Chapter 1
Introducing R

Prerequisites and goals of this chapter

- You may find it useful to read the chapter on installing R in the Appendix first.
- This chapter presents the origins, objectives and specificities of R.

SECTION 1.1

Presentation of the Software

1.1.1 Origins

R is a piece of statistical software created by Ross Ihaka and Robert Gentleman [21]. R is both a programming language and a work environment. Commands are executed using descriptive code. Results are displayed as text and the plots are visualized directly in their own window. R is clone of the statistical software S-plus. S-plus is an object-oriented programming language S developed by AT&T Bell Laboratories in 1988 [3]. S-plus is used to manipulate data, draw plots and perform statistical analyses of data.

1.1.2 Why Use R*?*

First of all, R is **free** and **open-source**. It works under UNIX (and Linux), Microsoft Windows and Macintosh Mac OS: it is **cross-platform**. It is being developed in the

P. Lafaye de Micheaux et al., *The R Software: Fundamentals of Programming and Statistical Analysis*, Statistics and Computing 40, DOI 10.1007/978-1-4614-9020-3_1,

free software movement by a large and growing community of eager volunteers. Anyone can contribute to and improve R by integrating more functionalities or analysis methods. It is thus a quickly and constantly evolving piece of software.

R is a very powerful statistical tool. The learning curve in R is steeper than other statistical software on the market such as SPSS, SAS or Minitab. R is not the kind of statistical package, which you can use with a few clicks of the mouse in the menus. In order to use it, you need to understand the statistical method that you are trying to implement, so R is a didactic program. R is also very efficient and easy to implement once you have mastered it. You will be able to create your own tools and you will be able to handle and work on very sophisticated data analyses.

Warning

R is harder to comprehend than other software on the market. You need to spend time learning the syntax and commands.

R is especially powerful for data manipulation, calculations and plots. Its features include:

- an integrated and very well-conceived documentation system (in English)
- Efficient procedures for data treatment and storage;
- a suite of operators for calculations on tables, especially matrices;
- a vast and coherent collection of statistical procedures for data analysis;
- advanced graphical capabilities;
- a simple and efficient programming language, including conditioning, loops, recursion, and input-output possibilities.

Note

For the readers already used to SAS, SPSS or Stata, we advise to read the books [32, 33] and also to consult the two following Internet websites:

- http://rforsasandspssusers.com
- http://www.statmethods.net

Note also that it is possible to call R functions directly from Matlab using the `R.matlab` package and from Excel using the `RExcelInstaller` package. Reading of [20] might be useful in this context. Finally, a similar tool for OpenOffice, called `R00o`, exists; see the Internet website http://rcom.univie.ac.at.

SECTION 1.2

R and Statistics

Many classical and modern statistical techniques are implemented in R. The most common methods for statistical analysis, such as

- descriptive statistics;
- hypothesis testing;
- analysis of variance;
- linear regression methods (simple and multiple)

are directly included at the core of the system. It should be noted that most advanced statistical methods are also available through external packages. These are easy to install, directly from a menu. They are all grouped and can be browsed on the website of the *comprehensive R archive network* (CRAN) (http://cran.r-project.org). This website also includes, for some large domains of interest, a commented list of packages associated with a theme (called Task View). This facilitates the search for a package on a specific statistical method. Furthermore, detailed documentation for each package is available on the CRAN.

It should also be noted that recent statistical methods are added on a regular basis by the statistics community itself.

See also

Section A.2, p. 532, gives details on the procedure to install a new package.

SECTION 1.3

R and Plots

One of the main strengths of R is its capacity (much greater than that of other software on the market) to combine a programming language with the ability to draw high-quality plots. Usual plots are easily drawn using predefined functions. These functions also include many parameters, for example to add titles, captions and colours. But it is also possible to create more sophisticated plots to represent complex data such as contour lines, volumes with a 3D effect, density curves, and many other things. It is also possible to add mathematical formulae. You can arrange or overlay several plots in the same window and use many colour palettes.

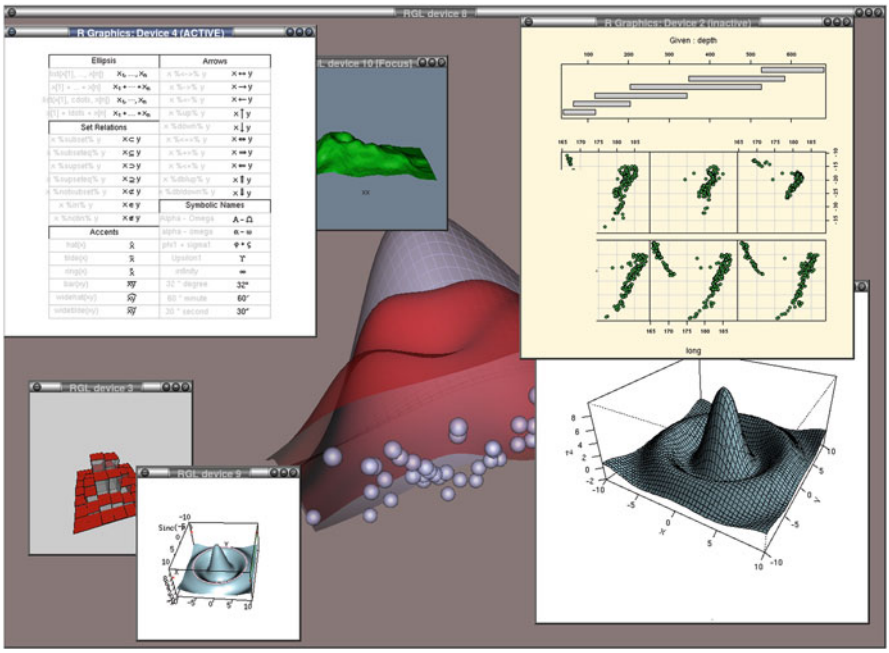


Fig. 1.1: A few of the graphical possibilities offered by R

You can get a demonstration of the graphical possibilities in R by typing in the following instructions:

```
demo(image)
example(contour)
demo(graphics)
demo(persp)
demo(plotmath)
demo(Hershey)
require("lattice") # Load the package, which you must have
                   # previously installed by using the menu
                   # Packages/Install packages.
demo(lattice)
example(wireframe)
require("rgl")     # Same remark as above.
demo(rgl)          # You can interact by using your mouse.
example(persp3d)
```

Figure 1.1 above shows a few of these plots.

