

# R FAQ

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Frequently Asked Questions on R  
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# Table of Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
1.1	Legalese	1
1.2	Obtaining this document	1
1.3	Citing this document	1
1.4	Notation	1
1.5	Feedback	1
<b>2</b>	<b>R Basics</b>	<b>2</b>
2.1	What is R?	2
2.2	What machines does R run on?	2
2.3	What is the current version of R?	3
2.4	How can R be obtained?	3
2.5	How can R be installed?	3
2.5.1	How can R be installed (Unix)	3
2.5.2	How can R be installed (Windows)	4
2.5.3	How can R be installed (Macintosh)	4
2.6	Are there Unix binaries for R?	5
2.7	What documentation exists for R?	5
2.8	Citing R	7
2.9	What mailing lists exist for R?	7
2.10	What is CRAN?	8
2.11	Can I use R for commercial purposes?	9
2.12	Why is R named R?	9
2.13	What is the R Foundation?	9
<b>3</b>	<b>R and S</b>	<b>10</b>
3.1	What is S?	10
3.2	What is S-PLUS?	10
3.3	What are the differences between R and S?	11
3.3.1	Lexical scoping	11
3.3.2	Models	14
3.3.3	Others	14
3.4	Is there anything R can do that S-PLUS cannot?	16
3.5	What is R-plus?	17
<b>4</b>	<b>R Web Interfaces</b>	<b>18</b>

<b>5</b>	<b>R Add-On Packages</b>	<b>19</b>
5.1	Which add-on packages exist for R?	19
5.1.1	Add-on packages in R	19
5.1.2	Add-on packages from CRAN	19
5.1.3	Add-on packages from Omegahat	40
5.1.4	Add-on packages from Bioconductor	42
5.1.5	Other add-on packages	46
5.2	How can add-on packages be installed?	47
5.3	How can add-on packages be used?	47
5.4	How can add-on packages be removed?	48
5.5	How can I create an R package?	49
5.6	How can I contribute to R?	49
<b>6</b>	<b>R and Emacs</b>	<b>50</b>
6.1	Is there Emacs support for R?	50
6.2	Should I run R from within Emacs?	50
6.3	Debugging R from within Emacs	51
<b>7</b>	<b>R Miscellanea</b>	<b>52</b>
7.1	How can I set components of a list to NULL?	52
7.2	How can I save my workspace?	52
7.3	How can I clean up my workspace?	52
7.4	How can I get eval() and D() to work?	52
7.5	Why do my matrices lose dimensions?	53
7.6	How does autoloading work?	53
7.7	How should I set options?	53
7.8	How do file names work in Windows?	54
7.9	Why does plotting give a color allocation error?	54
7.10	How do I convert factors to numeric?	54
7.11	Are Trellis displays implemented in R?	54
7.12	What are the enclosing and parent environments?	55
7.13	How can I substitute into a plot label?	55
7.14	What are valid names?	56
7.15	Are GAMs implemented in R?	56
7.16	Why is the output not printed when I source() a file?	56
7.17	Why does outer() behave strangely with my function?	57
7.18	Why does the output from anova() depend on the order of factors in the model?	57
7.19	How do I produce PNG graphics in batch mode?	58
7.20	How can I get command line editing to work?	58
7.21	How can I turn a string into a variable?	58
7.22	Why do lattice/trellis graphics not work?	59
7.23	How can I sort the rows of a data frame?	59
7.24	Why does the help.start() search engine not work?	59
7.25	Why did my .Rprofile stop working when I updated R?	59
7.26	Where have all the methods gone?	59
7.27	How can I create rotated axis labels?	60

<b>8</b>	<b>R Programming</b>	<b>61</b>
8.1	How should I write summary methods?	61
8.2	How can I debug dynamically loaded code?	61
8.3	How can I inspect R objects when debugging?	61
8.4	How can I change compilation flags?	61
8.5	How can I debug S4 methods?	61
<b>9</b>	<b>R Bugs</b>	<b>62</b>
9.1	What is a bug?	62
9.2	How to report a bug	62
<b>10</b>	<b>Acknowledgments</b>	<b>64</b>

# 1 Introduction

This document contains answers to some of the most frequently asked questions about R.

## 1.1 Legalese

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A copy of the GNU General Public License is available via WWW at

<http://www.gnu.org/copyleft/gpl.html>.

You can also obtain it by writing to the Free Software Foundation, Inc., 59 Temple Place — Suite 330, Boston, MA 02111-1307, USA.

## 1.2 Obtaining this document

The latest version of this document is always available from

<http://CRAN.R-project.org/doc/FAQ/>

From there, you can obtain versions converted to [plain ASCII text](#), [DVI](#), [GNU info](#), [HTML](#), [PDF](#), [PostScript](#) as well as the [Texinfo source](#) used for creating all these formats using the [GNU Texinfo system](#).

You can also obtain the R FAQ from the ‘[doc/FAQ](#)’ subdirectory of a CRAN site (see [Section 2.10 \[What is CRAN?\]](#), page 8).

## 1.3 Citing this document

In publications, please refer to this FAQ as Hornik (2004), “The R FAQ”, and give the above, *official* URL and the ISBN 3-900051-08-9.

## 1.4 Notation

Everything should be pretty standard. ‘R>’ is used for the R prompt, and a ‘\$’ for the shell prompt (where applicable).

## 1.5 Feedback

Feedback via email to [Kurt.Hornik@R-project.org](mailto:Kurt.Hornik@R-project.org) is of course most welcome.

In particular, note that I do not have access to Windows or Macintosh systems. Features specific to the Windows and Mac OS X ports of R are described in the [“R for Windows FAQ”](#) and the [“R for Mac OS X FAQ”](#). If you have information on Macintosh or Windows systems that you think should be added to this document, please let me know.

## 2 R Basics

### 2.1 What is R?

R is a system for statistical computation and graphics. It consists of a language plus a run-time environment with graphics, a debugger, access to certain system functions, and the ability to run programs stored in script files.

The design of R has been heavily influenced by two existing languages: Becker, Chambers & Wilks' S (see [Section 3.1 \[What is S?\]](#), page 10) and Sussman's [Scheme](#). Whereas the resulting language is very similar in appearance to S, the underlying implementation and semantics are derived from Scheme. See [Section 3.3 \[What are the differences between R and S?\]](#), page 11, for further details.

The core of R is an interpreted computer language which allows branching and looping as well as modular programming using functions. Most of the user-visible functions in R are written in R. It is possible for the user to interface to procedures written in the C, C++, or FORTRAN languages for efficiency. The R distribution contains functionality for a large number of statistical procedures. Among these are: linear and generalized linear models, nonlinear regression models, time series analysis, classical parametric and nonparametric tests, clustering and smoothing. There is also a large set of functions which provide a flexible graphical environment for creating various kinds of data presentations. Additional modules ("add-on packages") are available for a variety of specific purposes (see [Chapter 5 \[R Add-On Packages\]](#), page 19).

R was initially written by [Ross Ihaka](#) and [Robert Gentleman](#) at the Department of Statistics of the University of Auckland in Auckland, New Zealand. In addition, a large group of individuals has contributed to R by sending code and bug reports.

Since mid-1997 there has been a core group (the "R Core Team") who can modify the R source code archive. The group currently consists of Doug Bates, John Chambers, Peter Dalgaard, Robert Gentleman, Kurt Hornik, Stefano Iacus, Ross Ihaka, Friedrich Leisch, Thomas Lumley, Martin Maechler, Duncan Murdoch, Paul Murrell, Martyn Plummer, Brian Ripley, Duncan Temple Lang, and Luke Tierney.

R has a home page at <http://www.R-project.org/>. It is free software distributed under a GNU-style copyleft, and an official part of the GNU project ("GNU S").

### 2.2 What machines does R run on?

R is being developed for the Unix, Windows and Mac families of operating systems. Support for Mac OS Classic ended with R 1.7.1.

The current version of R will configure and build under a number of common Unix platforms including *cpu-linux-gnu* for the i386, alpha, arm, hppa, ia64, m68k, mips/mipsel, powerpc, s390, sparc (e.g., <http://buildd.debian.org/build.php?&pkg=r-base>), and x86\_64 CPUs, i386-freebsd, i386-sun-solaris, powerpc-apple-darwin, mips-sgi-irix, rs6000-ibm-aix, hppa-hp-hpux, and sparc-sun-solaris.

