Introduction to the R Project for Statistical Computing for use at ITC

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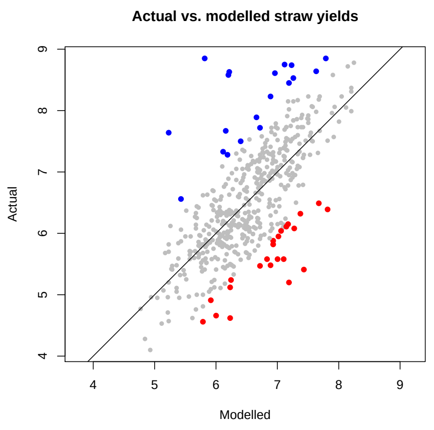
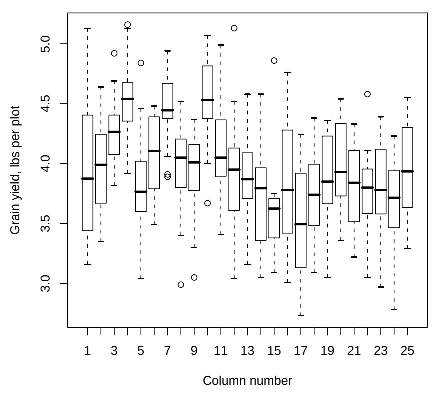
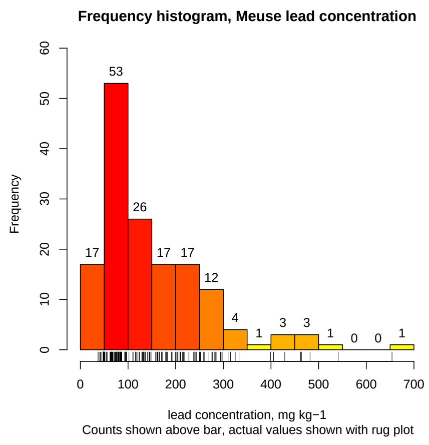
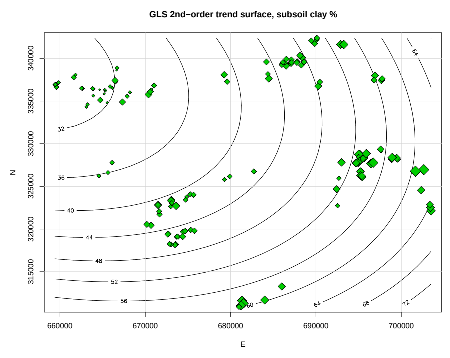








Contents

List of Figures

List of Tables

0 If you are impatient . . .

1. Install R and RStudio on your MS-Windows, Mac OS/X or Linux system (§A);

2. Run RStudio; this will automatically start R within it;

3. Follow one of the tutorials (§10.2) such as my "Using the R Environment for Statistical Computing: An example with the Mercer & Hall wheat yield dataset"[1] [48];

4. Experiment!

5. Use this document as a reference.

1 What is R?

R is an open-source environment for statistical computing and visualisation. It is based on the S language developed at Bell Laboratories in the 1980's [20], and is the product of an active movement among statisticians for a powerful, programmable, portable, and open computing environment, applicable to the most complex and sophsticated problems, as well as "routine" analysis, without any restrictions on access or use. Here is a description from the R Project home page:[2]

> "R is an **integrated suite of software facilities** for data manipulation, calculation and graphical display. It includes:
>
> · an effective **data handling and storage** facility,
>
> · a suite of **operators for calculations on arrays**, in particular **matrices**,
>
> · a large, coherent, integrated collection of **intermediate tools for data analysis**,
>
> · **graphical facilities** for data analysis and display either on-screen or on hardcopy, and
>
> · a well-developed, simple and effective **programming language** which includes conditionals, loops, user-defined recursive functions and input and output facilities."

The last point has resulted in another major feature:

· **Practising statisticians** have implemented hundreds of **spe-**

[1] `http://www.itc.nl/personal/rossiter/pubs/list.html#pubs_m_R`, item 2
[2] `http://www.r-project.org/`

cialised statistical produres for a wide variety of applications as **contributed packages**, which are also freely-available and which integrate directly into R.

A few examples especially relevant to ITC's mission are:

- the `gstat`, `geoR` and `spatial` packages for geostatistical analysis, contributed by Pebesma [33], Ribeiro, Jr. & Diggle [39] and Ripley [40], respectively;
- the `spatstat` package for spatial point-pattern analysis and simulation;
- the `vegan` package of ordination methods for ecology;
- the `circular` package for directional statistics;
- the `sp` package for a programming interface to spatial data;
- the `rgdal` package for GDAL-standard data access to geographic data sources;

There are also packages for the most modern statistical techniques such as:

- sophisticated modelling methods, including generalized linear models, principal components, factor analysis, bootstrapping, and robust regression; these are listed in §4.19;
- wavelets (`wavelet`);
- neural networks (`nnet`);
- non-linear mixed-effects models (`nlme`);
- recursive partitioning (`rpart`);
- splines (`splines`);
- random forests (`randomForest`)

2 Why R for ITC?

"ITC" is an abbreviation for University of Twente, Faculty of Geo-information Science& Earth Observation. It is a faculty of the University of Twente located in Enschede, the Netherlands, with a thematic focus on geo-information science and earth observation in support of development. Thus the two pillars on which ITC stands are *development-related* and *geo-information*. R supports both of these.

2.1 Advantages

R has several major **advantages** for a typical ITC student or collaborator:

item It is **completely free** and will always be so, since it is issued under the GNU Public License;[3]It is **freely-available over the internet**, via a large network of *mirror* servers; see Appendix A for how to obtain R; It runs on many **operating systems**: Unix© and derivatives including Darwin, Mac OS X, Linux, FreeBSD, and Solaris; most flavours of Microsoft Windows; Apple Macintosh OS; and even some mainframe OS. It is the product of **international collaboration** between **top computational statisticians** and computer language designers; It allows **statistical analysis** and **visualisation** of **unlimited sophistication**; you are not restricted to a small set of procedures or options, and because of the contributed packages, you are not limited to one method of accomplishing a given computation or graphical presentation; It can work on **objects of unlimited size and complexity** with a consistent, logical **expression language**; It is supported by comprehensive **technical documentation** and user-contributed tutorials (§10). There are also several good textbooks on statistical methods that use R (or S) for illustration. Every computational step is **recorded**, and this history can be saved for later use or documentation. It stimulates **critical thinking** about problem-solving rather than a "push the button" mentality. It is **fully programmable**, with its own sophisticated computer language (§4). Repetitive procedures can easily be automated by user-written **scripts** (§3.5). It is easy to write your own **functions** (§B), and not too difficult to write whole **packages** if you invent some new analysis; All **source code** is published, so you can see the exact algorithms being used; also, expert statisticians can make sure the code is correct; It can **exchange data** in MS-Excel, text, fixed and delineated formats (e.g. CSV), so that existing datasets are easily imported (§6), and results computed in R are easily exported (§8). Most programs written for the commercial **S-PLUS** program will run unchanged, or with minor changes, in R (§2.3.1).

[3] http://www.gnu.org/copyleft/gpl.html

2.2 Disadvantages

R has its **disadvantages** (although "every disadvantage has its advantage"):

1. The default Windows and Mac OS X **graphical user interface** (GUI) (§3.2) is limited to simple system interaction and does not include statistical procedures. The user must **type commands** to enter data, do analyses, and plot graphs. This has the advantage that the user has complete control over the system. The `Rcmdr` add-on package (§3.6) provides a reasonable GUI for common tasks, and there are various development environments for R, such as RStudio (§3.1).

2. The user must decide on the **analysis sequence** and execute it **step-by-step**. However, it is easy to create **scripts** with all the steps in an analysis, and run the script from the command line or menus (§3.5); scripts can be preared in code editors built into GUI versions of R or separate front-ends such as Tinn-R (§3.5) or RStudio (§3.1). A major advantage of this approach is that intermediate results can be reviewed, and scripts can be edited and run as batch processes.

3. The user must learn a **new way of thinking about data**, as **data frames** (§4.7) and **objects** each with its **class**, which in turn supports a set of **methods** (§4.13). This has the advantage common to object-oriented languages that you can only operate on an object according to methods that make sense[4] and methods can adapt to the type of object.[5]

4. The user must learn the **S language** (§4), both for commands and the notation used to specify **statistical models** (§4.17). The S statistical modelling language is a *lingua franca* among statisticians, and provides a compact way to express models.

2.3 Alternatives

There are many ways to do computational statistics; this section discusses them in relation to R. None of these programs are open-source, meaning that you must trust the company to do the computations correctly.

2.3.1 S-PLUS

S-PLUS is a commercial program distributed by the Insightful corporation,[6] and is a popular choice for large-scale commerical statistical computing. Like R, it is a dialect of the original S language developed at Bell Laborato-

[4] For example, the `t` (transpose) function only can be applied to matrices
[5] For example, the `summary` and `plot` methods give different results depending on the class of object.
[6] `http://www.insightful.com/`

ries.[7] S-PLUS has a full graphical user interface (GUI); it may be also used like R, by typing commands at the command line interface or by running scripts. It has a rich interactive graphics environment called Trellis, which has been emulated with the `lattice` package in R (§5.2). S-PLUS is licensed by local distributors in each country at prices ranging from moderate to high, depending factors such as type of licensee and application, and how many computers it will run on. The important point for ITC R users is that their expertise will be immediately applicable if they later use S-PLUS in a commercial setting.

2.3.2 Statistical packages

There are many statistical packages, including MINITAB, SPSS, Statistica, Systat, GenStat, and BMDP,[8] which are attractive if you are already familiar with them or if you are required to use them at your workplace. Although these are programmable to varying degrees, it is not intended that specialists develop completely new algorithms. These must be purchased from local distributors in each country, and the purchaser must agree to the license terms. These often have common analyses built-in as menu choices; these can be convenient but it is tempting to use them without fully understanding what choices they are making for you.

SAS is a commercial competitor to S-PLUS, and is used widely in industry. It is fully programmable with a language descended from PL/I (used on IBM mainframe computers).

2.3.3 Special-purpose statistical programs

Some programs adress specific statistical issues, e.g. geostatistical analysis and interpolation (SURFER, `gslib`, GEO-EAS), ecological analysis (FRAGSTATS), and ordination (CONOCO). The algorithms in these programs have or can be programmed as an R package; examples are the `gstat` program for geostatistical analysis[9] [35], which is now available within R [33], and the `vegan` package for ecological statistics.

2.3.4 Spreadsheets

Microsoft Excel is useful for data manipulation. It can also calculate some statistics (means, variances, . . .) directly in the spreadsheet. This is also an add-on module (menu item Tools | Data Analysis. . .) for some common statistical procedures including random number generation. Be aware that

[7] There are differences in the language definitions of S, R, and S-PLUS that are important to programmers, but rarely to end-users. There are also differences in how some algorithms are implemented, so the numerical results of an identical method may be somewhat different.

[8] See the list at `http://www.stata.com/links/stat_software.html`

[9] `http://www.gstat.org/`

Excel was not designed by statisticians. There are also some commercial add-on packages for Excel that provide more sophisticated statistical analyses. Excel's default graphics are easy to produce, and they may be customized via dialog boxes, but their design has been widely criticized. Least-squares fits on scatterplots give no regression diagnostics, so this is not a serious linear modelling tool.

OpenOffice[10] includes an open-source and free spreadsheet (Open Office Calc) which can replace Excel.

2.3.5 Applied mathematics programs

MATLAB is a widely-used applied mathematics program, especially suited to matrix maniupulation (as is R, see §4.6), which lends itself naturally to programming statistical algorithms. Add-on packages are available for many kinds of statistical computation. Statistical methods are also programmable in Mathematica.

[10] http://www.openoffice.org/

3 Using R

There are several ways to work with R:

- with the **RStudio** integrated development environment (IDE) (§3.1); this is recommended for the typical UT/ITC user;
- with the **R console GUI** (§3.2);
- with the **Tinn-R editor** (§3.4);
- from another IDE such as JGR;
- from a command line R interface (CLI) (§3.3);
- from the ESS (Emacs Speaks Statistics) module of the Emacs editor.

Of these, RStudio is the best choice for most ITC users; it contains an R command line interface but with a code editor, help text, a workspace browser, and graphic output.

3.1 The RStudio integrated development environment

RStudio[11] is an excellent cross-platform[12] integrated development environment (IDE) for R. A screenshot is shown in Figure 1. This environment includes the command line interface, a code editor, output graphs, history, help, workspace contents, and package manager all in one atttractive interface. The typical use is: (1) open a script or start a new script; (2) change the working directory to this script's location; (3) write R code in the script; (4) pass lines of code from the script to the command line interface and evaluate the output; (5) examine any graphs and save for later use. If you chose to use RStudio, you first install R, and then RStudio[13].

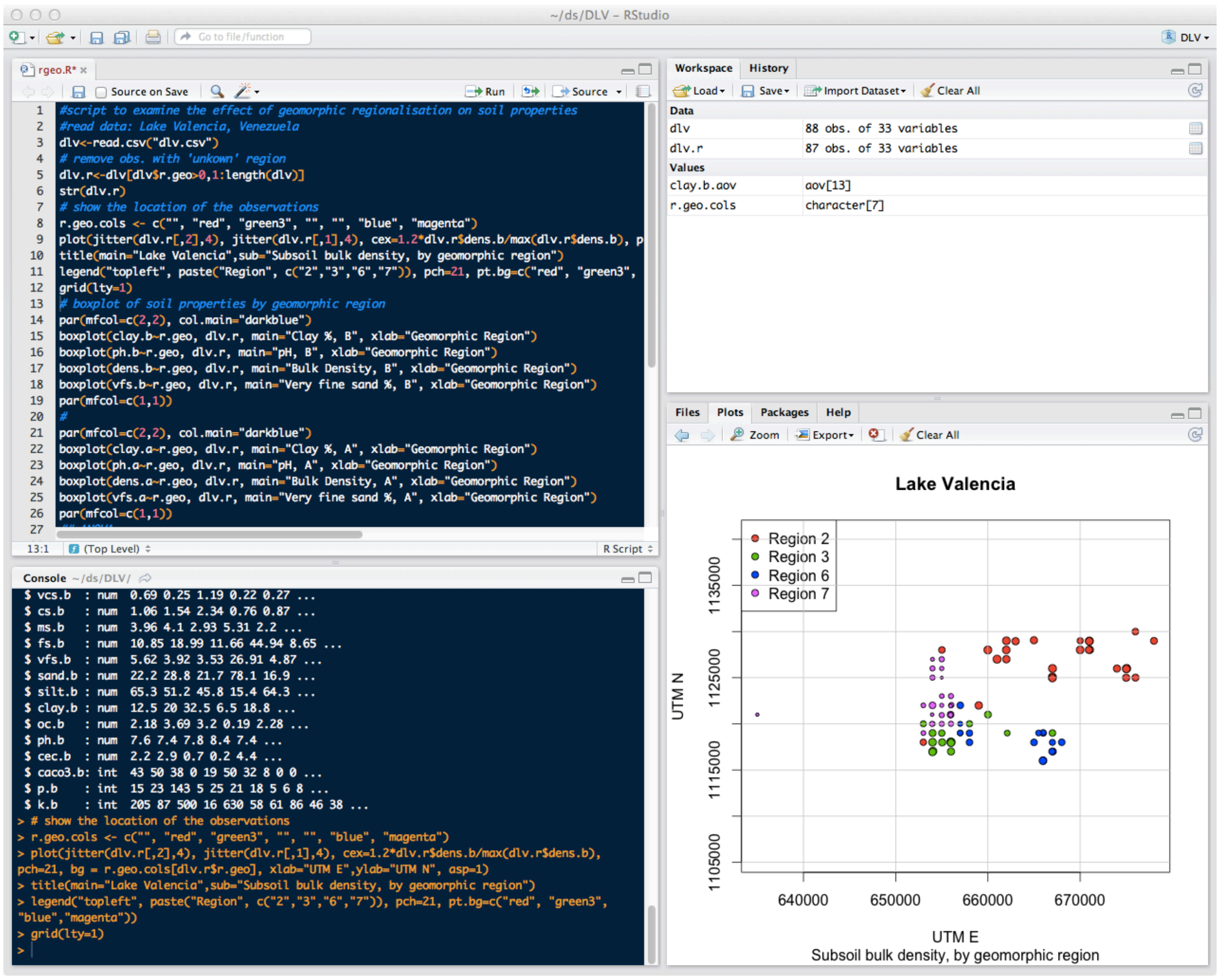
3.2 R console GUI

The default interface for both Windows and Mac OS/X is a simple GUI. We refer to these as "R console GUI" because they provide an easy-to-use interface to the R command line, a simple script editor, graphics output, and on-line help; they do not contain any menus for data manipulation or statistical procedures.

R for Linux has no GUI; however, several independent Linux programs[14] provide a GUI development environment; an example is RStudio (§3.1).

You can download and install R as instructed in §A. On Windows the in-

[11] http://www.rstudio.org/
[12] Windows, Mac OS/X, Linux
[13] from http://www.rstudio.org/
[14] http://www.linuxlinks.com/article/20110306113701179/GUIsforR.html



```
#script to examine the effect of geomorphic regionalisation on soil properties
#read data: Lake Valencia, Venezuela
dlv<-read.csv("dlv.csv")
# remove obs. with 'unkown' region
dlv.r<-dlv[dlv$r.geo>0,1:length(dlv)]
str(dlv.r)
# show the location of the observations
r.geo.cols <- c("", "red", "green3", "", "", "blue", "magenta")
plot(jitter(dlv.r[,2],4), jitter(dlv.r[,1],4), cex=1.2*dlv.r$dens.b/max(dlv.r$dens.b), p
title(main="Lake Valencia",sub="Subsoil bulk density, by geomorphic region")
legend("topleft", paste("Region", c("2","3","6","7")), pch=21, pt.bg=c("red", "green3",
grid(lty=1)
# boxplot of soil properties by geomorphic region
par(mfcol=c(2,2), col.main="darkblue")
boxplot(clay.b~r.geo, dlv.r, main="Clay %, B", xlab="Geomorphic Region")
boxplot(ph.b~r.geo, dlv.r, main="pH, B", xlab="Geomorphic Region")
boxplot(dens.b~r.geo, dlv.r, main="Bulk Density, B", xlab="Geomorphic Region")
boxplot(vfs.b~r.geo, dlv.r, main="Very fine sand %, B", xlab="Geomorphic Region")
par(mfcol=c(1,1))
#
par(mfcol=c(2,2), col.main="darkblue")
boxplot(clay.a~r.geo, dlv.r, main="Clay %, A", xlab="Geomorphic Region")
boxplot(ph.a~r.geo, dlv.r, main="pH, A", xlab="Geomorphic Region")
boxplot(dens.a~r.geo, dlv.r, main="Bulk Density, A", xlab="Geomorphic Region")
boxplot(vfs.a~r.geo, dlv.r, main="Very fine sand %, A", xlab="Geomorphic Region")
par(mfcol=c(1,1))
```

```
 $ vcs.b  : num  0.69 0.25 1.19 0.22 0.27 ...
 $ cs.b   : num  1.06 1.54 2.34 0.76 0.87 ...
 $ ms.b   : num  3.96 4.1 2.93 5.31 2.2 ...
 $ fs.b   : num  10.85 18.99 11.66 44.94 8.65 ...
 $ vfs.b  : num  5.62 3.92 3.53 26.91 4.87 ...
 $ sand.b : num  22.2 28.8 21.7 78.1 16.9 ...
 $ silt.b : num  65.3 51.2 45.8 15.4 64.3 ...
 $ clay.b : num  12.5 20 32.5 6.5 18.8 ...
 $ oc.b   : num  2.18 3.69 3.2 0.19 2.28 ...
 $ ph.b   : num  7.6 7.4 7.8 8.4 7.4 ...
 $ cec.b  : num  2.2 2.9 0.7 0.2 4.4 ...
 $ caco3.b: int  43 50 38 0 19 50 32 8 0 0 ...
 $ p.b    : int  15 23 143 5 25 21 18 5 6 8 ...
 $ k.b    : int  205 87 500 16 630 58 61 86 46 38 ...
> # show the location of the observations
> r.geo.cols <- c("", "red", "green3", "", "", "blue", "magenta")
> plot(jitter(dlv.r[,2],4), jitter(dlv.r[,1],4), cex=1.2*dlv.r$dens.b/max(dlv.r$dens.b),
pch=21, bg = r.geo.cols[dlv.r$r.geo], xlab="UTM E",ylab="UTM N", asp=1)
> title(main="Lake Valencia",sub="Subsoil bulk density, by geomorphic region")
> legend("topleft", paste("Region", c("2","3","6","7")), pch=21, pt.bg=c("red", "green3",
"blue","magenta"))
> grid(lty=1)
> 
```

```
Data
dlv          88 obs. of 33 variables
dlv.r        87 obs. of 33 variables
Values
clay.b.aov   aov[13]
r.geo.cols   character[7]
```

Figure 1: The RStudio screen

stallation will create a Start menu item and a desktop shortcut. Within the ITC network, R can be installed with the ITC Software Manager.

3.2.1 Running the R console GUI

This section §3.2.1 is only relevant if you run R by itself, not within an IDE such as RStudio.

R GUI for Windows is started like any Windows program: from the Start menu, from a desktop shortcut, or from the application's icon in Explorer.

By default, R starts in the directory where it was installed, which is not where you should store your projects. So, you will probably want to change your workspace, as explained in §3.2.2. You can also create a desktop shortcut or Start menu item for R, also as explained in §3.2.2.

To stop an R session, type `q()` at the command prompt[15], or select the `File | Exit` menu item in the Windows GUI.

3.2.2 Setting up a workspace in Windows

An important concept in R is the **workspace**, which contains the local data and procedures for a given statistics project. Under Windows this is usually determined by the folder from which R is started.

Under Windows, the easiest way to set up a statistics project is:

1. Create a **shortcut** to `RGui.exe` on your desktop;

2. Modify its **properties** so that its in your working directory rather than the default (e.g. `P:\R\bin`).

Now when you double-click on the shortcut, it will start R in the directory of your choice. So, you can set up a different shortcut for each of your projects.

Another way to set up a new statistics project in R is:

1. Start R as just described: **double-click the icon** for program `RGui.exe` in the Explorer;

2. Select the `File | Change Directory ...` menu item in R;

3. Select the directory where you want to work;

4. Exit R by selecting the `File | Exit` menu item in R, or typing the `q()` command; R will ask "Save workspace image?"; Answer **y** (Yes). This will create two files in your working directory: `.Rhistory` and `.RData`.

The next time you want to work on the same project:

1. Open Explorer and navigate to the working directory

2. **Double-click on the icon** for file `.RData`

R should open in that directory, with your previous workspace already loaded. (If R does not open, instead Explorer will ask you what programs should open files of type `.RData`; navigate to the program `RGui.exe` and select it.)

If you don't see the file `.RData` in your Explorer, this is because Windows

[15] This is a special case of the `q` function

Revealing hidden files in Windows

considers any file name that begins with "." to be a 'hidden' file. You need to select the `Tools | Folder options` in Explorer, then the `View` tab, and *click the radio button* for `Show hidden files and folders`. You must also *un-check the box* for `Hide file extensions for known file types`.

3.2.3 Saving your analysis steps

The `File | Save to file ...` menu command will save the entire console contents, i.e. both your commands and R's response, to a text file, which you can later review and edit with any text editor. This is useful for cutting-and-pasting into your reports or thesis, and also for writing scripts to repeat procedures.

3.2.4 Saving your graphs

In the Windows version of R, you can save any graphical output for insertion into documents or printing. If necessary, bring the graphics window to the front (e.g. click on its title bar), select menu command `File | Save as ...`, and then one of the formats. Most useful for insertion into MS-Word documents is Metafile; most useful for LaTeX is Postscript; most useful for `PDFLaTeX` and stand-alone printing is PDF. You can later review your saved graphics with programs such as Windows Picture Editor. If you want to add other graphical elements, you may want to save as a PNG or JPEG; however in most cases it is cleaner to add annotations within R itself.

You can also review graphics within the Windows R GUI itself. Create the first graph, bring the graphics window to foreground, and then select the menu command `History | Recording`. After this all graphs are automatically saved within R, and you can move through them with the up and down arrow keys.

You can also write your graphics commands directly to a graphics file in many formats, e.g. PDF or JPEG. You do this by opening a graphics device, writing the commands, and then closing the device. You can get a list of graphics devices (formats) available on your system with `?Devices` (note the upper-case `D`).

For example, to write a PDF file, we open a PDF graphics device with the `pdf` function, write to it, and then close it with the `dev.off` function:

```
pdf("figure1.pdf", h=6, w=6)
hist(rnorm(100), main="100 random values from N[0,1])")
dev.off()
```

Note the use of the optional `height=` and `width=` arguments (here abbreviated `h=` and `w=`) to specifiy the size of the PDF file (in US inches); this affects the font sizes. The defaults are both 7 inches (17.18 cm).

3.3 Working with the R command line

These instructions apply to the simple R GUI and the R command line interface window within RStudio. One of the windows in these interfaces is the command line, also called the R console.

It is also possible to work directly with the command line and no GUI:

- Under Linux and Mac OS/X, at the shell prompt just type `R`; there are various startup options which you can see with `R -help`.
- Under Windows, find and open the executable `Rterm`; this opens R in a terminal (non-graphics) window.

3.3.1 The command prompt

You perform most actions in R by typing **commands** in a **command line interface window**,[16] in response to a **command prompt**, which usually looks like this:

```
>
```

The `>` is a **prompt symbol** displayed by R, *not typed by you*. This is R's way of telling you it's ready for you to type a command.

Type your command and press the `Enter` or `Return` keys; R will execute your command.

If your entry is not a complete R command, R will prompt you to complete it with the **continuation prompt symbol**:

```
+
```

R will accept the command once it is *syntactically complete*; in particular the parentheses must balance. Once the command is complete, R then presents its results in the same command line interface window, directly under your command.

If you want to abort the current command (i.e. not complete it), press the `Esc` ("escape") key.

For example, to draw 500 samples from a binomial distribution of 20 trials with a 40% chance of success[17] you would first use the `rbinom` function and then summarize it with the `summary` function, as follows:[18]

[16] An alternative for some analyses is the `Rcmdr` GUI explained in §3.6.
[17] This simulates, for example, the number of women who would be expected, by chance, to present their work at a conference where 20 papers are to be presented, if the women make up 40% of the possible presenters.
[18] Your output will probably be somewhat different; why?

```
> x <- rbinom(500,20,.4)
> summary(x)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  2.000   7.000   8.000   8.232  10.000  15.000
```

This could also have been entered on several lines:

```
> x <- rbinom(
+ 500,20,.4
+ )
```

You can use any white space to increase legibility, *except* that the assignment symbol <- must be written together:

```
> x  <-   rbinom(500,         20,  0.4)
```

R is **case-sensitive**; that is, function `rbinom` must be written just that way, not as `Rbinom` or `RBINOM` (these might be different functions). Variables are also case-sensitive: `x` and `X` are different names.

Some functions produce output in a separate graphics window:

```
> hist(x)
```

3.3.2 On-line help in R

Both the base R system and contributed packages have extensive help within the running R environment. In RStudio the “Help” tab in the lower-right window pane gives access to the help system and (via the “home” button) to the R manuals. From the command prompt you can also get help on any function with the `?` function; this is a shorthand for the `help` function:

For example, if you don’t know the format of the `rbinom` function used above. Either of these two forms:

```
> ?rbinom
> help(rbinom)
```

will display a text page with the syntax and options for this function. There are **examples** at the end of many help topics, with executable code that you can experiment with to see just how the function works.

Searching for functions

If you don’t know the function name, you can search the help for relevant functions using the `help.search` function[19]:

```
> help.search("binomial")
```

[19] also available via the `Help | Search help ...` menu item

will show a window with all the functions that include this word in their description, along with the packages where these functions are found, whether already loaded or not.

In the list shown as a result of the above function, we see the `Binomial (stats)` topic; we can get more information on it with the `?` function; this is written as the `?` character *immediately* followed by the function name:

```
> ?Binomial
```

This shows the named topic, which explains the `rbinom` (among other) functions.

Vignettes

Packages have a long list of functions, each of which has its own documentation as explained above. Some packages are documented as a whole by so-called **vignettes**[20]; for now most packages do not have one, but more will be added over time.

You can see a list of the vignettes installed on your system with the `vignette` function with an empty argument:

```
> vignette()
```

and then view a specific vignette by naming it:

```
> vignette("sp")
```

3.4 The Tinn-R code editor

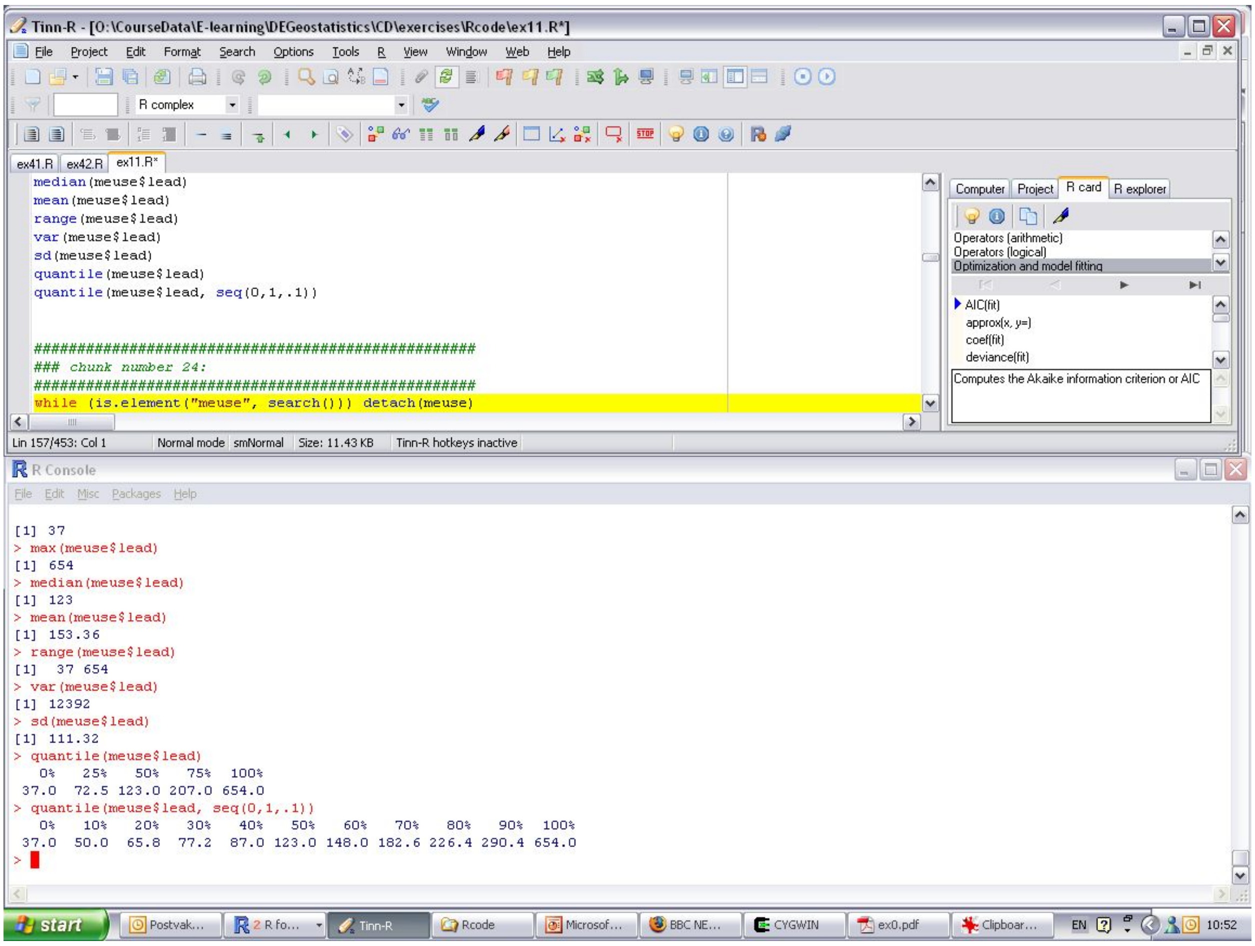
For Windows user, the Tinn-R code editor for Windows[21] is recommended for those who do not choose to use RStudio. This is tightly integrated with the Windows R GUI, as shown in Figure 2. R code is syntax-highlighted and there is extensive help within the editor to select the proper commands and arguments. Commands can be sent directly from the editor to R, or saved in a file and sourced.

3.5 Writing and running scripts

After you have worked out an analysis by typing a sequence of commands, you will probably want to re-run them on edited data, new data, subsets etc. This is easy to do by means of **scripts**, which are simply lists of commands in a file, written exactly as you would type them at the command line interface. They are run with the `source` function. A useful feature of scripts is that you can include comments (lines that begin with the #

[20] from the OED meaning "a brief verbal description of a person, place, etc.; a short descriptive or evocative episode in a play, etc."

[21] http://www.sciviews.org/Tinn-R/


Tinn-R - [O:\CourseData\E-learning\DEGeostatistics\CD\exercises\Rcode\ex11.R*]
File Project Edit Format Search Options Tools R View Window Web Help
R complex
ex41.R ex42.R ex11.R*
Computer Project R card R explorer
Operators (arithmetic)
Operators (logical)
Optimization and model fitting
AIC(fit)
approx(x, y=)
coef(fit)
deviance(fit)
Computes the Akaike information criterion or AIC
Lin 157/453: Col 1
Normal mode smNormal
Size: 11.43 KB
Tinn-R hotkeys inactive
R Console
File Edit Misc Packages Help
start
Postvak...
2 R fo...
Tinn-R
Rcode
Microsof...
BBC NE...
CYGWIN
ex0.pdf
Clipboar...
EN
10:52

```
median(meuse$lead)
mean(meuse$lead)
range(meuse$lead)
var(meuse$lead)
sd(meuse$lead)
quantile(meuse$lead)
quantile(meuse$lead, seq(0,1,.1))


########################################################
### chunk number 24:
########################################################
while (is.element("meuse", search())) detach(meuse)
```

```
[1] 37
> max(meuse$lead)
[1] 654
> median(meuse$lead)
[1] 123
> mean(meuse$lead)
[1] 153.36
> range(meuse$lead)
[1]  37 654
> var(meuse$lead)
[1] 12392
> sd(meuse$lead)
[1] 111.32
> quantile(meuse$lead)
   0%   25%   50%   75%  100%
 37.0  72.5 123.0 207.0 654.0
> quantile(meuse$lead, seq(0,1,.1))
   0%   10%   20%   30%   40%   50%   60%   70%   80%   90%  100%
 37.0  50.0  65.8  77.2  87.0 123.0 148.0 182.6 226.4 290.4 654.0
>
```

Figure 2: The Tinn-R screen, with the R command line interface also visible

character) to explain to yourself or others what the script is doing and why.