SECTION 1.4

The R Graphical User Interface

The R graphical user interface (GUI) (i.e. its set of menus) is very limited, and completely nonexistent on some operating systems, when compared to other standard software. This minimality can set back some new users. However, this drawback is limited since:

- it has the didactic advantage that it incites users to know well the statistical procedures they wish to use;
- there are additional tools which extend the GUI.

In the next section, we present the package `Rcmdr`, which can be installed from the menu `Packages` and which allows standard graphical and statistical analyses with a more user-friendly interface, which includes drop-down menus. Furthermore, the R instructions for the analysis chosen from the `RCommander` menus are displayed in dedicated panel. This can be useful if you do not know (or remember) the R instruction for a specific task.

Tip

Note that after you have learnt R thoroughly, you will be able to develop yourself tools similar to `Rcmdr`, made for a final users who do not desire to learn R but only to use, in the most user-friendly way, a procedure created by you. To this end, you can use the package `tcltk`.

Warning

Note that by using `RCommander`, we are distancing ourselves from what makes the strength and flexibility of R. We therefore advise against using such a tool if you wish to become an advanced user.

SECTION 1.5

First Steps in R

1.5.1 Using RCommander

In this section, we offer a brief introduction to the package `Rcmdr`. We then present some functionalities given by this interface for statistical manipulations. We conclude by explaining how to add functionalities to the `RCommander` interface.

1.5.1.1 Launching RCommander

Follow these steps to start RCommander.

- Double-click on the R icon on your Desktop.
- In the console, type `install.packages("Rcmdr")`. Choose a nearby mirror.
- In the console, type `require("Rcmdr")`. Answer `Yes` to all the questions you may be asked. The RCommander graphical interface then opens. Another option is to click on the menu `Packages`, then `Load package...`, then `Rcmdr`.
- In the `Messages` panel, you should see `WARNING: the Windows version of R Commander works better under RGui with the single document interface (SDI)`.
- To remedy this issue, close RCommander.
- In RGui, go to `Edit`, then `Preferences`. Check `SDI` then click on `Save...` and on `Save`. You can take this opportunity to customize R.
- Close R and save an image of the session.
- Restart R, then RCommander by typing `require("Rcmdr")` in the R console.

See also

We refer the reader to Sect. A.2 which details how to install the package Rcmdr.

Mac

Macintosh users may find useful the instructions at http://socserv.mcmaster.ca/jfox/Misc/Rcmdr/installation-notes.html, after installing package tcltk which is available on the CRAN.

The graphical interface of RCommander includes four parts as shown on Fig. 1.2:

(a) Drop-down menus to perform specific tasks
(b) A `Script window` which presents the code executed thanks to click on a drop-down menu
(c) An `Output window` which gives the output of the executed code
(d) A `Messages` window giving a message on the last task

1.5.1.2 Handling Data with RCommander

To perform statistical analyses, you need data.

• Entering data by band

Follow these steps to enter data by hand.

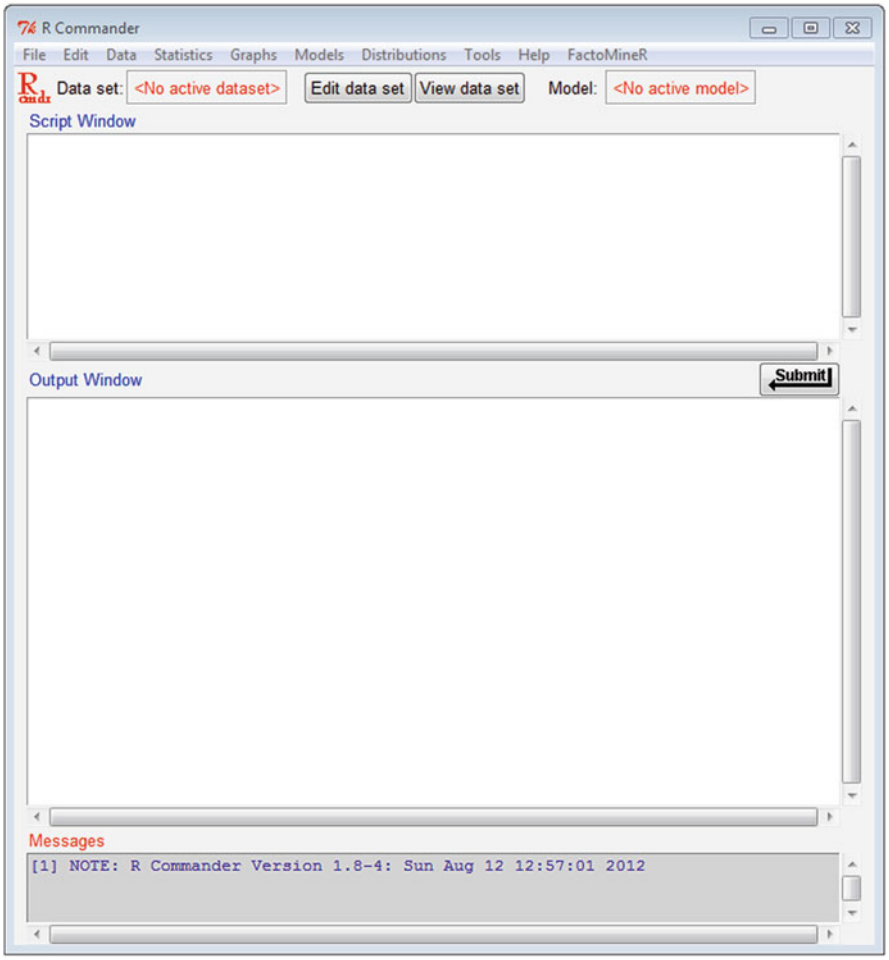


Fig. 1.2: The `RCommander` graphical interface

- In the menu `Data`, choose `New data set...`.
- In the window `New data table`, choose a name for your data set, for example `Data1`.
- A data editor appears. Click on `var1` and replace it with `Name`. Enter a few names for this variable: Peter, Jack, Ben (see Fig. 1.3).
- Create a variable `Height` of type `numeric` with the following values: 182, 184, 190.
- Click on the cross (X) at the top-right corner of the active window to close the data editor.
- You can visualize your data set by clicking on `View`.

We can now calculate some basic statistics.