If you know about other platforms, please drop us a note.

## 2.3 What is the current version of R?

The current released version is 2.0.1. Based on this ‘major.minor.patchlevel’ numbering scheme, there are two development versions of R, a patched version of the current release (‘r-patched’) and one working towards the next minor or eventually major (‘r-devel’) releases of R, respectively. Version r-patched is for bug fixes mostly. New features are typically introduced in r-devel.

## 2.4 How can R be obtained?

Sources, binaries and documentation for R can be obtained via CRAN, the “Comprehensive R Archive Network” (see [Section 2.10 \[What is CRAN?\]](#), page 8).

Sources are also available via <https://svn.r-project.org/R/>, the R Subversion repository, but currently not via anonymous rsync (nor CVS).

Tarballs with daily snapshots of the r-devel and r-patched development versions of R can be found at <ftp://ftp.stat.math.ethz.ch/Software/R>.

## 2.5 How can R be installed?

### 2.5.1 How can R be installed (Unix)

If R is already installed, it can be started by typing `R` at the shell prompt (of course, provided that the executable is in your path).

If binaries are available for your platform (see [Section 2.6 \[Are there Unix binaries for R?\]](#), page 5), you can use these, following the instructions that come with them.

Otherwise, you can compile and install R yourself, which can be done very easily under a number of common Unix platforms (see [Section 2.2 \[What machines does R run on?\]](#), page 2). The file ‘INSTALL’ that comes with the R distribution contains a brief introduction, and the “R Installation and Administration” guide (see [Section 2.7 \[What documentation exists for R?\]](#), page 5) has full details.

Note that you need a FORTRAN compiler or perhaps `f2c` in addition to a C compiler to build R. Also, you need Perl version 5 to build the R object documentations. (If this is not available on your system, you can obtain a PDF version of the object reference manual via CRAN.)

In the simplest case, untar the R source code, change to the directory thus created, and issue the following commands (at the shell prompt):

```
$ ./configure
$ make
```

If these commands execute successfully, the R binary and a shell script front-end called ‘R’ are created and copied to the ‘bin’ directory. You can copy the script to a place where users can invoke it, for example to ‘/usr/local/bin’. In addition, plain text help pages as well as HTML and LaTeX versions of the documentation are built.

Use `make dvi` to create DVI versions of the R manuals, such as ‘`refman.dvi`’ (an R object reference index) and ‘`R-exts.dvi`’, the “R Extension Writers Guide”, in the ‘`doc/manual`’ subdirectory. These files can be previewed and printed using standard programs such as `xdvi` and `dvips`. You can also use `make pdf` to build PDF (Portable Document Format)

version of the manuals, and view these using e.g. Acrobat. Manuals written in the GNU Texinfo system can also be converted to info files suitable for reading online with Emacs or stand-alone GNU Info; use *make info* to create these versions (note that this requires Makeinfo version 4.5).

Finally, use *make check* to find out whether your R system works correctly.

You can also perform a “system-wide” installation using *make install*. By default, this will install to the following directories:

```
'${prefix}/bin'
    the front-end shell script

'${prefix}/man/man1'
    the man page

'${prefix}/lib/R'
    all the rest (libraries, on-line help system, ...). This is the “R Home Directory”
    (R_HOME) of the installed system.
```

In the above, `prefix` is determined during configuration (typically `/usr/local`) and can be set by running `configure` with the option

```
$ ./configure --prefix=/where/you/want/R/to/go
```

(E.g., the R executable will then be installed into `/where/you/want/R/to/go/bin`.)

To install DVI, info and PDF versions of the manuals, use *make install-dvi*, *make install-info* and *make install-pdf*, respectively.

## 2.5.2 How can R be installed (Windows)

The `bin/windows` directory of a CRAN site contains binaries for a base distribution and a large number of add-on packages from CRAN to run on Windows 95, 98, ME, NT4, 2000, and XP (at least) on Intel and clones (but not on other platforms). The Windows version of R was created by Robert Gentleman and Guido Masarotto, and is now being developed and maintained by [Duncan Murdoch](#) and [Brian D. Ripley](#).

For most installations the Windows installer program will be the easiest tool to use.

See the [“R for Windows FAQ”](#) for more details.

## 2.5.3 How can R be installed (Macintosh)

The `bin/macosx` directory of a CRAN site contains a standard Apple installer package named `RAqua.pkg.sit` compressed in Aladdin Stuffit format. Once downloaded, uncompressed and executed, the installer will install the current non-developer release of R. RAqua is a native Mac OS X Darwin version of R with an Aqua GUI. Inside `bin/macosx/x.y` there are prebuilt binary packages to be used with RAqua corresponding to the “x.y” release of R. The installation of these packages is available through the “Package” menu of the RAqua GUI. This port of R for Mac OS X is maintained by [Stefano Iacus](#). The [“R for Mac OS X FAQ”](#) has more details.

The `bin/macos` directory of a CRAN site contains bin-hexed (`hqx`) and stuffit (`sit`) archives for a base distribution and a large number of add-on packages of R 1.7.1 to run under Mac OS 8.6 to Mac OS 9.2.2. This port of R for Macintosh is no longer supported.



## 2.6 Are there Unix binaries for R?

The ‘bin/linux’ directory of a CRAN site contains Mandrake 9.1/9.2/10.0 i386 packages by Michele Alzetta, Red Hat 8.x/9/Fedora1/Fedora2 i386 and Fedora1 x86\_64 packages by Martyn Plummer and James Henstridge, respectively, SuSE 7.3/8.0/8.1/8.2 i386 and 9.0/9.1 i586 packages by Detlef Steuer, and VineLinux 2.6 i386 packages by Susunu Tanimura. Debian packages, maintained by Dirk Eddelbuettel, have long been part of the Debian distribution, and can be accessed through APT, the Debian package maintenance tool.

No other binary distributions are currently publically available.

## 2.7 What documentation exists for R?

Online documentation for most of the functions and variables in R exists, and can be printed on-screen by typing `help(name)` (or `?name`) at the R prompt, where *name* is the name of the topic help is sought for. (In the case of unary and binary operators and control-flow special forms, the name may need to be quoted.)

This documentation can also be made available as one reference manual for on-line reading in HTML and PDF formats, and as hardcopy via LaTeX, see [Section 2.5 \[How can R be installed?\]](#), [page 3](#). An up-to-date HTML version is always available for web browsing at <http://stat.ethz.ch/R-manual/>.

Printed copies of the R reference manual for some version(s) are available from Network Theory Ltd, at <http://www.network-theory.co.uk/R/base/>. For each set of manuals sold, the publisher donates USD 10 to the R Foundation (see [Section 2.13 \[What is the R Foundation?\]](#), [page 9](#)).

The R distribution also comes with the following manuals.

- “An Introduction to R” (‘R-intro’) includes information on data types, programming elements, statistical modeling and graphics. This document is based on the “Notes on S-PLUS” by Bill Venables and David Smith.
- “Writing R Extensions” (‘R-exts’) currently describes the process of creating R add-on packages, writing R documentation, R’s system and foreign language interfaces, and the R API.
- “R Data Import/Export” (‘R-data’) is a guide to importing and exporting data to and from R.
- “The R Language Definition” (‘R-lang’), a first version of the “Kernighan & Ritchie of R”, explains evaluation, parsing, object oriented programming, computing on the language, and so forth.
- “R Installation and Administration” (‘R-admin’).

Books on R include

P. Dalgaard (2002), “Introductory Statistics with R”, Springer: New York, ISBN 0-387-95475-9.

<http://www.biostat.ku.dk/~pd/ISwR.html>.

J. Fox (2002), “An R and S-PLUS Companion to Applied Regression”, Sage Publications, ISBN 0-761-92280-6 (softcover) or 0-761-92279-2 (hardcover),

<http://socserv.socsci.mcmaster.ca/jfox/Books/Companion/>.

J. Maindonald and J. Braun (2003), “Data Analysis and Graphics Using R: An Example-Based Approach”, Cambridge University Press, ISBN 0-521-81336-0, <http://www.maths.anu.edu.au/~johnm/>.