Here's a step-by-step description of how to create and run a simple script which draws two random samples from a normal distribution and computes their correlation:[22]

1. if you are using RStudio or Tinn-R open a new script. If using RGui, open a new document in a **plain-text** editor, i.e., one that does not insert any formatting. Under MS-Windows you can use Notepad or Wordpad;

2. Type in the following lines in the script editor:

```
x <- rnorm(100, 180, 20)
y <- rnorm(100, 180, 20)
```

[22] What is the expected value of this correlation coefficient?

```
plot(x, y)
cor.test(x, y)
```

3. Save the file with the name `test.R`, in a convenient directory.

4. In RStudio, click the "run script" button; in RGui, select menu command `File | Source R code ...`

5. In the file selection dialog, locate the file `test.R` that you just saved (changing directories if necessary) and select it; R will run the script.

6. Examine the output.

You can source the file directly from the command line. Instead of steps 5 and 6 above, just type `source("test.R")` at the R command prompt (assuming you've switched to the directory where you saved the script).

Appendix B contains an example of a more sophisticated script.

For serious work with R you should use a more powerful text editor. The R for Windows, R for Mac OS X and JGR interfaces include built-in editors; another choice on Windows is WinEdt[23]. And both RStudio (§3.1) and Tinn_R (§3.4) have code editors. For the ultimate in flexibility and power, try `emacs`[24] with the ESS (Emacs Speaks Statistics) module[25]; learning `emacs` is not trivial but rather an investment in a lifetime of efficient computing.

3.6 The Rcmdr GUI

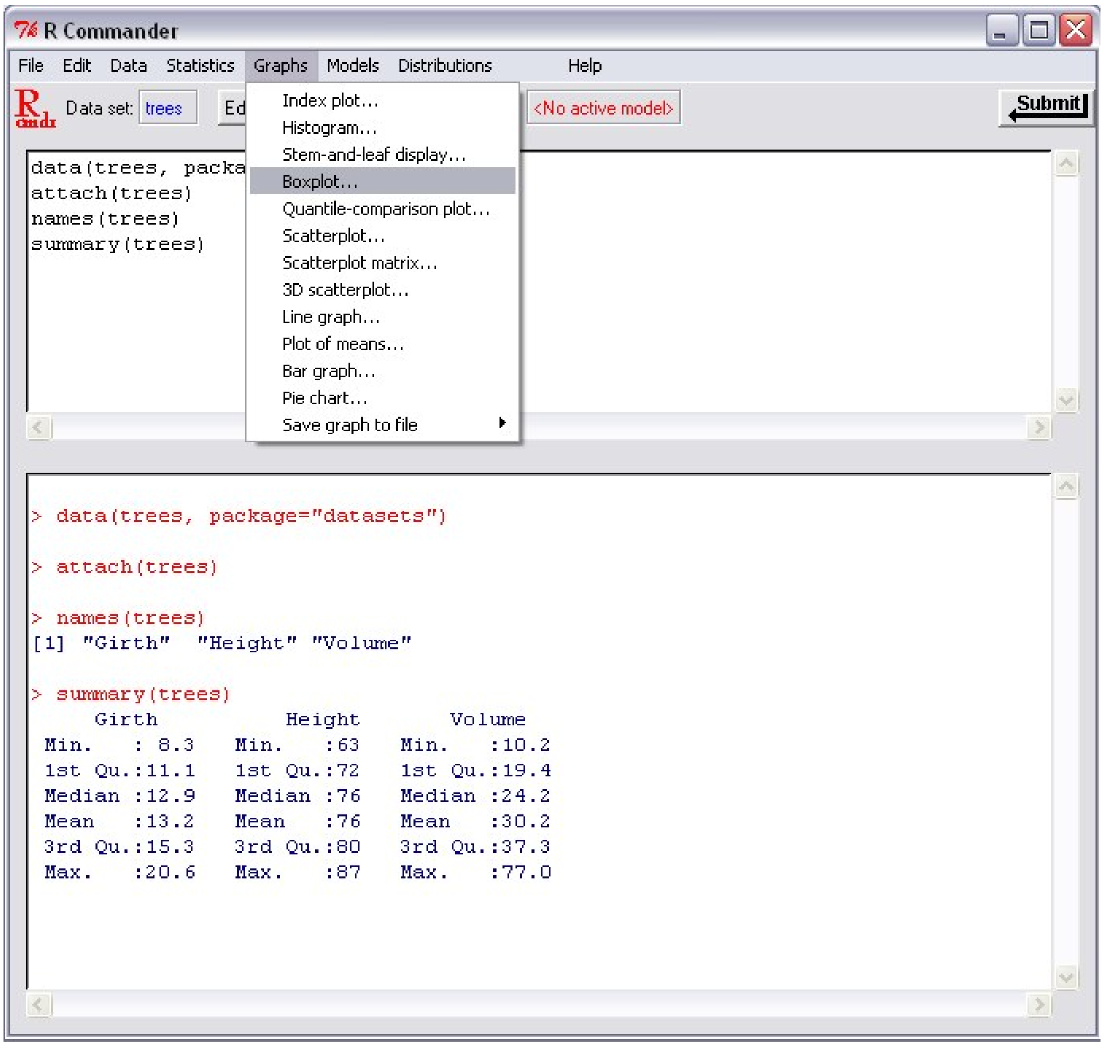
The `Rcmdr` add-on package, written by John Fox of McMaster University, provides a GUI for common data management and statistical analysis tasks. It is loaded like any other package, with the `require` function:

```
> require("Rcmdr")
```

As it is loaded, it starts up in another window, with its own menu system. You can run commands from these menus, but you can also continue to type commands at the R prompt. Figure 3 shows an R Commander screen shot.

To use `Rcmdr`, you first import or activate a dataset using one of the commands on `Rcmdr`'s `Data` menu; then you can use procedures in the `Statistics`, `Graphs`, and `Models` menus. You can also create and graph probability distributions with the `Distributions` menu.

[23] http://www.winedt.com/
[24] http://en.wikipedia.org/wiki/Emacs
[25] http://stat.ethz.ch/ESS/



```
data(trees, packa
attach(trees)
names(trees)
summary(trees)
```

```
> data(trees, package="datasets")

> attach(trees)

> names(trees)
[1] "Girth"  "Height" "Volume"

> summary(trees)
     Girth          Height       Volume
 Min.   : 8.3   Min.   :63   Min.   :10.2
 1st Qu.:11.1   1st Qu.:72   1st Qu.:19.4
 Median :12.9   Median :76   Median :24.2
 Mean   :13.2   Mean   :76   Mean   :30.2
 3rd Qu.:15.3   3rd Qu.:80   3rd Qu.:37.3
 Max.   :20.6   Max.   :87   Max.   :77.0
```

Figure 3: The R Commander screen: Menu bar at the top; a top panel showing commands submitted to R by the menu commands; a bottom panel showing the results after execution by R

When using `Rcmdr`, observe the commands it formats in response to your menu and dialog box choices. Then you can modify them yourself at the R command line or in a script.

`Rcmdr` also provides some nice graphics options, including scatterplots (2D and 3D) where observations can be coloured by a classifying factor.

3.7 Loading optional packages

R starts up with a `base` package, which provides basic statistics and the R language itself. There are a large number of optional packages for specific statistical procedures which can be loaded during a session. Some of these are quite common, e.g. MASS ("Modern Applied Statistics with S" [57]) and lattice (Trellis graphics [50], §5.2). Others are more specialised, e.g. for geostatistics and time-series analysis, such as gstat. Some are loaded by default in the base R distribution (see Table 4).

If you try to run a function from one of these packages before you load it, you will get the error message

```
Error: object not found
```

You can see a list of the packages installed on your system with the library function with an empty argument:

```
> library()
```

To see what functions a package provides, use the library function with the named argument. For example, to see what's in the geostatistical package gstat:

```
> library(help=gstat)
```

To load a package, simply give its name as an argument to the require function, for example:

```
> require(gstat)
```

Once it is loaded, you can get help on any function in the package in the usual way. For example, to get help on the variogram method of the gstat package, once this package has been loaded:

```
> ?variogram
```

3.8 Sample datasets

R comes with many example datasets (part of the default datasets package) and most add-in packages also include example datasets. Some of the datasets are classics in a particular application field; an example is the iris dataset used extensively by R A Fisher to illustrate multivariate methods.

To see the list of installed datasets, use the data method with an empty argument:

```
> data()
```

To see the datasets in a single add-in package, use the package= argument:

```
> data(package="gstat")
```

To load one of the datasets, use its name as the argument to the `data` method:

```
> data(iris)
```

The dataframe representing this dataset is now in the workspace.

4 The S language

R is a dialect of the S language, which has a syntax similar to ALGOL-like programming languages such as C, Pascal, and Java. However, S is object-oriented, and makes vector and matrix operations particularly easy; these make it a modern and attractive user and programming environment. In this section we build up from simple to complex commands, and break down their anatomy. A full description of the language is given in the *R Language Definition* [38][26] and a comprehensive introduction is given in the *Introduction to R* [36].[27] This section reviews the most outstanding features of S.

All the functions, packages and datasets mentioned in this section (as well as the rest of this note) are indexed (§C) for quick reference.

4.1 Command-line calculator and mathematical operators

The simplest way to use R is as an interactive calculator. For example, to compute the number of radians in one Babylonian degree of a circle:

```
> 2*pi/360
[1] 0.0174533
```

As this example shows, S has a few built-in constants, among them `pi` for the mathematical constant π. The Euler constant e is not built-in, it must be calculated with the `exp` function as `exp(1)`.

If the assignment operator (explained in the next section) is not present, the *expression* is evaluated and its value is displayed on the console. S has the usual arithmetic operators `+`, `-`, `*`, `/`, `^` and some less-common ones like `%%` (modulus) and `%/%` (integer division). Expressions are evaluated in accordance with the usual *operator precedence*; parentheses may be used to change the precedence or make it explicit:

```
> 3 / 2^2 + 2 * pi
[1] 7.03319
> ((3 / 2)^2 + 2) * pi
[1] 13.3518
```

Spaces may be used freely and do not alter the meaning of any S expression.

Common **mathematical functions** are provided as *functions* (see §4.3), including `log`, `log10` and `log2` functions to compute logarithms; `exp` for exponentiation; `sqrt` to extract square roots; `abs` for absolute value; `round`, `ceiling`, `floor` and `trunc` for rounding and related operations; trigonometric functions such as `sin`, and inverse trigonometric functions such as

[26] In `RGui`, menu command `Help | Manuals | R Language Manual`
[27] In `RGui`, menu command `Help | Manuals | R Introduction`

asin.

```
> log(10); log10(10); log2(10)
[1] 2.3026
[1] 1
[1] 3.3219
> round(log(10))
[1] 2
> sqrt(5)
[1] 2.2361
sin(45 * (pi/180))
[1] 0.7071
> (asin(1)/pi)*180
[1] 90
```

4.2 Creating new objects: the assignment operator

New objects in the workspace are created with the *assignment operator* `<-`, which may also be written as =:

```
> mu <- 180
> mu = 180
```

The symbol on the left side is given the value of the *expression* on the right side, creating a new object (or redefining an existing one), here named `mu`, in the workspace and *assigning* it the value of the expression, here the scalar value `180`, which is stored as a one-element vector. The two-character symbol `<-` *must* be written as two adjacent characters with no spaces..

Now that `mu` is defined, it may be printed at the console as an expression:

```
> print(mu)
[1] 180
> mu
[1] 180
```

and it may be used in an expression:

```
> mu/pi
[1] 57.2958
```

More complex objects may be created:

```
> s <- seq(10)
> s
[1]  1  2  3  4  5  6  7  8  9 10
```

This creates a new object named `s` in the workspace and *assigns* it the vector `(1 2 ...10)`. (The syntax of `seq(10)` is explained in the next section.)

Multiple assignments are allowed in the same expression:

```
> (mu <- theta <- pi/2)
[1] 1.5708
```

The final value of the expression, in this case the value of `mu`, is printed, because the parentheses force the expression to be evaluated as a unit.

Removing objects from the workspace You can remove objects when they are no longer needed with the `rm` function:

```
> rm(s)
> s
Error: Object "s" not found
```

4.3 Functions and their arguments

In the command `s <- seq(10)`, `seq` is an example of an S *function* by analogy with mathematical functions, which has the form:

```
function.name ( arguments )
```

Some functions do not need arguments, e.g. to list the objects in the workspace use the `ls` function with an *empty* argument list:

```
> ls()
```

Note that the empty argument list, i.e. nothing between the `(` and `)` is still needed, otherwise the computer code for the function itself is printed.

Optional arguments Most functions have *optional arguments*, which may be *named* like this:

```
> s <- seq(from=20, to=0, by=-2)
> s
[1] 20 18 16 14 12 10  8  6  4  2  0
```

Named arguments have the form `name = value`.

Arguments of many functions can also be *positional*, that is, their meaning depends on their position in the argument list. The previous command could be written:

```
> s <- seq(20, 0, by=-2); s
[1] 20 18 16 14 12 10  8  6  4  2  0
```

because the `seq` function expects its first un-named argument to be the starting point of the vector and its second to be the end.

The command separator This example shows the use of the `;` *command separator*. This allows several commands to be written on one line. In this case the first command computes the sequence and stores it in an object, and the second displays this object. This effect can also be achieved by enclosing the entire expression in parentheses, because then S prints the value of the expression, which in this case is the new object:

```
> (s <- seq(from=20, to=0, by=-2))
[1] 20 18 16 14 12 10  8  6  4  2  0
```

Named arguments give more flexibility; this could have been written with names:

```
> (s <- seq(to=0, from=20, by=-2))
[1] 20 18 16 14 12 10  8  6  4  2  0
```

but if the arguments are specified only by position the starting value must be before the ending value.

For each function, the list of arguments, both positional and named, and their meaning is given in the on-line help:

```
> ? seq
```

Any element or group of elements in a vector can be accessed by using subscripts, very much like in mathematical notation, with the `[ ]` (select array elements) operator:

```
> samp[1]
[1] -1.239197
> samp[1:3]
[1] -1.23919739  0.03765046  2.24047546
> samp[c(1,10)]
[1] -1.239197  9.599777
```

The notation `1:3`, using the `:` *sequence operator*, produces the sequence from 1 to 3.

The catenate function The notation `c(1, 10)` is an example of the very useful `c` or *catenate* (“make a chain”) function, which makes a *list* out of its arguments, in this case the two integers representing the indices of the first and last elements in the vector.

4.4 Vectorized operations and re-cycling

A very powerful feature of S is that most operations work on vectors or matrices with the same syntax as they work on scalars, so there is rarely any need for explicit looping commands (which are provided, xe.g. `for`).

These are called *vectorized* operations. As an example of vectorized operations, consider simulating a noisy random process:

```
> (sample <- seq(1, 10) + rnorm(10))
 [1] -0.1878978  1.6700122  2.2756831  4.1454326
 [5]  5.8902614  7.1992164  9.1854318  7.5154372
 [9]  8.7372579  8.7256403
```

This adds a random noise (using the `rnorm` function) with mean 0 and standard deviation 1 (the default) to each of the 10 numbers `1..10`. Note that both vectors have the same length (10), so they are added *element-wise*: the first to the first, the second to the second and so forth

If one vector is shorter than the other, its elements are *re-cycled* as needed:

```
> (samp <- seq(1, 10) + rnorm(5))
 [1] -1.23919739  0.03765046  2.24047546  4.89287818
 [5]  4.59977712  3.76080261  5.03765046  7.24047546
 [9]  9.89287818  9.59977712
```

This perturbs the first five numbers in the sequence the same as the second five.

A simple example of re-cycling is the computation of sample variance directly from the definition, rather than with the `var` function:

```
> (sample <- seq(1:8))
[1] 1 2 3 4 5 6 7 8
> (sample - mean(sample))
[1] -3.5 -2.5 -1.5 -0.5  0.5  1.5  2.5  3.5
> (sample - mean(sample))^2
[1] 12.25  6.25  2.25  0.25  0.25  2.25  6.25 12.25
> sum((sample - mean(sample))^2)
[1] 42
> sum((sample - mean(sample))^2)/(length(sample)-1)
[1] 6
> var(sample)
[1] 6
```

In the expression `sample - mean(sample)`, the mean `mean(sample)` (a scalar) is being subtracted from `sample` (a vector). The scalar is a one-element vector; it is shorter than the eight-element sample vector, so it is re-cycled: the same mean value is subtracted from each element of the sample vector in turn; the result is a vector of the same length as the sample. Then this entire vector is squared with the `^` operator; this also is applied element-wise.

The `sum` and `length` functions are examples of functions that *summarise* a vector and reduce it to a scalar.

Other functions transform one vector into another. Useful examples are `sort`, which sorts the vector, and `rank`, which returns a vector with the rank (order) of each element of the original vector:

```
> data(trees)
> trees$Volume
 [1] 10.3 10.3 10.2 16.4 18.8 19.7 15.6 18.2 22.6 19.9
[11] 24.2 21.0 21.4 21.3 19.1 22.2 33.8 27.4 25.7 24.9 34.5
[22] 31.7 36.3 38.3 42.6 55.4 55.7 58.3 51.5 51.0 77.0
> sort(trees$Volume)
 [1] 10.2 10.3 10.3 15.6 16.4 18.2 18.8 19.1 19.7 19.9
[11] 21.0 21.3 21.4 22.2 22.6 24.2 24.9 25.7 27.4 31.7 33.8
[22] 34.5 36.3 38.3 42.6 51.0 51.5 55.4 55.7 58.3 77.0
> rank(trees$Volume)
 [1]  2.5  2.5  1.0  5.0  7.0  9.0  4.0  6.0 15.0 10.0
[11]  16.0 11.0 13.0 12.0  8.0 14.0 21.0 19.0 18.0 17.0 22.0
[22] 20.0 23.0 24.0 25.0 28.0 29.0 30.0 27.0 26.0 31.0
```

Note how `rank` averages tied ranks by default; this can be changed by the optional `ties.method` argument.

This example also illustrates the `$` operator for extracting fields from dataframes; see §4.7.

4.5 Vector and list data structures

Many S functions create complicated *data structures*, whose structure must be known in order to use the results in further operations. For example, the `sort` function sorts a vector; when called with the optional `index=TRUE` argument it also returns the ordering index vector:

```
> ss <- sort(samp, index=TRUE)
> str(ss)
List of 2
 $ x : num [1:10] -1.2392  0.0377  2.2405  3.7608 ...
 $ ix: int [1:10] 1 2 3 6 5 4 7 8 10 9
```

This example shows the very important `str` function, which displays the S *structure* of an object.

Lists In this case the object is a *list*, which in S is an arbitrary collection of other objects. Here the list consists of two objects: a ten-element vector of sorted values `ss$x` and a ten-element vector of the indices `ss$ix`, which are the positions in the original list where the corresponding sorted value was found. We can display just one element of the list if we want:

```
> ss$ix
 [1]  1  2  3  6  5  4  7  8 10  9
```

This shows the syntax for accessing named components of a data frame or list using the `$` operator: `object $ component`, where the `$` indicates that the component (or field) is to be found *within* the named object.

We can combine this with the vector indexing operation:

```
> ss$ix[length(ss$ix)]
[1] 9
```

So the largest value in the sample sequence is found in the ninth position. This example shows how *expressions may contain other expressions*, and S evaluates them from the inside-out, just like in mathematics. In this case:

- The innermost expression is `ss$ix`, which is the vector of indices in object `ss`;
- The next enclosing expression is `length(...)`; the `length` function *returns* the length of its argument, which is the vector `ss$ix` (the innermost expression);
- The next enclosing expression is `ss$ix[ ...]`, which converts the result of the expression `length(ss$ix)` to a subscript and extracts that element from the vector `ss$ix`.

The result is the array position of the maximum element. We could go one step further to get the actual value of this maximum, which is in the vector `ss$x`:

```
> samp[ss$ix[length(ss$ix)]]
[1] 9.599777
```

but of course we could have gotten this result much more simply with the `max` function as `max(ss$x)` or even `max(samp)`.

4.6 Arrays and matrices

An *array* is simply a vector with an associated *dimension* attribute, to give its shape. *Vectors* in the mathematical sense are one-dimensional arrays in S; *matrices* are two-dimensional arrays; higher dimensions are possible.

For example, consider the sample confusion matrix of Congalton *et al.* [6], also used as an example by Skidmore [53] and Rossiter [43]:[28]

		Reference Class			
		A	B	C	D
Mapped Class	A	35	14	11	1
	B	4	11	3	0
	C	12	9	38	4
	D	2	5	12	2

This can be entered as a list in *row-major* order:

```
> cm <- c(35,14,11,1,4,11,3,0,12,9,38,4,2,5,12,2)
> cm
```

[28] This matrix is also used as an example in §6.1

```
 [1] 35 14 11  1  4 11  3  0 12  9 38  4  2  5 12 2
> dim(cm)
NULL
```

Initially, the list has no dimensions; these may be added with the `dim` function:

```
> dim(cm) <- c(4, 4)
> cm
     [,1] [,2] [,3] [,4]
[1,]   35    4   12    2
[2,]   14   11    9    5
[3,]   11    3   38   12
[4,]    1    0    4    2
> dim(cm)
[1] 4 4
> attributes(cm)
$dim
[1] 4 4
> attr(cm, "dim")
[1] 4 4
```

The `attributes` function shows any object's attributes; in this case the object only has one, its dimension; this can also be read with the `attr` or `dim` function.

Note that the list was converted to a matrix in *column-major* order, following the usual mathematical convention that a matrix is made up of column vectors. The `t` (*transpose*) function must be used to specify row-major order:

```
> cm <- t(cm)
> cm
     [,1] [,2] [,3] [,4]
[1,]   35   14   11    1
[2,]    4   11    3    0
[3,]   12    9   38    4
[4,]    2    5   12    2
```

A new matrix can also be created with the `matrix` function, which in its simplest form fills a matrix of the specified dimensions (rows, columns) with the value of its first argument:

```
 > (m <- matrix(0, 5, 3))
     [,1] [,2] [,3]
[1,]    0    0    0
[2,]    0    0    0
[3,]    0    0    0
[4,]    0    0    0
[5,]    0    0    0
```

This value may also be a vector:

```
> (m <- matrix(1:15, 5, 3, byrow=T))
     [,1] [,2] [,3]
```

```
[1,]    1    2    3
[2,]    4    5    6
[3,]    7    8    9
[4,]   10   11   12
[5,]   13   14   15

> (m <- matrix(1:5, 5, 3))
     [,1] [,2] [,3]
[1,]    1    1    1
[2,]    2    2    2
[3,]    3    3    3
[4,]    4    4    4
[5,]    5    5    5
```

In this last example the shorter vector `1:5` is *re-cycled* as many times as needed to match the dimensions of the matrix; in effect it fills each column with the same sequence.

A matrix element's rows and column are given by the `row` and `col` functions, which are also vectorized and so can be applied to an entire matrix:

```
> col(m)
     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    1    2    3
[3,]    1    2    3
[4,]    1    2    3
[5,]    1    2    3
```

The `diag` function applied to an existing matrix extracts its diagonal as a vector:

```
> (d <- diag(cm))
[1] 35 11 38  2
```

The `diag` function applied to a vector creates a square matrix with the vector on the diagonal:

```
(d <- diag(seq(1:4)))
     [,1] [,2] [,3] [,4]
[1,]    1    0    0    0
[2,]    0    2    0    0
[3,]    0    0    3    0
[4,]    0    0    0    4
```

And finally `diag` with a scalar argument creates an indentity matrix of the specified size:

```
> (d <- diag(3))
     [,1] [,2] [,3]
[1,]    1    0    0
[2,]    0    1    0
[3,]    0    0    1
```

Arithmetic operators such as `*` operate element-wise on matrices as on any vector; if matrix multiplication is desired the `%*%` operator must be used:

```
> cm*cm
     [,1] [,2] [,3] [,4]
[1,] 1225  196  121    1
[2,]   16  121    9    0
[3,]  144   81 1444   16
[4,]    4   25  144    4
> cm%*%cm
     [,1] [,2] [,3] [,4]
[1,] 1415  748  857   81
[2,]  220  204  191   16
[3,]  920  629 1651  172
[4,]  238  201  517   54
> cm%*%c(1,2,3,4)
     [,1]
[1,]  100
[2,]   35
[3,]  160
[4,]   56
```

As the last example shows, `%*%` also multiplies matrices and vectors.

Matrix inversion

A matrix can be *inverted* with the `solve` function, usually with little accuracy loss; in the following example the `round` function is used to show that we recover an identity matrix:

```
> solve(cm)
             [,1]        [,2]         [,3]         [,4]
[1,]  0.034811530 -0.03680710 -0.004545455 -0.008314856
[2,] -0.007095344  0.09667406 -0.018181818  0.039911308
[3,] -0.020399113  0.02793792  0.072727273 -0.135254989
[4,]  0.105321508 -0.37250554 -0.386363636  1.220066519
> solve(cm)%*%cm
              [,1]          [,2]          [,3]          [,4]
[1,]  1.000000e+00 -4.683753e-17 -7.632783e-17 -1.387779e-17
[2,] -1.110223e-16  1.000000e+00 -2.220446e-16 -1.387779e-17
[3,]  1.665335e-16  1.110223e-16  1.000000e+00  5.551115e-17
[4,] -8.881784e-16 -1.332268e-15 -1.776357e-15  1.000000e+00
> round(solve(cm)%*%cm, 10)
     [,1] [,2] [,3] [,4]
[1,]    1    0    0    0
[2,]    0    1    0    0
[3,]    0    0    1    0
[4,]    0    0    0    1
```

Solving linear equations

The same `solve` function applied to a matrix **A** and column vector b solves the linear equation $b = \mathbf{A}x$ for x:

```
> b <- c(1, 2, 3, 4)
> (x <- solve(cm, b))
[1] -0.08569845  0.29135255 -0.28736142  3.08148559
> cm %*% x
     [,1]
[1,]    1
[2,]    2
```

```
[3,]    3
[4,]    4
```

Applying functions to matrix margins

The `apply` function *applies* a function to the *margins* of a matrix, i.e. the rows (1) or columns (2). For example, to compute the row and column sums of the confusion matrix, use `apply` with the `sum` function as the function to be applied:

```
> (rsum <- apply(cm, 1, sum))
[1] 61 18 63 21
> (csum <- apply(cm, 2, sum))
[1] 53 39 64  7
```

These can be used, along with the `diag` function, to compute the producer's and user's classification accuracies, since `diag(cm)` gives the correctly-classified observations:

```
> (pa <- round(diag(cm)/csum, 2))
[1] 0.66 0.28 0.59 0.29
> (ua <- round(diag(cm)/rsum, 2))
[1] 0.57 0.61 0.60 0.10
```

The `apply` function has several variants: `lapply` and `sapply` to apply a user-written or built-in function to each element of a list, `tapply` to apply a function to groups of values given by some combination of factor levels, and `by`, a simplified version of this. For example, here is how to standardize a matrix "by hand", i.e., subtract the mean of each column and divide by the standard deviation of each column:

```
> apply(cm, 2, function(x) sapply(x, function(i) (i-mean(x))/sd(x)))
          [,1]     [,2]     [,3]   [,4]
[1,]  1.381930 -0.10742 -0.24678 -0.689
[2,] -0.087464  1.39642 -0.44420 -0.053
[3,] -0.297377 -0.32225  1.46421  1.431
[4,] -0.997089 -0.96676 -0.77323 -0.689
```

The outer `apply` applies a function to the second margin (i.e., columns). The function is defined with the `function` command.

The structure is clearer if braces are used (optional here because each function only has one command) and the command is written on several lines to show the matching braces and parentheses:

```
> apply(cm, 2, function(x)
+      {
+        sapply(x, function(i)
+               { (i-mean(x))/sd(x)
+               }  # end function
+               )  # end sapply
+      }  # end function
+      )  # end apply
```

This particular result could have been better achieved with the `scale`

"scale a matrix" function, which in addition to scaling a matrix column-wise (with or without centring, with or without scaling) returns attributes showing the central values (means) and scaling values (standard deviations) used:

```
> scale(cm)
          [,1]     [,2]     [,3]   [,4]
[1,]  1.381930 -0.10742 -0.24678 -0.689
[2,] -0.087464  1.39642 -0.44420 -0.053
[3,] -0.297377 -0.32225  1.46421  1.431
[4,] -0.997089 -0.96676 -0.77323 -0.689
attr(,"scaled:center")
[1] 15.25  4.50 15.75  5.25
attr(,"scaled:scale")
[1] 14.2916  4.6547 15.1959  4.7170
```

Other matrix functions

There are also functions to compute the determinant (`det`), eigenvalues and eigenvectors (`eigen`), the singular value decomposition (`svd`), the QR decomposition (`qr`), and the Choleski factorization (`chol`); these use long-standing numerical codes from LINPACK, LAPACK, and EISPACK.

4.7 Data frames

The fundamental S data structure for statistical modelling is the *data frame*. This can be thought of as a matrix where the *rows* are *cases*, called *observations* by S (whether or not they were field observations), and the *columns* are the *variables*. In standard database terminology, these are *records* and *fields*, respectively. Rows are generally accessed by the row number (although they can have names), and columns by the variable *name* (although they can also be accessed by number). A data frame can also be considerd a *list* whose members are the fields; these can be accessed with the `[[ ]]` (list access) operator.

Sample data R comes with many example datasets (§3.8) organized as data frames; let's load one (`trees`) and examine its structure and several ways to access its components:

```
> ?trees
> data(trees)
> str(trees)
`data.frame':   31 obs. of  3 variables:
 $ Girth : num  8.3 8.6 8.8 10.5 10.7 10.8 11 ...
 $ Height: num  70 65 63 72 81 83 66 75 80 75 ...
 $ Volume: num  10.3 10.3 10.2 16.4 18.8 19.7 ...
```

The help text tells us that this data set contains measurements of the girth (diameter in inches[29], measured at 4.5 ft[30] height), height (feet) and timber

[29] 1 inch = 2.54 cm

[30] 1 ft = 30.48 cm

volume (cubic feet[31]) in 31 felled black cherry trees. The data frame has 31 observations (rows, cases, records) each of which has three variables (columns, attributes, fields). Their names can be retrieved or changed by the `names` function. For example, to name the fields `Var.1`, `Var.2` etc. we could use the `paste` function to build the names into a list and then assign this list to the names attribute of the data frame:

```
> (saved.names <- names(trees))
[1] "Girth"  "Height" "Volume"
> (names(trees) <- paste("Var", 1:dim(trees)[2], sep="."))
[1] "Var.1" "Var.2" "Var.3''
> names(trees)[1] <- "Perimeter"
> names(trees)
[1] "Perimeter" "V.2"       "V.3"
> (names(trees) <- saved.names)
[1] "Girth"  "Height" "Volume"
> rm(saved.names)
```

Note in the `paste` function how the shorter vector `"Var"` was *re-cycled* to match the longer vector `1:dim(trees)[2]`. This was just an example of how to name fields; at the end we restore the original names, which we had saved in a variable which, since we no longer need it, we remove from the workspace with the `rm` function.

The data frame can accessed various ways:

```
>    # most common: by field name
> trees$Height
 [1] 70 65 63 72 81 83 66 75 80 75 79 76 76 69
[15] 75 74 85 86 71 64 78 80 74 72 77 81 82 80
[29] 80 80 87
>    # the result is a vector, can select elements of it
> trees$Height[1:5]
[1] 70 65 63 72 81
>    # but this is also a list element
>  trees[[2]]
 [1] 70 65 63 72 81 83 66 75 80 75 79 76 76 69
[15] 75 74 85 86 71 64 78 80 74 72 77 81 82 80
[ 29] 80 80 87
> trees[[2]][1:5]
[1] 70 65 63 72 81
>    # as a matrix, first by row....
> trees[1,]
  Girth Height Volume
1   8.3     70   10.3
>    # ... then by column
> trees[,2]
>  trees[[2]]
 [1] 70 65 63 72 81 83 66 75 80 75 79 76 76 69
[15] 75 74 85 86 71 64 78 80 74 72 77 81 82 80
[ 29] 80 80 87
>    # get one element
> trees[1,2]
[1] 70
```

[31] 1 ft^3 = 28.3168 dm^3

```
> trees[1,"Height"]
[1] 70
> trees[1,]$Height
[1] 70
```

The forms like `$Height` use the `$` operator to select a *named field* within the frame. The forms like `[1, 2]` show that this is just a matrix with column names, leading to forms like `trees[1,"Height"]`. The forms like `trees[1,]$Height` show that each row (observation, case) can be considered a list with named items. The forms like `trees[[2]]` show that the data frame is also a list whose elements can be accessed with the `[[ ]]` operator.

Attaching data frames to the search path To simplify access to named columns of data frames, S provides an `attach` function that makes the names visible in the outer namespace:

```
> attach(trees)
> Height[1:5]
[1] 70 65 63 72 81
```

Building a data frame S provides the `data.frame` function for creating data frames from smaller objects, usually vectors. As a simple example, suppose the number of trees in a plot has been measured at five plots in each of two transects on a regular spacing. We enter the x-coördinate as one list, the y-coördinate as another, and the number of trees in each plot as the third:

```
> x <- rep(seq(182,183, length=5), 2)*1000
> y <- rep(c(381000, 310300), 5)
> n.trees <- c(10, 12, 22, 4, 12, 15, 7, 18, 2, 16)
> (ds <- data.frame(x, y, n.trees))
        x      y n.trees
1  182000 381000      10
2  182250 310300      12
3  182500 381000      22
4  182750 310300       4
5  183000 381000      12
6  182000 310300      15
7  182250 381000       7
8  182500 310300      18
9  182750 381000       2
10 183000 310300      16
```

Note the use of the `rep` function to repeat a sequence. Also note that an arithmetic expression (in this case `* 1000`) can be applied to an entire vector (in this case `rep(seq(182,183, length=5), 2)`).

In practice, this data frame would probably be prepared outside R and then imported, see §6.