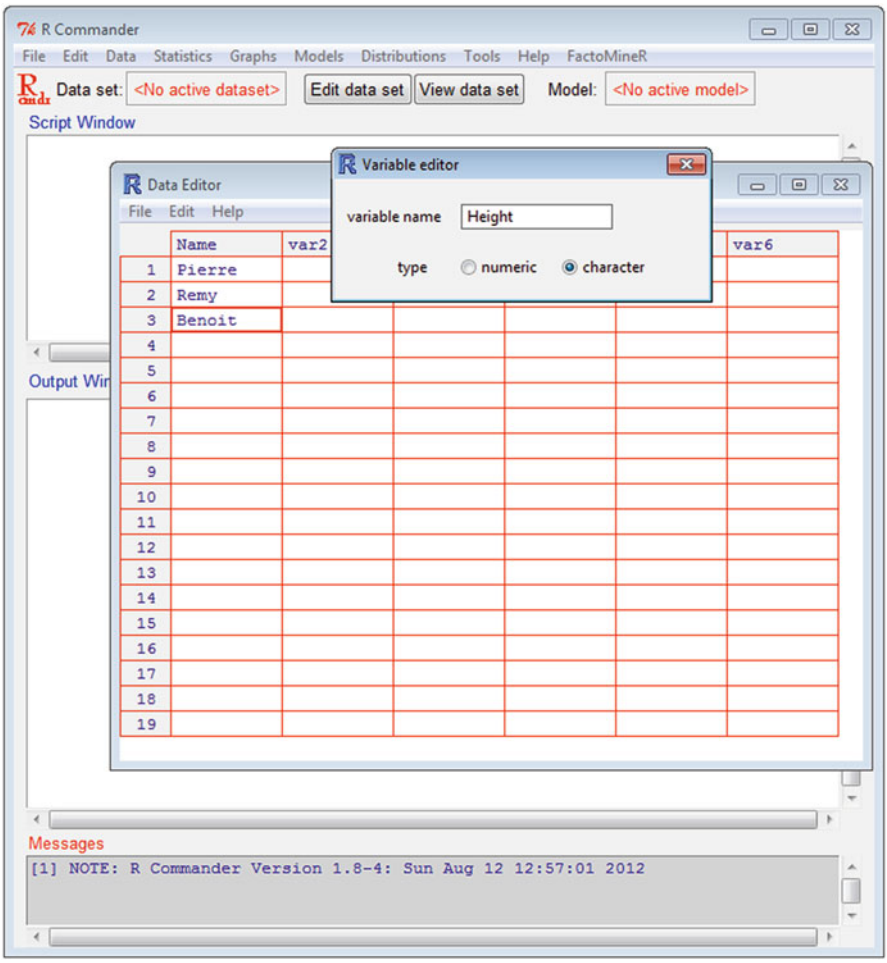


Fig. 1.3: Entering data with the `RCommander` graphical interface

• **Basic statistics**

Follow these steps to get some basic statistics on your data set:

- ► In the menu `Statistics`, choose `Summary`, then `Descriptive statistics ...`.
- ► A window called `General statistics` opens up; the only `numeric` variable in our data set is the variable `Height`.
- ► Choose the statistics `Mean`, `Standard deviation` and `Quantiles` and click on `OK`.
- ► The result is displayed in the `Output window`. Note that you can check the R instruction which was used for this task in the `Script window` (see Fig. 1.4).

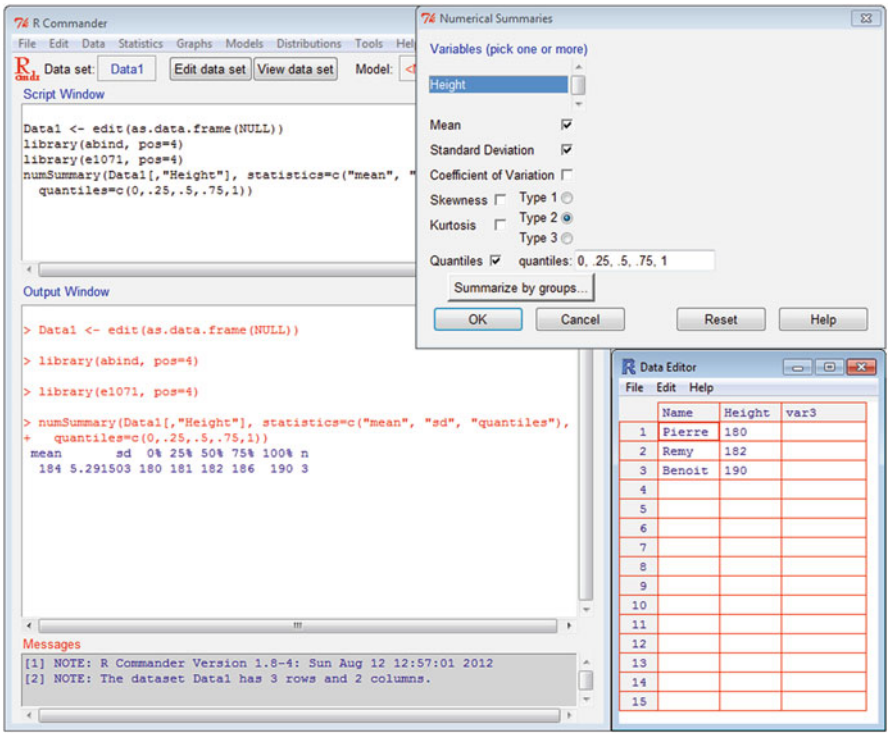


Fig. 1.4: Basic statistics with RCommander

Note that it is also possible to type an instruction directly in the `Script window` without using a menu. Here is an example.

► Type in the `Script window`:

```
numSummary(Data1[,"Height"],statistics=c("mean","sd"))
```

► Click on that line so that the cursor is displayed there, then click on `Submit`.
► You have just computed the mean and standard deviation of variable `Height` which contains 3 observations. The result appears in the `Output window`:

```
mean       sd % n
 184 5.291503 0 3
```

• Manipulating the data set

In our toy example, suppose that we also have the weight and wish to compute the body mass index: $BMI = Weight/Height^2$ (height in metres).