S. M. Iacus and G. Masarotto (2002), “Laboratorio di statistica con R”, McGraw-Hill, ISBN 88-386-6084-0 (in Italian), [http://www.ateneonline.it/LibroAteneo.asp?item\\_id=1436](http://www.ateneonline.it/LibroAteneo.asp?item_id=1436).

The book

W. N. Venables and B. D. Ripley (2002), “Modern Applied Statistics with S. Fourth Edition”. Springer, ISBN 0-387-95457-0

has a home page at <http://www.stats.ox.ac.uk/pub/MASS4/> providing additional material. Its companion is

W. N. Venables and B. D. Ripley (2000), “S Programming”. Springer, ISBN 0-387-98966-8

and provides an in-depth guide to writing software in the S language which forms the basis of both the commercial S-PLUS and the Open Source R data analysis software systems. See <http://www.stats.ox.ac.uk/pub/MASS3/Sprog/> for more information.

In addition to material written specifically or explicitly for R, documentation for S/S-PLUS (see [Chapter 3 \[R and S\]](#), [page 10](#)) can be used in combination with this FAQ (see [Section 3.3 \[What are the differences between R and S?\]](#), [page 11](#)). Introductory books include

P. Spector (1994), “An introduction to S and S-PLUS”, Duxbury Press.

A. Krause and M. Olsen (2002), “The Basics of S-PLUS” (Third Edition). Springer, ISBN 0-387-95456-2

The book

J. C. Pinheiro and D. M. Bates (2000), “Mixed-Effects Models in S and S-PLUS”, Springer, ISBN 0-387-98957-0

provides a comprehensive guide to the use of the **nlme** package for linear and nonlinear mixed-effects models.

As an example of how R can be used in teaching an advanced introductory statistics course, see

D. Nolan and T. Speed (2000), “Stat Labs: Mathematical Statistics Through Applications”, Springer Texts in Statistics, ISBN 0-387-98974-9

This integrates theory of statistics with the practice of statistics through a collection of case studies (“labs”), and uses R to analyze the data. More information can be found at <http://www.stat.Berkeley.EDU/users/statlabs/>.

Last, but not least, Ross’ and Robert’s experience in designing and implementing R is described in Ihaka & Gentleman (1996), “R: A Language for Data Analysis and Graphics”, *Journal of Computational and Graphical Statistics*, **5**, 299–314.

An annotated bibliography (BibTeX format) of R-related publications which includes most of the above references can be found at

<http://www.R-project.org/doc/bib/R.bib>

## 2.8 Citing R

To cite R in publications, use

```
@Manual{,
  title      = {R: A language and environment for statistical
                computing},
  author     = {{R Development Core Team}},
  organization = {R Foundation for Statistical Computing},
  address    = {Vienna, Austria},
  year       = 2004,
  note       = {3-900051-07-0},
  url        = {http://www.R-project.org}
}
```

Citation strings (or BibTeX entries) for R and R packages can also be obtained by `citation()`.

## 2.9 What mailing lists exist for R?

Thanks to [Martin Maechler](#), there are four mailing lists devoted to R.

### R-announce

A moderated list for major announcements about the development of R and the availability of new code.

### R-packages

A moderated list for announcements on the availability of new or enhanced contributed packages.

### R-help

The ‘main’ R mailing list, for discussion about problems and solutions using R, announcements (not covered by ‘R-announce’ and ‘R-packages’) about the development of R and the availability of new code, enhancements and patches to the source code and documentation of R, comparison and compatibility with S and S-PLUS, and for the posting of nice examples and benchmarks.

### R-devel

This list is for discussions about the future of R, proposals of new functionality, and pre-testing of new versions. It is meant for those who maintain an active position in the development of R.

Convenient access to information on these lists, subscription, and archives is provided by the web interface at <http://stat.ethz.ch/mailman/listinfo/>. One can also subscribe (or unsubscribe) via email, e.g. to R-help by sending ‘subscribe’ (or ‘unsubscribe’) in the *body* of the message (not in the subject!) to [R-help-request@lists.R-project.org](mailto:R-help-request@lists.R-project.org).

Send email to [R-help@lists.R-project.org](mailto:R-help@lists.R-project.org) to send a message to everyone on the R-help mailing list. Subscription and posting to the other lists is done analogously, with ‘R-help’ replaced by ‘R-announce’, ‘R-packages’, and ‘R-devel’, respectively. Note that the R-announce and R-packages lists are gatewayed into R-help. Hence, you should subscribe to either of them only in case you are not subscribed to R-help.

It is recommended that you send mail to R-help rather than only to the R Core developers (who are also subscribed to the list, of course). This may save them precious time they can

use for constantly improving R, and will typically also result in much quicker feedback for yourself.

Of course, in the case of bug reports it would be very helpful to have code which reliably reproduces the problem. Also, make sure that you include information on the system and version of R being used. See [Chapter 9 \[R Bugs\]](#), [page 62](#) for more details.

Please read the [posting guide](#) *before* sending anything to any mailing list.

See <http://www.R-project.org/mail.html> for more information on the R mailing lists.

The R Core Team can be reached at [R-core@lists.R-project.org](mailto:R-core@lists.R-project.org) for comments and reports.

## 2.10 What is CRAN?

The “Comprehensive R Archive Network” (CRAN) is a collection of sites which carry identical material, consisting of the R distribution(s), the contributed extensions, documentation for R, and binaries.

The CRAN master site at TU Wien, Austria, can be found at the URL

<http://cran.R-project.org/>

Daily mirrors are available at URLs including

<a href="http://cran.at.R-project.org/">http://cran.at.R-project.org/</a>	(TU Wien, Austria)
<a href="http://cran.au.R-project.org/">http://cran.au.R-project.org/</a>	(PlanetMirror, Australia)
<a href="http://cran.br.R-project.org/">http://cran.br.R-project.org/</a>	(Universidade Federal de Paraná, Brazil)
<a href="http://cran.ch.R-project.org/">http://cran.ch.R-project.org/</a>	(ETH Zürich, Switzerland)
<a href="http://cran.dk.R-project.org/">http://cran.dk.R-project.org/</a>	(SunSITE, Denmark)
<a href="http://cran.es.R-project.org/">http://cran.es.R-project.org/</a>	(Spanish National Research Network, Madrid, Spain)
<a href="http://cran.fr.R-project.org/">http://cran.fr.R-project.org/</a>	(INRA, Toulouse, France)
<a href="http://cran.hu.R-project.org/">http://cran.hu.R-project.org/</a>	(Semmelweis U, Hungary)
<a href="http://cran.pt.R-project.org/">http://cran.pt.R-project.org/</a>	(Universidade do Porto, Portugal)
<a href="http://cran.uk.R-project.org/">http://cran.uk.R-project.org/</a>	(U of Bristol, United Kingdom)
<a href="http://cran.us.R-project.org/">http://cran.us.R-project.org/</a>	(pair Networks, USA)
<a href="http://cran.za.R-project.org/">http://cran.za.R-project.org/</a>	(Rhodes U, South Africa)

See <http://cran.R-project.org/mirrors.html> for a complete list of mirrors. Please use the CRAN site closest to you to reduce network load.

From CRAN, you can obtain the latest official release of R, daily snapshots of R (copies of the current source trees), as gzipped and bziped tar files, a wealth of additional contributed code, as well as prebuilt binaries for various operating systems (Linux, Mac OS Classic, Mac OS X, and MS Windows). CRAN also provides access to documentation on R, existing mailing lists and the R Bug Tracking system.

To “submit” to CRAN, simply upload to <ftp://cran.R-project.org/incoming/> and send an email to [cran@R-project.org](mailto:cran@R-project.org). Note that CRAN generally does not accept submissions of precompiled binaries due to security reasons. In particular, binary packages for Windows and Mac OS X are provided by the respective binary package maintainers.

**Note:** It is very important that you indicate the copyright (license) information (GPL, BSD, Artistic, . . .) in your submission.

Please always use the URL of the master site when referring to CRAN.

## 2.11 Can I use R for commercial purposes?

R is released under the [GNU General Public License \(GPL\)](#). If you have any questions regarding the legality of using R in any particular situation you should bring it up with your legal counsel. We are in no position to offer legal advice.

