rm()` to delete all the R objects you have created in your work environment.

4.7- Import the file blisters.txt with the function `read.table()` and display the data.

Solution.
4.1- Type `blisters <- as.data.frame(de(""))` (Section 4.3.3): in the spreadsheet window, click each header cell to rename the columns `trt1`, …, `trt5` and set them to numeric, type the six values of each column, then close the window. `de()` needs a graphical device, so it cannot run in a script; the non-interactive instruction below builds the same data frame, and is what the remaining answers use.

```
blisters <- data.frame(trt1 = c(5, 8, 7, 7, 10, 8), trt2 = c(4, 6, 6, 3, 5, 6),
                       trt3 = c(6, 4, 4, 5, 4, 3), trt4 = c(7, 4, 6, 6, 3, 5),
                       trt5 = c(9, 3, 5, 7, 7, 6))
blisters
```

```
  trt1 trt2 trt3 trt4 trt5
1    5    4    6    7    9
2    8    6    4    4    3
3    7    6    4    6    5
4    7    3    5    6    7
5   10    5    4    3    7
6    8    6    3    5    6
```

4.2- After `attach()` the columns are visible as ordinary variables, so `mean()` works on each by name:

```
attach(blisters)
c(mean(trt1), mean(trt2), mean(trt3), mean(trt4), mean(trt5))
detach(blisters)
```

```
[1] 7.500000 5.000000 4.333333 5.166667 6.166667
```

4.3- `colMeans()` gives all five means in one call, with names:

```
colMeans(blisters)
```

```
    trt1     trt2     trt3     trt4     trt5
7.500000 5.000000 4.333333 5.166667 6.166667
```

The placebo has the longest mean healing time (7.5 days) and `trt3` the shortest (4.33 days); Chapter 15 tests whether these differences are significant.
4.4- The file is written to the working directory (`getwd()`):

```
write.table(blisters, file = "blisters.txt")
```

4.5- Any text editor shows the contents; here they are printed from R with `readLines()`:

```
cat(readLines("blisters.txt"), sep = "\n")
```

```
"trt1" "trt2" "trt3" "trt4" "trt5"
"1" 5 4 6 7 9
"2" 8 6 4 4 3
"3" 7 6 4 6 5
"4" 7 3 5 6 7
"5" 10 5 4 3 7
"6" 8 6 3 5 6
```

The file is correct. The row names are written as a first column, which is why the header line has one field less than the data lines.
4.6- `ls()` lists every object, so the call below removes them all; the empty `ls()` afterwards confirms it:

```
rm(list = ls())
ls()
```

```
character(0)
```

4.7- Read the file back with its header:

```
blisters <- read.table("blisters.txt", header = TRUE)
blisters
```

```
  trt1 trt2 trt3 trt4 trt5
1    5    4    6    7    9
2    8    6    4    4    3
```

```
3    7    6    4    6    5
4    7    3    5    6    7
5   10    5    4    3    7
6    8    6    3    5    6
```

Since the header line is one field short, `read.table()` reads the first column as row names, and we get back the same data frame we saved.

2.5 Worksheet 4.W.A.2 — Risk factors for atherosclerosis (entering data from a hard copy)

Problem 4.W.A.2. Worksheet 4.W.A.2 — Entering data from a hard copy — Risk factors for atherosclerosis

Risk factors for atherosclerosis: As part of a study on risk factors for atherosclerosis, data were collected and are summed up in this contingency table:

GENDER	tobacco	nondrinker	occasional-drinker	regular-drinker
M	non-smoker	6	19	7
M	former smoker	0	9	0
M	smoker	1	6	5
F	non-smoker	12	26	2
F	former smoker	3	5	1
F	smoker	1	6	1

It would be interesting to know whether there is a dependence between smoking and drinking, according to gender. To enter these data in R, there are several steps.

4.1- Use the function `scan()` to get a matrix `X` of size 6×3. This matrix will contain the data only.

4.2- Use the instruction `class(X) <- "ftable"` to specify that it is a contingency table.

4.3- Type the two instructions:

```
attributes(X)$col.vars <- list(alcohol=c("nondrinker",
            "occasional-drinker","regular-drinker"))
attributes(X)$row.vars <- list(GENDER=c("M","F"),tobacco=
               c("non-smoker","former smoker","smoker"))
```

4.4- Display the contingency table you have created.

4.5- Use the function `write.ftable()` to save the contingency table in a file called athero.txt.

4.6- Open the file in a text editor and check that there was no problem.

4.7- Use the function `rm()` to delete all the R objects you have created in your work environment.

4.8- Import the file athero.txt with the function `read.table()` and display the data.

Solution.

4.1- Type `X <- matrix(scan(), ncol = 3, byrow = TRUE)` and enter the 18 counts row by row, ending with an empty line (Section 4.3.3); `byrow = TRUE` fills the matrix one table row at a time. Here the typed input is given to `scan()` through its `text` argument so that the code can be rerun:

```
X <- matrix(scan(text = "6 19 7  0 9 0  1 6 5  12 26 2  3 5 1  1 6 1"),
            ncol = 3, byrow = TRUE)
X
```

```
Read 18 items
     [,1] [,2] [,3]
[1,]    6   19    7
[2,]    0    9    0
[3,]    1    6    5
[4,]   12   26    2
[5,]    3    5    1
[6,]    1    6    1
```

4.2- and 4.3- These two steps give `X` its class and the two attributes (`row.vars`, `col.vars`) that `print.ftable()` needs to label the table:

```
class(X) <- "ftable"
attributes(X)$col.vars <- list(alcohol=c("nondrinker",
            "occasional-drinker","regular-drinker"))
attributes(X)$row.vars <- list(GENDER=c("M","F"),tobacco=
```

```
                c("non-smoker","former smoker","smoker"))
```

4.4- Typing the object's name prints it as a flat table:

```
X
```

```
                     alcohol nondrinker occasional-drinker regular-drinker
GENDER tobacco
M      non-smoker                    6                 19               7
       former smoker                 0                  9               0
       smoker                        1                  6               5
F      non-smoker                   12                 26               2
       former smoker                 3                  5               1
       smoker                        1                  6               1
```

It matches the printed table.

4.5- The table is written in the working directory:

```
write.ftable(X, file = "athero.txt")
```

4.6- Here the file is printed from R:

```
cat(readLines("athero.txt"), sep = "\n")
```

```
                        "alcohol" "nondrinker" "occasional-drinker" "regular-drinker"
"GENDER" "tobacco"
"M"      "non-smoker"                      6                    19                  7
         "former smoker"                   0                     9                  0
         "smoker"                          1                     6                  5
"F"      "non-smoker"                     12                    26                  2
         "former smoker"                   3                     5                  1
         "smoker"                          1                     6                  1
```

The file holds the flat table with every label quoted. The `GENDER` label is written only on the first row of each block, so the lines do not all have the same number of fields.

4.7- Remove every object; the empty `ls()` confirms it:

```
rm(list = ls())
ls()
```

```
character(0)
```

4.8- `read.table()` fails on this file because its lines have different numbers of fields. This is an erratum in the book: the intended import function is `read.ftable()` (Section 4.1.1.2), which reads the labels back from the file's own header:

```
try(read.table("athero.txt"))
X <- read.ftable("athero.txt")
X
```

```
Error in scan(file = file, what = what, sep = sep, quote = quote, dec = dec,  :
  line 1 did not have 5 elements
                     alcohol nondrinker occasional-drinker regular-drinker
GENDER tobacco
M      non-smoker                    6                 19               7
       former smoker                 0                  9               0
       smoker                        1                  6               5
F      non-smoker                   12                 26               2
       former smoker                 3                  5               1
       smoker                        1                  6               1
```

We get back the contingency table of 4.4 exactly.

2.6 Worksheet 4.W.B — Importing from other software

Problem 4.W.B. Worksheet 4.W.B — Importing from other software — BMI of children
During a study of BMI (Body Mass Index) of children, a team of statisticians collected data in different formats. As an exercise, we are going to read these various formats. There are several files called bmichild, but with different file extensions.

4.1- Import the file bmichild.xls into a data.frame called `bmi.XLS`.
4.2- Import the file bmichild.xpt into a data.frame called `bmi.SAS`.
4.3- Import the file bmichild.sav into a data.frame called `bmi.SPSS`.
4.4- Import the file bmichild.mat into a data.frame called `bmi.MAT`. The procedure is trickier for this file, so here are detailed instructions:

```
x <- readMat("bmichild.mat")
class(x) # x is a list
x        # you can see that the data are in $bmi[,,1]
x <- x$bmi[,,1]
  # Note that the elements of GENDER and zep
  # are recorded in a list.
x$GENDER
class(x$GENDER) <- "character"
x$GENDER
class(x$zep) <- "character"
bmi.MAT <- as.data.frame(x)
```

4.5- To check that there was no problem during importation, use the function `summary()` on all these data.frames. This will display a few numerical summaries.
4.6- All these data.frames are identical. Save one of them in a file called bmichild.txt.

Solution.
4.1- The book's `read.xls()` (package `gdata`, Section 4.1.2.3) was removed from `gdata` 3.0, so use `read_excel()` from `readxl`, which reads only local files, hence the `download.file()` first.

```
library(readxl)
url <- "http://www.biostatisticien.eu/springeR/"
download.file(paste0(url, "bmichild.xls"), "bmichild.xls", mode = "wb", quiet = TRUE)
bmi.XLS <- as.data.frame(read_excel("bmichild.xls"))
head(bmi.XLS, 3)
```

```
  GENDER zep weight year month height
1      F   Y   16.0    3     5  100.0
2      F   Y   14.0    3    10   97.0
3      M   Y   13.5    3     5   95.5
```

4.2- `read.xport()` from `foreign` (Table 4.3). As the Warning in Section 4.1.3 says, it cannot read from a URL, so the file is downloaded first. `lookup.xport()` gives the variable names.

```
library(foreign)
download.file(paste0(url, "bmichild.xpt"), "bmichild.xpt", mode = "wb", quiet = TRUE)
lookup.xport("bmichild.xpt")$SAS$name
bmi.SAS <- read.xport("bmichild.xpt")
head(bmi.SAS, 3)
```

```
[1] "SEXE"   "ZEP"    "POIDS"  "AN"     "MOIS"   "TAILLE"
  SEXE ZEP POIDS AN MOIS TAILLE
1    F   O  16.0  3    5  100.0
2    F   O  14.0  3   10   97.0
3    G   O  13.5  3    5   95.5
```

The .xpt, .sav and .mat files come from the French edition of the book. Their variables are SEXE (gender, coded F/G for fille/garçon), ZEP (priority-education zone, coded O/N for oui/non), POIDS (weight), AN and MOIS (age in years and months) and TAILLE (height). So G stands for M and O stands for Y.
4.3- `read.spss()` from `foreign` reads directly from the URL. The argument `to.data.frame = TRUE` returns a data.frame instead of the default list.

```
bmi.SPSS <- read.spss(paste0(url, "bmichild.sav"), to.data.frame = TRUE)
head(bmi.SPSS, 3)
```

```
  SEXE zep poids an mois taille
1    F   O  16.0  3    5  100.0
2    F   O  14.0  3   10   97.0
3    G   O  13.5  3    5   95.5
```

4.4- `readMat()` from `R.matlab` (Table 4.3; installed from CRAN for this run). This part of the book's

instructions no longer works as printed. The served file stores the data in `$imc` (with French names SEXE and zep), not `$bmi` (GENDER and zep). Also, each SEXE and zep entry is a list holding a 1×1 matrix. In current R, `class(x$SEXE) <- "character"` deparses these entries into strings like `"list(\"F\")"`, so `unlist()` is used to flatten them.

```
library(R.matlab)
download.file(paste0(url, "bmichild.mat"), "bmichild.mat", mode = "wb", quiet = TRUE)
x <- readMat("bmichild.mat")
class(x)
names(x)
x <- x$imc[,,1]
names(x)
x$SEXE[1:2]
x$SEXE <- unlist(x$SEXE)
x$zep <- unlist(x$zep)
bmi.MAT <- as.data.frame(x)
head(bmi.MAT, 3)
```

```
[1] "list"
[1] "imc"
[1] "SEXE"   "zep"    "poids"  "an"     "mois"   "taille"
[[1]]
[[1]][[1]]
     [,1]
[1,] "F"


[[2]]
[[2]][[1]]
     [,1]
[1,] "F"


  SEXE zep poids an mois taille
1    F   0  16.0  3    5  100.0
2    F   0  14.0  3   10   97.0
3    G   0  13.5  3    5   95.5
```

4.5- Apply `summary()` to all four data.frames. The two coded columns are converted to factors first, so that `summary()` counts their levels.

```
bmi <- list(XLS = bmi.XLS, SAS = bmi.SAS, SPSS = bmi.SPSS, MAT = bmi.MAT)
bmi <- lapply(bmi, function(d) {d[1:2] <- lapply(d[1:2], factor); d})
lapply(bmi, summary)
```

```
$XLS
 GENDER zep         weight           year           month
 F:71   N: 41   Min.   :10.50   Min.   :3.000   Min.   : 0.000
 M:81   Y:111   1st Qu.:15.00   1st Qu.:3.000   1st Qu.: 3.000
               Median :16.00   Median :3.000   Median : 6.000
               Mean   :16.28   Mean   :3.303   Mean   : 5.618
               3rd Qu.:17.50   3rd Qu.:4.000   3rd Qu.: 9.000
               Max.   :22.80   Max.   :4.000   Max.   :11.000
    height
 Min.   : 88.5
 1st Qu.: 98.0
 Median :101.0
 Mean   :100.7
 3rd Qu.:103.6
 Max.   :111.5

## ... $SAS, $SPSS and $MAT truncated: identical numbers, printed under
## the French names and codes (F:71 G:81, N:41 O:111)
```

The truncated summaries are easiest to compare side by side:

```
sapply(bmi, function(d) c(table(d[[1]]), table(d[[2]]), colMeans(d[3:6])))
```

```
              XLS        SAS       SPSS        MAT
```

```
F       71.000000  71.000000  71.000000  71.000000
M       81.000000  81.000000  81.000000  81.000000
N       41.000000  41.000000  41.000000  41.000000
Y      111.000000 111.000000 111.000000 111.000000
weight  16.280263  16.280263  16.280263  16.280263
year     3.302632   3.302632   3.302632   3.302632
month    5.618421   5.618421   5.618421   5.618421
height 100.748026 100.748026 100.748026 100.748026
```

All four imports agree: 152 children, 71 girls and 81 boys, 111 in a ZEP, weights from 10.5 to 22.8 kg and heights from 88.5 to 111.5 cm, so no problem occurred during importation.

4.6- `write.table()` (Section 4.2.1) saves the data. Here `bmi.XLS` is saved, with tab separators and no row names.

```r
write.table(bmi.XLS, file = "bmichild.txt", sep = "\t", quote = FALSE,
            row.names = FALSE)
readLines("bmichild.txt", n = 3)
```

```
[1] "GENDER\tzep\tweight\tyear\tmonth\theight"
[2] "F\tY\t16\t3\t5\t100"
[3] "F\tY\t14\t3\t10\t97"
```

2.7 Worksheet 4.W.C — Importing more complex data files

Problem 4.W.C. Worksheet 4.W.C — Importing more complex data files

Statisticians often encounter data files in non-standard formats. This section therefore provides training in reading several non-standard files on which we wish to perform statistical analysis.

4.1- Import the file `raf98.gra` into the most relevant structure. To this end, you will need to read the associated file `geoidformat.txt` which describes the file format.

4.2- Import the file `Infarction.xls` into a data.frame. Make sure you handle missing values correctly.

4.3- The file `nutrition_elderly.txt` contains thirteen variables measured on 226 individuals. Import the file into a data.frame (hint: use the functions `t()` and `as.data.frame()`).

4.4- The file `Birth_weight.txt` contains ten variables measured on 189 individuals. Import it into a data.frame, which will contain the names of the variables as well as the names of the individuals (these are available in the column `Id`). Remember that you can use the online help!

Solution.

4.1- The file is a grid, so the natural structure is a 381×421 matrix of geoid heights (rows = latitudes from north to south, columns = longitudes from west to east), read with `scan()` (Section 4.1.1.3) since the values are not laid out as a rectangular table. According to `geoidformat.txt`, the first three lines hold the bounds and steps, and the values then follow row by row regardless of line breaks (52 lines of 8 plus one line of 5 per latitude, i.e. $52 \times 8 + 5 = 421$).

```r
url <- "http://www.biostatisticien.eu/springeR/"
header <- scan(paste0(url, "raf98.gra"), nlines = 3)
z <- scan(paste0(url, "raf98.gra"), skip = 3)
lat <- seq(header[2], header[1], by = -header[5])   # north to south
long <- seq(header[3], header[4], by = header[6])   # west to east
raf98 <- matrix(z, nrow = length(lat), ncol = length(long), byrow = TRUE,
                dimnames = list(round(lat, 3), round(long, 3)))
header
dim(raf98)
raf98[1:3, 1:4]
range(raf98)
```

```
Read 6 items
Read 160401 items
[1] 42.00000000 51.50000000 -5.50000000  8.50000000  0.02500000  0.03333333
[1] 381 421
          -5.5  -5.467  -5.433    -5.4
51.5   53.3573 53.3569 53.3546 53.3481
51.475 53.3284 53.3277 53.3259 53.3209
```

```
51.45  53.3056 53.3023 53.2990 53.2940
[1] 41.8493 55.4308
```

The $160401 = 381 \times 421$ values fill the grid exactly, and the geoid heights over France range from about 41.8 m to 55.4 m.

4.2- The spreadsheet codes missing values as a dot `.`, so declare it with `na = "."` (the equivalent of `na.strings = "."` in `read.table()`). We use `read_excel()` from readxl, which needs a local copy of the file. The authors' companion solution uses `read.xls()` from gdata (Section 4.1.2.3), which was removed in gdata 3.0; the missing-value handling is the same.

```
library(readxl)
tmp <- tempfile(fileext = ".xls")
download.file("http://www.biostatisticien.eu/springeR/Infarction.xls", tmp,
              mode = "wb", quiet = TRUE)
infarct <- as.data.frame(read_excel(tmp, na = "."))
str(infarct)
colSums(is.na(infarct))
```

```
'data.frame':        449 obs. of  10 variables:
 $ NUMBER : num  1 2 3 4 5 6 7 8 9 10 ...
 $ INFARCT: num  0 0 0 0 0 0 0 0 0 0 ...
 $ CO     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ TOBACCO: num  0 0 0 0 0 0 0 0 0 0 ...
 $ AGE    : num  47 17 35 82 50 31 60 30 44 38 ...
 $ WEIGHT : num  48 NA 53 78 52 47 60 75 68 NA ...
 $ HEIGHT : num  173 162 163 157 172 184 169 174 164 167 ...
 $ BMI    : num  16 NA 19.9 31.6 17.6 ...
 $ ATCD   : num  0 0 0 0 NA 0 0 0 0 0 ...
 $ HTA    : num  0 0 0 0 0 0 0 0 0 0 ...
 NUMBER INFARCT      CO TOBACCO     AGE  WEIGHT  HEIGHT     BMI    ATCD     HTA
      0       0       0       0       0      12       0      12       7       0
```

All ten variables are now numeric, with 12 missing weights (hence 12 missing BMIs) and 7 missing `ATCD`; without `na = "."` the columns `WEIGHT`, `BMI` and `ATCD` would have been read as character strings.

4.3- The file stores one variable per line (name followed by its 226 values), so read it with the names as row names, then transpose with `t()` and convert with `as.data.frame()`.

```
url <- "http://www.biostatisticien.eu/springeR/"
tmp <- read.table(paste0(url, "nutrition_elderly.txt"), row.names = 1)
dim(tmp)
nutri <- as.data.frame(t(tmp))
rownames(nutri) <- NULL
dim(nutri)
head(nutri, 3)
```

```
[1]  13 226
[1] 226  13
  gender situation tea coffee height weight age mea fish raw_fruits
1      2         1   0      0    151     58  72   4    3          1
2      2         1   1      1    162     60  68   5    2          5
3      2         1   0      4    162     75  78   3    1          5
  cooked_fruits_veg chocol fat
1                 4      5   6
2                 5      1   4
3                 2      5   4
```

The data.frame has the expected 226 individuals (rows) and 13 variables (columns).

4.4- `readLines()` shows the traps: the header is space-separated while the data are separated by `;`, and (looking at the end of the file) a line of dashes follows the 189 records. So read the names with `scan()`, then the data with `sep = ";"`, `skip = 1`, `nrows = 189`, and use `row.names = "ID"` to turn the identifier column into row names (the column is printed `Id` in the book but is called `ID` in the file).

```
url <- "http://www.biostatisticien.eu/springeR/"
readLines(paste0(url, "Birth_weight.txt"), n = 3)
nm <- scan(paste0(url, "Birth_weight.txt"), what = "", nlines = 1)
birth <- read.table(paste0(url, "Birth_weight.txt"), sep = ";", skip = 1,
                    nrows = 189, col.names = nm, row.names = "ID")
dim(birth)
```

```
head(birth, 3)
```

```
[1] "\"ID\" \"AGE\" \"LWT\" \"RACE\" \"SMOKE\" \"PTL\" \"HT\" \"UI\" \"FVT\" \"BWT\" \"LOW\""
[2] "85;19;182;2;0;0;0;1;0;2523;0"
[3] "86;33;155;3;0;0;0;0;3;2551;0"
Read 11 items
[1] 189  10
   AGE LWT RACE SMOKE PTL HT UI FVT  BWT LOW
85  19 182    2     0   0  0  1   0 2523   0
86  33 155    3     0   0  0  0   3 2551   0
87  20 105    1     1   0  0  0   1 2557   0
```

The result has the 189 individuals named by their `ID` and the ten variables named from the header; without `nrows = 189`, `read.table()` stops with "line 193 did not have 11 elements" because of the trailing dashes.

3 Data manipulation, functions

Contents

3.1 Exercises 5.1–5.7

Problem 5.1. What is the output of this instruction: `c(1,4)*c(2,3)`?

Solution. The output is the vector `2 12`: `*` multiplies term by term, it is not a scalar product.

```
c(1,4)*c(2,3)
```

```
[1]  2 12
```

Problem 5.2. What is the output of this instruction: `matrix(1:2,ncol=2,nrow=2)`?

Solution. A 2×2 matrix whose two columns both equal `1:2`, because the vector is filled column by column and recycled.

```
matrix(1:2,ncol=2,nrow=2)
```

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

Problem 5.3. How can you retrieve the names of rows and columns of a `data.frame`?

Solution. With `rownames()` and `colnames()` (or `names()` for the columns), or both at once with `dimnames()`.

```
df <- data.frame(a = 1:2, b = 3:4, row.names = c("r1", "r2"))
rownames(df); colnames(df)
```

```
[1] "r1" "r2"
[1] "a" "b"
```

Problem 5.4. Give the instruction to merge these two tables:

```
> X
      Gender Weight
Jack       M     80
Julia      F     60
> Y
        Eyes Height
Jack    Blue    180
Julia  Green    160
```

Solution. `merge(X, Y, by = "row.names")` merges the two tables on their common row names (`cbind(X, Y)` also works here because the rows are already in the same order).

```
X <- data.frame(Gender = c("M", "F"), Weight = c(80, 60),
                row.names = c("Jack", "Julia"))
Y <- data.frame(Eyes = c("Blue", "Green"), Height = c(180, 160),
                row.names = c("Jack", "Julia"))
merge(X, Y, by = "row.names")
```

```
  Row.names Gender Weight  Eyes Height
1      Jack      M     80  Blue    180
2     Julia      F     60 Green    160
```

Problem 5.5. Give the instruction to calculate the product of all the elements (respectively: of all the elements of each column) of a numerical matrix `X`.

Solution. `prod(X)` gives the product of all the elements, and `apply(X, 2, prod)` the product of each column.

```r
X <- matrix(1:6, nrow = 2)
prod(X)
apply(X, 2, prod)
```

```
[1] 720
[1]  2 12 30
```

Problem 5.6. What is the output of this instruction: `vec<-c(2,4,6,8,3);vec[2];vec[-2]`?

Solution. `vec[2]` is the second element, `4`, and `vec[-2]` is the vector without its second element.

```r
vec<-c(2,4,6,8,3);vec[2];vec[-2]
```

```
[1] 4
[1] 2 6 8 3
```

Problem 5.7. The height and weight of several men were measured. The measurements are stored in the vectors `weight` and `height`. Give the R instruction to get the weight of the men whose height is greater than 180 cm.

Solution. `weight[height > 180]`: the logical vector indexes `weight`. With some illustrative values:

```r
weight <- c(70, 85, 92, 64); height <- c(175, 183, 190, 168)
weight[height > 180]
```

```
[1] 85 92
```

3.2 Exercises 5.8–5.14

Problem 5.8. What is the output of this instruction `Mat<-matrix(1:12,nrow=4,byrow=TRUE);Mat[3,];Mat[2,2:3]`?

Solution. `Mat[3,]` is the third row `7 8 9` and `Mat[2,2:3]` is `5 6`, since `byrow=TRUE` fills the rows `1:3`, `4:6`, `7:9`, `10:12`.

```r
Mat<-matrix(1:12,nrow=4,byrow=TRUE);Mat[3,];Mat[2,2:3]
```

```
[1] 7 8 9
[1] 5 6
```

Problem 5.9. How could you replace the fourth component of the following list with `1:10`?
`L<-list(12,c(34,67),Mat,1:15,list(10,11))`

Solution. `L[[4]] <- 1:10` (the double bracket addresses the component itself; `Mat` is the matrix of Exercise 5.8).

```r
L<-list(12,c(34,67),Mat,1:15,list(10,11))
L[[4]] <- 1:10
L[[4]]
```

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

Problem 5.10. What is the output of this instruction: `L[[2]][2]`?

Solution. `67`: `L[[2]]` is the vector `c(34,67)` and `[2]` takes its second element.

```r
L[[2]][2]
```

```
[1] 67
```

Problem 5.11. Give the R instruction which outputs the weights and heights of all women in the following table (you can use the function `attach()`):

	weight	height	gender
1	79	163	M
2	90	163	F
3	87	198	M
4	63	164	F
5	90	168	F
6	71	178	F
7	58	191	M
8	80	194	F
9	91	185	F
10	89	176	M

Solution. `subset(X, gender =` "F", select = c(weight, height))=, or equivalently `attach(X); X[gender =` "F", c("weight", "height")]; detach(X)= (in this session `subset()` avoids `attach()`'s masking clash with the vectors `weight`, `height` of Exercise 5.7).

```
X <- data.frame(weight = c(79, 90, 87, 63, 90, 71, 58, 80, 91, 89),
                height = c(163, 163, 198, 164, 168, 178, 191, 194, 185, 176),
                gender = c("M", "F", "M", "F", "F", "F", "M", "F", "F", "M"))
subset(X, gender == "F", select = c(weight, height))
```

```
  weight height
2     90    163
4     63    164
5     90    168
6     71    178
8     80    194
9     91    185
```

Problem 5.12. What is the output of this instruction: `(1:3)[any(c(T,F,T))]`? And this one: `(1:3)[all(c(T,F,T))]`?

Solution. The first gives `1 2 3` (`any()` is `TRUE`, recycled over all indices) and the second `integer(0)` (`all()` is `FALSE`, so nothing is selected).

```
(1:3)[any(c(T,F,T))]
(1:3)[all(c(T,F,T))]
```

```
[1] 1 2 3
integer(0)
```

Problem 5.13. What is the output of this instruction: `c(T,T,F) | c(F,T,F)`? And this one: `c(T,T,F) || c(F,T,F)`?

Solution. `|` is term-wise and gives `TRUE TRUE FALSE`; `||` expects single values: in R 4.3.0 and later it throws an error on length-3 operands, whereas in the R version used by the book it compared only the first elements and returned `TRUE`. The authors' companion solution gives `TRUE` for the second instruction; that is the pre-4.3.0 behaviour, reproduced today by `c(T,T,F)[1] || c(F,T,F)[1]`.

```
c(T,T,F) | c(F,T,F)
c(T,T,F) || c(F,T,F)
```

```
[1]  TRUE  TRUE FALSE
Error in c(T, T, F) || c(F, T, F) :
  'length = 3' in coercion to 'logical(1)'
```

Problem 5.14. What is the output of this instruction: `nchar(c("abcd","efgh"))`?

Solution. `4 4`: `nchar()` is vectorised and counts the characters of each string.

```
nchar(c("abcd","efgh"))
```

```
[1] 4 4
```

3.3 Exercises 5.15–5.20

Problem 5.15. What is the output of this instruction?
`paste(c("a","b"),c("c","d"),collapse="",sep="")`

Solution. `"acbd"`: `sep""`= first pastes term by term into `"ac"`, `"bd"`, then `collapse""`= joins these into one string.

```
paste(c("a","b"),c("c","d"),collapse="",sep="")
```

```
[1] "acbd"
```

Problem 5.16. What is the output of this instruction: `strsplit(c("ab;cd"),";")`?

Solution. A list with one component, the vector `"ab" "cd"`: `strsplit()` always returns a list, one component per input string.

```
strsplit(c("ab;cd"),";")
```

```
[[1]]
[1] "ab" "cd"
```

Problem 5.17. What is the output of this instruction: `substring("abcdef",3,c(2,4))`?

Solution. The vector `"" "cd"`: the string is recycled against `last = c(2,4)`, and the sub-string from character 3 to character 2 is empty.

```
substring("abcdef",3,c(2,4))
```

```
[1] ""   "cd"
```

Problem 5.18. How could you transform the upper case into lower case in the following vector?
`c("Jack","Julia","William")`

Solution. With `tolower()` (`casefold(x, upper = FALSE)` is equivalent).

```
tolower(c("Jack","Julia","William"))
```

```
[1] "jack"    "julia"   "william"
```

Problem 5.19. Which function is used to retrieve a date from a character string?

Solution. `strptime()`, whose `format` argument describes how the date is written in the string (`as.Date()` does the same for dates without a time).

```
strptime("24/09/2026", format = "%d/%m/%Y", tz = "UTC")
```

```
[1] "2026-09-24 UTC"
```

Problem 5.20. Can you explain why the second number of the last output is not equal to 36.21313?

```
> logp <- function(x) log(max(x,exp(1)))
> x <- -2.4
> delta <- 0.1
> (abs(x))^(4+delta)/(logp(abs(x)))^2
[1] 36.21313
> x <- seq(from=-2.8,to=-2,length=3)
> x
[1] -2.8 -2.4 -2.0
> (abs(x))^(4+delta)/(logp(abs(x)))^2
[1] 64.26795 34.15959 16.17594
```

Propose a solution to this problem.

Solution. `max()` is not vectorised: it returns the single largest value of all its arguments, here $\max(2.8, 2.4, 2, e) = 2.8$, so every element is divided by $(\log 2.8)^2$ instead of its own $(\log \max(|x_i|, e))^2$. The fix is the term-wise maximum `pmax()`.

```r
logp <- function(x) log(max(x,exp(1)))
x <- seq(from=-2.8,to=-2,length=3); delta <- 0.1
logp(abs(x))
logp <- function(x) log(pmax(x, exp(1)))
(abs(x))^(4+delta)/(logp(abs(x)))^2
```

```
[1] 1.029619
[1] 64.26795 36.21313 17.14838
```

3.4 Worksheet 5.W.A — Manipulating a few data sets presented at the beginning of the book

Problem 5.W.A. Worksheet 5.W.A — Manipulating a few data sets presented at the beginning of the book — Manipulating various data sets

These files can be downloaded from the URL http://www.biostatisticien.eu/springeR/. Note that you can also append the file name at the end of this URL to download the file directly from R (e.g. http://www.biostatisticien.eu/springeR/nutrien1.xls).

Data set NE:

The data file `nutrition_elderly.xls`, described earlier in this book, is in fact the merge of two initial files, entered by different operators. We propose to reconstruct the file for the following cases. You will only use R, and will not edit the file by hand.

5.1- The individuals are initially listed separately in two files (`nutrien1.xls` and `nutrien2.xls`). Note that the variable names are in upper case in the first file, and in lower case in the second.

5.2- Some individuals are listed in both files (`nutrien3.xls` and `nutrien4.xls`). The variable names are identical.

5.3- Same question as 5.2, but errors have slipped in and you will need to detect the corresponding individuals, for example those with a weight greater than 200 kg (`nutrien5.xls` and `nutrien6.xls`).

5.4- The variables are split between two files (`nutrien7.xls` and `nutrien8.xls`), which contain the same individuals.

5.5- Same question as 5.4, but for one variable, too many values are missing. Remove that variable (`nutrien9.xls` and `nutrien10.xls`).

5.6- Same question as 5.4, but for one individual, too many values are missing. Remove that individual (`nutrien11.xls` and `nutrien12.xls`).

5.7- In the file `nutrition_elderly.xls`, how many people are vegetarians (no meat, no fish)?

File `Intima_Media_Thickness.xls`:

5.1- Add a column BMI to the data.frame, with the BMI of each individual in the data file.

5.2- Retrieve the thickness of intima for the people with a `BMI>30`.

5.3- Extract the "athletic" women.

5.4- Extract the "non-obese" people aged 50 or other (obese = `BMI>30`).

File `bmichild.xls`:

5.1- Add a column `BMI`.
5.2- Extract the children with a `BMI < 15` and an age < 3.5= years.
5.3- How many such children are there?
File `Birth_weight.xls`:
5.1- Add a variable `PTL1` (number of children born before term), with three modalities (where the third modality, coded 2, corresponds to "2 or more" pre-term births).
5.2- Same question with `FVT` (number of visits to a physician), to add `FVT1`.
5.3- Sort the file by increasing weight at birth (`BWT`).
5.4- Extract the individuals whose mothers are black or white and smoke.

Solution. Data set NE (all files are read straight from the book's URL with `read_excel()` from readxl; the helper `get.xls()` is reused below).
5.1- Give both files the column names of `nutrition_elderly.xls`, then stack them with `rbind()` (Section 5.1.4.2); `toupper()=/=tolower()` alone is not enough because the second operator also typed `vmeat` and the target file uses `raw_fruit`.

```
library(readxl)
url <- "http://www.biostatisticien.eu/springeR/"
get.xls <- function(f) {
  tf <- tempfile(fileext = ".xls")
  download.file(paste0(url, f), tf, mode = "wb", quiet = TRUE)
  as.data.frame(read_excel(tf))
}
ne <- get.xls("nutrition_elderly.xls")
n1 <- get.xls("nutrien1.xls"); n2 <- get.xls("nutrien2.xls")
rbind(n1 = names(n1), n2 = names(n2), ne = names(ne))[, 8:11]
names(n1) <- names(n2) <- names(ne)
NE1 <- rbind(n1, n2)
dim(NE1)
all.equal(NE1, ne)
```

```
   [,1]    [,2]   [,3]         [,4]
n1 "MEAT"  "FISH" "RAW_FRUITS" "COOKED_FRUITS_VEG"
n2 "vmeat" "fish" "raw_fruits" "cooked_fruits_veg"
ne "meat"  "fish" "raw_fruit"  "cooked_fruit_veg"
[1] 226  13
[1] TRUE
```

The 109 + 117 rows rebuild `nutrition_elderly.xls` exactly.
5.2- `merge(..., all = TRUE)` on all the common columns (Section 5.1.4.2) is a full outer join, so each of the 5 individuals present in both files is kept once.

```
n3 <- get.xls("nutrien3.xls"); n4 <- get.xls("nutrien4.xls")
c(nrow(n3), nrow(n4))
intersect(n3$Subject, n4$Subject)
NE2 <- merge(n3, n4, all = TRUE)   # outer join on all 14 common columns
dim(NE2)
NE2 <- NE2[order(NE2$Subject), -1]; names(NE2) <- names(ne)
nrow(merge(NE2, ne))               # every reconstructed row is found in ne
```

```
[1] 112 119
[1]  51 137  85  30 156
[1] 226  14
[1] 226
```

The 112 + 119 - 5 = 226 individuals are exactly those of `nutrition_elderly.xls` (`unique(rbind(n3, n4))` gives the same table).
5.3- The same merge now returns 227 rows, because one duplicated subject was typed differently; the printed rule "weight greater than 200 kg" finds nobody (the faulty weight is exactly 200, a small erratum), so we flag every value outside the coding of the data description (gender in {1, 2}, frequencies 0 to 5, fat 1 to 8) or physically implausible for elderly adults.

```
n5 <- get.xls("nutrien5.xls"); n6 <- get.xls("nutrien6.xls")
nrow(merge(n5, n6, all = TRUE))   # 227, not 226: a duplicated subject disagrees
```

```r
X <- rbind(n5, n6)
sum(X$weight > 200)               # the printed rule alone finds nothing
freq <- c("vmeat", "fish", "raw_fruits", "cooked_fruits_veg", "chocol")
bad <- !(X$gender %in% 1:2) | X$height < 130 | X$weight < 30 |
  X$weight >= 200 | X$age < 60 | X$fat > 8 | apply(X[, freq] > 5, 1, any)
X[bad, c("Subject", "gender", "height", "weight", "age", "vmeat", "chocol", "fat")]
NE3 <- unique(X[!bad, ])          # drop flagged rows, then exact duplicates
dim(NE3)
setdiff(X$Subject[bad], NE3$Subject)   # individuals to re-check at source
```

```
[1] 227
[1] 0
    Subject gender height weight age vmeat chocol fat
51      165      2 158.00    200  69     5      1   4
81      195     21 175.00     50  77     3      4   2
91      205      1 170.00     69   8     3      0   4
97      211     12 175.00     85  77     4      5   2
101     215      2   1.67     69  71     5      5   5
111     225      2 163.00     75  89     3      7   2
121       9      1 181.00     76  78     4      6   5
129      17      2 164.00     54   7     5      1   2
132      20      1 172.00     78  84     3      1   9
138      25     12 174.00     73  69     4      5   4
143      30     21 140.00     56  84     3      4   3
155      41      2 160.00      8  69     4      1   3
182      68      2 162.00     71  73     6      0   8
223     109      2 100.00     64  75     4      5   5
[1] 213  14
 [1] 165 195 205 211 215 225   9  17  20  25  41  68 109
```

Fourteen faulty records are detected (typing slips such as gender 21 or 12, a height typed in metres (1.67), age 8 for 84, chocolate score 7). Subject 30 is the conflicting duplicate: its correct copy survives, giving 213 clean individuals; the 13 subjects listed last must be corrected from the source questionnaires before the file is complete (comparison with `nutrien3/4` confirms that these 14 rows are exactly the ones that differ). The authors' companion solution repairs only subject 30 and misses the height of 100 cm for subject 109, which also differs from its copy in `nutrien4.xls`.

5.4- Both files hold the same 226 individuals in the same order, so the columns are glued with `cbind()` (demographics first, as in the target file).

```r
n7 <- get.xls("nutrien7.xls"); n8 <- get.xls("nutrien8.xls")
names(n7); names(n8)
NE4 <- cbind(n8, n7)
names(NE4) <- names(ne)
all.equal(NE4, ne)
```

```
[1] "meat"              "fish"              "raw_fruits"
[4] "cooked_fruits_veg" "chocol"            "fat"
[1] "gender"    "situation" "tea"       "coffee"    "height"    "weight"
[7] "age"
[1] TRUE
```

5.5- After `cbind()`, count the missing values per column with `colSums(is.na())` and keep only columns with few of them: `chocol` (29 of 226 missing) is removed.

```r
n9 <- get.xls("nutrien9.xls"); n10 <- get.xls("nutrien10.xls")
NE5 <- cbind(n10, n9)
colSums(is.na(NE5))
NE5 <- NE5[, colSums(is.na(NE5)) < 10]   # removes chocol (29 NAs)
dim(NE5)
```

```
          gender         situation               tea            coffee
               1                 1                 2                 1
          height            weight               age             meat
               0                 2                 2                 0
            fish        raw_fruits cooked_fruits_veg            chocol
               1                 0                 2                29
             fat
               0
```

```
[1] 226  12
```

5.6- The same idea by rows with `rowSums(is.na())`: individual 86 has 7 of its 13 values missing (every other row has at most one) and is removed.

```
n11 <- get.xls("nutrien11.xls"); n12 <- get.xls("nutrien12.xls")
NE6 <- cbind(n12, n11)
nNA <- rowSums(is.na(NE6))
table(nNA)
NE6[nNA == max(nNA), ]
NE6 <- NE6[nNA < max(nNA), ]
dim(NE6)
```

```
nNA
  0   1   7
209  16   1
   gender situation tea coffee height weight age meat fish raw_fruits
86      2        NA   3     NA     NA     58  NA    3   NA          5
   cooked_fruits_veg chocol fat
86                NA      0  NA
[1] 225  13
```

5.7- Nobody: `sum(meat = 0 & fish = 0)` is 0 — one person never eats meat and four never eat fish, but none avoids both.

```
table(meat0 = ne$meat == 0, fish0 = ne$fish == 0)
sum(ne$meat == 0 & ne$fish == 0)
```

```
       fish0
meat0   FALSE TRUE
  FALSE   221    4
  TRUE      1    0
[1] 0
```

File `Intima_Media_Thickness.xls`:

5.1- BMI = weight/height^2 with height in metres, added with `transform()` (Section 5.1.4.7).

```
imt <- get.xls("Intima_Media_Thickness.xls")
imt <- transform(imt, BMI = weight / (height / 100)^2)
head(round(imt$BMI, 2))
```

```
[1] 24.22 21.39 23.42 26.61 23.37 20.20
```

5.2- Nine people are obese; their intima-media thicknesses (mm) are

```
imt$measure[imt$BMI > 30]
```

```
[1] 0.62 0.52 0.55 0.59 0.59 0.65 0.63 0.79 0.63
```

5.3- Athletic women are `GENDER = 2`= (female) with `SPORT = 1`=: 23 of them. The authors' companion solution filters on `SPORT = 1`= only, which returns the 49 athletic people of both sexes rather than the women the question asks for.

```
athl <- imt[imt$GENDER == 2 & imt$SPORT == 1, ]
nrow(athl); head(athl, 3)
```

```
[1] 23
   GENDER AGE height weight tobacco packyear SPORT measure alcohol      BMI
4       2  42    169     76       1       26     1    0.48       1 26.60971
8       2  26    162     61       1       20     1    0.45       1 23.24341
15      2  39    156     52       0       NA     1    0.45       1 21.36752
```

5.4- Reading "aged 50 or other" as the intended "aged 50 or older" (a typo), `subset()` returns 24 non-obese people with `AGE > 50`=.

```
nonob50 <- subset(imt, BMI <= 30 & AGE >= 50)
nrow(nonob50); head(nonob50, 3)
```

```
[1] 24
  GENDER AGE height weight tobacco packyear SPORT measure alcohol      BMI
3      2  53    164     63       1       30     0    0.65       0 23.42356
5      2  53    152     54       0       NA     0    0.45       1 23.37258
6      2  50    162     53       2       10     0    0.49       1 20.19509
```

File `bmichild.xls`:

5.1- The same formula, assigned to a new column.

```
bmi <- get.xls("bmichild.xls")
bmi$BMI <- bmi$weight / (bmi$height / 100)^2
head(bmi, 3)
```

```
  GENDER zep weight year month height      BMI
1      F   Y   16.0    3     5  100.0 16.00000
2      F   Y   14.0    3    10   97.0 14.87937
3      M   Y   13.5    3     5   95.5 14.80223
```

5.2- Age is stored in two columns, so the age in years is `year + month/12`.

```
small <- bmi[bmi$BMI < 15 & bmi$year + bmi$month / 12 <= 3.5, ]
small
```

```
    GENDER zep weight year month height      BMI
3        M   Y   13.5    3     5   95.5 14.80223
68       F   Y   12.0    3     3   90.5 14.65157
82       M   Y   15.0    3     6  101.0 14.70444
83       F   Y   14.0    3     5   97.0 14.87937
91       F   Y   12.0    3     2   90.0 14.81481
124      M   N   13.5    3     2   96.2 14.58759
145      M   N   13.7    3     2   96.0 14.86545
150      F   N   14.3    3     4   98.0 14.88963
```

5.3- There are 8 such children. The authors' companion solution counts 7 because its condition `month < 5`= drops the boy aged exactly 3 years 6 months (row 82), who satisfies "age <= 3.5 years".

```
nrow(small)
```

```
[1] 8
```

File `Birth_weight.xls`:

5.1- `pmin(PTL, 2)` caps the count at 2, and `factor()` turns it into a three-level variable (0, 1, "2 or more").

```
bw <- get.xls("Birth_weight.xls")
bw$PTL1 <- factor(pmin(bw$PTL, 2))
table(bw$PTL, bw$PTL1)
```

```
    0   1   2
0 159   0   0
1   0  24   0
2   0   0   5
3   0   0   1
```

5.2- The same for the number of first-trimester visits.

```
bw$FVT1 <- factor(pmin(bw$FVT, 2))
table(bw$FVT, bw$FVT1)
```

```
    0   1   2
0 100   0   0
1   0  47   0
2   0   0  30
3   0   0   7
4   0   0   4
6   0   0   1
```

5.3- `order()` gives the row permutation (Section 5.1.3).

```
bw <- bw[order(bw$BWT), ]
head(bw[, c("ID", "BWT", "LOW")], 3)
```

```
    ID  BWT LOW
131  4  709   1
132 10 1021   1
133 11 1135   1
```

5.4- White is `RACE = 1`= and black is `RACE = 2`=, so the selection is `RACE %in% 1:2 & SMOKE = 1`=: 62 smoking mothers (52 white, 10 black), still sorted by birth weight.

```r
sel <- bw[bw$RACE %in% 1:2 & bw$SMOKE == 1, ]
nrow(sel); table(sel$RACE)
head(sel, 3)
```

```
[1] 62

 1  2
52 10
    ID AGE LWT RACE SMOKE PTL HT UI FVT  BWT LOW PTL1 FVT1
133 11  34 187    2     1   0  1  0   0 1135   1    0    0
140 20  21 165    1     1   0  1  0   1 1790   1    0    1
141 22  32 105    1     1   0  0  0   0 1818   1    0    0
```

3.5 Worksheet 5.W.B — Handling missing values

Problem 5.W.B. Worksheet 5.W.B — Handling missing values — Infarction.xls
Import into a `data.frame` the following file: http://www.biostatisticien.eu/springeR/Infarction.xls
5.1- Which rows include missing values?
5.2- Which individuals have more than one missing value?
5.3- Which variables include missing values?
5.4- Give at least one solution to remove all rows of this `data.frame` which include at least one missing value. In addition to logical operators and the extracting function, you are only allowed to use: a) the functions `is.na()`, `prod()`, `apply()` and `as.logical()`; b) the functions `is.na()`, `apply()` and `any()`; c) the functions `is.na()`, `apply()` and `all()`; d) the function `complete.cases()`; e) the function `na.omit()`.

Solution. The file codes its missing values as `"."`, so it is imported with `na = "."`; without it `WEIGHT`, `BMI` and `ATCD` come in as character columns with no `NA` at all. The authors' companion solution uses `read.xls(url, na.strings = ".")` from `gdata`, which gdata 3.0 removed, so `read_excel()` from `readxl` is used here instead.

```r
library(readxl)
url <- "http://www.biostatisticien.eu/springeR/Infarction.xls"
download.file(url, f <- tempfile(fileext = ".xls"), mode = "wb", quiet = TRUE)
infarct <- as.data.frame(read_excel(f, na = "."))
dim(infarct)
```

```
[1] 449  10
```

5.1- Eighteen rows contain at least one missing value: rows 2, 5, 10, 20, 29, 33, 38, 49, 62, 71, 153, 195, 200, 202, 344, 346, 362 and 426.

```r
miss <- apply(is.na(infarct), 1, any)
which(miss)
sum(miss)
```

```
[1]   2   5  10  20  29  33  38  49  62  71 153 195 200 202 344 346 362 426
[1] 18
```

5.2- Twelve individuals have more than one missing value; they are identified by their `NUMBER` (2, 10, 29, 38, 49, 71, 239, 314, 362, 414, 191, 426), which differs from the row number from row 153 on. In every case `WEIGHT` is missing, hence `BMI` too, and individual 426 also lacks `ATCD`.

```r
nmiss <- apply(is.na(infarct), 1, sum)
infarct[nmiss > 1, ]
```

```
    NUMBER INFARCT CO TOBACCO AGE WEIGHT HEIGHT BMI ATCD HTA
2        2       0  0       0  17     NA    162  NA    0   0
10      10       0  0       0  38     NA    167  NA    0   0
29      29       0  0       0  40     NA    153  NA    0   0
38      38       0  0       0  67     NA    165  NA    0   0
49      49       0  0       0  41     NA    165  NA    0   0
71      71       0  0       0  53     NA    152  NA    0   1
153    239       0  1       0  46     NA    158  NA    0   0
```

```
195    314       1  0       0  53     NA    170  NA    1   0
200    362       1  1       0  47     NA    158  NA    0   0
346    414       1  1       1  37     NA    160  NA    1   0
362    191       0  0       2  26     NA    175  NA    0   0
426    426       1  1       2  33     NA    164  NA   NA   0
```

5.3- Three variables contain missing values: `WEIGHT` (12), `BMI` (12) and `ATCD` (7).

```r
nacol <- apply(is.na(infarct), 2, sum)
nacol[nacol > 0]
```

```
WEIGHT    BMI   ATCD
    12     12      7
```

5.4- All five solutions keep the same 431 complete rows ($449 - 18$). In a) the product of the 0/1 indicators of a row is 1 only if every value is present; b) drops rows where `any()` value is missing; c) keeps rows where `all()` values are present; d) and e) are the built-in shortcuts (`na.omit()` only adds an `"na.action"` attribute, hence `check.attributes = FALSE`).

```r
infa <- infarct[as.logical(apply(!is.na(infarct), 1, prod)), ]   # a)
infb <- infarct[!apply(is.na(infarct), 1, any), ]                # b)
infc <- infarct[apply(!is.na(infarct), 1, all), ]                # c)
infd <- infarct[complete.cases(infarct), ]                       # d)
infe <- na.omit(infarct)                                         # e)
sapply(list(a = infa, b = infb, c = infc, d = infd, e = infe), nrow)
identical(infa, infb) && identical(infa, infc) && identical(infa, infd)
all.equal(infa, infe, check.attributes = FALSE)
```

```
  a   b   c   d   e
431 431 431 431 431
[1] TRUE
[1] TRUE
```

3.6 Worksheet 5.W.C — Handling character strings

Problem 5.W.C. Worksheet 5.W.C — Handling character strings
5.1- Import the file `www.biostatisticien.eu/springeR/dept-pop.csv` into a data.frame called `dept`.
5.2- Replace the first column with two new columns: one called `numdep` with the French *département* numbers, and another with the names.

Solution.
5.1- Use `read.csv()` with `dec = ","`, because the areas are written with a French decimal comma (`"5762,44"`), which would otherwise be read as character strings:

```r
dept <- read.csv("http://www.biostatisticien.eu/springeR/dept-pop.csv",
                 dec = ",", encoding = "UTF-8")
str(dept)
```

```
'data.frame':        96 obs. of  3 variables:
 $ Departement: chr  "01 Ain" "02 Aisne" "03 Allier" "04 Alpes-de-Hte-Provence" ...
 $ Superficie : num  5762 7369 7340 6925 5549 ...
 $ Population : int  559 536 342 153 132 1064 302 287 146 298 ...
```

5.2- Every entry of `Departement` has a two-character number, then a space, then the name. So `substr()` gives the number and `substring()` from character 4 onwards gives the name:

```r
numdep <- substr(dept$Departement, 1, 2)
nom <- substring(dept$Departement, 4)
dept <- data.frame(numdep, nom, dept[, -1])
head(dept, 3)
dept[20:22, ]
```

```
  numdep    nom Superficie Population
1     01    Ain    5762.44        559
2     02  Aisne    7369.12        536
3     03 Allier    7340.11        342
```

```
   numdep          nom Superficie Population
20     2A Corse-du-Sud    4014.22        128
21     2B  Haute-Corse    4665.57        149
22     21    Côte-d'Or    8763.21        513
```

`numdep` has to stay a character vector because of Corsica's codes `2A` and `2B`.

3.7 Worksheet 5.W.D — Influenza epidemics in France since 1984

Problem 5.W.D. Worksheet 5.W.D — Manipulating various data sets — Influenza epidemics in France since 1984 (source: http://www.sentiweb.fr/?lang=en)
5.1- Import the file http://www.biostatisticien.eu/springeR/flu.csv into a data.frame called `flu`. Make sure that you are handling missing values correctly.
5.2- Type `names(flu)`. As you can see, `flu$Date` includes dates in the format year (with century; for example: 2003) followed by the week number (two digits).
5.3- Determine the list of possible week numbers (hint: use the functions `sort()`, `substring()` and `unique()`).
5.4- First, you need to retrieve these dates in R in an object of class `POSIXlt`, for example with the function `strptime()`. Using Table 5.3, and this function, transform the first (oldest) date into the `POSIX` format.
5.5- The data are in fact updated every Monday, since the first week. Determine which is the oldest date (Day, Month, Year) for which observations exist (hint: use the calendar http://sentiweb.fr/calendrier.php).
5.6- You should notice that there is a difference with the answer to question 5.4. To solve this problem, try adding a "1" at the end of the first date, and transforming it again with the function `strptime()`.
5.7- Display the ten first dates from the data files. Use the hint from the previous question to transform them with the function `strptime()`. Is the last date correct? If not, do you have an idea to solve this problem?
5.8- At this point, you should realize that the format of the dates in this file is not compatible with the POSIX format (which takes week numbers between 00 and 53). It is therefore not possible to directly use the function `strptime()` or `as.POSIXlt()` to transform these dates into an object type easy to handle by R. Type in the instruction `date1 <- as.POSIXlt("Day,Month,Year",format`"to be specified")= where you will replace *Day*, *Month* and *Year* with the oldest date, and *to be specified* with the relevant date format.
5.9- Type in the instruction `date1` then `date1+7`. What do you notice?
5.10- Find a way to add seven days to `date1` (hint: how many seconds are there in a day?).
5.11- Now, create the vector `dates` containing all the dates in the POSIX format, sorted from most ancient to newest (hint: use the function `nrow()`).
5.12- Use the function `substring()` on the vector `dates` to replace the first column of the data.frame `flu` with dates in the format `"year-month-day"` (for example: `"1992-12-07"`).
5.13- Use the vector `dates` and what you have learnt about extraction to select only the portion of the data.frame `flu` for dates between 15 September 1992 and 3 November 1993. Store this sub-table in an object called `portion`.
5.14- Calculate the number of cases of influenza over this period for each french region (hint: pay attention to missing values; use the argument `na.rm`). Store the results in a vector called `flucases`.

Solution.
5.1- Missing values are coded `"-"` in the file, so pass `na.strings = "-"` to `read.csv()` (otherwise every column containing a dash would be read as character).

```
flu <- read.csv("http://www.biostatisticien.eu/springeR/flu.csv",
                na.strings = "-")
flu[1:3, 1:6]
sum(is.na(flu))
```

```
      Date Alsace Aquitaine Auvergne Basse.Normandie Bourgogne
```

```
1 198444   1828       768       462              NA        NA
2 198445   1908       988       330              NA      1631
3 198446   2421      2198       330              NA      4381
[1] 1111
```

The 1276 weekly rows (1984 week 44 to 2009 week 15) are numeric for all 22 regions, with 1111 missing counts.

5.2- The first column is `Date` (an integer `yyyyww`), followed by the 22 regions of metropolitan France; `read.csv()` has replaced dashes and spaces in the names by dots.

```
names(flu)
```

```
 [1] "Date"                        "Alsace"
 [3] "Aquitaine"                   "Auvergne"
 [5] "Basse.Normandie"             "Bourgogne"
 [7] "Bretagne"                    "Centre"
 [9] "Champagne.Ardenne"           "Corse"
[11] "Franche.Comté"               "Haute.Normandie"
[13] "Languedoc.Roussillon"        "Limousin"
[15] "Lorraine"                    "Midi.Pyrénées"
[17] "Nord.Pas.de.Calais"          "Pays.de.la.Loire"
[19] "Picardie"                    "Poitou.Charentes"
[21] "Provence.Alpes.Côte.d.Azur" "Ile.de.France"
[23] "Rhône.Alpes"
```

5.3- The week numbers run from 01 to 53 (week 00 never occurs):

```
sort(unique(substring(flu$Date, 5, 6)))
```

```
 [1] "01" "02" "03" "04" "05" "06" "07" "08" "09" "10" "11" "12" "13" "14" "15"
[16] "16" "17" "18" "19" "20" "21" "22" "23" "24" "25" "26" "27" "28" "29" "30"
[31] "31" "32" "33" "34" "35" "36" "37" "38" "39" "40" "41" "42" "43" "44" "45"
[46] "46" "47" "48" "49" "50" "51" "52" "53"
```

5.4- With the codes `%Y` (year with century) and `%W` (week of the year) of Table 5.3:

```
strptime(flu$Date[1], format = "%Y%W", tz = "GMT")
```

```
[1] "1984-09-24 GMT"
```

The week number is silently ignored because no day of the week is given, so R fills in today's day and month (this was run on 24 September 2026); the result changes with the day you run it.

5.5- The oldest observation is for the week starting Monday 29 October 1984: the Sentiweb calendar numbers weeks as in ISO 8601 (week 1 contains the first Thursday of the year), and 29 October 1984 is the Monday of ISO week 1984-44, which R can confirm with the output-only codes `%G` and `%V`:

```
format(as.Date("1984-10-29"), "%A %G-W%V")
```

```
[1] "Monday 1984-W44"
```

5.6- Appending the day of the week `1` (Monday, code `%u`) makes `%W` effective and gives the right date:

```
strptime(paste0(flu$Date[1], "1"), format = "%Y%W%u", tz = "GMT")
```

```
[1] "1984-10-29 GMT"
```

5.7- The first nine dates are correct but the tenth, week `198501`, is converted to 7 January 1985 instead of Monday 31 December 1984:

```
flu$Date[1:10]
strptime(paste0(flu$Date[1:10], "1"), format = "%Y%W%u", tz = "GMT")
```

```
 [1] 198444 198445 198446 198447 198448 198449 198450 198451 198452 198501
 [1] "1984-10-29 GMT" "1984-11-05 GMT" "1984-11-12 GMT" "1984-11-19 GMT"
 [5] "1984-11-26 GMT" "1984-12-03 GMT" "1984-12-10 GMT" "1984-12-17 GMT"
 [9] "1984-12-24 GMT" "1985-01-07 GMT"
```

With `%W` week 1 starts on the first Monday of the year (7 January 1985), whereas the file uses ISO 8601 weeks, whose week 1 of 1985 starts on 31 December 1984; worse, the ISO weeks `198753`, `199253`, `199853` and `200453` give `NA` under `%W`. Since R reads the ISO codes `%G%V` only on output, the fix is to build the dates ourselves: start from the first Monday and add one week per row (questions 5.8 to 5.11).

5.8- The oldest date is given with the day, month and year codes `%d`, `%m`, `%Y` (`tz = "GMT"` avoids

daylight-saving shifts when seconds are added later):

```
date1 <- as.POSIXlt("29,10,1984", format = "%d,%m,%Y", tz = "GMT")
```

5.9- Adding 7 to a `POSIXlt` object adds 7 *seconds*, not 7 days:

```
date1
date1 + 7
```

```
[1] "1984-10-29 GMT"
[1] "1984-10-29 00:00:07 GMT"
```

5.10- A day has $24 \times 3600 = 86400$ seconds, so one week later is:

```
date1 + 7 * 24 * 3600
```

```
[1] "1984-11-05 GMT"
```

5.11- The rows are consecutive weeks in chronological order, so the i-th date is `date1` plus $(i - 1)$ weeks:

```
dates <- date1 + (0:(nrow(flu) - 1)) * 7 * 24 * 3600
head(dates, 3); tail(dates, 3)
all(format(dates, "%G%V") == flu$Date)
```

```
[1] "1984-10-29 GMT" "1984-11-05 GMT" "1984-11-12 GMT"
[1] "2009-03-23 GMT" "2009-03-30 GMT" "2009-04-06 GMT"
[1] TRUE
```

Formatting `dates` back as ISO year-week reproduces all 1276 codes of `flu$Date`, so the file has no missing week and the vector is correct.

5.12- The first 10 characters of each date are `"yyyy-mm-dd"`:

```
flu[, 1] <- substring(dates, 1, 10)
head(flu[, 1:4], 3)
```

```
        Date Alsace Aquitaine Auvergne
1 1984-10-29   1828       768      462
2 1984-11-05   1908       988      330
3 1984-11-12   2421      2198      330
```

5.13- A logical index built from `dates` selects the rows:

```
portion <- flu[dates >= as.POSIXlt("1992-09-15", tz = "GMT") &
               dates <= as.POSIXlt("1993-11-03", tz = "GMT"), ]
dim(portion); range(portion$Date)
```

```
[1] 59 23
[1] "1992-09-21" "1993-11-01"
```

The period covers 59 weekly reports, from the week of 21 September 1992 to that of 1 November 1993.

5.14- Sum each regional column with `na.rm = TRUE`, since Corse (10 weeks) and Limousin (1 week) have missing counts over the period, and a plain sum would return `NA` for them:

```
flucases <- colSums(portion[, -1], na.rm = TRUE)
flucases
```

```
          Alsace                Aquitaine
           74436                   147578
        Auvergne           Basse.Normandie
           75177                    45585
       Bourgogne                 Bretagne
           65885                   247188
         Centre          Champagne.Ardenne
          122898                    53265
          Corse              Franche.Comté
           3007                    69107
 Haute.Normandie       Languedoc.Roussillon
           70135                   107797
       Limousin                  Lorraine
           17427                    75718
  Midi.Pyrénées         Nord.Pas.de.Calais
          109458                   220433
Pays.de.la.Loire                  Picardie
```

```
          122803                      79289
Poitou.Charentes Provence.Alpes.Côte.d.Azur
           53101                     148653
   Ile.de.France                Rhône.Alpes
          400794                     317269
```

Ile-de-France (400794 estimated cases) and Rhône-Alpes (317269) had the most cases over the 1992-93 season, Corse the fewest (3007, partly because of its 10 unreported weeks).