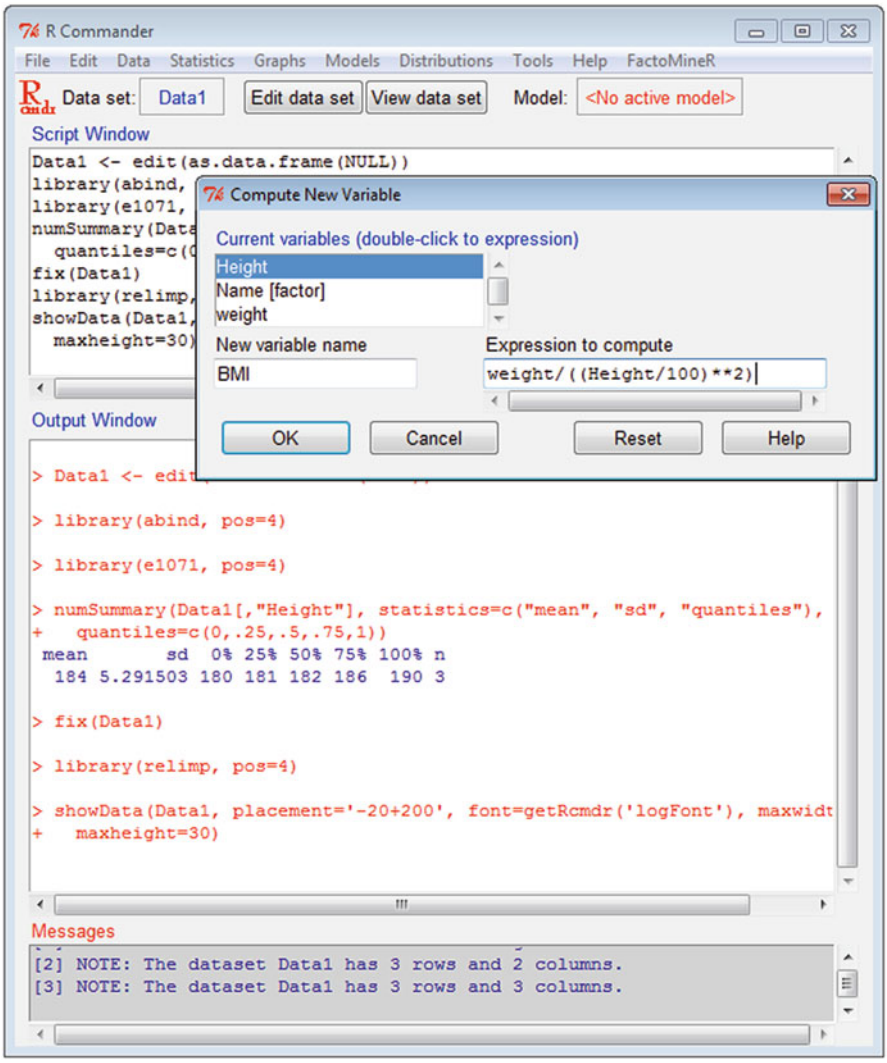


Fig. 1.5: Manipulating a data set with RCommander

- Click on `Edit` (below the RCommander menus).
- The data editor opens up and you can add the numeric variable `Weight`, with the following values: 70, 72 and 75. Now close the data editor.
- In the `Data` menu, choose `Manage variables in the active data set`, then `Calculate a new variable...`. A window opens.
- For `Name of new variable`, type `BMI` and for `Expression to calculate`: `Weight/((Height/100)**2)` (see Fig. 1.5). Click on `OK` to complete the calculation.
- Click on `View` to see the result for your data set.

You are starting to feel tired and need a coffee break! But before you take one, follow these steps to save your data set.

- In the Data menu, choose Active dataset, then Save active dataset....
- A window opens. You can choose a location to save your data set. We shall call it BMI and by default it has the .RData extension.
- Close RCommander and answer OK to the question Do you wish to quit?, No to Save script file? and No to Save output file?.
- You can now close R and answer No to the question Save session image?.

After a well-deserved break, you wish to add new data to your file BMI.RData.

- Open an R session. Type library("Rcmdr").
- In the Data menu, choose Load data set....
- A window opens. Navigate to and open the file BMI.RData.
- Click on View to display your data set.
- Add the information for a new person ("Julia", Height=150, Weight=52) by clicking on Edit.
- After closing the editor, you can check the changes by clicking on View. You then see the value NA (*not available*) for Julia's BMI.
- To get Julia's BMI, you need to go through the steps of section *manipulating the data set* again. We shall see later on how to create a function which calculates the BMI in a more user-friendly fashion.

You now wish to send your data set to a colleague who does not use R yet.

- In the Data menu, choose Active dataset, then Export active data set ....
- A first window opens. Uncheck the box Write names of individuals (rows) since we have not defined these. Choose Spaces for the field separator.
- Click on OK. A second window opens. You can choose a place to save your data set. We shall call it BMI and it has the default extension .txt.
- You can now send your data set BMI.txt to your colleague and use this opportunity to mention the wonderfulness of R, which has a rather user-friendly interface for data manipulation.

1.5.1.3 A Few Statistical Tasks with RCommander

In this section, we present a brief overview of how to use RCommander for statistical tasks. We start with a mean comparison test and a chi-square test of independence. We then show how to use RCommander to visualize the standard distributions (binomial, poisson, normal, gamma, etc.). We conclude with a linear model fit.

• **Mean comparison test**

We propose to use data already available in R. Follow these steps to load a data set:

- In the `Data` menu, choose `Data in packages`, then `Read data from an attached package...`.
- A window opens. Double-click on `datasets` in the `Package` section, then on `sleep` in the right column.
- `sleep` appears in the box `Enter a dataset name` (see Fig. 1.6).
- You can now click on `Help on the selected dataset` to have some information about it.
- Click on `OK` to close the previous window, then visualize the data set by clicking on `View`.

These data are used to compare the effect on sleep of a soporific drug, compared to a control group. We shall first visualize the distribution of sleep gain in both groups, then do a mean comparison test to see whether there is any statistical significant difference between the drug and the control.

- In the `Graphs` menu, choose `Box plot...`.
- A window opens. Click on `Plot by group...`, then on the variable `group`, then on `OK` twice.
- You can now see two box plots representing the sleep time gain in both groups.
- You can save this plot by clicking on `File`, then `Save as`. Several formats are possible.

You can also enhance this plot, for example, by adding colours. In the script window, type

```
boxplot(extra~group,ylab="extra",xlab="group",data=sleep,
        col=c("red","blue"))
```

then click on `Submit`.

See also

Chapter 7 is dedicated to plots in R.

We now perform a mean comparison test.

- In the `Statistics` menu, choose `Means`, then `independent t-test...`.
- Click on `group` in section `Groups (one)`. You now see specified the difference `1-2` (group 1 *vs.* group 2).
- Click on `OK` to see the result in the `Output window` (see also Fig. 1.6).

The p-value of this test (greater than 5 %) does not allow us to conclude that there is a significant difference between the sleep gains given by the drug and the control.