It is the opinion of the R Core Team that one can use R for commercial purposes (e.g., in business or in consulting). The GPL, like all Open Source licenses, permits all and any use of the package. It only restricts distribution of R or of other programs containing code from R. This is made clear in clause 6 (“No Discrimination Against Fields of Endeavor”) of the [Open Source Definition](#):

The license must not restrict anyone from making use of the program in a specific field of endeavor. For example, it may not restrict the program from being used in a business, or from being used for genetic research.

It is also explicitly stated in clause 0 of the GPL, which says in part

Activities other than copying, distribution and modification are not covered by this License; they are outside its scope. The act of running the Program is not restricted, and the output from the Program is covered only if its contents constitute a work based on the Program.

Most add-on packages, including all recommended ones, also explicitly allow commercial use in this way. A few packages are restricted to “non-commercial use”; you should contact the author to clarify whether these may be used or seek the advice of your legal counsel.

None of the discussion in this section constitutes legal advice. The R Core Team does not provide legal advice under any circumstances.

## 2.12 Why is R named R?

The name is partly based on the (first) names of the first two R authors (Robert Gentleman and Ross Ihaka), and partly a play on the name of the Bell Labs language ‘S’ (see [Section 3.1 \[What is S?\]](#), page 10).

## 2.13 What is the R Foundation?

The R Foundation is a not for profit organization working in the public interest. It was founded by the members of the R Core Team in order to provide support for the R project and other innovations in statistical computing, provide a reference point for individuals, institutions or commercial enterprises that want to support or interact with the R development community, and to hold and administer the copyright of R software and documentation. See <http://www.R-project.org/foundation/> for more information.

## 3 R and S

### 3.1 What is S?

S is a very high level language and an environment for data analysis and graphics. In 1998, the Association for Computing Machinery (ACM) presented its Software System Award to John M. Chambers, the principal designer of S, for

the S system, which has forever altered the way people analyze, visualize, and manipulate data . . .

S is an elegant, widely accepted, and enduring software system, with conceptual integrity, thanks to the insight, taste, and effort of John Chambers.

The evolution of the S language is characterized by four books by John Chambers and coauthors, which are also the primary references for S.

- Richard A. Becker and John M. Chambers (1984), “S. An Interactive Environment for Data Analysis and Graphics,” Monterey: Wadsworth and Brooks/Cole.

This is also referred to as the “*Brown Book*”, and of historical interest only.

- Richard A. Becker, John M. Chambers and Allan R. Wilks (1988), “The New S Language,” London: Chapman & Hall.

This book is often called the “*Blue Book*”, and introduced what is now known as S version 2.

- John M. Chambers and Trevor J. Hastie (1992), “Statistical Models in S,” London: Chapman & Hall.

This is also called the “*White Book*”, and introduced S version 3, which added structures to facilitate statistical modeling in S.

- John M. Chambers (1998), “Programming with Data,” New York: Springer, ISBN 0-387-98503-4 (<http://cm.bell-labs.com/cm/ms/departments/sia/Sbook/>).

This “*Green Book*” describes version 4 of S, a major revision of S designed by John Chambers to improve its usefulness at every stage of the programming process.

See <http://cm.bell-labs.com/cm/ms/departments/sia/S/history.html> for further information on “Stages in the Evolution of S”.

There is a huge amount of user-contributed code for S, available at the [S Repository](#) at CMU.

### 3.2 What is S-PLUS?

S-PLUS is a value-added version of S sold by Insightful Corporation. Based on the S language, S-PLUS provides functionality in a wide variety of areas, including robust regression, modern non-parametric regression, time series, survival analysis, multivariate analysis, classical statistical tests, quality control, and graphics drivers. Add-on modules add additional capabilities.

See the [Insightful S-PLUS page](#) for further information.

### 3.3 What are the differences between R and S?

We can regard S as a language with three current implementations or “engines”, the “old S engine” (S version 3; S-PLUS 3.x and 4.x), the “new S engine” (S version 4; S-PLUS 5.x and above), and R. Given this understanding, asking for “the differences between R and S” really amounts to asking for the specifics of the R implementation of the S language, i.e., the difference between the R and S *engines*.

For the remainder of this section, “S” refers to the S engines and not the S language.

#### 3.3.1 Lexical scoping

Contrary to other implementations of the S language, R has adopted an evaluation model in which nested function definitions are lexically scoped. This is analogous to the evaluation model in Scheme.

This difference becomes manifest when *free* variables occur in a function. Free variables are those which are neither formal parameters (occurring in the argument list of the function) nor local variables (created by assigning to them in the body of the function). In S, the values of free variables are determined by a set of global variables (similar to C, there is only local and global scope). In R, they are determined by the environment in which the function was created.

Consider the following function:

```
cube <- function(n) {
  sq <- function() n * n
  n * sq()
}
```

Under S, `sq()` does not “know” about the variable `n` unless it is defined globally:

```
S> cube(2)
Error in sq(): Object "n" not found
Dumped
S> n <- 3
S> cube(2)
[1] 18
```

In R, the “environment” created when `cube()` was invoked is also looked in:

```
R> cube(2)
[1] 8
```

As a more “interesting” real-world problem, suppose you want to write a function which returns the density function of the  $r$ -th order statistic from a sample of size  $n$  from a (continuous) distribution. For simplicity, we shall use both the cdf and pdf of the distribution as explicit arguments. (Example compiled from various postings by Luke Tierney.)

The S-PLUS documentation for `call()` basically suggests the following:



```
dorder <- function(n, r, pfun, dfun) {
  f <- function(x) NULL
  con <- round(exp(lgamma(n + 1) - lgamma(r) - lgamma(n - r + 1)))
  PF <- call(substitute(pfun), as.name("x"))
  DF <- call(substitute(dfun), as.name("x"))
  f[[length(f)]] <-
    call("*", con,
          call("*", call("^", PF, r - 1),
                call("*", call("^", call("-", 1, PF), n - r),
                      DF)))
  f
}
```

Rather tricky, isn't it? The code uses the fact that in S, functions are just lists of special mode with the function body as the last argument, and hence does not work in R (one could make the idea work, though).

A version which makes heavy use of `substitute()` and seems to work under both S and R is

```
dorder <- function(n, r, pfun, dfun) {
  con <- round(exp(lgamma(n + 1) - lgamma(r) - lgamma(n - r + 1)))
  eval(substitute(function(x) K * PF(x)^a * (1 - PF(x))^b * DF(x),
                    list(PF = substitute(pfun), DF = substitute(dfun),
                        a = r - 1, b = n - r, K = con)))
}
```

(the `eval()` is not needed in S).

However, in R there is a much easier solution:

```
dorder <- function(n, r, pfun, dfun) {
  con <- round(exp(lgamma(n + 1) - lgamma(r) - lgamma(n - r + 1)))
  function(x) {
    con * pfun(x)^(r - 1) * (1 - pfun(x))^(n - r) * dfun(x)
  }
}
```

This seems to be the “natural” implementation, and it works because the free variables in the returned function can be looked up in the defining environment (this is lexical scope).

Note that what you really need is the function *closure*, i.e., the body along with all variable bindings needed for evaluating it. Since in the above version, the free variables in the value function are not modified, you can actually use it in S as well if you abstract out the closure operation into a function `MC()` (for “make closure”):

```
dorder <- function(n, r, pfun, dfun) {
  con <- round(exp(lgamma(n + 1) - lgamma(r) - lgamma(n - r + 1)))
  MC(function(x) {
    con * pfun(x)^(r - 1) * (1 - pfun(x))^(n - r) * dfun(x)
  },
    list(con = con, pfun = pfun, dfun = dfun, r = r, n = n))
}
```



Given the appropriate definitions of the closure operator, this works in both R and S, and is much “cleaner” than a substitute/eval solution (or one which overrules the default scoping rules by using explicit access to evaluation frames, as is of course possible in both R and S).

For R, `MC()` simply is

```
MC <- function(f, env) f
```

(lexical scope!), a version for S is

```
MC <- function(f, env = NULL) {
  env <- as.list(env)
  if (mode(f) != "function")
    stop(paste("not a function:", f))
  if (length(env) > 0 && any(names(env) == ""))
    stop(paste("not all arguments are named:", env))
  fargs <- if(length(f) > 1) f[1:(length(f) - 1)] else NULL
  fargs <- c(fargs, env)
  if (any(duplicated(names(fargs))))
    stop(paste("duplicated arguments:", paste(names(fargs)),
      collapse = ", "))
  fbody <- f[length(f)]
  cf <- c(fargs, fbody)
  mode(cf) <- "function"
  return(cf)
}
```

Similarly, most optimization (or zero-finding) routines need some arguments to be optimized over and have other parameters that depend on the data but are fixed with respect to optimization. With R scoping rules, this is a trivial problem; simply make up the function with the required definitions in the same environment and scoping takes care of it. With S, one solution is to add an extra parameter to the function and to the optimizer to pass in these extras, which however can only work if the optimizer supports this.