Adding rows to a data frame The `rbind` ("row bind") function is used to add rows to a data frame, and to combine two data frames with the same structure. For example, to add one more trees to the data frame:

```
> (ds <- rbind(ds, c(183500, 381000, 15)))
        x      y n.trees
1  182000 381000      10
2  182250 310300      12
3  182500 381000      22
4  182750 310300       4
5  183000 381000      12
6  182000 310300      15
7  182250 381000       7
8  182500 310300      18
9  182750 381000       2
10 183000 310300      16
11 183500 381000      15
```

This can also be accomplished by directly assigning to the next row:

```
> ds[12,] <- c(183400, 381200, 18)
> ds
        x      y n.trees
1  182000 381000      10
2  182250 310300      12
3  182500 381000      22
4  182750 310300       4
5  183000 381000      12
6  182000 310300      15
7  182250 381000       7
8  182500 310300      18
9  182750 381000       2
10 183000 310300      16
11 183500 381000      12
12 183400 381200      18
```

Adding fields to a data frame A vector with the same number of rows as an existing data frame may be added to it with the `cbind` ("column bind") function. For example, we could compute a height-to-girth ratio for the trees (a measure of a tree's shape) and add it as a new field to the data frame; we illustrate this with the `trees` example dataset introduced in §4.7:

```
> attach(trees)
>  HG.Ratio <- Height/Girth;  str(HG.Ratio)
 num [1:31] 8.43 7.56 7.16 6.86 7.57 ...
> trees <- cbind(trees, HG.Ratio);  str(trees)
`data.frame': 31 obs. of  4 variables:
 $ Girth   : num  8.3 8.6 8.8 10.5 10.7 10.8 ...
 $ Height  : num  70 65 63 72 81 83 66 75 80 75 ...
 $ Volume  : num  10.3 10.3 10.2 16.4 18.8 19.7 ...
 $ HG.Ratio: num  8.43 7.56 7.16 6.86 7.57 ..
> rm(HG.Ratio)
```

Note that this new field is not visible in an `attached` frame; the frame must be detached (with the `detach` function) and re-attached:

```
> summary(HG.Ratio)
Error: Object "HG.Ratio" not found
> detach(trees); attach(trees)
> summary(HG.Ratio)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   4.22    4.70    6.00    5.99    6.84    8.43
```

Sorting a data frame This is most easily accomplished with the `order` function, naming the field(s) on which to sort, and then using the returned indices to extract rows of the data frame in sorted order:

```
> trees[order(trees$Height, trees$Girth),]
   Girth Height Volume
3    8.8     63   10.2
20  13.8     64   24.9
2    8.6     65   10.3
...
4   10.5     72   16.4
24  16.0     72   38.3
16  12.9     74   22.2
23  14.5     74   36.3
...
18  13.3     86   27.4
31  20.6     87   77.0
```

Note that the trees are first sorted by height, then any ties in height are sorted by girth.

4.8 Factors

Some variables are *categorical*: they can take only a defined set of values. In S these are called *factors* and are of two types: *unordered* (nominal) and *ordered* (ordinal). An example of the first is a soil type, of the second soil structure grade, from "none" through "weak" to "strong" and "very strong"; there is a natural order in the second case but not in the first. Many analyses in R depend on factors being correctly identified; some such as `table` (§4.15) only work with categorical variables.

Factors are defined with the `factor` and `ordered` functions. They may be converted from existing character or numeric vectors with the `as.factor` and `as.ordered` function; these are often used after data import if the `read.table` or related functions could not correctly identify factors; see §7.1 for an example. The levels of an existing factor are extracted with the `levels` function.

For example, suppose we have given three tests to each of three students and we want to rank the students. We might enter the data frame as follows (see also §6.1):

```
> student <- rep(1:3, 3)
> score <- c(9, 6.5, 8, 8, 7.5, 6, 9.5, 8, 7)
> tests <- data.frame(cbind(student, score))
> str(tests)
`data.frame': 9 obs. of  2 variables:
 $ student: num  1 2 3 1 2 3 1 2 3
 $ score  : num  9 6.5 8 8 7.5 6 9.5 8 7
```

We have the data but the student is just listed by a number; the `table` function won't work and if we try to predict the score from the student using the `lm` function (see §4.17) we get nonsense:

```
> lm(score ~ student, data=tests)
Coefficients:
(Intercept)      student
      9.556       -0.917
```

The problem is that the student is considered as a continuous variable when in fact it is a factor. We do much better if we make the appropriate conversion:

```
> tests$student <- as.factor(tests$student)
> str(tests)
`data.frame': 9 obs. of  2 variables:
 $ student: Factor w/ 3 levels "1","2","3": 1 2 3 1 2 3 1 2 3
 $ score  : num  9 6.5 8 8 7.5 6 9.5 8 7
> lm(score ~ student, data=tests)
Coefficients:
(Intercept)     student2     student3
       8.83        -1.50        -1.83
```

This is a meaningful one-way linear model, showing the difference in mean scores of students 2 and 3 from student 1 (the intercept).

Factor names can be any string; so to be more descriptive we could have assigned names with the `labels` argument to the `factor` function:

```
> tests$student <- factor(tests$student, labels=c("Harley", "Doyle", "JD"))
> str(tests)
'data.frame': 9 obs. of  2 variables:
 $ student: Factor w/ 3 levels "Harley","Doyle",..: 1 2 3 1 2 3 1 2 3
 $ score  : num  9 6.5 8 8 7.5 6 9.5 8 7
> table(tests)
        score
student   6 6.5 7 7.5 8 9 9.5
  Harley 0   0 0   0 1 1   1
  Doyle  0   1 0   1 1 0   0
  JD     1   0 1   0 1 0   0
```

An existing factor can be **recoded** with an additional call to `factor` and different labels:

```
> tests$student <- factor(tests$student, labels=c("John", "Paul", "George"))
> str(tests)
`data.frame': 9 obs. of  2 variables:
 $ student: Factor w/ 3 levels "John","Paul",..: 1 2 3 1 2 3 1 2 3
 $ score  : num  9 6.5 8 8 7.5 6 9.5 8 7
> table(tests)
        score
student  6 6.5 7 7.5 8 9 9.5
  John   0   0 0   0 1 1   1
  Paul   0   1 0   1 1 0   0
  George 1   0 1   0 1 0   0
```

The levels have the same internal numbers but different labels. This use of `factor` with the optional `labels` argument does not change the order of the factors, which will be presented in the original order. If for example we want to present them alphabetically, we need to re-order the levels, extracting them with the `levels` function in the order we want (as indicated by subscripts), and then setting these (in the new order) with the optional `levels` argument to `factor`:

```
> tests$student <- factor(tests$student, levels=levels(tests$student)[c(3,1,2)])
> str(tests)
'data.frame': 9 obs. of  2 variables:
 $ student: Factor w/ 3 levels "George","John",..: 2 3 1 2 3 1 2 3 1
 $ score  : num  9 6.5 8 8 7.5 6 9.5 8 7
> table(tests)
        score
student  6 6.5 7 7.5 8 9 9.5
  George 1   0 1   0 1 0   0
  John   0   0 0   0 1 1   1
  Paul   0   1 0   1 1 0   0
```

Now the three students are presented in alphabetic order, because the underlying codes have been re-ordered. The `car` package contains a useful `recode` function which also allows grouping of factors.

Factors require special care in statistical models; see §4.17.1.

4.9 Selecting subsets

We often need to examine subsets of our data, for example to perform a separate analysis for several strata defined by some factor, or to exclude outliers defined by some criterion.

Selecting known elements If we know the observation numbers, we simply name them as the first subscript, using the `[ ]` (select array elements) operator:

```
> trees[1:3,]
  Girth Height Volume
1   8.3     70   10.3
2   8.6     65   10.3
3   8.8     63   10.2
> trees[c(1, 3, 5),]
  Girth Height Volume
```

```
1   8.3     70   10.3
3   8.8     63   10.2
5  10.7     81   18.8
> trees[seq(1, 31, by=10),]
   Girth Height Volume
1    8.3     70   10.3
11  11.3     79   24.2
21  14.0     78   34.5
31  20.6     87   77.0
```

A *negative* subscript in this syntax *excludes* the named rows and includes all the others:

```
> trees[-(1:27),]
   Girth Height Volume
28  17.9     80   58.3
29  18.0     80   51.5
30  18.0     80   51.0
31  20.6     87   77.0
```

Selecting with a logical expression The simplest way to select subsets is with a *logical expression* on the *row* subscript which gives the criterion. For example, in the `trees` example dataset introduced in §4.7, there is only one tree with volume greater than 58 cubic feet, and it is substantially larger; we can see these in order with the `sort` function:

```
> attach(trees)
> sort(Volume)
 [1]   10.2 10.3 10.3 15.6 16.4 18.2 18.8 19.1 19.7
 [11]  19.9 21.0 21.3 21.4 22.2 22.6 24.2 24.9 25.7
 [21]  27.4 31.7 33.8 34.5 36.3 38.3 42.6 51.0 51.5
 [31]  55.4 55.7 58.3 77.0
```

To analyze the data without this "unusual" tree, we use a logical expression to select rows (observations), here using the < (less than) *logical comparaison operator*, and then the `[ ]` (select array elements) operator to extract the array elements that are selected:

```
> tr <- trees[Volume < 60,]
```

Note that there is no condition for the second subscript, so all columns are selected.

To make a list of the observation numbers where a certain condition is met, use the `which` function:

```
> which(trees$Volume > 60)
[1] 31
> trees[which(trees$Volume > 60),]
   Girth Height Volume
31  20.6     87     77
```

Logical expressions may be combined with *logical operators* such as & (logical AND) and | (logical OR), and their truth sense inverted with ! (logical NOT). For example, to select trees with volumes between 20 and 40 cubic feet:

```
> tr <- trees[Volume >=20 & Volume <= 40,]
```

Note that &, like S arithmetical operators, is *vectorized*, i.e. it operates on each pair of elements of the two logical vectors separately.

Parentheses should be used if you are unclear about operator precedence. Since the logical comparaison operators (e.g. >=) have precedence over binary logical operators (e.g. &), the previous expression is equivalent to:

```
> tr <- trees[(Volume >=20) & (Volume <= 40),]
```

Another way to select elements is to make a *subset*, with the `subset` function:

```
> (tr.small <- subset(trees, Volume < 18))
  Girth Height Volume
1   8.3     70   10.3
2   8.6     65   10.3
3   8.8     63   10.2
4  10.5     72   16.4
7  11.0     66   15.6
```

Selecting random elements of an array Random elements of a vector can be selected with the `sample` function:

```
> trees[sort(sample(1:dim(trees)[1], 5)), ]
   Girth Height Volume
13  11.4     76   21.4
18  13.3     86   27.4
22  14.2     80   31.7
23  14.5     74   36.3
26  17.3     81   55.4
```

Each call to `sample` will give a different result.

By default sampling is *without* replacement, so the same element can not be selected more than once; for sampling *with* replacement use the `replace=T` optional argument.

In this example, the command `dim(trees)` uses the `dim` function to give the dimensions of the data frame (rows and columns); the first element of this two-element list is the number of rows: `dim(trees)[1]`.

Splitting on a factor Another common operation is to split a dataset into several *strata* defined by some factor. For this, S provides the `split` function, which we illustrate with the `iris` dataset which has one factor, the species of Iris:

```
> data(iris); str(iris)
`data.frame': 150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versic..",..: 1 1  ...
> attach(iris)
> ir.s <- split(iris, Species); str(ir.s)
List of 3
 $ setosa    :`data.frame': 50 obs. of  5 variables:
  ..$ Sepal.Length: num [1:50] 5.1 4.9 4.7 4.6 5 5.4 4.6 5  ...
  ..$ Sepal.Width : num [1:50] 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4  ...
  ..$ Petal.Length: num [1:50] 1.4 1.4 1.3 1.5 1.4 1.7 1.4  ...
  ..$ Petal.Width : num [1:50] 0.2 0.2 0.2 0.2 0.2 0.4 0.3  ...
  ..$ Species     : Factor w/ 3 levels "setosa","versic..",..: 1 1  ...
 $ versicolor:`data.frame': 50 obs. of  5 variables:
  ..$ Sepal.Length: num [1:50] 7 6.4 6.9 5.5 6.5 5.7 6.3 4.9  ...
  ..$ Sepal.Width : num [1:50] 3.2 3.2 3.1 2.3 2.8 2.8 3.3 2.4  ...
  ..$ Petal.Length: num [1:50] 4.7 4.5 4.9 4 4.6 4.5 4.7 3.3  ...
  ..$ Petal.Width : num [1:50] 1.4 1.5 1.5 1.3 1.5 1.3 1.6 1  ...
  ..$ Species     : Factor w/ 3 levels "setosa","versic..",..: 2 2 ...
 $ virginica :`data.frame': 50 obs. of  5 variables:
  ..$ Sepal.Length: num [1:50] 6.3 5.8 7.1 6.3 6.5 7.6 4.9 7.3  ...
  ..$ Sepal.Width : num [1:50] 3.3 2.7 3 2.9 3 3 2.5 2.9 2.5  ...
  ..$ Petal.Length: num [1:50] 6 5.1 5.9 5.6 5.8 6.6 4.5 6.3  ...
  ..$ Petal.Width : num [1:50] 2.5 1.9 2.1 1.8 2.2 2.1 1.7 1.8  ...
  ..$ Species     : Factor w/ 3 levels "setosa","versic..",..: 3 3 ...
```

The `split` function builds a *list* of data frames named by the level of the factor on which the original data frame was split. Here the original 150 observations have been split into three lists of 50, one for each species. These can be accessed by name:

```
> summary(ir.s$setosa$Petal.Length)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00    1.40    1.50    1.46    1.58    1.90
```

4.9.1 Simultaneous operations on subsets

We often want to apply some computation to all subsets of a data frame. For example, to compute the mean petal length of the `iris` data set for each species separately, we could first split the set as shown in the previous section (§4.9), compute each subset's mean, and join them in one vector. This can be accomplished in one step using the `by` function:

```
> by(Petal.Length, Species, mean)
INDICES: setosa
[1] 1.462
------------------------------------------------
INDICES: versicolor
[1] 4.26
```

```
------------------------------------------------
INDICES: virginica
[1] 5.552
```

In this example, we applied the `mean` function to the `Petal.Length` field in the attached data frame, grouping the petal lengths by the `Species` categorical factor.

A function can be applied to several fields at the same time, and the results can be saved to the workspace:

```
> iris.m <- by(iris[,1:4], Species, mean)
> class(iris.m)
[1] "by"
> str(iris.m)
List of 3
 $ setosa    : Named num [1:4] 5.006 3.428 1.462 0.246
  ..- attr(*, "names")= chr [1:4] "Sepal.Length" "Sepal.Width" ...
 $ versicolor: Named num [1:4] 5.94 2.77 4.26 1.33
  ..- attr(*, "names")= chr [1:4] "Sepal.Length" "Sepal.Width" ...
 $ virginica : Named num [1:4] 6.59 2.97 5.55 2.03
  ..- attr(*, "names")= chr [1:4] "Sepal.Length" "Sepal.Width" ...
 - attr(*, "dim")= int 3
 - attr(*, "dimnames")=List of 1
  ..$ Species: chr [1:3] "setosa" "versicolor" "virginica"
 - attr(*, "call")= language by.data.frame(data = iris[, 1:4],
                                   INDICES = Species, FUN = mean)
 - attr(*, "class")= chr "by"
> iris.m$setosa
Sepal.Length  Sepal.Width Petal.Length  Petal.Width
       5.006        3.428        1.462        0.246
> iris.m$setosa[3]
Petal.Length
       1.462
> iris.m$setosa["Petal.Length"]
Petal.Length
       1.462
```

As this example shows, the result is one list for each level of the grouping factor (here, the *Iris* species). Each list is a vector with named elements (the `dimnames` attribute).

4.10 Rearranging data

As explained above (§4.7), the *data frame* is the object class on which most analysis is performed. Sometimes the same data must be arranged different ways into data frames, depending on what we consider the observations and columns.

A typical re-arrangement is *stacking* and its inverse, *unstacking*. In stacking, several variables are combined into one, coded by the original variable name; unstacking is the reverse.

For example, consider the data from a small plant growth experiment:

```
> data(PlantGrowth); str(PlantGrowth)
`data.frame':  30 obs. of  2 variables:
 $ weight: num  4.17 5.58 5.18 6.11 4.5 4.61 5.17 4.53  ...
 $ group : Factor w/ 3 levels "ctrl","trt1",..: 1 1 1 1 1 1 1  ...
```

There were two treatments and one control, and the weights are given in one column. If we want to find the maximum growth in the control group, we could select just the controls and then find the maximum:

```
> max(PlantGrowth$weight[PlantGrowth$group == "ctrl"])
[1] 6.11
```

But we could also *unstack* this two-column frame into a frame with three variables, one for each treatment, and then find the maximum of one (new) column; for this we use the `unstack` function:

```
> pg <- unstack(PlantGrowth, weight ~ group; str(pg)
`data.frame':  10 obs. of  3 variables:
 $ ctrl: num  4.17 5.58 5.18 6.11 4.5 4.61 5.17 4.53 5.33 5.14
 $ trt1: num  4.81 4.17 4.41 3.59 5.87 3.83 6.03 4.89 4.32 4.69
 $ trt2: num  6.31 5.12 5.54 5.5 5.37 5.29 4.92 6.15 5.8 5.26
> max(pg$ctrl)
[1] 6.11
```

The names of the groups in the unstacked frame become the names of the variables in the stacked frame; the formula `weight ~group` told the `unstack` function that `group` was the column with the new column names.

This process also works in reverse, when we have a frame with several variables to make into one, we use the `stack` function:

```
> pg.stacked <- stack(pg); str(pg.stacked)
`data.frame':  30 obs. of  2 variables:
 $ values: num  4.17 5.58 5.18 6.11 4.5 4.61 5.17 4.53  ...
 $ ind   : Factor w/ 3 levels "ctrl","trt1",..: 1 1 1 1 1 1  ...
> names(pg.stacked) <- c("weight", "group"); str(pg.stacked)
`data.frame':  30 obs. of  2 variables:
 $ weight: num  4.17 5.58 5.18 6.11 4.5 4.61 5.17 4.53  ...
 $ group : Factor w/ 3 levels "ctrl","trt1",..: 1 1 1 1 1 1  ...
```

The stacked frame has two columns with default names `value` (for the variables which were combined) and `ind` (for their names); these can be changed with the `names` function.

A more general function for data re-shaping is `reshape`.

4.11 Random numbers and simulation

R includes functions to evaluate a cumulative distribution function (CDF), the probability density function (PDF) and the quantiles, and to draw random samples, from a large number of distributions including the *uniform* (R name `unif`), *normal* (R name `norm`), *Student's t* (R name `t`), *binomial* (R name binom), *Poisson* (R name pois), and many others; see Chapter 8 of [36] for a complete list.

The names of the functions are built from two parts:

1. A *prefix* indicating the type of function: p for the CDF, d for the density, q for the quantile, and r for random samples;

2. The *R name* of the distribution, as listed above, e.g. norm for the normal distribution.

So the functions for the normal distribution are:

p	pnorm for the CDF;
d	dnorm for the density;
q	qnorm for the quantiles (inverse probability);
r	rnorm to draw random numbers.

For example, to find the proportion of people in a normally-distributed population with mean height 170 cm and standard deviation 15 cm shorter than 200 cm use pnorm:

```
> pnorm(200, 170, 15)
[1] 0.9772499
```

To plot the bell-shaped normal curve use dnorm:

```
> q <- seq(-3, 3, by=.05)
> plot(q, dnorm(q), type="l", xlab="z", ylab="Prob(z)")
```

To find which normal score corresponds to a list of critical Type I error probabilities use qnorm:

```
> alpha <- c(0.1, 0.05, 0.01, 0.001)
> qnorm(1-alpha/2)
[1] 1.644854 1.959964 2.575829 3.290527
```

Finally, to simulate sampling ten individuals from a normally-distributed population with mean height 170 cm and standard deviation 15 cm, with a measurement precision of 1 cm, use rnorm draw the sample and then round the results to the nearest integer:

```
> sort(round(rnorm(10, 170, 15)))
 [1] 147 159 166 169 169 174 176 180 183 185
```

Each time this command is issued it will give different results, because the sample is *random*:

```
> sort(round(rnorm(10, 170, 15)))
 [1] 155 167 170 177 181 182 185 186 188 199
```

To start a simulation at the same point (e.g. for testing) use the `set.seed` function:

```
> set.seed(61921)
> sort(round(rnorm(10, 170, 15)))
 [1] 129 157 157 166 168 170 173 175 185 193
> set.seed(61921)
> sort(round(rnorm(10, 170, 15)))
 [1] 129 157 157 166 168 170 173 175 185 193
```

Now the results are the same every time.

4.12 Character strings

R can work with *character vectors*, also known as *strings*. These are often used in graphics as labels, titles, and explanatory text. A string is created by the " *quote* operator:

```
> (label <- "A good graph")
[1] "A good graph"
```

Strings can be built from smaller pieces with the `paste` function; parts can be extracted or replaced with the `substring` function; strings can be split into pieces with the `strsplit` function:

```
> paste(label, ":", 15, "x", 20, "cm")
[1] "A nice graph : 15 x 20 cm"
> (labels <- paste("B", 1:8, sep=""))
 [1] "B1"  "B2"  "B3"  "B4"  "B5"  "B6"  "B7"  "B8"
> substring(label, 1, 4)
[1] "A go"
> substring(label, 3) <- "nice"; label
[1] "A nice graph"
> strsplit(label, " ")
[[1]]
[1] "A"     "nice"  "graph"
> unlist(strsplit(label, " "))
[1] "A"     "nice"  "graph"
> unlist(strsplit(label, " "))[3]
[1] "graph
```

Note the use of the `unlist` function to convert the list (of one element) returned by `strsplit` into a vector.

Numbers or factors can be converted to strings with the `as.character` function; however this conversion is performed automatically by many functions, so an explicit conversion is rarely needed.

4.13 Objects and classes

S is an *object-oriented* computer language: everything in S (including variables, results of expressions, results of statistical models, and functions) is an *object*, each with a *class*, which says what the object is and also controls the way in which it may be manipulated. The class of an object may be inspected with the `class` function:

```
> class(lm)
[1] "function"
> class(letters)
[1] "character"
> class(seq(1:10))
[1] "integer"
> class(seq(1,10,  by=.01))
[1] "numeric"
> class(diag(10))
[1] "matrix"
> class(iris)
[1] "data.frame"
> class(iris$Petal.Length)
[1] "numeric"
> class(iris$Species)
[1] "factor"
> class(iris$Petal.Length > 2)
[1] "logical"
> class(lm(iris$Petal.Width ~ iris$Petal.Length))
[1] "lm''
> class(hist(iris$Petal.Width))
[1] "histogram"
> class(table(iris$Species))
[1] "table"
```

The `letters` built-in constant in this example is a convenient way to get the 26 lower-case Roman letters; for upper-case use `LETTERS`.

As the last three examples show, many S functions create their own classes. These then can be used by *generic* functions such as `summary` to determine appropriate behaviour:

```
> summary(iris$Petal.Length)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00    1.60    4.35    3.76    5.10    6.90

> summary(iris$Species)
    setosa versicolor  virginica
        50         50         50

> summary(lm(iris$Petal.Width ~ iris$Petal.Length))
Call:
lm(formula = iris$Petal.Width ~ iris$Petal.Length)

Residuals:
   Min     1Q Median     3Q    Max
-0.565 -0.124 -0.019  0.133  0.643
```

```
Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       -0.36308    0.03976   -9.13  4.7e-16
iris$Petal.Length  0.41576    0.00958   43.39  < 2e-16

Residual standard error: 0.206 on 148 degrees of freedom
Multiple R-Squared: 0.927,Adjusted R-squared: 0.927
F-statistic: 1.88e+03 on 1 and 148 DF,  p-value: <2e-16

> summary(table(iris$Species))
Number of cases in table: 150
Number of factors: 1
```

S has functions for testing if an object is in a specific class or mode, and for converting modes or classes, as long as such a conversion makes sense. These have the form `is.` (test) or `as.` (convert), followed by the class name. For example:

```
> is.factor(iris$Petal.Width)
[1] FALSE
> is.factor(iris$Species)
[1] TRUE
> as.factor(iris$Petal.Width)
  [1] 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 0.2 0.2 0.1 0.1
...
[145] 2.5 2.3 1.9 2   2.3 1.8
22 Levels: 0.1 0.2 0.3 0.4 0.5 0.6 1 1.1 1.2 1.3 1.4  ... 2.5
> as.numeric(iris$Species)
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
...
[149] 3 3
```

The `is.factor` and `is.numeric` class test functions return a logical value (`TRUE` or `FALSE`) depending on the class their argument. The `as.factor` class conversion function determined the unique values of petal length (22) and then coded each observation; this is not too useful here; in practice you would use the `cut` function. The `as.numeric` conversion function extracts the *level number* of the factor for each object; this can be useful if we want to give a numeric argument derived from the factor

4.13.1 The S3 and S4 class systems

S has two class systems, referred to as *S3* (old-style) and *S4* (new-style). Most R functions still use S3 classes, as presented in the previous section, but most new and rewritten packages use the more powerful and modern S4 classes. The difference between the two systems is readily apparent in the output of both the `class` and `str` functions.

A good example of S4 classes is the class structure of the `sp` spatial statistics package [34]. First we look at an R object that is an old-style (S3) class. Note the use of the `require` function instead of `library`; this ensures that the library is loaded only once.

```
> require(sp)
> data(meuse)
> class(meuse)
[1] "data.frame"
> str(meuse)
`data.frame': 155 obs. of  14 variables:
 $ x      : num  181072 181025 181165 181298 181307 ...
 $ y      : num  333611 333558 333537 333484 333330 ...
 $ cadmium: num  11.7 8.6 6.5 2.6 2.8 3 3.2 2.8 2.4 1.6 ...
...
 $ dist.m : num  50 30 150 270 380 470 240 120 240 420 ...
```

The sample data `meuse` is imported as an S3 class, namely a `data.frame`. Notice that the coördinates of each point are listed as fields. However, `sp` has defined some S4 classes to make the spatial nature of the data explicit.

`sp` also provides a `coordinates` function to set the spatial coördinates and thereby create explict spatial data.

```
> coordinates(meuse) <- ~ x + y
>    # alternate command format: coordinates(meuse) <- c("x", "y")
> class(meuse)
[1] "SpatialPointsDataFrame"
attr(,"package")
[1] "sp"
> str(meuse)
Formal class 'SpatialPointsDataFrame' [package "sp"] with 5 slots
  ..@ data       :Formal class 'AttributeList' [package "sp"] with 1 slots
  .. .. ..@ att:List of 12
  .. .. .. ..$ cadmium: num [1:155] 11.7 8.6 6.5 2.6 2.8 3 3.2 2.8 2.4 1.6 ...
...
  .. .. .. ..$ dist.m : num [1:155] 50 30 150 270 380 470 240 120 240 420 ...
  ..@ coords.nrs : int [1:2] 1 2
  ..@ coords     : num [1:155, 1:2] 181072 181025 181165 181298 181307 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : NULL
  .. .. ..$ : chr [1:2] "x" "y"
  ..@ bbox       : num [1:2, 1:2] 178605 329714 181390 333611
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:2] "x" "y"
  .. .. ..$ : chr [1:2] "min" "max"
  ..@ proj4string:Formal class 'CRS' [package "sp"] with 1 slots
  .. .. ..@ projargs: chr NA
```

The object `meuse` has been *promoted* to an S4 class `SpatialPointsDataFrame`, which is shown as being a *formal class* defined by `sp`.

The class hierarchy may be examined with the `getClass` function:

```
> getClass("SpatialPointsDataFrame")

Slots:

Name:          data   coords.nrs      coords        bbox proj4string
Class:  data.frame     numeric      matrix      matrix         CRS

Extends:
```

```
Class "SpatialPoints", directly
Class "Spatial", by class "SpatialPoints", distance 2

Known Subclasses:
Class "SpatialPixelsDataFrame", directly, with explicit coerce
```

This shows that this class inherits from class `SpatialPoints` and in turn can be extended as class `SpatialPixelsDataFrame`.

S4 classes have named *slots*, marked by the `@` sign in the output of `str` and also shown in the output of `getClass`; these can also be listed with the `slotNames` function:

```
> slotNames(meuse)
[1] "data"        "coords.nrs"  "coords"      "bbox"        "proj4string"
```

The contents of these slots are explained in the help for the S4 class:

```
> ?"SpatialPointsDataFrame-class"
```

Each slot is either a primitive S object (e.g. slot `bbox` which is a matrix) or another S4 class (e.g. slot `data` which is an object of class `AttributeList` also defined by the `sp` package):

```
> class(meuse@bbox)
[1] "matrix"
> class(meuse@data)
[1] "AttributeList"
attr(,"package")
[1] "sp"
```

Slots may be accessed directly with the `@` operator, just as fields in data frames are accessed with the `$` operator. For example, to extract the bounding box (limiting coördinates) of this spatial data set:

```
> meuse@bbox
     min    max
x 178605 181390
y 329714 333611
> meuse@bbox["x","min"]
[1] 178605
```

However, it is better practice to use *access functions*:

```
 > bbox(meuse)
     min    max
x 178605 181390
y 329714 333611
```

Each S4 class has a set of *methods* that apply to it; `bbox` is an example that applies not only to objects of class `SpatialPointsDataFrame`, but to objects of the generalised class from which class `SpatialPointsDataFrame` is specialised, namely class `SpatialPoints` and class `Spatial`.

To determine the methods that can apply to a class, review the help, using the `class?<class name>` syntax:

```
> class?SpatialPointsDataFrame
> class?SpatialPoints
> class?Spatial
```

As this example shows, classes may be organised in an *inheritance structure*, so that the behaviour of a more *generalised* class is automatically inherited by a more *specialised* class; these are said to *extend* the base class.

For example class `SpatialPointsDataFrame` extends class `SpatialPoints`, which in turn extends the base class `Spatial`. These have appropriate slots and methods:

`Spatial` Only has a bounding box (slot `bbox` and projection (slot `proj4string`); no spatial objects as such;

`SpatialPoints` Also has coördinates (slot `coords`) of each point; at this level of hierarchy there are also class `SpatialLines` and class `SpatialPolygons`;

`SpatialPointsDataFrame` Also has attributes (slot `data`) for each point;

`SpatialGridDataFrame` Points are on a regular grid, inherited from class `GridTopology` as well as class `SpatialPointsDataFrame`.

The real power of this approach is seen when generic methods are applied to objects of the various classes; each class then specialises the generic method appropriately. For example, the `spplot` plotting method gives a different kind of plot for each class that inherits from class `Spatial`; we can see this with the `showMethods` method:

```
> showMethods(spplot)

Function "spplot":
obj = "SpatialPixelsDataFrame"
obj = "SpatialGridDataFrame"
obj = "SpatialPolygonsDataFrame"
obj = "SpatialLinesDataFrame"
obj = "SpatialPointsDataFrame"
```

For more on the S4 class system, see Chambers [3, Ch. 7 & 8] and Venables & Ripley [56, Ch. 5].

4.14 Descriptive statistics

Numeric vectors can be described by a set of functions with self-evident names, e.g. `min`, `max`, `median`, `mean`, `length`:

```
> data(trees); attach(trees)
> min(Volume); max(Volume); median(Volume);
+ mean(Volume); length(Volume)
[1] 10.2
[1] 77
[1] 24.2
[1] 30.17097
[1] 31
```

Another descriptive function is `quantile`:

```
> quantile(Volume)
  0%  25%  50%  75% 100%
10.2 19.4 24.2 37.3 77.0
> quantile(Volume, .1)
 10%
15.6
> quantile(Volume, seq(0,1,by=.1))
  0%  10%  20%  30%  40%  50%  60%  70%  80%  90% 100%
10.2 15.6 18.8 19.9 21.4 24.2 27.4 34.5 42.6 55.4 77.0
```

The `summary` function applied to data frames combines several of these descriptive functions:

```
> summary(Volume)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  10.20   19.40   24.20   30.17   37.30   77.00
```

Some summary functions are *vectorized* and can be applied to an entire data frame:

```
> mean(trees)
   Girth   Height   Volume
13.24839 76.00000 30.17097
> summary(trees)
     Girth           Height       Volume
 Min.   : 8.30   Min.   :63   Min.   :10.20
 1st Qu.:11.05   1st Qu.:72   1st Qu.:19.40
 Median :12.90   Median :76   Median :24.20
 Mean   :13.25   Mean   :76   Mean   :30.17
 3rd Qu.:15.25   3rd Qu.:80   3rd Qu.:37.30
 Max.   :20.60   Max.   :87   Max.   :77.00
```

Others are not, but can be *applied* to margins of a matrix or data frame with the `apply` function:

```
> apply(trees, 2, median)
 Girth Height Volume
  12.9   76.0   24.2
```

The margin is specified in the second argument: 1 for rows, 2 for columns (fields in the case of data frames).

Surprisingly, base R has no functions for skewness and kurtosis; these are provided by the e1071 package written by TU Wien[32].

```
> require(e1071)
> skewness(trees$Volume)
[1] 1.0133
> kurtosis(trees$Volume)
[1] 0.24604
```

The kurtosis here is "excess" kurtosis, i.e., subtracting 3 from the kurtosis.

4.15 Classification tables

For data items that are classified by one or more *factors*, the `table` function counts the number of observations at each factor level or combination of levels. We illustrate this with the `meuse` dataset included with the `sp` package. This dataset includes four factors:

```
> require(sp); data(meuse); str(meuse)
`data.frame': 155 obs. of  14 variables:
...
 $ ffreq  : Factor w/ 3 levels "1","2","3": 1 1 1 1 1 1 1 1 1 1 ...
 $ soil   : Factor w/ 3 levels "1","2","3": 1 1 1 2 2 2 2 1 1 2 ...
 $ lime   : Factor w/ 2 levels "0","1": 2 2 2 1 1 1 1 1 1 1 ...
 $ landuse: Factor w/ 15 levels "Aa","Ab","Ag",..: 4 4 4 11 4 11  ...
...
> attach(meuse)
> table(ffreq)
ffreq
 1  2  3
84 48 23
> round(100*table(ffreq)/length(ffreq), 1)
ffreq
   1    2    3
54.2 31.0 14.8
> table(ffreq, landuse)
     landuse
ffreq Aa Ab Ag Ah Am  B Bw DEN Fh Fw Ga SPO STA Tv  W
    1  0  8  5 19  6  3  3   0  1  5  3   0   0  0 30
    2  1  0  0 14 11  0  1   1  0  4  0   1   2  1 12
    3  1  0  0  6  5  0  2   0  0  1  0   0   0  0  8
```

The last example is the *cross-classification* or *contingency table* showing which land uses are associated with which flood frequency classes.