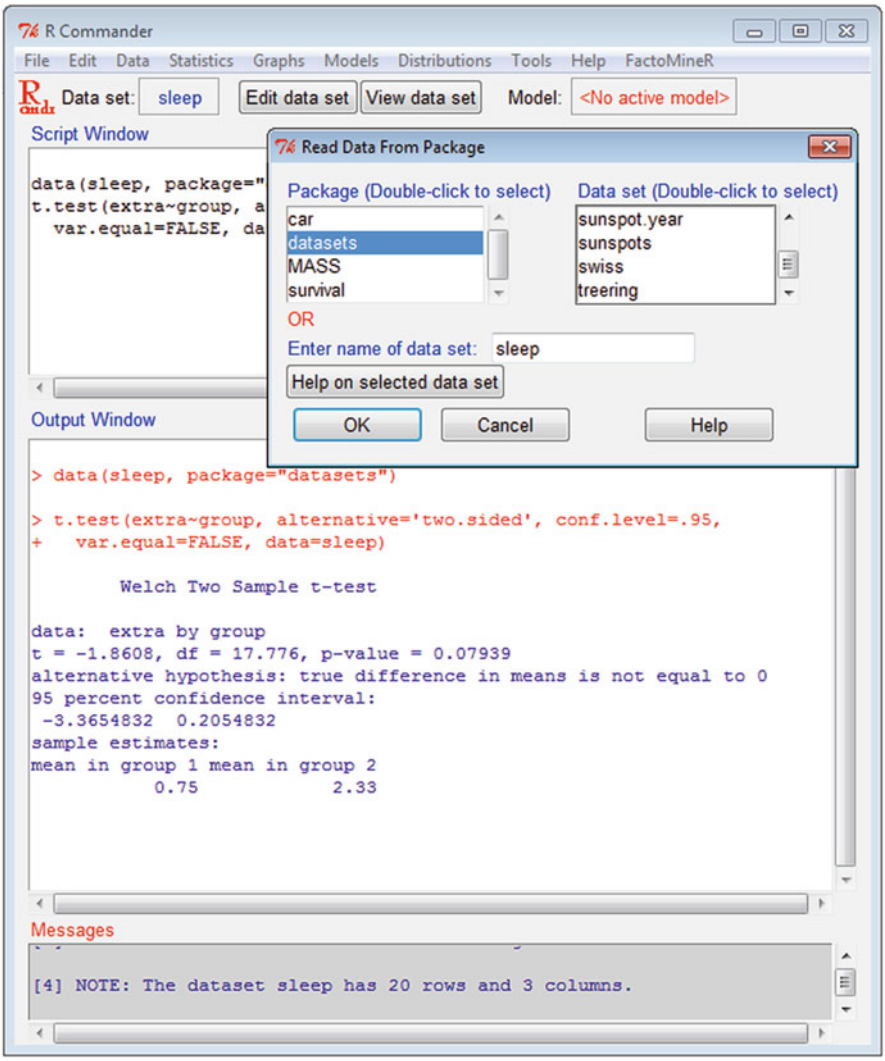


Fig. 1.6: Mean comparison test with `RCommander`

• Test on a double entry table

In a therapeutic test, the underlying question is whether a treatment on HIV-positive mothers has an effect on the HIV status of the child. If it does not, then the HIV status of the child is independent of the treatment taken by the mother. In this test, out of 391 children, 100 are HIV negative, 193 have mothers under treatment and 41 are HIV positive and have mothers under treatment. To know whether the treatment has an effect, follow these steps:

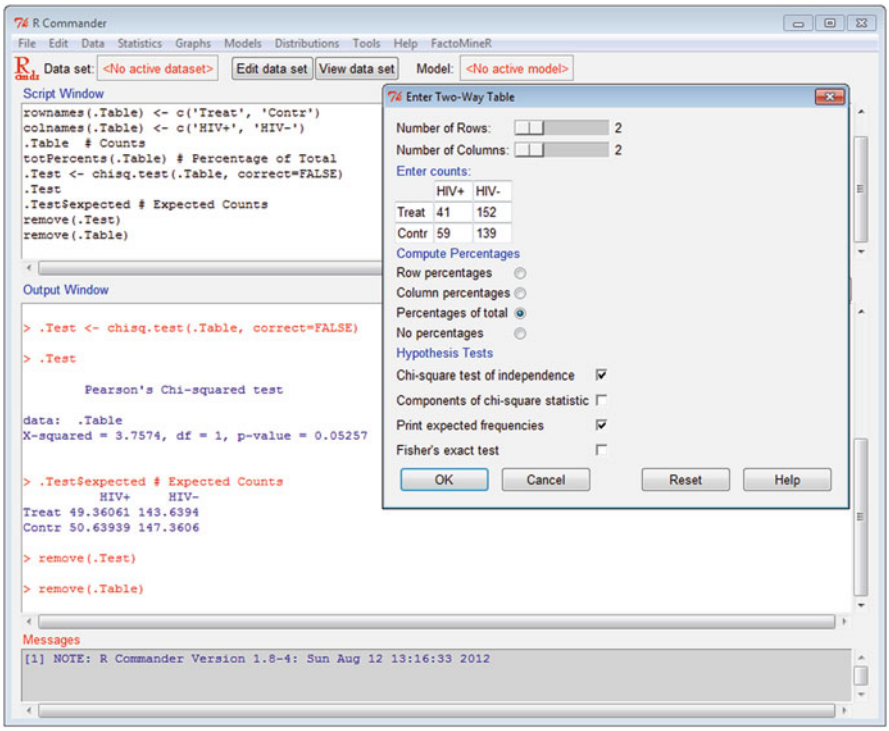


Fig. 1.7: Independence test with RCommander

- In the Statistics menu, choose Contingency tables, then Fill and analyse a double entry table....
- A window opens. Fill the table as indicated in Fig. 1.7. Choose Total percentages and Print expected frequencies.
- Click on OK to see the result in the Output window.

At the 5 % risk level, we cannot conclude that the treatment has an effect on the child's HIV status.

• Exploring distributions

RCommander can be used to visualize standard distributions.

- In the Distributions menu, choose Continuous distributions, the Normal distribution, then Plot of normal distribution....
- A window opens. Specify a mean of 4 and a standard deviation of 2. Click on OK.
- The curve of the density of a normal distribution centred at 4 and with standard deviation 2 appears in a graphical window.

You can follow the same steps for other probability distributions.

• Fitting a linear model

RCommander can be used to easily fit standard regression models. We illustrate this with the linear model. We shall first download a data set from an Internet address (URL). It contains the measures, for 80 patients with a disabling illness, of the variables GENDER (1 = Male, 2 = Female), WEIGHT (in kg), HEIGHT (in cm), PAIN (ordinal variable: a=least pain), DISTANCE (number of metres walked), MOBILITY (self-evaluation of mobility; 1=most mobile) and STAIRS (number of steps climbed).