Nested lexically scoped functions allow using function closures and maintaining local state. A simple example (taken from Abelson and Sussman) is obtained by typing `demo("scoping")` at the R prompt. Further information is provided in the standard R reference “R: A Language for Data Analysis and Graphics” (see [Section 2.7 \[What documentation exists for R?\]](#), page 5) and in Robert Gentleman and Ross Ihaka (2000), “Lexical Scope and Statistical Computing”, *Journal of Computational and Graphical Statistics*, **9**, 491–508.

Nested lexically scoped functions also imply a further major difference. Whereas S stores all objects as separate files in a directory somewhere (usually ‘.Data’ under the current directory), R does not. All objects in R are stored internally. When R is started up it grabs a piece of memory and uses it to store the objects. R performs its own memory management of this piece of memory, growing and shrinking its size as needed. Having everything in memory is necessary because it is not really possible to externally maintain all relevant “environments” of symbol/value pairs. This difference also seems to make R *faster* than S.

The down side is that if R crashes you will lose all the work for the current session. Saving and restoring the memory “images” (the functions and data stored in R’s internal memory at any time) can be a bit slow, especially if they are big. In S this does not happen, because everything is saved in disk files and if you crash nothing is likely to happen to them. (In fact, one might conjecture that the S developers felt that the price of changing their approach to persistent storage just to accommodate lexical scope was far too expensive.) Hence, when doing important work, you might consider saving often (see [Section 7.2 \[How can I save my workspace?\]](#), page 52) to safeguard against possible crashes. Other possibilities are logging your sessions, or have your R commands stored in text files which can be read in using `source()`.

**Note:** If you run R from within Emacs (see [Chapter 6 \[R and Emacs\]](#), page 50), you can save the contents of the interaction buffer to a file and conveniently manipulate it using `ess-transcript-mode`, as well as save source copies of all functions and data used.

### 3.3.2 Models

There are some differences in the modeling code, such as

- Whereas in S, you would use `lm(y ~ x^3)` to regress  $y$  on  $x^3$ , in R, you have to insulate powers of numeric vectors (using `I()`), i.e., you have to use `lm(y ~ I(x^3))`.
- The `glm` family objects are implemented differently in R and S. The same functionality is available but the components have different names.
- Option `na.action` is set to `"na.omit"` by default in R, but not set in S.
- Terms objects are stored differently. In S a terms object is an expression with attributes, in R it is a formula with attributes. The attributes have the same names but are mostly stored differently.
- Finally, in R `y~x+0` is an alternative to `y~x-1` for specifying a model with no intercept. Models with no parameters at all can be specified by `y~0`.

### 3.3.3 Others

Apart from lexical scoping and its implications, R follows the S language definition in the Blue and White Books as much as possible, and hence really is an “implementation” of S. There are some intentional differences where the behavior of S is considered “not clean”. In general, the rationale is that R should help you detect programming errors, while at the same time being as compatible as possible with S.

Some known differences are the following.

- In R, if `x` is a list, then `x[i] <- NULL` and `x[[i]] <- NULL` remove the specified elements from `x`. The first of these is incompatible with S, where it is a no-op. (Note that you can set elements to NULL using `x[i] <- list(NULL)`.)
- In S, the functions named `.First` and `.Last` in the `‘.Data’` directory can be used for customizing, as they are executed at the very beginning and end of a session, respectively.

In R, the startup mechanism is as follows. R first sources the system startup file `‘$R_HOME/library/base/R/Rprofile’`. Then, it searches for a site-wide startup profile unless the command line option `‘--no-site-file’` was given. The name of this file

is taken from the value of the `R_PROFILE` environment variable. If that variable is unset, the default is `'$R_HOME/etc/Rprofile.site'` (`'$R_HOME/etc/Rprofile'` in versions prior to 1.4.0). This code is loaded in package `base`. Then, unless `'--no-init-file'` was given, R searches for a file called `'.Rprofile'` in the current directory or in the user's home directory (in that order) and sources it into the user workspace. It then loads a saved image of the user workspace from `'.RData'` in case there is one (unless `'--no-restore'` was specified). If needed, the functions `.First()` and `.Last()` should be defined in the appropriate startup profiles.

- In R, `T` and `F` are just variables being set to `TRUE` and `FALSE`, respectively, but are not reserved words as in S and hence can be overwritten by the user. (This helps e.g. when you have factors with levels `"T"` or `"F"`.) Hence, when writing code you should always use `TRUE` and `FALSE`.
- In R, `dyn.load()` can only load *shared objects*, as created for example by R CMD SHLIB.
- In R, `attach()` currently only works for lists and data frames, but not for directories. (In fact, `attach()` also works for R data files created with `save()`, which is analogous to attaching directories in S.) Also, you cannot attach at position 1.
- Categories do not exist in R, and never will as they are deprecated now in S. Use factors instead.
- In R, `For()` loops are not necessary and hence not supported.
- In R, `assign()` uses the argument `'envir='` rather than `'where='` as in S.
- The random number generators are different, and the seeds have different length.
- R passes integer objects to C as `int *` rather than `long *` as in S.
- R has no single precision storage mode. However, as of version 0.65.1, there is a single precision interface to C/FORTRAN subroutines.
- By default, `ls()` returns the names of the objects in the current (under R) and global (under S) environment, respectively. For example, given

```
x <- 1; fun <- function() {y <- 1; ls()}
```

then `fun()` returns `"y"` in R and `"x"` (together with the rest of the global environment) in S.

- R allows for zero-extent matrices (and arrays, i.e., some elements of the `dim` attribute vector can be 0). This has been determined a useful feature as it helps reducing the need for special-case tests for empty subsets. For example, if `x` is a matrix, `x[, FALSE]` is not `NULL` but a “matrix” with 0 columns. Hence, such objects need to be tested for by checking whether their `length()` is zero (which works in both R and S), and not using `is.null()`.
- Named vectors are considered vectors in R but not in S (e.g., `is.vector(c(a = 1:3))` returns `FALSE` in S and `TRUE` in R).
- Data frames are not considered as matrices in R (i.e., if `DF` is a data frame, then `is.matrix(DF)` returns `FALSE` in R and `TRUE` in S).
- R by default uses treatment contrasts in the unordered case, whereas S uses the Helmert ones. This is a deliberate difference reflecting the opinion that treatment contrasts are more natural.

- In R, the argument of a replacement function which corresponds to the right hand side must be named ‘value’. E.g., `f(a) <- b` is evaluated as `a <- "f<-"(a, value = b)`. S always takes the last argument, irrespective of its name.
- In S, `substitute()` searches for names for substitution in the given expression in three places: the actual and the default arguments of the matching call, and the local frame (in that order). R looks in the local frame only, with the special rule to use a “promise” if a variable is not evaluated. Since the local frame is initialized with the actual arguments or the default expressions, this is usually equivalent to S, until assignment takes place.
- In S, the index variable in a `for()` loop is local to the inside of the loop. In R it is local to the environment where the `for()` statement is executed.
- In S, `tapply(simplify=TRUE)` returns a vector where R returns a one-dimensional array (which can have named dimnames).
- In S(-PLUS) the C locale is used, whereas in R the current operating system locale is used for determining which characters are alphanumeric and how they are sorted. This affects the set of valid names for R objects (for example accented chars may be allowed in R) and ordering in sorts and comparisons (such as whether `"aA" < "Bb"` is true or false). From version 1.2.0 the locale can be (re-)set in R by the `Sys.setlocale()` function.
- In S, `missing(arg)` remains TRUE if `arg` is subsequently modified; in R it doesn’t.
- From R version 1.3.0, `data.frame` strips `I()` when creating (column) names.
- In R, the string "NA" is not treated as a missing value in a character variable. Use `as.character(NA)` to create a missing character value.
- R disallows repeated formal arguments in function calls.
- In S, `dump()`, `dput()` and `deparse()` are essentially different interfaces to the same code. In R from version 2.0.0, this is only true if the same `control` argument is used, but by default it is not. By default `dump()` tries to write code that will evaluate to reproduce the object, whereas `dput()` and `deparse()` default to options for producing deparsed code that is readable.