The χ^2 test for conditional independence may be performed with the `chisq.test` function:

```
 > chisq.test(ffreq, lime)

Pearson's Chi-squared test

data:  ffreq and lime
```

[32] No, I don't know what the name stands for, either!

```
X-squared = 26.81, df = 2, p-value = 1.508e-06
```

Both the χ^2 statistic and the probability that a value this large could occur by chance in the null hypothesis of no association is true (the “p-value”) are given; the second is from the χ^2 table with the appropriate degrees of freedom (“df”). Here it is highly unlikely, meaning the flood frequency and liming are not independent factors.

4.16 Sets

S has several functions for working with lists (including vectors) as *sets*, i.e. a collection of elements; these include the `is.element`, `union`, `intersect`, `setdiff`, `setequal` functions. The `unique` function removes duplicate elements from a list; the `duplicated` function returns the indices of the duplicate elements in the original list.

The `setdiff` function can be used to select the *complement* of a defined set. For example, in §4.9 we selected random elements of the `trees` example dataset. We repeat that here; suppose this is a subsample, perhaps for calibration of some model. We select 2/3 of the trees for this set at random, rounded down to the nearest integer with the `floor` function:

```
> dim(trees)[1]
[1] 31 3
> floor(dim(trees)[1]*2/3)
[1] 20
> (tr.calib <- trees[sort(sample(1:dim(trees)[1], floor(dim(trees)[1]*2/3))), ])
   Girth Height Volume
2    8.6     65   10.3
4   10.5     72   16.4
...
30  18.0     80   51.0
```

If we now want to select the *validation* set, i.e. the remaining trees, we use the `setdiff` function on the two *sets* of row names (extracted with the `rownames` function:

```
> rownames(trees)
 [1] "1"  "2"  "3"  "4"  "5"  "6"  "7"  "8"  "9"  "10" "11" "12" "13" "14" "15"
[16] "16" "17" "18" "19" "20" "21" "22" "23" "24" "25" "26" "27" "28" "29" "30"
[31] "31"
> rownames(tr.calib)
 [1] "2"  "4"  "5"  "8"  "10" "11" "12" "13" "14" "16" "18" "20" "21" "22" "23"
[16] "26" "27" "28" "29" "30"
> setdiff(rownames(trees), rownames(tr.calib))
 [1] "1"  "3"  "6"  "7"  "9"  "15" "17" "19" "24" "25" "31"
> (tr.valid <- trees[setdiff(rownames(trees), rownames(tr.calib)),])
   Girth Height Volume
1    8.3     70   10.3
3    8.8     63   10.2
6   10.8     83   19.7
...
31  20.6     87   77.0
```

```
> dim(tr.calib)
[1] 20  3
> dim(tr.valid)
[1] 11  3
```

The dataframe has been split into mutually-exclusive frames for calibration (20 observations) and validation (11 observations).

4.17 Statistical models in S

Statistical models in S are specified in *symbolic* form with *model formulae*. These formulae are arguments to many statistical functions, most notably the `lm` (linear models) and `glm` (generalised linear models) functions, but also in base graphics (§5.1) functions such as `plot` and `boxplot` and trellis graphics (§5.2) functions such as `levelplot`.

The simplest form is where a (mathematically) *dependent* variable is (mathematically) explained by one (mathematically) *independent* variable; like all model formulae this uses the ~ *formula operator* to separate the left (dependent) from the right (independent) sides of the expression:

```
> (model <- lm(trees$Volume ~ trees$Height))
Call:
lm(formula = trees$Volume ~ trees$Height)

Coefficients:
 (Intercept)  trees$Height
      -87.12          1.54
```

This is to be read like a mathematical function, where the left-hand side is the result ("dependent") and the right-hand side is the expression ("independent"). In other words, a formula is read as:

- a *response* variable (left-hand side) . . .
- . . . is *explained* by (the ~ symbol) . . .
- . . . a *formula* including one or more *predictor* variables

In this example, the tree volume is to be explained as a linear function of its height; this is just a first-order linear regression, with the best-fit least-squares line $y = -87.12 + 1.54x$: for every foot increase in height, the volume increases by 1.54 ft^3; also, a zero-height tree would have a negative volume[33].

If the data frame has been attached, this can be written more simply:

```
> attach(trees)
```

[33] Nicely illustrating the risks of extrapolating outside the range of calibration; this data set only has trees from 63 to 87 feet tall, so the fitted relation says nothing about shorter trees

```
> model <- lm(Volume ~ Height)
```

but even if not, the variable names can be referred to a frame with the `data=` named argument:

```
> model <- lm(Volume ~ Height, data=trees)
```

Additive effects More complicated models include *additive effects*, using the + formula operator:

```
> model <- lm(Volume ~ Height + Girth, data=trees)
```

Note this is *not* an arithmetic addition, but rather a special use in the model notation. Here the tree volume is explained by by both its height and girth, considered as independent predictors.

Interactions The `:` formula operator is used to indicate *interactions*; usually these are used in addition to additive terms:

```
> model <- lm(Volume ~ Height + Girth + Height:Girth, data=trees)
```

Here the tree volume is explained by both its height and girth, as well as their interaction, i.e. that the effect of girth is different at different heights.

The `*` formula operator is shorthand for all linear terms and interactions of the named independent variables, so that the previous example could have been more simply written as:

```
> model <- lm(Volume ~ Height * Girth, data=trees)
```

The `^` formula operator is used to indicate predictor crossing to the specified degree:

```
> model <- lm(Volume ~ (Height + Girth)^2, data=trees)
```

Here the `^2` expands to all interactions between the named predictors, since there are only two; this is equivlent to `Height + Girth + Height:Girth`, which in this two-predictor case is also the same as `Height * Girth`.

Removing terms Sometimes it is convenient to specify a model and then remove a term from it with the - formula operator. As a somewhat artificial example, to model tree volume by only tree girth and its interaction with height:

```
> model <- lm(Volume ~ Height*Girth - Height, data=trees)
```

This is equivalent to:

```
> model <- lm(Volume ~ Girth + Girth:Height, data=trees)
```

The - formula operator is often used to remove the intercept; see below.

Nested models The / operator is used to specify that the second-named predictor is *nested* within the first-named predictor, i.e. levels of the nested predictor are not independent factors. Nested models are often used in designed experiments such as split-plot designs or replicated measurements within an experimental unit. This is also used for the analysis of covariance (ANCOVA), where the covariates are nested within the treatment; in this case the intercept should be removed (see next ¶).

No intercept The intercept term (e.g. the mean) is implicit in model formulas. For regression through the origin, it must be explicitly removed with the - formula operator, in this case the implied intercept, with the expression -1. Or, the origin can be named explicitly with the + formula operator, with the expression +0. For example, it's certainly true that a tree with no girth has no height, so if we want to force the regression of height on girth to go through $(0, 0)$:

```
> model <- lm(Height ~ Girth - 1, data=trees)
> model <- lm(Height ~ 0 + Girth, data=trees)
```

Note: Although this seems logical, in the range of timber trees, this may give a poorer predictive relation than allowing a (physically impossible) intercept and only predicting in the range of the calibration data.

Arithmetic operations in formulas Since the characters +, *, ^, and / have special meaning in formulas, they must be "quoted" with the I operator if they are to interpreted as arithmetic operators. For example, to model tree volume from the height-to-girth ratio:

```
> model <- lm(Volume ~ I(Height / Girth), data=trees)
```

To model volume as the square of girth:

```
> model <- lm(Volume ~ I(Girth^2), data=trees)
```

This is only needed if there is a danger of mis-interpretation; most functions can be used directly in formulas, e.g. the log function to compute natural logarithms. For example, to fit a log-log regression of tree height by width:

```
> model <- lm( log(Height) ~ log(Girth) )
```

For further description of model formulae, see the help topic:

```
> ?formula
```

The design matrix For full control of linear modelling, R offers the ability to extract or build *design matrices* of linear models; this is discussed in most regression texts, for example Christensen [4].

The design matrix of a model is extracted with the `model.matrix` function:

```
> model <- lm(Volume ~ Height + Girth, data=trees)
> (X <- model.matrix(model))
   (Intercept) Height Girth
1            1     70   8.3
2            1     65   8.6
...
30           1     80  18.0
31           1     87  20.6
```

This matrix contains the values of the predictor variables for each observation. This provides a good check on your understanding of the model structure. The matrix can be used to directly compute the least-squares linear solution:

$$\beta = (X'X)^{-1}X'Y$$

using the `t` (matrix transpose) and `solve` (matrix inversion) function, and the `%*%` (matrix multiplication) operator. For example, to directly compute the regression coefficients for the model of tree volume predicted by height and girth in the `trees` dataset:

```
> Y <- trees$Volume
> ( beta <- solve( t(X) %*% X ) %*% t(X) %*% Y )
                 [,1]
(Intercept) -57.98766
Height        0.33925
Girth         4.70816
>    # check this is the same result as from lm()
> lm(trees$Volume ~ trees$Height + trees$Girth)
Coefficients:
 (Intercept)  trees$Height   trees$Girth
     -57.988         0.339         4.708
```

The direct computation may be numerically unstable and is certainly slow; `lm` uses more sophisticated numerical functions.

4.17.1 Models with categorical predictors

The `lm` and `glm` functions are also used for models with categorical predictors and for mixed models, as well as for models using only continuous predictors. The categorical variables must be ordered or unordered S *factors*; this can be checked with the `is.factor` function or examined directly with the `str` function.

Factors are included in the design matrix as *contrasts* which divide the observations according to the classifying factors. This is quite a technical subject, treated thoroughly in standard linear modelling texts such as those by Venables & Ripley [57], Fox [18], Christensen [4] and Draper & Smith [14]. The practical importance of contrasts is mainly the interpretation of the results that is possible with a given contrast, and secondly in the computational stability.

One of R's environment options is the default contrast type for unordered and ordered factors; these can be viewed and changed with the `options` function. Contrasts for specific factors can be viewed and set with the `contrasts` function, using the `contr.helmert`, `contr.poly`, `contr.sum`, and `contr.treatment` functions to build contrast matrices.

```
> options("contrasts")
$contrasts
        unordered           ordered
"contr.treatment"      "contr.poly"
```

Polynomial contrasts assume equal feature-space distance between levels of the ordered predictor; this may not be justified and so you may want to change the contrast type.

For example, the `meuse` soil pollution dataset includes a factor for flooding frequency; this is an unordered factor but the three levels are naturally ordered from least to most flooding. So we might want to change the data type.

```
> data(meuse)
> str(meuse$ffreq)
 Factor w/ 3 levels "1","2","3": 1 1 1 1 1 1 1  ...
> contrasts(meuse$ffreq)
  2 3
1 0 0
2 1 0
3 0 1
> lm(log(meuse$lead) ~ meuse$ffreq))
Coefficients:
(Intercept)       ffreq2       ffreq3
      5.106       -0.666       -0.626
> meuse$ffreq <- as.ordered(meuse$ffreq)
> str(meuse$ffreq)
 Ord.factor w/ 3 levels "1"<"2"<"3": 1 1 1 1 1 1 1 1 1 1 ...
> contrasts(meuse$ffreq)
           .L        .Q
1 -7.0711e-01  0.40825
2 -9.0738e-17 -0.81650
3  7.0711e-01  0.40825
> lm(log(meuse$lead) ~ meuse$ffreq))
Coefficients:
  (Intercept)  meuse$ffreq.L  meuse$ffreq.Q
        4.675         -0.443          0.288
```

The unordered factor has treatments contrasts (sometimes called "dummy variables") whereas the ordered factor has orthogonal polynomial contrasts. These result in different fitted coefficients.

4.17.2 Analysis of Variance (ANOVA)

The results of linear models can be expressed in the traditional language of ANOVA as found in many textbooks with the aov function; this calls lm and formats its results in a traditional ANOVA table:

```
> model <- aov(Volume ~ Height + Girth, data=trees)
> class(model)
[1] "aov" "lm"
> summary(model)
            Df Sum Sq Mean Sq F value  Pr(>F)
Height       1   2901    2901     193 4.5e-14
Girth        1   4783    4783     317 < 2e-16
Residuals   28    422      15
```

Two models on the same dataset may be compared with the anova function; this is one way to test if the more complicated model is significantly better than the simpler one:

```
> model.1 <- aov(Volume ~ Height + Girth, data=trees)
> model.2 <- aov(Volume ~ Height * Girth, data=trees)
> anova(model.1, model.2)
Analysis of Variance Table

Model 1: Volume ~ Height + Girth
Model 2: Volume ~ Height * Girth
  Res.Df RSS Df Sum of Sq    F  Pr(>F)
1     28 422
2     27 198  1       224 30.5 7.5e-06
```

In this case the interaction term of the more complicated model is highly significant.

4.18 Model output

The result of a lm (linear models) function is a data structure with detailed information about the model, how it was fitted, and its results. It can be viewed directly with the str function, but it is better to access the model with a set of *extractor* functions: coefficients to extract a list with the model coefficients, fitted to extract a vector of the fitted values (what the model predicts for each observation), residuals to extract a vector of the residuals at each observation, and formula to extract the model formula:

```
> model <- lm(Volume ~ Height * Girth, data=trees)
> coefficients(model)
 (Intercept)       Height        Girth Height:Girth
    69.39632     -1.29708     -5.85585      0.13465
> fitted(model)
      1       2       3       4       5 ...
 8.2311  9.9974 10.8010 16.3186 18.3800 ...
> residuals(model)
        1         2         3         4         5 ...
 2.068855  0.302589 -0.600998  0.081368  0.420047 ...
> formula(model)
Volume ~ Height * Girth
```

The results are best reviewed with the `summary` generic function, which for linear models is specialized into `summary.lm`:

```
> summary(model)
Call:
lm(formula = Volume ~ Height * Girth, data = trees)

Residuals:
   Min     1Q Median     3Q    Max
-6.582 -1.067  0.303  1.564  4.665

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   69.3963    23.8358    2.91  0.00713
Height        -1.2971     0.3098   -4.19  0.00027
Girth         -5.8558     1.9213   -3.05  0.00511
Height:Girth   0.1347     0.0244    5.52  7.5e-06

Residual standard error: 2.71 on 27 degrees of freedom
Multiple R-Squared: 0.976,Adjusted R-squared: 0.973
F-statistic:  359 on 3 and 27 DF,  p-value: <2e-16
```

This provides the most important information about the model; for more insight consult textbooks which explain linear modelling, e.g. Venables & Ripley [57], Fox [18], Christensen [4] or Draper & Smith [14]:

- The *model formula* with which `lm` was called;
- A summary of the *residuals*; by definition the mean is zero so is not reported;
- The *model coefficients* (first column);
- The *standard error* associated with each coefficient (second column); these can be used to construct *confidence intervals*;
- The *significance level* of each coefficient (third column); this is the probability that rejecting the *null hypothesis* for the listed coefficient would be a mistake;
- The *residual standard error*, which is defined as the square root of the estimated variance of the random error: $\sigma^2 = (1/(n-p)) * \sum(r_i{}^2)$ where r_i is one of the n residuals and p is the number of coefficients.
- The *coefficient of determination* R^2, both the unadjusted fraction of variance explained by the model $R^2 = 1 - (\text{Residual SS}/\text{Total SS})$ and

the coefficient adjusted for the number of parameters in the model, $1 - [(n-1)/(n-p) * (1-R^2)]$.

The AIC (Akaike's An Information Criterion) function is often used to compare models; the lower AIC is better:

```
> AIC(lm(Volume ~ Height * Girth))
[1] 155.47
> AIC(lm(Volume ~ Height + Girth))
[1] 176.91
> AIC(lm(Volume ~ Girth))
[1] 181.64
> AIC(lm(Volume ~ 1))
[1] 264.53
```

In this example the successively more complicated models have lower AIC, i.e. provide more information.

4.18.1 Model diagnostics

The model summary (§4.18) shows the overall fit of the model and a summary of the residuals, but gives little insight into difficulties with the model (e.g. non-linearity, heteroscedascity of the residuals). A graphical presentation of some common diagnostic plots is given by the `plot` function applied to the model object (note that the generic `plot` function in this case automatically calls the specific `plot.lm` function):

```
> model <- lm(Volume ~ Height * Girth, data=trees)
> par(mfrow=c(2,2))  # set up a 2x2 matrix for the 4 diagnostic graphs
> plot(model)
> par(mfrow=c(1,1))  # reset the graphics device to show just 1 graph
```

This shows four plots (Figure 4): (1) residuals vs. fitted; (2) normal QQ plot of the residuals; (3) scale vs. location of residuals; (4) residuals vs. leverage. The intepretation of these is explained in many regression textbooks. The `par` function sets up a matrix of graphs in one figure; here there are four diagnostic graphs produced by the default `plot.lm` function, so a 2x2 grid is set up. See §5.4 for more information.

Many other diagnostics are available. There are several functions to directly access these from the model itself: `dfbetas`, `dffits`, `covratio`, `cooks.distance` and `hatvalues`; methdods `rstandard` and `rstudent` return the standardized and Studentized residuals, respectively. These diagnostic measures are explained in regression texts [e.g. 14, 18]; many of these were developed or expanded by Cook & Weisberg [8].

For example, to plot the "hat" values (leverage) for each point, with the number of the most influential observations:

```
> h <- hatvalues(model)
> plot(h, type="h")
```

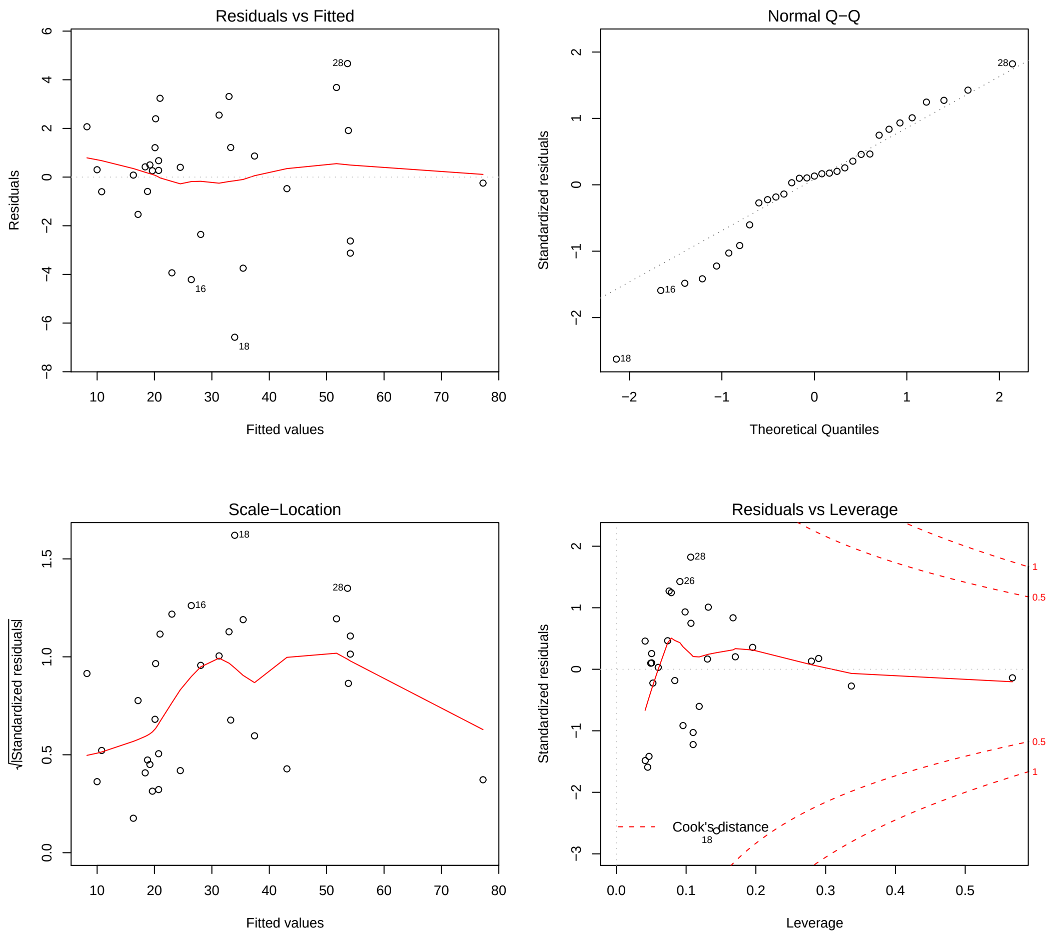


Figure 4: Regression diagnostic plots

```
> text(h, ifelse(h > 3*mean(h), seq(1:length(h)),""), pos=2)
```

A direct way to access diagnostics is with the `influence.measures` function applied to the fitted model:

```
> infl <- influence.measures(model)
> str(infl)
List of 3
 $ infmat: num [1:31, 1:8]  0.23213  0.06511 -0.15754  0.00173 -0.02461 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:31] "1" "2" "3" "4" ...
  .. ..$ : chr [1:8] "dfb.1_" "dfb.Hght" "dfb.Grth" "dfb.Hg:G" ...
 $ is.inf: logi [1:31, 1:8] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:31] "1" "2" "3" "4" ...
  .. ..$ : chr [1:8] "dfb.1_" "dfb.Hght" "dfb.Grth" "dfb.Hg:G" ...
 $ call  : language lm(formula = Volume ~ Height * Girth, data = trees)
 - attr(*, "class")= chr "infl"
```

The key field here is `is.inf`, which specifies which observations were especially influential in the fit, using eight different measures of influence, which are listed as attributes of this field.

```
> attr(infl$infmat, "dimnames")[[2]]
[1] "dfb.1_"   "dfb.Hght" "dfb.Grth" "dfb.Hg:G" "dffit"    "cov.r"
[7] "cook.d"   "hat"
```

The most common use here is to list the observations for which any of the influence measures were excessive:

```
> infl$is.inf[ which(apply(infl$is.inf, 1, any)) , ]
   dfb.1_ dfb.Hght dfb.Grth dfb.Hg:G dffit cov.r cook.d   hat
2   FALSE    FALSE    FALSE    FALSE FALSE  TRUE  FALSE FALSE
3   FALSE    FALSE    FALSE    FALSE FALSE  TRUE  FALSE FALSE
18  FALSE    FALSE    FALSE    FALSE  TRUE  TRUE  FALSE FALSE
20  FALSE    FALSE    FALSE    FALSE FALSE  TRUE  FALSE FALSE
31  FALSE    FALSE    FALSE    FALSE FALSE  TRUE  FALSE  TRUE
```

This example illustrates the use of the `which` function to return the indices in a vector where a logical condition is true, and the `any` function to perform a logical *or* on a set of logical vectors, in this case the eight diagnostics. In this example, observation `31` has a high leverage, `18` a high DFFITS value, and all five high COVRATIO.

Notice also the use of the `apply` function to apply the `any` "is any element of the vector `TRUE`?" function to each row.

4.18.2 Model-based prediction

The `fitted` function only gives values for the observations; often we want to predict at other values. For this the `predict` generic function is used; in the case of linear models this specialises to the `predict.lm` function. The first argument is the fitted model and the second is a *data frame* in which to look for variables with which to predict; these must have the same names as in the model formula. Both confidence and prediction intervals may be requested, with a user-specified confidence level.

For example, to predict tree volumes for all combinations of heights (in 10 foot increments) and girths (in 5 inch radius increments)[34] , along with the 99% confidence intervals of this prediction:

```
> model <- lm(Volume ~ Height * Girth, data=trees)
> new.data <- data.frame(expand.grid(Height = seq(50, 100, by=10),
     Girth = seq(5, 25, by=5)))
> pred <- predict(model, new.data, interval="prediction",
             level=0.99)
>    # add the predictor values for easy interpretation
> pred <- cbind(new.data, pred)
> str(pred)
```

[34] Some of these combinations would result in strange looking trees!

```
`data.frame': 30 obs. of  5 variables:
 $ Height: num  50 60 70 80 90 100 50 60 70 80 ...
 $ Girth : num  5 5 5 5 5 5 10 10 10 10 ...
 $ fit   : num    8.93   2.69  -3.55  -9.79 -16.03 ...
 $ lwr   : num   -7.37  -9.37 -12.74 -18.89 -27.88 ...
 $ upr   : num  25.222 14.743  5.639 -0.685 -4.167 ...
>    # fits for trees 50 feet tall
> pred[pred$Height==50,]
       fit     lwr    upr Height Girth
1   8.9265 -7.3694 25.222     50     5
7  13.3109  3.0322 23.590     50    10
13 17.6952  5.7180 29.672     50    15
19 22.0796  2.6126 41.547     50    20
25 26.4639 -2.0348 54.963     50    25
```

4.19 Advanced statistical modelling

The `lm` function is the workhorse of modelling in S, because of the importance of linear models and its versatility. However, R has many other modelling functions, including:

- `lm` implements *weighted* least squares if the weights are specified as an optional argument;
- `loess` for *local* fitting;
- `glm` for *generalised* linear models;
- `rlm` and `lqs` (in the `MASS` package) for *robust* fitting of linear models;
- `lm.ridge` (also in the `MASS` package) for *ridge* regression;
- `nls` for *non-linear* least squares fitting;
- `step` for *stepwise* regression; this is a dangerous procedure when applied blindly; `step` can select the “best” model, based on AIC, using forward or backward selection and a user-specified stopping and starting points;
- The `pls` package [27] implements *partial least squares regression* (PLSR) and *principal components regression* (PCR); these are often used in spectroscopy and chemometrics;
- The `boot` package provides bootstrapping functions;
- *Principal components* of multivariate matrices are computed by the `prcomp` function; the results can be visualised with the `biplot` and `screeplot` functions.

There are many other modelling functions; see §11.3 for some ideas on how to find the one you want. The advanced text of Venables & Ripley [57] has chapters on many sophisticated functions, all with theory, references, and S code. Many of these functions are implemented in the MASS package.

4.20 Missing values

A common problem in a statistical dataset is that not all variables are recorded for all records. R uses a special *missing value* value for all data types, represented as NA, which stands for 'not available'. Within R, it may be assigned to a variable.

For example, suppose the volume of the first tree in the trees dataset is unknown:

```
> trees$Volume[1] <- NA
> str(trees)
`data.frame': 31 obs. of  3 variables:
 $ Girth : num  8.3 8.6 8.8 10.5 10.7 10.8 11 11  ...
 $ Height: num  70 65 63 72 81 83 66 75 80 75 ...
 $ Volume: num  NA 10.3 10.2 16.4 18.8 19.7 15.6  ...
> summary(trees$Volume)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   10.2    19.8    24.5    30.8    37.8    77.0     1.0
```

As the example shows, some functions (like summary) can deal with NA's, but others can't. For example, if we try to compute the Pearson's correlation between tree volume and girth, using the cor function, with the missing value included:

```
> cor(trees$Volume, trees$Girth)
Error in cor(trees$Volume, trees$Girth) :
        missing observations in cov/cor
```

This message is explained in the help for cov, where several options are given for dealing with missing values within the function, the most common of which is to include a case in the computation only if no variables are missing:

```
> cor(trees$Volume, trees$Girth, use="complete.obs")
[1] 0.967397
```

To find out which cases have any missing value, S provides the complete.cases function:

```
> complete.cases(trees)
 [1] FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[14] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[27] TRUE TRUE TRUE TRUE TRUE
```

This shows that the first case (record) is not complete.

The na.omit function removes cases with a missing value in *any* variable:

```
> trees.complete <- na.omit(trees)
> str(trees.complete)
`data.frame': 30 obs. of  3 variables:
 $ Girth : num  8.6 8.8 10.5 10.7 10.8 11 11  ...
 $ Height: num  65 63 72 81 83 66 75 80 75 79 ...
 $ Volume: num  10.3 10.2 16.4 18.8 19.7 15.6  ...
```

The first observation, with the missing volume, was removed.

4.21 Control structures and looping

S is a powerful programming language with Algol-like syntax[35] and control structures.

Single statements may be grouped between the braces `{` and `}`, separated either by new lines or the *command separator* `;`. The value of the `{` and `}` expression is the value of its last statement.

The `if ...else` control structure allows *conditional execution*. These can be nested, i.e. the statement for either the `if` or `else` can itself contain a `if ...else` control structure.

The `for`, `while`, and `repeat` functions allow *looping*. Note however that because of R's many vectorized functions looping is much less common in R than in non-vectorized languages such as C.

For example, to convert the sample confusion matrix from counts to proportions, you might be tempted to try this:

```
> cmp <- cm
> for (i in 1:length(cm)) cmp[i] <- cm[i]/sum(cm)
> cmp
           [,1]       [,2]       [,3]        [,4]
[1,] 0.21472393 0.08588957 0.06748466 0.006134969
[2,] 0.02453988 0.06748466 0.01840491 0.000000000
[3,] 0.07361963 0.05521472 0.23312883 0.024539877
[4,] 0.01226994 0.03067485 0.07361963 0.012269939
```

But you can get the same result with a vectorized operation:

```
> cmp <- cm/sum(cm)
```

See Chapter 9 of [36] for more details.

An example of both the `for` and `if ...else` control structures is the following code to find the closest sample point to a given point. This also illustrates the `data.frame` function to create a new data frame, and the `runif` function to draw random numbers, by default in the range $0 \ldots 1$.

[35] also used in C and its derivatives such as C++ and Java; of Algol it has been aptly said that it was a great improvement over its successors.

Note also the use of the `ifelse` function to select one of two alternatives, in this case the colour to plot, based on some truth condition.

We also plot the sample points and target point, showing the nearest point and shift. This uses the `plot`, `points`, `text` and `arrows` base graphics functions. The result is shown in Figure 5.

```
> # simulate ten sample points
> n.pts <- 10
> sample.pts <- data.frame(x = runif(n.pts), y = runif(n.pts))
> # simulate the given point
> new.pt <-   data.frame(x = runif(1), y = runif(1))
> print(paste("Target point: x=", round(new.pt$x,4), ", y=", round(new.pt$y,4)))
[1] "Target point: x= 0.0756 , y= 0.8697"
> # the distance to the nearest point can't be further on a 1x1 grid
> min.dist <- sqrt(2); close.pt <- NULL
> for (pt in 1:n.pts)
+  d <- sqrt((sample.pts[pt,"x"] - new.pt$x)^2 + (sample.pts[pt,"y"] - new.pt$y)^2);
+  if (d < min.dist)
+    min.dist <- d;
+    closest.pt <- pt;
+    print(paste("Point ",pt," is closer: d=", round(d,4)))
+   else
+  print(paste("Point ",pt,"is not closer"))
[1] "Point  1  is closer: d= 0.4066"
[1] "Point  2 is not closer"
[1] "Point  3  is closer: d= 0.1478"
[1] "Point  4 is not closer"
[1] "Point  5 is not closer"
[1] "Point  6 is not closer"
[1] "Point  7 is not closer"
[1] "Point  8 is not closer"
[1] "Point  9 is not closer"
[1] "Point  10 is not closer"
> print(paste("Closest point: x=", round(sample.pts[closest.pt,"x"],4), ",
                          y=", round(sample.pts[closest.pt,"y"],4)))
[1] "Closest point: x= 0.2061 , y= 0.8003"
> plot(sample.pts, xlim=c(0,1), ylim=c(0,1), pch=20,
+    col=ifelse(row.names(sample.pts) == closest.pt, "red", "green"),
+    main="Finding the closest point")
> text(sample.pts, row.names(sample.pts), pos=3)
> points(new.pt, pch=20, col="blue", cex=1.2)
> text(new.pt, "target point", pos=3, col="blue")
> arrows(new.pt$x, new.pt$y, sample.pts[closest.pt,"x"],
+    sample.pts[closest.pt,"y"], length=0.05)
```

4.22 User-defined functions

An R user can use the `function` function to define *functions* with *arguments*, including *optional* arguments with *default* values. See the example in §C and a good introduction in Chapter 10 of [36]. These then are objects in the workspace which can be *called*.

For example, here's a function to compute the *harmonic mean* of a vector;

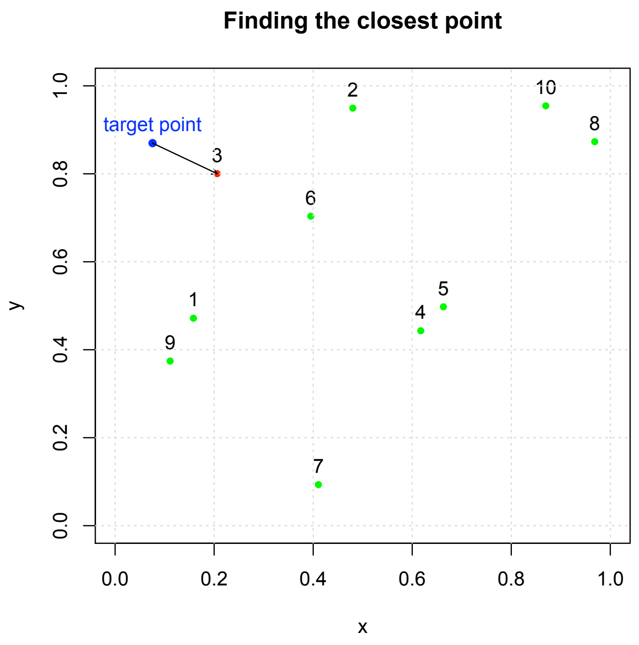


Figure 5: Finding the closest point

this is defined as

$$\bar{v}_h = \Big(\prod_{i=1 \dots n} v_i \Big)^{1/n}$$

where n is the length of the vector v, but is more reliably computed by taking logarithms, dividing by the length, and exponentiating:

```
> hm <- function(v) exp(sum(log(v))/length(v))
> hm(1:99)
[1] 37.6231
> mean(1:99)
[1] 50
```

As it stands, this function does not check its arguments; it only makes sense for a vector of positive numbers:

```
> hm(c(-1, -2, 1, 2))
[1] NaN
Warning message:
NaNs produced in: log(x)
```

To correct this behaviour we write a multi-line function with a conditional statement and the `return` function to leave the function:

```
> hm <- function(v) {
   if (!is.numeric(v)) {
     print("Argument must be numeric"); return(NULL)
     }
   else if (any(v <= 0)) {
     print("All elements must be positive"); return(NULL)
     }
   else return(exp(sum(log(v))/length(v)))
   }
> class(hm)
[1] "function"
> hm
function(v) {
  ...
   }
> hm(letters)
[1] "Argument must be numeric"
NULL
> hm(c(-1, -2, 1, 2))
[1] "All elements must be positive"
NULL
> hm(1:99)
[1] 37.6231
```

Note the use of the `any` function to check if any elements of the argument vector are not positive. Also note how simply typing the function name *lists* the function object (this is shorthand for the `print` function); to *call* the function you must supply the *argument list*.