- ► In the Data menu, choose Import data, then from a text file, the clipboard or a URL....
- ► A window opens. Call the data table Illness. Check the box Internet link (URL) in Data file and the box Tabulations for Field separator; click on OK.
- ► In the field Internet link (URL), type http://biostatisticien.eu/springeR/illness.txt.
- ► Click on OK and you should see the following in the Messages window: The illness data set contains 80 rows and 8 columns.

We shall fit a multiple regression model. Follow these steps.

- ► In the Statistics menu, choose Model fitting, then Linear regression ....
- ► Choose for example Model.1 as your model name in the field Enter a name for the model.
- ► Choose variable DISTANCE as the response variable, and variables WEIGHT and HEIGHT as the explanatory variables (keep the CTRL key pressed).
- ► Click on OK. The result of your linear model adjustment appears in the Output window. This result corresponds to the instructions

```
Model.1 <- lm(DISTANCE~WEIGHT+HEIGHT,data=Illness)
summary(Model.1)
```

which are shown in the Script window.

See also

Chapter 14 presents the linear model in further detail.

We now visualize the least squares plane corresponding to the fitted model.

- ► In the Plot menu, choose 3D plot, then 3D scatterplot....
- ► Choose variable DISTANCE as the response variable and the variables WEIGHT and HEIGHT as explanatory variables (use the CTRL key).
- ► Choose Ordinary least squares as the surface to fit. Click on OK.

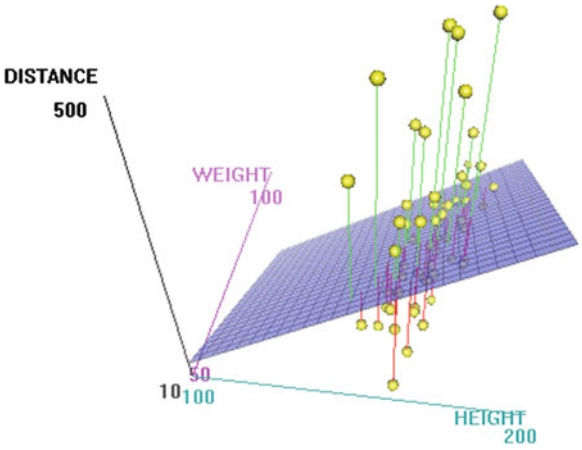


Fig. 1.8: Least squares plane

You can now see the 3D scatterplot (shown in Fig. 1.8) and the least squares plane. You can move the image with your mouse.

1.5.1.4 Adding Functionalities to the RCommander Interface

Some packages available on the official R website can also be integrated to the RCommander menus. They are easy to identify: their names start with RcmdrPlugin. We now illustrate how to use such a package.

See also

You can read the article [17] which explains how to build a package for RCommander integration.

• **The TeachingDemos package**

The RcmdrPlugin.TeachingDemos package can be used to illustrate some statistical concepts.

- Type `install.packages("RcmdrPlugin.TeachingDemos")` in the `Script window`. Click on `Submit` and choose a nearby mirror. Once the installation is complete, close and reopen RCommander using the instruction `Commander()`.
- In the `Tools` menu, choose `Load Rcmdr plug-ins...`, click on `OK` and answer `Yes` to the question `Restart now?`.
- There is a new menu called `Demos`. In this menu, you can choose for example the submenu `Simple Correlation` and explore the notion of correlation.

This plug-in also adds submenus to pre-existing menus. For example, in the `Distributions` menu, you can now choose `Visualize distributions`, then `t distributions`. By checking `Show Normal Distribution`, and by playing with the `d.f.` (*degree of freedom*) cursor, you can visualize the closeness of the Student distribution and the normal distribution.

• **The sos package**

The `RcmdrPlugin.sos` package can be used to ease the search for help on a given concept or function. Follow the same steps as before to install this plug-in. A new submenu called `Search R Help ... (sos)` appears in the `Help` menu. Explore this new `Rcommander` functionality, for example, by typing `linear model`.

See also

Chapter 6 describes how to search for information about R.

1.5.2 Using R *with the Console*

In the previous subsection, we saw how to use R through menus. In fact, this way of proceeding is far from optimal, since it imposes many limitations on the possibilities offered by R. Many analyses, either deeper or more recent and innovative, are not available in the `RCommander` menus. It is thus very useful to escape from the "button clicking" approach and master the R programming language. You will then be able to perform simulations and to code repetitive tasks. We have already encountered a few R instructions when using `RCommander`, which is itself a tool written in the R language. We now propose a brief introduction to a few elements of the R syntax, first through an analysis of complex data arising from a functional magnetic resonance imaging (MRI) experiment, then by letting the reader type a few R commands and think about the output.

1.5.2.1 The Strength of R Shown on an Example

Some neuroscientists work on finding which part of the brain deals with visual information on colour. To this end, a visual stimulus, consisting in an alternance of coloured and non-coloured moving patterns, is shown to a subject. During this time, volumic images of the subject's brain are acquired at time $t = 1, \ldots, T$ with an MRI scanner. Each 3D image is in fact a large (Rubik's!) cube made of many voxels, the 3D equivalents of 2D pixels. At time $t = 1, \ldots, T$, each voxel contains an electromagnetic measurement value $x(t)$. We can thus consider that in each voxel, we have observed a time series $\{x(t); t = 1, \ldots, T\}$ representing

electromagnetic variations. The acquired data (given in file Mond4D.nii, produced during a Mondrian experiment performed by M. Dojat and J. Huppé) thus consist in a 4-dimensional array, the concatenation of several volumic brain images measured through time.

We used R to find, in each brain slice, which voxel had temporal variations most correlated with the stimulus signal. The code below can be downloaded from http://biostatisticien.eu/springeR/brain-code.R and opened, thanks to the submenu `Open script...` of the `File` menu in R. The key combination CTRL+R then executes one by one the instructions of this script. You can try to execute these instructions to visualize the results. This will help you familiarize yourself with some of the possibilities offered by R.

We first download the data files we need (the files Mondanat.img and Mondanat.hdr contain an anatomical image of the subject's brain).

```
> getfile <- function(myfile)
+  download.file(paste("http://biostatisticien.eu/springeR/",
+  myfile,sep=""),paste(getwd(),"/",myfile,sep=""),mode="wb")
> getfile("Mond4D.nii")
> getfile("Mondanat.hdr")
> getfile("Mondanat.img")
```

We then install the package to read the data.