3.8 Worksheet 5.W.E — Combining tables or lists; other manipulations

Problem 5.W.E. Worksheet 5.W.E — Combining tables or lists; other manipulations — Combining tables or lists; other manipulations

5.1- Input into R the two following tables (check the row names).

```
> a
  [,1] [,2]
1    1    4
2    2    5
6    3    6
> b
  [,1] [,2]
3    1    5
4    2    6
5    3    7
7    4    8
```

5.2- Combine `a` and `b` into a new table called `ab` containing:

```
> ab
  [,1] [,2]
1    1    4
2    2    5
3    1    5
4    2    6
5    3    7
6    3    6
7    4    8
```

(hint: use `rbind()` and `order()`).

5.3- Concatenate the elements of `list1` as columns of one matrix:

```
> list1 <- list()
> list1[[1]] <- matrix(runif(25),nr=5)
> list1[[2]] <- matrix(runif(30),nr=5)
> list1[[3]] <- matrix(runif(15),nr=5)
```

(hint: use the function `unlist()` or the function `do.call()`).

5.4- Concatenate the elements of `list2` as rows of one matrix:

```
> list2 <- list()
> list2[[1]] <- matrix(runif(25),nc=5)
> list2[[2]] <- matrix(runif(35),nc=5)
> list2[[3]] <- matrix(runif(15),nc=5)
```

(hint: use the function `unlist()` or the function `do.call()`).

5.5- Automatically select the diseases which have tobacco as a risk factor.

```
> tmp
      Disease     RiskFactors
1  Infarction tobacco, alcohol
2   Hepatitis         alcohol
3 Lung cancer         tobacco
```

(hint: use the function `grep()`).

Solution.

5.1- Build each matrix with `matrix()` and set the row names (the columns stay unnamed) through the `dimnames` argument.

```r
a <- matrix(1:6, ncol = 2, dimnames = list(c(1, 2, 6), NULL))
b <- matrix(1:8, ncol = 2, dimnames = list(c(3, 4, 5, 7), NULL))
a
```

```
b
```

```
  [,1] [,2]
1    1    4
2    2    5
6    3    6
  [,1] [,2]
3    1    5
4    2    6
5    3    7
7    4    8
```

5.2- Stack the two tables with `rbind()`, then reorder the rows by their row names, converted to numbers so that the sort is numeric and not alphabetical.

```
ab <- rbind(a, b)
ab <- ab[order(as.numeric(rownames(ab))), ]
ab
```

```
  [,1] [,2]
1    1    4
2    2    5
3    1    5
4    2    6
5    3    7
6    3    6
7    4    8
```

5.3- `do.call(cbind, list1)` passes the three matrices to `cbind()` as separate arguments. This gives a 5×14 matrix. Method (2): all three matrices have 5 rows and are stored column by column, so `matrix(unlist(list1), nrow = 5)` returns the same matrix, as the check below confirms (seed 1).

```
set.seed(1)
list1 <- list()
list1[[1]] <- matrix(runif(25), nr = 5)
list1[[2]] <- matrix(runif(30), nr = 5)
list1[[3]] <- matrix(runif(15), nr = 5)
m1 <- do.call(cbind, list1)
dim(m1)
identical(m1, matrix(unlist(list1), nrow = 5))
```

```
[1]  5 14
[1] TRUE
```

5.4- `do.call(rbind, list2)` stacks the three matrices by rows, which gives a 15×5 matrix. Method (2): `unlist()` reads a matrix column by column, so transpose each element first and refill the result by rows.

```
list2 <- list()
list2[[1]] <- matrix(runif(25), nc = 5)
list2[[2]] <- matrix(runif(35), nc = 5)
list2[[3]] <- matrix(runif(15), nc = 5)
m2 <- do.call(rbind, list2)
dim(m2)
identical(m2, matrix(unlist(lapply(list2, t)), ncol = 5, byrow = TRUE))
```

```
[1] 15  5
[1] TRUE
```

5.5- `grep("tobacco", tmp$RiskFactors)` returns the row numbers whose risk-factor string contains "tobacco". Use these numbers to index `Disease`: infarction and lung cancer are the two diseases with tobacco as a risk factor.

```
tmp <- data.frame(Disease = c("Infarction", "Hepatitis", "Lung cancer"),
                  RiskFactors = c("tobacco, alcohol", "alcohol", "tobacco"))
tmp$Disease[grep("tobacco", tmp$RiskFactors)]
```

```
[1] "Infarction"  "Lung cancer"
```

4 R and its documentation

Contents

4.1 Exercises 6.1–6.7

Problem 6.1. Which R instruction should you type to get help on the function `mean()`?

Solution. Type `help(mean)`, or its alias `?mean` (Section 6.1.1); for names the `?` shortcut cannot parse, such as `function`, quote the name: `help("function")`.

Problem 6.2. Explain the purpose of the command `apropos()`.

Solution. `apropos()` returns the names of all objects on the search path whose names contain the character string (a regular expression) given as argument, which is useful when you remember only part of a function's name (Section 6.1.2).

```
1 apropos("mean")
```

```
[1] ".colMeans"     ".rowMeans"     "colMeans"      "kmeans"
[5] "mean"          "mean.Date"     "mean.default"  "mean.difftime"
[9] "mean.POSIXct"  "mean.POSIXlt"  "rowMeans"      "weighted.mean"
```

Problem 6.3. Explain the purpose of the command `example()`.

Solution. `example(f)` runs the code of the `Examples` section of the help file of `f`, echoing each instruction (prefixed by the function name) followed by its result, and drawing any graphs it produces, which help files themselves do not show (Section 6.1.2).

```
1 example(mean)
```

```
mean> x <- c(0:10, 50)

mean> xm <- mean(x)

mean> c(xm, mean(x, trim = 0.10))
[1] 8.75 5.50
```

Problem 6.4. Explain the purpose of the command `RSiteSearch()`.

Solution. `RSiteSearch("string")` sends the query `string` to the search engine of the official R website (search.r-project.org) directly from the R console and displays the matching help pages, manuals, vignettes and so on in your web browser (Section 6.2.1); unlike `help.search()`, it searches documentation of all CRAN packages, not only the installed ones. For example `RSiteSearch("trimmed mean")`; the argument `restrict` limits the search to, e.g., `"functions"` or `"vignettes"`.

Problem 6.5. How is a help file structured?

Solution. A help file (as displayed by `?mean`, Section 6.1.1) has nine standard parts, sometimes supplemented by sections such as `Details` or `Note`:

1. a header giving the function name, its package and the origin of the file (`mean package:base R Documentation`);
2. an explicit title (`Arithmetic Mean`);
3. `Description`: a brief description of what the function does;
4. `Usage`: how to call it, with its compulsory and optional arguments and their default values;
5. `Arguments`: a description of each argument;
6. `Value`: what the function returns;
7. `References`: related articles or books;
8. `See Also`: similar or related functions;

9. `Examples`: code illustrating its use, runnable with `example()`.

Problem 6.6. Which command would you use to get the list of functions available in the package `stats`?

Solution. `library(help = stats)` (equivalently `help(package = "stats")`) displays the package description followed by an index of all its documented functions with a one-line title each (Section 6.1.2); `ls("package:stats")` returns the exported object names as a character vector.

```
length(ls("package:stats"))
head(ls("package:stats"), 6)
```

```
[1] 454
[1] "acf"        "acf2AR"     "add.scope"  "add1"       "addmargins"
[6] "aggregate"
```

Problem 6.7. Explain how to display a dataset available in R.

Solution. `data()` lists all the datasets available (Section 6.1.2); `data(name)` loads one into the workspace, after which typing its name (or `head(name)`) displays it and `?name` describes its variables.

```
d <- data(package = "datasets")$results
nrow(d)
data(USArrests)
head(USArrests, 4)
```

```
[1] 108
           Murder Assault UrbanPop Rape
Alabama      13.2     236       58 21.2
Alaska       10.0     263       48 44.5
Arizona       8.1     294       80 31.0
Arkansas      8.8     190       50 19.5
```

4.2 Worksheet 6.W — Where to find information

Problem 6.W. Worksheet 6.W — Where to find information
6.1- Find the R function which lists all combinations of k elements out of n.
6.2- Use this function to list all combinations of three elements out of `c(5,8,2,9)`.
6.3- Find the dataset available in R which gives the rates of violent crimes in the USA.
6.4- Describe the contents of this dataset.
6.5- Subscribe to the mailing list https://stat.ethz.ch/mailman/listinfo/r-help.
6.6- Read the rules to follow before asking a question (http://www.r-project.org/posting-guide.html).
6.7- Find out how to unsubscribe from the mailing list.
6.8- Using the method of your choosing, join the IRC channel R and start a polite conversation with channel members.
6.9- Register on the message board http://r.789695.n4.nabble.com/.
6.10- Read the R FAQ for Windows. Try to understand the meaning of TAB completion.
6.11- Use TAB completion to list all files in the current directory.

Solution.
6.1- The function is `combn()` (package `utils`), found with `help.search()` (Section 6.1); restricting the search to the base packages keeps the list short, and `apropos("comb")` finds it too.

```
help.search("combinations", package = c("base", "utils", "stats"))$matches[, c("Topic",
↪  "Package")]
apropos("comb")
```

```
      Topic Package
```

```
1 expand.grid    base
2 expand.grid    base
3       combn   utils
4         ave   stats
[1] "anscombe" "combn"
```

6.2- `combn(x, m)` returns one combination per column: the $\binom{4}{3} = 4$ triples.

```
combn(c(5, 8, 2, 9), 3)
```

```
     [,1] [,2] [,3] [,4]
[1,]    5    5    5    8
[2,]    8    8    2    2
[3,]    2    9    9    9
```

6.3- The dataset is `USArrests` (package `datasets`), located by searching the help titles for "crime":

```
help.search("crime", package = "datasets", agrep = FALSE)$matches[, c("Topic", "Package",
↪  "Title")]
```

```
      Topic  Package                            Title
1 USArrests datasets Violent Crime Rates by US State
```

6.4- `USArrests` is a data frame of 50 rows (the US states, as row names) and 4 variables giving, for 1973, the arrests per 100,000 residents for murder (`Murder`), assault (`Assault`) and rape (`Rape`), plus the percentage of the population living in urban areas (`UrbanPop`); `?USArrests` gives this description and the sources (World Almanac 1975, Statistical Abstracts of the US 1975).

```
str(USArrests)
summary(USArrests)
```

```
'data.frame':        50 obs. of  4 variables:
 $ Murder  : num  13.2 10 8.1 8.8 9 7.9 3.3 5.9 15.4 17.4 ...
 $ Assault : int  236 263 294 190 276 204 110 238 335 211 ...
 $ UrbanPop: int  58 48 80 50 91 78 77 72 80 60 ...
 $ Rape    : num  21.2 44.5 31 19.5 40.6 38.7 11.1 15.8 31.9 25.8 ...
     Murder          Assault         UrbanPop          Rape
 Min.   : 0.800   Min.   : 45.0   Min.   :32.00   Min.   : 7.30
 1st Qu.: 4.075   1st Qu.:109.0   1st Qu.:54.50   1st Qu.:15.07
 Median : 7.250   Median :159.0   Median :66.00   Median :20.10
 Mean   : 7.788   Mean   :170.8   Mean   :65.54   Mean   :21.23
 3rd Qu.:11.250   3rd Qu.:249.0   3rd Qu.:77.75   3rd Qu.:26.18
 Max.   :17.400   Max.   :337.0   Max.   :91.00   Max.   :46.00
```

Assault is by far the most frequent of the three offences (median 159 arrests per 100,000 against 7.25 for murder and 20.1 for rape), and the states range from 32% to 91% urban.

6.5- Go to https://stat.ethz.ch/mailman/listinfo/r-help (Section 6.2.3), fill in the "Subscribing to R-help" form (e-mail address, optional name and password, digest mode or not) and click Subscribe; the subscription only becomes active after you answer the confirmation e-mail the list server sends you.

6.6- The posting guide (now at https://www.r-project.org/posting-guide.html) asks you, before posting, to search the help pages (`?`, `help.search()`, `RSiteSearch()`), the manuals, the FAQs and the list archives; to use an informative subject line, plain text only and no HTML; to give a minimal, self-contained, reproducible example (small data built in the code or with `dput()`, the commands run and the exact error message) together with the output of `sessionInfo()`; to post questions about contributed packages to the package maintainer first; and not to use R-help for homework.

6.7- Return to the same listinfo page: its last section ("R-help Subscribers") takes your subscription address and opens the options page, where the Unsubscribe button is (a confirmation e-mail follows); equivalently, send an e-mail with the word `unsubscribe` to r-help-request@r-project.org. The link to that page is also printed at the foot of every message distributed by the list.

6.8- The freenode network named in Section 6.2.4 (and in the authors' companion solution, via its web chat) has been abandoned by the R community: the channel `#R` now lives on Libera.Chat, so with any IRC client (HexChat, the successor of xchat, or irssi) type

```
/server irc.libera.chat
/join #R
```

or open the web client https://web.libera.chat/ and enter `#R` as the channel; then greet the

channel ("Hello, I am learning R from …") and ask a precise question, following the same etiquette as in 6.6. No conversation can be reproduced here.

6.9- The Nabble forum http://r.789695.n4.nabble.com/ no longer exists (Nabble closed its hosted forums), so the registration cannot be done; the R-help messages it mirrored are archived at https://stat.ethz.ch/pipermail/r-help/, and the active web message boards for R today are Stack Overflow (tag `[r]`, register at https://stackoverflow.com/) and Posit Community (https://forum.posit.co/).

6.10- The R for Windows FAQ is at https://cran.r-project.org/bin/windows/base/rw-FAQ.html (and `file.path(R.home("doc"), "html", "rw-FAQ.html")` in a Windows installation). TAB completion means that when you press the TAB key the console completes what you have started to type: the name of an object or function, an argument name after `f(`, a component after `$` or `@`, or a file name inside quotes; when several completions are possible, pressing TAB twice lists them all. Its behaviour is controlled with `rc.settings()` (package `utils`), for instance `rc.settings(files = TRUE)`.

6.11- Type an opening quote, for example `read.csv("`, and press TAB twice: the console lists every file of the current directory (`getwd()`). The same completion engine that the console calls on TAB can be run from a script to show what is displayed:

```
d <- tempfile(); dir.create(d); old <- setwd(d)  # a directory holding three files
invisible(file.create(c("data1.csv", "data2.csv", "notes.txt")))
line <- 'read.csv("'                  # what has been typed before TAB
utils:::.assignLinebuffer(line)
utils:::.assignEnd(nchar(line))
invisible(utils:::.guessTokenFromLine())
invisible(utils:::.completeToken())
utils:::.retrieveCompletions()        # what TAB TAB displays
setwd(old)
```

```
[1] "data1.csv" "data2.csv" "notes.txt"
```

Typing one more character (`read.csv("d` then TAB) narrows the list to `data1.csv` and `data2.csv` and completes the common prefix `data`; `list.files()` gives the same list without the keyboard.

5 Drawing curves and plots

Contents

5.1 Exercises 7.1–7.7

Problem 7.1. What is the command `windows()` used for? And the command `dev.off()`?

Solution. `windows()` opens a new graphics window (device), which becomes the active one (`X11()` under Linux, `quartz()` on a Mac); `dev.off()` closes the active device, or device `n` with `dev.off(n)`, and returns the number of the device that becomes active (Section 7.1.1). Run headless, with `pdf(NULL)` standing in for `windows()`:

```
pdf(NULL); pdf(NULL)   # headless stand-ins for two windows() calls
dev.list()
dev.off()
dev.list()
```

```
pdf pdf
  2   3
pdf
  2
pdf
  2
```

Problem 7.2. Suppose you drew a plot with the command `curve(cos(x))`. Which R instruction would you use to save this plot as a PDF in a file called myplot.pdf?

Solution. From the screen window: `savePlot(filename = "myplot.pdf", type = "pdf")` (Windows) or `dev.copy2pdf(file = "myplot.pdf")` (any screen device), Section 7.1.1. On any system, including a headless one, redraw the plot on a `pdf()` device and close it:

```
pdf(file = "myplot.pdf")
curve(cos(x))
dev.off()
```

```
null device
          1
```

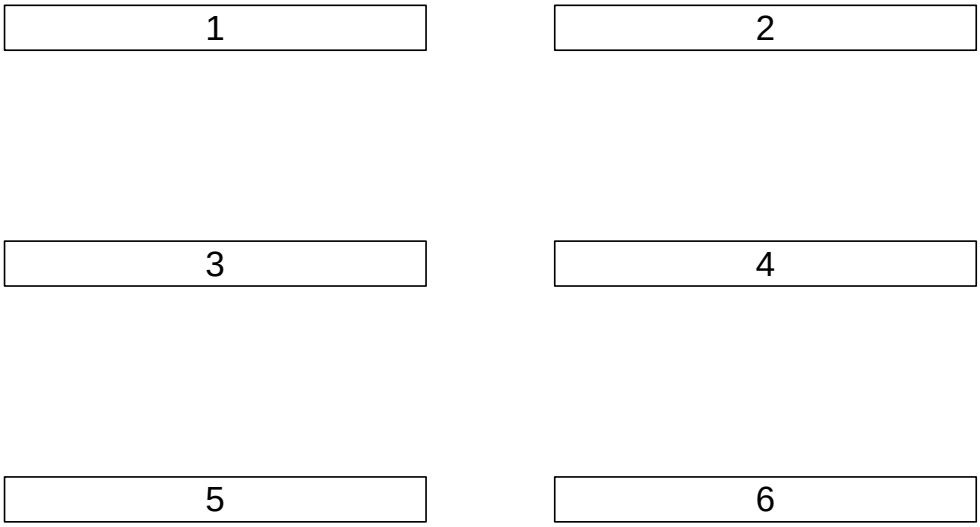
Problem 7.3. Give a detailed explanation of the effect of the instruction `par(mfrow=c(3,2))`.

Solution. It splits the active graphics window into a grid of 3 rows and 2 columns, that is 6 figure regions, which the next high-level plots fill one after the other row by row (`mfcol` would fill them column by column); a seventh plot clears the window and starts again in cell 1 (Section 7.1.2, Table 7.1). With three or more rows or columns R also shrinks the base character expansion `cex` to 0.66, and `par(mfrow = c(1, 1))` restores a single region.

```
par(mfrow = c(3, 2))
par("cex")
```

```
[1] 0.66
```

```
for (i in 1:6) { plot.new(); box(); text(0.5, 0.5, i, cex = 2) }
```



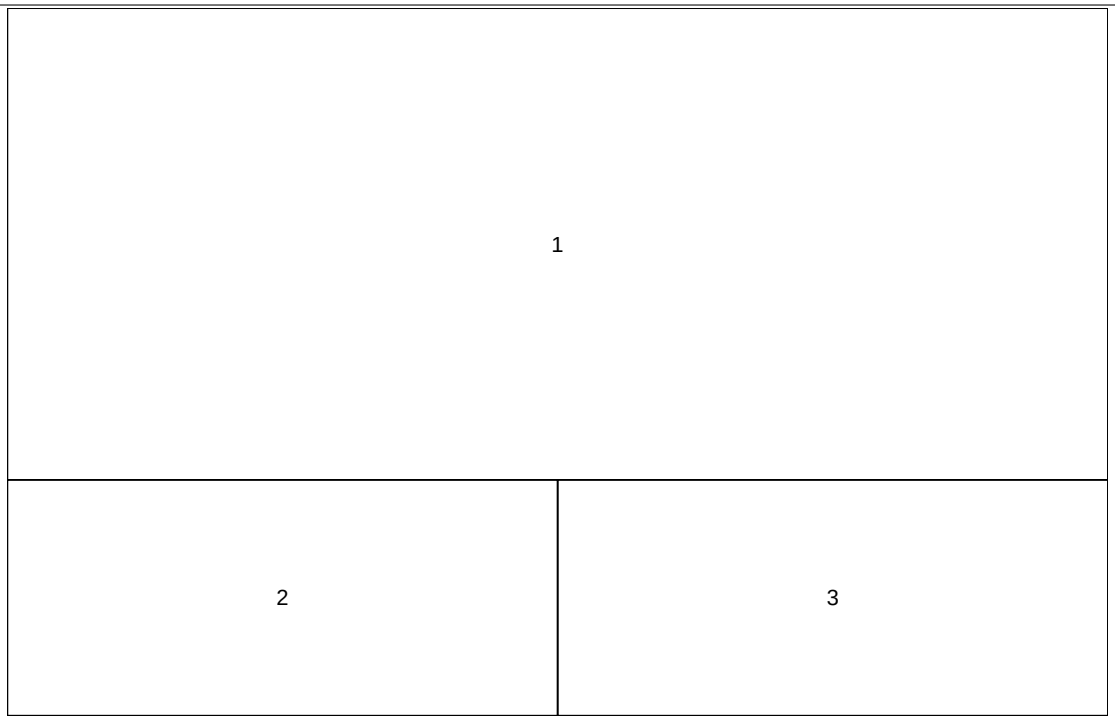
Problem 7.4. What is the function `layout()` used for?

Solution. `layout(mat)` splits the graphics window into regions of unequal size, which `par(mfrow)`= cannot do (Section 7.1.2). Each entry of the matrix `mat` gives the number of the plot drawn in that cell, equal numbers merge cells into one region, and 0 leaves a cell empty. The `widths` and `heights` arguments set relative column and row sizes, and `layout.show()` displays the result. Here plot 1 fills the whole top row:

```
nf <- layout(matrix(c(1, 1, 2, 3), nrow = 2, byrow = TRUE), heights = c(2, 1))
nf
```

```
[1] 3
```

```
layout.show(nf)
```



Problem 7.5. Which command would you use to add a scatter plot to a pre-existing plot?

Solution. `points(x, y)` adds the points to the current plot without erasing it; `type = "l"` or `"b"` also joins them with lines (Section 7.2.1).

Problem 7.6. Which argument of the function `plot()` would you use to get points with dashes between them?

Solution. The argument `type`: `type = "b"` draws both the points and the line segments joining them (`"o"` overplots points and lines), Section 7.2.1. For the segments to be drawn as actual dashes, add `lty = 2`, e.g. `plot(1:4, c(2, 3, 4, 1), type = "b", lty = 2)`. The authors' companion solution uses `type = "l"`, but that draws the lines alone without the points, so `"b"` is the value that answers the question.

Problem 7.7. Name a function which draws a straight line.

Solution. `abline()`, e.g. `abline(a = 0, b = 1)` for the line $y = x$, or `abline(h = 0)` and `abline(v = 0)` for horizontal and vertical lines; `segments()` and `lines()` draw finite line segments (Section 7.2.2).

5.2 Exercises 7.8–7.14

Problem 7.8. What is the function `curve()` used for?

Solution. `curve()` draws the graph of a function given by an expression in `x`, e.g. `curve(x^2 - 1, from = -2, to = 2)`, evaluated at `n = 101` points of the interval by default; `add = TRUE` overlays it on an existing plot (Section 7.2.5).

Problem 7.9. Which argument would you use to manage the colours in a plot?

Solution. The argument `col` (e.g. `col = "blue"`, a number, or a code such as `"#FF0000"`), with its variants `col.main`, `col.lab`, `col.axis`, `col.sub`, `fg` and `bg` for the other parts of the plot (Section 7.3, Table 7.2).

Problem 7.10. Which function would you use to display an image? Give an instruction to display an image, the values of which are given in a matrix `X`, so that the output is coherent with the way `X` is displayed in the console.

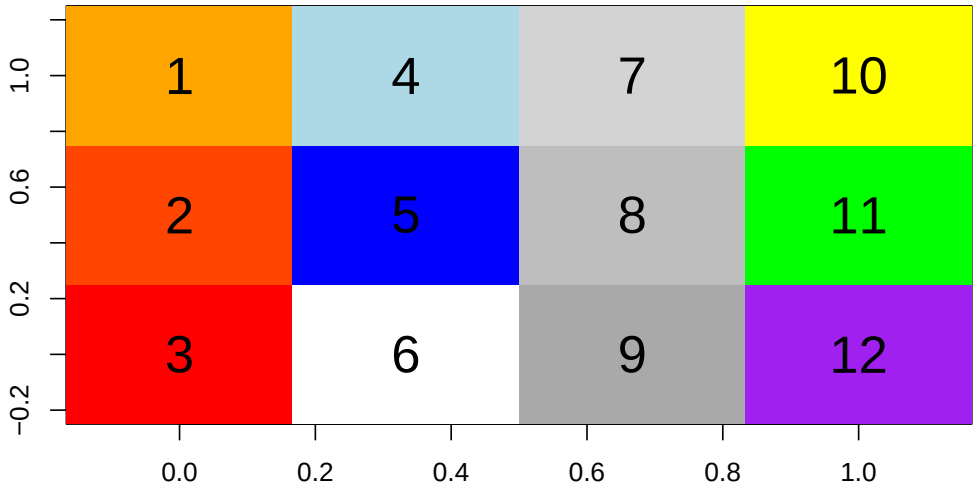
Solution. `image()`. It draws row 1 of `X` at the bottom and the columns from left to right, a 90-degree anticlockwise rotation of the console display (Section 7.3.3). So transpose `X` and reverse the columns of the result: `image(t(X)[, nrow(X):1])`. This is the same matrix as the book's `as.matrix(rev(as.data.frame(t(X))))`:

```
X <- matrix(1:12, nrow = 3)
t(X)[, nrow(X):1]
```

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

```
colours <- c("orange", "orangered", "red", "lightblue", "blue", "white",
             "lightgrey", "grey", "darkgrey", "yellow", "green", "purple")
image(t(X)[, nrow(X):1], col = colours)
```

```
text(rep(c(0, 1/3, 2/3, 1), each = 3), rep(c(1, 0.5, 0), 4), 1:12, cex = 2)
```



Problem 7.11. Which function would you use to add text to a plot?

Solution. `text(x, y, labels)` writes `labels` at the coordinates `(x, y)` inside the plot, and `labels` can be a mathematical expression such as `expression(hat(beta)[1])`. `mtext()` writes in the margins (Sections 7.4.1 and 7.4.2).

Problem 7.12. Which function would you use to find the coordinates of a point in a plot with a click of the mouse?

Solution. `locator()`: `locator(1)` waits for one click on the active window and returns the list `(x, y)` of its coordinates in the plot's scale, e.g. `text(locator(1), labels = "Here")` (Section 7.6.1). It needs an interactive screen device, so it cannot be run here. The authors' companion solution also lists `identify()`, but that function returns the index of the nearest existing data point rather than the coordinates of the click.

Problem 7.13. Give a detailed explanation of the effect of the instruction `par(ask=TRUE)`.

Solution. From then on, before each high-level plot that would erase the current window (a new page), R pauses, and the next plot is drawn only after the user presses Enter in the console or clicks the graphics window (Table 7.1). This lets you look at a series of plots one by one, e.g. `par(ask = TRUE); for (i in 1:3) hist(rnorm(100))`. The setting applies only to the active device and stays in force until `par(ask = FALSE)` or the device is closed. Table 7.1 recommends the newer equivalent `devAskNewPage(TRUE)`.

Problem 7.14. Which argument of the function `par()` would you use to specify the type of line drawn by the function `curve()`?

Solution. `lty` (0 blank, 1 solid, 2 dashed, 3 dotted, 4 dot-dash, 5 long dash, 6 two-dash, or a string such as `"1373"`), e.g. `par(lty = 2); curve(cos(x))`; its width is set by `lwd` (Section 7.7, Table 7.5).

5.3 Exercises 7.15–7.16

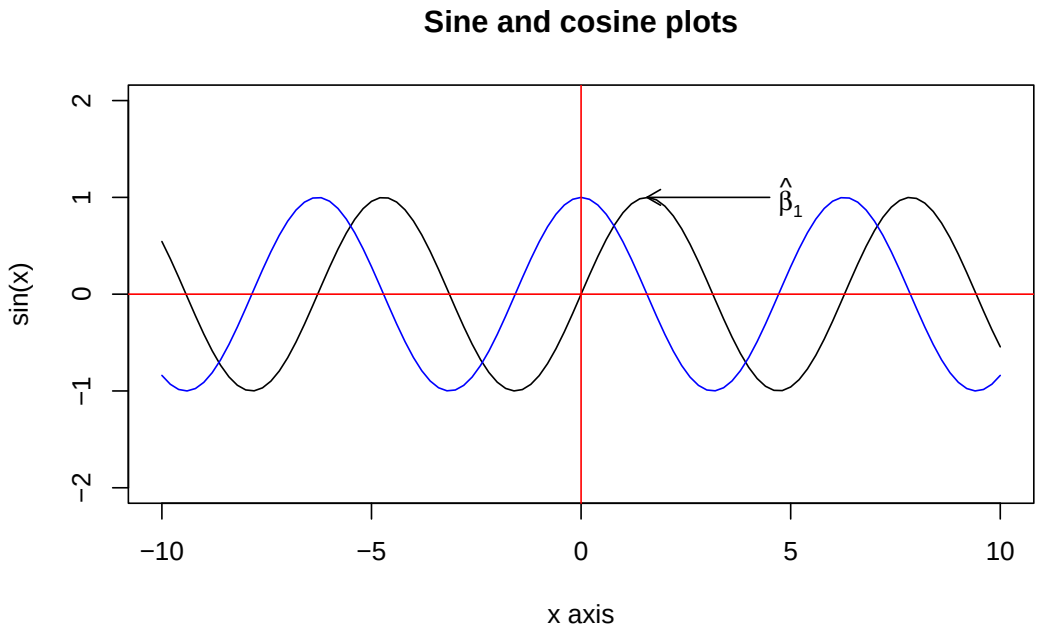
Problem 7.15. Which argument of the function `par()` would you use to display other symbols instead of small circles in a scatter plot?

Solution. `pch`, either a symbol code from 0 to 25 or a single character, e.g. `par(pch = 19)` for filled discs or `par(pch = "+")` (Section 7.7, Table 7.5); `cex` sets their size.

Problem 7.16. Give a list of instructions to display the following plot. The central axis system must be displayed in red. The cosine curve must be displayed in blue.
(The printed plot, titled "Sine and cosine plots", shows $\sin(x)$ in black and $\cos(x)$ in blue for $x \in [-10, 10]$, with the y-axis running from -2 to 2. The x-axis label is "x axis" and the y-axis label is "sin(x)". The lines $y = 0$ and $x = 0$ cross at the origin, and an arrow at height 1 points left to the peak of the sine curve at $x = \pi/2$, starting from the label $\hat{\beta}_1$.)

Solution. Use `curve()` twice, `abline()` for the red axes, `arrows()` and `text()` with a plotmath `expression()` for the label (Sections 7.2 and 7.4.1):

```
curve(sin(x), from = -10, to = 10, ylim = c(-2, 2),
      main = "Sine and cosine plots", xlab = "x axis")
curve(cos(x), add = TRUE, col = "blue")
abline(h = 0, v = 0, col = "red")
arrows(x0 = 4.5, y0 = 1, x1 = pi/2, y1 = 1, length = 0.1)
text(x = 5, y = 1, labels = expression(hat(beta)[1]))
```



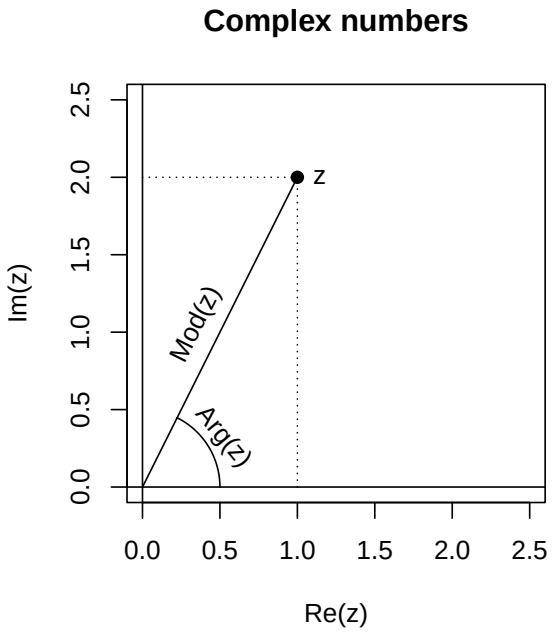
5.4 Worksheet 7.W.A — Complex numbers

Problem 7.W.A. Worksheet 7.W.A — Creating various plots — Complex numbers
7.1- Reproduce the plot on complex numbers in Chapter 3 (Figure 3.2, "Characteristics of a complex number", Section 3.2.1.2).

Solution.
7.1- Plot the point $z = 1 + 2i$ with `plot()`, then add the axes with `abline()`, the modulus and the dotted projections with `segments()`, the argument arc with `lines()` and the rotated labels with

`text(..., srt)`=; `par(pty = "s")` makes the plotting region square, as in the book.

```r
z <- 1 + 2i
op <- par(pty = "s")
plot(Re(z), Im(z), xlim = c(0, 2.5), ylim = c(0, 2.5), pch = 19,
     xlab = "Re(z)", ylab = "Im(z)", main = "Complex numbers")
abline(h = 0, v = 0)                                  # real and imaginary axes
text(Re(z), Im(z), "z", pos = 4)
segments(0, 0, Re(z), Im(z))                          # the modulus
segments(c(0, Re(z)), c(Im(z), 0), Re(z), Im(z), lty = "dotted")
theta <- seq(0, Arg(z), length.out = 100)
lines(0.5 * cos(theta), 0.5 * sin(theta))             # arc for the argument
text(0.35, 1.05, "Mod(z)", srt = Arg(z) * 180 / pi)
text(0.52, 0.32, "Arg(z)", srt = -50)
par(op)
```



The segment from the origin has length `Mod(z)` $= \sqrt{5} \approx 2.236$ and makes the angle `Arg(z)` ≈ 1.107 rad with the real axis; the `Mod(z)` label is rotated by that angle converted to degrees.

5.5 Worksheet 7.W.B — Flag of Canada

Problem 7.W.B. Worksheet 7.W.B — Creating various plots — Flag of Canada
7.1- Install the package `caTools`.
7.2- Use the function `read.gif()` to read the image http://www.biostatisticien.eu/springeR/canada.gif
7.3- Display the image with the function `image()`.
7.4- Re-draw this flag in another window, using the functions `plot()`, `rect()` and `polygon()` (hint: use the function `locator()`).

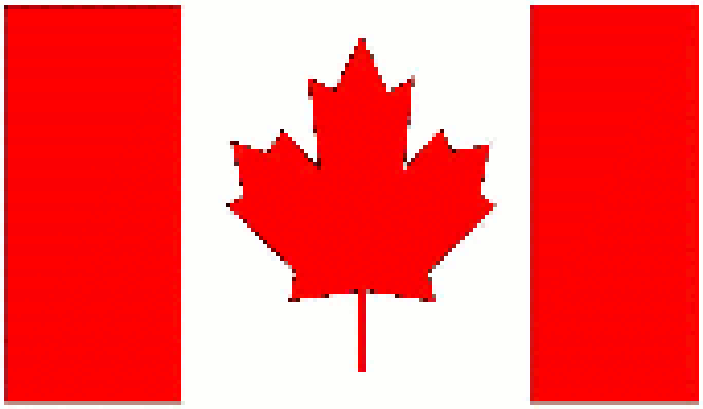
Solution.
7.1- `install.packages("caTools")`, then `library(caTools)` in each session (Section 9.5); the installed version 1.18.3 still exports `read.gif()`.
7.2- `read.gif()` returns a list whose `image` component is a matrix of colour indices (0 to 255, one per pixel, rows running from the top of the picture) and whose `col` component is the 256-colour palette.

```r
library(caTools)
canada <- read.gif("http://www.biostatisticien.eu/springeR/canada.gif")
str(canada, max.level = 1)
```

```
List of 4
 $ image      : int [1:172, 1:228] 255 255 255 255 255 255 255 255 255 255 ...
 $ col        : chr [1:256] "#170401FF" "#230100FF" "#330402FF" "#3B0101FF" ...
 $ transparent: NULL
 $ comment    : chr "Created with The GIMP"
```

7.3- Call `image()` on the transposed matrix with its columns reversed: `image()` puts the matrix rows along the x-axis and draws row 1 at the bottom, so the plain `image(canada$image, col = canada$col)` shows the flag rotated a quarter turn. Index k must get colour `col[k + 1]`, which the half-integer `breaks` guarantee, and `asp` keeps the 172 by 228 pixel shape.

```r
m <- canada$image
par(mar = c(0, 0, 0, 0))
image(t(m)[, nrow(m):1], col = canada$col, breaks = (-1:255) + 0.5,
      axes = FALSE, asp = nrow(m) / ncol(m), useRaster = TRUE)
```



7.4- Use pixel coordinates, x = column and $y = 173 -$ row, so the red bands are two `rect()` calls and the maple leaf is one `polygon()`. With a graphics window open, `pts <- locator(type = "l")` collects the leaf vertices by clicking and `polygon(pts, col = "red")` fills them. `locator()` needs a mouse and cannot run in a headless build, so the vertices below were read from the pixel matrix instead. The leaf is symmetric about $x = 118$, so we list only its left half, from the top tip round the left edge down to the stem, and mirror it.

```r
left <- cbind(p = c(34, 29, 27.5, 21, 22, 22.5, 23.5, 14, 12, 10, 3, 4, 5, 2, 6,
                    18, 17, 17, 25, 33, 33),
              r = c(41.5, 51, 54.5, 51.5, 55, 64, 73.5, 64.5, 68, 69.5, 67.5, 74,
                    80, 82.5, 86, 97.5, 101, 105, 105, 103, 123))
leaf <- rbind(left, cbind(68 - rev(left[, "p"]), rev(left[, "r"])))
x <- 84 + leaf[, 1]; y <- 173 - leaf[, 2]
dev.new()   # "another window"
plot(0, type = "n", xlim = c(31, 200), ylim = c(43, 139), asp = 1,
     axes = FALSE, xlab = "", ylab = "")
rect(31, 43, 200, 139, col = "white", border = "grey")
rect(31, 43, 74, 139, col = "red", border = NA)
rect(159, 43, 200, 139, col = "red", border = NA)
polygon(x, y, col = "red", border = NA)
```

5.6 Worksheet 7.W.C — Frequency tables

Problem 7.W.C. Worksheet 7.W.C — Frequency tables — Burning sensation under a hydrogel bandage

The following table represents scores of burning sensation for sixteen subjects in a study to test a new hydrogel bandage. The first column gives the subject number. The next columns give the score of burning sensation (on a scale from 1 to 4) for weeks 1 (`W1`) to 7 (`W7`).

Nr	W1	W2	W3	W4	W5	W6	W7
1	1	1	1	1	1	1	1
2	1	1	1	1	1	1	2
3	1	1	1	1	1	2	3
4	1	1	1	1	1	3	4
5	1	1	1	1	2	3	3
6	1	1	1	1	1	1	1
7	1	1	1	3	4	2	2
8	1	1	1	1	1	1	1
9	1	1	1	1	1	1	1
10	1	1	1	1	1	1	4
11	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1
13	1	2	1	3	2	3	4
14	1	1	1	2	2	4	4
15	1	1	1	1	1	1	1
16	1	1	1	1	1	1	1

We shall propose an interesting way to display these data.

7.1- For week `W7`, calculate the vector $(f_1, 1-f_1, f_2, 1-f_2, f_3, 1-f_3, f_4, 1-f_4)$ where f_i is the frequency of modality i ($1 \leq i \leq 4$) observed in week `W7` over the sixteen subjects. (Hint: use the functions `tabulate()`, `cbind()`, `t()` and `as.vector()`.)

7.2- Now, use the function `apply()` to do the same calculation for all other weeks. Store the result in a matrix.

7.3- Use the function `barplot()` and the argument `col=c("black","white")` on this matrix. The plot you get gives an overview of the evolution of the variable `Burning sensation` over time.

7.4- Change the previous plot so that the bars representing frequencies are in red. Week numbers should be in blue, and at the top of the plot instead of the bottom. Modality numbers should be on the left, in blue. Add a title to the plot.

Solution.
7.1- In week `W7` the frequencies are $f_1 = 0.5$, $f_2 = f_3 = 0.125$ and $f_4 = 0.25$; `cbind(f, 1 - f)` makes a 4×2 matrix whose transpose, read column by column by `as.vector()`, interleaves each f_i with $1 - f_i$. The argument `nbins = 4` makes `tabulate()` count a score that never occurs as 0.

```r
burn <- data.frame(
  W1 = rep(1, 16),
  W2 = c(1,1,1,1,1,1,1,1,1,1,1,2,1,1,1),
  W3 = rep(1, 16),
  W4 = c(1,1,1,1,1,1,3,1,1,1,1,1,3,2,1,1),
  W5 = c(1,1,1,1,2,1,4,1,1,1,1,1,2,2,1,1),
  W6 = c(1,1,2,3,3,1,2,1,1,1,1,1,3,4,1,1),
  W7 = c(1,2,3,4,3,1,2,1,1,4,1,1,4,4,1,1))
f <- tabulate(burn$W7, nbins = 4) / 16
v7 <- as.vector(t(cbind(f, 1 - f)))
v7
```

```
[1] 0.500 0.500 0.125 0.875 0.125 0.875 0.250 0.750
```

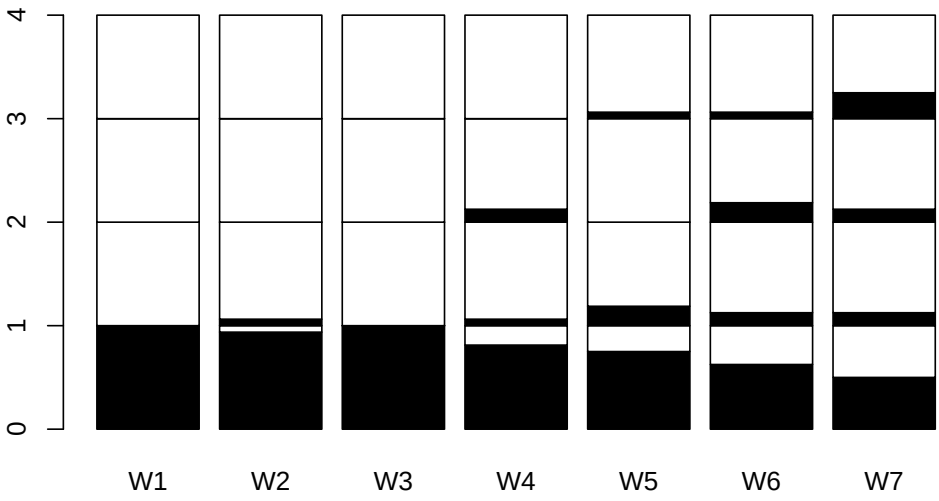
7.2- Wrap the calculation in a function and apply it to each column (`MARGIN = 2`); the result is an 8×7 matrix with one column per week, and every column sums to 4.

```r
freqs <- function(w) {
  f <- tabulate(w, nbins = 4) / length(w)
  as.vector(t(cbind(f, 1 - f)))
}
M <- apply(burn, 2, freqs)
rownames(M) <- paste0(rep(c("f", "1-f"), 4), rep(1:4, each = 2))
M
```

```
     W1     W2 W3     W4     W5     W6    W7
f1    1 0.9375  1 0.8125 0.7500 0.6250 0.500
1-f1  0 0.0625  0 0.1875 0.2500 0.3750 0.500
f2    0 0.0625  0 0.0625 0.1875 0.1250 0.125
1-f2  1 0.9375  1 0.9375 0.8125 0.8750 0.875
f3    0 0.0000  0 0.1250 0.0000 0.1875 0.125
1-f3  1 1.0000  1 0.8750 1.0000 0.8125 0.875
f4    0 0.0000  0 0.0000 0.0625 0.0625 0.250
1-f4  1 1.0000  1 1.0000 0.9375 0.9375 0.750
```

7.3- `barplot()` stacks the eight entries of each column, alternating black and white, so each week becomes a bar made of four unit-high bands: the black part of band i (counted from the bottom) is the frequency of score i.

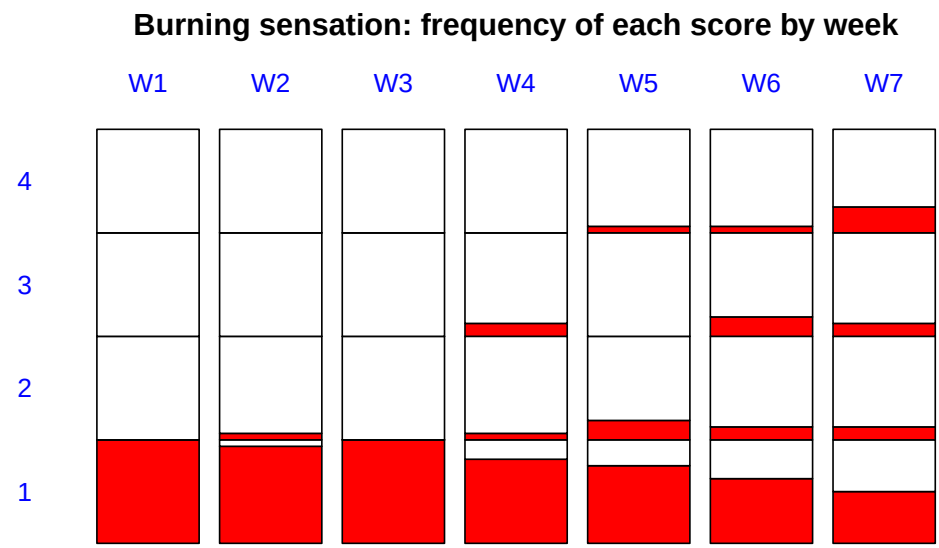
```r
barplot(M, col = c("black", "white"))
```



In weeks 1 and 3 every subject scores 1; from week 4 on the black share of band 1 shrinks (from 1 to 0.5 in week 7) while the higher bands fill, so the burning sensation gets steadily worse over the seven weeks.

7.4- Suppress the default axes and week names (`axes = FALSE`, `names.arg`), then add them back with `axis()` (Section 7.5.2): side 3 at the bar midpoints returned by `barplot()` for the weeks, side 2 at the band centres 0.5, 1.5, 2.5, 3.5 for the scores, both with `col.axis = "blue"`; the title is added with `title()` (Section 7.5.1), raised with `line = 3` so it clears the top axis.

```
bp <- barplot(M, col = c("red", "white"), axes = FALSE,
              names.arg = rep("", 7))
axis(3, at = bp, labels = colnames(M), col.axis = "blue", tick = FALSE)
axis(2, at = 0:3 + 0.5, labels = 1:4, col.axis = "blue", las = 1,
     tick = FALSE)
title("Burning sensation: frequency of each score by week", line = 3)
```



5.7 Worksheet 7.W.D — Anatomic images of the brain

Problem 7.W.D. Worksheet 7.W.D — Anatomic images of the brain
Data acquired during Magnetic Resonance Imaging (MRI) of the brain are usually stored as a binary file with extension `*.img`. We shall see how to read and display such data.
7.1- Import the file http://www.biostatisticien.eu/springeR/anat.img, which contains the image of a single brain section of 256×256 pixels, using the function `readBin()`. These data can be treated as a sequence of 256×256 byte pairs (`raw`). Store these data in an object called `bytes`.
7.2- When the data were recorded, each pair of bytes was in fact written in reverse (for example, the pair `02 56` was recorded as `56 02`). You therefore need to permute each byte pair. Store the result of this operation in `x`.
7.3- This sequence of byte pairs now needs to be transformed into numeric values which can be displayed graphically. With two bytes (such as `02 56`), you can use the instruction `as.numeric("0x0256")` to get the corresponding decimal value (in this case, the result is 598). Transform `x` into decimal values and store the result in an object called `values` (hint: use the functions `matrix()`, `apply()` and `paste()`).
7.4- Recreate the matrix of size 256×256 containing the observations stored in `values`. Call this matrix `X`.
7.5- Use the function `image()` on `X`. Use a colour gradient of shades of grey with about one hundred shades, using the function `gray()`.
7.6- Note that the R package `AnalyzeFMRI` does exactly that. After downloading the two files http://www.biostatisticien.eu/springeR/anat.img and http://www.biostatisticien.eu/springeR/anat.hdr, and after installing package `AnalyzeFMRI`, you could have got the exact same result by typing:

```
require(AnalyzeFMRI)
Y <- f.read.volume("/path/to/anat.img") # Replace path.
image(X,col=gray(0:1000 / 1000))
```

Solution.
7.1- Open a binary connection to the URL and read its $2 \times 256 \times 256 = 131072$ bytes as `raw`:

```
con <- url("http://www.biostatisticien.eu/springeR/anat.img", open = "rb")
bytes <- readBin(con, what = "raw", n = 2 * 256 * 256)
close(con)
length(bytes)
head(bytes)
```

```
[1] 131072
[1] 56 02 c4 02 64 02
```

7.2- Put the bytes in a two-row matrix (one column per pair), swap the rows and flatten back:

```
x <- as.vector(matrix(bytes, nrow = 2)[2:1, ])
head(x)
```

```
[1] 02 56 02 c4 02 64
```

7.3- For each column (byte pair) of the two-row matrix, `paste()` the two hexadecimal bytes behind `"0x"` and convert with `as.numeric()`:

```
values <- as.numeric(apply(matrix(x, nrow = 2), 2,
                           function(b) paste0("0x", b[1], b[2])))
head(values)
range(values)
```

```
[1] 598 708 612 624 429 576
[1]    93 24088
```

The first pixel is 598, the value quoted in the statement; intensities run from 93 to 24088.
7.4- The pixels are stored column by column, so `matrix()` with its default `byrow = FALSE` rebuilds the image:

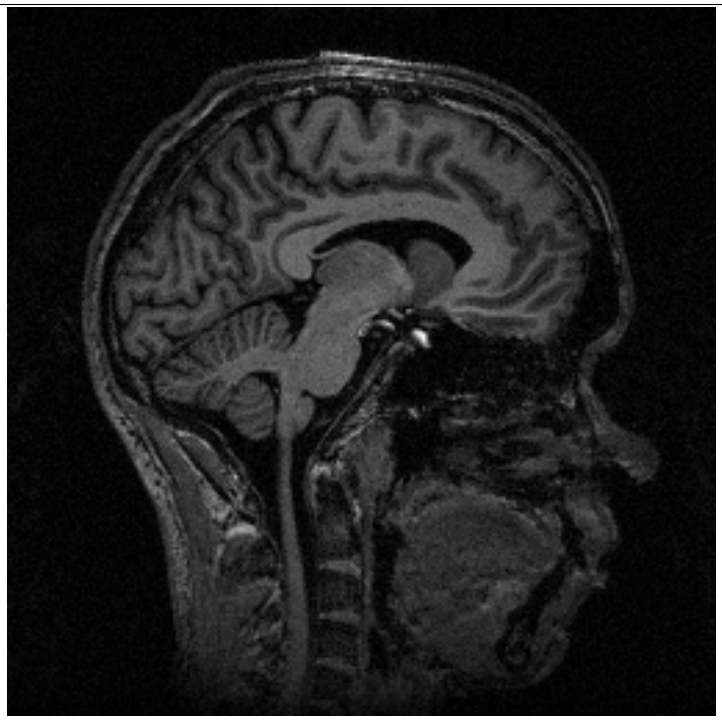
```
X <- matrix(values, nrow = 256, ncol = 256)
```

```
dim(X)
```

```
[1] 256 256
```

7.5- `image()` (Section 7.3.3) with `col = gray(0:100 / 100)`, i.e. 101 grey levels from black to white, shows a sagittal section of the head:

```
par(mar = c(0, 0, 0, 0))
image(X, col = gray(0:100 / 100), axes = FALSE, asp = 1, useRaster = TRUE)
```



7.6- With `AnalyzeFMRI` (version 1.1-26 from CRAN) `f.read.volume()` reads the Analyze header `anat.hdr` and returns a $256 \times 256 \times 1$ array whose single slice is identical to our `X`:

```
download.file("http://www.biostatisticien.eu/springeR/anat.img", "anat.img",
              mode = "wb", quiet = TRUE)
download.file("http://www.biostatisticien.eu/springeR/anat.hdr", "anat.hdr",
              mode = "wb", quiet = TRUE)
require(AnalyzeFMRI)
Y <- f.read.volume("anat.img")
dim(Y)
all.equal(Y[, , 1], X, check.attributes = FALSE)
```

```
[1] 256 256   1
[1] TRUE
```

So `image(Y[, , 1], col = gray(0:1000 / 1000))` redraws the figure of 7.5; the book's last line `image(X, ...)` should read `image(Y[, , 1], ...)` (erratum), since the object just read is `Y` and it is three-dimensional.

5.8 Worksheet 7.W.E — Drawing the map of a region of France

Problem 7.W.E. Worksheet 7.W.E — Drawing the map of a region of France
The package `maps` includes maps of various countries. We shall use it to draw the borders of a French *département*.
7.1- Install and load the packages `maps` and `mapdata`.
7.2- Draw the map of France: `map("france")`.
7.3- Get the data on borders of French regions: `france <- map("france",plot=FALSE)`
7.4- Display the contents of the object `france` and make sure you understand how it is organized. For example, note that latitude and longitude data are stored in `france$x` / `france$y` for each *département* in `france$names` (until the next `NA`).

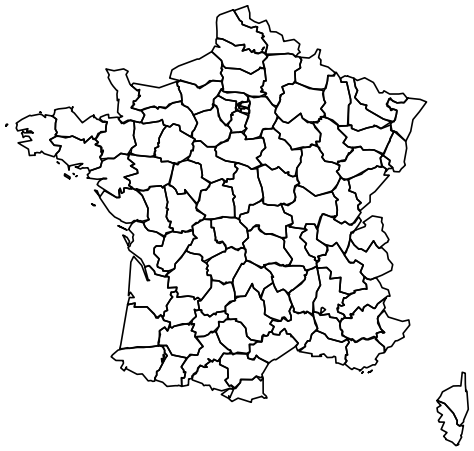
7.5- Create a vector `indNA` containing the indices of missing values.
7.6- Create an object containing the name of the *département* of your choice (for example `depname <- "Gard"`).
7.7- Create an object called `inddept` containing the *département* index `depname` in the vector `france$names`.
7.8- Draw the map of your *département*.
7.9- Add a point for a place on the map. You can get the coordinates (latitude and longitude) of a place on the website http://www.gpsvisualizer.com/geocode.

Solution.
7.1- `install.packages()` once, then `library()` in every session (`mapdata` only adds high-resolution databases such as `"worldHires"`; the `"france"` map itself ships with `maps`).

```
install.packages(c("maps", "mapdata"))
library(maps)
library(mapdata)
```

7.2- A single call draws the borders of the 96 metropolitan *départements* (Corsica included) held in the database.

```
map("france")
```



7.3- With `plot = FALSE`, `map()` returns the coordinates instead of drawing them.

```
france <- map("france", plot = FALSE)
```

7.4- `france` is a list of class `"map"` with four components: `x` (longitudes) and `y` (latitudes), both of length 13466, `range` (the bounding box) and `names` (114 polyline names).

```
str(france)
head(france$names, 6)
head(cbind(x = france$x, y = france$y), 3)
```

```
List of 4
 $ x    : num [1:13466] 2.56 2.58 2.61 2.63 2.63 ...
 $ y    : num [1:13466] 51.1 51 51 51 50.9 ...
 $ range: num [1:4] -5.14 9.56 41.37 51.1
 $ names: chr [1:114] "Nord" "Pas-de-Calais" "Somme" "Nord:1" ...
 - attr(*, "class")= chr "map"
[1] "Nord"           "Pas-de-Calais"  "Somme"          "Nord:1"
```

```
[5] "Ardennes"       "Seine-Maritime"
            x        y
[1,] 2.557093 51.09752
[2,] 2.579995 51.00298
[3,] 2.609101 50.98545
```

The `x=/=y` vectors are the 114 polygons laid end to end and separated by `NA`: the k-th stretch between two `NA` values is the outline named `france$names[k]`; a *département* drawn in several pieces (islands, enclaves) gets extra names such as `"Nord:1"`.

7.5- `which(is.na())` gives the 113 separators (`france$y` has its `NA` values at the same positions).

```
indNA <- which(is.na(france$x))
length(indNA)
head(indNA)
```

```
[1] 113
[1] 206 372 533 547 696 796
```

7.6- A character string of length 1:

```
depname <- "Gard"
```

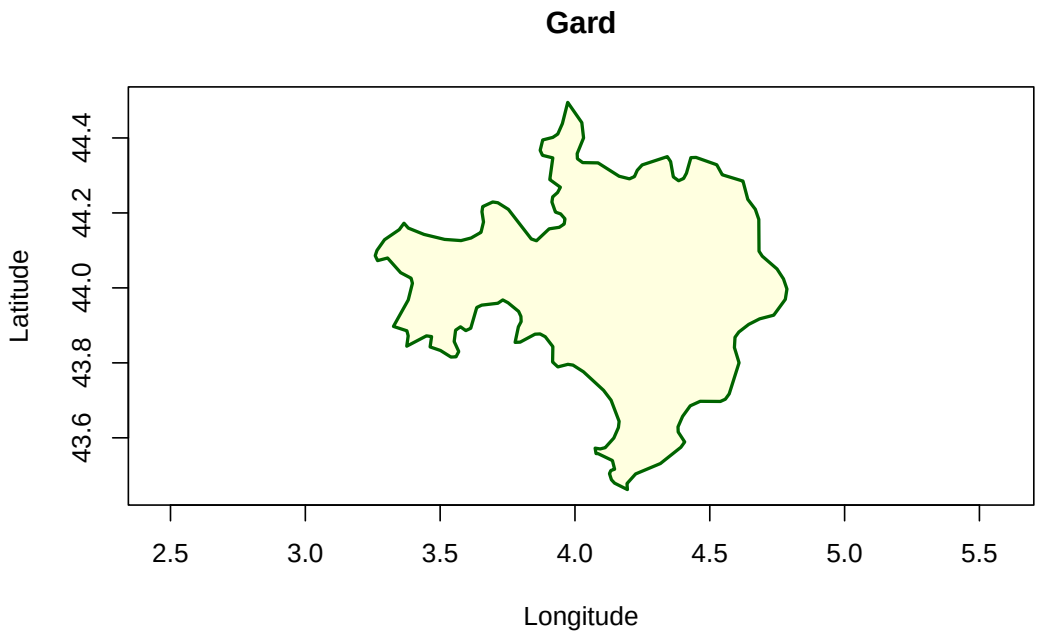
7.7- `which()` on a logical comparison; Gard is the 92nd outline and is drawn in one piece (no `"Gard:1"`).

```
inddept <- which(france$names == depname)
inddept
```

```
[1] 92
```

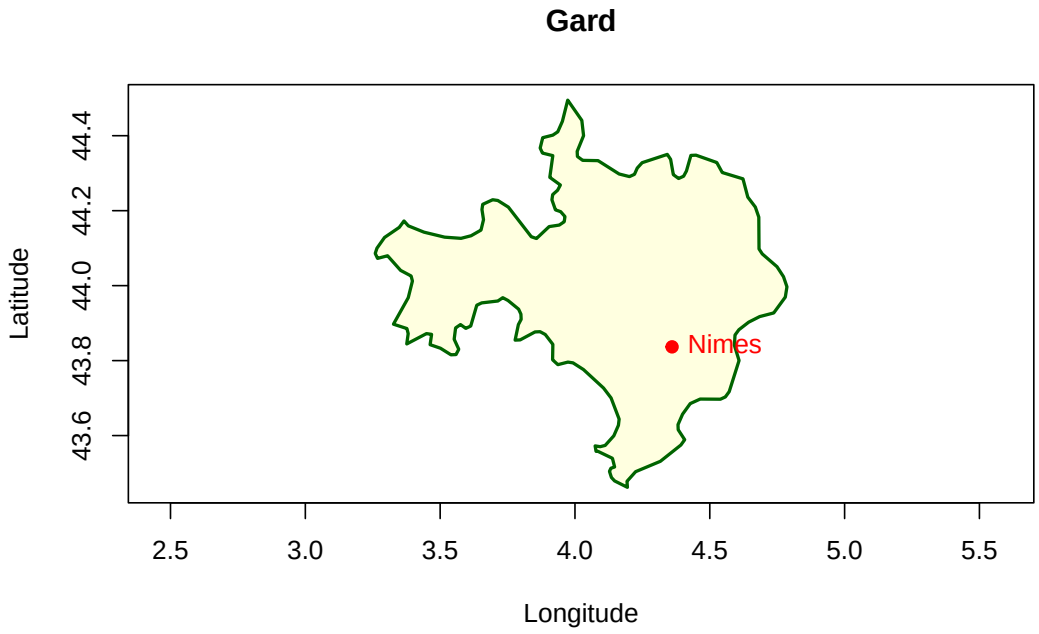
7.8- Padding `indNA` with 0 and `length(france$x) + 1` lets the k-th outline run from `bounds[k] + 1` to `bounds[k + 1] - 1`; `polygon()` then fills it, and `asp` $= 1/\cos(\text{latitude})$ keeps a degree of longitude to its true length (`map("france", regions = depname)` draws the same outline in one call).

```
bounds <- c(0, indNA, length(france$x) + 1)
ind <- (bounds[inddept] + 1):(bounds[inddept + 1] - 1)
x <- france$x[ind]; y <- france$y[ind]
plot(x, y, type = "n", asp = 1 / cos(mean(y) * pi / 180),
     xlab = "Longitude", ylab = "Latitude", main = depname)
polygon(x, y, col = "lightyellow", border = "darkgreen", lwd = 2)
```



7.9- `points()` adds the place with longitude on the x-axis and latitude on the y-axis; here Nîmes, the préfecture of the Gard, at latitude 43.8367 N and longitude 4.3601 E (its standard geocoded position; any place looked up on the gpsvisualizer site is added the same way).

```r
points(4.3601, 43.8367, pch = 19, col = "red")
text(4.3601, 43.8367, "Nimes", pos = 4, col = "red")
```



5.9 Worksheet 7.W.F — Representation of the geoid in France

Problem 7.W.F. Worksheet 7.W.F — Drawing curves and plots — Representation of the geoid in France
A geoid can be seen as a gravitation equipotential surface, going through the average sea level datum.
7.1- Import the file http://www.biostatisticien.eu/springeR/raf98.gra in a matrix, using the function `scan()`. First, read the associated file http://www.biostatisticien.eu/springeR/geoidformat.txt which gives a description of the file format.
7.2- Try to reproduce the plot available at http://www.biostatisticien.eu/springeR/geoid.png. Do not try to superpose the map of France yet (hint: use the functions `scan()`, `layout()`, `par()`, `image()`, `axis()`, `contour()`, `legend()` and `rainbow()`).