There are also differences which are not intentional, and result from missing or incorrect code in R. The developers would appreciate hearing about any deficiencies you may find (in a written report fully documenting the difference as you see it). Of course, it would be useful if you were to implement the change yourself and make sure it works.

### 3.4 Is there anything R can do that S-PLUS cannot?

Since almost anything you can do in R has source code that you could port to S-PLUS with little effort there will never be much you can do in R that you couldn’t do in S-PLUS if you wanted to. (Note that using lexical scoping may simplify matters considerably, though.)

R offers several graphics features that S-PLUS does not, such as finer handling of line types, more convenient color handling (via palettes), gamma correction for color, and, most importantly, mathematical annotation in plot texts, via input expressions reminiscent of  $\text{\TeX}$  constructs. See the help page for `plotmath`, which features an impressive on-line example. More details can be found in Paul Murrell and Ross Ihaka (2000), “An Approach

to Providing Mathematical Annotation in Plots”, *Journal of Computational and Graphical Statistics*, **9**, 582–599.

### 3.5 What is R-plus?

There is no such thing.

## 4 R Web Interfaces

**Rweb** is developed and maintained by **Jeff Banfield**. The **Rweb Home Page** provides access to all three versions of Rweb—a simple text entry form that returns output and graphs, a more sophisticated Javascript version that provides a multiple window environment, and a set of point and click modules that are useful for introductory statistics courses and require no knowledge of the R language. All of the Rweb versions can analyze Web accessible datasets if a URL is provided.

The paper “Rweb: Web-based Statistical Analysis”, providing a detailed explanation of the different versions of Rweb and an overview of how Rweb works, was published in the Journal of Statistical Software (<http://www.stat.ucla.edu/journals/jss/v04/i01/>).

**Ulf Bartel** is working on **R-Online**, a simple on-line programming environment for R which intends to make the first steps in statistical programming with R (especially with time series) as easy as possible. There is no need for a local installation since the only requirement for the user is a JavaScript capable browser. See <http://osvisions.com/r-online/> for more information.

**David Firth** has written **CGIwithR**, an R add-on package available from CRAN. It provides some simple extensions to R to facilitate running R scripts through the CGI interface to a web server. It is easily installed using Apache under Linux and in principle should run on any platform that supports R and a web server provided that the installer has the necessary security permissions.

**Rcgi** is a CGI WWW interface to R by **MJ Ray**. It had the ability to use “embedded code”: you could mix user input and code, allowing the HTML author to do anything from load in data sets to enter most of the commands for users without writing CGI scripts. Graphical output was possible in PostScript or GIF formats and the executed code was presented to the user for revision. However, it is not clear if the project is still active. Currently, a modified version of **Rcgi** by **Mai Zhou** (actually, two versions: one with (bitmap) graphics and one without) as well as the original code are available from <http://www.ms.uky.edu/~statweb>.

## 5 R Add-On Packages

### 5.1 Which add-on packages exist for R?

#### 5.1.1 Add-on packages in R

The R distribution comes with the following packages:

<b>base</b>	Base R functions (and datasets before R 2.0.0).
<b>datasets</b>	Base R datasets (added in R 2.0.0).
<b>grDevices</b>	Graphics devices for base and grid graphics (added in R 2.0.0).
<b>graphics</b>	R functions for base graphics.
<b>grid</b>	A rewrite of the graphics layout capabilities, plus some support for interaction.
<b>methods</b>	Formally defined methods and classes for R objects, plus other programming tools, as described in the Green Book.
<b>splines</b>	Regression spline functions and classes.
<b>stats</b>	R statistical functions.
<b>stats4</b>	Statistical functions using S4 classes.
<b>tcltk</b>	Interface and language bindings to Tcl/Tk GUI elements.
<b>tools</b>	Tools for package development and administration.
<b>utils</b>	R utility functions.

These “base packages” were substantially reorganized in R 1.9.0. The former **base** was split into the four packages **base**, **graphics**, **stats**, and **utils**. Packages **ctest**, **eda**, **modreg**, **mva**, **nls**, **stepfun** and **ts** were merged into **stats**, package **lqs** returned to the recommended package **MASS**, and package **mle** moved to **stats4**.

#### 5.1.2 Add-on packages from CRAN

The following packages are available from the CRAN ‘**src/contrib**’ area. (Packages denoted as *Recommended* are to be included in all binary distributions of R.)

**AlgDesign** Algorithmic experimental designs. Calculates exact and approximate theory experimental designs for D, A, and I criteria.

**AnalyzefMRI**

Functions for I/O, visualisation and analysis of functional Magnetic Resonance Imaging (fMRI) datasets stored in the ANALYZE format.

**Bhat** Functions for general likelihood exploration (MLE, MCMC, CIs).

**BradleyTerry**

Specify and fit the Bradley-Terry model and structured versions.

**BsMD** Bayes screening and model discrimination follow-up designs.

**CDNmoney**

Components of Canadian monetary aggregates.

<b>CGIwithR</b>	Facilities for the use of R to write CGI scripts.
<b>CircStats</b>	Circular Statistics, from “Topics in Circular Statistics” by S. Rao Jammalamadaka and A. SenGupta, 2001, World Scientific.
<b>CoCo</b>	Graphical modeling for contingency tables using CoCo.
<b>CoCoAn</b>	Constrained Correspondence Analysis.
<b>DAAG</b>	Various data sets used in examples and exercises in “Data Analysis and Graphics Using R” by John H. Maindonald and W. John Brown, 2003.
<b>DBI</b>	A common database interface (DBI) class and method definitions. All classes in this package are virtual and need to be extended by the various DBMS implementations.
<b>DCluster</b>	A set of functions for the detection of spatial clusters of diseases using count data.
<b>Davies</b>	Functions for the Davies quantile function and the Generalized Lambda distribution.
<b>Design</b>	Regression modeling, testing, estimation, validation, graphics, prediction, and typesetting by storing enhanced model design attributes in the fit. Design is a collection of about 180 functions that assist and streamline modeling, especially for biostatistical and epidemiologic applications. It also contains new functions for binary and ordinal logistic regression models and the Buckley-James multiple regression model for right-censored responses, and implements penalized maximum likelihood estimation for logistic and ordinary linear models. Design works with almost any regression model, but it was especially written to work with logistic regression, Cox regression, accelerated failure time models, ordinary linear models, and the Buckley-James model.
<b>Devore5</b>	Data sets and sample analyses from “Probability and Statistics for Engineering and the Sciences (5th ed)” by Jay L. Devore, 2000, Duxbury.
<b>Devore6</b>	Data sets and sample analyses from “Probability and Statistics for Engineering and the Sciences (6th ed)” by Jay L. Devore, 2003, Duxbury.
<b>EMV</b>	Estimation of missing values in a matrix by a $k$ -th nearest neighbors algorithm.
<b>GRASS</b>	An interface between the GRASS geographical information system and R, based on starting R from within the GRASS environment and chosen LOCATION_NAME and MAPSET. Wrapper and helper functions are provided for a range of R functions to match the interface metadata structures.
<b>GenKern</b>	Functions for generating and manipulating generalised binned kernel density estimates.
<b>GeneTS</b>	A package for analysing multiple gene expression time series data. Currently, implements methods for cell cycle analysis and for inferring large sparse graphical Gaussian models.
<b>HI</b>	Simulation from distributions supported by nested hyperplanes.



**HighProbability**

Estimation of the alternative hypotheses having frequentist or Bayesian probabilities at least as great as a specified threshold, given a list of  $p$ -values.

**Hmisc**

Functions useful for data analysis, high-level graphics, utility operations, functions for computing sample size and power, importing datasets, imputing missing values, advanced table making, variable clustering, character string manipulation, conversion of S objects to LaTeX code, recoding variables, and bootstrap repeated measures analysis.

**HyperbolicDist**

Basic functions for the hyperbolic distribution: probability density function, distribution function, quantile function, a routine for generating observations from the hyperbolic, and a function for fitting the hyperbolic distribution to data.