Note also the use of the `if ...else` control structure for conditional execution; these can be nested, i.e. the statement for either the `if` or `else` can itself contain a `if ...else` control structure.

4.23 Computing on the language

As explained in the R Language Definition:

> "R belongs to a class of programming languages in which subroutines have the ability to modify or construct other subroutines and evaluate the result as an integral part of the language itself." [38, Ch. 6]

This may seem quite exotic, but it has some practical applications even for the non-programmer R user, in addition to the deeper applications explained in the Definition.

For example, consider the problem of summarising a set of variables that are named `B1`, `B2`, ...`B256`[36] . To avoid writing `m[1] <- mean(B1)`, `m[2] <- mean(B2)` etc. we'd like to loop through the numbers and form the variable name (with the `B` prefix and a number) and perform the operation. We do this in three steps:

1. Build up a syntactically-correct string to be evaluated, using the `paste` function;

2. Parse this into an R language object with the `parse` function;

[36] Perhaps reflectances from a hyperspectral sensor

3. Evaluate it with the `eval` function.

```
>    # demonstrate how the string is built up
> paste("m[", b, "] <- mean(B", b, ")", sep="")
Error in paste("m[", b, "] <- mean(B", b, ")", sep = "") :
object "b" not found
>    # must define a value for b to see how this works
> b <- 4
> paste("m[", b, "] <- mean(B", b, ")", sep="")
[1] "m[4] <- mean(B4)"
>    # what does this look like as  a parse language object?
> parse(text=paste("m[", b, "] <- mean(B", b, ")", sep=""))
expression(m[4] <- mean(B4))
>    # initialise the results vector
> m <- NULL
>    # evaluate this one expression
> eval(parse(text=paste("m[", b, "] <- mean(B", b, ")", sep="")))
Error in mean(B4) : object "B4" not found
>    # must define this variable to compute its mean
> B4 <- 0:100
> eval(parse(text=paste("m[", b, "] <- mean(B", b, ")", sep="")))
>    # result so far
> m
[1] NA NA NA 50
>    # apply to all 256 variables; need B1 .. B256 defined
> for (b in 1:256)
      eval(
         parse(
            text =
                paste("m[", b, "] <- mean(B", b, ")", sep="")
         )
      )
```

Note that the `for` expression in this example does not need to be written on separate lines; it is so written here for clarity.

The result of the `parse` function is an expression; it is also possible to create an R expression, ready to be evaluated with the `eval` function, with the `expression` function. For example:

```
> tmp <- expression(2*pi/r)
> r <- 3
> eval(tmp)
[1] 2.0944
```

5 R graphics

R provides a rich environment for statistical visualisation [28]. There are (at least) four graphics systems:

1. the *base R graphics* system (in the `graphics` package, loaded by default when R starts)

2. the *Trellis* system (in the `lattice` package);

3. the *Grid* system [28] (in the `grid` package);

4. the *Grammer of Graphics* “ggplot” system [60] (in the `ggplot2` package).

The first of these is easiest to begin with; the second is especially suited to plots grouped by a factor, the third is for low-level graphic manipulation, and the last is more difficult to learn but very powerful. Only base R graphics are loaded by default when R starts. The `lattice` package is generally included in initial R distributions; the other two have to be installed before use.

R graphics are highly customizable; see each method’s help page for details and (for base graphics) the help page for graphics parameters: `?par`. Except for casual use, it’s best to create a script (§3.5) with the graphics commands; this can then be edited, and it also provides a way to produce the exact same graph later.

Multiple graphs can be placed in the same window for display or printing; see §5.4, and several graphics windows can be opened at the same time; see §5.3.

To get a quick appreciation of R graphics, run the demostration programs:

```
> demo(graphics)
> demo(lattice)
```

Packages `grid` and `ggplot2` have no demos, see the respective texts for an introduction.

5.1 Base R graphics

A technical introduction to base R graphics is given in Chapter 12 of [36]. Here we give an example of building up a sophisticated plot step-by-step, starting with the defaults and customizing.

The example is a scatter plot of petal length vs. width from the `iris` data set. A default scatterplot of two variables is produced by the `plot.default` method, which is automatically used by the generic `plot` command if two equal-length vectors are given as arguments:

```
> data(iris)
> str(iris)
`data.frame': 150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 ...
> attach(iris)
> plot(Petal.Length, Petal.Width)
```

In this form, the x- and y-axes are given by the first and second arguments, respectively. The same plot can be produced using a *formula* §4.17 showing the dependence, in which case the y-axis is given as the *dependent* variable on the left-hand side of the formula:

```
> plot(Petal.Width ~ Petal.Length)
```

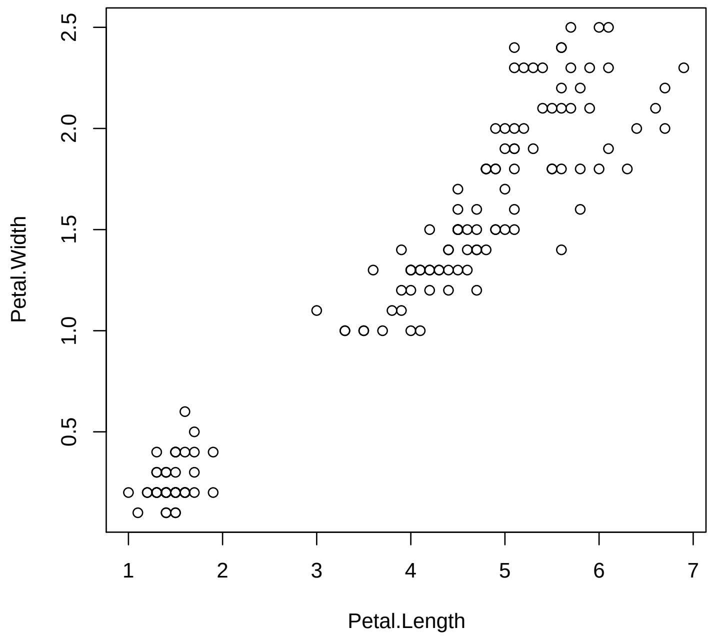


Figure 6: Default scatterplot

This default plot is shown in Figure 6. It is informative but not so attractive. We can customize the plotting symbol (`pch` argument), its colour and size (`col` and `cex` arguments), the axis labels (`xlab` and `ylab` arguments), and graph title (`main` argument).

Plotting symbols can be specified either by a single character (e.g. `"*"` for an asterisk) or an integer code for one of a set of graphics symbols. Figure

7 shows the symbols and their codes. Note that symbols 21–26 also have a *fill* (background) colour, specified by the bg argument; the main colour specified by the col argument specifies the border.

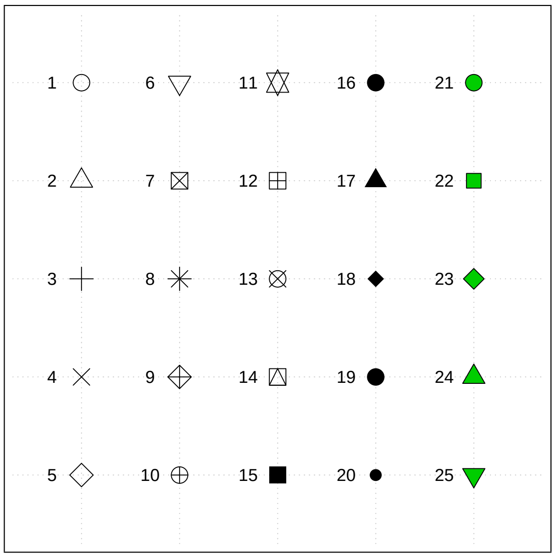


Figure 7: Plotting symbols

See §5.5 for details on how to specify colours.

We now produce a customized plot, showing the species:

```
> plot(Petal.Length, Petal.Width, pch=(21:23)[as.numeric(Species)], cex=1.2,
+   xlab="Petal length (cm)", ylab="Petal width (cm)",
+   main="Anderson Iris data",
+   col=c("slateblue", "firebrick", "darkolivegreen")[as.numeric(Species)]
+   )
```

It's clear that the species are of different sizes (*Setosa* smallest, *Versicolor* in the middle, *Virginica* largest) but that the ratio of petal length to width is about the same in all three.

Note the use of the as.numeric method to coerce the Species, which is a factor, to the corresponding level number (here, 1, 2 and 3), and then the use of this number to index a list of printing characters (pch argument) and colours (col argument).

The plot generic method is an example of a *high-level* plotting method which begins a new graph. Once the coördinate system is set up by plot, several *mid-level* plotting methods are available to add elements to the graph, such as lines, points, and text; Table 1 lists the principal methods; see the help for each one for more details.

For example, to add horizontal and vertical lines at the mean and median centroids, use the abline method:

```
> abline(v=mean(Petal.Length), lty=2, col="red")
```

`abline`	Add a Straight Line
`arrows`	Add Arrows
`axis`	Add an Axis
`box`	Draw a framing Box
`grid`	Add a Grid
`legend`	Add Legends
`lines`	Add Connected Line Segments
`mtext`	Write Text into the Margins
`points`	Add Points
`polygon`	Draw Polygons
`rect`	Draw Rectangles
`rug`	Add a Rug
`segments`	Add Line Segments
`symbols`	Draw Symbols
`text`	Add Text
`title`	Plot Annotation

Table 1: Methods for adding to an existing base graphics plot

```
> abline(h=mean(Petal.Width), lty=2, col="red")
> abline(v=median(Petal.Length), lty=2, col="blue")
> abline(h=median(Petal.Width), lty=2, col="blue")
```

The `lty` argument specifies the *line type* (style). These can be specified as a code (0=blank, 1=solid, 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as a descriptive name "blank", "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash").

To add light gray dotted grid lines at the axis ticks, use the `grid` method:

```
> grid()
```

To add the mean and median centroids as large filled diamonds, use the `points` method:

```
> points(mean(Petal.Length), mean(Petal.Width),
+       cex=2, pch=23,  col="black", bg="red")
> points(median(Petal.Length), median(Petal.Width),
+       cex=2, pch=23,  col="black", bg="blue")
```

Titles and axis labels can be added with the `title` method, if they were not already specified as arguments to the `plot` method:

```
> title(sub="Centroids: mean (green) and median (gray)")
```

Text can be added anywhere in the plot with the `text` method; the first two arguments are the coördinates as shown on the axes, the third argument is the text, and optional arguments specify the position of the text relative to the coördinates, the colour, text size, and font:

```
> text(1, 2.4, "Three species of Iris", pos=4, col="navyblue")
```

A special kind of text is the *legend*, added with the `legend` method;

```
> legend(1, 2.4, levels(Species), pch=21:23, bty="n",
+        col=c("slateblue", "firebrick", "darkolivegreen"))
```

The `abline` method can also add lines computed from a model, for example the least-squares regression (using the `lm` method) and a robust regression (using the `lqs` method of the `MASS` package):

```
> abline(lm(Petal.Width ~ Petal.Length), lty="longdash", col="red")
> require(MASS) # for lqs function
> abline(lqs(Petal.Width ~ Petal.Length), lty=2, col="blue")
```

This customized plot is shown in Figure 8.

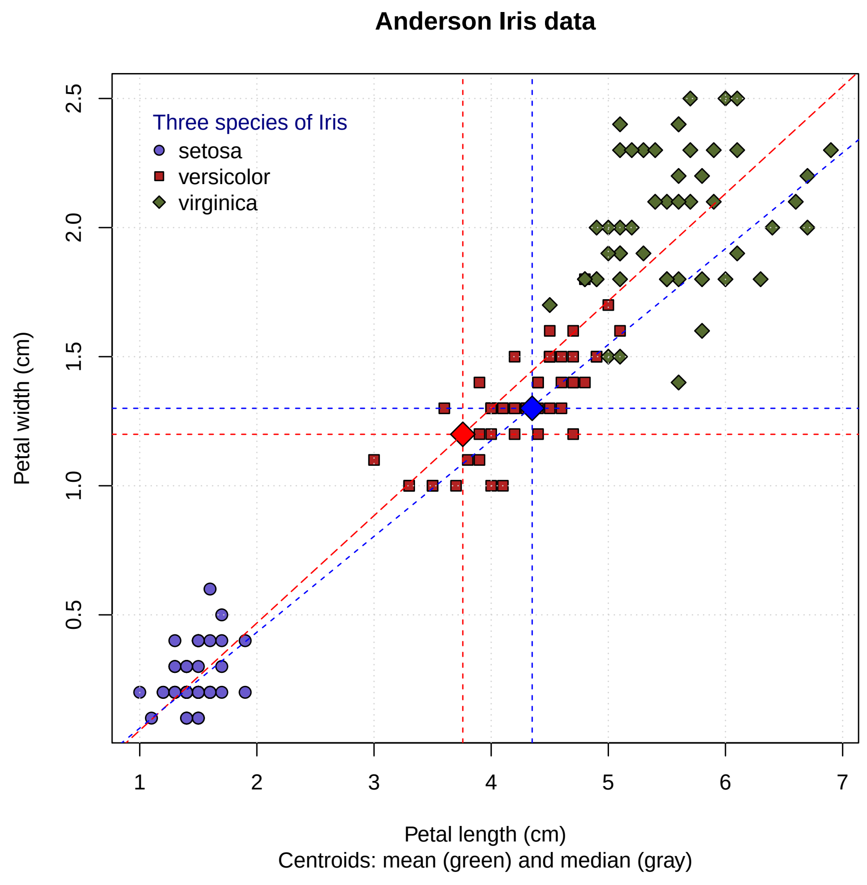


Figure 8: Custom scatterplot

5.1.1 Mathematical notation in base graphics

To include mathematical notation in one of the graphics functions that draw text, for example `text`, `axis` or `title`, there is a special syntax explained in the help for the `plotmath` function. The trick is to turn the argument into an R expression by using the `expression` function; in this case the text functions interpret the argument as a mathematical expression and the output will be formatted according to TEX-like rules. It is possible to produce many mathematical symbols, sub- or superscripts, fractions, operators, greek letters etc.; run `demo(plotmath)` to see examples.

> The `expression` function turns its argument into an R expression, ready to be evaluated with the `eval` function; more on this in §4.23.

Figure 9 shows an example of a graph with superscripts, e.g., "R^2", and math. notation, e.g. Greek letters such as β and a summation, produced with the following code. Note the use of the `substitute` function to place a numeric value (computed on-the-fly from a linear model result) into a text string, along with math. symbols. Note also the alignment of the text with the `pos` "position" argument to the `text` function.

```
> plot(single$SW ~single$SA, pch=as.numeric(single$spp),
     xlab=expression(paste("Stem area, ", plain(cm)^2)),
     ylab=expression(paste("Sapwood area, ", plain(cm)^2)),
     xlim=c(0,150), ylim=c(0,90))
> abline(0,coefficients(m.all.sw.sa.spp.i.st)[1])
> title(main="Sapwood area vs. stem area, smaller trees")
> for (i in 2:9) {
  abline(0,coefficients(m.all.sw.sa.spp.i.st)[1]
  +coefficients(m.all.sw.sa.spp.i.st)[i],lty=i-1)
  }
> legend(x=0,y=90, legend=spp, pch=c(2:length(spp),1), lty=c(2:length(spp),1))
> text(150,0,"S formula:  lm(SW ~ SA/spp - 1)",pos=2)
> text(150,6,substitute(plain(R)^2 == x,
  list(x=round(summary(m.all.sw.sa.spp.i.st)$adj.r.squared,3))), pos=2)
> text(150,12,expression(paste(plain(Model),
                              ~~ y == beta[1]*s + sum(beta[2]*x[k], k==1, n)
                              + epsilon)),
      pos=2)
```

5.1.2 Returning results from graphics methods

Many high-level graphics methods return results, which may be assigned to an S object or used directly in an expression. For example, the `hist` method returns the break and mid points, counts and densities:

```
> data(trees)
> h <- hist(trees$Volume)
> str(h)
List of 7
 $ breaks     : num [1:8] 10 20 30 40 50 60 70 80
 $ counts     : int [1:7] 10 9 5 1 5 0 1
 $ intensities: num [1:7] 0.03226 0.02903 0.01613 0.00323 0.01613 ...
 $ density    : num [1:7] 0.03226 0.02903 0.01613 0.00323 0.01613 ...
 $ mids       : num [1:7] 15 25 35 45 55 65 75
 $ xname      : chr "trees$Volume"
```

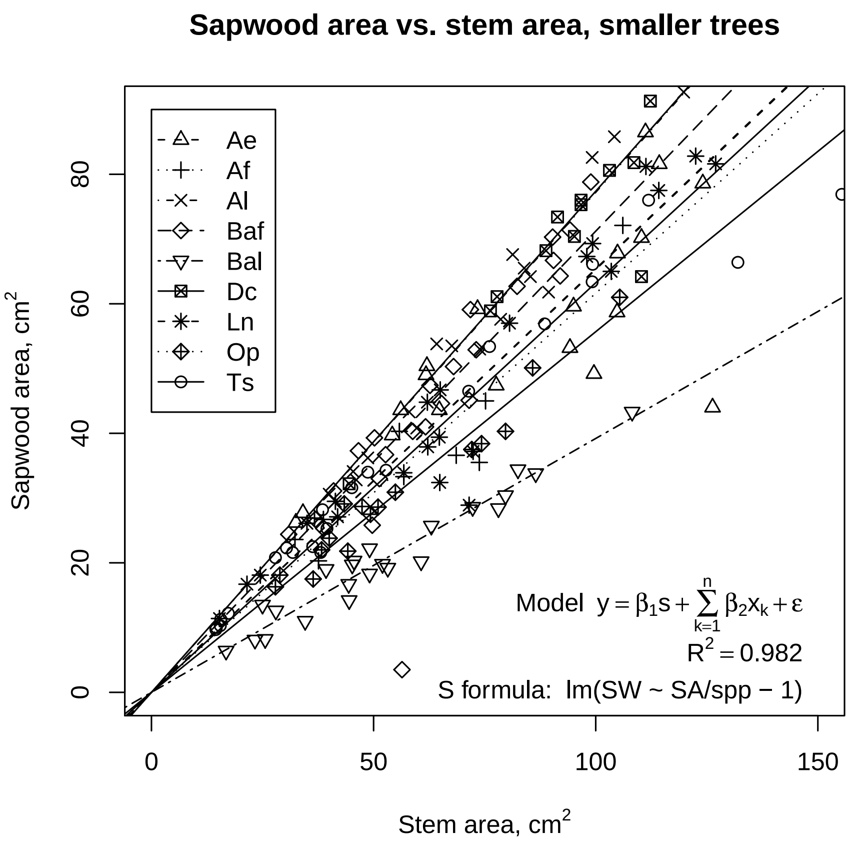


Figure 9: Scatterplot with math symbols, legend and model lines

```
 $ equidist   : logi TRUE
 - attr(*, "class")= chr "histogram"
> (hist(trees$Volume))$mids
[1] 15 25 35 45 55 65 75
```

5.1.3 Types of base graphics plots

Table 2 lists the principal plot types; see the help for each one for more details.

Figure 10 shows examples of a boxplot, a conditioning plot, a pairwise scatterplot, and a star plot, all applied to the Anderson `iris` dataset.

```
> boxplot(Petal.Length ~ Species, horizontal=T,
+    col="lightblue", boxwex=.5,
+    xlab="Petal length (cm)", ylab="Species",
+    main="Grouped box plot")
> coplot(Petal.Width ~ Petal.Length | Species,
+    col=as.numeric(Species), pch=as.numeric(Species))
> pairs(iris[,1:4], col=as.numeric(Species),
+    main="Pairwise scatterplot")
> stars(iris[,1:4], key.loc=c(2,35), mar=c(2, 2, 10, 2),
```

`assocplot`	Association Plots
`barplot`	Bar Plots
`boxplot`	Box Plots
`contour`	Contour Plots
`coplot`	Conditioning Plots
`dotchart`	Cleveland Dot Plots
`filled.contour`	Level (Contour) Plots
`fourfoldplot`	Fourfold Plots
`hist`	Histograms
`image`	Display a Colour Image
`matplot`	Plot Columns of Matrices
`mosaicplot`	Mosaic Plots
`pairs`	Scatterplot Matrices
`persp`	Perspective (3D) Plots
`plot`	Generic X-Y Plotting
`stars`	Star (Spider/Radar) Plots
`stem`	Stem-and-Leaf Plots
`stripchart`	1-D Scatter Plots
`sunflowerplot`	Sunflower Scatter Plots

Table 2: Base graphics plot types

```
+    main="Star plot of individuals", frame=T)
```

Some packages have implemented their own variations of these and other plots, for example `scatterplot` and `scatterplot.matrix` in the `car` package and `truehist` in the `MASS` package.

5.1.4 Interacting with base graphics plots

If the output graphics device is a screen, e.g. as initialised with the `windows` method, it is possible to *query* the graph with the `identify` method for scatterplots. This reads the position of the graphics pointer when the *left* mouse button is pressed, and searches the coördinates given as its for the closest point in the plot. If this point is close enough to the pointer, its index is added to a list to be returned, once the *right* mouse button is pressed.

The coördinate pairs for `identify` is normally the same as the scatterplot:

```
> plot(Petal.Length, Petal.Width)
> (p <- identify(Petal.Length, Petal.Width))
[1] 44 65 99
> iris[p,]
   Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
44          5.0         3.5          1.6         0.6     setosa
65          5.6         2.9          3.6         1.3 versicolor
99          5.1         2.5          3.0         1.1 versicolor
```

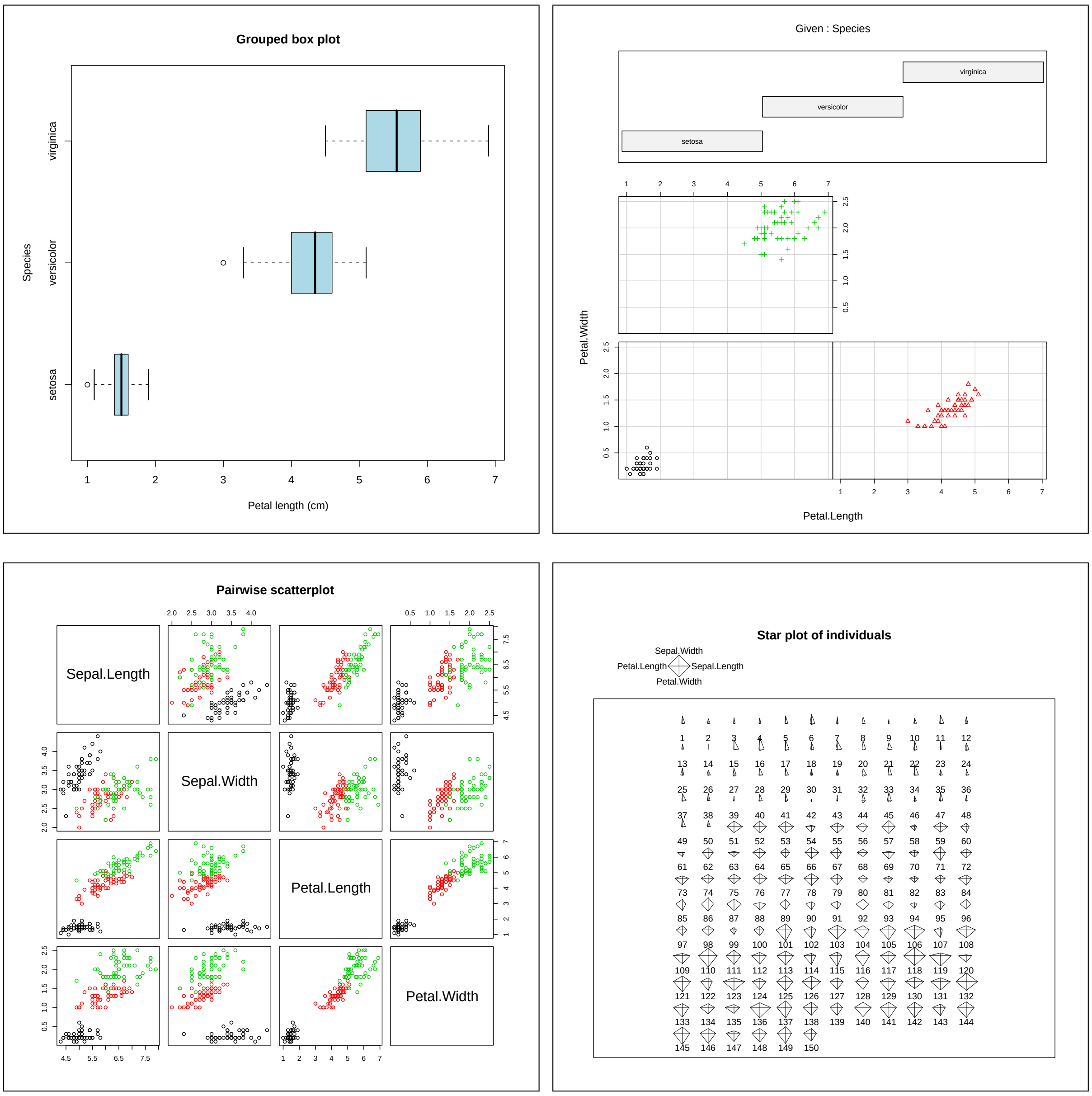


Figure 10: Some interesting base graphics plots

This is quite useful for identifying unusual points in the plot.

5.2 Trellis graphics

The Trellis graphics system is a framework for data visualization developed at Bell Labs (where S originated) based on the ideas in Cleveland [5]. It was implemented in S-PLUS and then in R with the `lattice` package; its design and basic use are well-explained by its author Sarkar [50] in the R Newsletter. It is harder to learn than R base graphics, but can produce higher-quality graphics, especially for *multivariate visualisation* when the relationship between variables changes with some grouping factor; this is called *conditioning* the graph on the factor. It uses *formulae* similar to the statistical formulae introduced in §4.17 to specify the variables to be plotted and their relation in the plot. Customization of Trellis graphics parameters (for example, default background and symbol colours) is explained in §5.2.6.

5.2.1 Univariate plots

As a simple example, consider the `iris` dataset. To produce a kernel density plot (a sophisticated histogram) on the whole dataset, use the `densityplot` method:

```
> densityplot(~ Petal.Length, data=iris)
```

The ~ operator here has no left-hand side, since there is no dependent variable in the plot; it is univariate. The petal length is the independent variable, and we get one plot; this is shown shown on the left side of Figure 11.

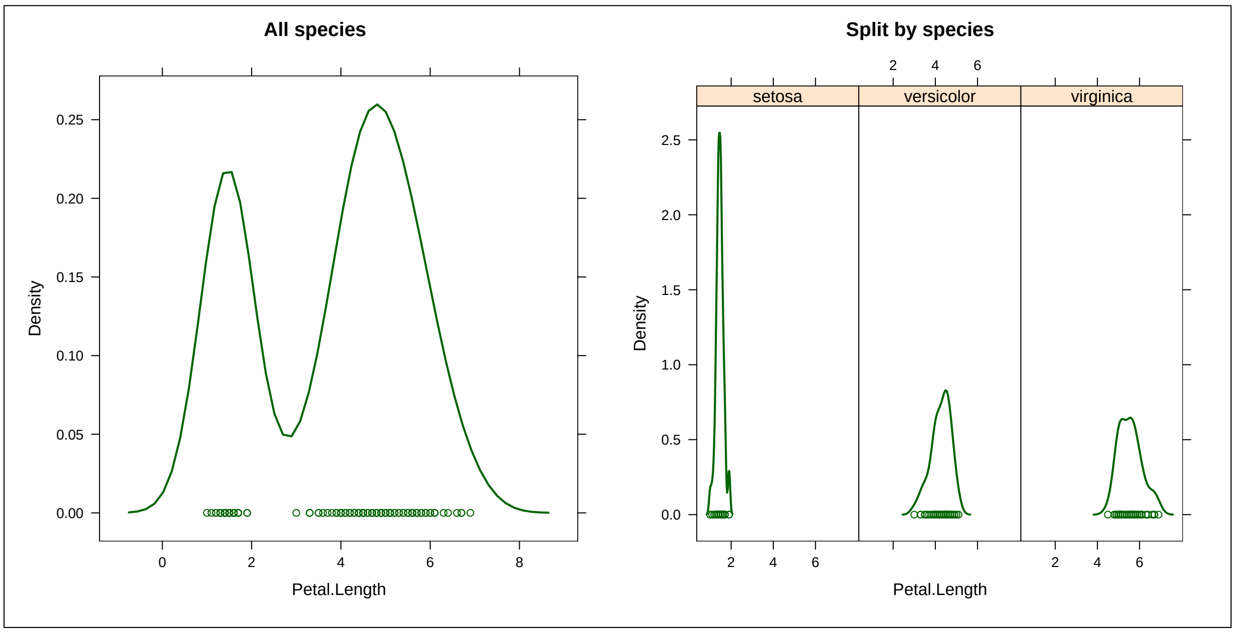


Figure 11: Trellis density plots, without and with a conditioning factor

To add *conditioning*, we use the | operator, which can be read as "conditioned on" the variable(s) named on its right side:

```
> densityplot(~ Petal.Length | Species, data=iris)
```

Here there is one *panel* per species; this is shown shown on the right side of Figure 11. We can clearly see that the multi-modal distribution of the entire data set is due to the different distributions for each species.

5.2.2 Bivariate plots

The workhorse here is the `xyplot` method, now with a dependent (y-axis) and independent (x-axis) variable; this can also be conditioned on one or more grouping factors:

```
> xyplot(Petal.Width ~ Petal.Length, data=iris,
+     groups=Species, auto.key=T)
> xyplot(Petal.Width ~ Petal.Length | Species, data=iris,
+     groups=Species)
```

These are shown in Figure 12. Note the use of the `groups` argument to specify a different graphic treatment (in this case colour) for each species, and the `auto.key` argument to get a simple key to the colours used for each species.

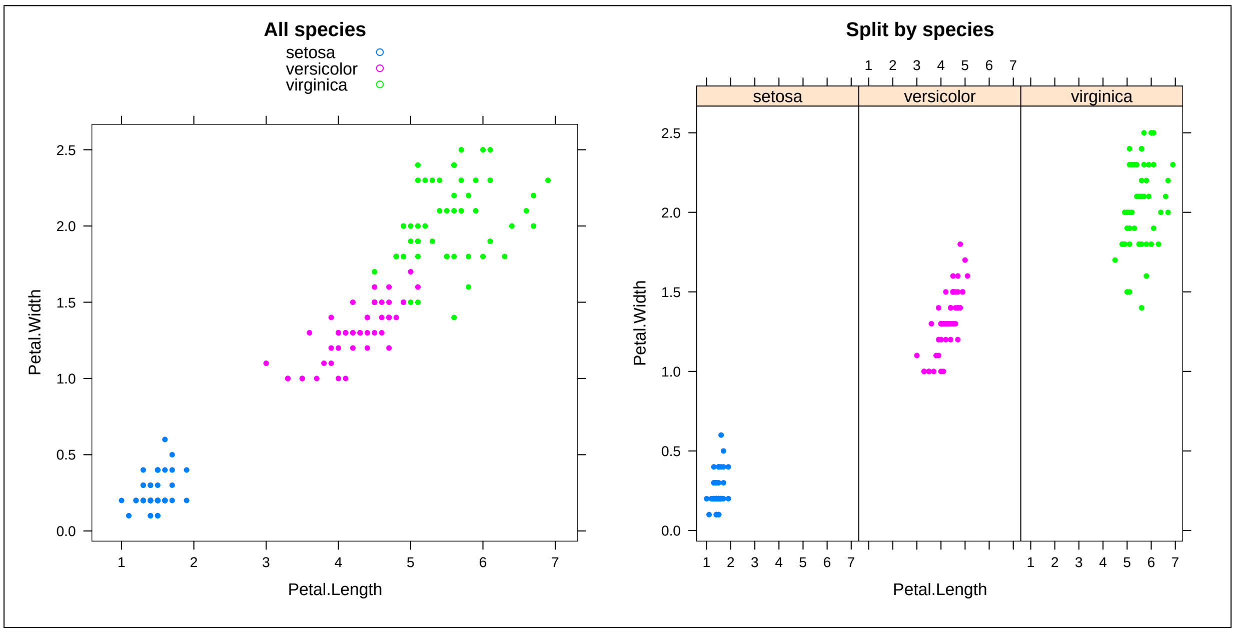


Figure 12: Trellis scatter plots, without and with a conditioning factor

5.2.3 Triivariate plots

The most useful plots here are the `levelplot` and `contourplot` methods for 2D plotting of one response variable on two continuous dependent variables (for example, elevation vs. two coördinates), the `wireframe` method for a 3D version of this, and the `cloud` method for a 3D scatterplot of three variables. All can be conditioned on a factor. Figure 13 shows some examples, produced by the following code:

```
> pl1 <- cloud(Sepal.Length ~ Petal.Length * Petal.Width,
+     groups=Species,
+     data=iris, pch=20, main="Anderson Iris data, all species",
+     screen=list(z=30, x=-60))
> data(volcano)
> pl2 <- wireframe(volcano,
+     shade = TRUE, aspect = c(61/87, 0.4),
+     light.source = c(10, 0, 10), zoom=1.1, box=F,
+     scales=list(draw=F), xlab="", ylab="", zlab="",
+     main="Wireframe plot, Maunga Whau Volcano, Auckland")
> pl3 <- levelplot(volcano,
+         col.regions=gray(0:16/16),
+         main="Levelplot, Maunga Whau Volcano, Auckland")
> pl4 <- contourplot(volcano, at=seq(floor(min(volcano)/10)*10,
+            ceiling(max(volcano)/10)*10, by=10),
+            main="Contourplot, Maunga Whau Volcano, Auckland",
+            sub="contour interval 10 m",
+            region=T,
+            col.regions=terrain.colors(100))
> print(pl1, split=c(1,1,2,2), more=T)
> print(pl2, split=c(2,1,2,2), more=T)
> print(pl3, split=c(1,2,2,2), more=T)
> print(pl4, split=c(2,2,2,2), more=F)
> rm(pl1, pl2, pl3, pl4)
```

Note that the `volcano` data set is just a matrix of elevations:

```
> str(volcano)
 num [1:87, 1:61] 100 101 102 103 104 105 105 106 107 108 ...
```

The `levelplot` method converts this into one response variable (the `z` values) and two predictors, i.e. the row and column of the matrix. (the `x` and `y` values).