Solution.
7.1- Read everything with `scan()`, drop the six header values and fill a 381×421 matrix `byrow = TRUE`. The format file says the header holds the south/north latitude limits (42, 51.5), the west/east longitude limits (-5.5, 8.5) and the steps (0.025 and 1/30 degree), and that the grid is stored latitude by latitude from north to south, each latitude running west to east.

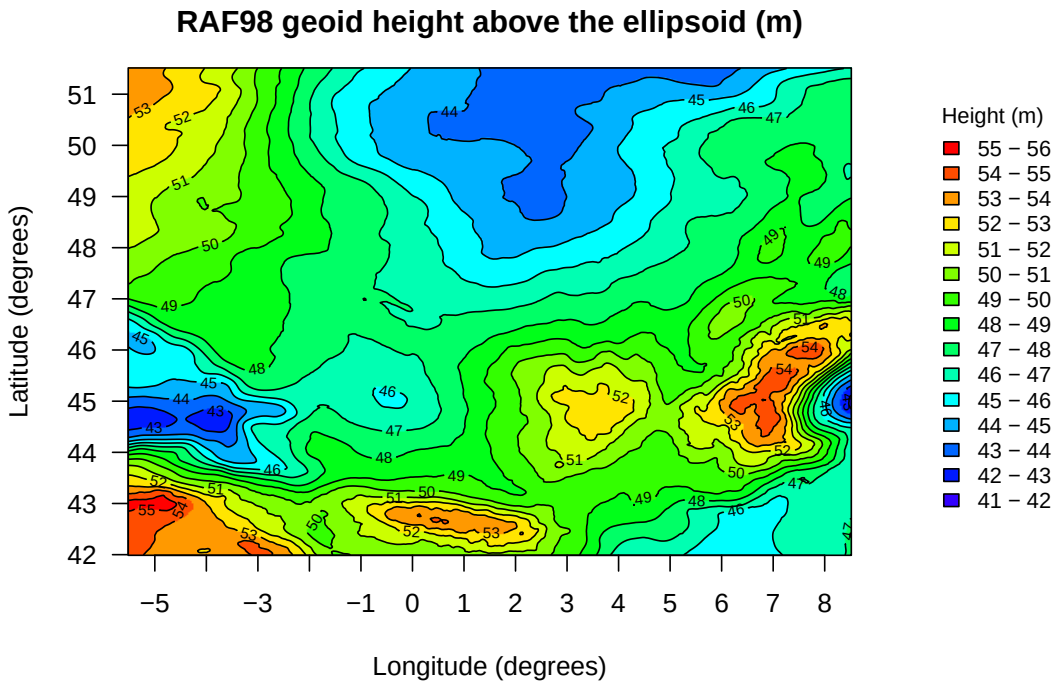
```r
x <- scan("http://www.biostatisticien.eu/springeR/raf98.gra", quiet = TRUE)
length(x)
hdr <- x[1:6]; hdr
geoid <- matrix(x[-(1:6)], nrow = 381, ncol = 421, byrow = TRUE)
dim(geoid)
range(geoid)
geoid[1:3, 1:4]
```

```
[1] 160407
[1] 42.00000000 51.50000000 -5.50000000  8.50000000  0.02500000  0.03333333
[1] 381 421
[1] 41.8493 55.4308
        [,1]    [,2]    [,3]    [,4]
[1,] 53.3573 53.3569 53.3546 53.3481
[2,] 53.3284 53.3277 53.3259 53.3209
[3,] 53.3056 53.3023 53.2990 53.2940
```

Since $160407 = 6 + 381 \times 421$, row 1 of `geoid` is the northern edge (51.5°N) and column 1 the western edge (5.5°W); geoid heights above the ellipsoid run from 41.8 m to 55.4 m.

7.2- The page `geoid.png` now returns HTTP 404, so the target could not be compared directly. The code below makes the plot the hints describe: a filled `image()` in `rainbow()` colours with `contour()` lines at 1 m intervals, custom `axis()` calls, and a `legend()` in a second panel created with `layout()`. `image()` expects rows indexed by x (longitude, increasing) and columns by y (latitude, increasing), so the matrix is flipped north to south and then transposed.

```
lon <- seq(-5.5, 8.5, length.out = 421)
lat <- seq(42, 51.5, length.out = 381)
z <- t(geoid[381:1, ])            # rows = longitudes W->E, cols = latitudes S->N
brk <- seq(41, 56, by = 1)
cols <- rev(rainbow(length(brk) - 1, end = 0.7))
layout(matrix(1:2, nrow = 1), widths = c(4, 1))
par(mar = c(4, 4, 3, 1))
image(lon, lat, z, breaks = brk, col = cols, axes = FALSE, useRaster = TRUE,
      xlab = "Longitude (degrees)", ylab = "Latitude (degrees)",
      main = "RAF98 geoid height above the ellipsoid (m)")
axis(1, at = seq(-5, 8, by = 1)); axis(2, at = seq(42, 51, by = 1), las = 1)
box()
contour(lon, lat, z, levels = brk, add = TRUE, labcex = 0.6)
par(mar = c(4, 0, 3, 0))
plot.new()
legend("center", legend = rev(paste(brk[-length(brk)], "–", brk[-1])),
       fill = rev(cols), title = "Height (m)", bty = "n", cex = 0.8)
```



The geoid is highest over the northern Spanish coast in the southwest corner (maximum 55.4 m near 4.8°W, 43°N), the Alps (about 54.6 m near 7°E, 45.5°N) and the Pyrenees (about 54 m). It is lowest, below 45 m, over the Paris Basin and Channel, in the Bay of Biscay near 4.5°W, 44.5°N, and off the Ligurian coast (minimum 41.8 m at 8.5°E, 45°N).

6 Programming in R

Contents

6.1 Exercises 8.1–8.7

Problem 8.1. For each of the following command lines, indicate the class of the returned R object. What is displayed upon execution of each of these command lines?

- `function(name) {name}`
- `(function(name) {name})("Ben")`
- `(function(name) {cat(name,"\n")})("Ben")`
- `(function(name) {invisible(name)})("Ben")`

Solution. The classes are `"function"`, `"character"`, `"NULL"` and `"character"`; only the first two lines auto-print their value, the third displays `Ben` as a side effect of `cat()` (its value is the invisible `NULL` of `cat()`) and the fourth displays nothing, since `invisible()` suppresses auto-printing of `"Ben"`.

```
function(name) {name}
(function(name) {name})("Ben")
(function(name) {cat(name,"\n")})("Ben")
(function(name) {invisible(name)})("Ben")
sapply(list(function(name) {name},
            (function(name) {name})("Ben"),
            (function(name) {cat(name,"\n")})("Ben"),
            (function(name) {invisible(name)})("Ben")), class)
```

```
function(name) {name}
[1] "Ben"
Ben
Ben
[1] "function"  "character" "NULL"      "character"
```

Problem 8.2. Is there a difference between

- `name <- function(name) name` and `name <- function(name) {name}`
- `name <- function(name) {name}` and `name <- function(name) {return(name)}`
- `name <- function(name) {name}` and `(function(name) {name}) -> name`

Solution. No difference in behaviour: all four declarations define a function returning its argument (Section 8.2). The braces only turn the body into a call to `"{"()` instead of the bare symbol, `return()` is redundant when it wraps the last instruction, and `->` is the right-to-left assignment of the same function object.

```
f1 <- function(name) name ; f2 <- function(name) {name}
f3 <- function(name) {return(name)}
(function(name) {name}) -> f4
c(f1("Ben"), f2("Ben"), f3("Ben"), f4("Ben"))
identical(f2, f4, ignore.srcref = TRUE)
```

```
[1] "Ben" "Ben" "Ben" "Ben"
[1] TRUE
```

Problem 8.3. Upon execution, is there a difference between `name()` and `name("Peter")` when

- `name <- function(name`“Peter”) name=
- `name <- function(name`“Peter”) name2 <- name=

For these two declarations of the function `name()`, is there a difference in the type of the R object `res` given by `res <- name("Ben")`?

Solution. No: in both declarations `name()` and `name("Peter")` are the same call, because `"Peter"` is the default value. The first version prints `[1] "Peter"`; the second prints nothing, since its last instruction is an assignment, whose value is returned invisibly.

```
name <- function(name="Peter") name
name(); name("Peter")
name <- function(name="Peter") name2 <- name
```

```r
name(); name("Peter")
res <- name("Ben"); class(res); (name("Ben"))
```

```
[1] "Peter"
[1] "Peter"
[1] "character"
[1] "Ben"
```

The type of `res` is the same: in both cases `res` is the character string `"Ben"`, because the value of the assignment `name2 <- name` is its right-hand side.

Problem 8.4. What R object is returned upon execution of `name()` when:

```r
name <- function(name="Peter") {
  name
  # The last instruction is a comment!
}
```

Solution. The character string `"Peter"`: a comment is not an instruction, so `name` is still the last evaluated expression of the block.

```r
name <- function(name="Peter") {
  name
  # The last instruction is a comment!
}
name()
```

```
[1] "Peter"
```

Problem 8.5. When `name <- function(firstname`“Peter”,name=“L”) {paste(firstname,name)}=, what R object is returned by

- `name(firstname`“Ben”)=
- `name(fir`“Ben”)=
- `name(n`“D”,f=“R”)=

Solution. The strings `"Ben L"`, `"Ben L"` and `"R D"`: arguments are matched by partial name (`fir`, `f` to `firstname`; `n` to `name`), and the missing one takes its default.

```r
name <- function(firstname="Peter",name="L") {
paste(firstname,name)}
name(firstname="Ben")
name(fir="Ben")
name(n="D",f="R")
```

```
[1] "Ben L"
[1] "Ben L"
[1] "R D"
```

Problem 8.6. Rewrite the following function declaration in one line, without using the command separator “;”:

```r
name <- function(name) { if(missing("name"))
name <- "Peter"; cat(name,"\n") }
```

Solution. Give the argument a default value: `name <- function(name = "Peter") cat(name, "\n")`; keeping `missing()` is also possible with `name <- function(name) cat(if (missing(name)) "Peter" else name, "\n")`.

```r
name <- function(name = "Peter") cat(name, "\n")
name(); name("Ben")
```

```
Peter
Ben
```

Problem 8.7. What is the output of the execution of `names("peteR","Ben","R")` when:

- `names <- function(...) c(...)`
- `names <- function(...) list(...)`
- `names <- function(...) for(name in c(...)) print(name)`
- `names <- function(...) for(name in list(...)) print(name)`

Same question upon execution of `names(c("peteR","L"),c("Ben","L"),c("R","D"))`.

Solution. With `c(...)` the arguments are concatenated into one character vector, with `list(...)` each argument stays a separate list element, and the `for` versions print element by element (then return `NULL` invisibly).

```
names <- function(...) c(...)
names("peteR","Ben","R")
names(c("peteR","L"),c("Ben","L"),c("R","D"))
names <- function(...) list(...)
names("peteR","Ben","R")
```

```
[1] "peteR" "Ben"   "R"
[1] "peteR" "L"     "Ben"   "L"     "R"     "D"
[[1]]
[1] "peteR"

[[2]]
[1] "Ben"

[[3]]
[1] "R"
```

With the three pairs, `list(...)` gives a list of three vectors of length 2:

```
names(c("peteR","L"),c("Ben","L"),c("R","D"))
```

```
[[1]]
[1] "peteR" "L"

[[2]]
[1] "Ben" "L"

[[3]]
[1] "R" "D"
```

For the loops, iterating over `c(...)` visits the six single strings, while iterating over `list(...)` visits the three vectors; with single strings as arguments both loops print the same three lines.

```
names <- function(...) for(name in c(...)) print(name)
names("peteR","Ben","R")
names(c("peteR","L"),c("Ben","L"),c("R","D"))
names <- function(...) for(name in list(...)) print(name)
names("peteR","Ben","R")
names(c("peteR","L"),c("Ben","L"),c("R","D"))
```

```
[1] "peteR"
[1] "Ben"
[1] "R"
[1] "peteR"
[1] "L"
[1] "Ben"
[1] "L"
[1] "R"
[1] "D"
[1] "peteR"
[1] "Ben"
[1] "R"
[1] "peteR" "L"
[1] "Ben" "L"
[1] "R" "D"
```

6.2 Exercises 8.8–8.11

Problem 8.8. When `names <- function(names=c("Ben","R"),...) c(names,...)`, which R objects are returned by `names("PeteR")`, `names(name="PeteR")` and `names(names="PeteR")`? Same question when `names <- function(...,names=c("Ben","R")) c(names,...)`.

Solution. With `names` placed before `...`, all three calls return `"PeteR"`: the first by position, the second by partial matching of `name` to `names`, the third by exact name. With `names` placed after `...`, it can only be matched by its exact name, so the first two calls put `"PeteR"` into `...` (keeping the tag `name` in the second) and the default `c("Ben","R")` is kept.

```r
names <- function(names=c("Ben","R"),...) c(names,...)
names("PeteR"); names(name="PeteR"); names(names="PeteR")
names <- function(...,names=c("Ben","R")) c(names,...)
names("PeteR"); names(name="PeteR"); names(names="PeteR")
rm(names)  # restore base::names()
```

```
[1] "PeteR"
[1] "PeteR"
[1] "PeteR"
[1] "Ben"   "R"     "PeteR"
                  name
  "Ben"     "R" "PeteR"
[1] "PeteR"
```

Problem 8.9. Create a constructor function `Male()` generating an object of class `"Male"` with fields `firstname` and `name` (in an object of type `list`). Create the method `hello.Male()` which displays `"Hello Mister FIRSTNAME NAME!"` (do not forget the `"\n"` at the end of the display!) for an object with values `"FIRSTNAME"` and `"NAME"` respectively for the fields `firstname` and `name`. When `man <- Male("Ben","L")`, what is produced upon execution of the following commands: `hello.Male(man)` and `hello(man)`? What code should you execute in addition for the two results to be identical?

Solution. `hello.Male(man)` displays `Hello Mister Ben L!` but `hello(man)` fails because the generic `hello()` does not exist; declaring it with `hello <- function(obj, ...) UseMethod("hello")` (Section 8.3) makes both calls identical.

```r
Male <- function(firstname, name) {
  obj <- list(firstname = firstname, name = name)
  class(obj) <- "Male"
  obj
}
hello.Male <- function(obj) cat("Hello Mister", obj$firstname, paste0(obj$name, "!"), "\n")
man <- Male("Ben", "L")
hello.Male(man)
hello(man)
```

```
Hello Mister Ben L!
Error in hello(man) : could not find function "hello"
```

```r
hello <- function(obj, ...) UseMethod("hello")
hello(man)
```

```
Hello Mister Ben L!
```

Problem 8.10. Create the analogous functions for the class `"Female"` (hint: do not forget to update the gender in `hello.Female()`). When `woman <- Female("Elsa","R")`, what is produced upon execution of the following commands: `hello.Male(woman)`, `hello.Female(woman)` and `hello(woman)`.

Solution. `hello.Male(woman)` displays `Hello Mister Elsa R!` (a method called directly does not check the class), whereas `hello.Female(woman)` and `hello(woman)` both display `Hello Madam Elsa R!`, the generic dispatching on the class `"Female"`.

```
Female <- function(firstname, name) {
  obj <- list(firstname = firstname, name = name)
  class(obj) <- "Female"
  obj
}
hello.Female <- function(obj) cat("Hello Madam", obj$firstname, paste0(obj$name, "!"), "\n")
woman <- Female("Elsa", "R")
hello.Male(woman)
hello.Female(woman)
hello(woman)
```

```
Hello Mister Elsa R!
Hello Madam Elsa R!
Hello Madam Elsa R!
```

Problem 8.11. When `welcome <- function(...) for(person in list(...)){hello(person)}`, what is returned by `welcome(man,woman)`? And when `welcome <- function(...) for(person in c(...)){hello(person)}`? Same question when `hello.default <- function(obj){cat("hello",obj,"!\n")}`.

Solution. With `list(...)` each person keeps its class, so the two greetings `Hello Mister Ben L!` and `Hello Madam Elsa R!` are displayed (the loop itself returns `NULL` invisibly). With `c(...)` the two objects are merged into a plain list of four character strings (the class attribute is dropped), so `hello()` is called on `"Ben"` and stops with an error.

```
welcome <- function(...) for(person in list(...)){
 hello(person)}
welcome(man,woman)
welcome <- function(...) for(person in c(...)){
 hello(person)}
welcome(man,woman)
```

```
Hello Mister Ben L!
Hello Madam Elsa R!
Error in UseMethod("hello") :
  no applicable method for 'hello' applied to an object of class "character"
```

Once `hello.default()` is defined, the `c(...)` version no longer fails: each of the four strings goes to the default method, while the `list(...)` version is unchanged.

```
hello.default <- function(obj){
 cat("hello",obj,"!\n")}
welcome(man,woman)
welcome <- function(...) for(person in list(...)){
 hello(person)}
welcome(man,woman)
```

```
hello Ben !
hello L !
hello Elsa !
hello R !
Hello Mister Ben L!
Hello Madam Elsa R!
```

6.3 Worksheet 8.W.A — Managing a bank account

Problem 8.W.A. Worksheet 8.W.A — Programming functions and object-oriented programming in R — Managing a bank account
The aim of this practical is to create three minimalist functions to manage bank accounts. The accounts will be stored in `data.frame` objects all called `account` and stored in different `.RData` files. All these files will be located in the same folder. The path to this folder should be saved in the R variable `.folder.accounts` and be accessible in all the functions you develop.
8.1- The instruction `file.path(.folder.accounts,paste(name,".RData",sep""))`= gives the path of the file associated with the account `name`. Create the function `path.account()`, which takes one formal argument `name` (representing the name of the account) and returns the complete path to the file (which contains the object `account` of class `data.frame`) with extension `.RData`.
8.2- Given that `factor(levels=c("Debit","Credit"))`, `numeric(0)` and `character(0)` respectively give empty vectors of explicit types, which expression would generate an empty data matrix with the predefined fields `amount`, `mode`, `date` and `remark`? Create the function `account()` (not to be confused with the variable `account` called in its body) which takes one argument `name` and creates a new account.
8.3- Create the functions `debit()` and `credit()` to respectively debit and credit an amount `amount` (second argument) from the account `name` (first argument). The third argument is any comment to put as `remark`. A fourth argument can represent the date; the default value is `format(Sys.time(),"%d/%m/%Y")` (i.e. the date of input). Remember to use the functions `load()` and `save()` to load and save the variable `account` in the body of each function.
8.4- If `account` is the data matrix containing information on the account, what is returned by `sum(account[account$mode=`"Credit","amount"])=? Modify the function `account()` so that it returns the current state of the account only when the file returned by `path.account(name)` exists (use the function `file.exists()` to test whether a file exists).
8.5- Complete account management by creating any additional functions you wish.
8.6- Optional question: Since most use of R is done with objects, adapt the previous functions in a way that respects the R object-oriented philosophy. You can use the next practicals for inspiration.

Solution.
8.1- `path.account()` just wraps the given `file.path()` call; `.folder.accounts` is a global whose leading dot hides it from `ls()`, and every function below reads it from the global environment without receiving it as an argument (Section 8.2.2.4). The folder is created once, here inside the session's temporary directory.

```
.folder.accounts <- file.path(tempdir(), "accounts")
dir.create(.folder.accounts)
path.account <- function(name)
  file.path(.folder.accounts, paste(name, ".RData", sep = ""))
basename(path.account("Ben"))
```

```
[1] "Ben.RData"
```

8.2- `data.frame(amount = numeric(0), mode = factor(levels = c("Debit", "Credit")), date = character(0), remark = character(0))` is a zero-row table whose four columns already carry their types (Section 3.2.2.4); `account()` builds it and saves it under the account's file name.

```
account <- function(name) {
  account <- data.frame(amount = numeric(0),
                        mode = factor(levels = c("Debit", "Credit")),
                        date = character(0), remark = character(0))
  save(account, file = path.account(name))
}
account("Ben")
load(path.account("Ben")); str(account)
```

```
'data.frame':        0 obs. of  4 variables:
 $ amount: num
```

```
$ mode  : Factor w/ 2 levels "Debit","Credit":
$ date  : chr
$ remark: chr
```

8.3- Each function loads the account, appends one row with `rbind()` and saves it back; `mode` is the only thing that differs, so `credit()` is `debit()` with `mode = "Credit"`. The date argument has the requested default, evaluated at call time (Section 8.2.2.3).

```
debit <- function(name, amount, remark = "",
                  date = format(Sys.time(), "%d/%m/%Y")) {
  load(path.account(name))
  account <- rbind(account, data.frame(amount = amount, mode = "Debit",
                                       date = date, remark = remark))
  save(account, file = path.account(name))
}
credit <- function(name, amount, remark = "",
                   date = format(Sys.time(), "%d/%m/%Y")) {
  load(path.account(name))
  account <- rbind(account, data.frame(amount = amount, mode = "Credit",
                                       date = date, remark = remark))
  save(account, file = path.account(name))
}
credit("Ben", 1000, "salary", "01/09/2026")
debit("Ben", 250.5, "rent", "03/09/2026")
credit("Ben", 80, "refund", "10/09/2026")
load(path.account("Ben")); account
```

```
  amount   mode       date remark
1 1000.0 Credit 01/09/2026 salary
2  250.5  Debit 03/09/2026   rent
3   80.0 Credit 10/09/2026 refund
```

8.4- The expression sums the `amount` column over the rows whose `mode` is `"Credit"`, i.e. the total credited, 1080 here. The modified `account()` tests `file.exists()` first and returns the stored table instead of overwriting it; for a new name it still creates the file and returns the empty table invisibly.

```
sum(account[account$mode == "Credit", "amount"])
account <- function(name) {
  if (file.exists(path.account(name))) {
    load(path.account(name))
    return(account)
  }
  account <- data.frame(amount = numeric(0),
                        mode = factor(levels = c("Debit", "Credit")),
                        date = character(0), remark = character(0))
  save(account, file = path.account(name))
  invisible(account)
}
account("Ben")
```

```
[1] 1080
  amount   mode       date remark
1 1000.0 Credit 01/09/2026 salary
2  250.5  Debit 03/09/2026   rent
3   80.0 Credit 10/09/2026 refund
```

8.5- Three natural additions: `balance()` (credits minus debits), `statement()` (the last `n` operations, via `tail()`) and `list.accounts()` (the `.RData` files in the folder, via `list.files()`).

```
balance <- function(name) {
  account <- account(name)
  sum(account[account$mode == "Credit", "amount"]) -
    sum(account[account$mode == "Debit", "amount"])
}
statement <- function(name, n = 5) tail(account(name), n)
list.accounts <- function()
  sub("\\.RData$", "", list.files(.folder.accounts, "\\.RData$"))
balance("Ben")
statement("Ben", 2)
```

```r
list.accounts()
```

```
[1] 829.5
  amount   mode       date remark
2  250.5  Debit 03/09/2026   rent
3   80.0 Credit 10/09/2026 refund
[1] "Ben"
```

8.6- In S3 style (Section 8.3) an account is an object of class `"Account"` holding its name and its table; `transaction()` and `balance()` are generics dispatched on that class, and `print.Account()` gives the object its own display. The file on disk is still updated by every transaction, so the two designs stay compatible.

```r
Account <- function(name) {
  obj <- list(name = name, account = account(name))
  class(obj) <- "Account"
  obj
}
transaction <- function(obj, ...) UseMethod("transaction")
transaction.Account <- function(obj, amount, mode = c("Debit", "Credit"),
                                remark = "",
                                date = format(Sys.time(), "%d/%m/%Y")) {
  mode <- match.arg(mode)
  obj$account <- rbind(obj$account, data.frame(amount = amount, mode = mode,
                                               date = date, remark = remark))
  account <- obj$account
  save(account, file = path.account(obj$name))
  obj
}
balance <- function(obj, ...) UseMethod("balance")
balance.Account <- function(obj, ...)
  with(obj$account, sum(amount[mode == "Credit"]) - sum(amount[mode == "Debit"]))
print.Account <- function(x, ...) {
  cat("Account of", x$name, "- balance:", balance(x), "\n")
  print(x$account)
}
ben <- Account("Ben")
ben <- transaction(ben, 45, "Debit", "groceries", "12/09/2026")
ben
```

```
Account of Ben - balance: 784.5
  amount   mode       date    remark
1 1000.0 Credit 01/09/2026    salary
2  250.5  Debit 03/09/2026      rent
3   80.0 Credit 10/09/2026    refund
4   45.0  Debit 12/09/2026 groceries
```

6.4 Worksheet 8.W.B — Organizing graphical objects

Problem 8.W.B. Worksheet 8.W.B — Organizing graphical objects — Organizing graphical objects When you think about it, plots in R do not really respect the object-oriented spirit: unlike most other entities, an R plot is not considered as an object which can be saved (and possibly modified) and on which certain methods can be applied. We shall attempt to propose a very basic prototype to draw a plot with circles and rectangles (and hence squares). You can enrich this library with graphical objects as you wish. Our aim is to maintain a list of graphical objects, with the possibility of changing any of its elements at any time.

8.1- R functions `plot.new()` and `plot.window()` are used to initialize a plot. The argument `asp` set to 1 creates plots with correct units for the x and y axes. Propose an object `Window` which gives the user the option of saving the dimensions of the graphics display window. The user can then call the constructor function (or method) `Window()` (which could have the same name as the class), which takes as arguments `x` and `y` (the coordinates of the centre), `width`, `height` (dimensions along the x and y axes respectively) and optionally `log` (logarithmic transformation). All these quantities

should be stored in an object `list`, returned by the constructor function `Window()`, after affecting its class to `"Window"`.

8.2- Similarly, propose constructor functions for objects of classes `Circle` and `Rectangle`. The fields `x` and `y` represent the coordinates of the centre of the object, `radius` is the radius of a circle and `width` and `height` are the dimensions of a rectangle.

8.3- Propose plotting methods `plot.Window()`, `plot.Rectangle()` and `plot.Circle()`. You can find inspiration in the following R treatments used to display a new plot with a circle and a square centred at the origin and of diameter and side length set to 1:

```
plot.new()
plot.window(xlim=c(-1,1),ylim=c(-1,1),asp=1)
rect(-.5,-.5,.5,.5)
symbols(0,0,circle=.5,inches=FALSE,add=TRUE)
```

8.4- Test the code you have developed by executing the code:

```
mywindow <- Window(0,0,2,2)
mycircle <- Circle(0,0,.5)
myrectangle <- Rectangle(0,0,1,1)
plot(mywindow);plot(mycircle);plot(myrectangle)
```

If all goes well, you should see a graphics window with a circle inside a square.

8.5- We now need to develop the methods associated with the class `MyPlot` which will contain the list of all graphical objects. First, propose a constructor function `MyPlot()` which initializes an object as `list(objects=list())` (where `objects` is the field containing the list of graphical objects), affects the class `"MyPlot"` and returns the object.

8.6- Propose a method `add.MyPlot()` which adds graphical objects. Remember to give a generic function `add()` to launch all associated methods. Use the functionalities of the list of supplementary arguments `...` and the function `c()` so that the method `add.MyPlot()` can initialize as many graphical objects as the user wishes. Propose a method `plot.MyPlot()` which executes the methods `plot()` for all graphical objects. The user can then enter the following lines to get the same result as earlier:

```
myplot <- MyPlot()
myplot <- add(myplot,Window(0,0,2,2),Circle(0,0,.5),
                    Rectangle(0,0,1,1))
plot(myplot)
```

8.7- To display a plot, you need to initialize an object of type `Window` and put it in first position of the list of graphical objects of the class `MyPlot`. It might be useful to initialize it directly inside the constructor function `MyPlot()`. The arguments of the function `Window()` can be proposed directly for the function `MyPlot()`. Another idea is to propose a list of graphical objects to the user upon creation of an object of class `MyPlot`. As we have done for the method `add.MyPlot()`, we could use the list of supplementary arguments `...`, which must be placed as first argument of the function `MyPlot()` so as to get the previous result with only two lines:

```
myplot <- MyPlot(Circle(),Rectangle())
plot(myplot)
```

However, note that in the first line, it is assumed that the default values of the arguments of the function `Window()`, `Circle()` and `Rectangle()` are appropriate.

8.8- The project is launched with this first prototype. You can complete it as you wish. If you need inspiration, you could try managing the list of graphical objects (for example, deleting or modifying an object), display styles, axes…

Solution.

8.1- `Window()` stores its five arguments in a list and sets the class attribute (S3 constructor, Section 8.3); the defaults (a 2×2 window centred at the origin) are chosen with question 8.7 in mind.

```
Window <- function(x = 0, y = 0, width = 2, height = 2, log = "") {
  obj <- list(x = x, y = y, width = width, height = height, log = log)
  class(obj) <- "Window"
  obj
}
str(Window(0, 0, 2, 2))
```

```
List of 5
 $ x     : num 0
 $ y     : num 0
 $ width : num 2
 $ height: num 2
 $ log   : chr ""
 - attr(*, "class")= chr "Window"
```

8.2- The two constructors follow the same pattern, with defaults giving the unit-diameter circle and the unit square of question 8.3.

```r
Circle <- function(x = 0, y = 0, radius = 0.5) {
  obj <- list(x = x, y = y, radius = radius)
  class(obj) <- "Circle"
  obj
}
Rectangle <- function(x = 0, y = 0, width = 1, height = 1) {
  obj <- list(x = x, y = y, width = width, height = height)
  class(obj) <- "Rectangle"
  obj
}
class(Circle(0, 0, .5)); unlist(Rectangle(0, 0, 1, 1))
```

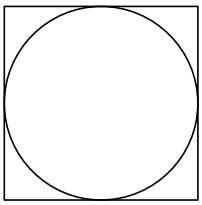
```
[1] "Circle"
     x      y  width height
     0      0      1      1
```

8.3- Each method converts the centre/size fields into the arguments of `plot.window()`, `rect()` and `symbols()`; since `plot()` is already generic, defining `plot.<class>()` is enough for dispatch. (The book's `circle`.5= works only through partial matching of the argument `circles`.)

```r
plot.Window <- function(x, ...) {
  plot.new()
  plot.window(xlim = x$x + c(-1, 1) * x$width / 2,
              ylim = x$y + c(-1, 1) * x$height / 2, asp = 1, log = x$log)
  invisible(x)
}
plot.Rectangle <- function(x, ...) {
  rect(x$x - x$width / 2, x$y - x$height / 2,
       x$x + x$width / 2, x$y + x$height / 2, ...)
  invisible(x)
}
plot.Circle <- function(x, ...) {
  symbols(x$x, x$y, circles = x$radius, inches = FALSE, add = TRUE, ...)
  invisible(x)
}
```

8.4- The test code draws the expected circle inscribed in the unit square.

```r
mywindow <- Window(0,0,2,2)
mycircle <- Circle(0,0,.5)
myrectangle <- Rectangle(0,0,1,1)
plot(mywindow);plot(mycircle);plot(myrectangle)
```



8.5- The first constructor simply wraps an empty list in the class `"MyPlot"`.

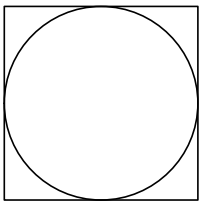
```
MyPlot <- function() {
  obj <- list(objects = list())
  class(obj) <- "MyPlot"
  obj
}
str(MyPlot())
```

```
List of 1
 $ objects: list()
 - attr(*, "class")= chr "MyPlot"
```

8.6- The generic `add()` dispatches with `UseMethod()`; `add.MyPlot()` appends `list(...)` to the field `objects` with `c()`, and `plot.MyPlot()` calls `plot()` on each element, which dispatches to the methods of 8.3. The book's three lines give the same figure as in 8.4.

```
add <- function(obj, ...) UseMethod("add")
add.MyPlot <- function(obj, ...) {
  obj$objects <- c(obj$objects, list(...))
  obj
}
plot.MyPlot <- function(x, ...) {
  for (o in x$objects) plot(o)
  invisible(x)
}
myplot <- MyPlot()
myplot <- add(myplot,Window(0,0,2,2),Circle(0,0,.5),
                    Rectangle(0,0,1,1))
sapply(myplot$objects, class)
plot(myplot)
```

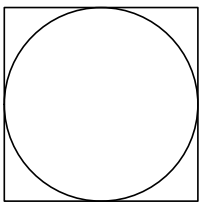
```
[1] "Window"    "Circle"    "Rectangle"
```



8.7- `MyPlot()` now takes `...` first, then the arguments of `Window()` (which must be named when called, since they follow `...`), puts the window in position 1 and hands the other objects to `add()`; the two-line call reproduces the figure.

```
MyPlot <- function(..., x = 0, y = 0, width = 2, height = 2, log = "") {
  obj <- list(objects = list(Window(x, y, width, height, log)))
  class(obj) <- "MyPlot"
  add(obj, ...)
}
myplot <- MyPlot(Circle(),Rectangle())
sapply(myplot$objects, class)
plot(myplot)
```

```
[1] "Window"    "Circle"    "Rectangle"
```

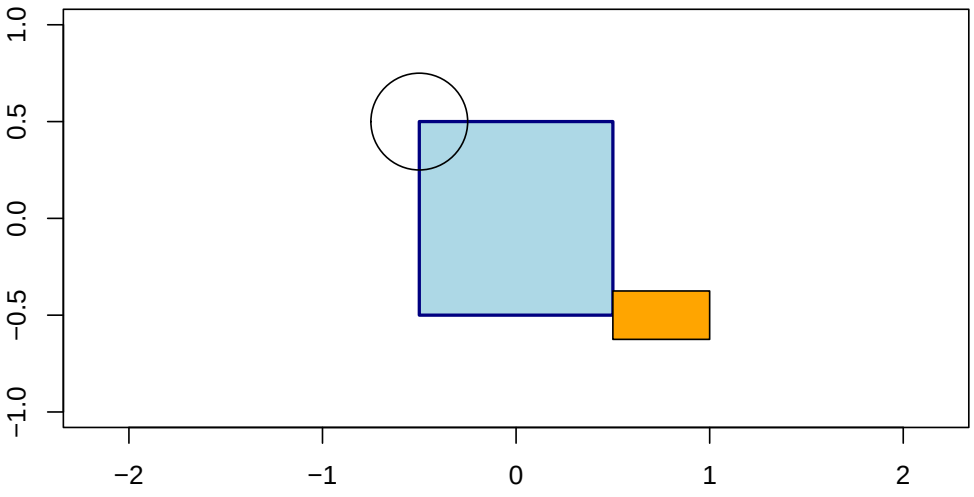


8.8- One possible extension: a `style` field whose entries are passed to `rect()=/=symbols()` through `do.call()`, an `axes` field for the window, and the new generics `delete()` and `modify()` for managing

the list (the window in position 1 is protected); in the figure the unit circle has been deleted, the square styled, the small circle moved and an orange rectangle added on a wider window with axes.

```
style <- function(obj, ...) {
  obj$style <- modifyList(as.list(obj$style), list(...)); obj
}
plot.Rectangle <- function(x, ...)
  do.call(rect, c(list(x$x - x$width/2, x$y - x$height/2,
                       x$x + x$width/2, x$y + x$height/2), x$style))
plot.Circle <- function(x, ...)
  do.call(symbols, c(list(x$x, x$y, circles = x$radius,
                          inches = FALSE, add = TRUE), x$style))
plot.Window <- function(x, ...) {
  plot.new()
  plot.window(xlim = x$x + c(-1, 1) * x$width / 2,
              ylim = x$y + c(-1, 1) * x$height / 2, asp = 1, log = x$log)
  if (isTRUE(x$axes)) { axis(1); axis(2); box() }
  invisible(x)
}
delete <- function(obj, ...) UseMethod("delete")
delete.MyPlot <- function(obj, i) {
  if (any(i == 1)) stop("the Window (object 1) cannot be deleted")
  obj$objects <- obj$objects[-i]; obj
}
modify <- function(obj, ...) UseMethod("modify")
modify.MyPlot <- function(obj, i, ...) {
  obj$objects[[i]] <- modifyList(obj$objects[[i]], list(...)); obj
}
myplot <- MyPlot(Circle(), Rectangle(), Circle(.5, .5, .25), width = 3)
myplot <- modify(myplot, 1, axes = TRUE)
myplot <- modify(myplot, 3, style = list(col = "lightblue", border = "navy", lwd = 2))
myplot <- modify(myplot, 4, x = -0.5)
myplot <- add(myplot, style(Rectangle(0.75, -0.5, 0.5, 0.25), col = "orange"))
myplot <- delete(myplot, 2)
sapply(myplot$objects, class)
plot(myplot)
```

```
[1] "Window"    "Rectangle" "Circle"    "Rectangle"
```



7 Managing sessions

Contents

7.1 Exercises 9.1–9.7

Problem 9.1. Name two R functions which return a list of objects in your session.

Solution. `ls()` and its synonym `objects()` (Section 9.1):

```
My.Weight <- 75; My.Height <- 1.90; foo <- 1:3
ls()
objects()
```

```
[1] "foo"       "My.Height" "My.Weight"
[1] "foo"       "My.Height" "My.Weight"
```

Problem 9.2. How would you delete the object `foo`?

Solution. With `rm(foo)` (Section 9.1); `rm(list = ls())` would delete every object in the workspace.

```
rm(foo)
ls()
```

```
[1] "My.Height" "My.Weight"
```

Problem 9.3. Which R command gives the current directory?

Solution. `getwd()` returns the current working directory (Section 9.2); here R was started in `/tmp`:

```
getwd()
```

```
[1] "/private/tmp"
```

Problem 9.4. Which R command changes the current directory?

Solution. `setwd("path/to/folder")` (Section 9.2); here it moves into a folder `Cars`, as in the book's example:

```
dir.create("Cars", showWarnings = FALSE)
setwd("Cars")
basename(getwd())
```

```
[1] "Cars"
```

Problem 9.5. What is the purpose of the function `save.image()`?

Solution. `save.image()` saves all the objects of the current workspace to a `.RData` file (by default `.RData` in the working directory), which `load()` restores in a later session (Section 9.2):

```
x <- c("FIAT", "VOLVO", "RENAULT", "PEUGEOT")
save.image("cars.RData")
rm(list = ls())
ls()
load("cars.RData")
x
```

```
character(0)
[1] "FIAT"    "VOLVO"   "RENAULT" "PEUGEOT"
```

Problem 9.6. What are the four things you can save before closing an R session?

Solution. The four things are:

1. the objects of the workspace, in a `.RData` file (`save.image()`, Section 9.2);

2. the command history, in a `.Rhistory` file (`savehistory()`, Section 9.3);
3. the plots (`dev.print()`, or `png()`, `pdf()`, … followed by `dev.off()`, Section 9.4);
4. the text output of the console (`sink(file = "myoutput.txt")`, or the menu File/Save to file… under Windows, Section 9.7).

Problem 9.7. What is the purpose of the command history? Which keys are necessary to use it?

Solution. It lets you recall, edit and re-execute the commands typed earlier (and, saved with `savehistory()` in a `.Rhistory` file, reuse them in a later session); the up and down arrow keys move backward and forward through it, and the left and right arrow keys edit the recalled line before pressing Enter (Section 9.3).

7.2 Exercises 9.8–9.12

Problem 9.8. What is the purpose of the function `history()`?

Solution. `history()` opens a window listing the commands typed in the current session (by default the last 25; `history(max.show = Inf)` shows them all, and `history(pattern = "plot")` only the matching ones), Section 9.3. It only works in an interactive session, so it is not run here.

Problem 9.9. Give the list of R instructions you would use to get a file called `myplot.png` containing a plot of the curve $y = x^2$.

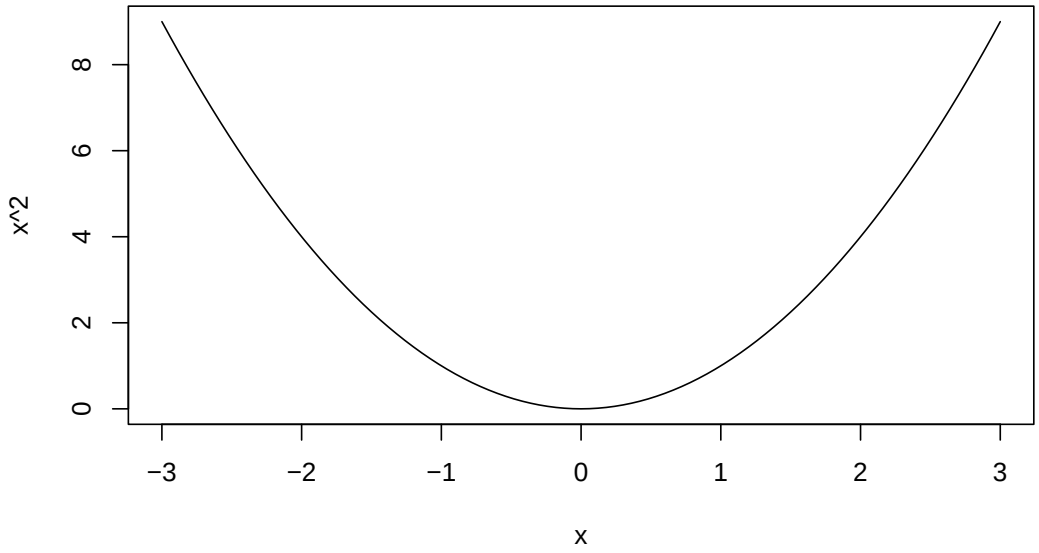
Solution. Open a `png()` device on the file, draw the curve, then close the device with `dev.off()` so that the file is written (Section 9.4):

```
png("myplot.png", width = 480, height = 480)
curve(x^2, from = -3, to = 3)
dev.off()
file.exists("myplot.png")
```

```
null device
          1
[1] TRUE
```

Equivalently, draw `curve(x^2, from = -3, to = 3)` on screen and copy it with `dev.print(png, file = "myplot.png", width = 480, height = 480)`. The plot stored in the file:

```
curve(x^2, from = -3, to = 3)
```



Problem 9.10. When is the function `attach()` useful for a data.frame?

Solution. When you work repeatedly with the variables of one data frame: `attach(mydata)` puts it in position 2 of the search path, so its columns can be called directly by name instead of `mydata$breaks` (Section 9.6); undo it with `detach(mydata)`.

```
mydata <- warpbreaks
attach(mydata)
search()[1:3]
tapply(breaks, tension, mean)
detach(mydata)
```

```
[1] ".GlobalEnv"    "mydata"        "package:stats"
       L        M        H
36.38889 26.38889 21.66667
```

Problem 9.11. Which R function is used to load an R package to the memory?

Solution. `require()` (or `library()`), for a package already installed on the disk; `require()` does nothing if the package is already loaded (Section 9.5):

```
require(MASS)
"package:MASS" %in% search()
```

```
Loading required package: MASS
[1] TRUE
```

Problem 9.12. What is the purpose of the function `source()`?

Solution. `source("myfile.R")` reads a file of R instructions and executes them all in the console, after checking their syntax (Section 9.7); `source(file.choose())` lets you pick the file interactively.

```
writeLines(c("sq <- function(x) x^2", "z <- sq(1:5)"), "myfile.R")
source("myfile.R")
z
```

```
[1]  1  4  9 16 25
```

7.3 Worksheet 9.W.A — Using the functions attach() and detach()

Problem 9.W.A. Worksheet 9.W.A — Managing and creating packages — Using the functions `attach()` and `detach()`
9.1- Download the file http://www.biostatisticien.eu/springeR/bmichild.xls.
9.2- Display the names of the variables of the data.frame.
9.3- Type `GENDER`. What do you observe?
9.4- Type `ls()`. Can you see the variable `GENDER`?
9.5- Use the function `attach()` on your data.frame, then type `GENDER`. What do you observe now?
9.6- Type `ls()` again. What do you observe?
9.7- Use the function `search()` to find the position at which your data.frame is attached.
9.8- Use the argument `pos` of the function `ls()` to list the objects present at this position.
9.9- Detach your data.frame and check (using the function `search()`) that it worked. Now type `GENDER` again and observe that this object has disappeared.
9.10- Create an object called `GENDER` containing the string `"Male"`. Display the contents of this object.
9.11- Use the function `attach()` on your data.frame then type `GENDER`. What do you observe?
9.12- Can you display the contents of the object `GENDER` of your data.frame? How about the object `weight`?
9.13- Type `ls()`. What do you observe? How about with `search()`?
9.14- Use the argument `pos` of the function `ls()` to check that the object `GENDER` of the data.frame does exist.
9.15- Use the function `get()` and its argument `pos` to display the contents of the object `GENDER` from your data.frame. Can you propose another approach?

Solution.
9.1- Download the file and read it into a data.frame `bmi`. The book used `read.xls()` from `gdata`, which newer `gdata` versions no longer provide, so this uses `readxl::read_excel()`. The `::` call avoids attaching `readxl`, which would shift the positions in `search()` below.

```
download.file("http://www.biostatisticien.eu/springeR/bmichild.xls",
              "bmichild.xls", mode = "wb", quiet = TRUE)
bmi <- as.data.frame(readxl::read_excel("bmichild.xls"))
```

9.2- `names(bmi)` lists the variables: gender, ZEP status, weight, age in years and months, and height.

```
names(bmi)
```

```
[1] "GENDER" "zep"    "weight" "year"   "month"  "height"
```

9.3- R cannot find `GENDER`. It exists only as a column inside `bmi`, and R does not look inside a data.frame when it resolves a name.

```
try(GENDER)
```

```
Error : object 'GENDER' not found
```

9.4- No. The workspace contains only the data.frame itself.

```
ls()
```

```
[1] "bmi"
```

9.5- `GENDER` now prints the 152 genders. `attach()` has put the columns of `bmi` on the search path (Section 9.6). Only the first 10 values are shown here.

```
attach(bmi)
head(GENDER, 10)
```

```
[1] "F" "F" "M" "F" "M" "M" "M" "M" "M" "M"
```

9.6- `ls()` still shows only `bmi`. `ls()` lists only the global environment. The attached columns are a copy that sits in a separate database further down the search path.

```
ls()
```

```
[1] "bmi"
```

9.7- The data.frame is attached at position 2, just after `.GlobalEnv`.

```
search()
match("bmi", search())
```

```
 [1] ".GlobalEnv"        "bmi"               "package:stats"
 [4] "package:graphics"  "package:grDevices" "package:utils"
 [7] "package:datasets"  "package:methods"   "Autoloads"
[10] "package:base"
[1] 2
```

9.8- `ls(pos = 2)` lists the six variables of the data.frame, in alphabetical order.

```
ls(pos = 2)
```

```
[1] "GENDER" "height" "month"  "weight" "year"   "zep"
```

9.9- After `detach()`, `"bmi"` is gone from `search()` and `GENDER` is again not found.

```
detach(bmi)
search()
try(GENDER)
```

```
[1] ".GlobalEnv"        "package:stats"     "package:graphics"
[4] "package:grDevices" "package:utils"     "package:datasets"
[7] "package:methods"   "Autoloads"         "package:base"
Error : object 'GENDER' not found
```

9.10- Assign the string, then print it.

```
GENDER <- "Male"
GENDER
```

```
[1] "Male"
```

9.11- R warns that the column `GENDER` of `bmi` is masked by the global object, and typing `GENDER` returns `"Male"`. R searches `.GlobalEnv` (position 1) before the attached data.frame (position 2).

```
attach(bmi)
GENDER
```

```
The following object is masked _by_ .GlobalEnv:

    GENDER

[1] "Male"
```

9.12- Typing `GENDER` cannot display the data.frame's column, because the global `"Male"` is always found first. `weight` has no global homonym, so it is found in the attached `bmi` and displays normally.

```
head(weight)
```

```
[1] 16.0 14.0 13.5 15.4 16.5 16.0
```

9.13- `ls()` now shows `bmi` and the global `GENDER`. `search()` shows `bmi` attached again at position 2. The data.frame's `GENDER` does not appear in `ls()`, which only lists position 1.

```
ls()
search()
```

```
[1] "bmi"    "GENDER"
 [1] ".GlobalEnv"        "bmi"               "package:stats"
 [4] "package:graphics"  "package:grDevices" "package:utils"
 [7] "package:datasets"  "package:methods"   "Autoloads"
[10] "package:base"
```

9.14- `ls(pos = 2)` confirms that the masked `GENDER` is still present in the attached data.frame.

```
ls(pos = 2)
```

```
[1] "GENDER" "height" "month"  "weight" "year"   "zep"
```

9.15- `get("GENDER", pos = 2)` reads `GENDER` directly from position 2, which bypasses the global object. A simpler alternative is to take the column from the data.frame itself with `bmi$GENDER`. `bmi[["GENDER"]]` and `with(bmi, GENDER)` also work, and none of the three needs `attach()`.

```r
head(get("GENDER", pos = 2), 10)
head(bmi$GENDER, 10)
```

```
[1] "F" "F" "M" "F" "M" "M" "M" "M" "M" "M"
[1] "F" "F" "M" "F" "M" "M" "M" "M" "M" "M"
```

7.4 Worksheet 9.W.B.1 — Creating a mini-package - Objects in the package

Problem 9.W.B.1. Worksheet 9.W.B.1 — Creating a mini-package — Objects in the package
9.1- Start R, then change the current directory to the Windows desktop, using the instruction `setwd(choose.dir())`.
9.2- Create the following functions and datasets:

```r
f <- function(x,y) x+y
g <- function(x,y) x-y
d <- data.frame(a=1,b=2)
e <- rnorm(1000)
```

Solution.
9.1- `setwd(choose.dir())` opens a folder chooser and makes the chosen folder (the desktop) the working directory; `choose.dir()` exists only under Windows, so on macOS or Linux type the path (or use `tcltk::tk_choose.dir()`):

```r
setwd("~/Desktop")   # Windows: setwd(choose.dir())
basename(getwd())
```

```
[1] "Desktop"
```

9.2- The four objects now live in the workspace, ready to be passed to `package.skeleton()` (seed 1 fixed so that `e` is reproducible):

```r
f <- function(x,y) x+y
g <- function(x,y) x-y
d <- data.frame(a=1,b=2)
set.seed(1)
e <- rnorm(1000)
ls()
sapply(list(f = f, g = g, d = d, e = e), class)
```

```
[1] "d" "e" "f" "g"
          f           g           d           e
 "function"  "function" "data.frame"   "numeric"
```

7.5 Worksheet 9.W.B.2 — Creating a mini-package - Package structure

Problem 9.W.B.2. Worksheet 9.W.B.2 — Creating a mini-package — Package structure
9.3- Use the function `package.skeleton()` to create the structure of your package.

```r
package.skeleton(name="SmallRPkg",list=c("f","g","d","e"))
```

A folder called SmallRPkg is created on your desktop. It contains three sub-folders (data, man and R) and two files (DESCRIPTION and Read-and-delete-me). The folder data contains the files d.RData and e.RData, which contain respectively the datasets (in binary form) d and e, which you imported from the R console. The folder R contains the files f.R and g.R, which contain the source code of the functions f and g defined earlier. The folder man contains help files for all objects included in the package.
9.4- You **must** edit the help files (`.Rd` extension files), even if they are not empty. Use the description of the help file for the function `mean` in Chapter 6. The fields to fill in are made apparent in all help files by lines starting with `%%`. Replace those lines (including the characters `%%`) with the appropriate information. Do not change the sentences starting with a single `%`. Furthermore, in fields of the form `keyword ~ kwd1`, you must replace `~ kwd1` with a reserved keyword; the list of reserved keywords is given by the instruction `file.show(file.path(R.home("doc"), "KEYWORDS"))`.

9.5- You should also change the file DESCRIPTION and fill in the relevant fields. For example, it is **very important** that you give a valid e-mail address.
9.6- You can then read and delete the file Read-and-delete-me.
Your package structure has now been created.

Solution.
9.3- One call builds the whole tree (Section 9.10); current R additionally writes a `NAMESPACE` file and a package-level help page, and saves the data as `d.rda` and `e.rda` rather than the `.RData` files the book describes:

```
package.skeleton(name = "SmallRPkg", list = c("f", "g", "d", "e"))
list.files("SmallRPkg", recursive = TRUE)
```

```
Creating directories ...
Creating DESCRIPTION ...
Creating NAMESPACE ...
Creating Read-and-delete-me ...
Saving functions and data ...
Making help files ...
Done.
Further steps are described in './SmallRPkg/Read-and-delete-me'.
 [1] "data/d.rda"                "data/e.rda"
 [3] "DESCRIPTION"               "man/d.Rd"
 [5] "man/e.Rd"                  "man/f.Rd"
 [7] "man/g.Rd"                  "man/SmallRPkg-package.Rd"
 [9] "NAMESPACE"                 "R/f.R"
[11] "R/g.R"                     "Read-and-delete-me"
```

9.4- Each `%%` placeholder is replaced by real text, the unused sections are removed, and the keyword is taken from the reserved list (`arith` for `f` and `g`, `datasets` for `d` and `e`):

```
kw <- readLines(file.path(R.home("doc"), "KEYWORDS"))
grep("arith|datasets", kw, value = TRUE)
```

```
[1] "\tdatasets\t&\tDatasets available by data(.)\t[!= S]"
[2] "\tarith\t\t&\tBasic Arithmetic and Sorting\t[!= S]"
```

The completed `man/f.Rd` (`g.Rd` is identical with "Difference", `x - y` and `g(5, 3)`; `d.Rd` and `e.Rd` keep their `\format` block and get a title, a `\description` and a `\source`):

```
\name{f}
\alias{f}
\title{Sum of Two Numbers}
\description{
Returns the sum of its two arguments.
}
\usage{
f(x, y)
}
\arguments{
  \item{x}{a numeric vector.}
  \item{y}{a numeric vector.}
}
\value{The numeric vector \code{x + y}.}
\author{John Doe}
\seealso{\code{\link{g}}}
\examples{
f(2, 3)
}
\keyword{arith}
```

In `SmallRPkg-package.Rd` the `%%` placeholder sections are simply deleted. `tools::checkRd()` reports no problem for any of the five files.
9.5- The completed `DESCRIPTION` (the `Depends` line is required because the data files use serialization format 3, and `LazyData` lets users type `e` without calling `data(e)`):

```
Package: SmallRPkg
Type: Package
Title: A Small Example Package
```

```
Version: 1.0
Date: 2026-09-24
Author: John Doe
Maintainer: John Doe <john.doe@example.org>
Description: Two arithmetic functions and two toy data sets, built as
    the worksheet of Chapter 9 of 'The R Software'.
License: GPL-2
Depends: R (>= 3.5.0)
LazyData: true
```

Replace the example address with your own working address. `Read-and-delete-me` also says to edit `NAMESPACE`; set it to `export("f", "g")` because `d` and `e` are data sets that users get through `data()`, not objects in the namespace.

9.6- The file lists the remaining steps; after reading it, delete it:

```
cat(readLines("SmallRPkg/Read-and-delete-me"), sep = "\n")
file.remove("SmallRPkg/Read-and-delete-me")
```

```
* Edit the help file skeletons in 'man', possibly combining help files
  for multiple functions.
* Edit the package 'DESCRIPTION'.
* Edit the exports in 'NAMESPACE', and add necessary imports.
* Put any C/C++/Fortran code in 'src'.
* If you have compiled code, add a useDynLib() directive to
  'NAMESPACE'.
* Run R CMD build to build the package tarball.
* Run R CMD check to check the package tarball.

Read "Writing R Extensions" for more information.
[1] TRUE
```

7.6 Worksheet 9.W.B.3 — Creating a mini-package - Creating the package file

Problem 9.W.B.3. Worksheet 9.W.B.3 — Creating a mini-package — Creating the package file

9.7- You have one final operation to perform: building the `.zip` file which will include your structure (modified by R). You first need to change a few system environment variables. Use the key combination `WINDOWS+PAUSE` to open the system properties window, go to the section `System Variables` and edit the variable `PATH`. At the beginning of this long list of semi-colon-separated paths, add the path to the executable Rgui.exe and the path to the executable hhc.exe (**be careful not to delete anything!**).

9.8- Open an MS-DOS command menu (using the menu `Start/Execute: command`) and execute the instructions

- `cd "C:\Documents and Settings\johndoe\Desktop"` (puts you in the folder containing the package structure).
- `R CMD check SmallRPkg` Check that there are no error or warning messages here. If there are, make the suggested changes.
- `R CMD build --binary --use-zip SmallRPkg`

If there were no errors, the package file SmallRPkg.zip is created.

9.9- Install it from the following menu: `Packages/Install package(s) from zip files...` Read the help files of your package.

You can follow this procedure to create more complex packages, which you can then publicize.

Solution.

9.7- Add R's `bin` folder (the one holding `R.exe`, next to `Rgui.exe`) to `PATH` so that the command `R CMD` is found, (the Rtools of Section 9.10 are needed only for a package with compiled code); the `hhc.exe` entry is obsolete, since R dropped compiled (CHM) help in version 2.10, and on macOS or Linux no editing is needed because `R` is already on the path. The folder to add is given by

```
R.home("bin")
```

```
[1] "/Library/Frameworks/R.framework/Resources/bin"
```

(on Windows this prints something like `C:/Program Files/R/R-4.5.1/bin`).

9.8- In a terminal opened in the folder that contains `SmallRPkg`, build the source tarball, check it, then build the binary; `R CMD build --binary --use-zip` no longer exists, and `R CMD INSTALL --build` replaces it (it writes `SmallRPkg_1.0.zip` on Windows, `SmallRPkg_1.0.tgz` on macOS):

```
cd ~/Desktop            # Windows: cd "C:\Users\johndoe\Desktop"
R CMD build SmallRPkg
R CMD check SmallRPkg_1.0.tar.gz
R CMD INSTALL --build SmallRPkg_1.0.tar.gz
```

Real output (macOS, R 4.5.1), trimmed to the last lines of each command:

```
* building 'SmallRPkg_1.0.tar.gz'
...
* checking examples ... OK
* checking PDF version of manual ... OK
* DONE

Status: OK
...
packaged installation of 'SmallRPkg' as 'SmallRPkg_1.0.tgz'
* DONE (SmallRPkg)
```

`R CMD check` returns `Status: OK`, with no error, warning or note, so no further change is needed.

9.9- Windows users choose `Packages > Install package(s) from local files...` and select the `.zip` file. The console equivalent, on any system, is `install.packages()` with `repos = NULL`:

```r
dir.create("mylib")
install.packages("SmallRPkg_1.0.tgz", repos = NULL, lib = "mylib")  # .zip on Windows
library(SmallRPkg, lib.loc = "mylib")
f(2, 3); g(5, 3); head(e, 3)
help(package = "SmallRPkg")
```

```
[1] 5
[1] 2
[1] -0.6264538  0.1836433 -0.8356286
...
Index:

SmallRPkg-package       A Small Example Package
d                       A Tiny Data Frame
e                       A Standard Normal Sample
f                       Sum of Two Numbers
g                       Difference of Two Numbers
```

The output is truncated at `...`, where `help(package)`= also lists the `DESCRIPTION` fields. `?f` then shows the help page written in 9.4, and its example `f(2, 3)` runs.

8 Basic mathematics: matrix operations, integration and optimization

Contents

8.1 Exercises 10.1–10.7

Problem 10.1. Which function calculates binomial coefficients?

Solution. `choose(n, k)` returns $\binom{n}{k}$ (Section 10.1).

```
choose(5, 2)
```

```
[1] 10
```

Problem 10.2. Give the instruction to compute the sum of the first n integers.

Solution. `sum(1:n)` (equivalently `n*(n+1)/2`); for example with $n = 10$:

```
n <- 10
sum(1:n)
```

```
[1] 55
```

Problem 10.3. Which function returns the range of a sample?

Solution. `range(x)` returns the minimum and maximum of the sample; the range as a single number max − min is `diff(range(x))`.

```
x <- c(4, 1, 9, 7)
range(x)
diff(range(x))
```

```
[1] 1 9
[1] 8
```

Problem 10.4. What is the output of this instruction?
`matrix(c(1,0,0,1),nrow=2)*matrix(1:4,nrow=2)`

Solution. The diagonal matrix diag(1, 4), because `*` multiplies element by element (not the matrix product), so the identity acts as a mask that keeps only the diagonal of `matrix(1:4,nrow=2)`.

```
matrix(c(1,0,0,1),nrow=2)*matrix(1:4,nrow=2)
```

```
     [,1] [,2]
[1,]    1    0
[2,]    0    4
```

Problem 10.5. What is the symbol for matrix multiplication?

Solution. `%*%` (Section 10.2.1); `*` is the element-wise product.

```
A <- matrix(1:4, nrow = 2)
A %*% A
```

```
     [,1] [,2]
[1,]    7   15
[2,]   10   22
```

Problem 10.6. Which function transposes a matrix? Which function inverses a matrix?

Solution. `t()` transposes and `solve()` inverts (`solve(A)` with no right-hand side returns A^{-1}; Section 10.2.1).

```
A <- matrix(c(2, 1, 4, 3), nrow = 2)
```

```
t(A)
solve(A)
```

```
     [,1] [,2]
[1,]    2    1
[2,]    4    3
     [,1] [,2]
[1,]  1.5   -2
[2,] -0.5    1
```

Problem 10.7. Give the instruction to create the identity matrix of size 5.

Solution. `diag(5)` (or `diag(rep(1, 5))`, the form used in Section 10.2.1).

```
diag(5)
```

```
     [,1] [,2] [,3] [,4] [,5]
[1,]    1    0    0    0    0
[2,]    0    1    0    0    0
[3,]    0    0    1    0    0
[4,]    0    0    0    1    0
[5,]    0    0    0    0    1
```

8.2 Exercises 10.8–10.13

Problem 10.8. Give the instructions to calculate the determinant and the trace of a matrix.

Solution. `det(A)` for the determinant and `sum(diag(A))` for the trace (Section 10.2.6).

```
A <- matrix(c(2, 1, 4, 3), nrow = 2)
det(A)
sum(diag(A))
```

```
[1] 2
[1] 5
```

Problem 10.9. Give the instruction to centre and scale a matrix $\mathcal{A}$.

Solution. `scale(A)` subtracts each column mean and divides by each column standard deviation (`center` and `scale` arguments switch either step off; Section 10.2.7).

```
A <- matrix(c(1, 2, 3, 4, 6, 11), nrow = 3)
scale(A)
```

```
     [,1]       [,2]
[1,]   -1 -0.8320503
[2,]    0 -0.2773501
[3,]    1  1.1094004
attr(,"scaled:center")
[1] 2 7
attr(,"scaled:scale")
[1] 1.000000 3.605551
```

Problem 10.10. Which function calculates the eigenvalues and eigenvectors of a matrix?