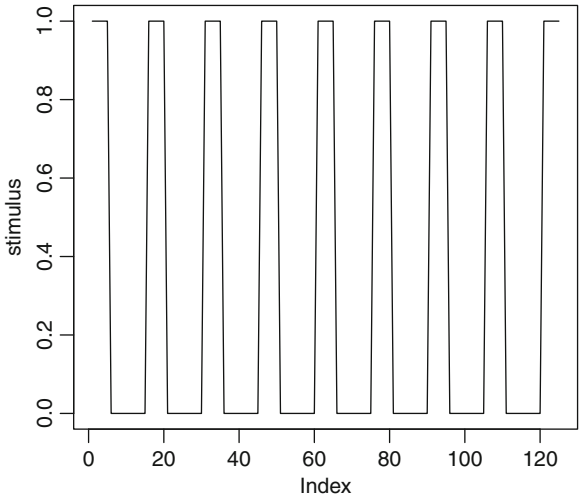
```
> install.packages("AnalyzeFMRI") # Choose a mirror.

> # File names.
> file.func <- paste(getwd(),"/","Mond4D.nii",sep="")
> file.anat <- paste(getwd(),"/","Mondanat.img",sep="")

> # Brain slice number.
> slice <- 10
```

The next instructions read the data.

```
> anat.slice <- f.read.nifti.slice(file.anat,slice,1)
> class(anat.slice)
[1] "matrix"
> dim(anat.slice)
[1] 128 128
> func.slice <- f.read.nifti.slice.at.all.timepoints(file.func,
    slice)
> class(func.slice)
[1] "array"
> dim(func.slice)
[1] 128 128 125
```

We now create the coding of the visual stimulus signal (1=colour, 0=no colour).

```
> stimulus <- c(rep(c(1,1,1,1,1,0,0,0,0,0,0,0,0,0,0),8),1,1,1,1,1)
> plot(stimulus,type="l")
```



We compute correlations between the observed time series in each voxel and the stimulus series.

```
> corMat <- matrix(NA,nrow=128,ncol=128)
> for (i in 1:128) {
+   for (j in 1:128) {
+     corMat[i,j] <- cor(func.slice[i,j,],stimulus)
+   }
+ }
```

We can now compute the coordinates of the voxel most strongly correlated with the stimulus

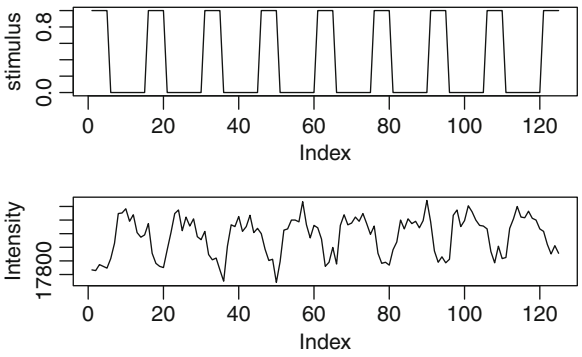
```
> which(abs(corMat)==max(abs(corMat),na.rm=TRUE),arr.ind=TRUE)
     row col
[1,]  67 117
```

and the correlation value of this voxel

```
> corMat[67,117]
[1] -0.6675017
```

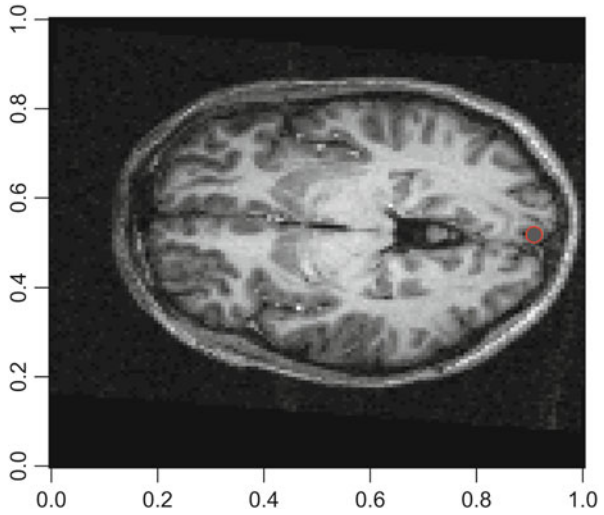
We can then plot the time series observed in this voxel.

```
> par(mfrow=c(2,1))
> plot(stimulus,type="l")
> plot(func.slice[67,117,],type="l",ylab="Intensity")
```



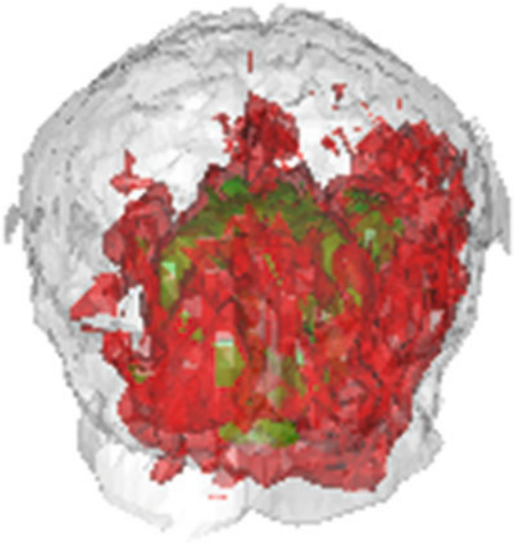
We are now able to identify on the anatomical image of the brain the most active voxel for the visual stimulus.

```
> image(as.matrix(rev(as.data.frame(t(anat.slice)))),
     col=gray((0:32)/32))
> points(117/128,67/128,col="red",cex=2,pch=19)
```



Note that you can also visualize these data in 3D. The following instructions, taken from the help file for the function `contour3d()` from package `misc3d`, give an interactive 3D view of the brain.

```
> install.packages("misc3d")

> require("misc3d")
> a <- f.read.analyze.volume(system.file("example.img",
+                  package="AnalyzeFMRI"))
> a <- a[,,,1]
> contour3d(a,1:64,1:64,1.5*(1:21),lev=c(3000, 8000, 10000),
+          alpha=c(0.2,0.5,1),color=c("white","red","green"))
```



You can try to move the image with your mouse.