This example shows that high-level `lattice` methods do not themselves draw a graph; they return an object of class `trellis` which can be printed with the `print` method. R's default behaviour when working interactively (at the console) is to print the results of any expression except an assignment, so the casual user doesn't see this behaviour. It is however quite useful to place multiple graphs on the same page as illustrated here and explained in more detail in §5.4.

5.2.4 Panel functions

A Trellis plot must be constructed in one go, unlike in the base graphics package, where elements can be added later. Each additional element beyond the default is specified by a so-called *panel function*. For example, suppose we want to add a least-squares regression line as well as regression lines for each species to the scatterplot of petal width and length:

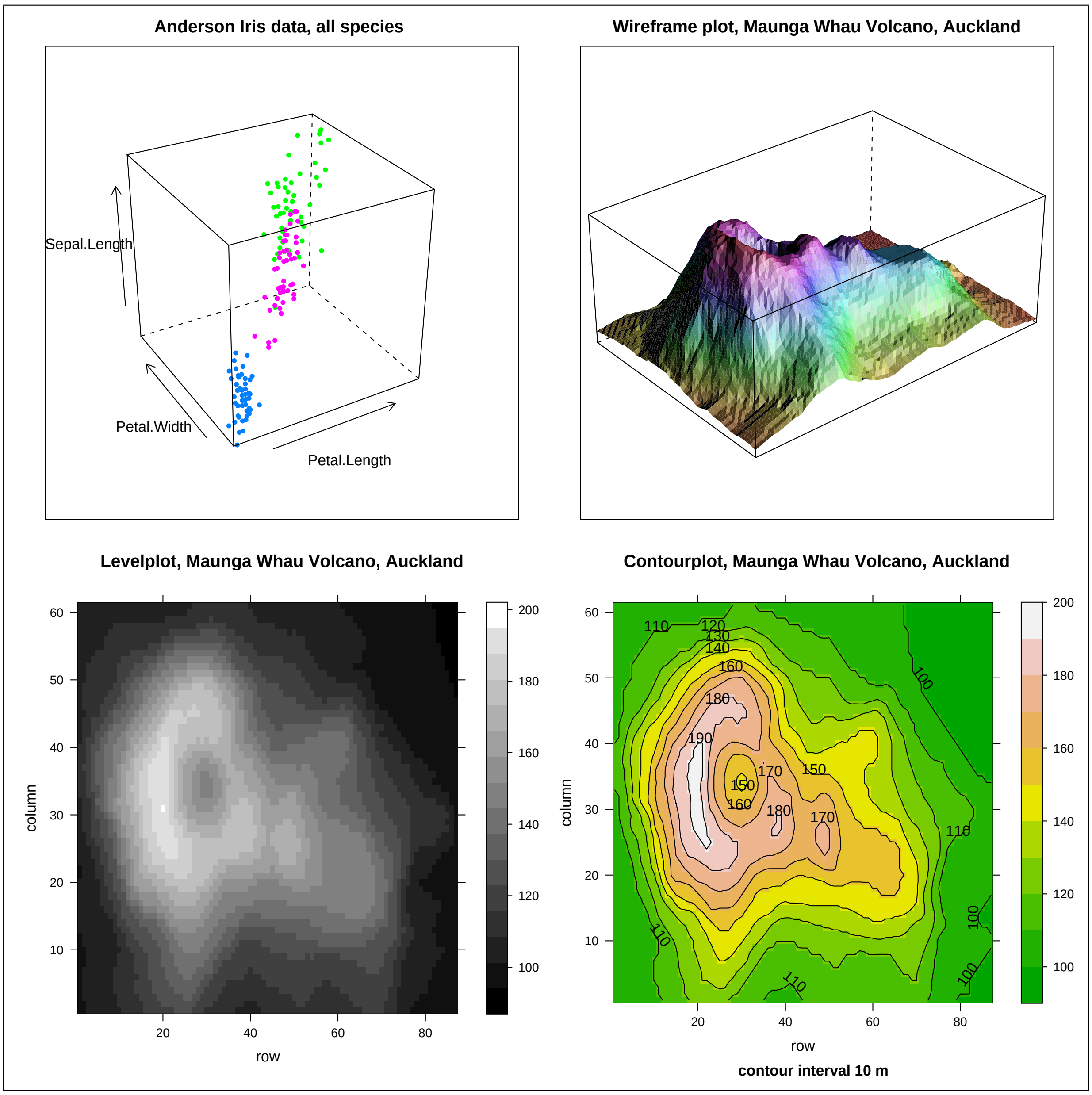


Figure 13: Trellis trivariate plots

```
> xyplot(Petal.Width ~ Petal.Length, data=iris,
+       col=c("darkgreen", "navyblue", "firebrick")
+               [as.numeric(iris$Species)], pch=20,
+       xlab="Petal length", ylab="Petal width",
+       main="Anderson Iris data",
+       panel = function(x, y, ...) {
+         panel.fill(col="antiquewhite3")
+         panel.xyplot(x, y, ...);
+         panel.abline(lm(y ~ x), col="black");
+         for (lvl in 1:length(levels(Species))) {
```

```
+            panel.abline(lm(y ~ x,
+              subset=(Species==levels(Species)[lvl])),
+              col=c("darkgreen", "navyblue", "firebrick")[lvl],
+              lty=2)
+        }
+     })
```

This plot is shown in Figure 14.

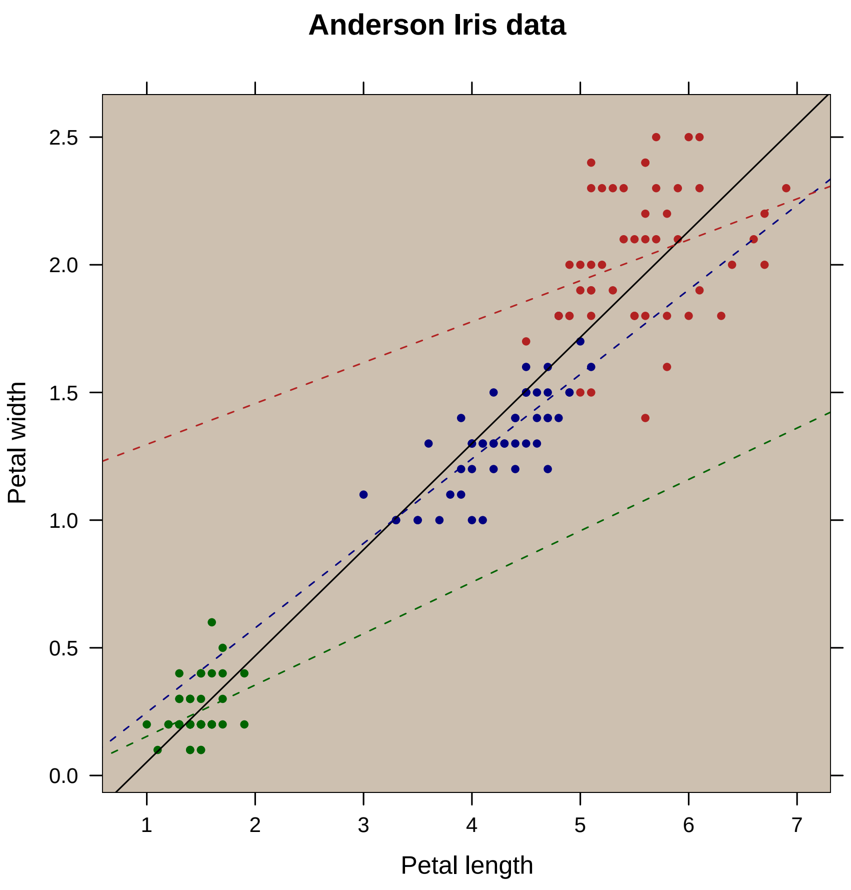


Figure 14: Trellis scatter plot with some added elements

The `panel` argument is used whenever we want to control the appearance of the panel beyond the default plot. Here it is a function, which takes as arguments the *dummy variables* `x` and `y`, which represent the two variables of the x-y plot. The `...` argument to the panel passes through all the extra arguments specified previously, e.g. `data=iris`. Within the un-named panel function, several pre-defined panel functions are called to add graphic elements. These all have names beginning with `panel.`. First we use `panel.fill` to change the main plot background, then `panel.xyplot` to draw the points; note that this must be called explicitly if there is a panel function. Then we add the regression lines with `panel.abline`. Note the use of the `for` loop to add one line for each species.

See `?panel.functions` and the explanation of the `panel` parameter in `?xyplot` for details.

5.2.5 Types of Trellis graphics plots

Table 3 lists the principal plot types; see the help for each one for more details.

Univariate

`assocplot`	Association Plots
`barchart`	bar plots
`bwplot`	box and whisker plots
`densityplot`	kernel density plots
`dotplot`	dot plots
`histogram`	histograms
`qqmath`	quantile plots against mathematical distributions
`stripplot`	1-dimensional scatterplot

Bivariate

`qq`	q-q plot for comparing two distributions
`xyplot`	scatter plots

Trivariate

`levelplot`	level plots
`contourplot`	contour plots
`cloud`	3-D scatter plots
`wireframe`	3-D surfaces

Hypervariate

`splom`	scatterplot matrix
`parallel`	parallel coördinate plots

Miscellaneous

`rfs`	residual and fitted value plot
`tmd`	Tukey Mean-Difference plot

Table 3: Trellis graphics plot types

5.2.6 Adjusting Trellis graphics parameters

The Trellis graphics environment as implemented in the `lattice` package sets reasonable defaults for its graphics parameters, based on the output device (screen, PDF file …). Changing these requires three steps: (1) retrieve the parameters into a data structure in memory; (2) modify them; (3) write the modified parameters back as permanent options.

Parameters are retrieved with the `trellis.par.get` method and set with the `trellis.par.set` method. In the following example we change the 'superposition' symbol which is used in the `xyplot` method to show groups of points, as in the example just above.

The current settings are shown graphically by the `show.settings` method.

```
> show.settings()
> options <- trellis.par.get()
> names(options)
 [1] "grid.pars"        "fontsize"         "background"
 [4] "clip"             "add.line"         "add.text"
 [7] "plot.polygon"     "box.dot"          "box.rectangle"
[10] "box.umbrella"     "dot.line"         "dot.symbol"
[13] "plot.line"        "plot.symbol"      "reference.line"
[16] "strip.background" "strip.shingle"    "strip.border"
[19] "superpose.line"   "superpose.symbol" "superpose.polygon"
[22] "regions"          "shade.colors"     "axis.line"
[25] "axis.text"        "axis.components"  "layout.heights"
[28] "layout.widths"    "box.3d"           "par.xlab.text"
[31] "par.ylab.text"    "par.zlab.text"    "par.main.text"
[34] "par.sub.text"
> options$superpose.symbol
$alpha
[1] 1 1 1 1 1 1 1
$cex
[1] 0.8 0.8 0.8 0.8 0.8 0.8 0.8
$col
[1] "#0080ff"   "#ff00ff"   "darkgreen" "#ff0000"   "orange"
[6] "#00ff00"   "brown"
$font
[1] 1 1 1 1 1 1 1
$pch
[1] 1 1 1 1 1 1 1
$fill
[1] "transparent" "transparent" "transparent" "transparent"
[5] "transparent" "transparent" "transparent"
> options$superpose.symbol$pch
[1] 1 1 1 1 1 1 1
> options$superpose.symbol$pch <- 20
> options$superpose.symbol$col <- c("blue","green","red","magenta",
+ "cyan","black","grey")
> options$superpose.symbol$cex <- 1.4
> trellis.par.set("superpose.symbol", options$superpose.symbol)
> xyplot(Sepal.Width ~ Sepal.Length, group=Species, iris)
```

There are a large number of options, each with sub-options. For example, the superposition symbol has a character code (`pch`), a vector of colours (`col`), a vector of fonts (`font`), and a character expansion fraction (`cex`). These can all be set and then written back as shown. Subsequent graphs use the changed parameters.

Colour options are often specified with **colour ramps**; see §5.5 for details.

5.3 Multiple graphics windows

To open several graphics windows at the same time, use the `windows` method. R opens the first graphics window automatically in response to the first graphics method such as `plot` or `hist`; in the following example we assume no such commands have yet been given.

```
> dev.list()
NULL
> windows()
> dev.list()
windows
  2
> dev.cur()
windows
  2
```

At this point, there is only one window and it is, of course, the current graphics device, i.e. number 2 (for some reason, 1 is not used). The results of any plotting commands will be displayed in this window.

Now we open another window; it becomes the current window:

```
> windows()
> dev.list()
windows windows
  2   3
> dev.cur()
windows
  3
```

At this point, any plot commands will go to the most recently-opened window, i.e. number 3.

5.3.1 Switching between windows

The `dev.set` method specifies which graphics device to use for the next graphics output. For example, to compare scatterplots of tree volume vs. two possible predictors (height and girth) in adjacent windows:

```
> dev.set(2)
> plot(Height, Volume)
> dev.set(3)
> plot(Girth, Volume)
```

5.4 Multiple graphs in the same window

This depends on the graphics system: *base* or *trellis* (§5.2), as implemented in the `lattice` R package. You can determine which system is used by a given graphics command at the top of its help page. For example:

```
> ?boxplot
```

shows the page title as `boxplot (graphics)` indicating that it's in the base graphics package, whereas

```
> ?xyplot
```

shows the page title as `xyplot (lattice)` indicating that it's a trellis plot.

5.4.1 Base graphics

The *parameters* of the active graphics device are set with the `par` method. One of these parameters is the number of rows and columns of indivual plots in the device. By default this is (1, 1), i.e. one plot per device. You can set up a matrix of any size with the `par(mfrow= ...)` or `par(mfcol= ...)` commands. The difference is the order in which figures will be drawn, either row- or column-wise.

For example, to set up a two-by-two matrix of four histograms, and fill them from left-to-right, top-to-bottom:

```
> # the `par' method refers to the active device
> par(mfrow=c(2, 2))
> hist(rnorm(100)); hist(rbinom(100, 20, .5))
> hist(rpois(100, 1)); hist(runif(100))
> par(mfrow=c(1,1))
> # next plot will fill the window
```

5.4.2 Trellis graphics

A trellis (§5.2) graphics window can also be split, but in this case the `print` method of the `lattice` package must be used on an object of class `trellis` (which might be built in the same command), using the `split` = optional argument to specify the position (x and y) within a matrix of plots. For all but the last plot on a page the `more=T` argument must be specified.

Repeating the previous example:

```
> print(histogram(rnorm(100)), split=c(1,1,2,2), more=T);
> print(histogram(rbinom(100, 20, .5)), split=c(2,1,2,2), more=T);
> print(histogram(rpois(100, 1)), split=c(1,2,2,2), more=T);
> print(histogram(runif(100)), split=c(2,2,2,2), more=F)
```

A more elegant way to do this is to create plots with any `lattice` method, including `levelplot`, `xyplot`, and `histogram`, but instead of displaying them directly, *saving* them (using the assignment operator <-) as *trellis objects* (this is the object type created by `lattice` graphics methods), and then print them with `lattice`'s `print` method. The advantage is that the same plot can be printed in a group of several plots, alone, or on different devices, without having to be recomputed.

For example:

```
> h1 <- histogram(rnorm(100), col="lightblue");
> h2 <- histogram(rbinom(100, 20, .5), col="snow3");
> h3 <- histogram(rpois(100, 1), col="springgreen1");
> h4 <- histogram(runif(100), col="red4");
> print(h1, split=c(1,1,2,2), more=T);
> print(h2, split=c(2,1,2,2), more=T);
> print(h3, split=c(1,2,2,2), more=T);
> print(h4, split=c(2,2,2,2), more=F);
> rm(h1, h2, h3, h4)
```

If you are printing to a file, `more=F` will end the page. The next call to the `print` method will start a new page. This is useful to produce a multi-page PDF file.

5.5 Colours

Both base (§5.1) and Trellis (§5.2) graphics have many places where colours can be specified, often with the `col` (foreground colour) or `bg` (background colour) optional arguments to graphics methods such as `plot`.

Colours may be specified either by name, by code (colour specification), or by their numeric position in the active *colour palette*. There are a large number of named colours, but only eight of these in the default palette.

To get a list of possible colour names use the `colours` method; to see the numeric colours in the active palette use the `palette` method:

```
> colours()
  [1] "white"          "aliceblue"      "antiquewhite"
  [4] "antiquewhite1"  "antiquewhite2"  "antiquewhite3"
...
[655] "yellow3"        "yellow4"        "yellowgreen"
> colours()[655]
[1] "yellow3"
> palette()
[1] "black"   "red"     "green3"  "blue"    "cyan"    "magenta"
[7] "yellow"  "gray"
> palette()[4]
[1] "blue"
```

The named colours can be visualised as a bar graph (Figure 15):

```
> tmp <- seq(1:length(colors()))
> plot(tmp, rep(1, length(tmp)), type="h", lwd=2,
          col=colors()[tmp], ylim=c(0,1), xlab="Colour number")
```

Then an individual colour number can be identified interactively by left-clicking on the vertical colour bar at the midpoint; right-click anywhere in the graph when done:

```
> abline(h=0.5, lwd=3)  # to aim at
> selected <- identify(tmp, rep(0.5, length(tmp)))
> selected                   # colour number
> colors()[selected]   # colour name
```

The Red, Green, Blue of any colour can be examined with the `col2rgb` method:

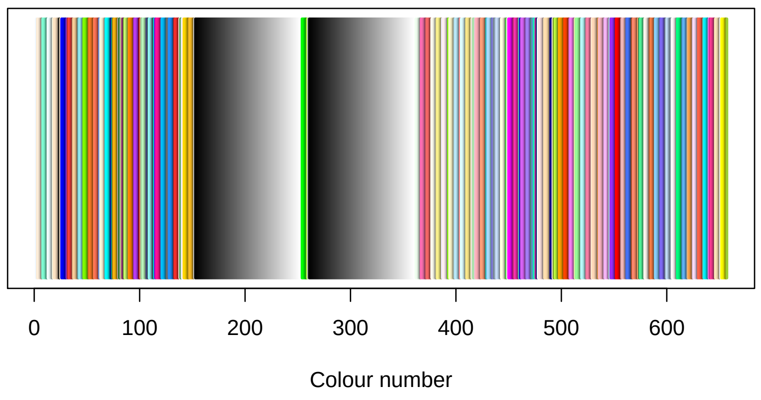


Figure 15: Available colours

```
> col2rgb("yellow3")
      [,1]
red    205
green  205
blue     0
```

Single colours can be created with the `rgb` method, specifying Red, Green and Blue contributions each in the range 0 . . . 1 (completely absent . . . saturated):

```
> rgb(0.25 0.5, 0)
[1] "#408000"
```

There are several built-in *colour ramps* (sequences of colours that give a pleasing visual impression); these are returned by the `heat.colors`, `terrain.colors`, `topo.colors`, and `cm.colors` methods; another palette is provided by the `bpy.colors` method of the `sp` package.[37] These all return a vector of colours from defined endpoints, according to the number of levels requested:

```
> terrain.colors(5)
[1] "#00A600" "#E6E600" "#EAB64E" "#EEB99F" "#F2F2F2"
> terrain.colors(10)
 [1] "#00A600" "#2DB600" "#63C600" "#A0D600" "#E6E600" "#E8C32E"
 [7] "#EBB25E" "#EDB48E" "#F0C9C0" "#F2F2F2"
> terrain.colors(10)[1]
 [1] "#00A600"
```

The hexidecimal codes here represent Red, Green, and Blue; from `00` (no colour) to `FF` (full colour); thus there are $256^3 = 16\ 777\ 216$ possible colours.

Grey scales use the slightly different `gray` method; its argument is a vector

[37] Note the American spelling of 'colour'.

of values between $0 \ldots 1$ giving the gray level:

```
> gray(seq(0, 1, by=.125))
[1] "#000000" "#202020" "#404040" "#606060" "#808080" "#9F9F9F"
[7] "#BFBFBF" "#DFDFDF" "#FFFFFF"
> gray(0:8 / 8)
[1] "#000000" "#202020" "#404040" "#606060" "#808080" "#9F9F9F"
[7]  "#BFBFBF" "#DFDFDF" "#FFFFFF"
> gray(c(0, .2, .3, 1))
[1] "#000000" "#333333" "#4D4D4D" "#FFFFFF"
> col2rgb(gray(0.4))
      [,1]
red    102
green  102
blue   102
```

Custom colour ramps can be produced with the `hsv` and `rainbow` methods; see their help for details.

All of these ramps can be indexed to get individual colours. They are most useful, however, when these colours are linked to data values. For example, to plot soil sample points in the `meuse` soil pollution data set, with the points coloured in order of their rank (from least to most polluted by cadmium):

```
> library(sp)
> data(meuse)
> attach(meuse)
> xyplot(y ~ x , data=meuse, asp="iso", pch=20,cex=2,
      col=topo.colors(length(cadmium))[rank(cadmium)])
```

This plot is shown in Figure 16. Note the use of the `asp` argument to `xyplot` to specify the *aspect* (ratio of axes), in this case proportional to the two scales ("isometric").

The key methods here are `topo.colors` to return a range of colours from dark blue through light pink, `length` to find the number of points and from this set the length of the colour ramp, and `rank` to return the rank of each sample, based on its cadmium content: the lowest pollution is rank 1, and so on to the most polluted with rank equal to the number of samples. Then the correct colour for each sample is extracted from the vector with the `[ ]` (subscript) operator.

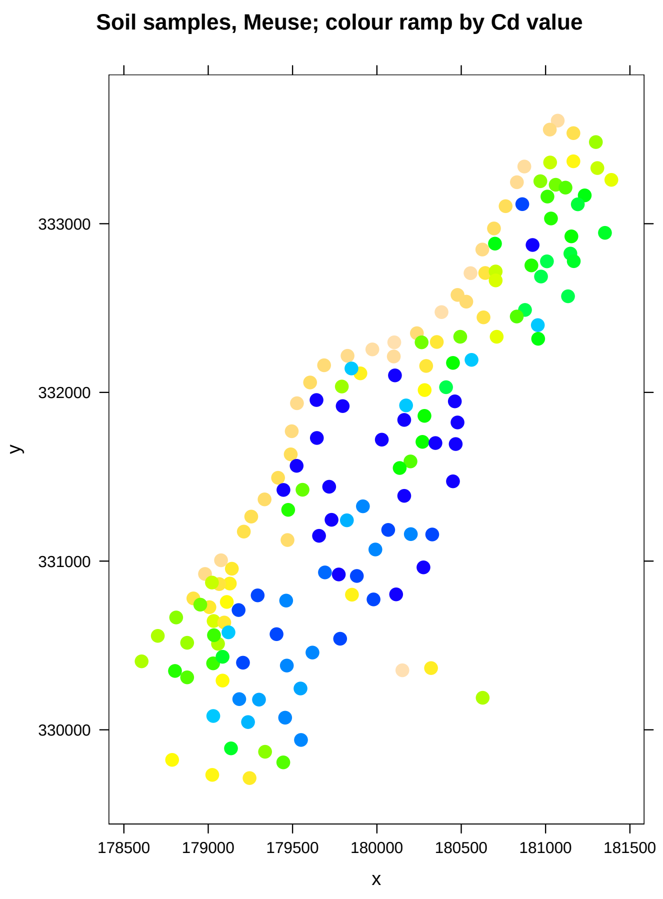


Figure 16: Example of a colour ramp

6 Preparing your own data for R

R comes with many interesting example datasets (§3.8), but of course you are most interested in your own data. There are many ways to prepare this for R; a comprehensive guide is given in the online **R Data Import/Export** manual[38], also provided as a PDF file [37].

6.1 Preparing data directly in R

A small dataset may be entered directly in R in several ways. Here we illustrate this with the winning times from the 100 m footrace in the modern Olympic games [55], which we will assemble into a data frame, with the cases being each year and the fields being the year number, the men's winning time, and the women's winning time.

One method is to assign a vector directly to a variable. In the case of regular data, this can be easily accomplished with the `seq` or `rep` functions. For irregular data, the `c` function must be used to create a list.

```
> yr <- seq(1900,2004,4)  # produces 1900, 1904, 1908, ... 2004
> men <- c(11, 11, 10.8, 10.8, NA, 10.8, 10.6, 10.8, 10.3,
+ 10.3, NA, NA,
+ 10.3, 10.4, 10.5, 10.2, 10, 9.95, 10.14, 10.06,
+ 10.25, 9.99, 9.92, 9.96, 9.84, 9.87, 9.85)
```

Note the + *continuation prompt* from R; as long as the list was not completed (not enough `)` to match the open `(`), R could determine that the expression was not complete, and prompted for more input.

Also note the use of the special `NA` value to indicate a *missing value*; no Olympic games were held in 1916, 1940 or 1944, so there is no time for those years.

Vectors can also be entered with the `scan` function. This waits for you to type at the console, until a blank line is entered. It shows the number of the next data item as a continuation prompt:

```
> women <- scan()
1: NA NA NA NA NA NA NA
8: 12.2 11.9 11.5 NA NA
13: 11.9 11.5 11.5 11 11.4 11.08 11.07 11.08 11.06 10.97
23: 10.54 10.82 10.94 10.75 10.93
28:
```

When the `28` was displayed, the user pressed the "Enter" key, and R realised the list was complete.

The three vectors are then gathered a data frame, and the local copies are discarded. By default the fields in the frame are named from the local

[38] In `RGui`, select menu command `Help | Manuals | R Data Import/Export`

variables, but new names can be given with the `fieldname = variable` syntax. For example:

```
> oly.100 <- data.frame(year=yr, men, women)
> str(oly.100)
`data.frame': 27 obs. of  3 variables:
 $ year  : num  1900 1904 1908 1912 1916 ...
 $ men   : num  11 11 10.8 10.8 NA 10.8 10.6 10.8 10.3 10.3 ...
 $ women: num  NA NA NA NA NA NA NA 12.2 11.9 11.5 ...
> rm(yr, men, women)
```

To enter a **matrix**, first enter the data with the `scan` function or as a list with the `c` function, and then place it in matrix form with the `matrix` ("create a matrix") function. We illustrate this with the sample confusion matrix of Congalton *et al.* [6], also used as an example by Skidmore [53] and Rossiter [43].[39] This example also illustrates the `rownames` and `colnames` functions to assign (or read) the row and column names of a matrix.

```
> cm <- scan()
1 : 35 14 11 1 4 11 3 0 12 9 38 4 2 5 12 2
17:
> cm <- matrix(cm, 4, 4, byrow=T)
> cm
     [,1] [,2] [,3] [,4]
[1,]   35   14   11    1
[2,]    4   11    3    0
[3,]   12    9   38    4
[4,]    2    5   12    2
> colnames(cm) <- c ("A", "B", "C", "D")
> rownames(cm) <- LETTERS[1:4]
> cm
   A  B  C D
A 35 14 11 1
B  4 11  3 0
C 12  9 38 4
D  2  5 12 2
> cm[1, ]
 A  B  C  D
35 14 11  1
> cm["A", "C"]
[1] 11
```

Note the use of the `byrow` optional argument to the `matrix` function, to indicate that we entered the data by row, also the use of the `rownames` and `colnames` functions to label the matrix with upper-case letters supplied conveniently by the `LETTERS` built-in constant.

6.2 A GUI data editor

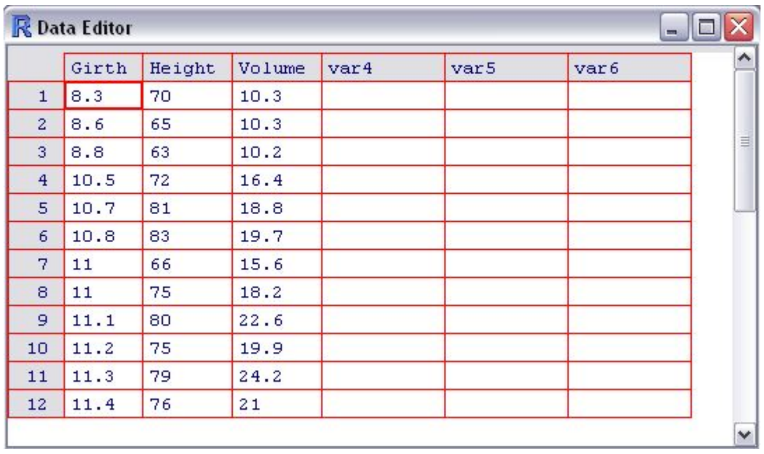
The `fix` function provides a simple graphical data editor for data frames. It can be used to correct data entry mistakes or to build new data frames.

[39] This matrix is also used as an example in §4.6

For example, to edit the sample `trees` dataset:

```
> data(trees)
> fix(trees)
```

This opens the data editor window (Figure 17). **Warning!**: any changes made to the frame will be stored in the object. You can change data values, add rows, add columns (new variables), change column names, and (if you give the optional `edit.row.names=T` argument) change row names.



	Girth	Height	Volume	var4	var5	var6
1	8.3	70	10.3			
2	8.6	65	10.3			
3	8.8	63	10.2			
4	10.5	72	16.4			
5	10.7	81	18.8			
6	10.8	83	19.7			
7	11	66	15.6			
8	11	75	18.2			
9	11.1	80	22.6			
10	11.2	75	19.9			
11	11.3	79	24.2			
12	11.4	76	21			

Figure 17: R graphical data editor

To edit a new data frame, you must first create it as a null data frame using the `as.data.frame` function, and then call the `fix` function:

```
> myNewFrame <- as.data.frame(NULL)
> fix(myNewFrame)
```

6.3 Importing data from Microsoft Excel

The `XLConnect` package uses an interface to Java to allow R to directly read (and write) Microsoft Excel worksheets. It includes a `loadWorkbook` function to load or create a workbook, a `readWorksheet` function to read all or part of one sheet of a workbook as a data frame, and a comparalbe `writeWorksheet` function.

Prior to this package, exchange with Excel was via CSV files, as explained in the next section.

6.4 Importing data from a CSV file

The *Comma-Separated Values* or "CSV" file is a common interchange format which can be prepared in many ways. For example, a CSV file can be created directly as a text file, using Notepad or some other plain-text editor. However, it is common to have data already in a spreadsheet such as

Excel. In this case the procedure is as follows:

1. Prepare the data as an Excel spreadsheet with named columns;
2. Export from Excel to a (CSV) file, using Excel's `File | Save As ...` menu item;
3. Import into R with the `read.csv` function;
4. Adjust data types in R if necessary.

We illustrate this with a simplified version of the `meuse` dataset from the `gstat` and `sp` packages, which has been prepared to illustrate some issues with import.

Here is a small CSV file written by Excel and viewed in a plain text editor such as Notepad:

```
x,y,cadmium,elev,dist,om,ffreq,soil,lime,landuse
181072,333611,11.7,7.909,0.00135803,13.6,1,1,1,Ah
181025,333558,8.6,6.983,0.0122243,14,1,1,1,Ah
181165,333537,6.5,7.8,0.103029,13,1,1,1,Ah
181298,333484,2.6,7.655,0.190094,8,1,2,0,Ga
181307,333330,2.8,7.48,0.27709,8.7,1,2,0,Ah
181390,333260,3,7.791,0.364067,7.8,1,2,0,Ga
```

Note that:

- There is one line per observation (*record*);
- Each record consists of the same number of *fields*, which are separated by commas;
- The first line has the same number of fields as the others but consists of the field *names*.

Suppose this file is named `example.csv`. To read into R, we first change to the directory where the file is stored and then read into an R object with the `read.csv` function[40].

```
> ds <- read.csv("example.csv")
> str(ds)
`data.frame': 6 obs. of  10 variables:
 $ x      : int  181072 181025 181165 181298 ...
 $ y      : int  333611 333558 333537 333484 ...
 $ cadmium: num  11.7 8.6 6.5 2.6 2.8 3
 $ elev   : num  7.91 6.98 7.80 7.66 7.48 ...
 $ dist   : num  0.00136 0.01222 0.10303 0.19009 ...
 $ om     : num  13.6 14 13 8 8.7 7.8
 $ ffreq  : int  1 1 1 1 1 1
 $ soil   : int  1 1 1 2 2 2
```

[40] `read.csv` is a specialised *wrapper* to the very general `read.table` function which can deal with tables in many other formats

```
 $ lime   : int  1 1 1 0 0 0
 $ landuse: Factor w/ 2 levels "Ah","Ga": 1 1 1 2 1 2
```

R could determine that `landuse` is a *factor* (categorical variable), because it was non-numeric. It could also determine the variable names from the first row. The other factors were not recognized, and in fact they have different R data types, which we now assign, using the `as.*` functions to change data types:

```
> ds$soil <- as.factor(ds$soil)
> ds$ffreq <- as.ordered(ds$ffreq)
> ds$lime <- as.logical(ds$lime)
> str(ds)
`data.frame': 6 obs. of  10 variables:
 $ x      : int  181072 181025 181165 181298 ...
 $ y      : int  333611 333558 333537 333484 ...
 $ cadmium: num  11.7 8.6 6.5 2.6 2.8 3
 $ elev   : num  7.91 6.98 7.80 7.66 7.48 ...
 $ dist   : num  0.00136 0.01222 0.10303 0.19009 ...
 $ om     : num  13.6 14 13 8 8.7 7.8
 $ ffreq  : Ord.factor w/ 3 levels "1"<"2"<"3": 1 ...
 $ soil   : Factor w/ 3 levels "1","2","3": 1 1 1 ...
 $ lime   : logi   TRUE  TRUE  TRUE FALSE FALSE FALSE
 $ landuse: Factor w/ 2 levels "Ah","Ga": 1 1 1 2 1 2
```

Using the correct data type is important for many modelling methods; here we inform R that `lime` was either applied (logical `TRUE`, associated by R with the number 1) or not (logical `FALSE`, associated by R with the number 0); that there are three soil types arbitrarily named “1”, “2” and “3”[41] (not in any order); and that there are three flood frequency classes named “1”, “2” and “3”, and these are in this order, from most to least flooded (n.b. we know this from the data documentation, not from anything we can see in the CSV file).

Missing values Missing values are expressed in CSV files by the two letters `NA` (without quotes). For example:

```
x,y,cadmium,elev,dist,om,ffreq,soil,lime,landuse
181072,333611,NA,7.909,0.00135803,NA,1,1,1,Ah
181025,333558,8.6,6.983,0.0122243,14,1,1,1,Ah
```

In the first record neither the cadmium concentration nor organic matter proportion are known; these will be imported as missing values, symbolized in R by `NA`.