Solution. `eigen()`, which returns a list with components `values` and `vectors` (eigenvectors in columns; Section 10.2.8).

```
eigen(matrix(c(2, 1, 1, 3), nrow = 2))
```

```
eigen() decomposition
$values
[1] 3.618034 1.381966
```

```
$vectors
          [,1]       [,2]
[1,] 0.5257311 -0.8506508
[2,] 0.8506508  0.5257311
```

Problem 10.11. Give the instruction to integrate numerically the function $3x^2 + 2$ over $[-1, 1]$.

Solution. `integrate(function(x) 3*x^2 + 2, lower = -1, upper = 1)` (Section 10.3); its value 6 agrees with the exact integral $\left[x^3 + 2x\right]_{-1}^{1} = 6$.

```
integrate(function(x) 3*x^2 + 2, lower = -1, upper = 1)
```

```
6 with absolute error < 6.7e-14
```

Problem 10.12. Give the instruction to find the maximum of the function $\sin^2(x)$ over $[0, 2]$.

Solution. `optimize(function(x) sin(x)^2, lower = 0, upper = 2, maximum = TRUE)` (Section 10.5.1): the maximum 1 is attained at $x \approx 1.5708 = \pi/2$.

```
optimize(function(x) sin(x)^2, lower = 0, upper = 2, maximum = TRUE)
```

```
$maximum
[1] 1.570779

$objective
[1] 1
```

Problem 10.13. Which function would you use to find where a function vanishes? Where a polynomial vanishes?

Solution. `uniroot()` finds a root of a function in an interval where it changes sign, and `polyroot()` returns all (possibly complex) roots of a polynomial given its coefficients in increasing order (Section 10.5.2).

```
uniroot(function(x) cos(x^2), lower = 0, upper = 2)$root
polyroot(c(3, -8, 1))   # roots of 3 - 8x + x^2
```

```
[1] 1.253319
[1] 0.3944487+0i 7.6055513+0i
```

8.3 Worksheet 10.W.A — A first optimization problem

Problem 10.W.A. Worksheet 10.W.A — Matrix operations, optimization, integration — A first optimization problem

The aim of this practical is to find the eigenvalues of the following matrix, using several methods.

```
> A
     [,1] [,2]
[1,]    2    5
[2,]    3    4
```

10.1- Create a function called `myf()` which evaluates the characteristic polynomial $P(x) = \det(\mathcal{A} - x\mathcal{I}_2)$ at point x (hint: use the function `det()`). Recall that the eigenvalues of a matrix are the roots of its characteristic polynomial.

10.2- Change the function `myf()` so that it takes vector values.

10.3- Plot the function `myf()` over the range $[-10, 10]$. Add axes.

10.4- Use the function `uniroot()` twice to find the two roots of this function.

10.5- Find the coefficients of the polynomial $P(x)$, then use the function `polyroot()` to calculate the roots of this polynomial.

10.6- Check your results with the function `eigen()`.

Solution.

10.1- `myf <- function(x) det(A - x * diag(2))`, where `diag(2)` is $\mathcal{I}_2$:

```
A <- matrix(c(2, 3, 5, 4), nrow = 2)
myf <- function(x) det(A - x * diag(2))
myf(0); myf(7)
```

```
[1] -7
[1] -2.220446e-15
```

$P(0) = \det \mathcal{A} = -7$, and $P(7)$ is zero up to rounding, so 7 is already a candidate eigenvalue.

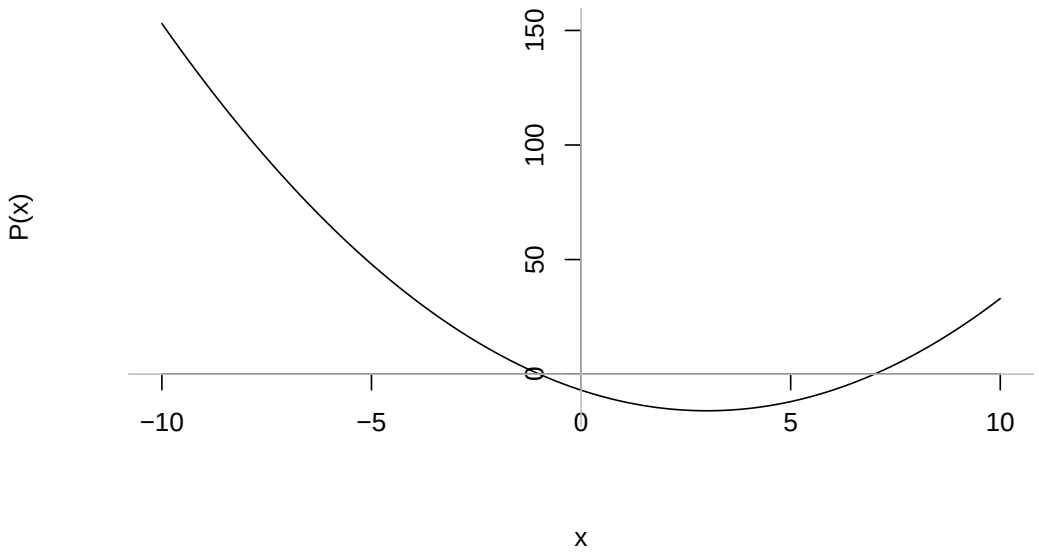
10.2- `det()` accepts one matrix only, so loop over the elements of `x` with `sapply()` (`Vectorize(myf)` works too):

```
myf <- function(x) sapply(x, function(xi) det(A - xi * diag(2)))
myf(c(-1, 0, 7))
```

```
[1]  0.000000e+00 -7.000000e+00 -2.220446e-15
```

10.3- `curve()` needs the vectorised version from 10.2; draw it without the default box, then add axes through the origin:

```
curve(myf, from = -10, to = 10, n = 401, xlab = "x", ylab = "P(x)",
      axes = FALSE)
axis(1, pos = 0); axis(2, pos = 0)
abline(h = 0, v = 0, col = "grey")
```



The parabola crosses zero near $x = -1$ and $x = 7$, which gives the brackets for 10.4.

10.4- Call `uniroot()` once on an interval around each sign change:

```
uniroot(myf, c(-5, 2))$root
uniroot(myf, c(2, 10))$root
uniroot(myf, c(2, 10), tol = 1e-10)$root
```

```
[1] -0.9999994
[1] 7.000003
[1] 7
```

The roots are -1 and 7. The default tolerance `.Machine$double.eps^0.25` explains the digits after the sixth decimal place.

10.5- For a 2×2 matrix, $P(x) = x^2 - \operatorname{tr}(\mathcal{A})\, x + \det \mathcal{A} = x^2 - 6x - 7$. `polyroot()` takes the coefficients in increasing order of degree:

```r
coefs <- c(det(A), -sum(diag(A)), 1)
coefs
polyroot(coefs)
Re(polyroot(coefs))
```

```
[1] -7 -6  1
[1] -1+6.878416e-17i  7-6.878416e-17i
[1] -1  7
```

The roots are again -1 and 7, since $P(x) = (x+1)(x-7)$. The imaginary parts are only rounding noise.

10.6- `eigen()` confirms both eigenvalues:

```r
eigen(A)
```

```
eigen() decomposition
$values
[1]  7 -1

$vectors
           [,1]       [,2]
[1,] -0.7071068 -0.8574929
[2,] -0.7071068  0.5144958
```

All three methods give the eigenvalues 7 and -1.

8.4 Worksheet 10.W.B — A second optimization problem

Problem 10.W.B. Worksheet 10.W.B — Matrix operations, optimization, integration — A second optimization problem

The following information is given about the figure below (a rectangle $ABCD$ with A, B on top and D, C at the bottom; M lies inside it, the triangle AMB is shaded, H is on $[DC]$ below M, Q is on $[BC]$ level with M, and the angle α is marked at M between $[MQ]$ and $[MB]$):

- (MH) is the perpendicular bisector of $[DC]$;
- Q is the orthogonal projection of M onto (BC);
- $g(\alpha) = MA + MB + MH$ with $\alpha = \widehat{AMB} \in]0; \pi/2]$;
- $AB = 10$ and $BC = 6$.

The aim of this practical is to find the angle α which minimizes $g(\alpha)$.

Recall the following trigonometric identities:

- $\cos(\theta) = \dfrac{\text{length of adjacent side}}{\text{length of hypotenuse}}$;
- $\sin(\theta) = \dfrac{\text{length of opposite side}}{\text{length of hypotenuse}}$;
- $\tan(\theta) = \dfrac{\text{length of opposite side}}{\text{length of adjacent side}} = \dfrac{\sin(\theta)}{\cos(\theta)}$;
- $\sin(\pi/2 - \theta) = \cos(\theta)$.

10.1- Reproduce the figure with R.

10.2- Show analytically that $g(\alpha) = 5(2 - \sin(\alpha))/\cos(\alpha) + 6$.

10.3- In R, create the function `g`.

10.4- Calculate numerically the value and argument of the minimum of $g(\alpha)$.

10.5- Calculate analytically $g'(\alpha)$.

10.6- Check your result with symbolic differentiation.

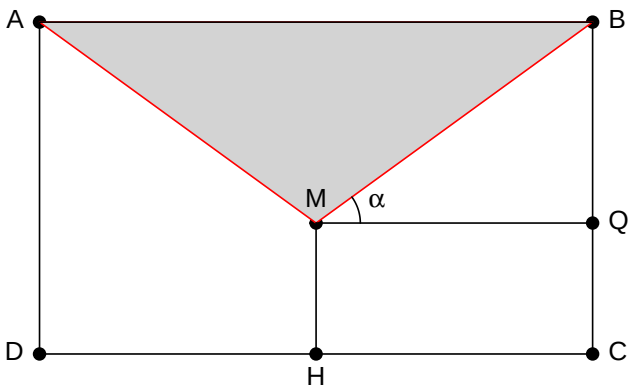
10.7- In R, create this function, which you can call `gprime`.

10.8- Calculate numerically the root of $g'(\alpha)$. Check that you get the same result as before.

Solution. Erratum: the printed $\alpha = \widehat{AMB}$ contradicts both the figure and the formula of 10.2; α is the angle $\widehat{QMB}$ (so $\widehat{AMB} = \pi - 2\alpha$), and since $MH = 6 - 5\tan\alpha \geq 0$ its range is really $]0; \arctan(6/5)]$.

10.1- Place D at the origin, so $A = (0, 6)$, $B = (10, 6)$, $C = (10, 0)$, $H = (5, 0)$ and $M = (5, 6 - 5\tan\alpha)$; `polygon()` shades the triangle and `segments()` draws the construction lines (here with $\alpha = \pi/5$).

```r
figure <- function(alpha = pi/5) {
  A <- c(0, 6); B <- c(10, 6); C <- c(10, 0); D <- c(0, 0)
  M <- c(5, 6 - 5 * tan(alpha)); H <- c(5, 0); Q <- c(10, M[2])
  P <- rbind(A, B, C, D, M, H, Q)
  plot(P, asp = 1, axes = FALSE, xlab = "", ylab = "", pch = 19,
       xlim = c(-0.5, 10.5), ylim = c(-0.5, 6.5))
  polygon(rbind(A, B, M), col = "lightgray", border = "red")
  rect(0, 0, 10, 6)
  segments(M[1], M[2], H[1], H[2]); segments(M[1], M[2], Q[1], Q[2])
  th <- seq(0, alpha, length = 30)
  lines(M[1] + 0.8 * cos(th), M[2] + 0.8 * sin(th))
  text(M[1] + 1.1, M[2] + 0.4, expression(alpha))
  text(P[, 1], P[, 2], c("A", "B", "C", "D", "M", "H", "Q"),
       pos = c(2, 4, 4, 2, 3, 1, 4))
}
figure()
```



10.2- M lies on the perpendicular bisector of $[DC]$ (which is also that of $[AB]$), so $MA = MB$ and $MQ = AB/2 = 5$. In the right triangle MQB, $\cos\alpha = MQ/MB$ and $\tan\alpha = BQ/MQ$, and $MH = QC = BC - BQ$:

$$MB = MA = \frac{5}{\cos\alpha}, \qquad BQ = 5\tan\alpha, \qquad MH = 6 - 5\,\frac{\sin\alpha}{\cos\alpha},$$
$$g(\alpha) = \frac{10}{\cos\alpha} - \frac{5\sin\alpha}{\cos\alpha} + 6 = \frac{5(2-\sin\alpha)}{\cos\alpha} + 6.$$

10.3- and 10.4- The one-dimensional minimizer `optimize()` of Section 10.5 does it; the search interval is the admissible range $]0; \arctan(6/5)]$:

```r
g <- function(alpha) 5 * (2 - sin(alpha)) / cos(alpha) + 6
optimize(g, lower = 0, upper = atan(6/5))
c(pi/6, 6 + 5 * sqrt(3))
```

```
$minimum
[1] 0.5235997

$objective
[1] 14.66025

[1]  0.5235988 14.6602540
```

The minimum is $g \approx 14.660$, reached at $\alpha \approx 0.5236$, which matches $\pi/6$ and $6 + 5\sqrt{3}$ (the last line).

10.5- By the quotient rule,

$$g'(\alpha) = 5\,\frac{-\cos\alpha\cos\alpha + (2-\sin\alpha)\sin\alpha}{\cos^2\alpha} = 5\,\frac{2\sin\alpha - (\sin^2\alpha + \cos^2\alpha)}{\cos^2\alpha}$$
$$= \frac{5(2\sin\alpha - 1)}{\cos^2\alpha},$$

which is negative then positive, vanishing only at $\sin\alpha = 1/2$, i.e. $\alpha = \pi/6$.
10.6- The symbolic derivative from `D()` (Section 10.4.1):

```
D(expression(5 * (2 - sin(alpha)) / cos(alpha) + 6), "alpha")
```

```
-(5 * cos(alpha)/cos(alpha) - 5 * (2 - sin(alpha)) * sin(alpha)/cos(alpha)^2)
```

This is $-5 + 5(2\sin\alpha - \sin^2\alpha)/\cos^2\alpha = 5(2\sin\alpha - \sin^2\alpha - \cos^2\alpha)/\cos^2\alpha$, which simplifies to the result of 10.5.
10.7- The function, checked against the gradient returned by `deriv()` on a grid of angles:

```
gprime <- function(alpha) 5 * (2 * sin(alpha) - 1) / cos(alpha)^2
dg <- deriv(~ 5 * (2 - sin(alpha)) / cos(alpha) + 6, "alpha",
            function.arg = TRUE)
a <- seq(0.1, 0.8, by = 0.1)
all.equal(as.vector(attr(dg(a), "gradient")), gprime(a))
```

```
[1] TRUE
```

10.8- `uniroot()` finds the root of `gprime` on the same interval:

```
r <- uniroot(gprime, lower = 0, upper = atan(6/5), tol = 1e-10)
c(root = r$root, g.root = g(r$root), diff = r$root - pi/6)
```

```
        root       g.root         diff
5.235988e-01 1.466025e+01 1.110223e-16
```

The root is $\alpha = \pi/6$ to machine precision and g there equals 14.66025, the same argument and minimum value as `optimize()` gave in 10.4.

8.5 Worksheet 10.W.C — Standard normal table

Problem 10.W.C. Worksheet 10.W.C — Standard normal table — Standard normal table
We shall use the function `integrate()` to create a table for the distribution $\mathcal{N}(0,1)$.
Let $\Phi(x) = \int_{-\infty}^{x} \frac{1}{\sqrt{2\pi}} e^{-t^2/2}\,dt$ be the cumulative distribution function of $\mathcal{N}(0,1)$. It is well known that $\Phi(-x) = 1 - \Phi(x)$. We shall thus only create the table for positive values of x.
10.1- Create a function `phi()` which takes as input a vector x of length n and returns the vector of values $\frac{1}{\sqrt{2\pi}} e^{-x_i^2/2}$, $i = 1, \ldots, n$.
10.2- Use the function `integrate()` to compute $\Phi(x)$ for all x in the following vector: `quantiles <- seq(0,5.5,by=0.1)`. Store these values in a vector called `probs`.
10.3- Use the function `all.equal()` to compare these results with those given by the function `pnorm()`.
10.4- Plot the values of $\Phi(x)$ for all x and all $-x$ in `quantiles` (hint: use the function `rev()`).
10.5- Plot the function `pnorm()` in blue over the previous curve. Check that the two plots coincide perfectly.

Solution.
10.1- Vectorised arithmetic makes `phi()` a one-liner:

```
phi <- function(x) exp(-x^2/2) / sqrt(2*pi)
phi(c(0, 1, 2))
```

```
[1] 0.39894228 0.24197072 0.05399097
```

10.2- `integrate()` takes a single upper bound, so we loop over `quantiles` with `sapply()` and keep the `$value` component:

```
quantiles <- seq(0, 5.5, by = 0.1)
probs <- sapply(quantiles, function(q) integrate(phi, -Inf, q)$value)
```

```r
head(round(probs, 4))
tail(round(probs, 7), 3)
```

```
[1] 0.5000 0.5398 0.5793 0.6179 0.6554 0.6915
[1] 0.9999999 1.0000000 1.0000000
```

These are the familiar table entries $\Phi(0) = 0.5$, $\Phi(0.5) = 0.6915$, and so on.

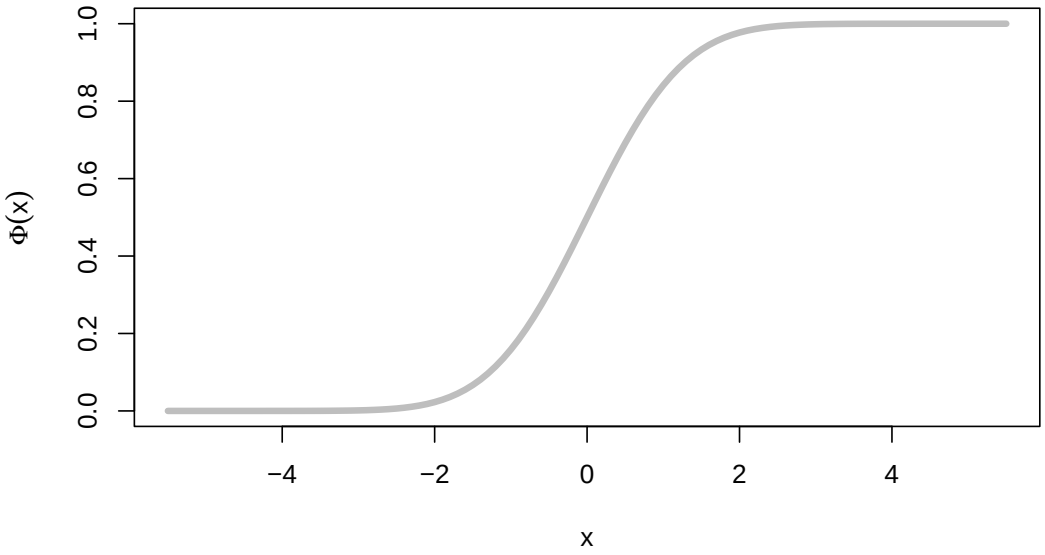
10.3- The numerical integrals agree with `pnorm()` to within `all.equal()`'s default tolerance (1.5×10^{-8}); the largest absolute discrepancy is about 4.6×10^{-9}:

```r
all.equal(probs, pnorm(quantiles))
max(abs(probs - pnorm(quantiles)))
```

```
[1] TRUE
[1] 4.559252e-09
```

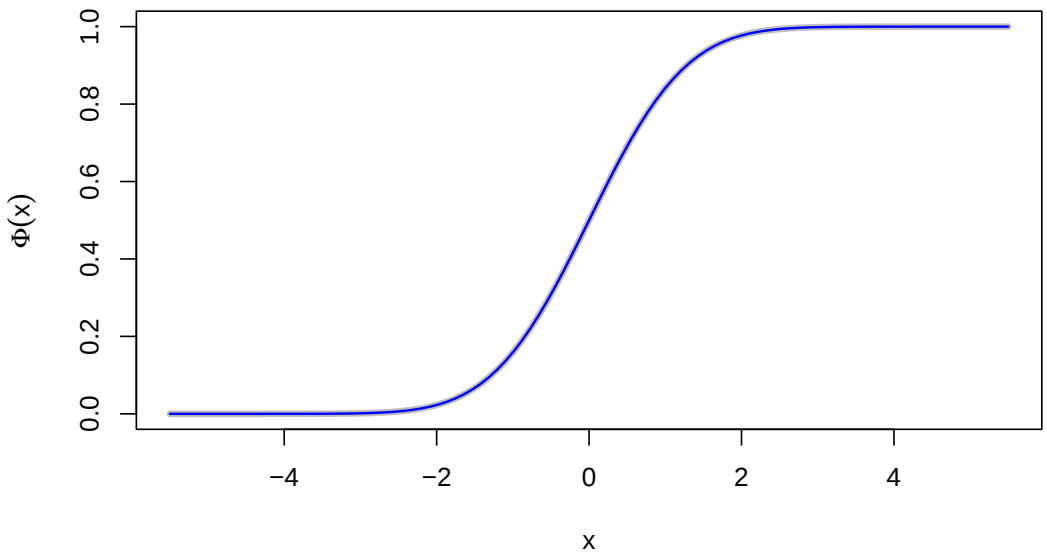
10.4- By symmetry $\Phi(-x) = 1 - \Phi(x)$, so the negative half is `1 - rev(probs)`. We drop the duplicated point $x = 0$ with `[-1]`:

```r
x <- c(-rev(quantiles[-1]), quantiles)
Phi <- c(1 - rev(probs[-1]), probs)
plot(x, Phi, type = "l", lwd = 4, col = "grey",
     xlab = "x", ylab = expression(Phi(x)))
```



10.5- We draw `pnorm()` in thin blue over the thick grey curve with `curve(..., add = TRUE)`. The blue line runs exactly along the grey one, and `all.equal()` confirms this over all 111 points:

```r
plot(x, Phi, type = "l", lwd = 4, col = "grey",
     xlab = "x", ylab = expression(Phi(x)))
curve(pnorm(x), add = TRUE, col = "blue", lwd = 1.5)
```




```
all.equal(Phi, pnorm(x))
```

```
[1] TRUE
```

8.6 Worksheet 10.W.D — Principal components analysis

Problem 10.W.D. Worksheet 10.W.D — Principal components analysis — Bordeaux climate and wine quality

Principal components analysis is used to describe the proximity of individuals on which several quantitative traits have been measured. This method requires many matrix operations, and is thus a good way to put into practice the notions introduced at the beginning of this chapter.

Data were collected in the wine region of Bordeaux. They include:

- four weather traits: `TEMPER` (sum of daily average temperatures, in degrees Celsius), `SUN` (length of insolation, in hours), `HEAT` (number of days of strong heat), `RAIN` (rainfall, in mm);
- wine quality (`QUALITY`), as determined by wine-tasters: 1 = good wine, 2 = average wine, 3 = mediocre wine.

We shall represent these quantitative data on a scatter plot after projecting the data onto a subspace (a plane) chosen so as to limit the loss of information caused by the projection.

10.1- Import into the variable `climatewine` the contents of the data file http://www.biostatisticien.eu/springeR/climatewine.csv

10.2- Store in matrix `X` the variables `TEMPER`, `SUN`, `HEAT`, `RAIN` (hint: `as.matrix()`).

10.3- Calculate the centre (of gravity) `g` of the scatter plot of individuals included in `X` (vector of column averages) with the function `colMeans()`. Display it with two decimal places.

10.4- Use the function `scale()` to calculate the matrix $\dot{X} = (\dot{x}_{ij})$ of centred data, and store it in the variable `Xdot`.

10.5- Calculate the global `inertia` of the scatter plot, which represents the dispersion of the points: $I = \frac{1}{n}\sum_{i=1}^{n}\sum_{j=1}^{n}\dot{x}_{ij}^2$, where n is the number of individuals in X.

10.6- The contribution of individual i to the global inertia is given by the formula $\frac{1}{nI}\sum_{j=1}^{p}\dot{x}_{ij}^2$, where p is the number of variables (four in this case). Calculate the vector `inertiacontr` of contributions to inertia from each individual.

10.7- Create the column matrix `onen` of length n, containing only 1's.

10.8- Check that the centre of gravity `g` of the scatter plot is also given by the formula $g = \frac{1}{n}X^T 1_n$.

10.9- Check that the matrix `Xdot` of centred data is also given by the formula $\dot{X} = X - 1_n g^T$.

10.10- Calculate the matrix of covariances `S` with the formula $S = \frac{1}{n}\dot{X}^T\dot{X}$. Try to reproduce this result with the function `cov()`.
10.11- Use the matrix `S` to calculate the diagonal matrix `Doneovers` containing the inverses of standard deviations: $D_{1/s} = \text{diag}(1/s_1, \ldots, 1/s_p)$.
10.12- Calculate the matrix `Z` of scaled and centred data with the formula $Z = \dot{X}D_{1/s}$.
10.13- Calculate the matrix of correlations `R` with the formula $R = \frac{1}{n}Z^TZ$. Try to reproduce this result with the function `cor()`.
10.14- Calculate the diagonal matrix `Lambda` of eigenvalues (Λ) and the matrix `W` of eigenvectors (W) of the correlation matrix R. The matrix `W` contains the coordinates of a new basis in which we shall represent the individuals.
10.15- Plot the circle of correlations, which is a circle of radius 1, over which you should overlay arrows starting at the origin and ending at the points with coordinates given by the first two columns of the matrix $W\Lambda^{1/2}$. On the same plot, add the names of the variables at the end of the four arrows.
10.16- The total inertia of the scaled and centred scatter plot is equal to the number of variables (four in this case). It can be decomposed into a sum of inertias contributed by each one of the four axes of the basis of W, which are given by the diagonal of Λ. Calculate the vector of percentages of total inertia explained by the first k axes ($1 \leq k \leq p$). What percentage of the inertia is explained by the first two axes?
10.17- Calculate the matrix `CW` of principal components with the formula $C_W = ZW$. The principal components are the coordinates of the individuals in the new basis described by `W`.
10.18- Open a new graphics window and plot the individuals projected onto the first principal plane, i.e. with coordinates given by the first two columns of C_W. Add the names of the individuals onto the plot.
10.19- Draw the last plot again, but this time plot in red (respectively blue, green) good wines (respectively average wines, mediocre wines). Add a caption.
10.20- The quality of representation of individual i on the first principal plane is given by the formula $\frac{c_{i1}^2+c_{i2}^2}{\sum_{j=1}^{p} c_{ij}^2}$, where c_{ij} is the entry at row i and column j of the matrix C_W. Calculate the vector `QLT` of qualities of representation of individuals on the first principal plane. Display `QLT` with two decimal places.
10.21- We shall briefly explore package `ade4` which performs PCA. Install and load this package.
10.22- Type the following instructions:

```
rownames(X) <- climatewine[,1]
res <- dudi.pca(X) # Answer 2 to the question you are asked.
scatter(res)
s.class(res$li,as.factor(climatewine[,6]))
```

Solution.
10.1- The file is tab-separated with a header line, so `read.table()` with `header = TRUE` reads it directly from the URL (34 years, 1924-1957).

```
climatewine <- read.table("http://www.biostatisticien.eu/springeR/climatewine.csv",
                          header = TRUE)
head(climatewine, 3)
dim(climatewine)
```

```
  YEAR TEMPER  SUN HEAT RAIN QUALITY
1 1924   3064 1201   10  361       2
2 1925   3000 1053   11  338       3
3 1926   3155 1133   19  393       2
[1] 34  6
```

10.2- Select the four weather columns and coerce with `as.matrix()`.

```
X <- as.matrix(climatewine[, c("TEMPER", "SUN", "HEAT", "RAIN")])
n <- nrow(X); p <- ncol(X)
```

10.3- The centre of gravity is the vector of column means.

```
g <- colMeans(X)
```

```
round(g, 2)
```

```
 TEMPER     SUN    HEAT    RAIN
3157.88 1247.32   18.82  360.44
```

10.4- `scale()` with `scale = FALSE` only subtracts the column means.

```
Xdot <- scale(X, center = TRUE, scale = FALSE)
```

10.5- The inner sum runs over the p variables, not n (the printed upper limit n on j is a typo): $I = \frac{1}{n}\sum_{i=1}^{n}\sum_{j=1}^{p}\dot{x}_{ij}^2$.

```
inertia <- sum(Xdot^2) / n
inertia
```

```
[1] 43114.48
```

The unscaled inertia is dominated by `TEMPER` and `SUN`, whose variances are in the tens of thousands.

10.6- Row sums of squares divided by nI; the contributions add to 1.

```
inertiacontr <- rowSums(Xdot^2) / (n * inertia)
round(head(inertiacontr), 4)
sum(inertiacontr)
```

```
[1] 0.0075 0.0432 0.0096 0.0640 0.0085 0.0339
[1] 1
```

10.7- A one-column matrix of 1's:

```
onen <- matrix(1, nrow = n, ncol = 1)
```

10.8- The matrix product $\frac{1}{n}X^T 1_n$ returns the same vector as `colMeans()`.

```
all.equal(g, drop(t(X) %*% onen / n))
```

```
[1] TRUE
```

10.9- The outer product $1_n g^T$ repeats `g` on each row; `check.attributes = FALSE` ignores the `"scaled:center"` attribute that `scale()` attaches.

```
all.equal(Xdot, X - onen %*% t(g), check.attributes = FALSE)
```

```
[1] TRUE
```

10.10- $S = \frac{1}{n}\dot{X}^T\dot{X}$ uses divisor n, whereas `cov()` uses $n-1$, so `cov(X)` must be rescaled by $(n-1)/n$ to match.

```
S <- t(Xdot) %*% Xdot / n
round(S, 1)
all.equal(S, cov(X) * (n - 1) / n, check.attributes = FALSE)
```

```
        TEMPER     SUN   HEAT    RAIN
TEMPER 19346.8 12360.3 1187.4 -5130.4
SUN    12360.3 15561.8  795.8 -5317.8
HEAT    1187.4   795.8   97.4  -356.5
RAIN   -5130.4 -5317.8 -356.5  8108.5
[1] TRUE
```

10.11- The standard deviations are the square roots of the diagonal of `S`; `diag()` builds the diagonal matrix of their inverses.

```
Doneovers <- diag(1 / sqrt(diag(S)))
round(Doneovers, 5)
```

```
        [,1]    [,2]    [,3]    [,4]
[1,] 0.00719 0.00000 0.00000 0.00000
[2,] 0.00000 0.00802 0.00000 0.00000
[3,] 0.00000 0.00000 0.10134 0.00000
[4,] 0.00000 0.00000 0.00000 0.01111
```

10.12- Right-multiplying by $D_{1/s}$ divides each centred column by its standard deviation.

```
Z <- Xdot %*% Doneovers
colnames(Z) <- colnames(X)
```

10.13- $R = \frac{1}{n}Z^T Z$ coincides with `cor(X)` (the n versus $n-1$ divisor cancels in a correlation).

```r
R <- t(Z) %*% Z / n
round(R, 3)
all.equal(R, cor(X), check.attributes = FALSE)
```

```
       TEMPER    SUN   HEAT   RAIN
TEMPER  1.000  0.712  0.865 -0.410
SUN     0.712  1.000  0.646 -0.473
HEAT    0.865  0.646  1.000 -0.401
RAIN   -0.410 -0.473 -0.401  1.000
[1] TRUE
```

The three heat-related traits are strongly positively correlated with one another and negatively with rainfall.

10.14- `eigen()` returns the eigenvalues in decreasing order and the unit eigenvectors in columns (each defined only up to sign).

```r
eig <- eigen(R)
Lambda <- diag(eig$values)
W <- eig$vectors
dimnames(W) <- list(colnames(X), paste0("Axis", 1:p))
round(diag(Lambda), 4)
round(W, 3)
```

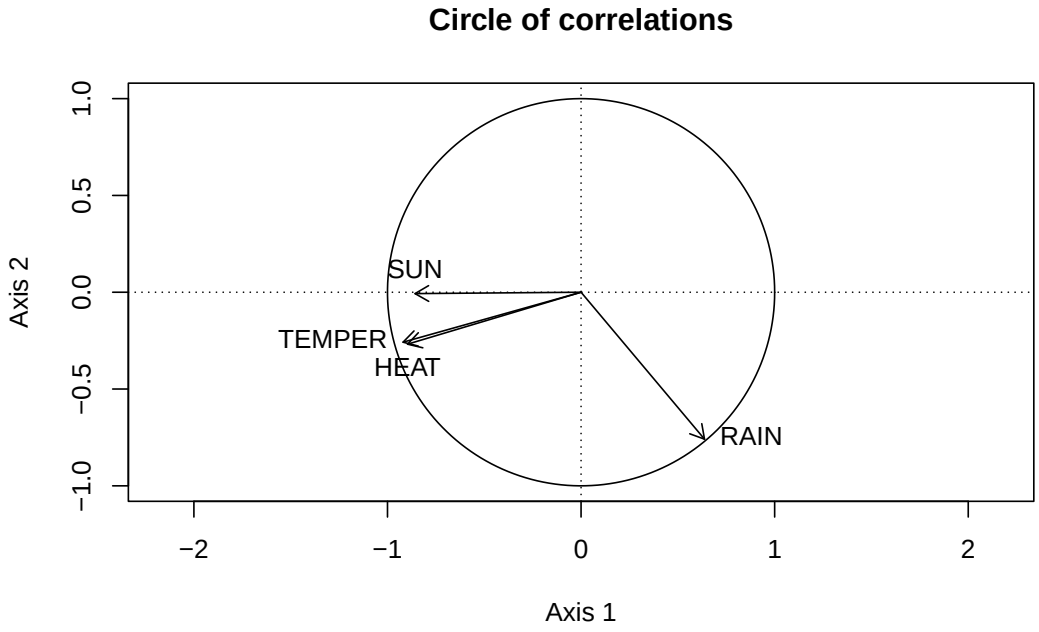
```
[1] 2.7915 0.7145 0.3659 0.1281
        Axis1  Axis2  Axis3  Axis4
TEMPER -0.550 -0.305 -0.208  0.749
SUN    -0.513 -0.008  0.846 -0.146
HEAT   -0.537 -0.317 -0.441 -0.646
RAIN    0.382 -0.898  0.218 -0.025
```

10.15- The first two columns of $W\Lambda^{1/2}$ are the correlations between each variable and the first two principal components.

```r
coords <- W %*% sqrt(Lambda)
round(coords[, 1:2], 3)
```

```
         [,1]   [,2]
TEMPER -0.920 -0.258
SUN    -0.858 -0.007
HEAT   -0.896 -0.268
RAIN    0.638 -0.759
```

```r
theta <- seq(0, 2 * pi, length.out = 200)
plot(cos(theta), sin(theta), type = "l", asp = 1, xlab = "Axis 1",
     ylab = "Axis 2", main = "Circle of correlations")
abline(h = 0, v = 0, lty = 3)
arrows(0, 0, coords[, 1], coords[, 2], length = 0.1)
text(coords[, 1], coords[, 2], labels = colnames(X), pos = c(2, 3, 1, 4))
```



All four arrows reach close to the circle, so the four variables are well represented on the first plane: axis 1 opposes warm, sunny years (`TEMPER`, `SUN`, `HEAT` on the left) to rainy years (`RAIN` on the right), and axis 2 is driven mainly by `RAIN`.

10.16- The cumulative sums of the eigenvalues, divided by $p = 4$:

```
round(100 * cumsum(diag(Lambda)) / p, 2)
```

```
[1]  69.79  87.65  96.80 100.00
```

The first two axes explain 87.65% of the total inertia, so the first principal plane loses little information.

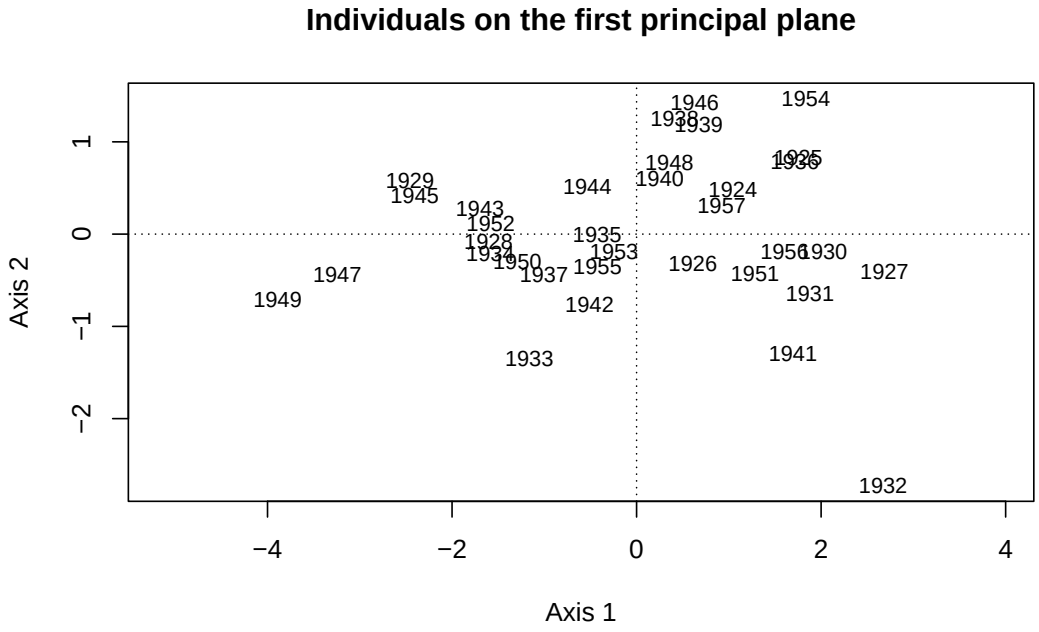
10.17- The principal components are $C_W = ZW$; the variance (divisor n) of column k equals the k-th eigenvalue.

```
CW <- Z %*% W
round(head(CW, 3), 3)
round(apply(CW, 2, var) * (n - 1) / n, 4)
```

```
     Axis1  Axis2  Axis3  Axis4
[1,] 1.044  0.487  0.222  0.126
[2,] 1.755  0.835 -0.787 -0.104
[3,] 0.610 -0.316 -0.700  0.098
 Axis1  Axis2  Axis3  Axis4
2.7915 0.7145 0.3659 0.1281
```

10.18- Open a new device with `dev.new()` (or `x11()=/=quartz()=/=windows()`) and label each point with its year.

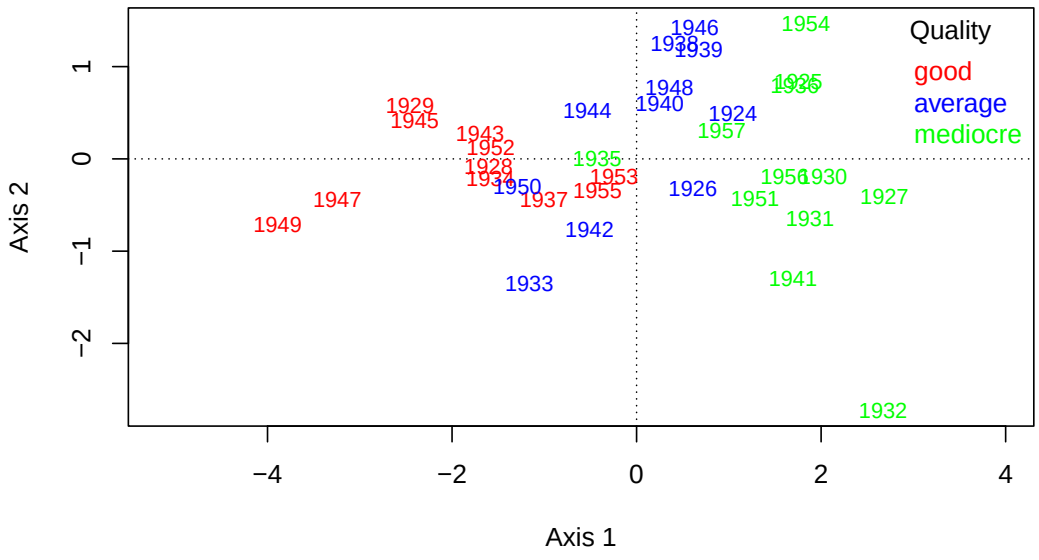
```
dev.new()
plot(CW[, 1], CW[, 2], type = "n", asp = 1, xlab = "Axis 1", ylab = "Axis 2",
     main = "Individuals on the first principal plane")
abline(h = 0, v = 0, lty = 3)
text(CW[, 1], CW[, 2], labels = climatewine$YEAR, cex = 0.8)
```



Years on the left (e.g. 1947, 1949) were hot and sunny; years on the right (e.g. 1927, 1932) were cool and wet.

10.19- Index a colour vector by `QUALITY` and add a legend.

```
cols <- c("red", "blue", "green")[climatewine$QUALITY]
plot(CW[, 1], CW[, 2], type = "n", asp = 1, xlab = "Axis 1", ylab = "Axis 2",
     main = "Individuals coloured by wine quality")
abline(h = 0, v = 0, lty = 3)
text(CW[, 1], CW[, 2], labels = climatewine$YEAR, col = cols, cex = 0.8)
legend("topright", legend = c("good", "average", "mediocre"),
       text.col = c("red", "blue", "green"), title = "Quality",
       title.col = "black", bty = "n")
```



Quality follows the first axis: good vintages sit on the hot, sunny left, mediocre ones on the cool, rainy right, and average ones in between.

10.20- Squared coordinates on axes 1-2 divided by the squared distance to the origin across all four axes:

```r
QLT <- rowSums(CW[, 1:2]^2) / rowSums(CW^2)
names(QLT) <- climatewine$YEAR
round(QLT, 2)
names(QLT)[QLT < 0.6]
```

```
1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939
0.95 0.86 0.49 0.83 0.65 0.94 0.67 0.89 0.99 0.99 0.95 0.13 0.97 0.52 0.87 0.76
1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955
0.32 0.88 0.76 0.95 0.77 0.93 0.97 0.86 0.78 1.00 0.95 0.96 0.91 0.86 0.96 0.61
1956 1957
0.81 0.91
[1] "1926" "1935" "1937" "1940"
```

Most years are well represented on the plane; the positions of 1926, 1935, 1937 and 1940 (quality below 0.6, 1935 only 0.13) should not be interpreted from this plot.

10.21- Install once from CRAN with `install.packages("ade4")`, then load it in each session.

```r
# install.packages("ade4")  # only once per R installation
library(ade4)
```

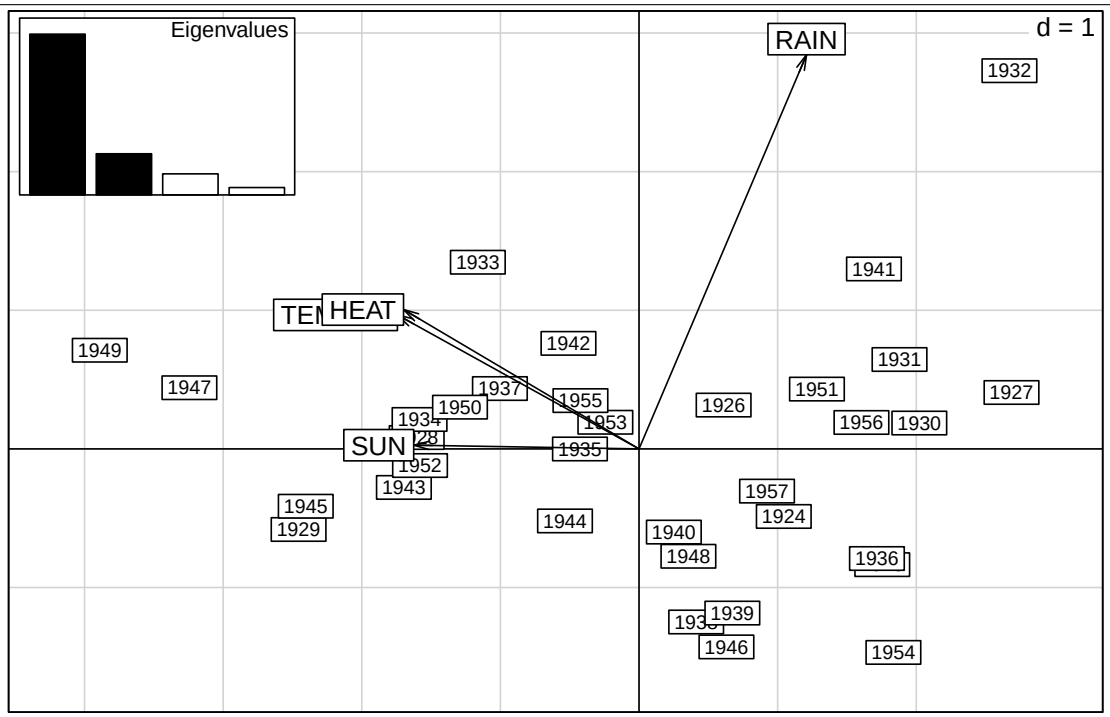
10.22- `dudi.pca()` centres and scales by default, so it reproduces our eigenvalues; answering 2 to its interactive question keeps two axes, which is what `scannf = FALSE, nf = 2` does non-interactively.

```r
rownames(X) <- climatewine[, 1]
res <- dudi.pca(X, scannf = FALSE, nf = 2)
round(res$eig, 4)
all.equal(abs(as.matrix(res$li)), abs(CW[, 1:2]), check.attributes = FALSE)
all.equal(abs(as.matrix(res$co)), abs(coords[, 1:2]), check.attributes = FALSE)
```

```
[1] 2.7915 0.7145 0.3659 0.1281
[1] TRUE
[1] TRUE
```

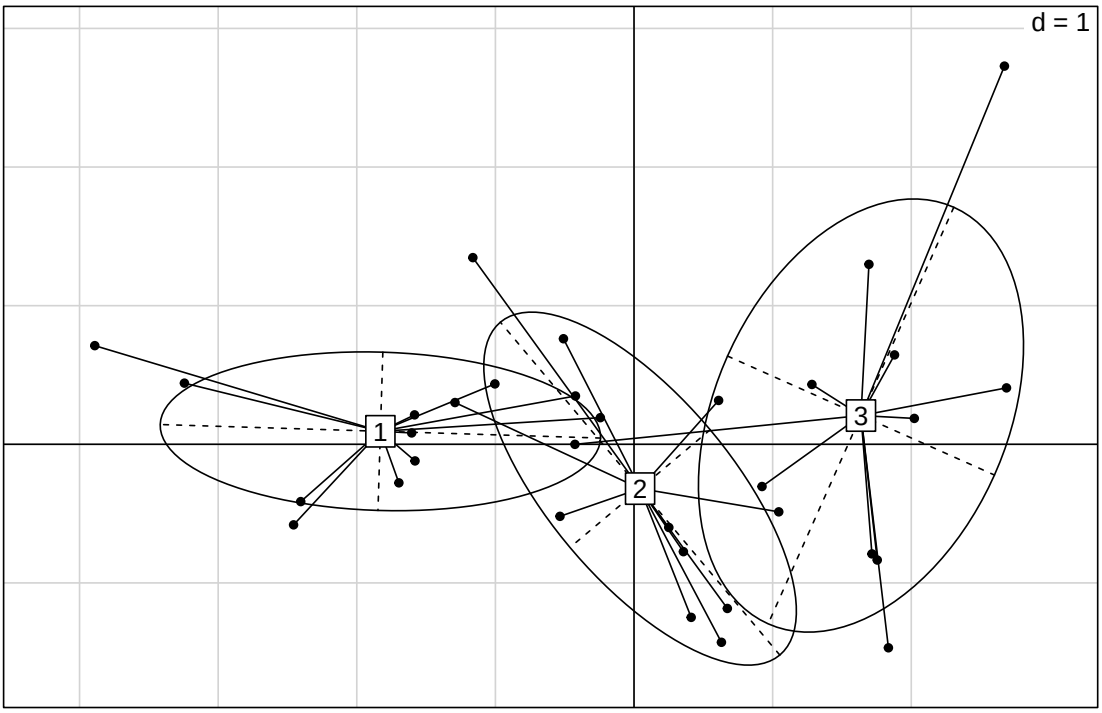
`res$li` (row coordinates) is C_W and `res$co` (column coordinates) is $W\Lambda^{1/2}$, up to the sign of each axis. `scatter(res)` draws the biplot (individuals plus variable arrows):

```r
scatter(res)
```



`s.class()` draws the individuals grouped by quality, with each group's centre of gravity and inertia ellipse:

```r
s.class(res$li, as.factor(climatewine[, 6]))
```



The three quality groups (1 = good, 2 = average, 3 = mediocre) are ordered along the first axis with only partial overlap of their ellipses, confirming that the climate traits largely separate the vintages by quality.

9 Descriptive statistics

Contents

9.1 Exercises 11.1–11.7

Problem 11.1. Give the instruction which returns the table of frequencies for a qualitative variable `x`.

Solution. `table(x)/length(x)` (equivalently `prop.table(table(x))`), as in Section 11.3.2; here `x` is the variable `fat` of the `nutrition_elderly` data used throughout the chapter (`gdata::read.xls()` no longer exists in current `gdata`, so the file is read with `readxl`).

```
library(readxl)
f <- tempfile(fileext = ".xls")
download.file("http://www.biostatisticien.eu/springeR/nutrition_elderly.xls",
              f, mode = "wb", quiet = TRUE)
NE <- as.data.frame(read_excel(f))
gender <- factor(NE$gender, labels = c("Male", "Female"))
fat <- factor(NE$fat, labels = c("butter", "margarine", "peanut",
  "sunflower", "olive", "Isio4", "rapeseed", "duck"))
weight <- NE$weight; height <- NE$height; tea <- NE$tea
x <- fat
round(table(x)/length(x), 3)
```

```
x
   butter margarine    peanut sunflower     olive     Isio4  rapeseed      duck
    0.066     0.119     0.212     0.301     0.177     0.102     0.004     0.018
```

Problem 11.2. Give the instruction which returns the contingency table for qualitative variables `x` and `y`.

Solution. `table(x, y)` (Section 11.3.4.1); with `x = gender` and `y = fat`:

```
genderfat <- table(gender, fat)
genderfat
```

```
        fat
gender   butter margarine peanut sunflower olive Isio4 rapeseed duck
  Male       10        10     16        21    20     5        0    3
  Female      5        17     32        47    20    18        1    1
```

Problem 11.3. Which function returns the marginal distributions from a contingency table?

Solution. `margin.table()`, with second argument `1` for the row margin and `2` for the column margin (Section 11.3.4.3).

```
margin.table(genderfat, 1)
margin.table(genderfat, 2)
```

```
gender
  Male Female
    85    141
fat
   butter margarine    peanut sunflower     olive     Isio4  rapeseed      duck
       15        27        48        68        40        23         1         4
```

Problem 11.4. Which function returns the conditional distributions from a contingency table?

Solution. `prop.table()`, with `margin = 1` for the distributions conditional on the rows (row profiles) and `margin = 2` for those conditional on the columns (Section 11.3.4.4).

```
round(prop.table(genderfat, 1), 3)
```

```
        fat
gender   butter margarine peanut sunflower olive Isio4 rapeseed  duck
```

```
Male    0.118     0.118  0.188     0.247 0.235 0.059    0.000 0.035
Female  0.035     0.121  0.227     0.333 0.142 0.128    0.007 0.007
```

Problem 11.5. Give the instruction which returns the mode of a distribution.

Solution. `names(which.max(table(x)))` returns a (the first) mode; `names(tab)[tab =` max(tab)]= with `tab <- table(x)` returns all of them when there are ties (Section 11.4.1.1). For the number of cups of tea per day, the mode is 0 cups:

```
tabtea <- table(tea)
names(which.max(tabtea))
names(tabtea)[tabtea == max(tabtea)]
```

```
[1] "0"
[1] "0"
```

Problem 11.6. Give the instruction which returns the range of a vector `x`.

Solution. `diff(range(x))` (or `max(x) - min(x)`); note that `range(x)` alone returns the pair (minimum, maximum), not the range (Section 11.4.2). For the heights:

```
x <- height
range(x)
diff(range(x))
```

```
[1] 140 188
[1] 48
```

Problem 11.7. Give the instruction which returns the interquartile range of a vector `x`.

Solution. `IQR(x)`, i.e. $q_{3/4} - q_{1/4}$ (Section 11.4.2).

```
IQR(x)
```

```
[1] 13
```

9.2 Exercises 11.8–11.14

Problem 11.8. Give the instruction which returns the (non empirical) variance of a vector `x`.

Solution. `var(x) * (length(x) - 1) / length(x)`, the book's `var.pop(x)`: the variance σ^2_{Pop} of the population, with divisor N (Section 11.4.2); `var(x)` alone is the unbiased sample estimator with divisor $n - 1$ (Note in Section 11.4.2).

```
var(x) * (length(x) - 1) / length(x)
var(x)
```

```
[1] 80.70195
[1] 81.06063
```

Problem 11.9. Give the code of a function which calculates the coefficient of variation.

Solution. The coefficient of variation is $cv = \sigma_{\text{Pop}}/\mu_X$ (Section 11.4.2):

```
co.var <- function(x) {
  sd.pop <- sqrt(mean((x - mean(x))^2))
  sd.pop / mean(x)
}
co.var(x)
```

```
[1] 0.0547903
```

Problem 11.10. Give the instruction which calculates the mean absolute deviation.

Solution. `mean(abs(x - mean(x)))`, i.e. $\frac{1}{N}\sum_{i=1}^{N}|x_i - \bar{x}|$ (Section 11.4.2; not to be confused with `mad()`, the median absolute deviation).

```
mean(abs(x - mean(x)))
```

```
[1] 7.312045
```

Problem 11.11. Which package includes functions to calculate skewness and kurtosis?

Solution. The package `moments`, through its functions `skewness()` and `kurtosis()` (Section 11.4.3); they return γ_1 and β_2 exactly as the book's `skew()` and `kurt()`.

```
library(moments)
skewness(x)
kurtosis(x)
```

```
[1] 0.4256203
[1] 2.778185
```

Problem 11.12. Give the instruction which returns Cramér's Φ^2.

Solution. `chisq.test(tab, correct = FALSE)$statistic/sum(tab)` (`correct = FALSE` stops a Yates correction on a 2 x 2 table), i.e. $\Phi^2 = \chi^2/N$ for a contingency table `tab` (Section 11.5.1.2). For `gender` by `fat`:

```
chi2 <- suppressWarnings(chisq.test(genderfat, correct = FALSE))$statistic
Phi2 <- unname(chi2 / sum(genderfat))
Phi2
```

```
[1] 0.06707265
```

Problem 11.13. Give the code of a function which calculates the correlation ratio $\eta^2_{Y|X}$.

Solution. The function below computes $\eta^2_{Y|X} = \sum_k n_k(\bar{y}_k - \bar{y})^2 / \sum_i (y_i - \bar{y})^2$ (Section 11.5.4.1):

```
eta2 <- function(y, gpe) {
  means <- tapply(y, gpe, mean)
  counts <- tapply(y, gpe, length)
  sum(counts * (means - mean(y))^2) / sum((y - mean(y))^2)
}
eta2(weight, gender)
```

```
[1] 0.3325501
```

So gender accounts for about 33% of the variation in weight.

Problem 11.14. Which function would you use to draw a Pareto chart?

Solution. `barplot()` applied to the sorted table of counts, `barplot(sort(table(x), decreasing = TRUE))` (Section 11.6.1.3).

9.3 Exercises 11.15–11.18

Problem 11.15. Which function would you use to draw a stacked bar chart?

Solution. `barplot()` with a matrix as its first argument (one column per bar, e.g. the `cbind()` of the frequency tables of each group), since `beside = FALSE` is the default (Section 11.6.1.4).

Problem 11.16. Which function would you use to draw a pie chart?

Solution. `pie()`, applied to a table of counts, e.g. `pie(table(x))` (Section 11.6.1.5).

Problem 11.17. Which function would you use to draw a box plot?

Solution. `boxplot()`, e.g. `boxplot(x)`, or `boxplot(y ~ g)` for one box per level of a factor `g` (Sections 11.6.3.5 and 11.6.4.3).

Problem 11.18. Which function would you use to draw a histogram?

Solution. `hist()`, with `breaks` to set the class boundaries and `freq = FALSE` for a density histogram (Section 11.6.4.4).

9.4 Worksheet 11.W.A — Thoughts on independence in descriptive statistics

Problem 11.W.A. Worksheet 11.W.A — Descriptive data studies — Thoughts on independence in descriptive statistics
11.1- Import the file http://www.biostatisticien.eu/springeR/snee74en.txt into an R object called `snee`.
11.2- Display the first and last lines of `snee` with the functions `head()` and `tail()`. How many individuals are there? How many variables? What type are the variables?
11.3- Use the function `attach()` on your data.frame then check with the functions `class()` and `levels()` that the structure of your variables is correct. What are the levels of the variables?
11.4- Perform a univariate descriptive study of each variable: numerical results and appropriate graphical representations.
11.5- We shall now study the dependence of variables `eyes` and `hair`. Create the contingency table `eyeshair` (observed counts) of variables `eyes` and `hair`.
11.6- Calculate the frequency of each level of the variable `hair` (profile by column). You get the distribution function `fhair` of hair colour in the population.
11.7- Now, include the second characteristic: eye colour. Calculate the number `nblue` of individuals with blue eyes in the entire population.
11.8- Suppose that eye colour and hair colour are independent. In other words, the fact that an individual has blue eyes bears no relation with the colour of their hair. In that case, the proportions calculated in 11.6 should still be the same within the subpopulation of people with blue eyes. Under this independence hypothesis, calculate the number of blue-eyed people who should have blond hair (respectively brown, black and red).
11.9- Do the same with other eye colours. You get a table `tab.ind1` of theoretical counts under the hypothesis of independence between eye and hair colour.
11.10- Repeat the entire process, but with the two characteristics inverted (i.e. start with the variable `eyes`). From table `eyeshair`, calculate the frequency of each level of the variable `eyes` (profiles by rows). You get the distribution function `feyes` of eye colours in the population.
11.11- Now include the second characteristic: hair colour. Calculate the number `nblond` of people with blond hair in the entire population.
11.12- Suppose that hair and eye colour are independent. In other words, the fact that an individual has blond hair bears no relation with their eye colour. In that case, the proportions calculated in 11.10 should still be the same within the subpopulation of people with blond hair. Under this independence hypothesis, calculate the number of blond people who should have blue eyes (respectively brown, hazel and green).
11.13- Do the same with other hair colours. You get a table `tab.ind2` of theoretical counts under the hypothesis of independence between hair and eye colour.

11.14- Use the function `all.equal()` to compare the two tables of theoretical counts. What do you observe?
11.15- Compare the table of observed counts `eyeshair` with the table of theoretical counts (for each entry, calculate the square of the difference).
11.16- Calculate the table of contributions to the χ^2.
11.17- Calculate all relevant link indicators. Conclude.
11.18- Independence can also be defined (and this is in fact the primary definition) as equality of all conditional distributions. Calculate the conditional distribution of the variable `hair` knowing that the eye colour is blue (i.e. the frequency of various hair colours knowing that eye colour is blue). Calculate the three other conditional distributions of the variable `hair`. Calculate the conditional distributions of the variable `eyes` knowing each of the levels of variable `hair`. Conclude.
11.19- Perform a descriptive study of variable `hair` as a function of variable `gender`.
11.20- Perform a descriptive study of variable `eyes` as a function of variable `gender`.
11.21- Analyze the dependence between eye colour and hair colour for the following contingency table (rows: Eyes; columns: Hair):

Eyes	Blond	Brown	Black	Red	Total
Blue	1768	807	189	47	2811
Grey/green	946	1387	746	53	3132
Brown	115	438	288	16	857
Total	2829	2632	1223	116	6800

Solution.
11.1- Use `read.table()` with `header = TRUE`; since R 4.0 strings are no longer converted to factors by default, so add `stringsAsFactors = TRUE` to get the qualitative variables as factors.

```
snee <- read.table("http://www.biostatisticien.eu/springeR/snee74en.txt",
                   header = TRUE, stringsAsFactors = TRUE)
```

11.2- There are 592 individuals and 3 variables (`hair`, `eyes`, `gender`), all qualitative (nominal), stored as factors.

```
head(snee)
tail(snee)
dim(snee)
```

```
   hair  eyes gender
1 Black Brown   Male
2 Blond  Blue Female
3 Black  Blue   Male
4 Brown Brown Female
5   Red Brown   Male
6 Brown  Blue   Male
     hair  eyes gender
587 Black Brown   Male
588 Blond Brown Female
589 Brown  Blue   Male
590 Brown Hazel   Male
591 Brown Hazel Female
592 Brown  Blue   Male
[1] 592   3
```

11.3- All three variables are factors, which is the correct structure for nominal data; `hair` has levels Black, Blond, Brown, Red, `eyes` has Blue, Brown, Green, Hazel, and `gender` has Female, Male.

```
attach(snee)
sapply(snee, class)
levels(hair); levels(eyes); levels(gender)
```

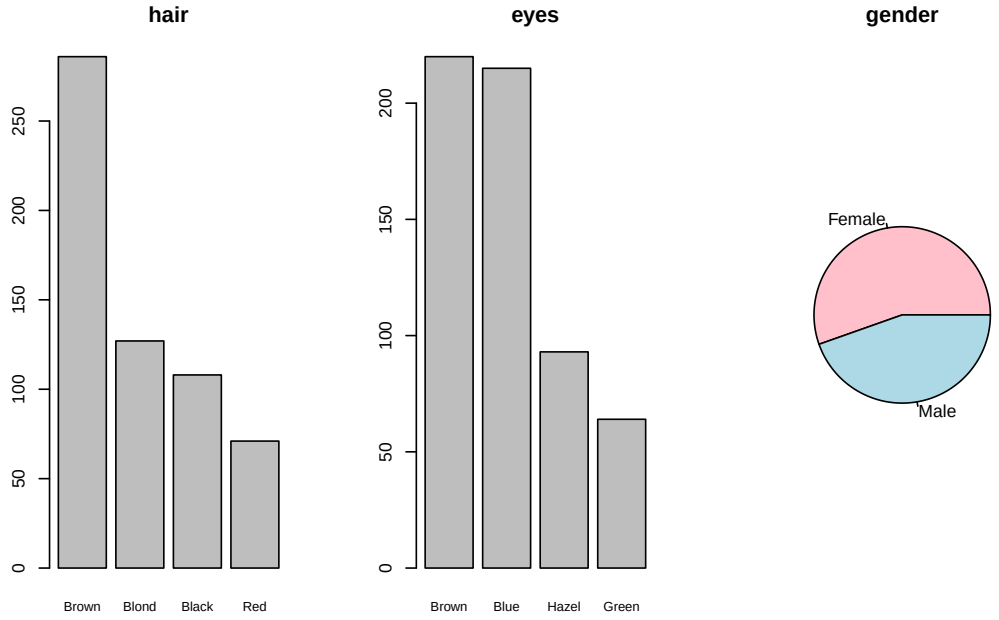
```
    hair     eyes   gender
"factor" "factor" "factor"
[1] "Black" "Blond" "Brown" "Red"
[1] "Blue"  "Brown" "Green" "Hazel"
[1] "Female" "Male"
```

11.4- For nominal variables the numerical summaries are the counts (`summary()`) and relative frequencies (`prop.table(table())`), and the appropriate graphics are Pareto/bar charts and pie charts (Section 11.6.1).

```
summary(snee)
lapply(snee, function(v) round(prop.table(table(v)), 3))
```

```
    hair        eyes        gender
 Black:108   Blue :215   Female:328
 Blond:127   Brown:220   Male  :264
 Brown:286   Green: 64
 Red  : 71   Hazel: 93
$hair
v
Black Blond Brown   Red
0.182 0.215 0.483 0.120

$eyes
v
 Blue Brown Green Hazel
0.363 0.372 0.108 0.157

$gender
v
Female   Male
 0.554  0.446
```

```
par(mfrow = c(1, 3))
barplot(sort(table(hair), decreasing = TRUE), main = "hair", col = "grey",
        cex.names = 0.8)
barplot(sort(table(eyes), decreasing = TRUE), main = "eyes", col = "grey",
        cex.names = 0.8)
pie(table(gender), main = "gender", col = c("pink", "lightblue"))
```



Brown is the modal hair colour (48.3%) and red the rarest (12.0%); brown and blue eyes dominate (37.2% and 36.3%), green is rare (10.8%); the sample is 55.4% female.