1.5.2.2 A Brief Introduction of R Syntax Through Some Instructions to Type

• Basic operations

We advise the reader to play with these commands and try to understand how they work.

```
> 1*2*3*4
[1] 24
> factorial(4)
[1] 24
> cos(pi)
[1] -1
> x <- 1:10
> x
 [1]  1  2  3  4  5  6  7  8  9 10
> exp(x)
 [1]     2.718282     7.389056    20.085537    54.598150
 [5]   148.413159   403.428793  1096.633158  2980.957987
 [9]  8103.083928 22026.465795
> x^2
 [1]   1   4   9  16  25  36  49  64  81 100
> chain <- "R is great!"
> chain
[1] "R is great!"
> nchar(chain)
[1] 11
> ?nchar
```

```
> M <- matrix(x,ncol=5,nrow=2)
> M
     [,1] [,2] [,3] [,4] [,5]
[1,]    1    3    5    7    9
[2,]    2    4    6    8   10
> M[2,3]
[1] 6
> L <- list(matrix=M,vector=x,chain=chain)
> L[[3]]
[1] "R is great!"
> while(TRUE) {
+  toguess <- sample(1:2,1)
+  {cat("Guess a number among 1, 2, 3: ") ; value <- readline()}
+   if (value == toguess) {print("Well done!") ; break()}
+   else print("Try again.")
+ }
> ls()
[1] "chain" "L"     "M"     "x"
> rm(chain)
```

The following commands perform matrix operations:

```
> A <- matrix(runif(9),nrow=3)
> 1/A
         [,1]     [,2]     [,3]
[1,] 2.270797 1.546875 1.422103
[2,] 1.268152 1.957924 1.057803
[3,] 1.642736 5.273120 2.174020
> A * (1/A)
     [,1] [,2] [,3]
[1,]    1    1    1
[2,]    1    1    1
[3,]    1    1    1
> B <- matrix(1:12,nrow=3)
> A * B
Error in A * B : non-conformable arrays
> A %*% B
         [,1]      [,2]      [,3]     [,4]
[1,] 3.842855  9.212923 14.582990 19.95306
[2,] 4.646105 11.380053 18.114001 24.84795
[3,] 2.367954  6.143031  9.918107 13.69318
> (invA <- solve(A))
          [,1]      [,2]      [,3]
[1,]  1.145642 -3.376148  5.187347
[2,]  4.379786 -4.641906  2.844607
[3,] -3.321872  6.381822 -5.863772
> A %*% invA
              [,1]          [,2] [,3]
[1,]  1.000000e+00 0.000000e+00    0
[2,]  0.000000e+00 1.000000e+00    0
[3,] -2.220446e-16 4.440892e-16    1
```

```
> det(A)
[1] 0.04857799
> eigen(A)
$values
[1]  1.6960690+0.000000i -0.1424863+0.091319i
[3] -0.1424863-0.091319i
$vectors
             [,1]                   [,2]                   [,3]
[1,] 0.5859852+0i  0.6140784-0.1816841i  0.6140784+0.1816841i
[2,] 0.7064296+0i  0.2234155+0.2505528i  0.2234155-0.2505528i
[3,] 0.3969616+0i -0.6908020+0.0000000i -0.6908020+0.0000000i
```

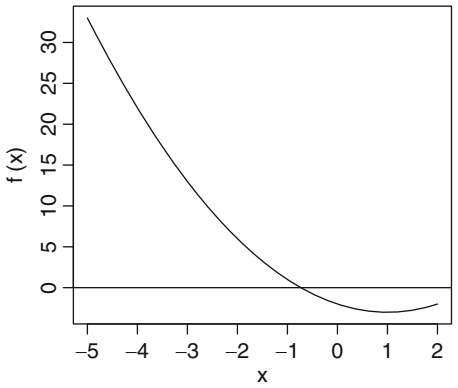
- **Statistics**

  Here are a few statistical calculations.

```
> weight <- c(70,75,74)
> mean(weight)
[1] 73
> height <- c(182,190,184)
> mat <- cbind(weight,height)
> mat
     weight height
[1,]     70    182
[2,]     75    190
[3,]     74    184
> apply(mat,MARGIN=2,FUN=mean)
  weight   height
 73.0000 185.3333
> ?apply
> colMeans(mat)
  weight   height
 73.0000 185.3333
> names <- c("Peter","Ben","John")
> data <- data.frame(Names=names,height,weight)
> summary(data)
   Names       height          weight
 Ben  :1   Min.   :182.0   Min.   :70.0
 John :1   1st Qu.:183.0   1st Qu.:72.0
 Peter:1   Median :184.0   Median :74.0
           Mean   :185.3   Mean   :73.0
           3rd Qu.:187.0   3rd Qu.:74.5
           Max.   :190.0   Max.   :75.0
```

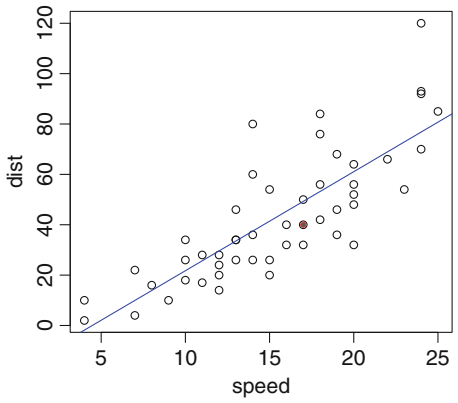
- **Some plots**

```
> f <- function(x) x^2-2*x-2
> curve(f,xlim=c(-5,2));abline(h=0)
> locator(1) # Click on the intersection of the two curves.
```

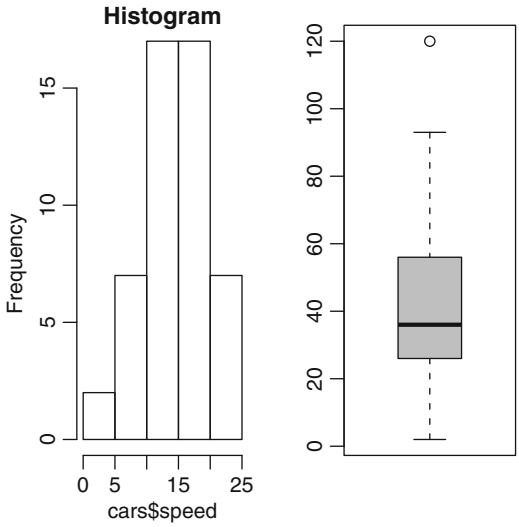



```
> uniroot(f,c(-5,2))
$root
[1] -0.7320503
$f.root
[1] -1.874450e-06
$iter
[1] 8
$estim.prec
[1] 6.103516e-05
```

```
> plot(cars)
> abline(lm(dist~speed,data=cars),col="blue")
> points(cars[30,],col="red",pch=20)
```




```
> par(mfrow=c(1,2))
> hist(cars$speed,main="Histogram")
> boxplot(cars$dist,col="orange")
```



See also

This link points to a reference card of the most useful R functions http://cran.r-project.org/doc/contrib/Short-refcard.pdf