**ISwR**

Data sets for “Introductory Statistics with R” by Peter Dalgaard, 2002, Springer.

**Icens**

Functions for computing the NPMLE for censored and truncated data.

**KMsurv**

Data sets and functions for “Survival Analysis, Techniques for Censored and Truncated Data” by Klein and Moeschberger, 1997, Springer.

**KernSmooth**

Functions for kernel smoothing (and density estimation) corresponding to the book “Kernel Smoothing” by M. P. Wand and M. C. Jones, 1995. *Recommended.*

**MASS**

Functions and datasets from the main package of Venables and Ripley, “Modern Applied Statistics with S”. Contained in the ‘VR’ bundle. *Recommended.*

**MCMCpack**

Markov chain Monte Carlo (MCMC) package: functions for posterior simulation for a number of statistical models.

**MNP**

Fitting Bayesian Multinomial Probit models via Markov chain Monte Carlo. Along with the standard Multinomial Probit model, it can also fit models with different choice sets for each observation and complete or partial ordering of all the available alternatives.

**MPV**

Data sets from the book “Introduction to Linear Regression Analysis” by D. C. Montgomery, E. A. Peck, and C. G. Vining, 2001, John Wiley and Sons.

**Malmig**

An implementation of Malecot migration model together with a number of related functions.

**Matching**

Multivariate and propensity score matching with formal tests of balance.

**Matrix**

A Matrix package.

**NADA**

Methods described in “Nondetects And Data Analysis: Statistics for Censored Environmental Data” by Dennis R. Helsel, 2004, John Wiley and Sons.

**NISTnls**

A set of test nonlinear least squares examples from NIST, the U.S. National Institute for Standards and Technology.

**Oarray** Arrays with arbitrary offsets.

**PBSmapping**

Software evolved from fisheries research conducted at the Pacific Biological Station (PBS) in Nanaimo, British Columbia, Canada. Draws maps and implements other GIS procedures.

**PHYLOGR**

Manipulation and analysis of phylogenetically simulated data sets (as obtained from PDSIMUL in package PDAP) and phylogenetically-based analyses using GLS.

**PTak**

A multiway method to decompose a tensor (array) of any order, as a generalisation of SVD also supporting non-identity metrics and penalisations. Also includes some other multiway methods.

**R2HTML** Functions for exporting R objects & graphics in an HTML document.

**R2WinBUGS**

Running WinBUGS from R: call a BUGS model, summarize inferences and convergence in a table and graph, and save the simulations in arrays for easy access in R.

**RArcInfo** Functions to import Arc/Info V7.x coverages and data.

**RColorBrewer**

ColorBrewer palettes for drawing nice maps shaded according to a variable.

**RCurl** Allows one to compose HTTP requests to fetch URIs, post forms, etc., and process the results returned by the Web server.

**RMySQL** An interface between R and the MySQL database system.

**RNetCDF** An interface to Unidata's NetCDF library functions (version 3) and furthermore access to Unidata's udunits calendar conversions.

**RODBC** An ODBC database interface.

**ROracle** Oracle Database Interface driver for R. Uses the ProC/C++ embedded SQL.

**RQuantLib**

Provides access to (some) of the QuantLib functions from within R; currently limited to some Option pricing and analysis functions. The QuantLib project aims to provide a comprehensive software framework for quantitative finance.

**RSQLite** Database Interface R driver for SQLite. Embeds the SQLite database engine in R.

**RScaLAPACK**

An interface to ScaLAPACK functions from R.

**RSvgDevice**

A graphics device for R that uses the new w3.org XML standard for Scalable Vector Graphics.

**RUnit** Functions implementing a standard Unit Testing framework, with additional code inspection and report generation tools.

**RadioSonde**

A collection of programs for reading and plotting SKEW-T,log p diagrams and wind profiles for data collected by radiosondes (the typical weather balloon-borne instrument).

**RandomFields**

Creating random fields using various methods.

**Rcmdr**

A platform-independent basic-statistics GUI (graphical user interface) for R, based on the **tcltk** package.

**Rmpi**

An interface (wrapper) to MPI (Message-Passing Interface) APIs. It also provides an interactive R slave environment in which distributed statistical computing can be carried out.

**Rstem**

Interface to Snowball implementation of Porter's word stemming algorithm.

**Rwave**

An environment for the time-frequency analysis of 1-D signals (and especially for the wavelet and Gabor transforms of noisy signals), based on the book "Practical Time-Frequency Analysis: Gabor and Wavelet Transforms with an Implementation in S" by Rene Carmona, Wen L. Hwang and Bruno Torresani, 1998, Academic Press.

**SASmixed**

Data sets and sample linear mixed effects analyses corresponding to the examples in "SAS System for Mixed Models" by R. C. Littell, G. A. Milliken, W. W. Stroup and R. D. Wolfinger, 1996, SAS Institute.

**SIN**

A SINful approach to selection of Gaussian Graphical Markov Models.

**SenSrivastava**

Collection of datasets from "Regression Analysis, Theory, Methods and Applications" by A. Sen and M. Srivastava, 1990, Springer.

**SoPhy**

Soil Physics Tools: simulation of water flux and solute transport in soil.

**SparseLogReg**

Sparse logistic regression.

**SparseM**

Basic linear algebra for sparse matrices.

**StatDataML**

Read and write StatDataML.

**SuppDists**

Ten distributions supplementing those built into R (Inverse Gauss, Kruskal-Wallis, Kendall's Tau, Friedman's chi squared, Spearman's rho, maximum F ratio, the Pearson product moment correlation coefficient, Johnson distributions, normal scores and generalized hypergeometric distributions).

**UNF**

Tools for creating universal numeric fingerprints for data.

**UsingR**

Data sets to accompany the textbook "Using R for Introductory Statistics" by J. Verzani, 2005, Chapman & Hall/CRC.

**VLMC**

Functions, classes & methods for estimation, prediction, and simulation (bootstrap) of VLMC (Variable Length Markov Chain) models.

**VaR**

Methods for calculation of Value at Risk (VaR).

<b>XML</b>	Facilities for reading XML documents and DTDs.
<b>Zelig</b>	Everyone's statistical software: an easy-to-use program that can estimate, and help interpret the results of, an enormous range of statistical models.
<b>abind</b>	Combine multi-dimensional arrays.
<b>accuracy</b>	A suite of tools designed to test and improve the accuracy of statistical computation.
<b>acepack</b>	ACE (Alternating Conditional Expectations) and AVAS (Additivity and VAriance Stabilization for regression) methods for selecting regression transformations.
<b>adapt</b>	Adaptive quadrature in up to 20 dimensions.
<b>ade4</b>	Multivariate data analysis and graphical display.
<b>adehabitat</b>	A collection of tools for the analysis of habitat selection by animals.
<b>agce</b>	Analysis of growth curve experiments.
<b>akima</b>	Linear or cubic spline interpolation for irregularly gridded data.
<b>amap</b>	Another Multidimensional Analysis Package.
<b>anm</b>	Analog model for statistical/empirical downscaling.
<b>ape</b>	Analyses of Phylogenetics and Evolution, providing functions for reading and plotting phylogenetic trees in parenthetic format (standard Newick format), analyses of comparative data in a phylogenetic framework, analyses of diversification and macroevolution, computing distances from allelic and nucleotide data, reading nucleotide sequences from GenBank via internet, and several tools such as Mantel's test, computation of minimum spanning tree, or the population parameter theta based on various approaches.
<b>ash</b>	David Scott's ASH routines for 1D and 2D density estimation.
<b>assist</b>	A suite of functions implementing smoothing splines.
<b>asypow</b>	A set of routines that calculate power and related quantities utilizing asymptotic likelihood ratio methods.
<b>aws</b>	Functions to perform adaptive weights smoothing.
<b>bayesSurv</b>	Bayesian survival regression with flexible error and (later on also random effects) distributions.
<b>bayesmix</b>	Bayesian mixture models of univariate Gaussian distributions using JAGS.
<b>betareg</b>	Beta regression for modeling rates and proportions.
<b>bim</b>	Bayesian interval mapping diagnostics: functions to interpret QTLCart and Bmapqtl samples.
<b>bindata</b>	Generation of correlated artificial binary data.
<b>blighty</b>	Function for drawing the coastline of the United Kingdom.