11.5- The observed contingency table (with margins from `addmargins()`):

```
eyeshair <- table(eyes, hair)
addmargins(eyeshair)
```

```
       hair
eyes    Black Blond Brown Red Sum
```

```
Blue     20    94    84  17 215
Brown    68     7   119  26 220
Green     5    16    29  14  64
Hazel    15    10    54  14  93
Sum     108   127   286  71 592
```

11.6- `fhair` is the column margin divided by the total:

```
fhair <- margin.table(eyeshair, 2) / sum(eyeshair)
round(fhair, 4)
```

```
hair
 Black  Blond  Brown    Red
0.1824 0.2145 0.4831 0.1199
```

11.7- There are `nblue` = 215 blue-eyed individuals.

```
nblue <- sum(eyeshair["Blue", ]); nblue
```

```
[1] 215
```

11.8- Under independence the 215 blue-eyed people split like the whole population: about 46.1 blond, 103.9 brown, 39.2 black and 25.8 red-haired.

```
nblue * fhair
```

```
hair
    Black     Blond     Brown       Red
 39.22297  46.12331 103.86824  25.78547
```

11.9- Repeating for every eye colour amounts to the outer product of the eye-colour counts with `fhair`:

```
neyes <- margin.table(eyeshair, 1)
tab.ind1 <- outer(neyes, fhair)
round(tab.ind1, 2)
```

```
       hair
eyes    Black Blond  Brown   Red
  Blue  39.22 46.12 103.87 25.79
  Brown 40.14 47.20 106.28 26.39
  Green 11.68 13.73  30.92  7.68
  Hazel 16.97 19.95  44.93 11.15
```

11.10- `feyes` is the row margin divided by the total:

```
feyes <- margin.table(eyeshair, 1) / sum(eyeshair)
round(feyes, 4)
```

```
eyes
  Blue  Brown  Green  Hazel
0.3632 0.3716 0.1081 0.1571
```

11.11- There are `nblond` = 127 blond-haired individuals.

```
nblond <- sum(eyeshair[, "Blond"]); nblond
```

```
[1] 127
```

11.12- Under independence the 127 blond people should comprise about 46.1 blue-eyed, 47.2 brown-eyed, 20.0 hazel-eyed and 13.7 green-eyed people.

```
nblond * feyes
```

```
eyes
    Blue    Brown    Green    Hazel
46.12331 47.19595 13.72973 19.95101
```

11.13- Repeating for every hair colour gives the outer product of `feyes` with the hair-colour counts:

```
nhair <- margin.table(eyeshair, 2)
tab.ind2 <- outer(feyes, nhair)
round(tab.ind2, 2)
```

```
       hair
eyes    Black Blond  Brown   Red
  Blue  39.22 46.12 103.87 25.79
  Brown 40.14 47.20 106.28 26.39
  Green 11.68 13.73  30.92  7.68
```

```
Hazel 16.97 19.95  44.93 11.15
```

11.14- The two tables are identical: both equal $E_{ij} = n_{i\cdot}\, n_{\cdot j}/N$, which is symmetric in the two variables, and they coincide with the expected counts returned by `chisq.test()` (Section 11.5.1).

```
all.equal(tab.ind1, tab.ind2)
all.equal(tab.ind1, chisq.test(eyeshair)$expected, check.attributes = FALSE)
```

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

11.15- The squared differences $(O_{ij} - E_{ij})^2$ are largest for blond hair (blue eyes: far more than expected; brown eyes: far fewer) and for black hair with brown eyes:

```
round((eyeshair - tab.ind1)^2, 2)
```

```
       hair
eyes      Black   Blond   Brown     Red
  Blue   369.52 2292.18  394.75   77.18
  Brown  776.45 1615.71  161.70    0.15
  Green   44.56    5.15    3.68   40.00
  Hazel    3.87   99.02   82.28    8.10
```

11.16- The contributions are $(O_{ij} - E_{ij})^2/E_{ij}$, i.e. the squared Pearson residuals of `chisq.test()`:

```
tab.contr <- (eyeshair - tab.ind1)^2 / tab.ind1
round(tab.contr, 2)
all.equal(c(tab.contr), c(chisq.test(eyeshair)$residuals^2))
```

```
       hair
eyes    Black Blond Brown   Red
  Blue   9.42 49.70  3.80  2.99
  Brown 19.35 34.23  1.52  0.01
  Green  3.82  0.38  0.12  5.21
  Hazel  0.23  4.96  1.83  0.73
[1] TRUE
```

The cells blond/blue (49.7), blond/brown (34.2) and black/brown (19.4) alone account for 75% of the total χ^2.

11.17- With $\chi^2 = 138.3$, $\Phi^2 = 0.234$, Cramér's $V^2 = 0.078$ and Pearson's $C = 0.435$ (formulas of Section 11.5.1.2), eye and hair colour are clearly associated.

```
chi2 <- sum(tab.contr)
N <- sum(eyeshair); p <- nrow(eyeshair); q <- ncol(eyeshair)
Phi2 <- chi2 / N
c(chi2 = chi2, Phi2 = Phi2, V2 = Phi2 / (min(p, q) - 1),
  C = sqrt(chi2 / (N + chi2)))
chisq.test(eyeshair)
```

```
       chi2        Phi2          V2           C
138.2898416   0.2335977   0.0778659   0.4351585

        Pearson's Chi-squared test

data:  eyeshair
X-squared = 138.29, df = 9, p-value < 2.2e-16
```

The association is of moderate strength ($C = 0.435$ against a maximum of $\sqrt{3/4} \approx 0.866$ for a 4×4 table), and the test of independence (H_0: eye and hair colour independent, 9 df) is rejected with $p < 2.2 \times 10^{-16}$.

11.18- `prop.table(eyeshair, 1)` gives the four conditional distributions of `hair` given each eye colour (row profiles), and `prop.table(eyeshair, 2)` those of `eyes` given each hair colour (column profiles):

```
round(prop.table(eyeshair, 1), 3)
round(prop.table(eyeshair, 2), 3)
```

```
       hair
eyes    Black Blond Brown   Red
  Blue  0.093 0.437 0.391 0.079
  Brown 0.309 0.032 0.541 0.118
```

```
  Green 0.078 0.250 0.453 0.219
  Hazel 0.161 0.108 0.581 0.151
       hair
eyes    Black Blond Brown   Red
  Blue  0.185 0.740 0.294 0.239
  Brown 0.630 0.055 0.416 0.366
  Green 0.046 0.126 0.101 0.197
  Hazel 0.139 0.079 0.189 0.197
```

The conditional distributions are far from equal (43.7% of blue-eyed people are blond against 3.2% of brown-eyed people; 74.0% of blonds have blue eyes against 18.5% of black-haired people), so the variables are not independent, in agreement with 11.17.

11.19- Hair colour distributions are very similar in both sexes (brown about 48% in each; women slightly more often blond, 24.7% vs 17.4%, men slightly more often black-haired, 21.2% vs 15.9%), and the link is negligible: $\Phi^2 = V^2 = 0.0105$, $C = 0.10$, and the χ^2 test (3 df) does not reject independence ($p = 0.10$).

```r
assoc <- function(tab) {
  chi2 <- chisq.test(tab)$statistic; N <- sum(tab)
  Phi2 <- chi2 / N
  round(c(chi2 = unname(chi2), Phi2 = unname(Phi2),
          V2 = unname(Phi2) / (min(dim(tab)) - 1),
          C = unname(sqrt(chi2 / (N + chi2)))), 4)
}
gh <- table(gender, hair)
addmargins(gh)
round(prop.table(gh, 1), 3)
assoc(gh)
chisq.test(gh)$p.value
```

```
        hair
gender   Black Blond Brown Red Sum
  Female    52    81   158  37 328
  Male      56    46   128  34 264
  Sum      108   127   286  71 592
        hair
gender   Black Blond Brown   Red
  Female 0.159 0.247 0.482 0.113
  Male   0.212 0.174 0.485 0.129
   chi2   Phi2     V2      C
6.2212 0.0105 0.0105 0.1020
[1] 0.1013296
```

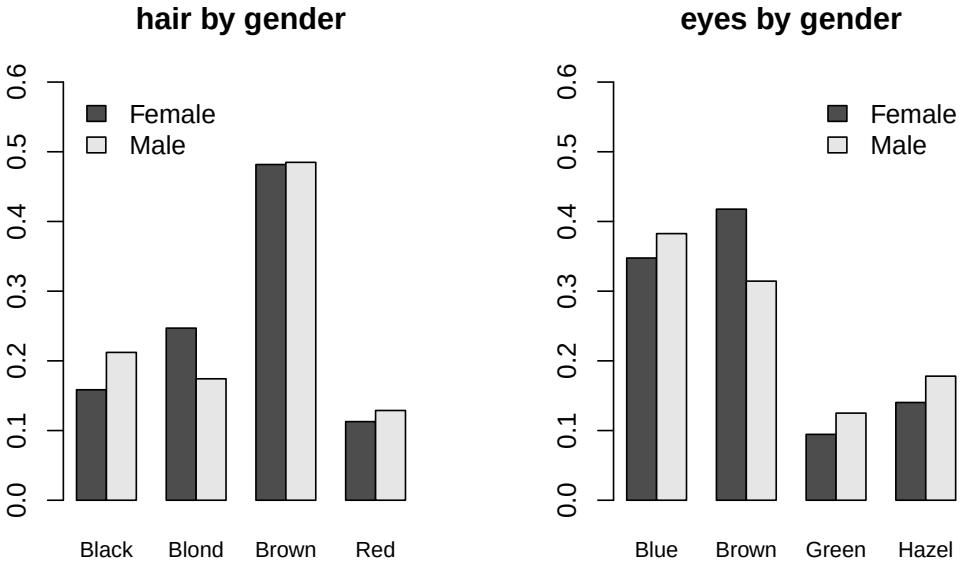
11.20- Eye colour depends only weakly on gender: women more often have brown eyes (41.8% vs 31.4%), men slightly more often blue, green or hazel eyes; $V^2 = 0.012$, $C = 0.11$, and the χ^2 test (3 df) is not significant at the 5% level ($p = 0.063$). The side-by-side bar charts of the row profiles (Section 11.6.5) display both studies.

```r
ge <- table(gender, eyes)
addmargins(ge)
round(prop.table(ge, 1), 3)
assoc(ge)
chisq.test(ge)$p.value
```

```
        eyes
gender   Blue Brown Green Hazel Sum
  Female  114   137    31    46 328
  Male    101    83    33    47 264
  Sum     215   220    64    93 592
        eyes
gender    Blue Brown Green Hazel
  Female 0.348 0.418 0.095 0.140
  Male   0.383 0.314 0.125 0.178
   chi2   Phi2     V2      C
7.2800 0.0123 0.0123 0.1102
[1] 0.06348869
```

```r
par(mfrow = c(1, 2))
```

```r
barplot(prop.table(gh, 1), beside = TRUE, ylim = c(0, 0.6), cex.names = 0.8,
        legend.text = TRUE, args.legend = list(x = "topleft", bty = "n"),
        main = "hair by gender")
barplot(prop.table(ge, 1), beside = TRUE, ylim = c(0, 0.6), cex.names = 0.8,
        legend.text = TRUE, args.legend = list(x = "topright", bty = "n"),
        main = "eyes by gender")
```



11.21- Eye and hair colour are strongly dependent in this population of 6800: $\chi^2 = 1073.5$ (6 df, p essentially 0), $\Phi^2 = 0.158$, $V^2 = 0.079$, $C = 0.369$; the contributions show that blue eyes go with blond hair and brown eyes with brown or black hair, while red hair is distributed independently of eye colour.

```r
eh <- matrix(c(1768,  807, 189, 47,
               946, 1387, 746, 53,
               115,  438, 288, 16), nrow = 3, byrow = TRUE,
             dimnames = list(Eyes = c("Blue", "Grey/green", "Brown"),
                             Hair = c("Blond", "Brown", "Black", "Red")))
round(chisq.test(eh)$expected, 1)
round(chisq.test(eh)$residuals^2, 1)
assoc(eh)
round(prop.table(eh, 1), 3)
```

```
           Hair
Eyes         Blond  Brown Black  Red
  Blue      1169.5 1088.0 505.6 48.0
  Grey/green 1303.0 1212.3 563.3 53.4
  Brown      356.5  331.7 154.1 14.6
           Hair
Eyes         Blond Brown Black Red
  Blue      306.3  72.6 198.2 0.0
  Grey/green  97.8  25.2  59.3 0.0
  Brown      163.6  34.1 116.3 0.1
     chi2      Phi2        V2         C
1073.5076    0.1579    0.0789    0.3692
           Hair
Eyes         Blond Brown Black   Red
  Blue      0.629 0.287 0.067 0.017
  Grey/green 0.302 0.443 0.238 0.017
  Brown      0.134 0.511 0.336 0.019
```

The row profiles confirm it: 62.9% of blue-eyed people are blond against 13.4% of brown-eyed people, whereas the proportion of red hair is 1.7-1.9% in every eye-colour group.

9.5 Worksheet 11.W.B — Descriptive analysis of the data set NUTRIELDERLY

Problem 11.W.B. Worksheet 11.W.B — Descriptive data studies — Descriptive analysis of data set NutriElderly
We now propose to solve the following questions on the dataset NutriElderly, in which deliberate errors were introduced.
11.1- Import the data file `nutrition_elderly.xls`.
11.2- Give the absolute mode of variables `situation`, `chocol` and `height`.
11.3- Choose classes for variable `height` and give the modal class.
11.4- Calculate the median of variable `chocol`.
11.5- Give frequency tables of variables `chocol` and `raw_fruit`.
11.6- Using **only** these frequency tables, give the median of these two variables.
11.7- Calculate the quartiles of variable `height` using the classes defined earlier.
11.8- Draw the cumulative frequency polygon for variable `height`. On this plot, estimate the quartiles of the distribution.
11.9- Using individual data, calculate the mean of variables `height`, `weight` and `age`.
11.10- Calculate the frequency table of variable `tea`. Using this table, calculate the mean of this variable.
11.11- Calculate the mean of variable `height` using the classes defined earlier.
11.12- Calculate the range of variable `weight`.
11.13- Draw a boxplot of variable `weight`.
11.14- Using individual data, calculate the standard deviation of variable `height`.
11.15- Using **only** its frequency table, calculate the coefficient of variation of variable `tea`.
11.16- Calculate the total variance, the within-group variance and the between-group variance of variable `coffee` with the population split into two groups: males and females. Calculate the coefficient η^2.

Solution.
11.1- Download the file and read it with `read_excel()` from readxl (the book's `gdata::read.xls()` was removed in gdata 3.0), check every code against its admissible set, then structure the variables as in Section 11.2.

```
library(readxl)
tf <- tempfile(fileext = ".xls")
download.file("http://www.biostatisticien.eu/springeR/nutrition_elderly.xls",
              tf, mode = "wb", quiet = TRUE)
ne <- as.data.frame(read_excel(tf))
dim(ne)
# Admissible codes (Section 11.2): any value outside them is an error
ok <- list(gender = 1:2, situation = 1:4, fat = 1:8, meat = 0:5, fish = 0:5,
           raw_fruit = 0:5, cooked_fruit_veg = 0:5, chocol = 0:5)
sapply(names(ok), function(v) sum(!ne[[v]] %in% ok[[v]]))
sapply(ne[c("tea", "coffee", "height", "weight", "age")], range)
sum(is.na(ne))
# Structuring (Section 11.2)
ne$gender <- factor(ne$gender, levels = 1:2, labels = c("Male", "Female"))
ne$situation <- factor(ne$situation, levels = 1:4,
                       labels = c("single", "couple", "family", "other"))
ne$fat <- factor(ne$fat, levels = 1:8, labels = c("butter", "margarine",
  "peanut", "sunflower", "olive", "Isio4", "rapeseed", "duck"))
mylevels <- c("never", "< 1/week.", "1/week.", "2-3/week.", "4-6/week.", "1/day")
for (v in c("meat", "fish", "raw_fruit", "cooked_fruit_veg", "chocol"))
  ne[[v]] <- factor(ne[[v]], levels = 0:5, labels = mylevels, ordered = TRUE)
ne$tea <- as.integer(ne$tea); ne$coffee <- as.integer(ne$coffee)
```

```
[1] 226  13
          gender        situation              fat             meat
               0                0                0                0
            fish        raw_fruit cooked_fruit_veg           chocol
               0                0                0                0
```

```
     tea coffee height weight age
[1,]   0      0    140     38  65
[2,]  10      5    188     96  91
[1] 0
```

The file has 226 individuals and 13 variables; every code is admissible, there are no missing values and the ranges of the quantitative variables are plausible, so the copy served at the book's URL (and the local mirror, identical) does not contain the deliberate errors announced by the worksheet; all answers below are computed on this clean file.

11.2- With the idiom of Section 11.4.1.1, the modes are `couple` for `situation`, `1/day` for `chocol` and 160 cm for `height` (22 individuals).

```r
modes <- function(x) { t <- table(x); names(t)[t == max(t)] }
modes(ne$situation); modes(ne$chocol); modes(ne$height)
max(table(ne$height))
```

```
[1] "couple"
[1] "1/day"
[1] "160"
[1] 22
```

11.3- Take the ten classes of width 5 cm from 140 to 190 (the Sturges classes of Section 11.3.3); the modal class is $]155, 160]$ with 50 individuals.

```r
brk <- seq(140, 190, by = 5)
tab.h <- table(cut(ne$height, brk, include.lowest = TRUE))
tab.h
names(which.max(tab.h))
```

```
[140,145] (145,150] (150,155] (155,160] (160,165] (165,170] (170,175] (175,180]
        1         7        37        50        46        31        27        17
(180,185] (185,190]
        4         6
[1] "(155,160]"
```

11.4- `chocol` is ordinal, so use the book's `my.median()` (Section 11.4.1.2): with $N = 226$ the observations of rank 113 and 114 are both `1/week.`, which is the median.

```r
my.median <- function(x) {
  if (is.numeric(x)) return(median(x))
  if (is.ordered(x)) {
    N <- length(x)
    if (N %% 2) return(sort(x)[(N + 1) / 2]) else {
      inf <- sort(x)[N / 2]; sup <- sort(x)[N / 2 + 1]
      if (inf == sup) return(inf) else return(c(inf, sup))
    }}
  stop("Cannot calculate the median for this type of data.")
}
my.median(ne$chocol)
```

```
[1] 1/week.
Levels: never < < 1/week. < 1/week. < 2-3/week. < 4-6/week. < 1/day
```

11.5- Divide the table of counts by N (Section 11.3.2).

```r
tf.chocol <- table(ne$chocol) / nrow(ne)
tf.fruit <- table(ne$raw_fruit) / nrow(ne)
round(rbind(chocol = tf.chocol, raw_fruit = tf.fruit), 3)
```

```
          never < 1/week. 1/week. 2-3/week. 4-6/week. 1/day
chocol    0.221     0.274   0.071     0.097     0.049 0.288
raw_fruit 0.009     0.035   0.035     0.062     0.097 0.761
```

Three quarters of the elderly eat raw fruit every day, while chocolate consumption is split between "never/rarely" and "every day".

11.6- The median of an ordinal variable is the first level whose cumulative frequency reaches 50 %: `1/week.` for `chocol` (cumulative frequency jumps from 0.496 to 0.566) and `1/day` for `raw_fruit` (from 0.239 to 1), in agreement with 11.4.

```r
med.ord.freq <- function(f) names(f)[which(cumsum(f) >= 0.5)[1]]
```

```
round(rbind(chocol = cumsum(tf.chocol), raw_fruit = cumsum(tf.fruit)), 3)
c(chocol = med.ord.freq(tf.chocol), raw_fruit = med.ord.freq(tf.fruit))
```

```
          never < 1/week. 1/week. 2-3/week. 4-6/week. 1/day
chocol    0.221     0.496   0.566     0.664     0.712     1
raw_fruit 0.009     0.044   0.080     0.142     0.239     1
   chocol raw_fruit
"1/week."   "1/day"
```

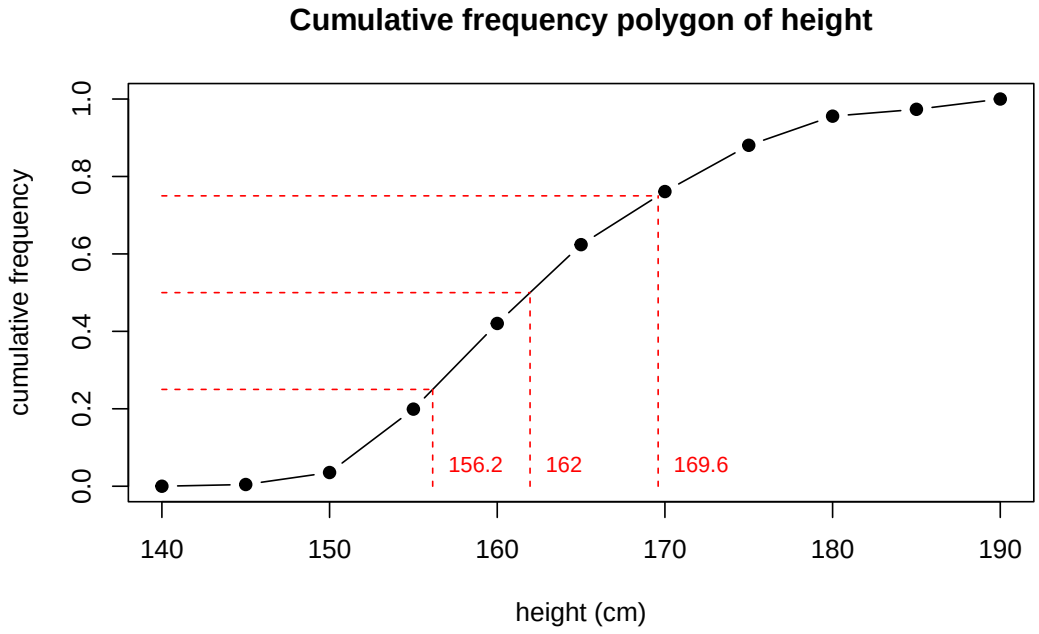
11.7- Interpolate linearly on the cumulative frequency polygon of the classes (the formula of Section 11.4.1.2, applied to 25 %, 50 % and 75 %), which `approx()` does in one call: $q_1 \approx 156.2$, $m_e \approx 162.0$ and $q_3 \approx 169.6$ cm. The book's `median.for.freq()` cannot be used as printed, since `is.numeric(names(x))` is always `FALSE` and it returns `NA` (as its own printed output shows).

```
cfp <- c(0, cumsum(tab.h)) / sum(tab.h)
q.h <- approx(cfp, brk, xout = c(0.25, 0.5, 0.75), ties = "ordered")$y
names(q.h) <- c("q1", "me", "q3"); round(q.h, 2)
```

```
    q1     me     q3
156.15 161.96 169.60
```

11.8- Plot the points $(e_k, \mathrm{CFP}(e_k))$ joined by segments and read the abscissae where the polygon crosses the levels 0.25, 0.5 and 0.75: about 156, 162 and 170 cm, the values of 11.7.

```
plot(brk, cfp, type = "b", pch = 19, xlab = "height (cm)",
     ylab = "cumulative frequency", main = "Cumulative frequency polygon of height")
segments(140, c(0.25, 0.5, 0.75), q.h, c(0.25, 0.5, 0.75), lty = 2, col = "red")
segments(q.h, 0, q.h, c(0.25, 0.5, 0.75), lty = 2, col = "red")
text(q.h, 0.05, round(q.h, 1), pos = 4, col = "red", cex = 0.8)
```



11.9- The mean height is 163.96 cm, the mean weight 66.48 kg and the mean age 74.48 years.

```
sapply(ne[c("height", "weight", "age")], mean)
```

```
   height    weight       age
163.96018  66.48230  74.47788
```

11.10- With frequencies f_k of the values x_k, the mean is $\bar{x} = \sum_k f_k x_k = 0.712$ cup of tea per day, the same as `mean(ne$tea)` since no information is lost for a discrete variable.

```
tf.tea <- table(ne$tea) / nrow(ne)
round(tf.tea, 3)
x.tea <- as.numeric(names(tf.tea))
sum(x.tea * tf.tea)
```

```
    0     1     2     3     4     5     6     9    10
0.721 0.058 0.128 0.035 0.040 0.004 0.004 0.004 0.004
[1] 0.7123894
```

Almost three quarters (72.1 %) of the elderly never drink tea.

11.11- Replace each observation by the midpoint of its class: the grouped mean is 163.23 cm, close to the exact 163.96 cm of 11.9.

```
mid <- (brk[-1] + brk[-length(brk)]) / 2
sum(mid * tab.h) / sum(tab.h)
```

```
[1] 163.2301
```

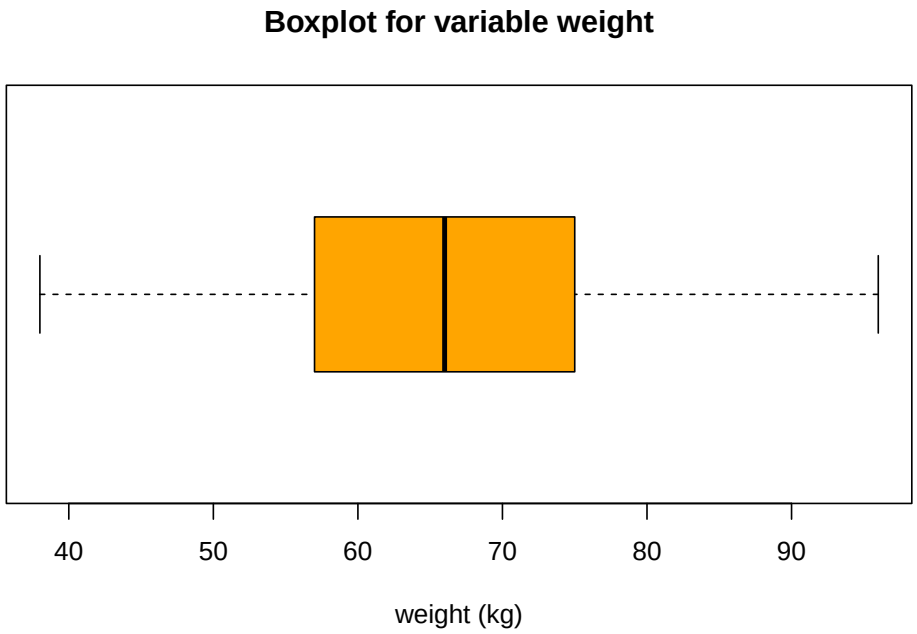
11.12- The range of `weight` is $96 - 38 = 58$ kg.

```
range(ne$weight); diff(range(ne$weight))
```

```
[1] 38 96
[1] 58
```

11.13- Use `boxplot()` (Section 11.6.3.5); the five numbers drawn are 38, 57, 66, 75 and 96 kg, and there is no outlier.

```
boxplot(ne$weight, col = "orange", horizontal = TRUE,
        xlab = "weight (kg)", main = "Boxplot for variable weight")
```




```
boxplot.stats(ne$weight)$stats; boxplot.stats(ne$weight)$out
```

```
[1] 38 57 66 75 96
numeric(0)
```

The distribution of weight is roughly symmetric around the median of 66 kg, with whiskers reaching the extreme values.

11.14- With the population standard deviation of Section 11.4.2, $\sigma = 8.98$ cm (`sd()`, which divides by $N - 1$, gives 9.00 cm).

```
var.pop <- function(x) var(x) * (length(x) - 1) / length(x)
sd.pop <- function(x) sqrt(var.pop(x))
sd.pop(ne$height); sd(ne$height)
```

```
[1] 8.983427
[1] 9.003368
```

11.15- From the frequency table of 11.10, $\mu = \sum_k f_k x_k$, $\sigma = \sqrt{\sum_k f_k (x_k - \mu)^2}$ and $cv = \sigma/\mu = 2.03$.

```
mu <- sum(x.tea * tf.tea)
sigma <- sqrt(sum(tf.tea * (x.tea - mu)^2))
```

```r
c(mean = mu, sd = sigma, cv = sigma / mu)
```

```
     mean        sd        cv
0.7123894 1.4456301 2.0292696
```

The standard deviation is twice the mean: tea consumption is very heterogeneous, most people drinking none and a few drinking up to 10 cups a day.

11.16- With $K = 2$ groups of sizes n_k, means $\bar{y}_k$ and (population) variances σ_k^2,

$$\sigma^2_{\text{within}} = \frac{1}{N}\sum_k n_k \sigma_k^2, \qquad \sigma^2_{\text{between}} = \frac{1}{N}\sum_k n_k (\bar{y}_k - \bar{y})^2,$$
$$\sigma^2_{\text{total}} = \sigma^2_{\text{within}} + \sigma^2_{\text{between}}, \qquad \eta^2 = \sigma^2_{\text{between}} / \sigma^2_{\text{total}}.$$

```r
y <- ne$coffee; g <- ne$gender
n.k <- tapply(y, g, length); m.k <- tapply(y, g, mean); v.k <- tapply(y, g, var.pop)
rbind(n = n.k, mean = m.k, var = v.k)
v.tot <- var.pop(y)
v.within <- sum(n.k * v.k) / length(y)
v.between <- sum(n.k * (m.k - mean(y))^2) / length(y)
c(total = v.tot, within = v.within, between = v.between,
  sum = v.within + v.between, eta2 = v.between / v.tot)
summary(lm(y ~ g))$r.squared
```

```
          Male     Female
n    85.000000 141.000000
mean  1.870588   1.468085
var   1.595017   1.483024
     total     within    between        sum       eta2
1.56316078 1.52514537 0.03801541 1.56316078 0.02431958
[1] 0.02431958
```

The total variance 1.563 splits into 1.525 within and 0.038 between the sexes, so $\eta^2_{\text{coffee|gender}} = 0.024$ (the same value as the R^2 of Section 11.5.4.1): although men drink slightly more coffee (1.87 vs 1.47 cups a day), gender explains only 2.4 % of the variation in coffee consumption. The authors' companion solution applies its η^2 function to `tea` rather than `coffee`; the statement asks for `coffee`, which is what is computed here.

9.6 Worksheet 11.W.C — Descriptive analysis of data sets

Problem 11.W.C. Worksheet 11.W.C — Descriptive analysis of data sets — Birth weight and myocardial infarction

The two data sets are described in Appendix B: B- is the weight-at-birth study (Section B.2, 189 mothers seen at the Baystate medical centre in 1986; file `Birth_weight.txt`) and I is the myocardial infarction study (Section B.5, 149 women who had an infarction and 300 controls; file `Infarction.xls`).

11.1- Perform a descriptive statistical analysis of data set B-.

11.2- Perform a descriptive statistical analysis of data set I.

Solution.

11.1- Birth weight averages 2945 g (sd 729 g, 31.2% of babies under 2500 g). The descriptors most strongly linked to it are uterine irritability ($\eta^2 = 0.080$), race (0.051) and smoking (0.036), and each explains only a few percent of its variance. Import this irregular text file as in question 4.4 of Worksheet 4.W.C, then recode the qualitative variables as factors (Section 11.2):

```r
url <- "http://www.biostatisticien.eu/springeR/Birth_weight.txt"
bw <- read.table(url, row.names = 1, skip = 1, header = FALSE, sep = ";",
                 nrows = 189, blank.lines.skip = TRUE)
colnames(bw) <- as.matrix(read.table(url, nrows = 1, row.names = 1))
bw$RACE <- factor(bw$RACE, labels = c("White", "Black", "Other"))
for (v in c("SMOKE", "HT", "UI", "LOW"))
  bw[[v]] <- factor(bw[[v]], levels = 0:1, labels = c("No", "Yes"))
```

```
dim(bw)
```

```
[1] 189  10
```

Univariate summaries of the quantitative variables (Section 11.4; `skewness()` and `kurtosis()` come from `e1071`):

```
library(e1071)
quanti <- bw[, c("AGE", "LWT", "PTL", "FVT", "BWT")]
round(t(sapply(quanti, function(x) c(mean = mean(x), sd = sd(x),
  quantile(x), IQR = IQR(x), cv = sd(x) / mean(x),
  skew = skewness(x), kurt = kurtosis(x)))), 2)
table(bw$PTL); table(bw$FVT)
```

```
       mean     sd  0%  25%  50%  75% 100%  IQR   cv  skew  kurt
AGE   23.24   5.30  14   19   23   26   45    7 0.23  0.71  0.53
LWT  129.81  30.58  80  110  121  140  250   30 0.24  1.38  2.25
PTL    0.20   0.49   0    0    0    0    3    0 2.52  2.76  8.17
FVT    0.79   1.06   0    0    0    1    6    1 1.33  1.56  3.00
BWT 2944.66 729.02 709 2414 2977 3475 4990 1061 0.25 -0.21 -0.14

  0   1   2   3
159  24   5   1

  0   1   2   3   4   6
100  47  30   7   4   1
```

The mothers are young (median 23 years) and the mother's weight is right-skewed (skewness 1.38). PTL and FVT are small counts heaped at 0: 84% of mothers had no previous premature birth and 53% had no first-trimester visit. BWT itself is nearly symmetric (skewness -0.21, excess kurtosis -0.14).

Frequency tables (in %) of the qualitative variables (Section 11.3):

```
round(100 * prop.table(table(bw$RACE)), 1)
sapply(bw[, c("SMOKE", "HT", "UI", "LOW")],
       function(f) round(100 * prop.table(table(f)), 1))
```

```
White Black Other
 50.8  13.8  35.4
    SMOKE   HT   UI  LOW
No   60.8 93.7 85.2 68.8
Yes  39.2  6.3 14.8 31.2
```

Half of the mothers are white, 39.2% smoked during pregnancy, and hypertension (6.3%) and uterine irritability (14.8%) are uncommon.

Measures of association with the birth weight (Section 11.5). For each factor, the output gives the conditional means and the correlation ratio $\eta^2_{\mathrm{BWT}|X}$ computed with the book's `eta2()`, followed by the linear correlations with the quantitative variables:

```
eta2 <- function(x, gpe) {
  means <- tapply(x, gpe, mean); counts <- tapply(x, gpe, length)
  sum(counts * (means - mean(x))^2) / (var(x) * (length(x) - 1))
}
lapply(bw[, c("SMOKE", "RACE", "HT", "UI")], function(g)
  round(c(tapply(bw$BWT, g, mean), eta2 = eta2(bw$BWT, g)), 3))
round(cor(quanti)["BWT", ], 2)
```

```
$SMOKE
      No      Yes     eta2
3054.957 2773.243    0.036

$RACE
   White    Black    Other     eta2
3103.740 2719.692 2804.015    0.051

$HT
      No      Yes     eta2
2972.311 2536.750    0.021
```

```
$UI
      No      Yes     eta2
3030.609 2450.429    0.080

  AGE   LWT   PTL   FVT   BWT
 0.09  0.19 -0.15  0.06  1.00
```

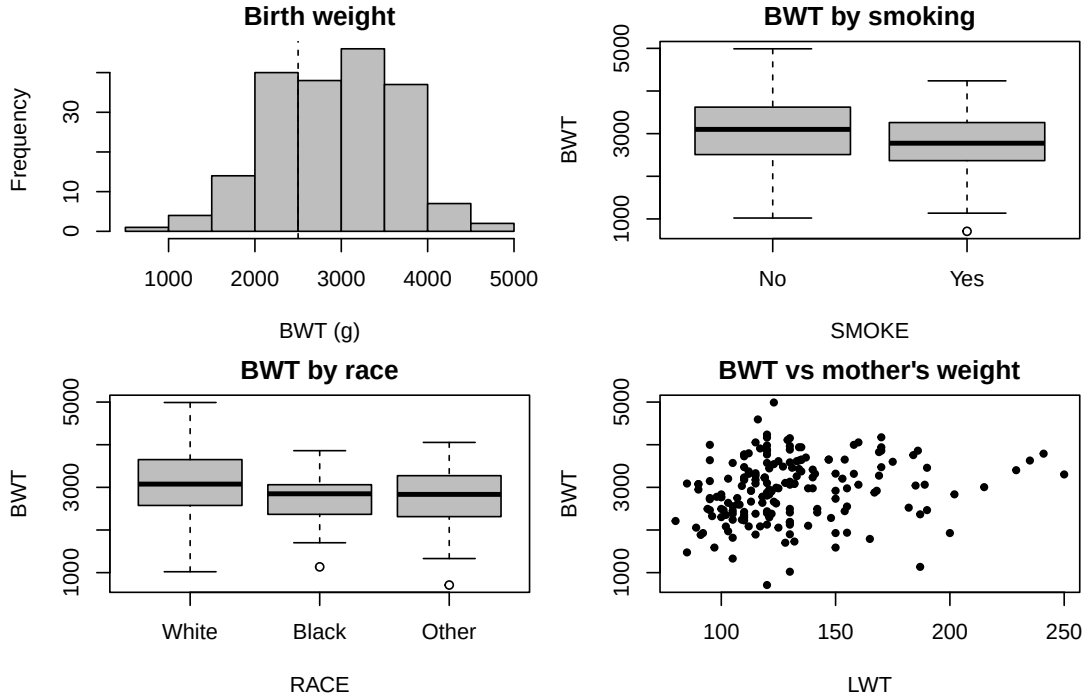
Babies of smokers are 282 g lighter on average. Babies of white mothers are about 300 to 385 g heavier than those of the other two groups, and hypertension and uterine irritability each lower the mean by 435 to 580 g. All the correlation ratios and correlations are small, the largest correlation being $r = 0.19$ with the mother's weight. The binary outcome LOW gives the same picture:

```
tab <- table(bw$SMOKE, bw$LOW, dnn = c("SMOKE", "LOW"))
round(100 * prop.table(tab, 1), 1)
chi <- chisq.test(tab, correct = FALSE)
c(chi2 = unname(chi$statistic), V2 = unname(chi$statistic) / sum(tab),
  p = chi$p.value)
```

```
     LOW
SMOKE   No  Yes
  No  74.8 25.2
  Yes 59.5 40.5
      chi2         V2          p
4.92370543 0.02605135 0.02649064
```

40.5% of smokers had a low-weight baby, compared with 25.2% of non-smokers. The link is weak ($V^2 = \Phi^2 = 0.026$) but it is significant at the 5% level ($\chi^2 = 4.92$, $p = 0.026$). Graphical summary (Section 11.6):

```
par(mfrow = c(2, 2), mar = c(4, 4, 2, 1))
hist(bw$BWT, main = "Birth weight", xlab = "BWT (g)", col = "grey")
abline(v = 2500, lty = 2)
boxplot(BWT ~ SMOKE, data = bw, main = "BWT by smoking", col = "grey")
boxplot(BWT ~ RACE, data = bw, main = "BWT by race", col = "grey")
plot(BWT ~ LWT, data = bw, main = "BWT vs mother's weight", pch = 20)
```



11.2- Infarction cases differ from controls mainly in their exposures. 56% of oral-contraceptive users are cases, compared with 14.9% of never-users ($V^2 = 0.189$), and tobacco (current or former) shows a similar gap ($V^2 = 0.132$). Age and height hardly differ between cases and controls. The book imports the file with `read.xls()`, which the current `gdata` no longer provides, so the equivalent `readxl` call is used here, again with "`.`" declared as the missing-value code:

```
library(readxl)
```

```
url <- "http://www.biostatisticien.eu/springeR/Infarction.xls"
tf <- tempfile(fileext = ".xls")
download.file(url, tf, mode = "wb", quiet = TRUE)
inf <- as.data.frame(read_excel(tf, na = "."))
inf$INFARCT <- factor(inf$INFARCT, labels = c("Control", "Case"))
inf$TOBACCO <- factor(inf$TOBACCO, labels = c("No", "Smoker", "Former"))
for (v in c("CO", "ATCD", "HTA"))
  inf[[v]] <- factor(inf[[v]], levels = 0:1, labels = c("No", "Yes"))
colSums(is.na(inf))[colSums(is.na(inf)) > 0]
```

```
WEIGHT    BMI   ATCD
    12     12      7
```

Twelve weights (and hence twelve BMIs) and seven family histories are missing. Each summary below therefore uses the available values only. Univariate summaries of the quantitative variables (Section 11.4):

```
library(e1071)
round(t(sapply(inf[, c("AGE", "WEIGHT", "HEIGHT", "BMI")], function(x) {
  x <- na.omit(x)
  c(n = length(x), mean = mean(x), sd = sd(x), quantile(x),
    cv = sd(x) / mean(x), skew = skewness(x), kurt = kurtosis(x))})), 2)
```

```
         n   mean    sd     0%    25%    50%    75%   100%   cv  skew  kurt
AGE    449  45.62 16.17  15.00  33.00  44.00  56.00 100.00 0.35  0.50  0.02
WEIGHT 437  66.07 17.96  33.00  51.00  64.00  79.00 128.00 0.27  0.65  0.00
HEIGHT 449 165.16  8.11 138.00 160.00 166.00 171.00 184.00 0.05 -0.33 -0.06
BMI    437  24.38  7.13  11.36  18.67  23.18  29.17  47.78 0.29  0.70 -0.03
```

The women are aged 15 to 100 (median 44). Weight and BMI are moderately right-skewed, while height is almost symmetric and has little spread (cv 0.05). Frequency tables (in %) of the qualitative variables (Section 11.3), where the cases make up $149/449 = 33.2\%$ of the sample by design:

```
round(100 * prop.table(table(inf$TOBACCO)), 1)
sapply(inf[, c("CO", "ATCD", "HTA")],
       function(f) round(100 * prop.table(table(f)), 1))
```

```
   No Smoker Former
 47.9   30.1   22.0
     CO ATCD  HTA
No  55.5   88 64.6
Yes 44.5   12 35.4
```

The next block compares cases with controls (Section 11.5). For the quantitative variables it gives the conditional means and the correlation ratio η^2, using the book's `eta2()`:

```
eta2 <- function(x, gpe) {
  means <- tapply(x, gpe, mean); counts <- tapply(x, gpe, length)
  sum(counts * (means - mean(x))^2) / (var(x) * (length(x) - 1))
}
round(t(sapply(c("AGE", "WEIGHT", "HEIGHT", "BMI"), function(v) {
  ok <- !is.na(inf[[v]])
  c(tapply(inf[[v]][ok], inf$INFARCT[ok], mean),
    eta2 = eta2(inf[[v]][ok], inf$INFARCT[ok]))})), 3)
```

```
       Control    Case  eta2
AGE     44.967  46.933 0.003
WEIGHT  63.510  71.214 0.041
HEIGHT 165.353 164.772 0.001
BMI     23.404  26.358 0.038
```

Cases are on average 7.7 kg heavier than controls (BMI 26.4 against 23.4), yet infarction status still explains only about 4% of the variance of weight. The age and height differences are negligible ($\eta^2 \leq 0.003$). For the qualitative variables, the next block gives the percentage of cases in each level, Cramér's V^2 and the χ^2 p-value:

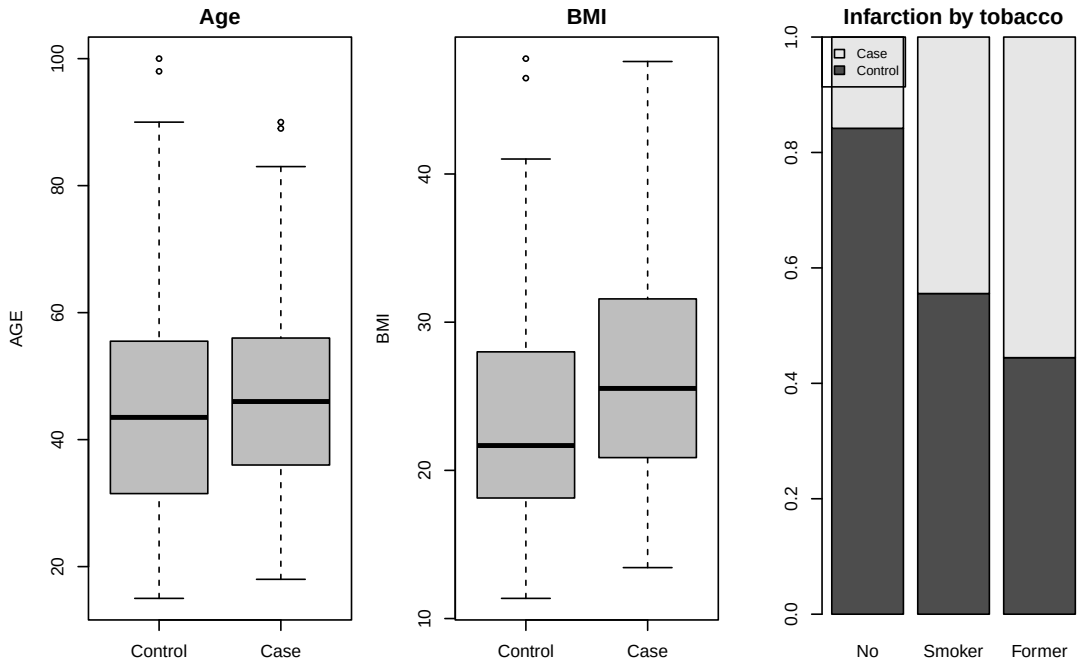
```
lapply(inf[, c("CO", "TOBACCO", "ATCD", "HTA")], function(g) {
  tab <- table(g, inf$INFARCT)
  chi <- chisq.test(tab, correct = FALSE)
```

```
  round(c(100 * prop.table(tab, 1)[, "Case"],
    V2 = unname(chi$statistic) / (sum(tab) * (min(dim(tab)) - 1)),
    p = chi$p.value), 4)})
```

```
$CO
     No     Yes      V2       p
14.8594 56.0000  0.1886  0.0000

$TOBACCO
     No  Smoker  Former      V2       p
15.8140 44.4444 55.5556  0.1321  0.0000

$ATCD
     No     Yes      V2       p
31.8766 41.5094  0.0044  0.1619

$HTA
     No     Yes      V2       p
29.3103 40.2516  0.0123  0.0185
```

Oral contraceptives and tobacco are the two clearly associated factors ($p < 10^{-4}$). Hypertension is weakly associated: 40.3% of hypertensive women are cases against 29.3% of the others ($p = 0.019$). Family history shows no significant link at the 5% level ($p = 0.16$). Graphical summary (Section 11.6):

```
par(mfrow = c(1, 3), mar = c(4, 4, 2, 1))
boxplot(AGE ~ INFARCT, data = inf, main = "Age", col = "grey", xlab = "")
boxplot(BMI ~ INFARCT, data = inf, main = "BMI", col = "grey", xlab = "")
barplot(prop.table(table(inf$INFARCT, inf$TOBACCO), 2),
        main = "Infarction by tobacco", legend.text = TRUE,
        args.legend = list(x = "topleft", cex = 0.8))
```



10 Random variables, distributions and simulations

Contents

10.1 Exercises 12.1–12.7

Problem 12.1. Which R function would you use to generate numbers from a $\mathcal{N}(0,1)$ distribution?

Solution. `rnorm()`, whose defaults `mean = 0, sd = 1` are exactly the $\mathcal{N}(0,1)$ distribution (Table 12.2), so only the sample size is needed (seed 1):

```
set.seed(1)
rnorm(5)
```

```
[1] -0.6264538  0.1836433 -0.8356286  1.5952808  0.3295078
```

Problem 12.2. Which R function would you use to generate numbers from a $\mathcal{N}(2,10)$ distribution?

Solution. `rnorm()` with `mean = 2` and `sd = sqrt(10)`: the book writes $\mathcal{N}(\mu, \sigma^2)$, but R's argument is the standard deviation σ, not the variance (seed 1):

```
set.seed(1)
rnorm(5, mean = 2, sd = sqrt(10))
```

```
[1]  0.01897911  2.58073118 -0.64248969  7.04472084  3.04199507
```

Problem 12.3. Which R function would you use to calculate the quantiles of a χ^2 distribution?

Solution. `qchisq(p, df)`, with the degrees of freedom in `df`; e.g. the 2.5%, 50% and 97.5% quantiles of a χ^2_5:

```
qchisq(c(0.025, 0.5, 0.975), df = 5)
```

```
[1]  0.8312116  4.3514602 12.8325020
```

Problem 12.4. Which R function would you use to calculate the density of a Fisher distribution?

Solution. `df(x, df1, df2)`, with the numerator and denominator degrees of freedom in `df1` and `df2`; e.g. for $\mathcal{F}(3,10)$:

```
df(c(0.5, 1, 2), df1 = 3, df2 = 10)
```

```
[1] 0.6340072 0.4041228 0.1482109
```

Problem 12.5. Which R function would you use to calculate the quantiles of a Student distribution?

Solution. `qt(p, df)`, with the degrees of freedom in `df`; e.g. the 2.5% and 97.5% quantiles of a $\mathcal{T}_{10}$:

```
qt(c(0.025, 0.975), df = 10)
```

```
[1] -2.228139  2.228139
```

Problem 12.6. How would you compute the probability that X lays between 3 and 5 given that $X \sim \mathcal{N}(4,2)$?

Solution. As a difference of the distribution function, $P(3 \leq X \leq 5) = F(5) - F(3)$, with `pnorm()` and `sd = sqrt(2)` since the second parameter is the variance:

```
pnorm(5, mean = 4, sd = sqrt(2)) - pnorm(3, mean = 4, sd = sqrt(2))
```

```
[1] 0.5204999
```

So $P(3 \leq X \leq 5) \approx 0.5205$; the authors' companion solution uses `mean = 2`, a slip for the stated mean of 4.

Problem 12.7. How would you calculate the quantile of order $p = 0.95$ of a $\mathcal{N}(0,1)$?

Solution. `qnorm(0.95)`, since `qnorm()` defaults to `mean = 0, sd = 1`:

```
qnorm(0.95)
```

```
[1] 1.644854
```

10.2 Worksheet 12.W.A — Simulations - Study of the distribution f(x) = (3/2) sqrt(x) on [0, 1]

Problem 12.W.A. Worksheet 12.W.A — Simulations — Study of the distribution $f(x) = \frac{3}{2}\sqrt{x}$ on $[0,1]$
12.1- Check that $f(x)$ is a density, using the function `integrate()`.
12.2- Simulate a sample of size 1,000 from the distribution defined by the density $f(x) = \frac{3}{2}\sqrt{x}$ over $[0,1]$.
12.3- Calculate the empirical mean and variance.
12.4- Compare with the theoretical values.
12.5- Calculate and compare the theoretical and empirical probabilities of the following classes: $[0, 0.30]$, $]0.30, 0.50]$, $]0.50, 0.70]$, $]0.70, 0.85]$, $]0.85, 1]$.

Solution.
12.1- $f \geq 0$ on $[0,1]$ and its integral is 1, so f is a density:

```
f <- function(x) 3/2 * sqrt(x)
integrate(f, lower = 0, upper = 1)
```

```
1 with absolute error < 0.00012
```

12.2- Use the inverse transform method of Section 12.5.2: $F(x) = x^{3/2}$ on $[0,1]$, so $F^{-1}(u) = u^{2/3}$ and $X = U^{2/3}$ with $U \sim U[0,1]$ has density f.

```
set.seed(1)
x <- runif(1000)^(2/3)
head(round(x, 4))
```

```
[1] 0.4131 0.5174 0.6898 0.9378 0.3439 0.9311
```

12.3- With `set.seed(1)`, the empirical mean is 0.6003 and the (unbiased, Section 12.4.1) empirical variance is 0.0677:

```
c(mean = mean(x), var = var(x))
```

```
      mean        var
0.60029442 0.06767857
```

12.4- The theoretical values are $E(X) = \int_0^1 \frac{3}{2}x^{3/2}\,dx = \frac{3}{5}$ and $\mathrm{Var}(X) = \frac{3}{7} - \frac{9}{25} = \frac{12}{175} \approx 0.0686$, computed here with `integrate()`:

```
mu <- integrate(function(x) x * f(x), 0, 1)$value
sigma2 <- integrate(function(x) x^2 * f(x), 0, 1)$value - mu^2
rbind(theoretical = c(mean = mu, var = sigma2),
      empirical = c(mean(x), var(x)))
```

```
                mean        var
theoretical 0.6000000 0.06857143
empirical   0.6002944 0.06767857
```

The empirical mean and variance agree with the theoretical ones to within about 0.0003 and 0.001, which is the sampling variation expected with $n = 1000$ (law of large numbers, Section 12.3.1).
12.5- The theoretical probability of $]a,b]$ is $F(b) - F(a) = b^{3/2} - a^{3/2}$; the empirical one is the proportion of the sample falling in the class, obtained with `cut()` and `table()`:

```
breaks <- c(0, 0.30, 0.50, 0.70, 0.85, 1)
F <- function(q) q^(3/2)
emp <- table(cut(x, breaks, include.lowest = TRUE)) / length(x)
```

```r
round(rbind(theoretical = diff(F(breaks)), empirical = emp), 4)
```

```
            [0,0.3] (0.3,0.5] (0.5,0.7] (0.7,0.85] (0.85,1]
theoretical  0.1643    0.1892    0.2321      0.198   0.2163
empirical    0.1610    0.1900    0.2410      0.198   0.2100
```

Every empirical frequency is within 0.01 of its theoretical probability (largest gap 0.009 on $]0.50, 0.70]$), so the simulated sample reproduces the distribution f well.

10.3 Worksheet 12.W.B — Study of the generalized Pareto distribution

Problem 12.W.B. Worksheet 12.W.B — Study of the generalized Pareto distribution
Let X be a random variable following a generalized Pareto distribution $GP(\mu, \sigma, \xi)$. The density of this distribution is

$$f_X(x) = \frac{1}{\sigma}\left(1 + \frac{\xi(x-\mu)}{\sigma}\right)^{-\frac{1}{\xi}-1}$$

with $x \geq \mu$ if $\xi \geq 0$ and $x \leq \mu - \sigma/\xi$ if $\xi < 0$. It is given that

$$\mathbb{E}(X) = \mu + \frac{\sigma}{1-\xi} \quad (\xi < 1)$$

and

$$\mathrm{Var}(X) = \frac{\sigma^2}{(1-\xi)^2(1-2\xi)} \quad (\xi < 1/2).$$

We can simulate from X with the following formula:

$$X = \mu + \frac{\sigma(U^{-\xi} - 1)}{\xi}$$

where U is a uniform random variable over $[0, 1]$.
12.1- Propose an R code to generate a sample of size n from a $GP(\mu, \sigma, \xi)$ distribution. Your source code should use the following variables: `n`, `mu`, `sigma` and `xi`.
12.2- Simulate a sample of size $n = 1{,}000$ from the distribution $GP(0, 1, 1/4)$.
12.3- Calculate the empirical mean and variance.
12.4- Compare with the theoretical values.
12.5- Repeat questions 2 to 3 with $n = 10{,}000$.
12.6- Plot in red the density histogram of your sample. Take 500 equidistant classes and limit the display of the histogram to the interval $[0, 10]$ on the x-axis.
12.7- Overlay the density plot of the $GP(0, 1, 1/4)$ distribution (in blue). Note that the plot is close to the histogram.

Solution.
12.1- Apply the given inversion formula to `runif()` draws, vectorised over the n uniforms:

```r
rGP <- function(n, mu, sigma, xi) mu + sigma * (runif(n)^(-xi) - 1) / xi
```

12.2- With `set.seed(1)`:

```r
set.seed(1)
n <- 1000; mu <- 0; sigma <- 1; xi <- 1/4
x <- rGP(n, mu, sigma, xi)
head(round(x, 4))
```

```
[1] 1.5724 1.1214 0.5978 0.0975 1.9689 0.1086
```

12.3- The empirical mean is 1.294 and the empirical variance 2.749 (seed 1):

```r
c(mean = mean(x), var = var(x))
```

```
    mean      var
1.293959 2.748602
```

12.4- The theoretical values are $\mathbb{E}(X) = 1/(3/4) = 4/3 \approx 1.333$ and $\mathrm{Var}(X) = 1/\big((9/16)(1/2)\big) =$

$32/9 \approx 3.556$:

```
c(mean = mu + sigma/(1 - xi), var = sigma^2/((1 - xi)^2 * (1 - 2*xi)))
```

```
    mean      var
1.333333 3.555556
```

The empirical mean is within 3% of 4/3, but the empirical variance undershoots 32/9 by about 23%: with $\xi = 1/4$ the fourth moment of X is infinite, so the sample variance converges slowly and is driven by rare large values.

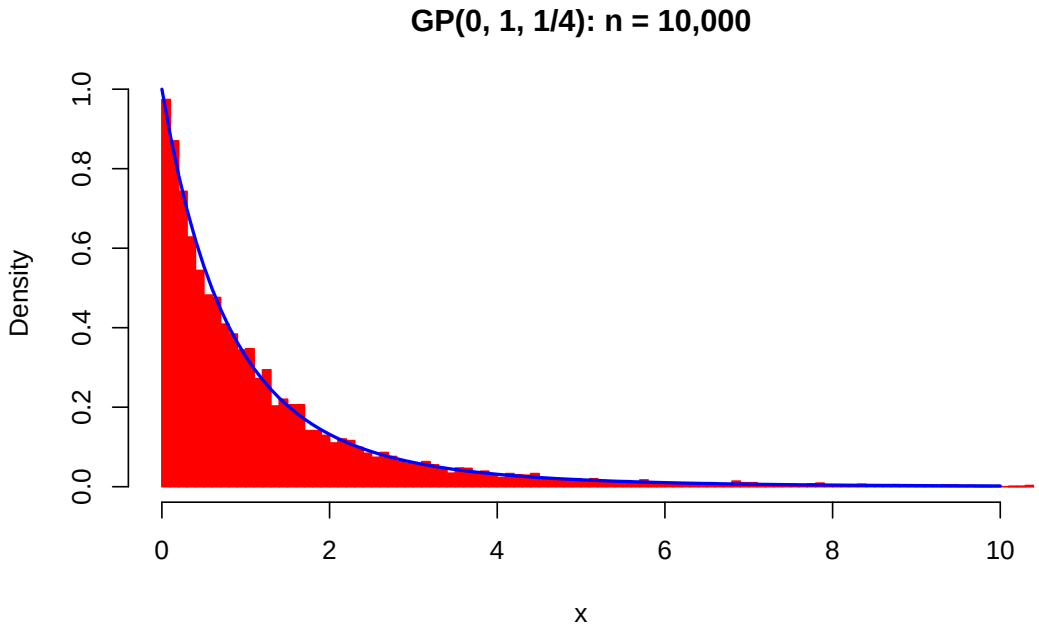
12.5- With $n = 10{,}000$ (seed 1) the mean is 1.348 and the variance 3.573, both now close to 4/3 and 32/9:

```
set.seed(1)
n <- 10000
x <- rGP(n, mu, sigma, xi)
c(mean = mean(x), var = var(x))
```

```
    mean      var
1.348422 3.573066
```

12.6- and 12.7- `hist(freq = FALSE)` draws the density histogram and `curve(add = TRUE)` overlays the density $f_X(x) = (1 + x/4)^{-5}$:

```
dGP <- function(x, mu, sigma, xi) (1 + xi * (x - mu) / sigma)^(-1/xi - 1) / sigma
hist(x, breaks = 500, freq = FALSE, col = "red", border = "red", xlim = c(0, 10),
     main = "GP(0, 1, 1/4): n = 10,000", xlab = "x")
curve(dGP(x, mu, sigma, xi), from = 0, to = 10, col = "blue", lwd = 2, add = TRUE)
```



The blue density follows the red histogram closely across $[0, 10]$, confirming that the inversion formula generates $GP(0, 1, 1/4)$ draws; `breaks = 500` splits the whole sample range (maximum 35.4 here) into classes, of which only those in $[0, 10]$ are displayed.

10.4 Worksheet 12.W.C — Uniform distribution on a square

Problem 12.W.C. Worksheet 12.W.C — Uniform distribution on a square — Uniform distribution on a square

12.1- Simulate 1,000 observations from (X_1, X_2) which follow the uniform distribution over the square $[0, 1] \times [0, 1]$.

12.2- Get an approximation of the probability that the distance between (X_1, X_2) and the nearest

edge is less than 0.25.
12.3- Same question for the distance to the nearest vertex.
12.4- Try to identify the theoretical distribution of the variable distance to the nearest edge: expected value, variance, density.