Matrices A matrix can also be prepared as a CSV file (perhaps exported from Excel) and imported into R with the `read.csv` function. The matrix can also be prepared with row and column labels,

For example here is the CSV file for a small confusion matrix, as prepared

[41] These are *not* the *numbers* 1, 2, and 3.

in a text editor; the first row has the column names (reference classes) and each of the other rows begins with the row name (mapped class); there is no entry for the very first column of the first row:

```
 ,"A","B","C","D"
"A",35,14,11,1
"B",4,11,3,0
"C",12,9,38,4
"D",2,5,12,2
```

Suppose this file is named `cm.csv`; it can be read in as follows; note that we inform R that the row names are in the first column, and convert the default class (data frame) to a matrix with the `as.matrix` function. The `attributes` function shows the correct data type and attributes, here the dimension names for the rows and columns.

```
> cm <- as.matrix(read.csv("cm.csv", row.names=1))
> cm
   A  B  C D
A 35 14 11 1
B  4 11  3 0
C 12  9 38 4
D  2  5 12 2
> class(cm)
[1] "matrix"
> attributes(cm)
$dim
[1] 4 4

$dimnames
$dimnames[[1]]
[1] "A" "B" "C" "D"

$dimnames[[2]]
[1] "A" "B" "C" "D"
```

6.5 Importing images

Some data, such as satellite imagery, is naturally organized as a *matrix* of data values on a regular grid. Many export formats write a *header* of several lines, giving information on the file contents, followed by the data values as one long *vector* or else with each row of the imagery as a row in the text file. An example is the ESRI `asciigrid` format.

Here is a small example of a 12 by 12 image, stored as ASCII text file `image.grd`. We display it within R with the `file.show` function:

```
> file.show("image.grd")
NCOLS 12
NROWS 12
XLLCORNER 180000
YLLCORNER 331000
CELLSIZE 40
NODATA_VALUE -9999
```

```
141 148 159 166 176 186 192 195 201 206 211 215
143 153 160 170 177 188 198 204 206 212 218 222
147 154 164 172 182 189 199 209 215 218 224 230
151 159 166 176 183 193 201 211 221 227 230 235
153 163 170 177 188 195 205 212 222 232 238 241
153 164 175 182 189 199 206 217 224 234 244 250
153 164 176 186 193 201 211 218 228 235 245 256
157 164 176 188 198 205 212 222 230 240 247 256
159 169 176 188 199 209 217 224 234 241 245 245
159 170 180 188 199 211 221 228 232 234 234 234
163 170 182 192 199 211 221 222 222 222 222 223
166 175 182 193 204 209 211 211 211 211 211 214
```

This format is documented by ESRI; there are six header lines with self-explanatory names, followed by one row per image row.

This specific format can be read directly into a spatial object with the `read.asciigrid` function of the `sp` package; however here we show how to read it using basic R commands.

The `scan` function, which we used above (§6.1) to read from the keyboard, can also be used to read from text files, if the first argument is the optional `file`. Lines can be skipped with the optional `skip` argument; and the number of lines to read can be specified with the optional `nlines` argument. The value to take as the missing values (`NA` in R) is specified with the optional `na.strings` argument. The separator between values is by default white space; that can be changed with the optional `sep` argument. Finally, `scan` expects to read double-precision numbers; this can be changed with the optional `what` argument.

In this example, we first read in the dimensions of the image. The header lines have both character strings (e.g. `NCOLS`) and numbers (e.g. `12`); we read them into a character vector and then extract the number with the `as.numeric` function. Note that we read the second line by specifying `skip=1` and then `nlines=1`:

```
> ncol <- scan(file="image.grd", nlines=1, what="character")
> ncol
[1] "NCOLS" "12"
> ncol <- as.numeric(ncol[2])
> ncol
[1] 12
> (nrow <- as.numeric(scan(file="image.grd", skip=1, nlines=1, what="character")[2]))
[1] 12
```

Now we read the image data into a matrix, as one vector:

```
> img <- scan(file="image.grd", skip=6, na.strings="-9999")
Read 144 items
> summary(img)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
    141     176     202     200     222     256 
> class(img)
[1] "numeric"
```

Although this small image has no missing values, in general we may expect them, so we need to specify the format of the missing values.

Finally, we specify the dimensions and format of the image, thereby promoting it to a matrix, with the `matrix` function. By default R interprets a matrix in *column-major* order (each column is a vector); but the image is stored by convention in *row-major* order; therefore we specify the optional `byrow=T` argument.

```
> img <- matrix(img, nrow, ncol, byrow=T)
> class(img)
[1] "matrix"
> str(img)
 num [1:12, 1:12] 141 143 147 151 153 153 153 157 159 159 ...
```

7 Exporting from R

Data frames are easily exported from R. For all the possibilities, see the R Data Import/Export manual. Here we explain the most common operation: exporting a data frame to a CSV file. This format can be read into Excel, ILWIS, and many other programs.

Prior to this package, exchange with Excel was via CSV files, as explained in the next section.

7.1 Importing data from a CSV file

The *Comma-Separated Values* or "CSV" file is a common interchange format which can be prepared in many ways. For example, a CSV file can be created directly as a text file, using Notepad or some other plain-text editor. However, it is common to have data already in a spreadsheet such as Excel. In this case the procedure is as follows:

1. Prepare the data as an Excel spreadsheet with named columns;
2. Export from Excel to a (CSV) file, using Excel's `File | Save As ...` menu item;
3. Import into R with the `read.csv` function;
4. Adjust data types in R if necessary.

We illustrate this with a simplified version of the `meuse` dataset from the `gstat` and `sp` packages, which has been prepared to illustrate some issues with import.

Here is a small CSV file written by Excel and viewed in a plain text editor such as Notepad:

```
x,y,cadmium,elev,dist,om,ffreq,soil,lime,landuse
181072,333611,11.7,7.909,0.00135803,13.6,1,1,1,Ah
181025,333558,8.6,6.983,0.0122243,14,1,1,1,Ah
181165,333537,6.5,7.8,0.103029,13,1,1,1,Ah
181298,333484,2.6,7.655,0.190094,8,1,2,0,Ga
181307,333330,2.8,7.48,0.27709,8.7,1,2,0,Ah
181390,333260,3,7.791,0.364067,7.8,1,2,0,Ga
```

Note that:

- There is one line per observation (*record*);
- Each record consists of the same number of *fields*, which are separated by commas;
- The first line has the same number of fields as the others but consists

of the field *names*.

Suppose this file is named `example.csv`. To read into R, we first change to the directory where the file is stored and then read into an R object with the `read.csv` function[42].

```
> ds <- read.csv("example.csv")
> str(ds)
`data.frame': 6 obs. of  10 variables:
 $ x      : int  181072 181025 181165 181298 ...
 $ y      : int  333611 333558 333537 333484 ...
 $ cadmium: num  11.7 8.6 6.5 2.6 2.8 3
 $ elev   : num  7.91 6.98 7.80 7.66 7.48 ...
 $ dist   : num  0.00136 0.01222 0.10303 0.19009 ...
 $ om     : num  13.6 14 13 8 8.7 7.8
 $ ffreq  : int  1 1 1 1 1 1
 $ soil   : int  1 1 1 2 2 2
 $ lime   : int  1 1 1 0 0 0
 $ landuse: Factor w/ 2 levels "Ah","Ga": 1 1 1 2 1 2
```

R could determine that `landuse` is a *factor* (categorical variable), because it was non-numeric. It could also determine the variable names from the first row. The other factors were not recognized, and in fact they have different R data types, which we now assign, using the `as.*` functions to change data types:

```
> ds$soil <- as.factor(ds$soil)
> ds$ffreq <- as.ordered(ds$ffreq)
> ds$lime <- as.logical(ds$lime)
> str(ds)
`data.frame': 6 obs. of  10 variables:
 $ x      : int  181072 181025 181165 181298 ...
 $ y      : int  333611 333558 333537 333484 ...
 $ cadmium: num  11.7 8.6 6.5 2.6 2.8 3
 $ elev   : num  7.91 6.98 7.80 7.66 7.48 ...
 $ dist   : num  0.00136 0.01222 0.10303 0.19009 ...
 $ om     : num  13.6 14 13 8 8.7 7.8
 $ ffreq  : Ord.factor w/ 3 levels "1"<"2"<"3": 1 ...
 $ soil   : Factor w/ 3 levels "1","2","3": 1 1 1 ...
 $ lime   : logi   TRUE  TRUE  TRUE FALSE FALSE FALSE
 $ landuse: Factor w/ 2 levels "Ah","Ga": 1 1 1 2 1 2
```

Using the correct data type is important for many modelling methods; here we inform R that `lime` was either applied (logical `TRUE`, associated by R with the number `1`) or not (logical `FALSE`, associated by R with the number `0`); that there are three soil types arbitrarily named “1”, “2” and “3”[43] (not in any order); and that there are three flood frequency classes named “1”, “2” and “3”, and these are in this order, from most to least flooded (n.b. we know this from the data documentation, not from anything we can see in the CSV file).

[42] `read.csv` is a specialised *wrapper* to the very general `read.table` function which can deal with tables in many other formats

[43] These are *not* the *numbers* 1, 2, and 3.

Missing values Missing values are expressed in CSV files by the two letters NA (without quotes). For example:

```
x,y,cadmium,elev,dist,om,ffreq,soil,lime,landuse
181072,333611,NA,7.909,0.00135803,NA,1,1,1,Ah
181025,333558,8.6,6.983,0.0122243,14,1,1,1,Ah
```

In the first record neither the cadmium concentration nor organic matter proportion are known; these will be imported as missing values, symbolized in R by NA.

Matrices A matrix can also be prepared as a CSV file (perhaps exported from Excel) and imported into R with the `read.csv` function. The matrix can also be prepared with row and column labels,

For example here is the CSV file for a small confusion matrix, as prepared in a text editor; the first row has the column names (reference classes) and each of the other rows begins with the row name (mapped class); there is no entry for the very first column of the first row:

```
 ,"A","B","C","D"
"A",35,14,11,1
"B",4,11,3,0
"C",12,9,38,4
"D",2,5,12,2
```

Suppose this file is named `cm.csv`; it can be read in as follows; note that we inform R that the row names are in the first column, and convert the default class (data frame) to a matrix with the `as.matrix` function. The `attributes` function shows the correct data type and attributes, here the dimension names for the rows and columns.

```
> cm <- as.matrix(read.csv("cm.csv", row.names=1))
> cm
   A  B  C D
A 35 14 11 1
B  4 11  3 0
C 12  9 38 4
D  2  5 12 2
> class(cm)
[1] "matrix"
> attributes(cm)
$dim
[1] 4 4

$dimnames
$dimnames[[1]]
[1] "A" "B" "C" "D"

$dimnames[[2]]
[1] "A" "B" "C" "D"
```

7.2 Importing images

Some data, such as satellite imagery, is naturally organized as a *matrix* of data values on a regular grid. Many export formats write a *header* of several lines, giving information on the file contents, followed by the data values as one long *vector* or else with each row of the imagery as a row in the text file. An example is the ESRI `asciigrid` format.

Here is a small example of a 12 by 12 image, stored as ASCII text file `image.grd`. We display it within R with the `file.show` function:

```
> file.show("image.grd")
NCOLS 12
NROWS 12
XLLCORNER 180000
YLLCORNER 331000
CELLSIZE 40
NODATA_VALUE -9999
141 148 159 166 176 186 192 195 201 206 211 215
143 153 160 170 177 188 198 204 206 212 218 222
147 154 164 172 182 189 199 209 215 218 224 230
151 159 166 176 183 193 201 211 221 227 230 235
153 163 170 177 188 195 205 212 222 232 238 241
153 164 175 182 189 199 206 217 224 234 244 250
153 164 176 186 193 201 211 218 228 235 245 256
157 164 176 188 198 205 212 222 230 240 247 256
159 169 176 188 199 209 217 224 234 241 245 245
159 170 180 188 199 211 221 228 232 234 234 234
163 170 182 192 199 211 221 222 222 222 222 223
166 175 182 193 204 209 211 211 211 211 211 214
```

This format is documented by ESRI; there are six header lines with self-explanatory names, followed by one row per image row.

This specific format can be read directly into a spatial object with the `read.asciigrid` function of the `sp` package; however here we show how to read it using basic R commands.

The `scan` function, which we used above (§6.1) to read from the keyboard, can also be used to read from text files, if the first argument is the optional `file`. Lines can be skipped with the optional `skip` argument; and the number of lines to read can be specified with the optional `nlines` argument. The value to take as the missing values (`NA` in R) is specified with the optional `na.strings` argument. The separator between values is by default white space; that can be changed with the optional `sep` argument. Finally, `scan` expects to read double-precision numbers; this can be changed with the optional `what` argument.

In this example, we first read in the dimensions of the image. The header lines have both character strings (e.g. `NCOLS`) and numbers (e.g. `12`); we read them into a character vector and then extract the number with the `as.numeric` function. Note that we read the second line by specifying `skip=1` and then `nlines=1`:

```
> ncol <- scan(file="image.grd", nlines=1, what="character")
> ncol
[1] "NCOLS" "12"
> ncol <- as.numeric(ncol[2])
> ncol
[1] 12
> (nrow <- as.numeric(scan(file="image.grd", skip=1, nlines=1, what="character")[2]))
[1] 12
```

Now we read the image data into a matrix, as one vector:

```
> img <- scan(file="image.grd", skip=6, na.strings="-9999")
Read 144 items
> summary(img)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    141     176     202     200     222     256
> class(img)
[1] "numeric"
```

Although this small image has no missing values, in general we may expect them, so we need to specify the format of the missing values.

Finally, we specify the dimensions and format of the image, thereby promoting it to a matrix, with the `matrix` function. By default R interprets a matrix in *column-major* order (each column is a vector); but the image is stored by convention in *row-major* order; therefore we specify the optional `byrow=T` argument.

```
> img <- matrix(img, nrow, ncol, byrow=T)
> class(img)
[1] "matrix"
> str(img)
 num [1:12, 1:12] 141 143 147 151 153 153 153 157 159 159 ...
```

8 Exporting from R

Data frames are easily exported from R. For all the possibilities, see the R Data Import/Export manual. Here we explain the most common operation: exporting a data frame to a CSV file. This format can be read into Excel, ILWIS, and many other programs.

The XLConnect package uses an interface to Java to allow R to directly read (and write) Microsoft Excel worksheets. It includes a loadWorkbook function to create a workbook, and a writeWorksheet function to write all or part of one sheet of a data frame to a worksheet.

A common reason for exporting is that you have computed some result in R which you want to use in another program. For example, suppose you've computed a kriging interpolation with the krige function of the gstat package:

```
>  # load sp library to support spatial classes
>  # load gstat for variograms and kriging
> library(sp); library(gstat)
>  # load sample data and interpolation grid
> data(meuse); data(meuse.grid)
>  # convert these to spatial objects
> coordinates(meuse) <- ~ x + y; coordinates(meuse.grid) <- ~ x + y
>  # krige using a known variogram model
> kxy <- krige(log(lead)~x+y, locations=meuse,
+       newdata=meuse.grid, maxdist=800,
+       model=vgm(0.34, "Sph", 1140, 0.08))
[using universal kriging]
> str(as.data.frame(kxy))
`data.frame':   3103 obs. of  4 variables:
 $ x        : num  181180 181140 181180 181220 181100 ...
 $ y        : num  333740 333700 333700 333700 333660 ...
 $ var1.pred: num  5.72 5.68 5.61 5.54 5.67 ...
 $ var1.var : num  0.293 0.225 0.239 0.257 0.173 ...
```

Note the use of the coordinates function to promote the meuse and meuse.grid data frames to objects of class SpatialPointsDataFrame as required by the krige function, and the as.data.frame function to extract the data frame from the kriged object as required by the write.table function.

To export this data frame we use the write.table function, specifying that a comma separate the fields by using the optional sep="," argument:

```
> write.table(round(as.data.frame(kxy), 4), file="KrigeResult.csv",
+    sep=",", quote=T, row.names=F,
+    col.names=c("E", "N", "LPb", "LPb.var"))
```

In this example the precision of the output was limited with the round function, and named the fields with the col.names= optional argument to write.table. We also specified that no row names be written, with the optionaol row.names=F argument, and that any strings be quoted with the optional `quote=T` argument.

Here are the first few lines of the file `KrigeResult.csv` viewed in a plain-text editor such as Notepad:

```
"E","N","LPb","LPb.var"
181180,333740,5.7214,0.2932
181140,333700, 5.6772,0.2254
181180,333700, 5.6064,0.2391
```

9 Reproducible data analysis

Since R is a programming language, it can be used to write scripts (§3.5) which can then be run at any time to **reproduce** the analysis. This is especially useful if the data changes, or to apply the same analysis to a different dataset. It also allows the exact same figure to be produced.

A step further is to integrate the R analysis into a text document. Rather than cutting and pasting, a better approach is to prepare the text document with LaTeX [23, 22][44] and incorporate executable R code into the document. This ingenious approach is known generically as "Weaving" or "literate programming" [21], and has been implemented for R as "Sweave" [24, 25] and more recently as "knitr" [61] implemented as the `knitr` package[45].

This approach has three steps: (1) preparing the source NoWeb document; (2) compiling this with Sweave into a LaTeX source file; (3) compiling the LaTeX source into a PDF document. Following is a brief introduction; for an extended discussion see Rossiter [47].

9.1 The NoWeb document

This is plain-text file with extension `.Rnw` ("R NoWeb"). It contains two kinds of commands:

1. LaTeXcommands, as in a standard LaTeX document;
2. R commands, to be executed.

The R commands are placed in **code chunks**, delimited with the special symbols < < > > = to begin a chunk, and `@` to end one.

Here is a minimal example, suppose this is in a text file named `example.Rnw`:

```
\documentclass{article}
\usepackage[pdftex,final]{graphicx}
\usepackage{Sweave}
\begin{document}
\title{Sweaving for reproducible data analysis}
\author{A Nonymous}
\date{14-November-2010}
\maketitle
Here is a simple example of R and Sweave:
<<>>=
data(trees)
str(trees)
summary(lm(Volume ~ Height*Girth, data=trees))$adj.r.squared
@
\end{document}
```

[44] http://www.latex-project.org/
[45] http://yihui.name/knitr/

The LaTeX commands begin with \, e.g., `\documentclass`. The R code is written as if at the R console, but between the <<>>= (beginning a code chunk) and the @ (ending it), e.g., `data(trees)`. Everything else is text, e.g., `Here is a simple example`.

This is processed in R with the `Sweave` function, which takes as its argument the name of the NoWeb file:

```
> Sweave("example.Rnw")
```

The result is a LaTeX input file, with the standard file extension `.tex` and the same first part of the name, where the NoWeb chunks have been evaluated. and formatted as both input and output. In this example the file is named `example.tex`.

9.2 The LaTeX document

This is now just a standard LaTeX input file. R code has been formatted in a special `Schunk` LaTeX enviroment, provided by the LaTeX `Sweave` package, as specificed in the `\usepackage{Sweave}` declaration in the preamble. In this example we have the following file:

```
\documentclass{article}
\usepackage[pdftex,final]{graphicx}
\usepackage{Sweave}
\begin{document}
\title{Sweaving for reproducible data analysis}
\author{A Nonymous}
\date{14-November-2010}
\maketitle
Here is a simple example of R and Sweave:
\begin{Schunk}
\begin{Sinput}
R> data(trees)
R> str(trees)
\end{Sinput}
\begin{Soutput}
'data.frame': 31 obs. of  3 variables:
 $ Girth : num  8.3 8.6 8.8 10.5 10.7 10.8 11 11 11.1 11.2 ...
 $ Height: num  70 65 63 72 81 83 66 75 80 75 ...
 $ Volume: num  10.3 10.3 10.2 16.4 18.8 19.7 15.6 18.2 22.6 19.9 ...
\end{Soutput}
\begin{Sinput}
R> summary(lm(Volume ~ Height * Girth, data = trees))$adj.r.squared
\end{Sinput}
\begin{Soutput}
[1] 0.97285
\end{Soutput}
\end{Schunk}
\end{document}
```

Note how the input code has been parsed and placed in the special `Sinput` LaTeX environment, e.g.:

```
\begin{Sinput}
> summary(lm(Volume ~ Height * Girth, data = trees))$adj.r.squared
\end{Sinput}
```

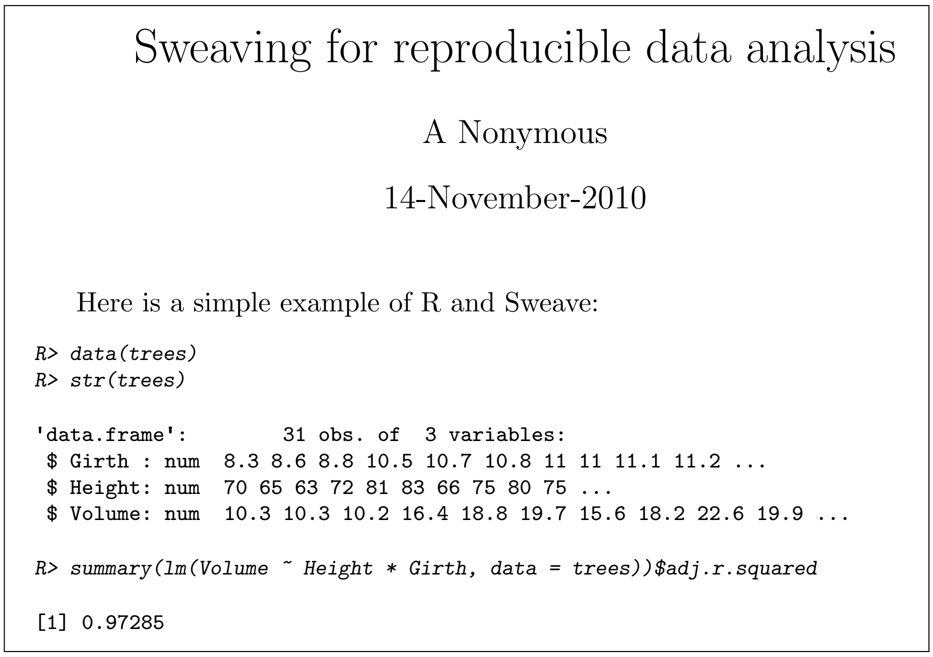
The code was executed by R, and the code that would produce output on the console was added to the document, again in a special LaTeX environment, `Soutput`.

```
\begin{Soutput}
[1] 0.97285
\end{Soutput}
```

There is no cut-and-paste here! The code was executed by R and produced the output. "What you asked for, you got." The LaTeX environments are defined in the `Sweave` LaTeX package; this was specified in the preamble.

9.3 The PDF document

The LaTeX document produced by Sweave is then processed as any LaTeX document, usually to to produce a PDF. Figure 18 shows the output from this example.



Sweaving for reproducible data analysis

A Nonymous

14-November-2010

Here is a simple example of R and Sweave:

```
R> data(trees)
R> str(trees)

'data.frame':        31 obs. of  3 variables:
 $ Girth : num  8.3 8.6 8.8 10.5 10.7 10.8 11 11 11.1 11.2 ...
 $ Height: num  70 65 63 72 81 83 66 75 80 75 ...
 $ Volume: num  10.3 10.3 10.2 16.4 18.8 19.7 15.6 18.2 22.6 19.9 ...

R> summary(lm(Volume ~ Height * Girth, data = trees))$adj.r.squared

[1] 0.97285
```

Figure 18: Example PDF produced by Sweave and LaTeX

Notice how the R input is formatted differently from the R output.

9.4 Graphics in Sweave

Since R produces graphs, Sweave can also produce them and incorporate them into documents. See Rossiter [47], Leisch [24, 25] and the Sweave web site[46] for many examples.

[46] `http://www.stat.uni-muenchen.de/~leisch/Sweave/`

10 Learning R

The present document explains the basics of using R (§3), the S language (§4), R graphics (§5), and the on-line help system (§3.3.2). There are many other resources for learning and applying R; this section explains the most useful.

10.1 Task views

Many applications are covered in on-line **Task Views**[47] . These are a summary by a task maintainer of the facilities in R to accomplish certain tasks. For example, Roger Bivand maintains a task view "Analysis of Spatial Data"[48] which discusses how to represent spatial data in R, how to read and write it, how to analyze point patterns, and geostatistical analysis. Another useful task view is "Multivariate Statistics"[49] maintained by Paul Hewson.

The **contributed documentation** at CRAN[50] has many introductions and reference cards for specific kinds of analysis, for example regression analysis[51] and time-series analysis[52].

10.2 R tutorials and introductions

From the R console, you can follow the introductory course "An Introduction to R" as follows.

1. **Select menu command** `Help | Html help`; a web page will appear in your web browser.

2. In this web page, **select the link** "An Introduction to R"; another web page will appear.

You will probably want to start with the section "Appendix A: A sample session" (scroll down the web page to find this in the table of contents). This will give you some familiarity with the style of R sessions and more importantly some instant feedback on what actually happens. Don't worry if you don't understand everything; this is just to give you a feel for how R works and what it can do. For individual commands, it is always best to look at its help topic.

Translations

The introductory tutorial or similar has been translated to many languages, including Chinese, Croatian, Farsi, French, German, Hungarian, Italian,

[47] http://cran.r-project.org/web/views/index.html
[48] http://cran.r-project.org/web/views/Spatial.html
[49] http://cran.r-project.org/web/views/Multivariate.html
[50] http://cran.r-project.org/other-docs.html
[51] http://cran.r-project.org/doc/contrib/Ricci-refcard-regression.pdf
[52] http://cran.r-project.org/doc/contrib/Ricci-refcard-ts.pdf

Japanese, Spanish, Polish, Portuguese and Vietnamese; these can be accessed by following the “CRAN” link on the R Project home page[53], and then “Contributed documentation” and “other languages”.

A good introduction to R concepts is the 100-page “R for Beginners” by Emmanuel Paradis of the University of Montpellier (F) [30]. This is also availble in his native French [32] and in a Spanish translation [31]; Correa & González [9]. is a Spanish-language introduction to R graphics. Dalgaard [11] is a clearly-written introductory statistics textbook, using R in all examples. Another useful introduction is “simpleR” by John Verzani of the City University of New York [58], also available as a set of web pages (§10.5). This shows how to use R for the usual univariate and bivariate statistics and tests, linear regression, and ANOVA. It has since been updated as a commercial textbook [59].

中文

中国语言文件可以在网站《R 文档》[54] 找到。 也有一个《R语言中文论坛》[55]

10.3 Textbooks using R

e-books in the ITC library

Crawley [10] is a good introduction to many kinds of analysis using R, with emphasis on statistical modelling.

Other books in the ITC library

The introductory text of Dalgaard [11] was mentioned above. Venables & Ripley [57] present a wide variety of up-to-date statistical methods (including spatial statistics) with algorithms coded in S, for both R and S-PLUS. There are a variety of other texts using S or S-PLUS, which are mostly applicable to R. Fox [19] explains how to use R for regression analysis, including advanced techniques; this is a companion to his text [18]. A more mathematically-sophisticated approach, but with a heavy emphasis on R techniques, is the free text by Faraway [15], which was expanded into two commercial texts [16, 17].

UseR! series

Springer publishes the **UseR!** series[56] with 39 titles[57], which includes practical texts, with many examples of R code; among the topics are time series [26], data prepration [54], spatial data analysis [2], Bayesian data anlysis [1], Lattice graphics [51], dynamic visualization [7], wavelet analysis [29], and non-linear regression [41].

It is increasingly common for sophisticated statistics texts to use R to illustrate their concepts; an example is the geostatistics text of Diggle & Ribeiro Jr. [13], which uses the authors’ `geoR` package [39]. So theory and practice go hand-in-hand.

[53] http://www.r-project.org/
[54] http://www.biosino.org/R/R-doc/
[55] http://rbbs.biosino.org/Rbbs/forums/list.page
[56] http://www.springer.com/series/6991?detailsPage=titles
[57] as of 13-August-2012

The text of Shumway & Stoffer [52] on time-series analysis uses R code for illustration; they also provide an on-line tutorial at the book's supporting website[58].

10.4 Technical notes using R

I have written several technical notes on statistical topics, using R to compute and graph; these are all available as PDF files on-line[59]. If you work through these and use them as starting points for your own analysis, you will have a good basis in R. One note [48] is designed as a tutorial on R and the S language. Another [46] is designed to show as many R techniques as possible: exploratory data analysis, univariate statistics, bivariate correlation and regression, multivariate analysis including PCA, and some geostatistics. Others are more specialised:

- land cover change with logistic regression [49];
- assessing map accuracy [43];
- co-kriging [45];
- fitting rational functions to time series [44];
- optimal partitioning of soil transects [42].

10.5 Web Pages to learn R

- `http://www.rseek.org/`

  The "RSeek" website is a unified portal to R discussion lists, books, FAQ, R Journal, user-contributed documentation, etc.

  Figure 19 shows the results of an RSeek search.

- `http://www.maths.bath.ac.uk/~jjf23/book/`

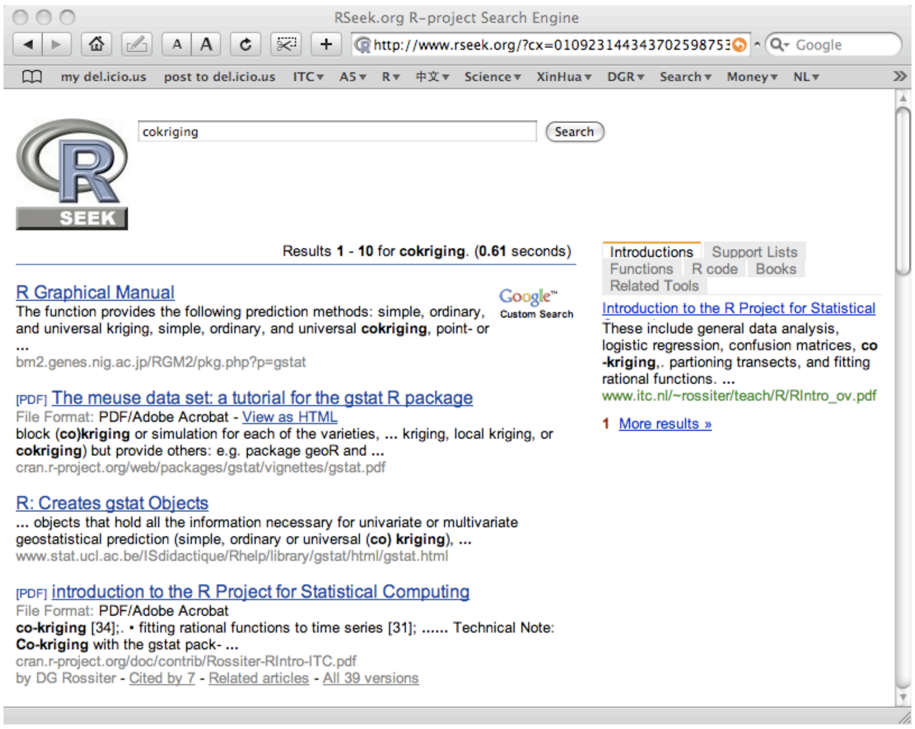
  "Practical Regression and Anova in R" by Julian Faraway (University of Bath, UK); this has been updated into two commerical textbooks: [16, 17]

- `http://rgm2.lab.nig.ac.jp/RGM2/`

  "R Graphical Manual", a huge collection of graphs produced with R, all with source code

- `http://addictedtor.free.fr/graphiques/`

[58] `http://www.stat.pitt.edu/stoffer/tsa2/index.html`
[59] `http://www.itc.nl/personal/rossiter/pubs/list.html#pubs_m_R`



Results **1** - **10** for **cokriging**. (**0.61** seconds)

R Graphical Manual
The function provides the following prediction methods: simple, ordinary, and universal kriging, simple, ordinary, and universal **cokriging**, point- or ...
bm2.genes.nig.ac.jp/RGM2/pkg.php?p=gstat

[PDF] The meuse data set: a tutorial for the gstat R package
File Format: PDF/Adobe Acrobat - View as HTML
block (**co**)**kriging** or simulation for each of the varieties, ... kriging, local kriging, or **cokriging**) but provide others: e.g. package geoR and ...
cran.r-project.org/web/packages/gstat/vignettes/gstat.pdf

R: Creates gstat Objects
... objects that hold all the information necessary for univariate or multivariate geostatistical prediction (simple, ordinary or universal (**co**) **kriging**), ...
www.stat.ucl.ac.be/ISdidactique/Rhelp/library/gstat/html/gstat.html

[PDF] introduction to the R Project for Statistical Computing
File Format: PDF/Adobe Acrobat
co-kriging [34];. • fitting rational functions to time series [31]; ...... Technical Note: **Co-kriging** with the gstat pack- ...
cran.r-project.org/doc/contrib/Rossiter-RIntro-ITC.pdf
by DG Rossiter - Cited by 7 - Related articles - All 39 versions

Introduction to the R Project for Statistical
These include general data analysis, logistic regression, confusion matrices, **co -kriging**,. partioning transects, and fitting rational functions. ...
www.itc.nl/~rossiter/teach/R/RIntro_ov.pdf

1 More results »

Figure 19: Results of an RSeek search

"Addicted to R" graphics gallery, also with source code

10.6 Keeping up with developments in R

R is a dynamic environment, with a large number of dedicated scientists working to make it both a rich statistical computing environment and a modern programming language. Almost every day brings new and modified packages added to CRAN. New versions of the R base appear regularly, about twice a year. This means the R user needs to invest some time to keep up with developments:

- Read the **R Journal**[60]. This is issued about four times a year, and is announced on R home page. It is an attractive PDF document with news, announcements, tutorials, programmer's tips, bibliographies and much more. Prior to 2009 it was known as the **R Newsletter**; this is archived along with the Journal. Many important developments in R were and are explained, and illustrated with examples, in the Journal and Newsletter.