Solution.
12.1- Fill a two-column matrix with `runif(2*n)` (seed 1), since X_1 and X_2 are independent $U[0,1]$:

```
set.seed(1)
n <- 1000
X <- matrix(runif(2 * n), ncol = 2, dimnames = list(NULL, c("X1", "X2")))
head(X, 3)
```

```
           X1        X2
[1,] 0.2655087 0.5308088
[2,] 0.3721239 0.6848609
[3,] 0.5728534 0.3832834
```

12.2- The estimate is 0.767. The distance to the nearest edge is $D = \min(X_1, 1-X_1, X_2, 1-X_2)$, and the probability is estimated by the proportion of simulated points with $D < 0.25$:

```
d.edge <- apply(cbind(X, 1 - X), 1, min)
mean(d.edge < 0.25)
```

```
[1] 0.767
```

This is close to the exact value $1 - (1 - 2 \times 0.25)^2 = 0.75$, the area of the square minus the central square of side 0.5 (see 12.4).
12.3- The estimate is 0.205. Take the minimum of the Euclidean distances to the four vertices:

```
V <- cbind(c(0, 1, 0, 1), c(0, 0, 1, 1))
d.vert <- apply(X, 1, function(p) min(sqrt((p[1] - V[, 1])^2 + (p[2] - V[, 2])^2)))
mean(d.vert < 0.25)
pi / 16
```

```
[1] 0.205
[1] 0.1963495
```

The exact probability is the total area of the four quarter-discs of radius 0.25 at the corners, $\pi(0.25)^2 = \pi/16 \approx 0.196$, which agrees with the simulation.
12.4- D has density $f_D(d) = 4(1-2d)$ on $[0, 1/2]$, with $\mathbb{E}(D) = 1/6$ and $\mathrm{Var}(D) = 1/72$. Indeed $D > d$ exactly when the point lies in the central square $[d, 1-d]^2$, so

$$P(D > d) = (1-2d)^2, \qquad F_D(d) = 1 - (1-2d)^2, \qquad f_D(d) = 4(1-2d),$$
$$\mathbb{E}(D) = \int_0^{1/2} (1-2d)^2 \, dd = \frac{1}{6}, \qquad \mathbb{E}(D^2) = \int_0^{1/2} 4d^2(1-2d) \, dd = \frac{1}{24},$$
$$\mathrm{Var}(D) = \frac{1}{24} - \frac{1}{36} = \frac{1}{72} \approx 0.0139.$$

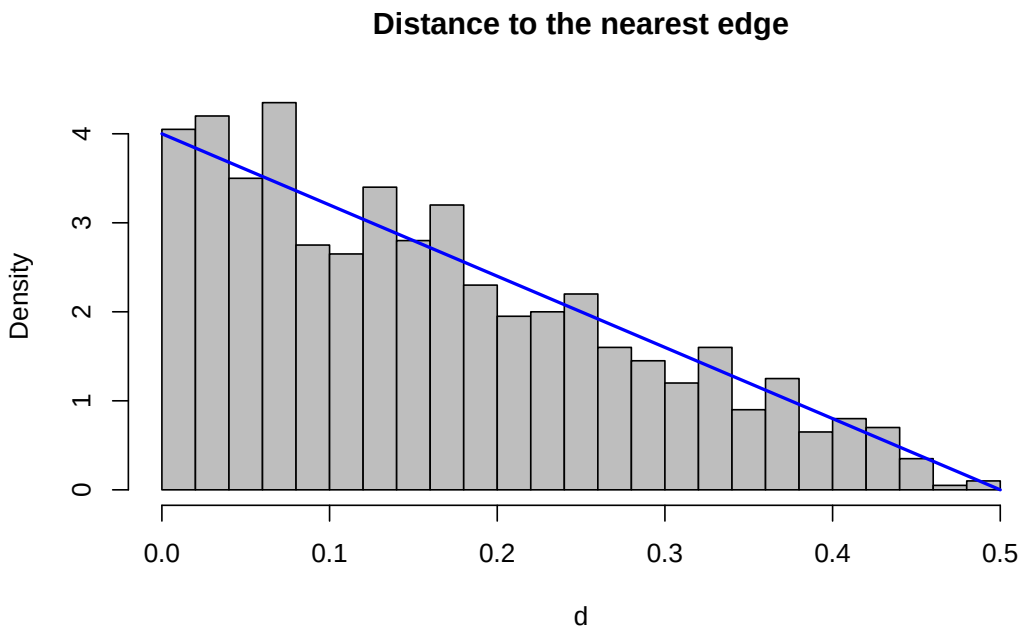
The simulated sample confirms this:

```
c(mean = mean(d.edge), var = var(d.edge))
c(mean = 1/6, var = 1/72)
integrate(function(d) 4 * (1 - 2 * d), 0, 0.5)$value
ks.test(d.edge, function(q) 1 - (1 - 2 * pmin(pmax(q, 0), 0.5))^2)
```

```
      mean        var
0.16175485 0.01360786
      mean        var
0.16666667 0.01388889
[1] 1

        Asymptotic one-sample Kolmogorov-Smirnov test

data:  d.edge
D = 0.033624, p-value = 0.2082
alternative hypothesis: two-sided
```

The empirical mean and variance are close to 1/6 and 1/72, and the Kolmogorov-Smirnov test (p-value 0.21) does not reject the proposed distribution. Its density fits the histogram well:

```r
hist(d.edge, breaks = 20, freq = FALSE, col = "grey",
     main = "Distance to the nearest edge", xlab = "d")
curve(4 * (1 - 2 * x), 0, 0.5, add = TRUE, col = "blue", lwd = 2)
```



10.5 Worksheet 12.W.D — Towards modelling

Problem 12.W.D. Worksheet 12.W.D — Towards modelling — Towards modelling
A statistician believes that the world around us and the phenomena that occur are a large entanglement of random events, which can be **modelled** in a simplified way by random variables.
12.1- Start with the simple, and classical, example, of a coin toss. The outcome of this experiment is the observation of HEAD or TAIL at each toss. This can be modelled by a random variable X with distribution a Bernoulli with parameter 1/2. This experiment can be reproduced with a computer. Create a function `X` which simulates a coin toss. You can toss your virtual coins a few times.
12.2- We can also propose a **modelling** of the throw of a die. The outcome of this experiment is the observation of the number on the upper side of the die at each throw. If the die is not weighted, this can be modelled by a random variable X with distribution a discrete uniform over $\{1, 2, 3, 4, 5, 6\}$. This experiment can be reproduced with a computer. Create a function `throw.die()` using the function `sample()`. You can throw your virtual die a few times.
12.3- To simulate the game of Yahtzee, we shall create a function `yahtzee()` which throws five virtual dice. Create this function using the parameters `size` and `replace` of the function `sample()`.
12.4- Estimate the probability of getting a *yahtzee*, i.e. five identical dice in one throw (hint: use the functions `apply()`, `replicate()` and `unique()`). You should get a value close to $\frac{1}{6^4}$.

Solution.
12.1- Draw a $\mathcal{B}(1/2)$ value with `rbinom(1, 1, 1/2)` (Table 12.1) and map 0/1 to TAIL/HEAD; `replicate()` tosses the coin repeatedly (seed 1).

```r
set.seed(1)
X <- function() c("TAIL", "HEAD")[rbinom(1, size = 1, prob = 1/2) + 1]
replicate(8, X())
```

```
[1] "TAIL" "TAIL" "HEAD" "HEAD" "TAIL" "HEAD" "HEAD" "HEAD"
```

12.2- `sample(1:6, 1)` draws one value uniformly from $\{1, \ldots, 6\}$, which is exactly the discrete uniform

model; ten throws with seed 1:

```r
set.seed(1)
throw.die <- function() sample(1:6, 1)
replicate(10, throw.die())
```

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

12.3- Five independent dice means drawing `size = 5` values **with** replacement (`replace = TRUE`), otherwise the five faces would be forced to differ; two throws with seed 1:

```r
set.seed(1)
yahtzee <- function() sample(1:6, size = 5, replace = TRUE)
yahtzee()
yahtzee()
```

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

12.4- The estimated probability is $\hat{p} = 0.00070$ from 10^5 simulated throws (seed 1), close to the exact $1/6^4 = 6/6^5 \approx 0.000772$. `replicate()` stores each throw as a column of a $5 \times n$ matrix, and `apply()` flags the columns with a single `unique()` value:

```r
set.seed(1)
n <- 100000
throws <- replicate(n, yahtzee())
p.hat <- mean(apply(throws, 2, function(d) length(unique(d)) == 1))
c(estimate = p.hat, exact = 1/6^4)
round(p.hat + c(-1, 1) * 1.96 * sqrt(p.hat * (1 - p.hat) / n), 6)
```

```
   estimate       exact
0.0007000000 0.0007716049
[1] 0.000536 0.000864
```

The exact value lies inside the approximate 95% confidence interval $[0.000536, 0.000864]$, so the simulation agrees with $1/6^4$ up to Monte Carlo error.

10.6 Worksheet 12.W.E — Box-Muller theorem

Problem 12.W.E. Worksheet 12.W.E — Box-Muller theorem — Box-Muller theorem
Let U_1 and U_2 be two independent random variables uniform over the interval $[0, 1]$. The variables

$$Z_1 = \sqrt{-2\log(U_1)}\,\cos(2\pi U_2)$$
$$Z_2 = \sqrt{-2\log(U_1)}\,\sin(2\pi U_2)$$

are then two independent standard normal random variables.
12.1- Generate $n = 1{,}000$ pairs of observations $(z_1, z_2)_1, \ldots, (z_1, z_2)_n$ using this algorithm.
12.2- Use the function `kde2d()` from package `MASS` to estimate the bivariate density of these data.
12.3- Use the functions `spheres3d()` and `surface3d()` from the package `rgl` to plot these observations and the surface of the estimated bivariate density of these data. Also plot the surface of the density of a bivariate standard normal distribution. Note that you get a bell plot, typical of the bivariate normal.

Solution.
12.1- Two vectors of `runif()` draws pushed through the transformation give the 1,000 pairs (seed 1):

```r
set.seed(1)
n <- 1000
u1 <- runif(n); u2 <- runif(n)
z1 <- sqrt(-2 * log(u1)) * cos(2 * pi * u2)
z2 <- sqrt(-2 * log(u1)) * sin(2 * pi * u2)
z <- cbind(z1, z2)
head(round(z, 4), 3)
round(c(mean(z1), mean(z2), sd(z1), sd(z2), cor(z1, z2)), 3)
```

```
          z1      z2
```

```
[1,] -1.5981 -0.3133
[2,] -0.5595 -1.2899
[3,] -0.7842  0.7066
[1]  0.043  0.003  0.971  1.016 -0.016
```

Means near 0, standard deviations near 1 and a correlation near 0 are what two independent $N(0,1)$ samples should show.

12.2- `kde2d()` returns a list with the grid `x`, `y` and the matrix `z` of estimated density values; here on a 50×50 grid over $[-3.5, 3.5]^2$, compared with the exact density $\phi(x)\phi(y)$:

```r
library(MASS)
est <- kde2d(z1, z2, n = 50, lims = c(-3.5, 3.5, -3.5, 3.5))
str(est, give.attr = FALSE)
round(max(est$z), 4); round(1 / (2 * pi), 4)
theo <- outer(est$x, est$y, function(x, y) dnorm(x) * dnorm(y))
round(max(abs(est$z - theo)), 4)
```

```
List of 3
 $ x: num [1:50] -3.5 -3.36 -3.21 -3.07 -2.93 ...
 $ y: num [1:50] -3.5 -3.36 -3.21 -3.07 -2.93 ...
 $ z: num [1:50, 1:50] 1.51e-19 8.44e-18 3.61e-16 1.17e-14 2.91e-13 ...
[1] 0.1668
[1] 0.1592
[1] 0.0333
```

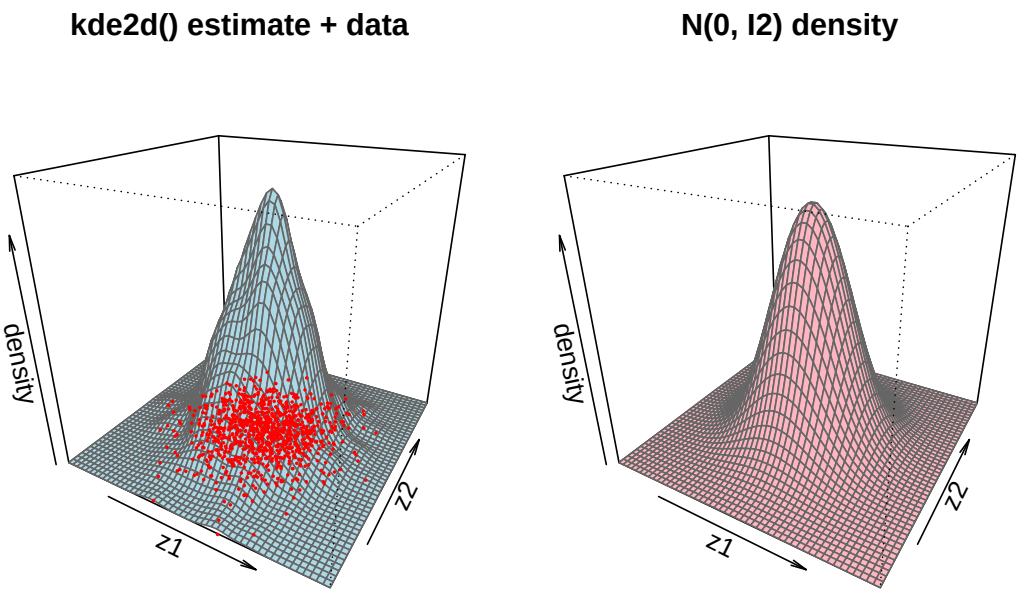
The estimated peak (0.167) is close to the theoretical maximum $1/(2\pi) \approx 0.159$, and the estimate never departs from $\phi(x)\phi(y)$ by more than 0.033 on the grid.

12.3- With `rgl` the requested plots are drawn by

```
library(rgl)
open3d()
spheres3d(z1, z2, 0, radius = 0.05, color = "red")
surface3d(est$x, est$y, 10 * est$z, color = "lightblue", alpha = 0.6)
open3d()
surface3d(est$x, est$y, 10 * theo, color = "pink")
```

(the factor 10 stretches the vertical axis so the bell is visible next to the points); since `rgl` cannot render headless, the static equivalent below uses `persp()`, with the observations projected onto the base plane by `trans3d()`:

```r
par(mfrow = c(1, 2), mar = c(1, 1, 2, 1))
pm <- persp(est$x, est$y, est$z, theta = 30, phi = 25, col = "lightblue",
            border = "grey40", xlab = "z1", ylab = "z2", zlab = "density",
            main = "kde2d() estimate + data", zlim = c(0, 0.18))
points(trans3d(z1, z2, 0, pm), pch = 16, cex = 0.3, col = "red")
persp(est$x, est$y, theo, theta = 30, phi = 25, col = "lightpink",
      border = "grey40", xlab = "z1", ylab = "z2", zlab = "density",
      main = "N(0, I2) density", zlim = c(0, 0.18))
```



Both surfaces are the same circularly symmetric bell centred at $(0, 0)$, confirming that the Box-Muller pairs behave as a bivariate standard normal sample.

11 Confidence intervals and hypothesis testing

Contents

11.1 Exercises 13.1–13.7

Problem 13.1. Which function would you use to get the quantiles of a binomial distribution?

Solution. `qbinom(p, size, prob)`, the "q" member of the `binom` family, returns the smallest integer x with $P(X \leq x) \geq p$; for $X \sim \mathcal{B}(20, 0.3)$:

```
qbinom(c(0.025, 0.5, 0.975), size = 20, prob = 0.3)
```

```
[1]  2  6 10
```

Problem 13.2. What is the use of the function `pnorm()`?

Solution. `pnorm(q, mean = 0, sd = 1)` evaluates the cumulative distribution function of the normal distribution, $P(X \leq q)$ for $X \sim N(\mu, \sigma^2)$ (with `lower.tail = FALSE` it gives $P(X > q)$, used for p-values):

```
pnorm(1.96)
pnorm(180, mean = 170, sd = 10)
```

```
[1] 0.9750021
[1] 0.8413447
```

Problem 13.3. Give the R instruction to get a confidence interval for the mean using a sample of size 50.

Solution. `t.test(x, conf.level = 0.95)$conf.int` (Section 13.2.1); with $n = 50 > 30$ the Student interval is valid even without normality. On a simulated sample (`set.seed(1)`):

```
set.seed(1)
x <- rnorm(50, mean = 10, sd = 2)
t.test(x, conf.level = 0.95)$conf.int
```

```
[1]  9.728337 10.673456
attr(,"conf.level")
[1] 0.95
```

The interval [9.73, 10.67] covers the true mean 10.

Problem 13.4. Explain the difference between the functions `prop.test()` and `binom.test()`.

Solution. `prop.test()` uses the normal (large-sample) approximation to the binomial, so it needs $np \geq 5$ and $n(1-p) \geq 5$, and it can also compare two or more proportions; `binom.test()` is the exact test/interval (Clopper-Pearson) based on the binomial distribution itself, valid for any n but for a single proportion only (Sections 13.2.2 and 13.3.1.3). On the book's 141 successes out of 226:

```
prop.test(141, 226)$conf.int
binom.test(141, 226)$conf.int
```

```
[1] 0.5569177 0.6865847
attr(,"conf.level")
[1] 0.95
[1] 0.5572321 0.6872590
attr(,"conf.level")
[1] 0.95
```

With $n = 226$ the approximate and exact intervals agree to two decimals.

Problem 13.5. Name two functions which compare two cumulative distribution functions using two samples.

Solution. `ks.test(x, y)` (two-sample Kolmogorov-Smirnov, $H_0 : F_X = F_Y$ via $\sup_x |\hat{F}_1(x) - \hat{F}_2(x)|$) and `wilcox.test(x, y)` (Mann-Whitney, $H_0 : F_X = F_Y$ against a shift), Table 13.4. On two simulated samples (`set.seed(1)`) differing by a shift of 1:

```
set.seed(1)
x <- rnorm(30); y <- rnorm(30, mean = 1)
ks.test(x, y)$p.value
wilcox.test(x, y)$p.value
```

```
[1] 0.0008995777
[1] 2.410166e-05
```

Both tests reject equality of the two distributions at the 5 % level.

Problem 13.6. Which function is used to test whether a sample follows a normal distribution?

Solution. `shapiro.test(x)`, the Shapiro-Wilk test of H_0: "the sample comes from a normal distribution" (Section 13.3.3.1; package `nortest` adds `lillie.test()`, `ad.test()`, …). On an exponential sample (`set.seed(1)`):

```
set.seed(1)
shapiro.test(rexp(40))
```

```

        Shapiro-Wilk normality test

data:  rexp(40)
W = 0.7696, p-value = 1.669e-06
```

The p-value 1.7×10^{-6} rejects normality, as it should for exponential data.

Problem 13.7. Which functions are used to test the dependence of qualitative variables?

Solution. `chisq.test()` on the contingency table (Pearson χ^2, with `correct=TRUE` for Yates' correction on a 2×2 table) and `fisher.test()` (Fisher's exact test, when theoretical counts are small), Section 13.3.2. For hair and eye colour:

```
tab <- margin.table(HairEyeColor, c(1, 2))
chisq.test(tab)
set.seed(1)
fisher.test(tab, simulate.p.value = TRUE, B = 1e4)$p.value
```

```

        Pearson's Chi-squared test

data:  tab
X-squared = 138.29, df = 9, p-value < 2.2e-16

[1] 9.999e-05
```

Both tests reject independence: hair colour and eye colour are associated (the Fisher p-value is a Monte Carlo estimate on this 4×4 table, seed 1, at its floor $1/(B+1)$).

11.2 Exercises 13.8–13.10

Problem 13.8. Which package includes functions to compute confidence intervals using bootstrap?

Solution. Package `boot`: `boot()` generates the bootstrap replicates and `boot.ci()` turns them into intervals (Section 13.2.1). For the mean of an exponential sample (`set.seed(1)`):

```
library(boot)
set.seed(1)
x <- rexp(50)
b <- boot(x, function(d, i) mean(d[i]), R = 2000)
```

```r
boot.ci(b, type = c("norm", "perc", "bca"))
```

```
BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
Based on 2000 bootstrap replicates

CALL :
boot.ci(boot.out = b, type = c("norm", "perc", "bca"))

Intervals :
Level      Normal             Percentile            BCa
95%   ( 0.7467,  1.2219 )   ( 0.7643,  1.2395 )   ( 0.7913,  1.2945 )
Calculations and Intervals on Original Scale
```

All three 95 % intervals for the mean, lying between 0.75 and 1.29, contain the true value 1 of the $\mathcal{E}(1)$ distribution; BCa is shifted right to follow the skewness of the sample.

Problem 13.9. Which formal argument of the function `t.test()` is used for a paired test?

Solution. `paired`: `t.test(x, y, paired = TRUE)` tests the mean of the differences `x - y` (Section 13.3.1.1). On the two drugs of the `sleep` data (same ten patients):

```r
drug1 <- sleep$extra[1:10]; drug2 <- sleep$extra[11:20]
t.test(drug2, drug1, paired = TRUE)
```

```
        Paired t-test

data:  drug2 and drug1
t = 4.0621, df = 9, p-value = 0.002833
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 0.7001142 2.4598858
sample estimates:
mean difference
           1.58
```

Drug 2 gives on average 1.58 more hours of sleep than drug 1 ($p = 0.003$).

Problem 13.10. What is the difference between a χ^2 for independence and a χ^2 for fit to a distribution? How would you perform these two tests in R?

Solution. The χ^2 for independence uses a two-way contingency table of two qualitative variables and tests H_0: "the variables are independent", with expected counts $n_{i\cdot}n_{\cdot j}/n$ estimated from the margins and $(I-1)(J-1)$ degrees of freedom; the χ^2 of fit uses the counts of one variable and tests H_0: "the category probabilities equal given $p_1, \ldots, p_K$", with expected counts np_k and $K-1$ degrees of freedom (Sections 13.3.2.1 and 13.3.3.1). In R: `chisq.test(table)` for the first, `chisq.test(counts, p = probs)` for the second. The independence test is 13.7's `chisq.test(tab)`; the fit test of equiprobable hair colours is:

```r
hair <- margin.table(HairEyeColor, 1)
hair
chisq.test(hair, p = rep(1/4, 4))
```

```
Hair
Black Brown   Red Blond
  108   286    71   127

        Chi-squared test for given probabilities

data:  hair
X-squared = 182.53, df = 3, p-value < 2.2e-16
```

The four hair colours are clearly not equally frequent ($\chi^2_3 = 182.5$).

11.3 Worksheet 13.W.A.1 — Study of confidence intervals - Study of the confidence interval for the mean

Problem 13.W.A.1. Worksheet 13.W.A.1 — Study of confidence intervals — Study of the confidence interval for the mean
The aim of this practical is to understand how to interpret a confidence interval. Indeed, for a confidence interval at level $1-\alpha$ of an unknown parameter, it is incorrect to say that there is a $100\times(1-\alpha)$ % chance that the parameter lies in the realized interval. The unknown parameter has a unique value which does not change: the probability that it lies in the realized interval is either 0 or 1. However, it is correct to say that there is a 5 % risk of being wrong by stating that the parameter lies in the realized confidence interval.
13.1- Simulate $M = 50{,}000$ samples of size $n = 20$ from a normal distribution with mean $\mu = -1.2$ and variance $\sigma^2 = 2$.
13.2- For each sample, compute a 90 % confidence interval of the mean μ.
13.3- Calculate the proportion of intervals which contain the value $\mu = -1.2$. What do you observe?
13.4- Repeat this procedure for the value $\mu = 1$, with samples of size $n = 100$ from a $\chi^2(1)$ distribution.
13.5- Same question with $n = 10$ and a $\chi^2(1)$ distribution. What do you observe? How do you explain this?
13.6- Simulate a sample of size $n = 20$ from a normal distribution with mean $\mu = -1.2$ and variance $\sigma^2 = 2$. Calculate a 95 % confidence interval for μ.
13.7- Repeat this operation for samples of increasing size: $n = 50$; 100; 1,000; 10,000; 100,000. What do you observe?
13.8- For each of the six samples above, calculate the observed value of the statistic for a Student test of hypothesis $\mathcal{H}_1 : \mu \neq 0$, as well as the p-value of the test (at significance level 5 %). What do you observe? How do you explain this?
13.9- For a sample of size $n = 100{,}000$, calculate a 95 % confidence interval and compute the p-value of the test of hypothesis $\mathcal{H}_1 : \mu \neq -1.1$. Compare this p-value to the one you found in the previous question with $n = 50$. What do you conclude?

Solution.
13.1- Store the M samples as the rows of a $50{,}000 \times 20$ matrix (seed 1).
13.2- The Student interval of Section 13.2.1, $\bar{x} \pm t_{n-1,\,0.95}\, s/\sqrt{n}$, computed row-wise; the first row agrees with `t.test(x, conf.level = 0.90)$conf.int`, which would be too slow to call 50,000 times.

```r
set.seed(1)
M <- 50000; n <- 20
X <- matrix(rnorm(M * n, mean = -1.2, sd = sqrt(2)), nrow = M)
ci <- function(X, level = 0.90) {
  n <- ncol(X); m <- rowMeans(X); s <- apply(X, 1, sd)
  h <- qt(1 - (1 - level) / 2, df = n - 1) * s / sqrt(n)
  cbind(lower = m - h, upper = m + h)
}
IC <- ci(X)
head(IC, 3)
t.test(X[1, ], conf.level = 0.90)$conf.int
```

```
         lower      upper
[1,] -1.675360 -0.9709107
[2,] -2.047374 -1.1885837
[3,] -1.827927 -0.8760421
[1] -1.6753598 -0.9709107
attr(,"conf.level")
[1] 0.9
```

13.3- 89.73 % of the intervals contain $\mu = -1.2$: the observed coverage matches the nominal 90 %, because the data are normal and the Student interval is exact. Each single interval either contains -1.2 or does not; the 90 % describes the procedure over repeated samples.

```r
mean(IC[, "lower"] <= -1.2 & -1.2 <= IC[, "upper"])
```

```
[1] 0.8973
```

13.4- With $n = 100$ draws from $\chi^2(1)$ (mean 1), the coverage is 88.7 %, a little under the nominal 90 % (seed 1).

```r
set.seed(1)
Y <- matrix(rchisq(M * 100, df = 1), nrow = M); IC <- ci(Y)
mean(IC[, 1] <= 1 & 1 <= IC[, 2])
```

```
[1] 0.88666
```

13.5- With $n = 10$ the coverage falls to 81.6 % (seed 1), far below 90 %; almost all misses are intervals lying entirely below 1.

```r
set.seed(1)
Y <- matrix(rchisq(M * 10, df = 1), nrow = M); IC <- ci(Y)
mean(IC[, 1] <= 1 & 1 <= IC[, 2])
c(below = mean(IC[, 2] < 1), above = mean(IC[, 1] > 1))
```

```
[1] 0.81552
  below   above
0.17650 0.00798
```

The Student interval assumes normal data or $n > 30$ (Table 13.3). The $\chi^2(1)$ distribution is strongly right-skewed. With $n = 10$, $\bar{x}$ is still far from normal. Also, a sample with a small mean tends to have a small s, so its interval is short and misses 1 from below. At $n = 100$ the central limit theorem has mostly taken effect, and coverage is nearly nominal.

13.6- and 13.7- For $n = 20$ the 95 % interval is $[-1.535, -0.326]$ (seed 1). As n increases the interval shrinks roughly like $1/\sqrt{n}$, and at $n = 100{,}000$ it is $[-1.210, -1.193]$, tightly around -1.2. All six intervals contain -1.2.

```r
set.seed(1)
sizes <- c(20L, 50L, 100L, 1000L, 10000L, 100000L)
samples <- lapply(sizes, function(n) rnorm(n, mean = -1.2, sd = sqrt(2)))
data.frame(n = sizes, t(sapply(samples, function(x)
  round(t.test(x)$conf.int, 4))), check.names = FALSE) |>
  setNames(c("n", "lower", "upper"))
```

```
       n   lower   upper
1     20 -1.5350 -0.3261
2     50 -1.3750 -0.6200
3    100 -1.5691 -1.0605
4   1000 -1.3417 -1.1578
5  10000 -1.2341 -1.1785
6 100000 -1.2104 -1.1928
```

13.8- The statistic is $T = \bar{x}/(s/\sqrt{n})$ under $\mathcal{H}_0 : \mu = 0$. We reject $\mathcal{H}_0$ at the 5 % level for every sample. The observed t grows in magnitude from -3.2 to -268, and the p-value falls from 0.0045 to below machine precision (printed as 0).

```r
data.frame(n = sizes, t(sapply(samples, function(x) {
  tt <- t.test(x, mu = 0)
  c(t = round(unname(tt$statistic), 2), p.value = signif(tt$p.value, 3))
})))
```

```
       n       t   p.value
1     20   -3.22  4.49e-03
2     50   -5.31  2.65e-06
3    100  -10.26  2.96e-17
4   1000  -26.68 8.32e-119
5  10000  -84.96  0.00e+00
6 100000 -268.14  0.00e+00
```

The explanation is that $T \approx \sqrt{n}\,(\mu - 0)/\sigma = \sqrt{n} \times (-1.2)/\sqrt{2} \approx -0.85\sqrt{n}$. So a fixed true difference from μ_0 produces a statistic that grows like $\sqrt{n}$, and a p-value that goes to 0: the power of the test goes to 1. The authors' companion solution says it becomes harder to show that $\mu \neq 0$ as n grows; the output shows the opposite, so that comment is a slip.

13.9- For $n = 100{,}000$ the 95 % interval is $[-1.2104, -1.1928]$. The test of $\mathcal{H}_0 : \mu = -1.1$ gives $t = -22.67$ and $p = 1.6 \times 10^{-113}$, so we reject $\mathcal{H}_0$ decisively.

```r
tt <- t.test(samples[[6]], mu = -1.1)
round(tt$conf.int, 4); round(tt$statistic, 2); tt$p.value
t.test(samples[[2]], mu = -1.1)$p.value
```

```
[1] -1.2104 -1.1928
attr(,"conf.level")
[1] 0.95
     t
-22.67
[1] 1.615433e-113
[1] 0.5878748
```

This p-value is far smaller than the 2.65×10^{-6} obtained at $n = 50$ against $\mu_0 = 0$, even though -1.1 is only 0.1 away from the true mean while 0 is 1.2 away. On the same $n = 50$ sample, the test against -1.1 gives $p = 0.59$ and does not reject. So a p-value measures the evidence against $\mathcal{H}_0$, which depends on n, and not the size of the departure. With a huge sample, even a practically negligible difference is highly significant. The confidence interval is what shows the size of the effect.

11.4 Worksheet 13.W.A.2 — Study of confidence intervals - Study of confidence intervals from bootstrap

Problem 13.W.A.2. Worksheet 13.W.A.2 — Study of confidence intervals — Study of confidence intervals from bootstrap
13.1- Simulate $M = 500$ samples of size $n = 20$ from an exponential distribution with expectation $1/\lambda = 10$.
13.2- For each sample, calculate a 90 % confidence interval of the mean $1/\lambda$ using the bootstrap method.
13.3- Using the method described above, check the level of the confidence interval.
13.4- Compare this level to the one you get with a standard confidence interval for the mean (procedure `t.test()`).

Solution.
13.1- and 13.2- The samples are the rows of `X` (seed 1, `rate = 1/10`). Each row goes through `boot()` with 999 replicates and `boot.ci()`, exactly as in Section 13.2.1. We keep the percentile and BCa 90 % intervals.

```r
library(boot)
set.seed(1)
M <- 500; n <- 20
X <- matrix(rexp(M * n, rate = 1/10), nrow = M)
mymean <- function(x, indices) mean(x[indices])
IC.boot <- t(apply(X, 1, function(x) {
  b <- boot(x, mymean, R = 999, stype = "i", sim = "ordinary")
  bc <- boot.ci(b, conf = 0.90, type = c("perc", "bca"))
  c(perc = bc$percent[4:5], bca = bc$bca[4:5])
}))
head(round(IC.boot, 3), 3)
```

```
     perc1  perc2   bca1   bca2
[1,] 5.569  8.599  5.715  8.924
[2,] 9.761 18.154 10.194 18.858
[3,] 5.402 12.498  5.882 13.470
```

13.3- As in the first study, the level is estimated by the proportion of the 500 intervals that contain the true mean 10. The coverage is 87.0 % for the percentile interval and 86.4 % for BCa (seed 1). Both are below the nominal 90 %: with $n = 20$ skewed observations, the bootstrap distribution of $\bar{x}$ is too narrow. The Monte Carlo standard error is $\sqrt{0.9 \times 0.1/500} \approx 0.013$.

```r
covers <- function(lo, up) mean(lo <= 10 & 10 <= up)
c(perc = covers(IC.boot[, 1], IC.boot[, 2]), bca = covers(IC.boot[, 3], IC.boot[, 4]))
```

```
 perc   bca
0.870 0.864
```

13.4- On the same 500 samples, the Student interval `t.test(x, conf.level = 0.90)$conf.int` covers 10 in 88.4 % of cases. This is as close to 90 % as the bootstrap intervals, or closer. The differences of about 1.5 points are within Monte Carlo error. So at $n = 20$ the bootstrap brings no gain over `t.test()` for the mean of an exponential, and all three intervals slightly undercover.

```
IC.t <- t(apply(X, 1, function(x) t.test(x, conf.level = 0.90)$conf.int))
covers(IC.t[, 1], IC.t[, 2])
```

```
[1] 0.884
```

11.5 Worksheet 13.W.B.1 — Study of risks in hypothesis testing - Study of risk of the first kind

Problem 13.W.B.1. Worksheet 13.W.B.1 — Study of risks in hypothesis testing — Study of risk of the first kind
The aim of this practical is to explore the risks associated with hypothesis testing: $P[\text{accept } \mathcal{H}_1 \mid \mathcal{H}_0 \text{ is true}] = \alpha$, the risk of deciding $\mathcal{H}_1$ when in reality $\mathcal{H}_0$ is true; and $P[\text{reject } \mathcal{H}_1 \mid \mathcal{H}_1 \text{ is true}] = \beta$, the risk of not deciding $\mathcal{H}_1$ when in reality $\mathcal{H}_1$ is true.
13.1- Simulate $M = 500$ samples of size $n = 20$ following a normal distribution with mean $\mu = 4$ and variance $\sigma^2 = 1.2$.
13.2- For each sample, perform a Student test for hypotheses $\mathcal{H}_0 : \mu = 4$ and $\mathcal{H}_1 : \mu \neq 4$ at level $\alpha = 5\,\%$.
13.3- Count how many times you decide $\mathcal{H}_1$. What result did you expect?
13.4- Increase the number M of simulations.
13.5- Repeat this procedure for the value $\mu = 1$, with samples of size $n = 100$ from a $\chi^2(1)$ distribution.
13.6- Same question with $n = 10$. What do you observe? How do you explain this?
13.7- In fact, for each of the $M = 500$ samples, we make the decision either to accept $\mathcal{H}_1$, or to reject it. Let d_j $(1 \leq j \leq M)$ be the random variable which takes the value 1 if we decide to accept $\mathcal{H}_1$ and 0 otherwise (based on the jth sample). The variable d_j follows a Bernoulli distribution with parameter $p = P[d_j = 1] = P[\text{accept } \mathcal{H}_1]$. The variables d_j are independent, hence the variable $d = \sum_{j=1}^{M} d_j$ follows a binomial distribution $\mathcal{B}in(M, p)$. It counts how many times we accept $\mathcal{H}_1$. If $\mathcal{H}_0$ is true, and the test is well constructed (well chosen critical value), then we should have $p = P[\text{accept } \mathcal{H}_1 \mid \mathcal{H}_0 \text{ is true}] = \alpha$. Calculate a 95 % confidence interval for parameter p and conclude.

Solution.
13.1- Store the M samples as the rows of a 500×20 matrix (seed 1 throughout):

```
set.seed(1)
M <- 500; n <- 20
X <- matrix(rnorm(M * n, mean = 4, sd = sqrt(1.2)), nrow = M)  # one sample per row
dim(X)
```

```
[1] 500  20
```

13.2- Apply `t.test(x, mu = 4)` (Section 13.3.1) to each row and keep its p-value; $\mathcal{H}_1$ is decided when $p < 0.05$:

```
pval <- apply(X, 1, function(x) t.test(x, mu = 4)$p.value)
head(round(pval, 4))
```

```
[1] 0.5750 0.1871 0.4083 0.5946 0.2462 0.4208
```

13.3- $\mathcal{H}_1$ is decided 28 times out of 500, i.e. 5.6 %:

```
d <- as.numeric(pval < 0.05)   # d_j = 1 when H1 is decided
sum(d); mean(d)
```

```
[1] 28
[1] 0.056
```

Since $\mathcal{H}_0$ is true here, every such decision is a type I error, and we expected about $\alpha M = 0.05 \times 500 = 25$

of them; 28 is close to that.

13.4- With $M = 50\,000$ samples the rejection rate is 0.0505, essentially the nominal $\alpha = 0.05$:

```
nreject <- function(M, n, rgen, mu0) {
  X <- matrix(rgen(M * n), nrow = M)
  sum(apply(X, 1, function(x) t.test(x, mu = mu0)$p.value) < 0.05)
}
set.seed(1)
nreject(50000, 20, function(k) rnorm(k, 4, sqrt(1.2)), mu0 = 4) / 50000
```

```
[1] 0.0505
```

The empirical level converges to α as M grows, because the Student test is exact for normal data.

13.5- For $\chi^2(1)$ samples (true mean 1, so $\mathcal{H}_0 : \mu = 1$ is true) of size $n = 100$, the rejection rate is 6.2 % with $M = 500$ and 6.49 % with $M = 50\,000$:

```
set.seed(1)
d100 <- nreject(500, 100, function(k) rchisq(k, df = 1), mu0 = 1)
d100 / 500
nreject(50000, 100, function(k) rchisq(k, df = 1), mu0 = 1) / 50000
```

```
[1] 0.062
[1] 0.06486
```

The level is close to 5 % but slightly too high: with $M = 50\,000$ the Monte Carlo standard error is $\sqrt{0.05 \times 0.95/50\,000} \approx 0.001$, so 0.0649 is clearly above α.

13.6- With $n = 10$ the test rejects the true $\mathcal{H}_0$ about 14 % of the time, nearly three times the nominal 5 %:

```
set.seed(1)
d10 <- nreject(500, 10, function(k) rchisq(k, df = 1), mu0 = 1)
d10 / 500
nreject(50000, 10, function(k) rchisq(k, df = 1), mu0 = 1) / 50000
```

```
[1] 0.138
[1] 0.13926
```

The Student test assumes normal data or, failing that, a sample large enough for the central limit theorem to make $T = \sqrt{n}(\bar{X} - \mu_0)/S$ approximately Student (Table 13.4: "$n > 30$ or normality"). The $\chi^2(1)$ distribution is very skewed (skewness $2\sqrt{2} \approx 2.8$). With $n = 10$, T is far from its $\mathcal{T}(n-1)$ reference distribution, so the critical value is wrong and the real type I risk is not controlled. At $n = 100$ the approximation is much better, which explains the small excess in 13.5.

13.7- Since $d \sim \mathcal{B}in(500, p)$, `binom.test(d, 500)$conf.int` gives the exact 95 % interval for p (Section 13.2.2); here it is computed for the three $M = 500$ experiments above:

```
ci <- sapply(c(normal.n20 = sum(d), chisq.n100 = d100, chisq.n10 = d10),
             function(k) binom.test(k, 500)$conf.int)
rownames(ci) <- c("lower", "upper")
round(ci, 4)
```

```
      normal.n20 chisq.n100 chisq.n10
lower     0.0375     0.0425    0.1090
upper     0.0799     0.0869    0.1714
```

For normal samples, [0.0375; 0.0799] contains $\alpha = 0.05$, so the data are consistent with a correctly calibrated test. For $\chi^2(1)$ samples with $n = 100$, the interval [0.0425; 0.0869] also contains 0.05; with $M = 500$ runs we cannot detect the slight excess that the larger simulation in 13.5 revealed. With $n = 10$, [0.1090; 0.1714] lies entirely above 0.05, so the real type I risk is significantly larger than α and the Student test is not valid for such small, skewed samples.

11.6 Worksheet 13.W.B.2 — Study of risks in hypothesis testing - Study of power

Problem 13.W.B.2. Worksheet 13.W.B.2 — Study of risks in hypothesis testing — Study of power
The aim of this practical is to explore the risks associated with hypothesis testing: $P[\text{accept } \mathcal{H}_1 \mid \mathcal{H}_0 \text{ is true}] = \alpha$, the risk of deciding $\mathcal{H}_1$ when in reality $\mathcal{H}_0$ is true; and $P[\text{reject } \mathcal{H}_1 \mid \mathcal{H}_1 \text{ is true}] = \beta$, the risk of not deciding $\mathcal{H}_1$ when in reality $\mathcal{H}_1$ is true.

13.1- Simulate $M = 500$ samples of size $n = 20$ from a normal distribution with mean $\mu = 5$ and variance $\sigma^2 = 1.2$.
13.2- On each sample, perform a Student test between $\mathcal{H}_0 : \mu = 4$ and $\mathcal{H}_1 : \mu \neq 4$ at level $\alpha = 5\,\%$.
13.3- Count the number of times you accept $\mathcal{H}_1$. Estimate the power of the test for the situation in $\mathcal{H}_1$ where $\mu = 5$.
13.4- Increase the size of the sample to $n = 100$ and estimate the power of the test. What do you observe?
13.5- Repeat the procedure for the test $\mathcal{H}_0 : \mu = 1$ and $\mathcal{H}_1 : \mu \neq 1$, with samples of size $n = 100$ from a $\chi^2(2)$ distribution.
13.6- Same question with $n = 10$. What do you observe? How do you explain this?

Solution.
13.1- The 500 samples are the rows of a 500×20 matrix (seed 1 throughout):

```r
set.seed(1)
M <- 500; n <- 20
X <- matrix(rnorm(M * n, mean = 5, sd = sqrt(1.2)), nrow = M)
dim(X)
```

```
[1] 500  20
```

13.2- Run `t.test(x, mu = 4)` on each row and keep the p-values:

```r
pval <- apply(X, 1, function(x) t.test(x, mu = 4)$p.value)
head(signif(pval, 3))
```

```
[1] 4.45e-03 3.06e-03 1.28e-02 1.42e-04 7.23e-03 9.32e-05
```

13.3- $\mathcal{H}_1$ is accepted 487 times out of 500, so the estimated power at $\mu = 5$ is $1 - \hat{\beta} = 0.974$, with exact 95 % interval $[0.956; 0.986]$:

```r
d <- sum(pval < 0.05)
d; d / M
binom.test(d, M)$conf.int
power.t.test(n = 20, delta = 1, sd = sqrt(1.2), type = "one.sample")$power
```

```
[1] 487
[1] 0.974
[1] 0.9559496 0.9860851
attr(,"conf.level")
[1] 0.95
[1] 0.9718466
```

The interval contains the theoretical power 0.972 returned by `power.t.test()`, so the simulation estimates the power correctly; the type II risk is $\hat{\beta} = 0.026$.
13.4- With $n = 100$ every one of the 500 tests accepts $\mathcal{H}_1$, so the estimated power is 1:

```r
power.hat <- function(M, n, rgen, mu0) {
  X <- matrix(rgen(M * n), nrow = M)
  mean(apply(X, 1, function(x) t.test(x, mu = mu0)$p.value) < 0.05)
}
set.seed(1)
power.hat(500, 100, function(k) rnorm(k, 5, sqrt(1.2)), mu0 = 4)
```

```
[1] 1
```

Power increases with n: the standard error $\sigma/\sqrt{n}$ shrinks, so a gap of 1 between $\mu = 5$ and $\mu_0 = 4$ becomes about 9 standard errors and is always detected.
13.5- A $\chi^2(2)$ variable has mean 2 and variance 4, so here $\mathcal{H}_1$ is true with $\mu = 2$. With $n = 100$ the estimated power is again 1:

```r
set.seed(1)
power.hat(500, 100, function(k) rchisq(k, df = 2), mu0 = 1)
```

```
[1] 1
```

With 100 observations, a shift of 1 is $1/(2/\sqrt{100}) = 5$ standard errors, so the test always detects it despite the skewness of the data.

13.6- With $n = 10$ the power falls to about 0.22 ($M = 500$), or 0.196 with $M = 50\,000$, which is well below the 0.29 that `power.t.test()` gives for normal data with the same mean shift and standard deviation:

```
set.seed(1)
power.hat(500, 10, function(k) rchisq(k, df = 2), mu0 = 1)
power.hat(50000, 10, function(k) rchisq(k, df = 2), mu0 = 1)
power.t.test(n = 10, delta = 1, sd = 2, type = "one.sample")$power
```

```
[1] 0.218
[1] 0.1963
[1] 0.2928286
```

There are two reasons. First, with only 10 observations the shift of 1 is only $1/(2/\sqrt{10}) \approx 1.6$ standard errors, so the test misses it about 80 % of the time ($\hat{\beta} \approx 0.8$). Second, the $\chi^2(2)$ distribution is skewed, so the Student statistic is not $\mathcal{T}(9)$-distributed, as in 13.W.B.1. For right-skewed data, a large $\bar{x}$ usually comes with a large s, so T rarely becomes large and positive. This reduces rejections in the direction of the truth ($\mu = 2 > 1$), and the power is even lower than the normal-theory value.

11.7 Worksheet 13.W.C.1 — A few practical examples - Cow study

Problem 13.W.C.1. Worksheet 13.W.C.1 — A few practical examples — Cow study
The quantity of bacteria per cm^3 of milk from eight different cows is estimated after milking and 24 hours later. We wish to test whether the quantity of bacteria significantly increases with time.

Cow	Just after milking	24 h after milking
1	12,000	11,000
2	13,000	20,000
3	21,500	31,000
4	17,000	28,000
5	15,000	26,000
6	22,000	30,000
7	11,000	16,000
8	21,000	29,000

13.1- Answer the question under the assumption of normality of the data.
13.2- Answer the question using a sign test.
13.3- Answer the question using a Mann-Whitney test.

Solution.
13.1- The two measurements are made on the same cows, so use a one-sided paired Student test (Section 13.3.1), `t.test(after, before, paired = TRUE, alternative = "greater")`, of $H_0 : \mu_D = 0$ against $H_1 : \mu_D > 0$, where $D =$ (24 h) − (just after milking):

```
before <- c(12000, 13000, 21500, 17000, 15000, 22000, 11000, 21000)
after  <- c(11000, 20000, 31000, 28000, 26000, 30000, 16000, 29000)
t.test(after, before, paired = TRUE, alternative = "greater")
```

```
        Paired t-test

data:  after and before
t = 5.2786, df = 7, p-value = 0.0005749
alternative hypothesis: true mean difference is greater than 0
95 percent confidence interval:
 4687.921      Inf
sample estimates:
mean difference
         7312.5
```

With $p = 0.0006 < 0.05$ we reject H_0: the bacteria count increases significantly over 24 hours, by about 7,300 per cm^3 on average.
13.2- The sign test for two paired samples (Section 13.3.3) counts the positive and negative differences and applies `binom.test()` with $p = 1/2$ under H_0:

```r
d <- after - before
nplus <- sum(d > 0); nminus <- sum(d < 0)
c(nplus = nplus, nminus = nminus)
binom.test(nplus, nplus + nminus, alternative = "greater")$p.value
```

```
nplus nminus
    7      1
[1] 0.03515625
```

Seven of the eight cows show an increase; $p = 0.035 < 0.05$, so the sign test also concludes that the bacteria count increases significantly.

13.3- The Mann-Whitney (Wilcoxon rank-sum) test is `wilcox.test()` with two samples (Section 13.3.3); `exact = FALSE` because of the ties:

```r
wilcox.test(after, before, alternative = "greater", exact = FALSE)
```

```
        Wilcoxon rank sum test with continuity correction

data:  after and before
W = 49.5, p-value = 0.037
alternative hypothesis: true location shift is greater than 0
```

With $p = 0.037 < 0.05$ we reject H_0 at the 5% level: counts 24 h after milking are shifted upwards. The authors' companion solution uses the paired signed-rank version, `wilcox.test(..., paired = TRUE)` ($V = 35$, $p = 0.010$), which respects the pairing by cow that Mann-Whitney ignores; both lead to the same conclusion.

11.8 Worksheet 13.W.C.2 — A few practical examples - East German athletes

Problem 13.W.C.2. Worksheet 13.W.C.2 — A few practical examples — East German athletes
In the 1970s, female athletes from East Germany were well known for their corpulence. The Olympic ethics committee of the time, intrigued by this "masculinity", required the services of Dr Volker Fischbach. He selected nine female athletes with identical morphological characteristics, then measured the quantity of androgens (hormones which stimulate male characteristics) per litre of blood. The results are: 3.22 3.07 3.17 2.91 3.40 3.58 3.23 3.11 3.62.

13.1- Given that for women who do not use performance-enhancing drugs, the mean quantity of androgens is 3.1, propose a way to test whether East German athletes used such drugs (assume normality of data).

13.2- What was Dr Fischbach conclusion?

Solution.

13.1- Use a one-sample, one-sided Student test (Section 13.3.1) of $H_0 : \mu = 3.1$ (no doping) against $H_1 : \mu > 3.1$ (doping raises androgen levels), where μ is the mean androgen level of the athletes:

```r
andro <- c(3.22, 3.07, 3.17, 2.91, 3.40, 3.58, 3.23, 3.11, 3.62)
t.test(andro, mu = 3.1, alternative = "greater")
```

```
        One Sample t-test

data:  andro
t = 1.9968, df = 8, p-value = 0.04046
alternative hypothesis: true mean is greater than 3.1
95 percent confidence interval:
 3.110771      Inf
sample estimates:
mean of x
 3.256667
```

13.2- Since $p = 0.040 < 0.05$, Dr Fischbach rejects H_0 at the 5% level: the athletes' mean androgen level (3.26) is significantly above 3.1, which is evidence that they used performance-enhancing drugs (though the evidence would not be significant at the 1% level).

11.9 Worksheet 13.W.C.3 — A few practical examples - Drinking and driving

Problem 13.W.C.3. Worksheet 13.W.C.3 — A few practical examples — Drinking and driving
To study the effect of alcohol on reflexes, fourteen subjects went through a test of dexterity before and after drinking 100 ml of wine. The before and after scores are given in the following table (these are reaction times: a higher score means slower reflexes).

Subject	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Before	57	54	62	64	71	65	70	75	68	70	77	74	80	83
After	55	60	68	69	70	73	74	74	75	76	76	78	81	90

Propose a way to test whether alcohol has an effect on reflexes (assume normality of the data).

Solution. Use a paired Student test (Section 13.3.1) on the differences $D = \text{after} - \text{before}$, testing $H_0 : \mu_D = 0$ (no effect) against $H_1 : \mu_D \neq 0$:

```r
bef <- c(57, 54, 62, 64, 71, 65, 70, 75, 68, 70, 77, 74, 80, 83)
aft <- c(55, 60, 68, 69, 70, 73, 74, 74, 75, 76, 76, 78, 81, 90)
t.test(aft, bef, paired = TRUE)
```

```
        Paired t-test

data:  aft and bef
t = 3.6927, df = 13, p-value = 0.002707
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 1.452372 5.547628
sample estimates:
mean difference
            3.5
```

With $p = 0.0027 < 0.05$ we reject H_0: alcohol has a significant effect on reflexes, increasing reaction time by 3.5 points on average (95% CI $[1.45, 5.55]$), i.e. slowing the subjects down.

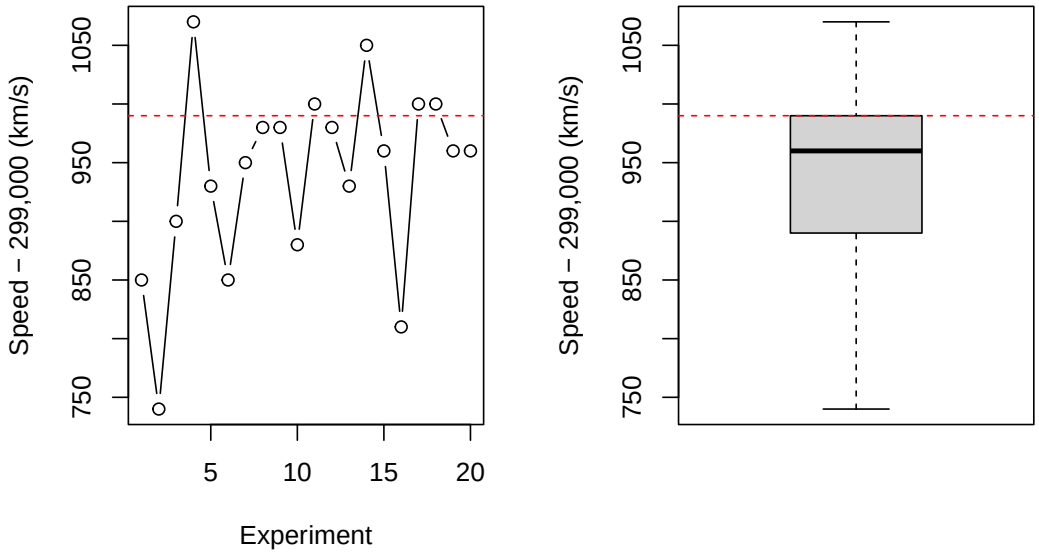
11.10 Worksheet 13.W.C.4 — A few practical examples - Speed of light

Problem 13.W.C.4. Worksheet 13.W.C.4 — A few practical examples — Speed of light
In 1879, American physicist Michelson performed several experiments to check the speed of light c proposed by French physicist Cornu in 1876. Cornu proposed a value of 299,990 km/s. Michelson got the 20 following measures (we subtracted 299,990 from Michelson's values, to avoid having to handle large numbers):
850 740 900 1,070 930 850 950 980 980 880 1,000 980 930 1050 960 810 1,000 1,000 960 960.
These twenty observations can be considered as the observed values of twenty random variables with identical but unknown mean μ. If the conditions to measure the speed of light are satisfactory, then it is reasonable to assume that μ is the true speed of light.
13.1- Plot the data. Comment.
13.2- Test the normality of the data.
13.3- Perform a Student test to check whether Michelson's measures invalidate the value of c proposed by Cornu.
13.4- What value for the speed of light could Michelson propose after these twenty experiments?

Solution. Erratum: the printed values are Michelson's measures minus 299,000 km/s, not minus 299,990 (the convention of R's `morley` data set, whose first run these values reproduce), since subtracting 299,990 would put c near 300,930 km/s, so Cornu's value corresponds to 990 in these units.
13.1- A sequence plot and a boxplot, with Cornu's value as a dashed line:

```r
light <- c(850, 740, 900, 1070, 930, 850, 950, 980, 980, 880,
           1000, 980, 930, 1050, 960, 810, 1000, 1000, 960, 960)
op <- par(mfrow = c(1, 2))
plot(light, type = "b", xlab = "Experiment", ylab = "Speed - 299,000 (km/s)")
abline(h = 990, lty = 2, col = "red")
```

```r
boxplot(light, ylab = "Speed − 299,000 (km/s)")
abline(h = 990, lty = 2, col = "red")
par(op)
```



The measures fluctuate between 740 and 1,070 with no visible trend over the experiments, so treating them as identically distributed is reasonable; the distribution is roughly symmetric with a slightly longer lower tail, and most measures (the whole box) lie at or below Cornu's value 990.

13.2- Shapiro-Wilk test (Section 13.3.3) of H_0: the data are normally distributed:

```r
shapiro.test(light)
```

```
        Shapiro-Wilk normality test

data:  light
W = 0.94593, p-value = 0.3095
```

With $p = 0.31 > 0.05$ normality is not rejected, so a Student test is justified.

13.3- Test $H_0 : \mu = 990$ (Cornu's $c = 299{,}990$ km/s) against $H_1 : \mu \neq 990$ with `t.test()` (Section 13.3.1):

```r
t.test(light, mu = 990)
```

```
        One Sample t-test

data:  light
t = -2.8189, df = 19, p-value = 0.01096
alternative hypothesis: true mean is not equal to 990
95 percent confidence interval:
 901.1333 976.8667
sample estimates:
mean of x
      939
```

With $p = 0.011 < 0.05$ we reject H_0: Michelson's measures invalidate Cornu's value at the 5% level (though not at the 1% level).

13.4- Michelson could propose the empirical mean, $c \approx 299{,}939$ km/s, with the 95% Student confidence interval of Section 13.2.1:

```r
299000 + c(estimate = mean(light), t.test(light)$conf.int)
```

```
estimate
299939.0 299901.1 299976.9
```

That is, $c \approx 299{,}939$ km/s with 95% confidence interval [299,901; 299,977] km/s.

11.11 Worksheet 13.W.C.5 — A few practical examples - Cholesterol levels

Problem 13.W.C.5. Worksheet 13.W.C.5 — A few practical examples — Cholesterol levels
Seventeen people with the same illness I are randomly assigned to two groups. The first group receives a placebo A and the second group receives a treatment B containing a vitamin. The relevant measure is capillary resistance. We get the following measurements:
Group A: 46.3 ; 42.5 ; 43.0 ; 43.9 ; 42.0 ; 41.5 ; 41.6 ; 44.4 ; 40.7
Group B: 47.1 ; 44.5 ; 45.8 ; 49.0 ; 44.6 ; 43.7 ; 44.5 ; 47.4
Assuming that the measure of capillary resistance is normally distributed, what can you conclude?

Solution. The vitamin treatment significantly increases capillary resistance ($p = 0.004$). The groups are independent, so compare the two means with a two-sample Student test (Section 13.3.1), after checking equality of variances with Fisher's test `var.test()`:

```r
A <- c(46.3, 42.5, 43.0, 43.9, 42.0, 41.5, 41.6, 44.4, 40.7)
B <- c(47.1, 44.5, 45.8, 49.0, 44.6, 43.7, 44.5, 47.4)
var.test(A, B)$p.value
t.test(A, B, var.equal = TRUE)
```

```
[1] 0.8710977

        Two Sample t-test

data:  A and B
t = -3.391, df = 15, p-value = 0.004032
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -4.799753 -1.094691
sample estimates:
mean of x mean of y
 42.87778  45.82500
```

Equal variances are not rejected ($p = 0.87$), and the Student test rejects $H_0 : \mu_A = \mu_B$ ($p = 0.004 < 0.05$): mean capillary resistance is about 2.9 units higher under treatment B (45.8 against 42.9; 95% CI for $\mu_A - \mu_B$: $[-4.80, -1.09]$), so the vitamin treatment is effective.

11.12 Worksheet 13.W.C.6 — A few practical examples - Treatment-death independence

Problem 13.W.C.6. Worksheet 13.W.C.6 — A few practical examples — Treatment-death independence
Two small groups of animals are infected by a virulent germ. The first group receives chemotherapy; the second group is not treated. We measure mortality after eight days in both groups.

	With treatment	Without treatment	Total
Dead	0	9	9
Survived	8	3	11
Total	8	12	20

Is mortality independent of treatment?

Solution. No: Fisher's exact test (Section 13.3.2) rejects independence with $p = 0.0014$. The expected counts under independence are below 5, so the χ^2 test is not valid here and `fisher.test()` is the right tool:

```r
tab <- matrix(c(0, 8, 9, 3), nrow = 2,
              dimnames = list(c("Dead", "Survived"), c("With", "Without")))
suppressWarnings(chisq.test(tab)$expected)
fisher.test(tab)$p.value
```

```
         With Without
Dead      3.6     5.4
Survived  4.4     6.6
```

```
[1] 0.001381281
```

We reject H_0: mortality and treatment are independent. Mortality depends on treatment: none of the 8 treated animals died, against 9 of the 12 untreated ones.

11.13 Worksheet 13.W.C.7 — A few practical examples - Number of patients in the emergency ward

Problem 13.W.C.7. Worksheet 13.W.C.7 — A few practical examples — Number of patients in the emergency ward
To study the variation of the number of emergency cases in a hospital, the number of patients was counted for the months of June, July and August. The results are:

	June	July	August
Number of patients	1,500	1,600	1,450
Number of emergency patients	675	720	610

Can we conclude that the proportion of emergency cases is the same every month?

Solution. We cannot reject that it is the same: the test of equality of several proportions, `prop.test()` (Section 13.3.1), does not reject $H_0 : p_{\text{June}} = p_{\text{July}} = p_{\text{August}}$ ($p = 0.18$):

```r
emerg <- c(June = 675, July = 720, August = 610)
total <- c(1500, 1600, 1450)
round(emerg / total, 3)
prop.test(emerg, total)
```

```
  June   July August
 0.450  0.450  0.421

        3-sample test for equality of proportions without continuity correction

data:  emerg out of total
X-squared = 3.4433, df = 2, p-value = 0.1788
alternative hypothesis: two.sided
sample estimates:
   prop 1    prop 2    prop 3
0.4500000 0.4500000 0.4206897
```

With $p = 0.18 > 0.05$ the observed proportions (45%, 45%, 42%) are compatible with a common proportion of emergency cases (about 44%) across the three months; the dip in August is within sampling variation. The authors' companion solution applies `chisq.test()` to the three proportions themselves, which is a goodness-of-fit test on non-counts and ignores the sample sizes; `prop.test()` is the correct test and reaches the same conclusion.

12 Simple and multiple linear regression

Contents

12.1 Exercises 14.1–14.7

Problem 14.1. Give the instruction to fit the model $Y = \beta_0 + \beta_1 X_1 + \epsilon$.

Solution. `lm(Y ~ X1)` (the intercept is included by default, Section 14.2). On simulated data (seed 1), reused in the following exercises:

```r
set.seed(1)
n <- 100
X1 <- runif(n, 0, 2); X2 <- rnorm(n)
Z <- factor(sample(c("a", "b", "c"), n, replace = TRUE))
Y <- 1 + 2*X1 - X2 + 0.5*X1*X2 + (Z == "b") + rnorm(n, sd = 0.5)
X3 <- rnorm(n)   # pure noise, used in 14.11–14.12
coef(lm(Y ~ X1))
```

```
(Intercept)          X1
   1.227759    2.081160
```

Problem 14.2. Give the instruction to fit the model $Y = \beta_1 X_1 + \epsilon$.