- Subscribe to one or more **mailing lists**: follow the "Mailing Lists" link on the R Project home page. The most relevant for most ITC users are:

  – *R-announce*: major announcements, e.g. new versions

[60] http://journal.r-project.org/

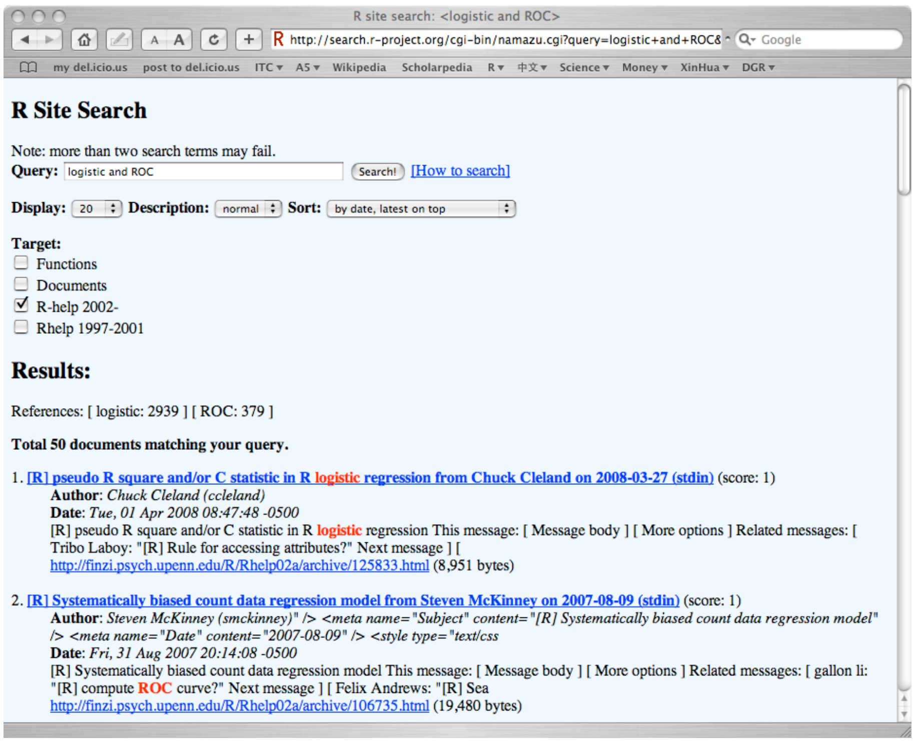
- *R-packages*: announcements of new or updated packages

- *R-help*: discussion about problems using R, and their solutions. The R gurus monitor this list and reply as necessary. A search through the archives is a good way to see if your problem was already discussed. You can access this search via the **Search** link on the R home page[61], or from within R with the `RSiteSearch` method:

```
> RSiteSearch("logistic and ROC",
+ restrict="Rhelp02a", sortby = "date:late")

A search query has been submitted to http://search.r-project.org
The results page should open in your browser shortly
```

Figure 20 shows the results of this search.


R site search: <logistic and ROC>
http://search.r-project.org/cgi-bin/namazu.cgi?query=logistic+and+ROC&
Google
my del.icio.us
post to del.icio.us
ITC
A5
Wikipedia
Scholarpedia
R
中文
Science
Money
XinHua
DGR

R Site Search

Note: more than two search terms may fail.
Query: logistic and ROC [Search!] [How to search]

Display: 20 **Description:** normal **Sort:** by date, latest on top

Target:
- ☐ Functions
- ☐ Documents
- ☑ R-help 2002-
- ☐ Rhelp 1997-2001

Results:

References: [logistic: 2939] [ROC: 379]

Total 50 documents matching your query.

1. [R] pseudo R square and/or C statistic in R logistic regression from Chuck Cleland on 2008-03-27 (stdin) (score: 1)
   Author: *Chuck Cleland (ccleland)*
   Date: *Tue, 01 Apr 2008 08:47:48 -0500*
   [R] pseudo R square and/or C statistic in R logistic regression This message: [Message body] [More options] Related messages: [Tribo Laboy: "[R] Rule for accessing attributes?" Next message] [
   http://finzi.psych.upenn.edu/R/Rhelp02a/archive/125833.html (8,951 bytes)

2. [R] Systematically biased count data regression model from Steven McKinney on 2007-08-09 (stdin) (score: 1)
   Author: *Steven McKinney (smckinney)" /> <meta name="Subject" content="[R] Systematically biased count data regression model" /> <meta name="Date" content="2007-08-09" /> <style type="text/css*
   Date: *Fri, 31 Aug 2007 20:14:08 -0500*
   [R] Systematically biased count data regression model This message: [Message body] [More options] Related messages: [gallon li: "[R] compute ROC curve?" Next message] [Felix Andrews: "[R] Sea
   http://finzi.psych.upenn.edu/R/Rhelp02a/archive/106735.html (19,480 bytes)

Figure 20: Results of an R site search

· Attend the **useR!** user's conference every two years since 2004. The papers from these meetings are available on-line[62].

[61] links to `http://finzi.psych.upenn.edu/search.html`
[62] `http://www.r-project.org/conferences.html`

11 Frequently-asked questions

11.1 Help! I got an error, what did I do wrong?

1. **Read the error message carefully**. Often it says exactly what is wrong. For example:

```
> x <- rnorm(100)
> summary(X)
Error in summary(X) : Object "X" not found
```

   This means exactly what it says: there is no object named X in the workspace nor in attached data frames, so R could not find it when it tried to execute the summary method. In this case the solution is clear: the variable is a lower-case x, not an upper-case X:

```
> summary(x)
    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-2.750  -0.561  -0.070  -0.014   0.745   2.350
```

2. If the command involves an **external file**, make sure your R session is in the right **directory**, or else use the **full path name**. For example, the read.csv method requires a file name:

```
> dlv <- read.csv("dlv.csv")
Error in file(file, "r") : unable to open connection
In addition: Warning message:
cannot open file 'dlv.csv'
```

   The "unable to open connection" message means that the file could not be found.

   Check the current working directory with the getwd method, and see if the file is there with the list.files method (or, you could look for the file in Windows Explorer):

```
> getwd()
[1] "/Users/rossiter/ds/DavisGeostats"
> list.files(pattern="dlv.csv")
character(0)
```

   In fact this file is in another directory. One way is to give the full path name; note the use of the front slash / as in Unix; R interprets this correctly for MS-Windows:

```
> dlv <- read.csv("/Users/rossiter/ds/DLV/dlv.csv")
> dim(dlv)
[1] 88 33
```

   Another way is to change the working directory with the setwd method:

```
> setwd("/Users/rossiter/ds/DLV")
> getwd()
[1] "/Users/rossiter/ds/DLV"
> dlv <- read.csv("dlv.csv")
> dim(dlv)
[1] 88 33
```

3. A common problem is the **attempt to use a method that is in an unloaded package**:

   For example, suppose we try to run a resistant regression with the `lqs` method:

```
> lqs(lead ~ om, data=meuse)
Error: couldn't find function "lqs"
```

   This error has two possible causes: either there is no such method anywhere (for example, if it had been misspelled `lqr`), or the method is available in an unloaded package.

   To find out if the method is available in any package, search for the topic with the `help.search` method:

```
> help.search("lqs")
```

   In this case, the list of matches to the search term `"lqs"` shows two, both associated with package `MASS`.

   Once the required package is loaded, the method is available:

```
> library(MASS)
> lqs(lead ~ om, data=meuse)
Coefficients:
(Intercept)           om
      -19.9         15.4
Scale estimates 46.9 45.9
```

4. If the command which produced the error is **compound**, break it down into small pieces, beginning with the innermost command and then working outwards.

5. **Review the documentation for the command**; it may explain situations in which an error will be produced. For example, if we try to compute the non-parametric correlation between lead and organic matter in the Meuse data set, we get an error:

```
> library(gstat); data(meuse)
> cor(meuse$lead, meuse$om, method="spearman")
Error in cor(lead, om) : missing observations in cov/cor
> ?cor
```

   The help for `cor` says: “If `use` is `"all.obs"`, then the presence of missing observations will produce an error”; in the usage section it shows that `use = "all.obs"` is the default; so we must have some missing values. We can check for these with the `is.na` method:

```
> sum(is.na(lead)); sum(is.na(om))
[1] 0
[1] 2
```

There are two missing values of organic matter (but none of lead). Then we must decide how to deal with them; one way is to compute the correlation without the missing cases:

```
> cor(lead, om, method="spearman", use="complete")
[1] 0.59759
```

11.2 Why didn't my command(s) do what I expected?

Because R does what you said, not what you meant! Some ideas to make the two match:

1. Review the **on-line documentation** for the command to see what the command actually does. Pay especial attention to the arguments and any defaults. All methods have examples; experiment with these to make sure you understand what the method really does.

2. Look for the same commands in a tutorial or text and follow the examples.

3. **Break down** the command into smaller parts; make sure each part does what you think.

4. **Experiment** with test data or "toy" examples to understand how the command really works.

5. Look at the **data structures** with `str` and `class`: sometimes it has a different structure than you thought.

6. Look at your **data** with `summary`, `head`, or `print`. Maybe your data is not what you thought.

7. A common problem occurs when a *variable defined in the workspace*, also called a *local* variable, has the same name as a *field in a data frame*. The local variable is found by R when it looks for the name, and *masks* the field name.

```
> data(trees); str(trees)
`data.frame': 31 obs. of  3 variables:
 $ Girth : num  8.3 8.6 8.8 10.5 10.7 10.8 11 11 11.1  ...
 $ Height: num  70 65 63 72 81 83 66 75 80 75 ...
 $ Volume: num  10.3 10.3 10.2 16.4 18.8 19.7 15.6 18.2  ...
> (Volume <- sample(1:31))
 [1]  6  7  3 21 22  1 24  9 11 14 19 13 20  8  5 30 29 31
```

```
[19]  18 10 23 15 12 27 16  2 26 17 28 4 25
> attach(trees)
> cor(Volume, Girth)
[1] 0.30725
```

This is not the expected value; it is very low, and we know that a tree's volume should be fairly well correlated with its girth. What is wrong? Listing the workspace gives a clue:

```
> ls()
[1] "Volume" "trees"
```

The name `Volume` occurs *twice*: once as a local variable, visible with `ls()`, and once as a field name, visible with `str(trees)`. Even though the `trees` frame is attached, the `Volume` field is masked by the `Volume` local variable, which in this case is just a random permutation of the integers from 1 to 31, so the `cor` method gives an incorrect result.

One way around this problem is to name the field explicitly within its frame using `$`, e.g. `trees$Volume`:

```
> cor(trees$Volume, Girth)
[1] 0.96712
```

Another way is to delete the workspace variable with `rm()`; this makes the field name in the attached frame visible:

```
> rm(Volume)
> cor(Volume, Girth)
[1] 0.96712
```

Another way is to use names for local variables that do not conflict with field names in the attached data frames.

11.3 How do I find the method to do what I want?

R has a very rich set of methods, and there are often several ways to accomplish the same thing, especially with contributed packages.

1. Look at the **help pages for methods you do know**; they often list related methods. For example, the help page for the linear models method (`?lm`) gives related methods for prediction, summary, regression diagnostics, analysis of variance, and generalised linear models, with hyperlinks (in the HTML help) to directly access their help.

2. **Search for keywords**. For example `help.search("sequence")` lists methods to generate sequences, vectors of sequences, and sequences of dates for time-series analysis.

3. Look at the **Task Views**[63]. These are a summary of the facilities in R to accomplish certain tasks (multivariate methods, spatial statistics . . .), including the names of the applicable packages and methods.

4. Review the **tutorials** (§10.2); they cover many common methods.

5. The **contributed documentation** at CRAN[64] has many introductions and reference cards for specific kinds of analysis, for example the brief reference cards by Vito Ricci for regression analysis[65] and time-series analysis[66].

6. Many **textbooks** use R to illustrate their discussion (§10.3), e.g., [11, 19, 57, 15, 13]; you can adapt their examples to your needs.

7. If you don't find what you're looking for, perhaps the method is in a **contributed package which has not yet been installed on your system**. You can **search for it on CRAN** (the R archive)[67].

   For example, the von Mises distribution is the circular analogue of the normal distribution [12, p. 322]. On R with the default installation, a search for this term with the `help.search` method will give no results:

```
> help.search("von Mises")
No help files found with alias or concept or title
     matching 'von Mises'
```

   However, you can search the R archive for the term "Von Mises" with the `RSiteSearch` method:

```
>  RSiteSearch("von Mises")
>  RSiteSearch("von Mises", restrict="functions")
```

   The second form restricts the search to just functions; by default documentation and the R-help mailing list archives are also searched. This opens the search page http://search.r-project.org/ in a browser.

   In this case, several matches are shown, including two packages. A review of their contents shows that the `circular` package for circular statistics is the more complete, so it should be installed on your system (§A.1).

   Once the new package is installed, its contents are available to be searched, and this time the term "von Mises" is found. Several methods in the `circular` package are relevant:

[63] http://cran.r-project.org/web/views/index.html
[64] http://cran.r-project.org/other-docs.html
[65] http://cran.r-project.org/doc/contrib/Ricci-refcard-regression.pdf
[66] http://cran.r-project.org/doc/contrib/Ricci-refcard-ts.pdf
[67] http://cran.r-project.org/

```
> help.search("von Mises")
dmixedvonmises(circular)
    Mixture of von Mises Distributions
mle.vonmises(circular)
    von Mises Maximum Likelihood Estimates
mle.vonmises.bootstrap.ci(circular)
    Bootstrap Confidence Intervals
pp.plot(circular)
    von Mises Probability-Probability Plot
dvonmises(circular)
    von Mises Density Function
```

You can get help on any of these by loading the package and viewing the help:

```
> library(circular)
> ?dvonmises
```

11.4 Memory problems

Information on memory usage is returned by the `object.size` method for individual objects, and the `gc` ("garbage collection") method for the whole workspace:

```
> object.size(meuse)
[1] 23344
> gc()
         used (Mb) gc trigger (Mb) max used (Mb)
Ncells 486087 13.0     818163 21.9   818163 21.9
Vcells 326301  2.5     905753  7.0   905753  7.0
```

If you work with large objects, such as images, you may well exceed R's default memory limits:

```
> tmp <- matrix(1, 10000, 100000)
Error in matrix matrix(1, 10000, 1e+05)  : cannot allocate vector of length 1000000000
```

There are other, similar, messages you may see. This topic is discussed in the help page for memory limits:

```
> help("Memory-limits")
```

MS-Windows limits the total memory that can be allocated to R; this can be reviewed with the `memory.size` method (on Windows only); with the optional `max=TRUE` argument it shows the maximum vector than can be allocated; the `memory.limit` method (on Windows only) shows the total memory that can be allocated for all objects:

```
> # running on MS-Windows
> memory.size(max=T)
[1] 917176320
> memory.limit()
[1] 1038856192
```

This is about 874 Mb for one object and almost 1 Gb total.

Memory can be increased up to about 2 Gb under Windows and indefinitely under better-designed operating systems; see the help:

```
> ?Memory
```

The easiest way to increase memory in Windows is by adding a command-line option to the `Target` field of a desktop shortcut or Start menu item. For example:

```
"C:\Program File\R\R-2.5.1\bin\Rgui.exe" --LANGUAGE=de --max-mem-size=2Gb
```

(Just for fun we specify a German-language GUI with the `LANGUAGE` flag.)

After re-starting R from the shortcut:

```
> memory.limit()
[1] 21474835648
```

If you are doing serious image processing, MS-Windows is unlikely to be a satisfactory platform. Fortunately, almost all your R code will run unchanged in R running under an OS that does not limit memory, such as some variety of Unix.

11.5 What version of R am I running?

The `R.version` system variable contains this information; if you want to report a possible program error it is always necessary to specify this:

```
> R.version

platform       x86_64-apple-darwin9.8.0
arch           x86_64
os             darwin9.8.0
system         x86_64, darwin9.8.0
status
major          2
minor          15.0
year           2012
month          03
day            30
svn rev        58871
language       R
version.string R version 2.15.0 (2012-03-30)
```

To determine the version of an installed package (whether loaded or not), use the `help` method with the optional `package=` argument:

```
> help(package="sp")

Information on package 'sp'
```

```
Description:

Package:           sp
Version:           0.9-98
Date:              2012-03-26
Title:             classes and methods for spatial data
Author:         Edzer Pebesma  <edzer.pebesma@uni-muenster.de>,
                     Roger Bivand <Roger.Bivand@nhh.no>
...
Depends:           R (>= 2.10.0), methods, graphics
Suggests:          lattice, RColorBrewer, rgdal, rgeos (>= 0.1-8)
Imports:           utils, lattice, grid
...
Index:

CRS-class              Class "CRS" of coordinate reference system
                       arguments
DMS-class              Class "DMS" for degree, minute, decimal second
                       values
...
zerodist           find point pairs with equal spatial coordinates
```

To find all packages loaded at a given time, use the `sessionInfo` command:

```
> sessionInfo()
R version 2.15.0 (2012-03-30)
Platform: x86_64-apple-darwin9.8.0/x86_64 (64-bit)

locale:
[1] C

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods
[7] base

other attached packages:
[1] gstat_1.0-10    spacetime_0.6-2 xts_0.8-6
[4] zoo_1.7-7       sp_0.9-98

loaded via a namespace (and not attached):
[1] grid_2.15.0    lattice_0.20-6 tcltk_2.15.0   tools_2.15.0
```

11.6 What statistical procedure should I use?

This of course depends on your application field, your research questions, and your dataset. You should always refer to textbooks and research papers. R is a computer program to carry out your computations, not a statistical wizard to design them.

Within R, each help page gives references to textbooks or articles which you should consult if you are unsure about the theory behind the method or its options. For example:

```
> help("glm")
```

```
glm                    package:stats                    R Documentation

Fitting Generalized Linear Models

Description:
     'glm' is used to fit generalized linear models, specified by
     giving a symbolic description of the linear predictor and a
     description of the error distribution.
...
References:
     Dobson, A. J. (1990) An Introduction to Generalized Linear
     Models. London: Chapman and Hall.

     Hastie, T. J. and Pregibon, D. (1992) Generalized linear models.
     Chapter 6 of Statistical Models in S eds J. M. Chambers and T.
     J. Hastie, Wadsworth & Brooks/Cole.

     McCullagh P. and Nelder, J. A. (1989) Generalized Linear Models.
     London: Chapman and Hall.

     Venables, W. N. and Ripley, B. D. (2002) Modern Applied
     Statistics with S. New York: Springer.
```

You can also look up technical terms in your favourite statistics textbook.

One of R's strongest points is that you are not limited to "textbook" or "routine" methods; you can use the most modern techniques that you see referenced in papers, usually with contributed packages. As a last resort, you can program a procedure yourself.

A Obtaining your own copy of R

Within the ITC computing environment R can be installed via the Software Manager.

From anywhere in the world, everything R is found via the R Project Home Page[68], which has links to:

- **Download** R and additional packages from CRAN (The Comprehensive R ArchiveNetwork)[69]; the first time you attempt to download you will be asked to select a *mirror*, i.e. one of the many servers that host the R distribution;
- Installation instructions;
- Manuals;
- Frequently Asked Questions (FAQ);
- The R Journal, including innovative statistical applications, clever uses of R, and R programming.

If you want to use an IDE such as RStudio, it should be installed *after* installing R itself.

Installing R for Windows To install R on Windows, download the setup program from CRAN by following the links for “Windows”, then the “base” package, then selecting the setup program, the exact name depending on the version). Download the file (about 32 Mb) and run it; this will install R and its base packages.

This link will redirect to the current Windows binary release:

`http://mirrors.dotsrc.org/cran/bin/windows/base/release.htm`.

> Note for Windows system managers: the “R Windows FAQ” in the same directory as the setup program has extensive information on administering R for Windows.

The setup installs the base R system and some of the most common libraries (Table 4).

[68] `http://www.r-project.org/`
[69] `http://cran.r-project.org/`

base	The R Base Package
chron	Chronological objects which can handle dates and times
class	Functions for classification
cluster	Functions for clustering
datasets	The R Datasets Package
foreign	Read data stored by Minitab, S, SAS, SPSS, Stata, ...
graphics	The R Graphics Package
grDevices	The R graphics devices;s upport for colours and fonts
grid	The Grid Graphics Package
KernSmooth	Functions for kernel smoothing
lattice	Lattice Graphics
MASS	Main Library of Venables and Ripley's MASS
methods	Formal Methods and Classes
mle	Maximum likelihood estimation
multcomp	Multiple Tests and Simultaneous Confidence Intervals
mvtnorm	Multivariate Normal and T Distribution
nlme	Linear and nonlinear mixed effects models
nnet	Feed-forward neural networks
rgl	3D visualization device system (OpenGL)
rpart	Recursive partitioning
SparseM	Sparse Linear Algebra
spatial	Functions for Kriging and point pattern analysis
splines	Regression Spline Functions and Classes
stats	The R Stats Package (includes classical tests, exploratory data anlysis, smoothing and local methods for regression, multivariate analysis, non-linear least squares, time series analysis)
stepfun	Step Functions, including Empirical Distributions
survival	Survival analysis, including penalised likelihood.
utils	R Utilities

Table 4: Packages in the base R distribution for Windows; libraries loaded when R starts are shown in **boldface**.

It also installs **six manuals** in both PDF and HTML format: (1) An Introduction to R; (2) R Installation and Administration; (3) R Language Definition; (4) Reference Index; (5) R Data Import/Export; (6) Writing R Extensions.

Other operating systems For Mac OS/X or other Unix-based system, follow the appropriate links from the CRAN home page and read the installation instructions. The GUI for the Mac OS/X version has a code editor, data editor, data browser, and native Quartz graphics.

Cross-platform RStudio is explained in §3.1.

The JGR project at the University of Augsburg (D)[70] has developed a Java-based GUI which runs on any platform with industry-standard Java Runtime Engine, including Mac OS X and most Windows systems. This includes the `iplots` interactive graphics package.

A.1 Installing new packages

The ITC network installation includes the optional packages requested by ITC users. If you need to install packages on your own copy of R, use the `Packages | Install Package(s) from CRAN ...` menu item while connected to the Internet. You need administrator privledges on your system; if you can install the base program, you can install packages.

A brief description and full documentation of the available packages is available from the CRAN home page; click on the link for "Packages".

If you need a new package on the ITC network, contact the person who maintains the R distribution[71].

A.2 Customizing your installation

Many aspects of R's interactive behaviour can be changed to suit your preferences. For example, you can set up your own copy of R to load libraries at startup, and you can also change many default options. You do this by creating a file named `.Rprofile` either in your *home directory*, or in a *working directory* from which you will start R, or both. The second of these is used if it exists, otherwise the master copy in the home directory.

To see the current options setings, use the `options` function without any arguments; it's easier to review these by viewing its structure. Individual settings can then be viewed by their field name.

```
> str(options())
List of 45
```

[70] http://www.rosuda.org/
[71] As of the date of these notes, their author

```
 $ prompt              : chr "> "
 $ continue            : chr "+ "
...
 $ htmlhelp            : logi TRUE
> options()$digits
[1] 5
```

Here is an example `.Rprofile` which sets some options and loads some libraries that will always be used in a project:

```
options(show.signif.stars = FALSE);
options(html.help=TRUE);
options(digits = 5);
options(prompt = "R> "); options(continue = "R+ ");
options(timeout = 20);
library(gstat); library(lattice);
         # optional: function to run at startup
.First <- function() {
  print("Welcome to R, you've made a wise choice") };
         # optional: function to run at shutdown
.Last <- function() { graphics.off(); print("Get a life!") }
```

A.3 R in different human languages

R’s menus and messages have been translated to several common languages; the codes of these are listed as folders under folder `share/locale` in the R installation.

MS-Windows If your system is set up to work in a non-English language (e.g. Spanish, code `es`), R GUI will automatically display its menus, and R its messages, in that language.

If you’d like R to work in a different language than your overall system, the simplest method is to:

1. Create a desktop shortcut to R Gui (probably created during installation);

2. Open its properties;

3. In the the Target field, add the environment variable `LANGUAGE` and the code for the language you want; for example to force English: `LANGUAGE=en`. Note the format: upper-case variable name, language name exactly as in the list of available languages, no quotes; the whole thing after the program name.

See the R for Windows FAQ Questions 2.2 and 2.15 for more details; this FAQ is available via the Help menu in RGui.

Mac OS/X The R for Mac OS X FAQ[72] explains that R detects the language settings from the Language & Text section of the System Preferences, and presents translated messages and GUI if they are available in the selected language. The Formats information for numbers is also used.

This can be over-ridden on a system-wide basis (not per-session). by setting the `force.LANG` defaults setting. For example, to force the US English text on a system running another language, open the Terminal (i.e., a shell) and enter this command:

```
defaults write org.R-project.R force.LANG en_US.UTF-8
```

Other languages and encodings can be specified with the International Organization for Standardization (ISO) standard for the identification of languages (ISO 639-1 or -2)[73] and locales (ISO 3166-1).

B An example script

This is an example of a moderately complicated script, which gives both a numerical and a visual impression of the variability of small random samples. The output is shown in Figure 21 on the following page. If you want to experiment with the script, cut-and-paste it into a text editor (for example, Tinn-R or the built-in editor of RStudio or R console), modify it as you like (for example, change the sample size `n` or the number of replications), save it as a command file, and run it with the `source` function as explained in §3.5.

You prepare this with a plain-text editor as a text file, for example `plot4.R`[74] and then "source" it into R, which executes the commands immediately.

```
> source("plot4.R")
```

If you want to change the plotting parameters, you have to change the script and re-source it. The next section offers a better solution.

A note on R style It is good practice to make all parameters into variables at the beginning of the script, so they can be easily adjusted. If you find yourself repeating the same number in many expressions, it probably should be converted to a variable. Examples here are the sample size and parameters of the normal distribution. You could write:

```
v <- rnorm(30, 180, 20)
hist(v, breaks = seq(800, 280, by=(20/3)))
points(x, dnorm(x, 180, 20)*(30*(20/3)))
```

[72] http://cran.r-project.org/bin/macosx/RMacOSX-FAQ.html
[73] http://www.loc.gov/standards/iso639-2/php/English_list.php
[74] The `.R` file extension is customary for R scripts.

but it is more elegant to write:

```
n <- 30; mu <- 180; sd <- 20; bin.width <- sd/3
v <- rnorm(n, mu, sd)
hist(v, breaks = seq(mu-5*sd, mu+5*sd, by=bin.width))
points(x, dnorm(x, mu, sd)*(n*bin.width))
```

```
### visualise the variability of small random samples
                              # sample size
n <- 30
                              # number of plot rows, columns
rows <- 2; cols <- 2; reps <- rows*cols
                              # parameters of the normal distribution
mu <- 180; sd <- 20
                              # set up graphic display
par(mfrow=c(rows, cols))
                              # number of s.d.'s for histogram display
sdd <- 3.5
                              # compute bin width from s.d and
                              #  the number of bars for each
bin.width=sd/3
                              # scale x-axis
x.min <- mu-(sdd*sd); x.max <- mu+(sdd*sd)
                              # scale y-axis
y.max <- n*0.5*bin.width/sd
                              # compute and display each graph
for (i in 1:reps) {
  v <- rnorm(n, mu, sd)
  hist(v, xlim=c(x.min,x.max), ylim=c(0, y.max),
       breaks = seq(mu-5*sd, mu+5*sd, by=bin.width),
       main="", xlab=paste("Sample",i)) ;
  x <- seq(x.min, x.max, length=120)
                              # true normal distribution
  points(x,dnorm(x, mu, sd)*(n*bin.width),
         type="l", col="blue", lty=1, lwd=1.8)
                              # distribution estimated from sample
  points(x,dnorm(x, mean(v), sd(v))*(n*bin.width),
         type="l", col="red", lty=2, lwd=1.8)
                              # print sample params.
                              # and Pr(Type I error)
  text(x.min, 0.9*y.max, paste("mean:", round(mean(v),2)),pos=4)
  text(x.min, 0.8*y.max, paste("sdev:", round(sd(v),2)),pos=4)
  text(x.min, 0.7*y.max,
       paste("Pr(t):", round((t.test(v, mu=mu))$p.value,2)),pos=4)
}
                              # clean up
par(mfrow=c(1,1))
rm(n, rows, cols, reps, mu, sd, v, i, sdd, bin.width, x.min, x.max, y.max, x)
```

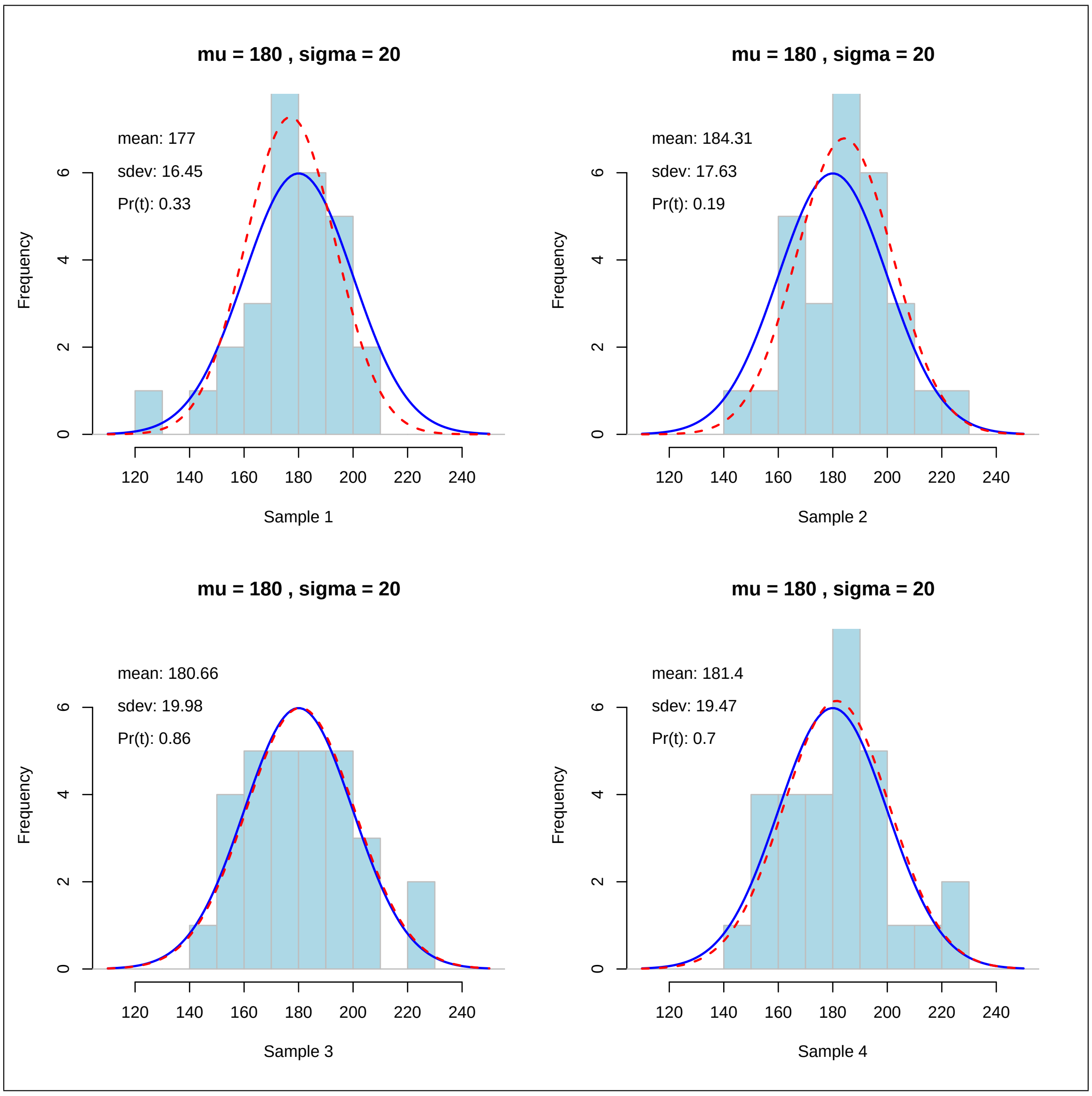


Figure 21: A visualisation of the variability of small random samples. Each sample of 30 has been divided into ten histogram bins on [130...230]. The blue (solid) normal curves all have $\mu = 180$ and $\sigma = 20$; the red (dashed) normal curves are estimated from each sample. Note the bias (left or right of the blue curves) and variances (narrower or wider than the blue curves).

C An example function

A more powerful approach than writing and sourcing a script is to write a *function* which is loaded into the workspace with the `source` function and then run as if it were a built-in R function. The main advantage is that you can make the function adaptable with a set of *arguments* (parameters that can be sent to the function), so you don't have to edit the script.

Here we have converted the script of Appendix B into a function, with only one required *argument* (the sample size) and six optional arguments which control aspects of the display, for example the number of samples to compare on one plot.

You prepare this with a plain-text editor in the same way as a script, for example creating a file named `plot_normals.R` and then read it into R with the `source` function. This is a script; as it is executed it defines the function. Once the function is defined in the workspace (which you can verify with the `ls` function), you run it just like a built-in R function.

```
> source("plot_normals.R")
> ls()
plot.normals
> plot.normals(60)
> plot.normals(60, mu=100, sd=15)
> plot.normals(60, rows=3, cols=3, mu=100, sd=15)
```

```
### function to visualise the variability of small random samples
##  required arguments:
##     n : sample size
##  arguments with reasonable defaults:
##     rows,cols : dimensions of display
##     mu, sd : mean, s.d. of normal distribution to sample
##     bsd : histogram bins to represent each s.d.
##     sdd : +/- number of s.d. to display
plot.normals <- function(n, rows=2, cols=2, mu=0, sd=1,
                       bsd = 2, sdd=3.5) {
                              # set up graphic display
par(mfrow=c(rows, cols))
                              # number of random samples
reps <- rows*cols
                              # histogram bin width
bin.width=sd/bsd
                              # scale x-axis
x.min <- mu-(sdd*sd); x.max <- mu+(sdd*sd)
                              # scale y-axis; max. dnorm(1,0)=0.3989
                              #  adjust to sample and bin sizes
                              #  and normalize by s.d.
                              #  and leave room for higher bars
y.max <- n*0.5*bin.width/sd
                              # compute and display each graph
for (i in 1:reps) {
  v <- rnorm(n, mu, sd)
  hist(v, xlim=c(x.min,x.max), ylim=c(0,y.max),
       breaks = seq(mu-5*sd, mu+5*sd, by=bin.width),
       main=paste("mu =", mu, ", sigma =", sd),
       xlab=paste("Sample",i), col="lightblue", border="gray",
       freq=TRUE)
  x <- seq(x.min,x.max,length=120)
                              # true normal distribution
  points(x,dnorm(x, mu, sd)*(n*bin.width),
         type="l", col="blue", lty=1, lwd=1.8)
                              # normal dist. estimated from sample
  points(x,dnorm(x, mean(v), sd(v))*(n*bin.width),
         type="l", col="red", lty=2, lwd=1.8)
                              # print sample params.
                              # and Pr(Type I error)
  text(x.min, 0.9*y.max, paste("mean:", round(mean(v),2)),pos=4)
  text(x.min, 0.8*y.max, paste("sdev:", round(sd(v),2)),pos=4)
  text(x.min, 0.7*y.max,
       paste("Pr(t):", round((t.test(v, mu=mu))$p.value,2)),pos=4)
}
                              # clean up
par(mfrow=c(1,1))
}
```

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Index of R concepts