Solution. `lm(Y ~ -1 + X1)` (equivalently `lm(Y ~ X1 + 0)`): the `-1` removes the intercept.

```r
coef(lm(Y ~ -1 + X1))
```

```
      X1
3.018764
```

Problem 14.3. Give the instruction to fit the model $Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \epsilon$.

Solution. `lm(Y ~ X1 + X2)` (Section 14.3).

```r
coef(lm(Y ~ X1 + X2))
```

```
(Intercept)          X1          X2
  1.1301441   2.1661711  -0.5443446
```

Problem 14.4. Give the instruction to fit the model $Y = \beta_0 + \beta_1 X_1 \times \beta_2 X_2 + \beta_3 X_1 + \beta_4 X_2 + \epsilon$.

Solution. `lm(Y ~ X1 * X2)`, i.e. `lm(Y ~ X1 + X2 + X1:X2)` (Section 14.3.6); the printed "$\beta_1 X_1 \times \beta_2 X_2$" is a typo for the interaction term $\beta_1 X_1 X_2$, and a product of two coefficients would not be identifiable.

```r
coef(lm(Y ~ X1 * X2))
```

```
(Intercept)          X1          X2       X1:X2
  1.1014228   2.1782534  -0.9182888   0.3694867
```

Problem 14.5. Give the instruction to fit the model $Y = \beta_0 + \beta_1 X_1 + \beta_2 X_1^2 + \beta_3 X_1^4 + \epsilon$.

Solution. `lm(Y ~ X1 + I(X1^2) + I(X1^4))`: `I()` makes `^` an arithmetic power rather than a formula operator (Section 14.3.10).

```r
coef(lm(Y ~ X1 + I(X1^2) + I(X1^4)))
```

```
 (Intercept)           X1      I(X1^2)      I(X1^4)
1.4025191267 1.6061815730 0.2324587625 0.0006218695
```

Problem 14.6. Which instruction performs a partial Fisher test?

Solution. `anova(mod1, mod2)`, where `mod1` is the sub-model nested in `mod2` (Section 14.3.4, Table 14.2). Testing $H_0 : \beta_2 = \beta_3 = 0$ in $Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_1 X_2 + \epsilon$:

```r
mod1 <- lm(Y ~ X1)
mod2 <- lm(Y ~ X1 + X2 + X1:X2)
anova(mod1, mod2)
```

```
Analysis of Variance Table

Model 1: Y ~ X1
Model 2: Y ~ X1 + X2 + X1:X2
  Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1     98 80.038
2     96 50.770  2    29.268 27.671 3.242e-10 ***
```

With $F = 27.67$ on $(2, 96)$ degrees of freedom and $p \approx 3 \times 10^{-10}$, H_0 is rejected: X_2 and the interaction jointly contribute to explaining Y given X_1.

Problem 14.7. Which function recovers the residuals of a model?

Solution. `residuals()` (alias `resid()`), applied to the fitted `lm` object; `rstandard()` and `rstudent()` give the standardized and studentized versions (Section 14.3.9).

```r
head(round(residuals(mod2), 3), 4)
```

```
    1     2     3     4
0.385 -0.972 -0.235 -0.177
```

12.2 Exercises 14.8–14.12

Problem 14.8. Which function gives the estimates of a regression model?

Solution. `coef()` (alias `coefficients()`) returns the estimated coefficients $\hat{\beta}_j$; `summary(lm())` (or its `$coefficients` component) adds their standard errors, t statistics and p-values.

```r
coef(mod2)
round(summary(mod2)$coefficients, 4)
```

```
(Intercept)          X1          X2       X1:X2
  1.1014228   2.1782534  -0.9182888   0.3694867
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.1014     0.1600  6.8820    0.000
X1            2.1783     0.1372 15.8773    0.000
X2           -0.9183     0.1641 -5.5974    0.000
X1:X2         0.3695     0.1426  2.5915    0.011
```

Problem 14.9. Let Z be a qualitative variable. Which function should you use to fit a regression model with Z as the explanatory variable?

Solution. `factor()` inside the formula, `lm(Y ~ factor(Z))`, so that Z is coded by indicator variables against a reference level (Section 14.3.5; `relevel()` changes the reference).

```r
coef(lm(Y ~ factor(Z)))
```

```
(Intercept)  factor(Z)b  factor(Z)c
  2.8932267   1.4785262   0.2750768
```

Problem 14.10. Give the instruction to fit the polynomial model $Y = \beta_0 + \beta_1 X^1 + \beta_2 X^2 + \beta_3 X^3 + \epsilon$.

Solution. `lm(Y ~ poly(X, 3, raw = TRUE))`, or equivalently `lm(Y ~ X + I(X^2) + I(X^3))` (Section 14.3.10); `raw = TRUE` gives the plain powers rather than orthogonal polynomials. With `X1` as X:

```r
coef(lm(Y ~ poly(X1, 3, raw = TRUE)))
```

```
             (Intercept) poly(X1, 3, raw = TRUE)1 poly(X1, 3, raw = TRUE)2
              1.38012619               1.72726144               0.08161453
poly(X1, 3, raw = TRUE)3
              0.05228201
```

Problem 14.11. Which function performs forward selection?

Solution. `add1(..., test = "F")`, applied repeatedly from the null model, adding at each step the most significant variable while its p-value is below α (Section 14.3.8); `step(..., direction = "forward")` automates the search with the AIC.

```r
add1(lm(Y ~ 1), ~ X1 + X2 + X3 + Z, test = "F")
fw <- step(lm(Y ~ 1), scope = ~ X1 + X2 + X3 + Z,
           direction = "forward", trace = 0)
formula(fw)
```

```
Single term additions

Model:
Y ~ 1
       Df Sum of Sq     RSS     AIC  F value    Pr(>F)
<none>              202.846  72.728
X1      1   122.809  80.038 -18.267 150.3694 < 2.2e-16 ***
X2      1    16.530 186.316  66.228   8.6947   0.00399 **
X3      1     0.000 202.846  74.728   0.0002   0.98793
Z       2    37.512 165.334  56.280  11.0041 4.931e-05 ***
Y ~ X1 + X2 + Z
```

X_1 enters first (largest F, $p < 2.2 \times 10^{-16}$), and the automated search stops at `Y ~ X1 + X2 + Z`, correctly leaving out the pure-noise X_3.

Problem 14.12. Which function performs backward selection?

Solution. `drop1(..., test = "F")`, applied repeatedly from the full model, deleting at each step the least significant variable while its p-value exceeds α (Section 14.3.8); `step(..., direction = "backward")` automates it with the AIC.

```r
drop1(lm(Y ~ X1 + X2 + X3 + Z), test = "F")
bw <- step(lm(Y ~ X1 + X2 + X3 + Z), direction = "backward", trace = 0)
formula(bw)
```

```
Single term deletions

Model:
Y ~ X1 + X2 + X3 + Z
       Df Sum of Sq     RSS     AIC  F value    Pr(>F)
<none>               34.560 -94.248
X1      1   113.487 148.047  49.236 308.6774 < 2.2e-16 ***
X2      1    25.060  59.620 -41.718  68.1624 9.241e-13 ***
X3      1     0.028  34.588 -96.168   0.0758    0.7837
Z       2    19.739  54.299 -53.067  26.8445 5.993e-10 ***
Y ~ X1 + X2 + Z
```

X_3 has the largest p-value (0.78) and is deleted; all remaining terms are significant, so both procedures select `Y ~ X1 + X2 + Z`.

12.3 Worksheet 14.W.A.1 — Study of simple linear regression - Study of synthetic data

Problem 14.W.A.1. Worksheet 14.W.A.1 — Study of simple linear regression — Study of synthetic data

14.1- Simulate a dataset (x_i, y_i), $i = 1, \ldots, n$ from a simple linear regression model. To this end:

- choose the true parameters β_0 and β_1, as well as $\sigma > 0$;
- simulate the vector of errors e of size n from a normal distribution $\mathcal{N}(0, \sigma^2)$;
- simulate the vector of values of the explanatory variable x of size n from a uniform distribution over $[0, t]$ where t is a positive real number of your choosing;
- construct the vector of values of the explained variable y of size n from the linear regression model.

14.2- Plot the n points (x_i, y_i).

14.3- Give an estimate of the regression parameters and of the error variance.

14.4- Analyse the residuals to validate the model:

- plot the residuals against the fitted values;
- plot the fitted values against the observed values;
- draw a plot to check the normality of residuals.

14.5- Change the values of n and σ to understand the consequences on the precision of the regression parameter estimates (in terms of variance).

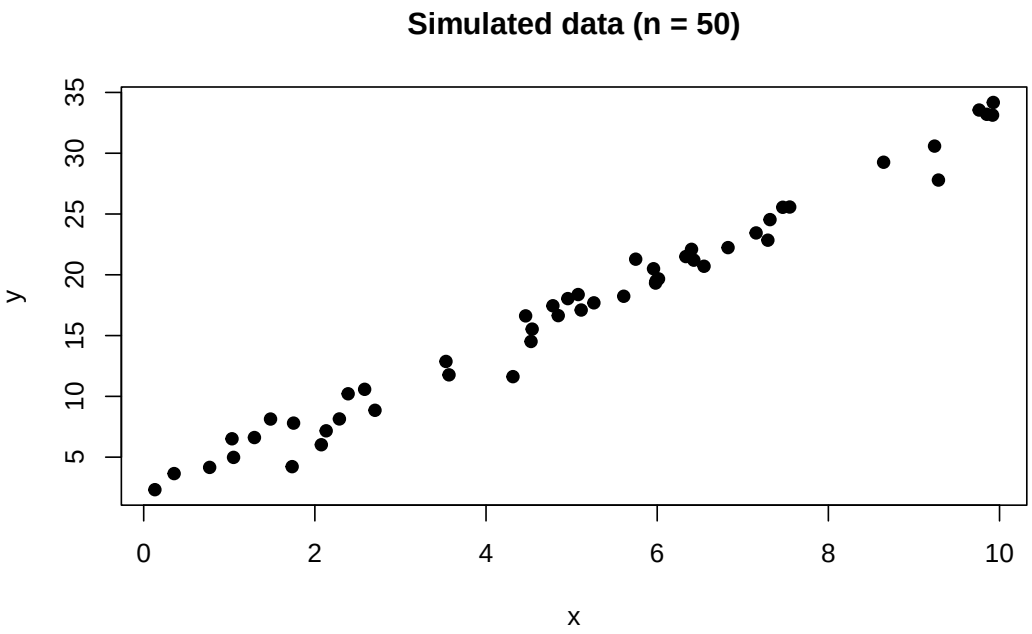
Solution.

14.1- With $\beta_0 = 2$, $\beta_1 = 3$, $\sigma = 1.5$, $n = 50$ and $t = 10$ (seed 1), the model $y_i = \beta_0 + \beta_1 x_i + e_i$ is simulated by:

```r
set.seed(1)
n <- 50; beta0 <- 2; beta1 <- 3; sigma <- 1.5; t <- 10
e <- rnorm(n, mean = 0, sd = sigma)
x <- runif(n, min = 0, max = t)
y <- beta0 + beta1 * x + e
```

14.2- The points lie along a straight line of slope about 3 with a roughly constant spread.

```r
plot(x, y, pch = 19, main = "Simulated data (n = 50)")
```



14.3- $\hat{\beta}_0 = 1.53$, $\hat{\beta}_1 = 3.12$ and $\hat{\sigma}^2 = 1.47$ (the residual mean square, Section 14.2.2), to be compared with the true values 2, 3 and $1.5^2 = 2.25$; with only 48 residual degrees of freedom the variance estimate

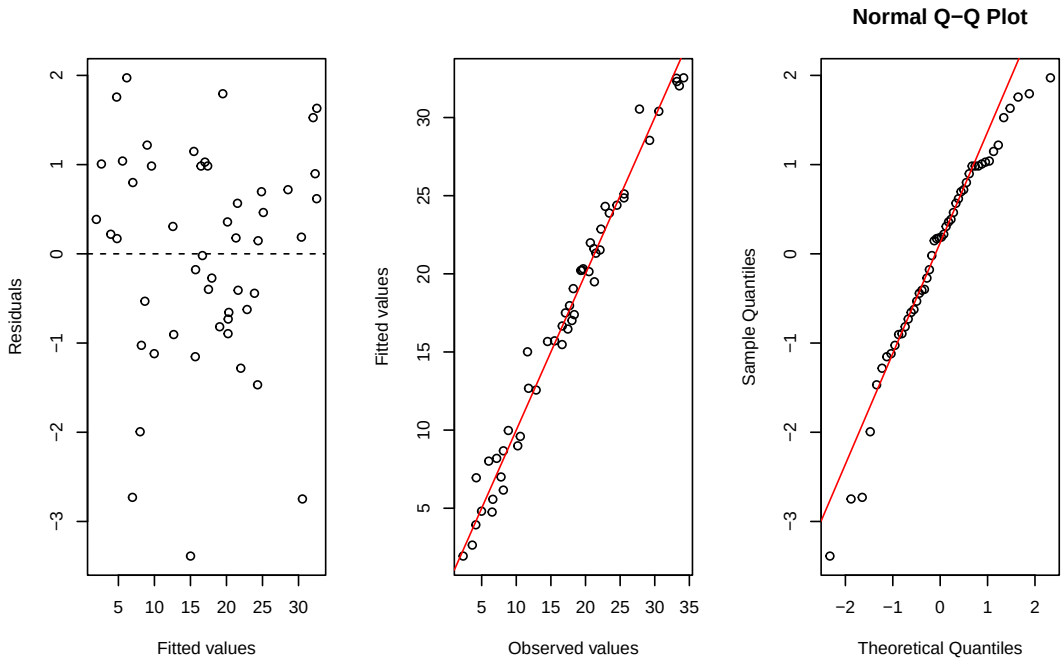
is the least precise of the three.

```r
model <- lm(y ~ x)
coef(model)
summary(model)$sigma^2
```

```
(Intercept)           x
   1.530688    3.124003
[1] 1.466543
```

14.4- The residuals scatter randomly around 0 with constant spread, the fitted values follow the line $\hat{y} = y$, and the normal Q-Q plot is close to a straight line (Shapiro-Wilk $p = 0.057$), so the model is validated, as expected for data generated from it (Section 14.2.4).

```r
par(mfrow = c(1, 3))
plot(fitted(model), residuals(model), xlab = "Fitted values", ylab = "Residuals")
abline(h = 0, lty = 2)
plot(y, fitted(model), xlab = "Observed values", ylab = "Fitted values")
abline(0, 1, col = "red")
qqnorm(residuals(model)); qqline(residuals(model), col = "red")
shapiro.test(residuals(model))
```




```
        Shapiro-Wilk normality test

data:  residuals(model)
W = 0.95534, p-value = 0.05673
```

14.5- Repeating the simulation 1000 times for each (n, σ) (seed 1) and taking the empirical variance of the estimates shows that both variances grow like σ^2 and shrink like $1/n$: multiplying σ by 10 multiplies them by about 100, multiplying n by 25 divides them by about 25, in line with $\text{Var}(\hat{\beta}_1) = \sigma^2 / \sum_i (x_i - \bar{x})^2$.

```r
sim <- function(n, sigma, B = 1000, t = 10) {
  est <- replicate(B, {
    x <- runif(n, 0, t)
    y <- 2 + 3 * x + rnorm(n, 0, sigma)
    coef(lm(y ~ x))
  })
  apply(est, 1, var)
}
set.seed(1)
grid <- expand.grid(n = c(20, 100, 500), sigma = c(0.5, 1.5, 5))
res <- t(mapply(sim, grid$n, grid$sigma))
```

```r
colnames(res) <- c("var(b0)", "var(b1)")
cbind(grid, signif(res, 3))
```

```
    n sigma var(b0)  var(b1)
1  20   0.5 0.05060 1.60e-03
2 100   0.5 0.01090 3.41e-04
3 500   0.5 0.00204 6.07e-05
4  20   1.5 0.46800 1.44e-02
5 100   1.5 0.08710 2.51e-03
6 500   1.5 0.01780 5.35e-04
7  20   5.0 5.29000 1.51e-01
8 100   5.0 0.99800 2.96e-02
9 500   5.0 0.21500 6.53e-03
```

12.4 Worksheet 14.W.A.2 — Study of simple linear regression - Study of intima-media

Problem 14.W.A.2. Worksheet 14.W.A.2 — Study of simple linear regression — Study of intima-media
In the "Intima-media" study, we wish to study the relationship between intima-media thickness and age.
14.1- Download the intima-media data file.
14.2- Plot variable `measure` as a function of variable `AGE`. Describe this scatter plot.
14.3- Is there a link between these variables? Explain how to measure the severeness of the link.
14.4- We now wish to fit a regression line on this scatter plot:

- propose a regression model and estimate the parameters of the model;
- draw the regression line over the scatter plot.

14.5- Analyse the residuals to validate the model.
14.6- Give a prediction interval for intima-media thickness for a 33 years old person.
14.7- Give a confidence interval for the average intima-media thickness of 33 years old people.
14.8- Propose a model to increase the predictive power of intima-media thickness, using only `AGE` as an explanatory variable.

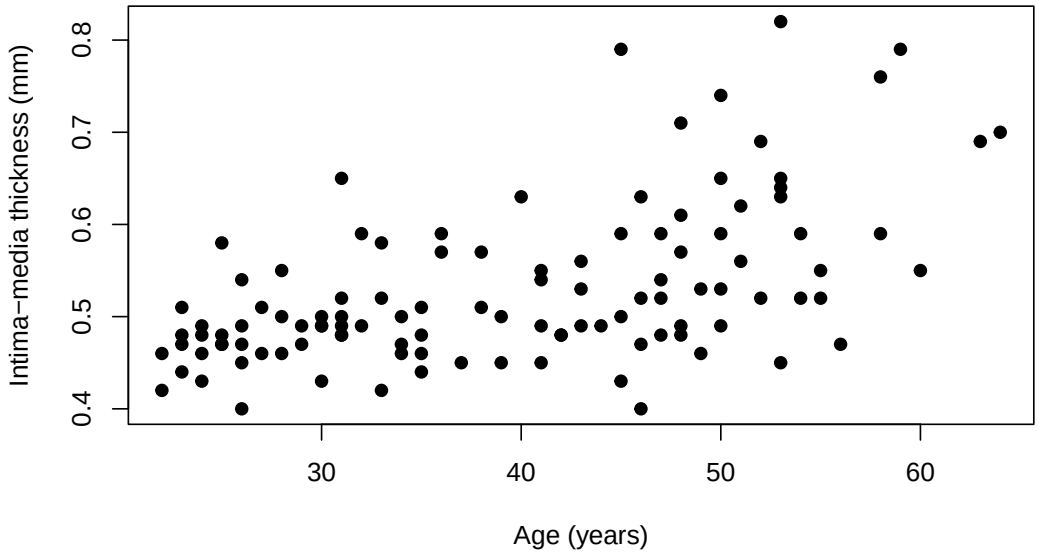
Solution.
14.1- The file uses single spaces as separators (empty fields are missing values) and a decimal comma, so it is read with `sep = " "` and `dec = ","`:

```r
url <- "http://www.biostatisticien.eu/springeR/Intima_Media_Thickness.txt"
intima <- read.table(url, header = TRUE, sep = " ", dec = ",")
str(intima[, c("AGE", "measure")])
```

```
'data.frame':        110 obs. of  2 variables:
 $ AGE    : int  33 33 53 42 53 50 22 26 50 47 ...
 $ measure: num  0.52 0.42 0.65 0.48 0.45 0.49 0.42 0.45 0.65 0.52 ...
```

14.2- The cloud of the 110 subjects (aged 22 to 64, thickness 0.40 to 0.82 mm) rises with age and fans out: thickness is tightly grouped around 0.45-0.50 mm before 35 and much more dispersed, with several high values, after 45.

```r
plot(measure ~ AGE, data = intima, pch = 19,
     xlab = "Age (years)", ylab = "Intima-media thickness (mm)")
```



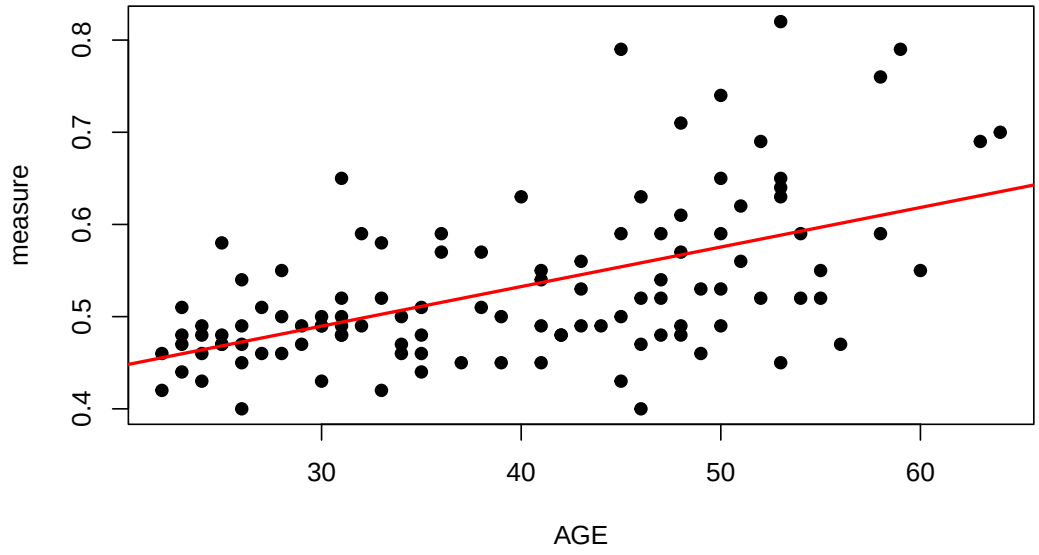
14.3- Yes: the link is positive and roughly linear. Its strength is measured by Pearson's linear correlation coefficient $r = 0.55$, and $H_0 : \rho = 0$ is rejected ($p = 4 \times 10^{-10}$); equivalently $R^2 = r^2 = 0.31$ of the variability of thickness is explained by age.

```r
cor.test(~ AGE + measure, data = intima)
```

```
        Pearson's product-moment correlation

data:  AGE and measure
t = 6.8862, df = 108, p-value = 3.953e-10
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.4072451 0.6702836
sample estimates:
      cor
0.5523669
```

14.4- The model is $\text{measure}_i = \beta_0 + \beta_1 \text{AGE}_i + \epsilon_i$ with ϵ_i i.i.d. $\mathcal{N}(0, \sigma^2)$ (Section 14.2). The fit gives $\hat{\beta}_0 = 0.361$ mm, $\hat{\beta}_1 = 0.00429$ mm per year (about 0.043 mm per decade, significantly non-zero, $p = 4 \times 10^{-10}$) and $\hat{\sigma} = 0.0726$.

```r
model <- lm(measure ~ AGE, data = intima)
summary(model)
plot(measure ~ AGE, data = intima, pch = 19)
abline(model, col = "red", lwd = 2)
```

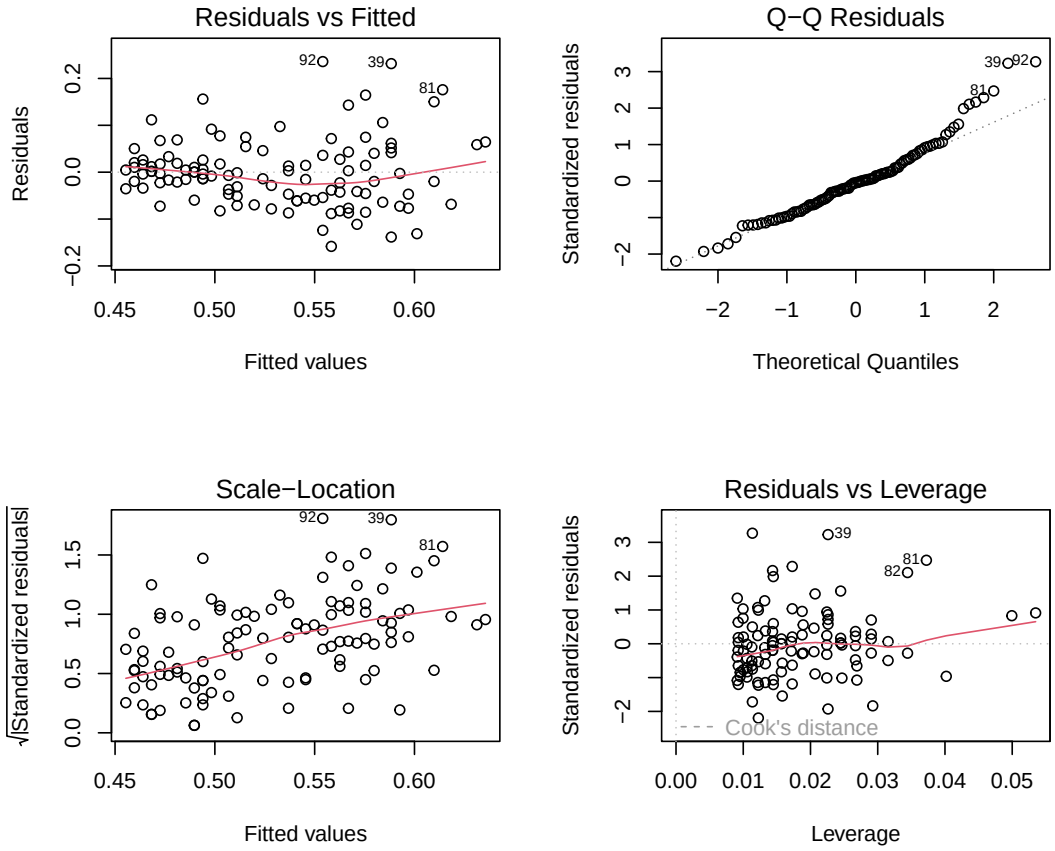



```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.3610255  0.0255330  14.140  < 2e-16 ***
AGE         0.0042897  0.0006229   6.886 3.95e-10 ***
...
Residual standard error: 0.07257 on 108 degrees of freedom
Multiple R-squared:  0.3051,        Adjusted R-squared:  0.2987
F-statistic: 47.42 on 1 and 108 DF,  p-value: 3.953e-10
```

(output truncated to the coefficient table and fit summary)

14.5- The model is only partly validated. The residuals are centred with no strong trend, but their spread grows with the fitted values (Scale-Location plot; Breusch-Pagan $p = 0.0004$), and the Q-Q plot bends upwards at the right with subjects 39, 81, 92 standing out, so the residuals are right-skewed rather than normal (Shapiro-Wilk $p = 0.002$). No point has a large leverage or Cook's distance (Section 14.2.4), so the line itself is trustworthy, but intervals based on normality with constant variance should be read with caution.

```r
par(mfrow = c(2, 2))
plot(model)
shapiro.test(residuals(model))
library(lmtest)
bptest(model)
```




```
        Shapiro-Wilk normality test

data:  residuals(model)
W = 0.95936, p-value = 0.002005

        studentized Breusch-Pagan test

data:  model
BP = 12.51, df = 1, p-value = 0.0004048
```

14.6- A 95% prediction interval for the thickness of one 33-year-old is $[0.358, 0.647]$ mm, around the prediction 0.503 mm (Section 14.2.3).

```r
new <- data.frame(AGE = 33)
predict(model, new, interval = "prediction")
```

```
        fit       lwr      upr
1 0.5025848 0.3578677 0.647302
```

14.7- A 95% confidence interval for the mean thickness of 33-year-olds is $[0.487, 0.518]$ mm, much narrower than the prediction interval because it ignores the individual error ϵ.

```r
predict(model, new, interval = "confidence")
```

```
        fit       lwr       upr
1 0.5025848 0.4867222 0.5184474
```

14.8- Since the cloud curves upwards after 45, a polynomial regression in `AGE` (Section 14.3.10), measure $= \beta_0 + \beta_1 \text{AGE} + \beta_2 \text{AGE}^2 + \epsilon$, is proposed. It raises the adjusted R^2 from 0.299 to 0.315, although the quadratic term is only borderline (partial Fisher test $p = 0.061$), and a cubic term brings nothing more ($p = 0.41$).

```r
model2 <- lm(measure ~ poly(AGE, 2, raw = TRUE), data = intima)
model3 <- lm(measure ~ poly(AGE, 3, raw = TRUE), data = intima)
anova(model, model2)
anova(model2, model3)
```

```r
sapply(list(model, model2, model3), function(m) summary(m)$adj.r.squared)
```

```
Analysis of Variance Table

Model 1: measure ~ AGE
Model 2: measure ~ poly(AGE, 2, raw = TRUE)
  Res.Df     RSS Df Sum of Sq      F  Pr(>F)
1    108 0.56876
2    107 0.55031  1  0.018452 3.5878 0.06091 .
...
Analysis of Variance Table

Model 1: measure ~ poly(AGE, 2, raw = TRUE)
Model 2: measure ~ poly(AGE, 3, raw = TRUE)
  Res.Df     RSS Df Sum of Sq      F Pr(>F)
1    107 0.55031
2    106 0.54684  1  0.003473 0.6732 0.4138
[1] 0.2986750 0.3150862 0.3129880
```

12.5 Worksheet 14.W.B.1 — Study of multiple linear regression - Study of intima-media

Problem 14.W.B.1. Worksheet 14.W.B.1 — Study of multiple linear regression — Study of intima-media

In the previous practical, we looked at the relationship between intima-media thickness and age. We now wish to fit a regression model on all variables which may explain variations in intima-media thickness. The study will rely on the following variables: `AGE`, `SPORT`, `alcohol`, `packyear` and the variable `BMI` which you must create from variables `height`, `weight`.

We are mostly interested in tobacco, through the variable `packyear` as main exposure factor. We therefore decide to keep this variable in the model even if it is not significant.

14.1- Draw scatter plots of all pairs of variables (explained and explanatory). Do you suspect any issues with collinearity?

14.2- Perform a univariate analysis of intima-media thickness of each explanatory variable.

14.3- We only keep the explanatory variables associated with significance level $p < 0.25$ in the univariate analysis. One by one, test all possible interactions between the selected explanatory variables and the main exposure variable `packyear`.

14.4- Estimate and analyse the model with all variables which were declared significant in the univariate analyses ($\alpha = 25\%$) and all interaction terms significant at the 10% level.

14.5- Are the interaction terms still significant? Remove interaction terms which are no longer significant at the 10% level.

14.6- Starting with the model from the previous question, remove one by one all variables which are not significant at the 5% level, making sure that the removals do not make a big difference on the estimate of the coefficient associated with tobacco status.

14.7- Interpret the final model.

Solution. Read the intima-media file of Worksheet A with `read.table()` (Chapter 4); `packyear` is `NA` exactly for the 72 non-smokers (`tobacco` = 0), so it is set to 0, `BMI` is weight (kg) over squared height (m), and `alcohol` (coded 0, 1, 2) is a factor.

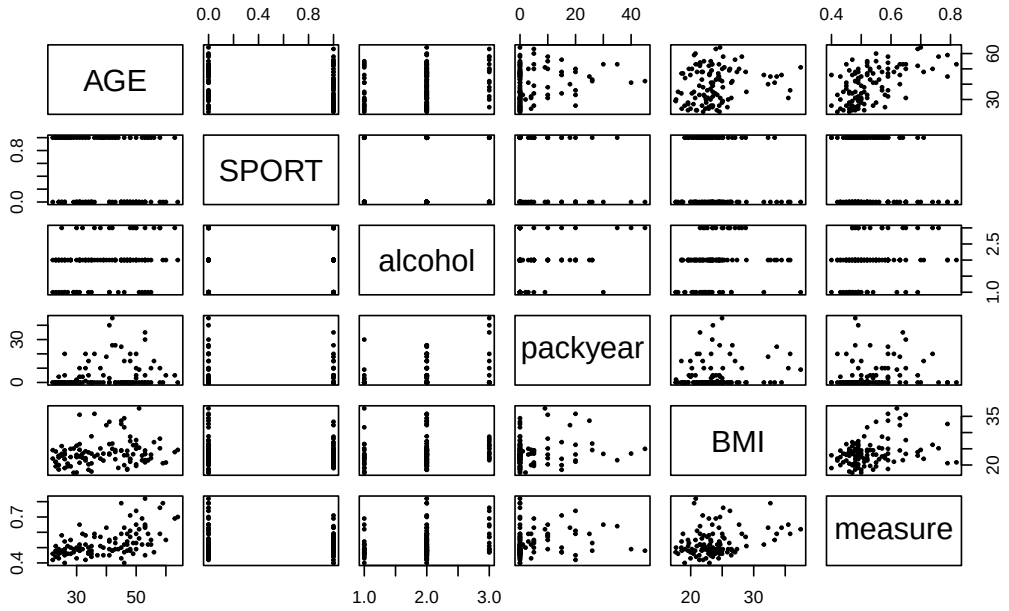
```r
url <- "http://www.biostatisticien.eu/springeR/Intima_Media_Thickness.txt"
im <- read.table(url, header = TRUE, sep = " ", dec = ",")
table(tobacco = im$tobacco, packyear.NA = is.na(im$packyear))
im$packyear[is.na(im$packyear)] <- 0
im$BMI <- im$weight / (im$height / 100)^2
my.data <- data.frame(AGE = im$AGE, SPORT = im$SPORT,
                      alcohol = factor(im$alcohol), packyear = im$packyear,
                      BMI = im$BMI, measure = im$measure)
```

```
       packyear.NA
tobacco FALSE TRUE
```

```
0     0   72
1    18    0
2    20    0
```

14.1- `pairs()` draws every pairwise scatter plot; the correlation matrix quantifies what it shows.

```r
pairs(my.data, pch = 20, cex = 0.6)
round(cor(data.matrix(my.data)), 2)
```




```
          AGE SPORT alcohol packyear   BMI measure
AGE      1.00 -0.17    0.24     0.19  0.18    0.55
SPORT   -0.17  1.00    0.03    -0.06 -0.13   -0.10
alcohol  0.24  0.03    1.00     0.26  0.15    0.24
packyear 0.19 -0.06    0.26     1.00  0.17    0.15
BMI      0.18 -0.13    0.15     0.17  1.00    0.31
measure  0.55 -0.10    0.24     0.15  0.31    1.00
```

The `measure` row shows a clear linear trend with `AGE` ($r = 0.55$) and a weaker one with `BMI` (0.31). Some pairs of explanatory variables show mild linear trends (`AGE`, `alcohol` and `packyear` are pairwise correlated at about 0.2 to 0.26), so a little collinearity is present, but every correlation between regressors is below 0.3: no serious collinearity problem is expected (this will be confirmed by the stability of the estimates below).

14.2- Fit one simple regression (one-way ANOVA for the factor `alcohol`) per explanatory variable and collect the p-value of its overall F test:

```r
vars <- c("AGE", "SPORT", "alcohol", "packyear", "BMI")
p.uni <- sapply(vars, function(v)
  anova(lm(reformulate(v, "measure"), data = my.data))[1, "Pr(>F)"])
round(p.uni, 4)
```

```
   AGE    SPORT  alcohol packyear      BMI
0.0000   0.3072   0.0448   0.1108   0.0011
```

Taken one at a time, `AGE` ($p < 10^{-4}$), `BMI` ($p = 0.001$) and `alcohol` ($p = 0.045$) are significantly associated with intima-media thickness at the 5% level, `packyear` is not ($p = 0.11$), and `SPORT` shows no association ($p = 0.31$).

14.3- At the 25% level we keep `AGE`, `alcohol`, `BMI` and `packyear` and drop `SPORT`. Each interaction with `packyear` is tested by a partial Fisher test (Section 14.3.4) comparing the additive model with the model containing the interaction:

```r
p.inter <- sapply(c("AGE", "alcohol", "BMI"), function(v) {
  m0 <- lm(reformulate(c(v, "packyear"), "measure"), data = my.data)
  m1 <- lm(reformulate(paste0(v, "*packyear"), "measure"), data = my.data)
  anova(m0, m1)[2, "Pr(>F)"]
```

```
})
round(p.inter, 4)
round(coef(summary(lm(measure ~ alcohol * packyear, data = my.data)))[5:6, ], 4)
```

```
    AGE alcohol     BMI
 0.7453  0.1031  0.5473
                 Estimate Std. Error t value Pr(>|t|)
alcohol1:packyear  -0.0048     0.0031 -1.5633   0.1210
alcohol2:packyear  -0.0066     0.0031 -2.1373   0.0349
```

The `AGE:packyear` and `BMI:packyear` interactions are clearly not significant. The `alcohol:packyear` interaction is borderline: its global test gives $p = 0.103$, but the coefficient for heavy drinkers (`alcohol2:packyear`) has $p = 0.035 < 0.10$, so we retain this interaction for the next step (as does the authors' companion solution).

14.4- The model contains `AGE`, `BMI`, `alcohol`, `packyear` and the `alcohol:packyear` interaction:

```
model.inter <- lm(measure ~ AGE + BMI + alcohol * packyear, data = my.data)
summary(model.inter)
```

```
Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)        0.2640114  0.0468079   5.640 1.52e-07 ***
AGE                0.0037386  0.0006504   5.748 9.44e-08 ***
BMI                0.0042187  0.0018080   2.333   0.0216 *
alcohol1           0.0185379  0.0187008   0.991   0.3239
alcohol2           0.0409030  0.0277387   1.475   0.1434
packyear           0.0028237  0.0024036   1.175   0.2428
alcohol1:packyear -0.0025591  0.0026442  -0.968   0.3354
alcohol2:packyear -0.0036977  0.0026613  -1.389   0.1677
...
Residual standard error: 0.07119 on 102 degrees of freedom
Multiple R-squared:  0.3685,        Adjusted R-squared:  0.3252
F-statistic: 8.503 on 7 and 102 DF,  p-value: 3.589e-08
```

(Call, residual quantiles and significance codes truncated.) The model is globally significant ($F = 8.50$ on 7 and 102 df, $p = 3.6 \times 10^{-8}$) and explains 37% of the variance; once adjusted for the other variables, only `AGE` and `BMI` have significant coefficients.

14.5- No: in the adjusted model neither interaction coefficient is significant ($p = 0.34$ and 0.17), and the partial Fisher test of both together gives $p = 0.37$, so the interaction is removed.

```
model.without.inter <- lm(measure ~ AGE + BMI + alcohol + packyear, data = my.data)
anova(model.without.inter, model.inter)
round(coef(summary(model.without.inter)), 5)
```

```
Analysis of Variance Table

Model 1: measure ~ AGE + BMI + alcohol + packyear
Model 2: measure ~ AGE + BMI + alcohol * packyear
  Res.Df     RSS Df Sum of Sq      F Pr(>F)
1    104 0.52700
2    102 0.51688  2  0.010127 0.9993 0.3717
            Estimate Std. Error  t value Pr(>|t|)
(Intercept)  0.25938    0.04637  5.59416  0.00000
AGE          0.00385    0.00064  5.98157  0.00000
BMI          0.00451    0.00178  2.53417  0.01276
alcohol1     0.01309    0.01729  0.75736  0.45055
alcohol2     0.02397    0.02471  0.97007  0.33426
packyear     0.00000    0.00078 -0.00150  0.99881
```

14.6- `packyear` is kept by design, so the only candidate for removal is `alcohol` (both of its coefficients have $p > 0.3$); a partial Fisher test compares the models with and without it:

```
model.final <- lm(measure ~ AGE + BMI + packyear, data = my.data)
anova(model.final, model.without.inter)
rbind(with.alcohol = coef(model.without.inter)["packyear"],
      without.alcohol = coef(model.final)["packyear"])
```

```
Analysis of Variance Table
```

```
Model 1: measure ~ AGE + BMI + packyear
Model 2: measure ~ AGE + BMI + alcohol + packyear
  Res.Df     RSS Df Sum of Sq      F Pr(>F)
1    106 0.53209
2    104 0.52700  2 0.0050855 0.5018 0.6069
                     packyear
with.alcohol    -1.167391e-06
without.alcohol  1.549257e-04
```

`alcohol` adds nothing once `AGE`, `BMI` and `packyear` are in the model ($p = 0.61$), so it is removed. The `packyear` coefficient moves from -0.000001 to 0.00015 mm per pack-year, a change that is tiny compared with its standard error (0.00076), so the removal does not alter the tobacco estimate. `AGE` and `BMI` remain significant at 5%, so the procedure stops.

14.7- The final model is measure $= \beta_0 + \beta_1\,\text{AGE} + \beta_2\,\text{BMI} + \beta_3\,\text{packyear} + \epsilon$:

```r
summary(model.final)
round(confint(model.final), 5)
```

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.2623458  0.0451913   5.805 6.77e-08 ***
AGE         0.0039677  0.0006272   6.325 6.14e-09 ***
BMI         0.0046588  0.0017665   2.637  0.00962 **
packyear    0.0001549  0.0007559   0.205  0.83800
...
Residual standard error: 0.07085 on 106 degrees of freedom
Multiple R-squared:  0.3499,        Adjusted R-squared:  0.3315
F-statistic: 19.02 on 3 and 106 DF,  p-value: 6.087e-10
               2.5 %  97.5 %
(Intercept)  0.17275 0.35194
AGE          0.00272 0.00521
BMI          0.00116 0.00816
packyear    -0.00134 0.00165
```

(Call, residual quantiles and significance codes truncated.) Intima-media thickness is explained by `AGE` and `BMI`, adjusted for tobacco exposure: whatever the number of pack-years smoked, the thickness increases on average by 0.0040 mm per year of age (95% CI 0.0027 to 0.0052), i.e. about 0.04 mm per decade, and by 0.0047 mm per unit of BMI (95% CI 0.0012 to 0.0082). Adjusted for age and BMI, tobacco has no detectable effect ($p = 0.84$, CI $[-0.0013, 0.0017]$ mm per pack-year): its weak crude association ($r = 0.15$) is absorbed by age, which is correlated with both. The model explains 35% of the variability of the thickness.

12.6 Worksheet 14.W.B.2 — Study of multiple linear regression - Study of unemployment rates

Problem 14.W.B.2. Worksheet 14.W.B.2 — Study of multiple linear regression — Study of unemployment rates

This practical studies unemployment rates from 1960 to 1993. The dataset `unemployment` is made of $n = 34$ yearly observations (from 1960 to 1993). Here is a description of the variables:

- `year`: year;
- `unemp`: unemployment rate;
- `gdprate`: rate of variation of Gross domestic product (GDP), representing economic growth;
- `govspend`: ratio of government spending and GDP, representing the degree of intervention of the state in the economy;
- `taxb`: tax burden, to see whether taxation of businesses has an impact on hiring policy, and hence on unemployment rates;
- `salav`: ratio of salaries to added value, to know the influence of cost at hiring;
- `infl`: inflation rate, to verify the inverse relationship between unemployment and inflation, defined in the Philips curve.

14.1- We consider a linear model explaining variable `unemp` as a function of variable `gdprate` only. Download the dataset http://www.biostatisticien.eu/springeR/unemployment.RData.

Perform a complete analysis of the underlying simple linear regression model.
14.2- We consider a multiple linear model explaining variable `unemp` as a function of all explanatory variables in the dataset (except variable `year`). Give the correlation matrix of all these variables.
14.3- Draw scatter plots of all pairs of variables.
14.4- Which explanatory variables seem to make the biggest contribution? Do you suspect collinearity between regressors?
14.5- Present the results of the multiple linear regression model with explanatory variables.
14.6- Calculate the `VIF` associated with each explanatory variable.
14.7- Perform backward variable selection with threshold $\alpha = 0.2$.
14.8- Present the final model.
14.9- Suppose we do not know the value of `unemp` in 1993. Can you predict its value, and calculate a 95% prediction interval?
14.10- What is the observed value of `unemp` in 1993? Is this surprising?
C- Study of polynomial regression — Study of synthetic data
14.1- Simulate a sample of size $n = 100$ from the following model:

$$Y = X + 2X^2 + 3.5X^3 - 2.3X^4 + \epsilon$$

where X follows a uniform distribution over $[-2, +2]$ and ϵ follows a $\mathcal{N}(0, 1)$ distribution.
14.2- Draw the scatter plot and the simulated polynomial line.
14.3- Fit a simple linear regression model. Remember to analyse the residuals.
14.4- Fit a polynomial regression, using a polynomial of degree 4. Draw the estimated model over the scatter plot.

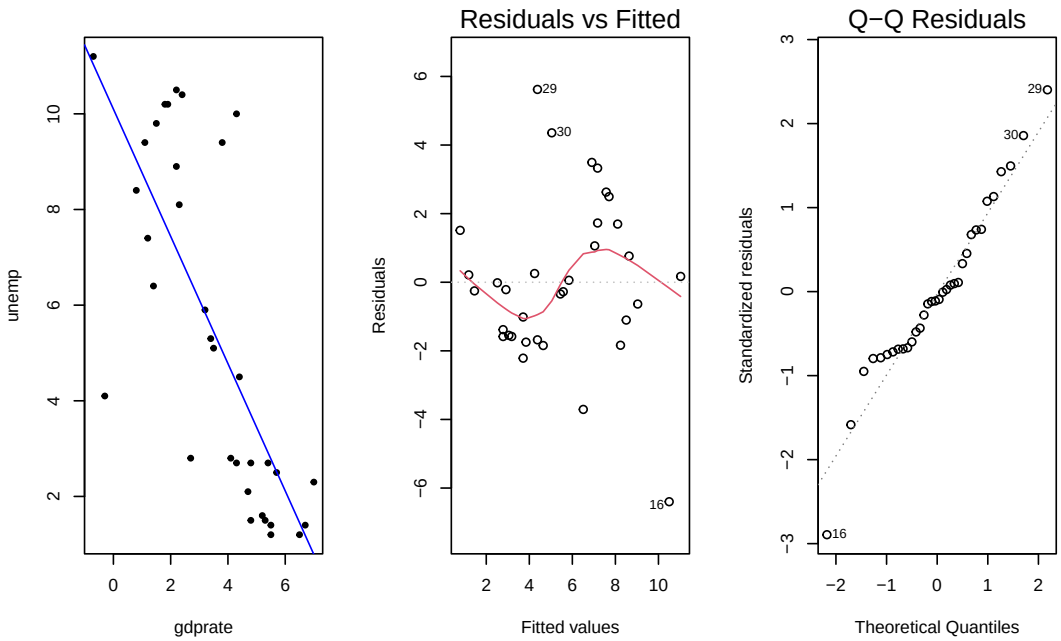
Solution.
14.1- The model is $\text{unemp}_i = \beta_0 + \beta_1\, \text{gdprate}_i + \epsilon_i$; load the file with `load()`, then fit it with `lm()` and validate it with the residual plots of Section 14.2:

```
load(url("http://www.biostatisticien.eu/springeR/unemployment.RData"))
model.gdprate <- lm(unemp ~ gdprate, data = unemployment)
summary(model.gdprate)
confint(model.gdprate)
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  10.0996     0.8293   12.18 1.48e-13 ***
gdprate      -1.3304     0.2069   -6.43 3.14e-07 ***
...
Residual standard error: 2.381 on 32 degrees of freedom
Multiple R-squared:  0.5637,        Adjusted R-squared:  0.5501
F-statistic: 41.34 on 1 and 32 DF,  p-value: 3.144e-07

                2.5 %     97.5 %
(Intercept)  8.410412 11.7888025
gdprate     -1.751865 -0.9089548
```

(Call, residual quantiles and significance codes truncated.) Growth has a highly significant negative effect ($H_0 : \beta_1 = 0$ rejected, $p = 3 \times 10^{-7}$): each extra point of GDP growth goes with 1.33 points less unemployment (95% CI $[-1.75, -0.91]$), and the model explains 56% of the variance.

```
par(mfrow = c(1, 3))
plot(unemp ~ gdprate, data = unemployment, pch = 20)
abline(model.gdprate, col = "blue")
plot(model.gdprate, which = 1:2)
shapiro.test(residuals(model.gdprate))$p.value
lmtest::dwtest(model.gdprate)$p.value
```




```
[1] 0.3019621
[1] 8.392195e-06
```

The residuals are compatible with normality (Shapiro-Wilk $p = 0.30$), but the residuals-versus-fitted plot shows a wave rather than a horizontal band and the Durbin-Watson test ($p = 8 \times 10^{-6}$) detects strong positive autocorrelation of these yearly residuals: the model is misspecified (unemployment trends upwards over the period for reasons growth alone does not capture), so its standard errors and p-values are over-optimistic, which motivates the multiple model.

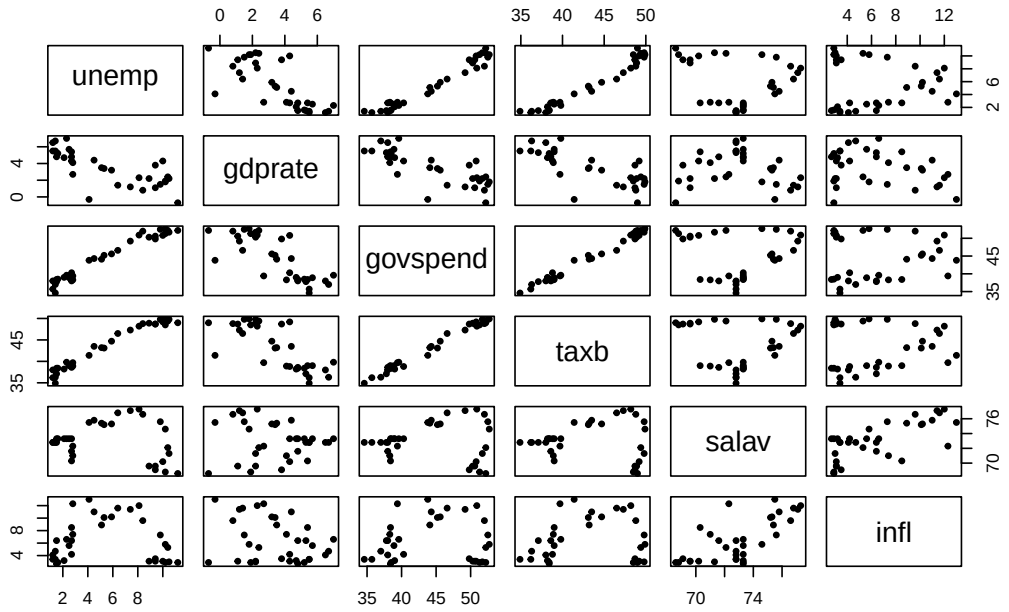
14.2- `cor()` on columns 2 to 7 (all but `year`):

```
round(cor(unemployment[, 2:7]), 2)
```

```
         unemp gdprate govspend  taxb salav  infl
unemp     1.00   -0.75     0.98  0.98 -0.17 -0.05
gdprate  -0.75    1.00    -0.78 -0.75 -0.11 -0.30
govspend  0.98   -0.78     1.00  0.99 -0.01  0.07
taxb      0.98   -0.75     0.99  1.00 -0.04  0.07
salav    -0.17   -0.11    -0.01 -0.04  1.00  0.70
infl     -0.05   -0.30     0.07  0.07  0.70  1.00
```

14.3- `pairs()`:

```
pairs(unemployment[, 2:7], pch = 20)
```



14.4- `govspend` and `taxb` ($r = 0.98$ with `unemp`) and then `gdprate` ($r = -0.75$) seem to contribute most; `salav` and `infl` are almost uncorrelated with `unemp`. Collinearity is strongly suspected: `govspend` and `taxb` are almost perfectly correlated ($r = 0.99$, the points lie on a line in the scatter plot), both are correlated with `gdprate` ($r \approx -0.75$ to -0.78), and `salav` and `infl` are correlated ($r = 0.70$).

14.5- The model is unemp $= \beta_0 + \beta_1$ gdprate $+ \beta_2$ govspend $+ \beta_3$ taxb $+ \beta_4$ salav $+ \beta_5$ infl $+ \epsilon$:

```
full.model <- lm(unemp ~ gdprate + govspend + taxb + salav + infl,
                 data = unemployment)
summary(full.model)
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -5.80283    3.86147  -1.503 0.144098
gdprate     -0.07188    0.07753  -0.927 0.361820
govspend     0.35855    0.12702   2.823 0.008665 **
taxb         0.22751    0.14324   1.588 0.123432
salav       -0.19195    0.05079  -3.779 0.000757 ***
infl        -0.03131    0.03961  -0.791 0.435873
...
Residual standard error: 0.469 on 28 degrees of freedom
Multiple R-squared:  0.9852,        Adjusted R-squared:  0.9826
F-statistic: 372.7 on 5 and 28 DF,  p-value: < 2.2e-16
```

(Call, residual quantiles and significance codes truncated.) The model is globally highly significant ($F = 372.7$, $p < 2.2 \times 10^{-16}$) and explains 98.5% of the variance. Adjusted for the others, only `govspend` (positive effect) and `salav` (negative effect) are significant at 5%; `gdprate`, strongly significant alone in 14.1, is no longer significant ($p = 0.36$) because its information is carried by the correlated `govspend` and `taxb`, and `taxb` itself is not significant ($p = 0.12$) despite $r = 0.98$ with `unemp`, a symptom of collinearity.

14.6- `vif()` from package `car` (Section 14.3.7):

```
library(car)
round(vif(full.model), 2)
```

```
gdprate govspend     taxb    salav     infl
   3.62    91.78    81.14     2.38     2.71
```

`govspend` (VIF 91.8) and `taxb` (VIF 81.1) are far above the usual threshold of 10: the variance of their estimates is inflated about 80 to 90 times by their collinearity, confirming 14.4; the other three VIFs are small.

14.7- Backward selection (Section 14.3.8) repeatedly applies `drop1(..., test = "F")` and removes the variable with the largest partial-F p-value while it exceeds 0.2:

```
model <- full.model
repeat {
  tab <- drop1(model, test = "F")[-1, c("F value", "Pr(>F)")]
  print(data.frame(F = round(tab[, 1], 3), p = signif(tab[, 2], 3),
                   row.names = rownames(tab)))
  worst <- rownames(tab)[which.max(tab[, "Pr(>F)"])]
  if (max(tab[, "Pr(>F)"]) <= 0.2) break
  cat("-> remove", worst, "\n\n")
  model <- update(model, as.formula(paste(". ~ . -", worst)))
}
```

```
             F        p
gdprate   0.859 0.362000
govspend  7.968 0.008660
taxb      2.523 0.123000
salav    14.282 0.000757
infl      0.625 0.436000
-> remove infl

             F        p
gdprate   0.398 5.33e-01
govspend 11.718 1.86e-03
taxb      1.984 1.70e-01
salav    43.079 3.44e-07
-> remove gdprate

             F        p
govspend 15.875 3.99e-04
taxb      1.714 2.00e-01
salav    43.597 2.62e-07
-> remove taxb

               F        p
govspend 1826.785 4.01e-29
salav      48.863 7.61e-08
```

`infl`, then `gdprate`, then `taxb` (by a hair: $p = 0.2005$) are removed; `govspend` and `salav` are both kept.

14.8- The final model is $\text{unemp} = \beta_0 + \beta_1\,\text{govspend} + \beta_2\,\text{salav} + \epsilon$:

```
final.model <- lm(unemp ~ govspend + salav, data = unemployment)
summary(final.model)
confint(final.model)
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.83284    2.46623  -1.149    0.259
govspend     0.56373    0.01319  42.741  < 2e-16 ***
salav       -0.22872    0.03272  -6.990 7.61e-08 ***
...
Residual standard error: 0.4665 on 31 degrees of freedom
Multiple R-squared:  0.9838,        Adjusted R-squared:  0.9827
F-statistic: 940.2 on 2 and 31 DF,  p-value: < 2.2e-16

                2.5 %     97.5 %
(Intercept) -7.8627567  2.1970816
govspend     0.5368330  0.5906335
salav       -0.2954518 -0.1619867
```

(Call, residual quantiles and significance codes truncated.) With only two regressors the model still explains 98.4% of the variance (adjusted R^2 0.983, as high as the full model's). Other things being equal, one more point of government spending in GDP goes with 0.56 more points of unemployment (95% CI $[0.54, 0.59]$), and one more point of the share of salaries in added value with 0.23 fewer points (95% CI $[-0.30, -0.16]$).

14.9- Yes: refit the final model without 1993 (as if `unemp` were unknown that year) and use

`predict(..., interval = "prediction")` (Section 14.3.3) at the 1993 values of `govspend` and `salav`:

```
model.92 <- lm(unemp ~ govspend + salav, data = unemployment,
               subset = year < 1993)
new93 <- unemployment[unemployment$year == 1993, c("govspend", "salav")]
new93
predict(model.92, newdata = new93, interval = "prediction")
```

```
   govspend salav
34     52.2  68.6
        fit      lwr      upr
34 10.84117 9.783461 11.89887
```

The predicted 1993 unemployment rate is 10.8%, with 95% prediction interval [9.8%, 11.9%]. (Predicting with `final.model`, fitted on all 34 years as in the book's solution, gives 10.9%, interval [9.9%, 11.9%].)

14.10- The observed value is 11.2%:

```
unemployment[unemployment$year >= 1990, ]
```

```
   year unemp gdprate govspend taxb salav infl
31 1990   8.9     2.2     50.3 48.9  69.6  3.1
32 1991   9.4     1.1     50.6 48.7  69.6  3.1
33 1992  10.2     1.9     51.3 48.5  68.8  2.9
34 1993  11.2    -0.7     52.2 49.0  68.6  2.9
```

It is not surprising: 11.2% lies inside the 95% prediction interval [9.8, 11.9], only 0.36 points above the prediction, even though 1993 was a recession year (`gdprate` $= -0.7$) that the model sees only through the rise in `govspend`.

C- Study of polynomial regression — Study of synthetic data

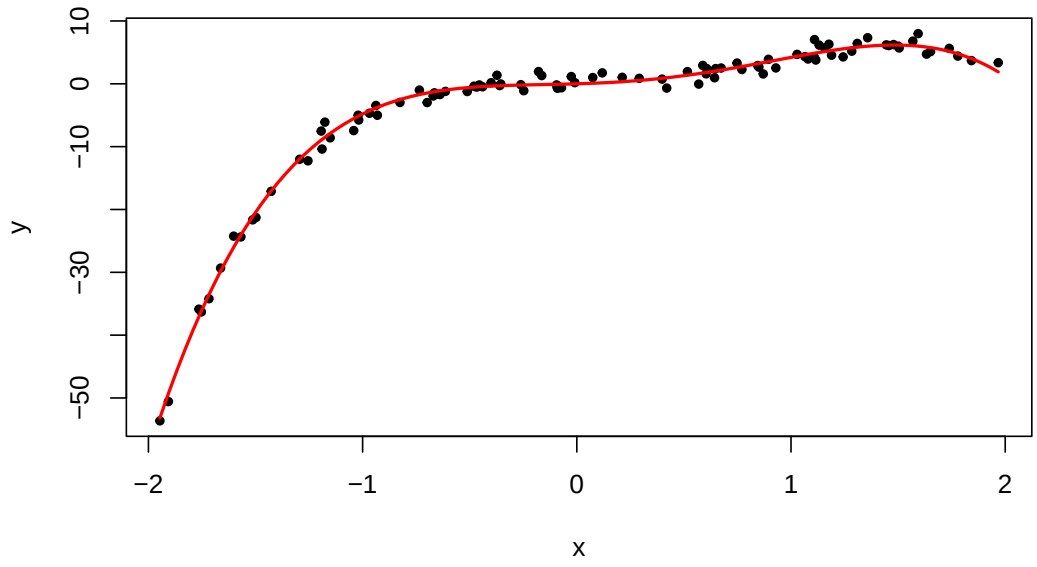
14.1- Draw X with `runif()` and ϵ with `rnorm()` (seed 1):

```
set.seed(1)
n <- 100
x <- runif(n, min = -2, max = 2)
eps <- rnorm(n)
y <- x + 2 * x^2 + 3.5 * x^3 - 2.3 * x^4 + eps
summary(y)
```

```
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-53.6361  -2.1966   0.4616  -2.6843   3.8145   7.9844
```

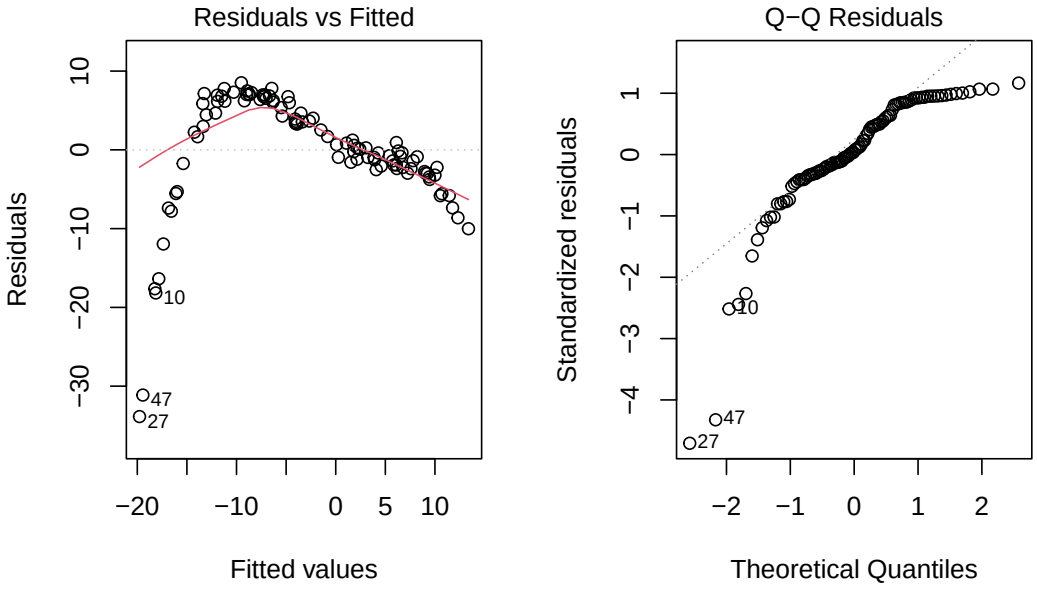
14.2- `plot()` for the points and `curve(..., add = TRUE)` for the true polynomial:

```
plot(y ~ x, pch = 20)
curve(x + 2 * x^2 + 3.5 * x^3 - 2.3 * x^4, add = TRUE, col = "red", lwd = 2)
```



14.3- The simple linear model $Y = \beta_0 + \beta_1 X + \epsilon$ is fitted with `lm(y ~ x)`:

```
simple.model <- lm(y ~ x)
summary(simple.model)
shapiro.test(residuals(simple.model))$p.value
par(mfrow = c(1, 2))
plot(simple.model, which = 1:2)
```

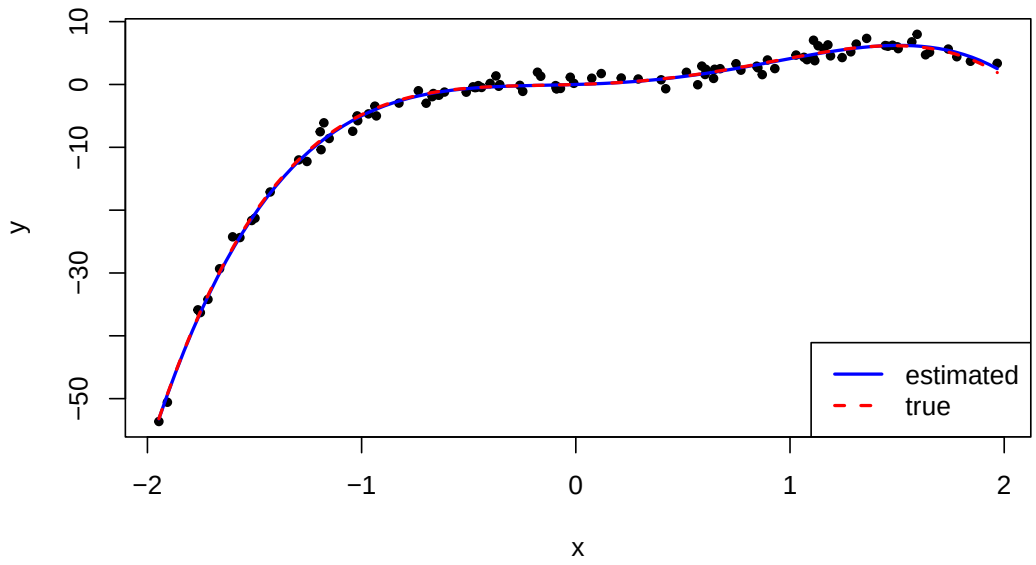



```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -3.2890     0.7382  -4.455 2.23e-05 ***
x             8.4705     0.6916  12.247  < 2e-16 ***
...
Residual standard error: 7.366 on 98 degrees of freedom
Multiple R-squared:  0.6048,        Adjusted R-squared:  0.6008
F-statistic:   150 on 1 and 98 DF,  p-value: < 2.2e-16

[1] 6.072915e-10
```

(Call, residual quantiles and significance codes truncated.) The slope is highly significant and $R^2 = 0.60$, yet the model is wrong: the residuals-versus-fitted plot shows a strong curved pattern instead of a horizontal band, the Q-Q plot a long left tail, and the Shapiro-Wilk test rejects normality ($p = 6 \times 10^{-10}$); the residual standard error (7.37) is far above the true $\sigma = 1$.

14.4- The degree-4 model without intercept, $Y = \beta_1 X + \beta_2 X^2 + \beta_3 X^3 + \beta_4 X^4 + \epsilon$, is `lm(y ~ -1 + poly(x, 4, raw = TRUE))` (Section 14.3.10):

```
poly.model <- lm(y ~ -1 + poly(x, 4, raw = TRUE))
summary(poly.model)
b <- coef(poly.model)
plot(y ~ x, pch = 20)
curve(b[1] * x + b[2] * x^2 + b[3] * x^3 + b[4] * x^4, add = TRUE,
      col = "blue", lwd = 2)
curve(x + 2 * x^2 + 3.5 * x^3 - 2.3 * x^4, add = TRUE, col = "red",
      lty = 2, lwd = 2)
legend("bottomright", c("estimated", "true"), col = c("blue", "red"),
       lty = 1:2, lwd = 2)
```




```
Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
poly(x, 4, raw = TRUE)1  1.00522    0.20608   4.878 4.25e-06 ***
poly(x, 4, raw = TRUE)2  1.79451    0.19309   9.294 4.90e-15 ***
poly(x, 4, raw = TRUE)3  3.53967    0.08800  40.223  < 2e-16 ***
poly(x, 4, raw = TRUE)4 -2.22662    0.07057 -31.554  < 2e-16 ***
...
Residual standard error: 0.9444 on 96 degrees of freedom
Multiple R-squared:  0.994,        Adjusted R-squared:  0.9937
F-statistic:  3950 on 4 and 96 DF,  p-value: < 2.2e-16
```

(Call, residual quantiles and significance codes truncated.) The estimates $(1.01, 1.79, 3.54, -2.23)$ are close to the true $(1, 2, 3.5, -2.3)$, the residual standard error 0.94 matches $\sigma = 1$, and the estimated curve is almost indistinguishable from the true one over the scatter plot.

12.7 Worksheet 14.W.B.3 — Study of multiple linear regression - Fitting a scatter plot with a polynomial

Problem 14.W.B.3. Worksheet 14.W.B.3 — Study of multiple linear regression — Fitting a scatter plot with a polynomial
Suppose you are asked to propose a model to predict a variable Y given an explanatory variable X. You are given a sample of size n.
14.1- Download the data file http://www.biostatisticien.eu/springeR/fitpoly.RData.
14.2- Draw a scatter plot of variable Y as a function of variable X.
14.3- Is there a linear relationship between these two variables? Fit a regression line on the previous plot.
14.4- Perform polynomial regression to fit the data better.
14.5- Draw the estimated polynomial over the scatter plot. Draw the confidence curve for the mean of Y for $X \in [-3.5, 3.5]$. Add the prediction interval of the model for $X \in [-3.5, 3.5]$.

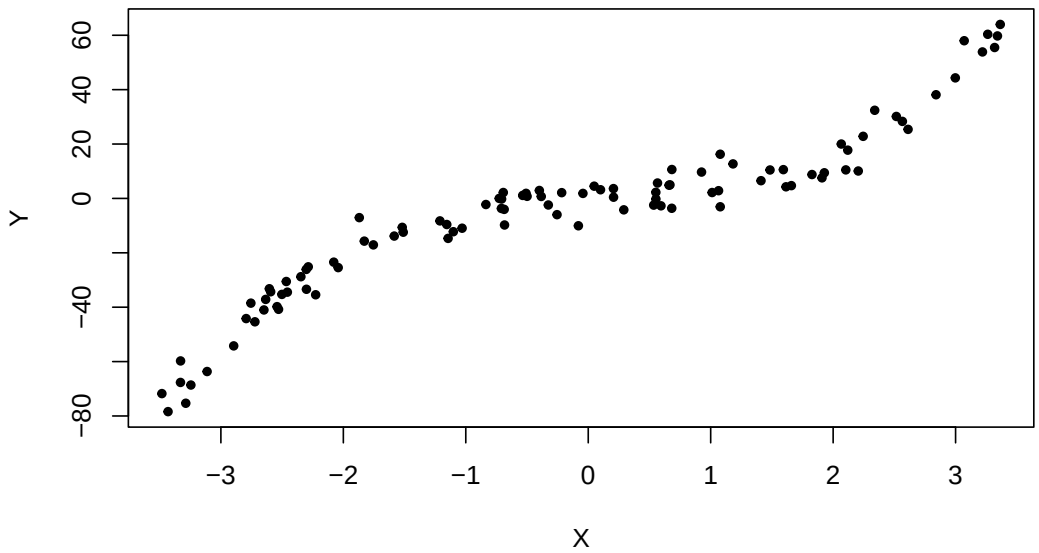
Solution.
14.1- `load()` the file straight from its URL; it contains the data frame `fitpoly` with $n = 100$ pairs (X, Y):

```
load(url("http://www.biostatisticien.eu/springeR/fitpoly.RData"))
head(fitpoly, 3)
dim(fitpoly)
```

```
          Y         X
1  16.25158  1.077938
2  32.40916  2.339643
3 -33.41027 -2.301348
[1] 100   2
```

14.2- A formula in `plot()`:

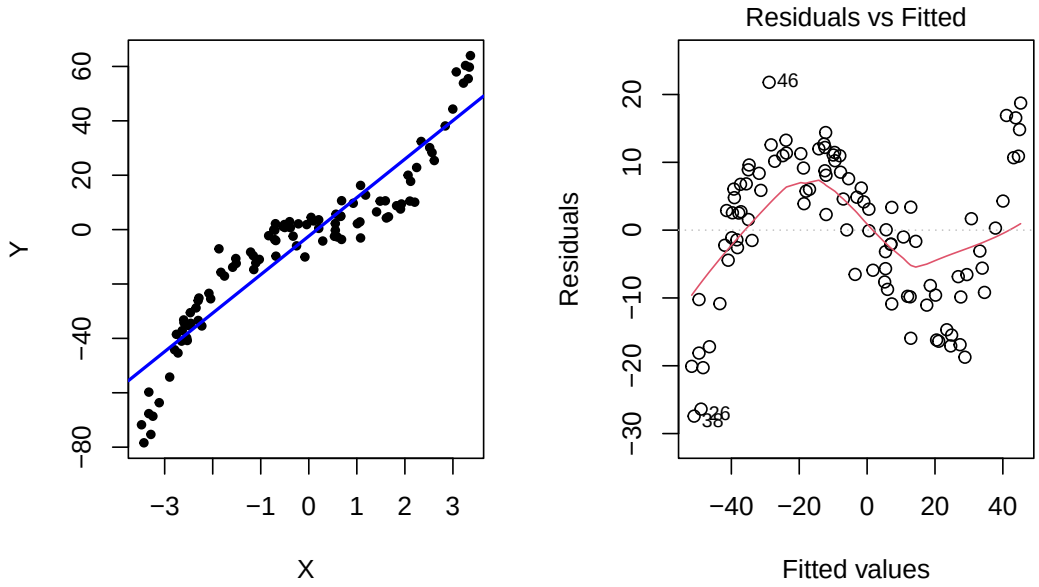
```
plot(Y ~ X, data = fitpoly, pch = 20)
```



14.3- Not really: Y increases with X, but along an S-shaped curve (flat near 0, steep at both ends), so a straight line is only a first approximation.

```
lin.model <- lm(Y ~ X, data = fitpoly)
summary(lin.model)
par(mfrow = c(1, 2))
plot(Y ~ X, data = fitpoly, pch = 20)
```

```r
abline(lin.model, col = "blue", lwd = 2)
plot(lin.model, which = 1)
```




```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.3948     1.0840  -2.209   0.0295 *
X            14.1570     0.5471  25.876   <2e-16 ***
...
Residual standard error: 10.76 on 98 degrees of freedom
Multiple R-squared:  0.8723,        Adjusted R-squared:  0.871
F-statistic: 669.5 on 1 and 98 DF,  p-value: < 2.2e-16
```

(Call, residual quantiles and significance codes truncated.) The slope is highly significant and $R^2 = 0.87$, but the residuals follow a clear systematic wave (negative at the left end, positive for moderately negative X, negative for moderately positive X, positive again at the right end), so the linear model is inadequate.

14.4- Polynomials of increasing degree are fitted with `poly(X, k, raw = TRUE)` (Section 14.3.10) and compared by partial Fisher tests on the nested models:

```r
m2 <- lm(Y ~ poly(X, 2, raw = TRUE), data = fitpoly)
poly.model <- lm(Y ~ poly(X, 3, raw = TRUE), data = fitpoly)
m4 <- lm(Y ~ poly(X, 4, raw = TRUE), data = fitpoly)
anova(lin.model, m2, poly.model, m4)
summary(poly.model)
```

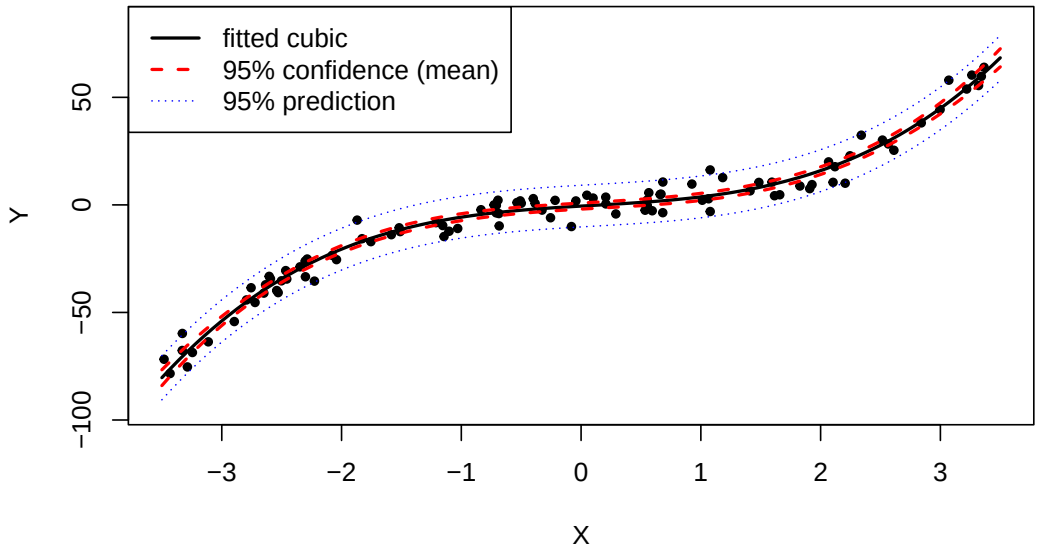
```
  Res.Df     RSS Df Sum of Sq        F    Pr(>F)
1     98 11337.0
2     97 10879.5  1     457.5  20.2334 1.939e-05 ***
3     96  2237.3  1    8642.2 382.1794 < 2.2e-16 ***
4     95  2148.2  1      89.1   3.9382   0.05009 .
...
Coefficients:
                        Estimate Std. Error t value Pr(>|t|)
(Intercept)              -0.5513     0.7071  -0.780  0.43750
poly(X, 3, raw = TRUE)1   3.2447     0.6117   5.305 7.23e-07 ***
poly(X, 3, raw = TRUE)2  -0.4425     0.1328  -3.331  0.00123 **
poly(X, 3, raw = TRUE)3   1.4694     0.0763  19.257  < 2e-16 ***
...
Residual standard error: 4.828 on 96 degrees of freedom
Multiple R-squared:  0.9748,        Adjusted R-squared:  0.974
F-statistic:  1238 on 3 and 96 DF,  p-value: < 2.2e-16
```

(Model formulae, call, residual quantiles and significance codes truncated.) Adding X^2 and above

all X^3 improves the fit enormously (the cubic term alone divides the residual sum of squares by almost 5), while the quartic term is not significant at 5% ($p = 0.050$). We retain the cubic model $\hat{Y} = -0.55 + 3.24X - 0.44X^2 + 1.47X^3$: $R^2 = 0.975$ and the residual standard error falls from 10.8 to 4.8.

14.5- `curve()` draws the fitted cubic, and `predict()` with `interval = "confidence"` and `interval = "prediction"` (Section 14.3.3) on a grid of 100 points of $[-3.5, 3.5]$ gives the two bands, drawn with `matlines()`:

```
plot(Y ~ X, data = fitpoly, pch = 20, xlim = c(-3.5, 3.5), ylim = c(-95, 85))
b <- coef(poly.model)
curve(b[1] + b[2] * x + b[3] * x^2 + b[4] * x^3, add = TRUE, lwd = 2)
x <- seq(-3.5, 3.5, length = 100)
conf.int <- predict(poly.model, data.frame(X = x), interval = "confidence")
pred.int <- predict(poly.model, data.frame(X = x), interval = "prediction")
matlines(x, cbind(conf.int[, 2:3], pred.int[, 2:3]), lty = c(2, 2, 3, 3),
         col = c("red", "red", "blue", "blue"), lwd = c(2, 2, 1, 1))
legend("topleft", c("fitted cubic", "95% confidence (mean)", "95% prediction"),
       lty = c(1, 2, 3), lwd = c(2, 2, 1), col = c("black", "red", "blue"))
x <- c(-3.5, 0, 3.5)
round(cbind(X = x, predict(poly.model, data.frame(X = x), interval = "confidence"),
      predict(poly.model, data.frame(X = x), interval = "prediction")[, 2:3]), 2)
```




```
     X    fit    lwr    upr    lwr    upr
1 -3.5 -80.33 -84.00 -76.66 -90.59 -70.07
2  0.0  -0.55  -1.95   0.85 -10.24   9.13
3  3.5  68.38  64.18  72.59  57.92  78.85
```

The cubic follows the S shape of the cloud closely. The confidence band for the mean of Y (first `lwr=/=upr` pair) is narrow in the centre (± 1.4 at $X = 0$) and widens at the edges of the data (± 4 at $X = \pm 3.5$); the prediction band for a new observation (second pair) is much wider (± 9.7 to ± 10.5) because it adds the error variance $\hat{\sigma}^2 = 4.83^2$, and it contains almost all the observed points, as expected of a 95% prediction interval.

13 Elementary analysis of variance

Contents

13.1 Exercises 15.1–15.7

Problem 15.1. Give the instruction to perform ANOVA with one factor (noted `A`).

Solution. `summary(aov(Y ~ A))` (equivalently `anova(lm(Y ~ A))`), with `A` stored as a `factor` (Section 15.1). On the scarring-time data of Section 15.1:

```r
X <- data.frame(Placebo = c(5,8,7,7,10,8), T2 = c(4,6,6,3,5,6),
                T3 = c(6,4,4,5,4,3), T4 = c(7,4,6,6,3,5), T5 = c(9,3,5,7,7,6))
Y <- stack(X)$values ; A <- stack(X)$ind
summary(aov(Y ~ A))
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
A            4  36.47   9.117   3.896 0.0136 *
Residuals   25  58.50   2.340
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

With $p = 0.0136 < 0.05$ we reject $H_0 : \mu_1 = \cdots = \mu_5$: at least two treatments have different mean scarring times.

Problem 15.2. Give the instruction to perform ANOVA with two factors (noted `A` and `B`) without interaction.

Solution. `summary(aov(Y ~ A + B))` (or `anova(lm(Y ~ A + B))`): the `+` in the formula gives the additive model with main effects only. On the wheat data of Section 15.2.2 (`A` = region, `B` = fertilizer):

```r
yield <- c(15,14,17,21,20,21,14,15,14,16,17,17,16,19,20,23,
           24,25,15,14,14,12,11,12,18,17,17,20,21,21,17,19,17,12,13,13)
B <- gl(3, 12, 36, labels = paste("Fertilizer", 1:3))
A <- gl(4, 3, 36, labels = paste("Region", 1:4))
summary(aov(yield ~ A + B))
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
A            3  327.2  109.06  26.625 1.35e-08 ***
B            2    0.9    0.44   0.108    0.898
Residuals   30  122.9    4.10
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Under the additive model the region effect is highly significant ($p = 1.35 \times 10^{-8}$) while the fertilizer effect is not ($p = 0.898$); Exercise 15.3 shows this model omits a strong interaction.

Problem 15.3. Give the instruction to perform ANOVA with two factors (noted `A` and `B`) with interaction.

Solution. `summary(aov(Y ~ A * B))` (or `anova(lm(Y ~ A * B))`, or `car::Anova(lm(Y ~ A * B))`), where `A * B` stands for `A + B + A:B` (Section 15.2.3). On the wheat data of Exercise 15.2 (same session):

```r
summary(aov(yield ~ A * B))
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
A            3  327.2  109.06 112.181 2.95e-14 ***
B            2    0.9    0.44   0.457    0.638
A:B          6   99.6   16.59  17.067 1.36e-07 ***
Residuals   24   23.3    0.97
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The interaction is highly significant ($p = 1.36 \times 10^{-7}$): the effect of the fertilizer depends on the region, so the non-significant main effect of fertilizer must not be read as "no fertilizer effect".

Problem 15.4. Which test would you use to check for homoscedasticity in an ANOVA model?

Solution. Bartlett's test, `bartlett.test(Y ~ A)`, or, when normality is doubtful, the more robust Levene test (Section 15.1.4); the `levene.test()` of the book and of the authors' companion solution is defunct in current `car`, whose function is now `leveneTest()`.

```
X <- data.frame(Placebo = c(5,8,7,7,10,8), T2 = c(4,6,6,3,5,6),
                T3 = c(6,4,4,5,4,3), T4 = c(7,4,6,6,3,5), T5 = c(9,3,5,7,7,6))
Y <- stack(X)$values ; A <- stack(X)$ind
bartlett.test(Y ~ A)
car::leveneTest(Y ~ A)
```

```
        Bartlett test of homogeneity of variances

data:  Y by A
Bartlett's K-squared = 2.4197, df = 4, p-value = 0.6591

Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  4  0.5851 0.6763
      25
```

Both p-values (0.66 and 0.68) are large, so equality of the five group variances is not rejected for the scarring-time data.

Problem 15.5. Which instruction performs pairwise tests after single-factor ANOVA?

Solution. `pairwise.t.test(Y, A, p.adjust = "bonf")`, which uses the pooled residual standard deviation and corrects for multiple testing through `p.adjust` (Section 15.1.5); `TukeyHSD(aov(Y ~ A))` is the Tukey alternative. On the data of Exercise 15.4:

```
pairwise.t.test(Y, A, p.adjust = "bonf")
```

```
        Pairwise comparisons using t tests with pooled SD

data:  Y and A

   Placebo T2    T3    T4
T2 0.090   -     -     -
T3 0.014   1.000 -     -
T4 0.140   1.000 1.000 -
T5 1.000   1.000 0.483 1.000

P value adjustment method: bonferroni
```

After Bonferroni correction only the Placebo/T3 difference is significant at 5 % (adjusted $p = 0.014$).

Problem 15.6. Which function gives the estimates for a single-factor ANOVA model?

Solution. `lm()`, read through `summary(lm(Y ~ A))` (or `coef()`); by default R imposes the constraint $\alpha_1 = 0$, so the intercept estimates μ_1 and each other coefficient estimates $\mu_i - \mu_1$ (Section 15.1.3). On the data of Exercise 15.4:

```
round(coef(summary(lm(Y ~ A))), 4)
```

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   7.5000     0.6245 12.0096   0.0000
AT2          -2.5000     0.8832 -2.8307   0.0090
AT3          -3.1667     0.8832 -3.5855   0.0014
AT4          -2.3333     0.8832 -2.6420   0.0140
AT5          -1.3333     0.8832 -1.5097   0.1437
```

The placebo mean is estimated at 7.5 days, and treatments T2, T3 and T4 shorten it significantly at

the unadjusted 5 % level (by 2.5, 3.2 and 2.3 days), T5 does not ($p = 0.14$).

Problem 15.7. Which function is used to choose the constraint in ANOVA?

Solution. `C()`, applied to the factor inside the formula: `C(A, base = 2)` makes level 2 the reference ($\alpha_2 = 0$) and `C(A, sum)` imposes $\sum_i \alpha_i = 0$ (Section 15.1.3); the `contrasts` argument of `lm()` does the same, e.g. `contrasts = list(A = contr.sum)`.

```
round(coef(summary(lm(Y ~ C(A, sum)))), 4)
```

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.6333     0.2793 20.1706   0.0000
C(A, sum)1    1.8667     0.5586  3.3419   0.0026
C(A, sum)2   -0.6333     0.5586 -1.1338   0.2676
C(A, sum)3   -1.3000     0.5586 -2.3274   0.0283
C(A, sum)4   -0.4667     0.5586 -0.8355   0.4114
```

Under $\sum_i \alpha_i = 0$ the intercept is the grand mean 5.63 days and each coefficient is a deviation of a treatment mean from it (the fifth is $-\sum_{i \le 4} \hat{\alpha}_i = 0.53$); the F test of Exercise 15.1 is unchanged.

13.2 Worksheet 15.W.A.1 — Study of one-way ANOVA - Study of noise levels

Problem 15.W.A.1. Worksheet 15.W.A.1 — Study of one-way ANOVA — Study of noise levels
In order to study the influence of the factor "level of surrounding noise" on the ability of a subject to solve a problem, the following experiment is designed: twenty-four school children are randomly allocated to four rooms. Street noises were previously recorded and are played in each room at a specific noise level. The children must solve a series of problems. The response variable is the final grade for the series of problems. The results are given in the following table (columns are the noise levels):

1	2	3	4
62	56	63	68
60	62	67	66
63	60	71	71
59	61	64	67
63	63	65	68
59	64	66	68

We wish to know whether there is an effect of the factor "level of surrounding noise" on a subject's ability to solve a problem.
15.1- Input the data set in an adequate structure to perform ANOVA.
15.2- Write down the ANOVA model to answer the question.
15.3- Perform the analysis corresponding to your model.
15.4- Perform all pairwise comparisons of noise levels; remember to take into account the problem of multiplicity of tests.

Solution.
15.1- A data frame in "long" format, one row per child, with the grade as a numeric column and the noise level as a `factor`; `stack()` does the reshaping, as in Section 15.1.2.

```
noise <- data.frame(N1 = c(62,60,63,59,63,59), N2 = c(56,62,60,61,63,64),
                    N3 = c(63,67,71,64,65,66), N4 = c(68,66,71,67,68,68))
grades <- stack(noise)
names(grades) <- c("grade", "level")
str(grades)
tapply(grades$grade, grades$level, mean)
```

```
'data.frame':        24 obs. of  2 variables:
 $ grade: num  62 60 63 59 63 59 56 62 60 61 ...
 $ level: Factor w/ 4 levels "N1","N2","N3",..: 1 1 1 1 1 1 2 2 2 2 ...
N1 N2 N3 N4
```

```
61 61 66 68
```

15.2- The one-way ANOVA model of Section 15.1.1, with $I = 4$ noise levels and $n_i = 6$ children per level:

$$Y_{ik} = \mu + \alpha_i + \varepsilon_{ik}, \qquad i = 1, \ldots, 4,\ k = 1, \ldots, 6,$$

where Y_{ik} is the grade of child k in room i, the errors ε_{ik} are independent $\mathcal{N}(0, \sigma^2)$, and R imposes the constraint $\alpha_1 = 0$. The question is the test of $H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4$ (i.e. $\alpha_2 = \alpha_3 = \alpha_4 = 0$) against H_1: at least two means differ.

15.3- Fisher's F test rejects H_0: $F = 13.57$ on 3 and 20 df, $p = 4.7 \times 10^{-5}$, so the noise level has a significant effect on the grade.

```r
mod <- aov(grade ~ level, data = grades)
summary(mod)
bartlett.test(grade ~ level, data = grades)$p.value
shapiro.test(residuals(mod))$p.value
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
level        3    228    76.0   13.57 4.66e-05 ***
Residuals   20    112     5.6
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
[1] 0.5836931
[1] 0.862856
```

The assumptions hold: Bartlett's test does not reject equal variances ($p = 0.58$) and the Shapiro-Wilk test does not reject normality of the residuals ($p = 0.86$).

15.4- `pairwise.t.test()` with Bonferroni's correction (Section 15.1.5):

```r
pairwise.t.test(grades$grade, grades$level, p.adjust = "bonf")
```

```
        Pairwise comparisons using t tests with pooled SD

data:  grades$grade and grades$level

   N1      N2      N3
N2 1.00000 -       -
N3 0.00934 0.00934 -
N4 0.00031 0.00031 0.95266

P value adjustment method: bonferroni
```

Since the design is balanced, Tukey's method, which Section 15.1.5 calls the most accurate here, gives simultaneous intervals:

```r
round(TukeyHSD(mod)$level, 4)
```

```
      diff     lwr     upr  p adj
N2-N1    0 -3.8241  3.8241 1.0000
N3-N1    5  1.1759  8.8241 0.0078
N4-N1    7  3.1759 10.8241 0.0003
N3-N2    5  1.1759  8.8241 0.0078
N4-N2    7  3.1759 10.8241 0.0003
N4-N3    2 -1.8241  5.8241 0.4766
```

Both corrections give the same conclusion at the 5 % level: levels 1 and 2 do not differ, levels 3 and 4 do not differ, but each of levels 3 and 4 gives significantly higher mean grades (by 5 and 7 points) than each of levels 1 and 2. The noise levels therefore form two groups, $\{1, 2\}$ and $\{3, 4\}$.

13.3 Worksheet 15.W.A.2 — Study of one-way ANOVA - Study of intima-media

Problem 15.W.A.2. Worksheet 15.W.A.2 — Study of one-way ANOVA — Study of intima-media
In the "Intima-media" study, we are interested in the relationship between intima-media thickness and alcohol consumption.

15.1- Download the intima-media data file.

15.2- Suggest a plot to visualize the differences in intima-media thickness depending on alcohol

consumption.
15.3- Is there a difference of mean intima-media thickness depending on alcohol consumption?
15.4- Analyse the residuals to validate the assumptions of your statistical study.

Solution.
15.1- `read.table()` with `sep = " "` (missing values are empty fields) and `dec = ","`; `alcohol` is recoded as a factor with the labels of Appendix B.3 (0 = non-drinker, 1 = occasional, 2 = regular drinker).

```
intima <- read.table("http://www.biostatisticien.eu/springeR/Intima_Media_Thickness.txt",
                     sep = " ", header = TRUE, dec = ",")
intima$alcohol <- factor(intima$alcohol, levels = 0:2,
                         labels = c("non-drinker", "occasional", "regular"))
table(intima$alcohol, useNA = "ifany")
round(tapply(intima$measure, intima$alcohol, mean), 3)
```

```
non-drinker  occasional     regular
         23          71          16
non-drinker  occasional     regular
      0.501       0.530       0.571
```

15.2- Parallel boxplots, `plot(measure ~ alcohol)` (Table 15.1), here with the group means added as red crosses.

```
plot(measure ~ alcohol, data = intima, xlab = "Alcohol consumption",
     ylab = "Intima-media thickness (mm)", col = "grey90")
points(1:3, tapply(intima$measure, intima$alcohol, mean), pch = 4, col = "red", cex = 1.5)
```

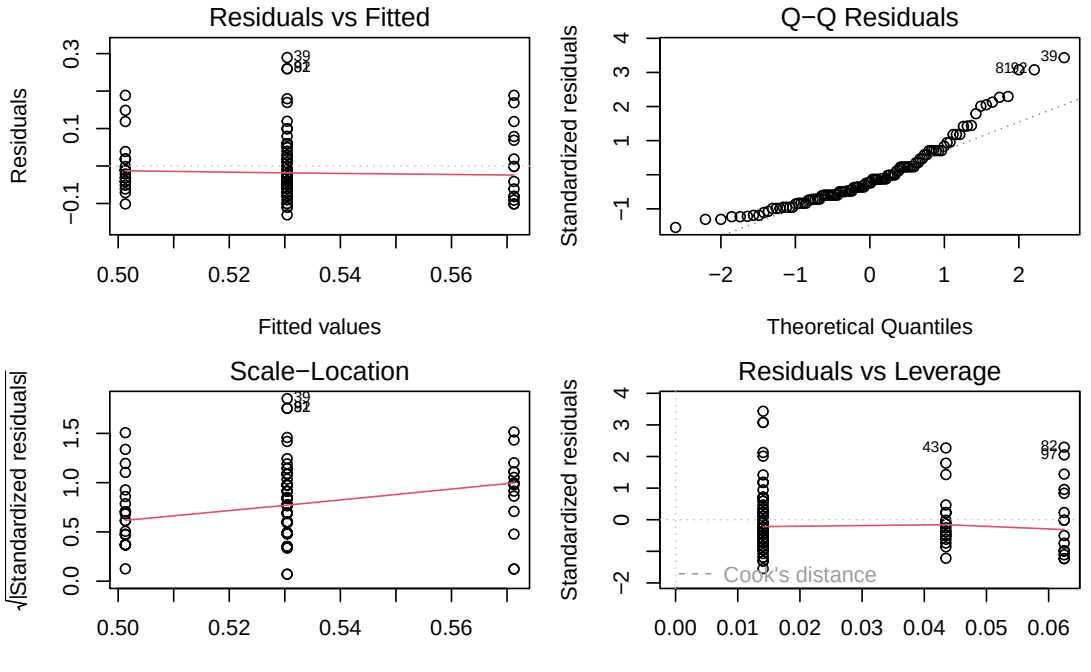
Thickness tends to increase with alcohol consumption, and the distributions are right-skewed (upper outliers).
15.3- Yes, at the 5 % level: in the model $Y_{ik} = \mu + \alpha_i + \varepsilon_{ik}$ (i = alcohol class, ε_{ik} i.i.d. $\mathcal{N}(0, \sigma^2)$), Fisher's test of $H_0 : \mu_1 = \mu_2 = \mu_3$ gives $F = 3.198$ on 2 and 107 df, $p = 0.045$.

```
mod <- aov(measure ~ alcohol, data = intima)
summary(mod)
```

```
             Df Sum Sq  Mean Sq F value Pr(>F)
alcohol       2 0.0462 0.023084   3.198 0.0448 *
Residuals   107 0.7723 0.007218
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

We reject H_0 (just): mean intima-media thickness differs between alcohol classes, rising from 0.501 mm (non-drinkers) to 0.571 mm (regular drinkers).
15.4- Homoscedasticity holds but normality of the residuals does not: the four diagnostic plots of Section 15.1.4, Bartlett's and Levene's tests (the book's `levene.test()` is now `leveneTest()` in `car`) and a Shapiro-Wilk test:

```
par(mfrow = c(2, 2))
plot(mod)
```




```
shapiro.test(residuals(mod))$p.value
bartlett.test(measure ~ alcohol, data = intima)$p.value
library(car)
leveneTest(measure ~ alcohol, data = intima)
kruskal.test(measure ~ alcohol, data = intima)$p.value
```

```
[1] 4.472462e-07
[1] 0.307024
Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group   2  1.6941 0.1887
      107
[1] 0.04435345
```

Homoscedasticity is acceptable (Bartlett $p = 0.31$, Levene $p = 0.19$; the "Residuals vs Fitted" spreads are comparable), but normality is not: the Q-Q plot bends upwards in the right tail (observations 39, 81, 92) and Shapiro-Wilk rejects with $p = 4.5 \times 10^{-7}$. With $n = 110$ the F test is fairly robust to this skewness, and the rank-based Kruskal-Wallis test, which does not assume normality, reaches the same conclusion ($p = 0.044$), so the alcohol effect found in 15.3 stands, though only marginally.

13.4 Worksheet 15.W.A.3 — Study of one-way ANOVA - Study of physical activity

Problem 15.W.A.3. Worksheet 15.W.A.3 — Study of one-way ANOVA — Study of physical activity
In a study of risky behaviour amongst people aged 14 to 25, a scientist observed offences (theft, racketeering, brawls…) committed by youngsters and weekly physical activity. Risky behaviour was measured on a scale from 0 to 100. A subset of the data is available at the URL http://www.biostatisticien.eu/springeR/sports.RData:

```
> print(sports[sample(1:105,10),],row.names=FALSE)
```

```
 score  time
     9 [2;3[
    75 [0;1[
     0 [3;4[
    21 [2;3[
    67 [4;5[
    69 [1;2[
    36 [2;3[
     0 [3;4[
    87 [0;1[
    16 [2;3[
```

15.1- Describe the factors involved and write down the model (and the underlying assumptions).
15.2- Perform a test at the 5 % level to decide whether there is a significant effect between physical activity and risky behaviour.
We call "not athletic" youngsters who play sports for less than 2 hours per week, "somewhat athletic" those with weekly physical activity in the interval [2,4[and "very athletic" those who play sports at least 4 hours per week. The scientist makes the following research assumptions:
research assumption 1: "not athletic" youngsters have more risky behaviour than "somewhat athletic" youngsters;
research assumption 2: risky behaviour is different between "very athletic" and "not athletic" youngsters.
15.3- Translate the research assumptions into contrasts.
15.4- Test these two assumptions at the 5 % level.

Solution.
15.1- There is one factor, `time` (weekly hours of physical activity), with $I = 7$ modalities $[0;1[$, $[1;2[$, …, $[6;7[$, each observed on $n_i = 15$ youngsters; the response is the quantitative risky-behaviour `score` (0 to 100).

```
load(url("http://www.biostatisticien.eu/springeR/sports.RData"))
table(sports$time)
round(tapply(sports$score, sports$time, mean), 2)
```

```
[0;1[ [1;2[ [2;3[ [3;4[ [4;5[ [5;6[ [6;7[
   15    15    15    15    15    15    15
[0;1[ [1;2[ [2;3[ [3;4[ [4;5[ [5;6[ [6;7[
76.40 57.67 28.33 30.33 52.00 68.73 79.07
```

The one-way ANOVA model (Section 15.1.1) is

$$Y_{ik} = \mu_i + \varepsilon_{ik} = \mu + \alpha_i + \varepsilon_{ik}, \qquad i = 1, \ldots, 7,\ k = 1, \ldots, 15,$$

where Y_{ik} is the score of youngster k in activity class i, μ_i is the mean score of class i, and the errors ε_{ik} are assumed independent, normally distributed, with mean 0 and a common variance σ^2 (homoscedasticity); R uses the constraint $\alpha_1 = 0$.
15.2- Physical activity has a highly significant effect on risky behaviour: Fisher's test of $H_0 : \mu_1 = \cdots = \mu_7$ gives $F = 12.1$ on 6 and 98 df, $p = 3.9 \times 10^{-10} < 0.05$.

```
mod <- aov(score ~ time, data = sports)
summary(mod)
bartlett.test(score ~ time, data = sports)$p.value
oneway.test(score ~ time, data = sports)$p.value
kruskal.test(score ~ time, data = sports)$p.value
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
time         6  38300    6383    12.1 3.86e-10 ***
Residuals   98  51679     527
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
[1] 1.291906e-09
[1] 1.290315e-14
[1] 3.000801e-08
```

Bartlett's test rejects equal variances ($p = 1.3 \times 10^{-9}$; the group standard deviations range from 5.7 to 39.2), but the design is balanced, and Welch's heteroscedastic test (`oneway.test()`) and the Kruskal-Wallis test both confirm the effect ($p < 10^{-7}$).

15.3- With $\mu_1, \ldots, \mu_7$ the class means in the order above, "not athletic" is classes 1-2, "somewhat athletic" classes 3-4 and "very athletic" classes 5-7. The contrasts are

$$L_1 = \tfrac{1}{2}(\mu_1 + \mu_2) - \tfrac{1}{2}(\mu_3 + \mu_4), \qquad \lambda_1 = (\tfrac{1}{2}, \tfrac{1}{2}, -\tfrac{1}{2}, -\tfrac{1}{2}, 0, 0, 0)^T,$$
$$L_2 = \tfrac{1}{3}(\mu_5 + \mu_6 + \mu_7) - \tfrac{1}{2}(\mu_1 + \mu_2), \quad \lambda_2 = (-\tfrac{1}{2}, -\tfrac{1}{2}, 0, 0, \tfrac{1}{3}, \tfrac{1}{3}, \tfrac{1}{3})^T,$$

(coefficients summing to zero), and the research assumptions become the alternatives: assumption 1 is $H_0 : L_1 \leq 0$ against $H_1 : L_1 > 0$ (one-sided), assumption 2 is $H_0 : L_2 = 0$ against $H_1 : L_2 \neq 0$ (two-sided).

15.4- Assumption 1 is accepted, assumption 2 is not. `fit.contrast()` (Section 15.1.5; the book's `gregmisc` has since been split and the function now lives in `gmodels`) gives two-sided p-values; the one-sided p-value for L_1 is the upper tail of its t statistic.

```
library(gmodels)
cmat <- rbind(": not - somewhat" = c(1/2, 1/2, -1/2, -1/2, 0, 0, 0),
              ": very - not"     = c(-1/2, -1/2, 0, 0, 1/3, 1/3, 1/3))
res <- fit.contrast(mod, "time", cmat)
res
pt(res[1, "t value"], df = df.residual(mod), lower.tail = FALSE)
```

```
                      Estimate Std. Error     t value     Pr(>|t|)
time: not - somewhat 37.7000000   5.929258  6.35829987 6.495787e-09
time: very - not     -0.4333333   5.412647 -0.08005941 9.363533e-01
[1] 3.247894e-09
```

Research assumption 1: $\hat{L}_1 = 37.7 > 0$ with one-sided $p = 3.2 \times 10^{-9} < 0.05$, so "not athletic" youngsters have significantly more risky behaviour than "somewhat athletic" ones. Research assumption 2: $\hat{L}_2 = -0.43$, $p = 0.94 > 0.05$, so no difference in risky behaviour is detected between "very athletic" and "not athletic" youngsters; the relationship is U-shaped, with the lowest scores for 2 to 4 hours of sport per week.

13.5 Worksheet 15.W.B.1 — Study of two-way ANOVA - Study of batteries

Problem 15.W.B.1. Worksheet 15.W.B.1 — Study of two-way ANOVA — Study of batteries
In an experiment on battery lifetime, the aim is to find battery life as a function of type of battery. It is known that battery lifetime depends on temperature, so a plane with two factors (temperature and type of battery) is created. The following table gives battery lifetime depending on these two factors.

	15 °C	70 °C	125 °C
Type I	130 155	34 40	20 70
	74 180	80 75	82 58
Type II	150 188	136 122	25 70
	159 126	106 115	58 45
Type III	138 110	174 120	96 104
	168 160	150 139	82 60

15.1- Which factors are involved in this experiment? What are their modalities? What is the response variable?
15.2- Propose and define an ANOVA model for this data set.
15.3- Propose a graphical representation to visualize any interaction there may be in the model.
15.4- Estimate the parameters of the model.
15.5- Draw an ANOVA table for your model.
15.6- Perform the relevant tests to finalize this analysis.

Solution.

15.1- Two crossed factors: battery type (modalities I, II, III) and temperature (modalities 15 °C, 70 °C, 125 °C); the response is battery lifetime. Each of the 3×3 cells holds 4 observations, so the design is balanced ($n = 36$). The data are entered in the style of Section 15.2.2:

```
life <- c(130,155,74,180,  34,40,80,75,     20,70,82,58,
          150,188,159,126, 136,122,106,115, 25,70,58,45,
          138,110,168,160, 174,120,150,139, 96,104,82,60)
type <- gl(3, 12, labels = c("I", "II", "III"))
temp <- gl(3, 4, 36, labels = c("15C", "70C", "125C"))
battery <- data.frame(life, type, temp)
with(battery, tapply(life, list(type, temp), mean))
```

```
       15C    70C 125C
I   134.75  57.25 57.5
II  155.75 119.75 49.5
III 144.00 145.75 85.5
```

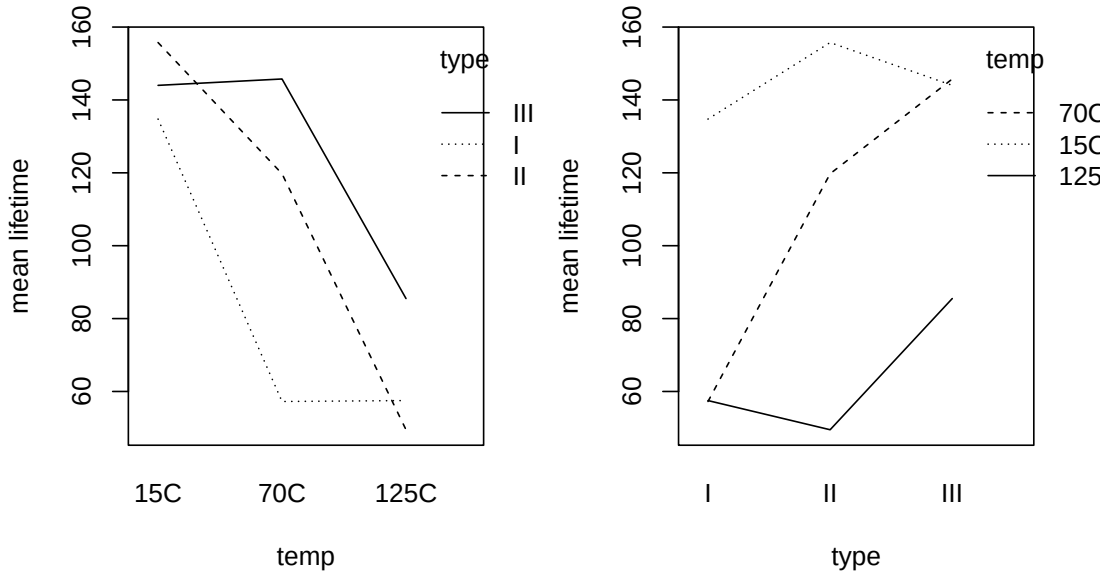
15.2- The two-way ANOVA model with interaction of Section 15.2.1:

$$Y_{ijk} = \mu_{\bullet\bullet} + \alpha_i^A + \alpha_j^B + \beta_{ij} + \varepsilon_{ijk}, \qquad i, j = 1, 2, 3, \quad k = 1, \ldots, 4,$$

where Y_{ijk} is the lifetime of the k-th battery of type i at temperature j, α_i^A is the differential effect of type i, α_j^B that of temperature j, β_{ij} the interaction effect, and the errors ε_{ijk} are independent $N(0, \sigma^2)$ (so $Y_{ijk} \sim N(\mu_{ij}, \sigma^2)$, a common variance in all nine cells).

15.3- An interaction plot (`interaction.plot()`, Section 15.2.2), drawn both ways round:

```
par(mfrow = c(1, 2))
with(battery, interaction.plot(temp, type, life, ylab = "mean lifetime"))
with(battery, interaction.plot(type, temp, life, ylab = "mean lifetime"))
```



The profiles are far from parallel: type I collapses already at 70 °C, whereas type III keeps its lifetime up to 70 °C, which suggests an interaction.

15.4- Under R's constraints $\alpha_1^A = \alpha_1^B = 0$, $\beta_{1j} = \beta_{i1} = 0$ (Section 15.2.3) the estimates are the `lm()=/=aov()` coefficients; `model.tables()` gives the grand and marginal means, from which the differential effects of Section 15.2.1 follow.

```
mod <- aov(life ~ type * temp, data = battery)
round(coef(mod), 2)
lapply(model.tables(mod, type = "means")$tables[1:3], round, 2)
sigma(lm(life ~ type * temp, data = battery))^2
```

```
     (Intercept)           typeII          typeIII          temp70C
          134.75            21.00             9.25           -77.50
         temp125C   typeII:temp70C  typeIII:temp70C  typeII:temp125C
          -77.25            41.50            79.25           -29.00
typeIII:temp125C
           18.75
$`Grand mean`
[1] 105.53

$type
type
     I     II    III
 83.17 108.33 125.08

$temp
temp
   15C    70C   125C
144.83 107.58  64.17

[1] 675.213
```

The intercept 134.75 is the mean lifetime of type I at 15 °C, and every other cell mean is the intercept plus its main-effect and interaction terms (e.g. type III at 70 °C: $134.75+9.25-77.5+79.25 = 145.75$). With the sum-to-zero constraints of Section 15.2.1, $\hat{\mu}_{\bullet\bullet} = 105.53$, $\hat{\alpha}^A = (-22.36,\ 2.81,\ 19.56)$ for types I, II, III, $\hat{\alpha}^B = (39.31,\ 2.06,\ -41.36)$ for 15, 70, 125 °C, and $\hat{\sigma}^2 = 675.2$ on 27 df.

15.5- The ANOVA table is given by `summary(aov())` (Section 15.2.3; the design is balanced, so the sequential decomposition is unique):

```r
summary(mod)
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
type         2  10684    5342   7.911  0.00198 **
temp         2  39119   19559  28.968 1.91e-07 ***
type:temp    4   9614    2403   3.560  0.01861 *
Residuals   27  18231     675
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

15.6- The interaction test ($H_0 : \beta_{ij} = 0$ for all i, j) gives $F = 3.56$, $p = 0.019 < 0.05$: the interaction between type and temperature is significant, so the model with interaction is kept and, as Section 15.2.3 advises, the main effects are not interpreted from the table; instead the type effect is tested at each temperature, dividing the one-way mean square by the residual mean square of the full model (27 df). The model assumptions are checked first (Bartlett test over the nine cells, Shapiro-Wilk on the residuals).

```r
bartlett.test(life ~ interaction(type, temp), data = battery)$p.value
shapiro.test(residuals(mod))$p.value
CMres <- deviance(mod) / df.residual(mod)
sapply(levels(battery$temp), function(t) {
  s <- summary(aov(life ~ type, data = battery, subset = temp == t))[[1]]
  F <- s[1, "Mean Sq"] / CMres
  c(F = F, p.value = pf(F, 2, df.residual(mod), lower.tail = FALSE))
}) |> signif(3)
library(emmeans)
pairs(emmeans(mod, ~ type | temp, at = list(temp = "70C")))
```

```
[1] 0.7321499
[1] 0.6117267
          15C      70C 125C
F       0.656 1.23e+01 2.12
p.value 0.527 1.63e-04 0.14
temp = 70C:
 contrast estimate   SE df t.ratio p.value
 I - II      -62.5 18.4 27  -3.402  0.0058
 I - III     -88.5 18.4 27  -4.817  0.0001
 II - III    -26.0 18.4 27  -1.415  0.3475
```

```
P value adjustment: tukey method for comparing a family of 3 estimates
```

Homoscedasticity ($p = 0.73$) and normality ($p = 0.61$) are not rejected, so the tests are valid. Battery type makes no significant difference at 15 °C ($p = 0.53$) or at 125 °C ($p = 0.14$), but it does at 70 °C ($p = 1.6 \times 10^{-4}$), where types II and III both last significantly longer than type I (Tukey-adjusted comparisons with the pooled residual variance) and do not differ from each other. Every type loses lifetime at 125 °C (interaction plot), and type III, never significantly worse than the others and with the highest mean at 70 °C and 125 °C, is the most robust choice.

13.6 Worksheet 15.W.B.2 — Study of two-way ANOVA - Milk yield

Problem 15.W.B.2. Worksheet 15.W.B.2 — Study of two-way ANOVA — Milk yield
We are interested in the influence of type and quantity of food on milk yield. We have observed these forty values:

	Straw	Hay	Grass	Silage
Low dose	8 11 11 10 7	12 13 14 11 10	10 12 12 13 14	17 13 17 14 13
High dose	8 9 8 10 9	10 7 10 12 11	11 9 11 11 12	13 12 11 15 14

15.1- Propose and define an ANOVA model to study the influence of type and quantity of food on milk yield.
15.2- Propose a graphical representation to visualize any interaction there may be in the model.
15.3- Estimate the parameters of the model.
15.4- Draw an ANOVA table for your model.
15.5- Perform the relevant tests to finalize this analysis.

Solution.
15.1- A two-way ANOVA with interaction (Section 15.2.1), with factor A = dose (low, high; $I = 2$) and factor B = type of food (straw, hay, grass, silage; $J = 4$), five cows per cell:

$$Y_{ijk} = \mu_{\bullet\bullet} + \alpha_i^A + \alpha_j^B + \beta_{ij} + \varepsilon_{ijk}, \qquad i = 1, 2, \quad j = 1, \dots, 4, \quad k = 1, \dots, 5,$$

where Y_{ijk} is the milk yield, α_i^A and α_j^B the differential effects of dose i and food j, β_{ij} their interaction, and ε_{ijk} independent $N(0, \sigma^2)$ errors.

```r
yield <- c(8,11,11,10,7, 12,13,14,11,10, 10,12,12,13,14, 17,13,17,14,13,
           8,9,8,10,9,   10,7,10,12,11,  11,9,11,11,12,  13,12,11,15,14)
dose <- gl(2, 20, labels = c("Low", "High"))
food <- gl(4, 5, 40, labels = c("Straw", "Hay", "Grass", "Silage"))
milk <- data.frame(yield, dose, food)
with(milk, tapply(yield, list(dose, food), mean))
```

```
     Straw Hay Grass Silage
Low    9.4  12  12.2   14.8
High   8.8  10  10.8   13.0
```

15.2- An interaction plot of the cell means:

```r
with(milk, interaction.plot(food, dose, yield, ylab = "mean milk yield"))
```

The two dose profiles are almost parallel (the high dose sits 0.6 to 2 units below the low dose for every food), so little or no interaction is expected.

15.3- With R's constraints (first level of each factor as reference, Section 15.2.3):

```r
mod <- aov(yield ~ dose * food, data = milk)
round(coef(mod), 2)
lapply(model.tables(mod, type = "means")$tables[1:3], round, 2)
deviance(mod) / df.residual(mod)
```

```
       (Intercept)            doseHigh             foodHay           foodGrass
               9.4                -0.6                 2.6                 2.8
        foodSilage    doseHigh:foodHay  doseHigh:foodGrass doseHigh:foodSilage
               5.4                -1.4                -0.8                -1.2
$`Grand mean`
[1] 11.38

$dose
dose
  Low  High
12.10 10.65

$food
food
 Straw    Hay  Grass Silage
   9.1   11.0   11.5   13.9

[1] 2.5125
```

The intercept 9.4 is the mean yield with a low dose of straw; e.g. high-dose silage has mean $9.4 - 0.6 + 5.4 - 1.2 = 13.0$. With the sum-to-zero constraints, $\hat{\mu}_{\bullet\bullet} = 11.38$, $\hat{\alpha}^A = (0.725, -0.725)$ for low/high dose, $\hat{\alpha}^B = (-2.275, -0.375, 0.125, 2.525)$ for straw, hay, grass, silage, and $\hat{\sigma}^2 = 2.51$ on 32 df.

15.4- The ANOVA table (balanced design):

```r
summary(mod)
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
dose         1  21.03   21.03   8.368  0.00682 **
food         3 117.07   39.02  15.532 2.07e-06 ***
dose:food    3   2.87    0.96   0.381  0.76705
Residuals   32  80.40    2.51
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

15.5- The interaction is not significant ($F = 0.38$, $p = 0.77 > 0.05$), so, following Section 15.2.3, the additive model $Y_{ijk} = \mu_{\bullet\bullet} + \alpha_i^A + \alpha_j^B + \varepsilon_{ijk}$ is fitted and its main effects tested; the assumptions and the pairwise food comparisons are checked on it.

```
mod2 <- aov(yield ~ dose + food, data = milk)
summary(mod2)
round(coef(mod2), 2)
bartlett.test(yield ~ interaction(dose, food), data = milk)$p.value
shapiro.test(residuals(mod2))$p.value
TukeyHSD(mod2, "food")$food |> round(4)
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
dose         1  21.03   21.03   8.837  0.00531 **
food         3 117.07   39.02  16.402 7.98e-07 ***
Residuals   35  83.27    2.38
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Intercept)    doseHigh     foodHay   foodGrass  foodSilage
       9.83       -1.45        1.90        2.40        4.80
[1] 0.8013939
[1] 0.3546157
             diff     lwr    upr  p adj
Hay-Straw     1.9  0.0396 3.7604 0.0438
Grass-Straw   2.4  0.5396 4.2604 0.0071
Silage-Straw  4.8  2.9396 6.6604 0.0000
Grass-Hay     0.5 -1.3604 2.3604 0.8865
Silage-Hay    2.9  1.0396 4.7604 0.0010
Silage-Grass  2.4  0.5396 4.2604 0.0071
```

Variances are homogeneous ($p = 0.80$) and the residuals normal ($p = 0.35$). Both factors act on milk yield: the dose effect is significant ($p = 0.005$, the high dose giving on average 1.45 units less than the low dose) and so is the type of food ($p = 8 \times 10^{-7}$). Silage gives the highest yield (significantly above all other foods), straw the lowest, and hay and grass do not differ ($p = 0.89$).

13.7 Worksheet 15.W.B.3 — Study of two-way ANOVA - Intima-media study

Problem 15.W.B.3. Worksheet 15.W.B.3 — Study of two-way ANOVA — Intima-media study
In practical A, we looked at a possible relationship between intima-media thickness and alcohol consumption in the “Intima-media” study. We now wonder whether intima-media thickness is linked to alcohol consumption and tobacco consumption.
15.1- Download the intima-media data set.
15.2- Propose and define an ANOVA model to study the influence of tobacco consumption and alcohol consumption on intima-media thickness.
15.3- Propose a graphical representation to visualize any interaction there may be in the model.
15.4- Is there a difference in intima-media thickness depending on alcohol consumption? Depending on tobacco consumption?

Solution.
15.1- `read.table()` on the book’s text file (Section 4.1.1: space separator, comma decimal mark), with the two codes turned into labelled factors (the book’s description of the data set codes tobacco 0/1/2 = non-smoker/former smoker/smoker, alcohol 0/1/2 = non-drinker/occasional/regular drinker):

```
imt <- read.table("http://www.biostatisticien.eu/springeR/Intima_Media_Thickness.txt",
                  header = TRUE, sep = " ", dec = ",")
imt$tobacco <- factor(imt$tobacco, levels = 0:2,
                      labels = c("non-smoker", "former smoker", "smoker"))
imt$alcohol <- factor(imt$alcohol, levels = 0:2,
                      labels = c("non-drinker", "occasional", "regular"))
with(imt, table(tobacco, alcohol))
```

```
              alcohol
tobacco        non-drinker occasional regular
  non-smoker             18         45       9
```

```
former smoker           3         14       1
smoker                  2         12       6
```

The 110 subjects are spread very unevenly over the nine cells (from 1 to 45 per cell): the design is unbalanced.

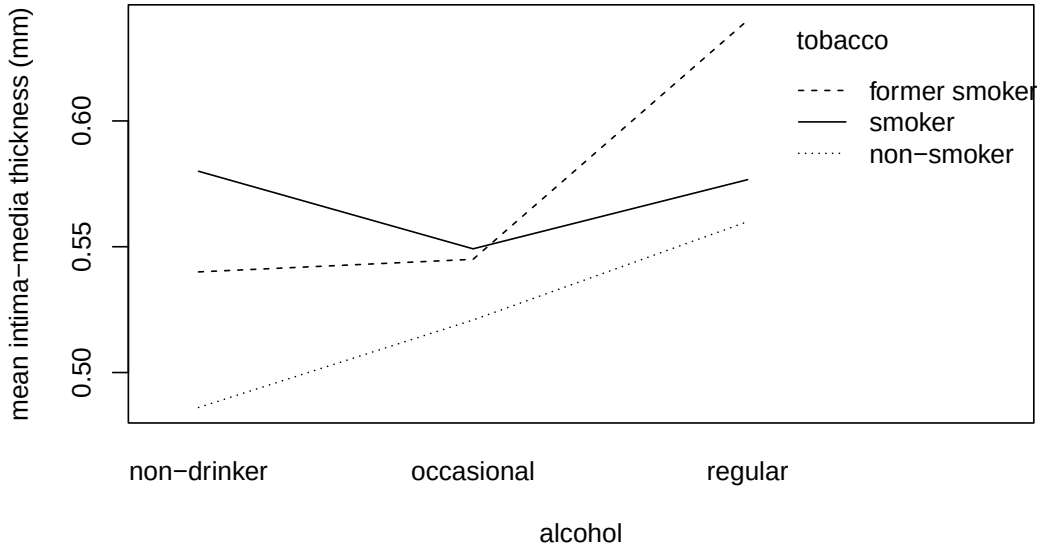
15.2- The two-way ANOVA model with interaction of Section 15.2.1, with A = tobacco ($I = 3$) and B = alcohol ($J = 3$):

$$Y_{ijk} = \mu_{\bullet\bullet} + \alpha_i^A + \alpha_j^B + \beta_{ij} + \varepsilon_{ijk}, \qquad i, j = 1, 2, 3, \quad k = 1, \ldots, n_{ij},$$

where Y_{ijk} is the intima-media thickness (mm) of the k-th subject with tobacco status i and alcohol consumption j, α_i^A, α_j^B and β_{ij} are the tobacco, alcohol and interaction effects, and the ε_{ijk} are independent $N(0, \sigma^2)$. Because n_{ij} varies, the tests use type III sums of squares (Section 15.2.2).

15.3- The interaction plot of the cell means:

```r
with(imt, interaction.plot(alcohol, tobacco, measure,
                           ylab = "mean intima-media thickness (mm)"))
```



The profiles cross (smokers do not follow the upward trend with alcohol seen in non-smokers), but the most extreme point, former smokers who drink regularly, rests on a single subject, so the apparent interaction may be noise.

15.4- Neither: once both factors are in the model, neither alcohol nor tobacco has a significant effect at the 5 % level. The interaction is tested first (type III, contrasts as in Section 15.2.3), then, since it is not significant, the additive model $Y_{ijk} = \mu_{\bullet\bullet} + \alpha_i^A + \alpha_j^B + \varepsilon_{ijk}$ is fitted and its main effects tested (type II, each adjusted for the other).

```r
library(car)
mod <- lm(measure ~ tobacco * alcohol, data = imt,
          contrasts = list(tobacco = contr.sum, alcohol = contr.sum))
options(show.signif.stars = FALSE)
Anova(mod, type = "III")
mod2 <- lm(measure ~ tobacco + alcohol, data = imt)
Anova(mod2, type = "II")
round(coef(mod2), 3)
shapiro.test(residuals(mod2))$p.value
Anova(lm(log(measure) ~ tobacco + alcohol, data = imt))[1:2, 4]
```

```
Anova Table (Type III tests)

Response: measure
                Sum Sq  Df   F value Pr(>F)
```

```
(Intercept)     10.6579   1 1466.6124 <2e-16
tobacco          0.0314   2    2.1608 0.1205
alcohol          0.0187   2    1.2892 0.2800
tobacco:alcohol  0.0118   4    0.4061 0.8039
Residuals        0.7340 101
Anova Table (Type II tests)

Response: measure
           Sum Sq  Df F value  Pr(>F)
tobacco   0.02655   2  1.8692 0.15934
alcohol   0.03531   2  2.4854 0.08818
Residuals 0.74577 105
         (Intercept) tobaccoformer smoker        tobaccosmoker
               0.494                0.033                0.033
   alcoholoccasional       alcoholregular
               0.024                0.063
[1] 2.254354e-07
[1] 0.09781140 0.08086831
```

There is no interaction ($p = 0.80$). In the additive model the alcohol effect ($p = 0.088$) and the tobacco effect ($p = 0.16$) are both non-significant, even though the estimated thickness rises with alcohol (+0.024 mm for occasional, +0.063 mm for regular drinkers) and is about 0.033 mm higher for smokers and former smokers than for non-smokers. So the alcohol effect found in the one-way analysis of practical A (15.W.A.2, $p = 0.045$) does not survive adjustment for tobacco, to which it is partly confounded. The residuals are not normal (Shapiro-Wilk $p = 2.3 \times 10^{-7}$, right skew), but with $n = 110$ the F tests are robust, and a log-transformed response gives the same verdict ($p = 0.098$ for tobacco, $p = 0.081$ for alcohol).