<b>boa</b>	Bayesian Output Analysis Program for MCMC.
<b>boolean</b>	Boolean logit and probit: a procedure for testing Boolean hypotheses.
<b>boot</b>	Functions and datasets for bootstrapping from the book “Bootstrap Methods and Their Applications” by A. C. Davison and D. V. Hinkley, 1997, Cambridge University Press. <i>Recommended.</i>
<b>bqtl</b>	QTL mapping toolkit for inbred crosses and recombinant inbred lines. Includes maximum likelihood and Bayesian tools.
<b>brlr</b>	Bias-reduced logistic regression: fits logistic regression models by maximum penalized likelihood.
<b>car</b>	Companion to Applied Regression, containing functions for applied regression, linear models, and generalized linear models, with an emphasis on regression diagnostics, particularly graphical diagnostic methods.
<b>cat</b>	Analysis of categorical-variable datasets with missing values.
<b>catspec</b>	Special models for categorical variables.
<b>cclust</b>	Convex clustering methods, including $k$ -means algorithm, on-line update algorithm (Hard Competitive Learning) and Neural Gas algorithm (Soft Competitive Learning) and calculation of several indexes for finding the number of clusters in a data set.
<b>cfa</b>	Analysis of configuration frequencies.
<b>chplot</b>	Augmented convex hull plots: informative and nice plots for grouped bivariate data.
<b>chron</b>	A package for working with chronological objects (times and dates).
<b>circular</b>	Circular statistics, from “Topics in Circular Statistics” by Rao Jammalamadaka and A. SenGupta, 2001, World Scientific.
<b>clac</b>	Clust Along Chromosomes, a method to call gains/losses in CGH array data.
<b>class</b>	Functions for classification ( $k$ -nearest neighbor and LVQ). Contained in the ‘VR’ bundle. <i>Recommended.</i>
<b>classPP</b>	Projection Pursuit for supervised classification.
<b>clim.pact</b>	Climate analysis and downscaling for monthly and daily data.
<b>clines</b>	Calculates Contour Lines.
<b>cluster</b>	Functions for cluster analysis. <i>Recommended.</i>
<b>cmprsk</b>	Estimation, testing and regression modeling of subdistribution functions in competing risks.
<b>cobs</b>	Constrained B-splines: qualitatively constrained (regression) smoothing via linear programming.
<b>coda</b>	Output analysis and diagnostics for Markov Chain Monte Carlo (MCMC) simulations.

<b>combinat</b>	Combinatorics utilities.
<b>concord</b>	Measures of concordance and reliability.
<b>conf.design</b>	A series of simple tools for constructing and manipulating confounded and fractional factorial designs.
<b>covRobust</b>	Robust covariance estimation via nearest neighbor cleaning.
<b>cramer</b>	Routine for the multivariate nonparametric Cramer test.
<b>crossdes</b>	Functions for the construction and randomization of balanced carryover balanced designs, to check given designs for balance, and for simulation studies on the validity of two randomization procedures.
<b>cyclones</b>	Cyclone identification.
<b>date</b>	Functions for dealing with dates. The most useful of them accepts a vector of input dates in any of the forms ‘8/30/53’, ‘30Aug53’, ‘30 August 1953’, . . . , ‘August 30 53’, or any mixture of these.
<b>dblcens</b>	Calculates the NPMLE of the survival distribution for doubly censored data.
<b>deal</b>	Bayesian networks with continuous and/or discrete variables can be learned and compared from data.
<b>debug</b>	Debugger for R functions, with code display, graceful error recovery, line-numbered conditional breakpoints, access to exit code, flow control, and full keyboard input.
<b>deldir</b>	Calculates the Delaunay triangulation and the Dirichlet or Voronoi tessellation (with respect to the entire plane) of a planar point set.
<b>diamonds</b>	Functions for illustrating aperture-4 diamond partitions in the plane, or on the surface of an octahedron or icosahedron, for use as analysis or sampling grids.
<b>dichromat</b>	Color schemes for dichromats: collapse red-green distinctions to simulate the effects of colour-blindness.
<b>digest</b>	Two functions for the creation of “hash” digests of arbitrary R objects using the md5 and sha-1 algorithms permitting easy comparison of R language objects.
<b>diptest</b>	Compute Hartigan’s dip test statistic for unimodality.
<b>dispmod</b>	Functions for modelling dispersion in GLMs.
<b>distr</b>	An object orientated implementation of distributions and some additional functionality.
<b>dr</b>	Functions, methods, and datasets for fitting dimension reduction regression, including pHd and inverse regression methods SIR and SAVE.
<b>drfit</b>	Dose-response data evaluation.
<b>dse</b>	Dynamic System Estimation, a multivariate time series package. Contains <b>dse1</b> (the base system, including multivariate ARMA and state space models), <b>dse2</b> (extensions for evaluating estimation techniques, forecasting, and for evaluating

forecasting model), **tframe** (functions for writing code that is independent of the representation of time). and **setRNG** (a mechanism for generating the same random numbers in S and R).

### **dynamicGraph**

Interactive graphical tool for manipulating graphs.

**e1071** Miscellaneous functions used at the Department of Statistics at TU Wien (E1071), including moments, short-time Fourier transforms, Independent Component Analysis, Latent Class Analysis, support vector machines, and fuzzy clustering, shortest path computation, bagged clustering, and some more.

**eba** Fitting and testing probabilistic choice models, especially the BTL, elimination-by-aspects (EBA), and preference tree (Pretree) models.

### **ebayesthresh**

Empirical Bayes thresholding and related methods.

**edci** Edge Detection and Clustering in Images.

**effects** Graphical and tabular effect displays, e.g., of interactions, for linear and generalised linear models.

**eha** A package for survival and event history analysis.

**ellipse** Package for drawing ellipses and ellipse-like confidence regions.

**emme2** Functions to read from and write to an EMME/2 databank.

**emplik** Empirical likelihood ratio for means/quantiles/hazards from possibly right censored data.

**energy** E-statistics (energy) tests for comparing distributions: multivariate normality, Poisson test, multivariate  $k$ -sample test for equal distributions, hierarchical clustering by e-distances.

**epitools** Basic tools for applied epidemiology.

**epsi** Edge Preserving Smoothing for Images.

**evd** Functions for extreme value distributions. Extends simulation, distribution, quantile and density functions to univariate, bivariate and (for simulation) multivariate parametric extreme value distributions, and provides fitting functions which calculate maximum likelihood estimates for univariate and bivariate models.

**evdbayes** Functions for the bayesian analysis of extreme value models, using MCMC methods.

**evir** Extreme Values in R: Functions for extreme value theory, which may be divided into the following groups; exploratory data analysis, block maxima, peaks over thresholds (univariate and bivariate), point processes, gev/gpd distributions.

### **exactLoglinTest**

Monte Carlo exact tests for log-linear models.

**exactRankTests**

Computes exact  $p$ -values and quantiles using an implementation of the Streitberg/Roehmel shift algorithm.

**fBasics**

The Rmetrics module for “Markets, basic statistics, and date and time management”. Rmetrics is an environment and software collection for teaching financial engineering and computational finance (<http://www.Rmetrics.org/>).

**fExtremes**

The Rmetrics module for “Beyond the Sample, Dealing with Extreme Values”.

**fOptions**

The Rmetrics module for “The Valuation of Options”.

**fSeries**

The Rmetrics module for “The Dynamical Process Behind Financial Markets”.

**faraway**

Functions and datasets for books by Julian Faraway.

**fastICA**

Implementation of FastICA algorithm to perform Independent Component Analysis (ICA) and Projection Pursuit.

**fda**

Functional Data Analysis: analysis of data where the basic observation is a function of some sort.

**fdim**

Functions for calculating fractal dimension.

**fields**

A collection of programs for curve and function fitting with an emphasis on spatial data. The major methods implemented include cubic and thin plate splines, universal Kriging and Kriging for large data sets. The main feature is that any covariance function implemented in R can be used for spatial prediction.

**flexmix**

Flexible Mixture Modeling: a general framework for finite mixtures of regression models using the EM algorithm.

**foreign**

Functions for reading and writing data stored by statistical software like Minitab, S, SAS, SPSS, Stata, Systat, etc. *Recommended*.

**fork**

Functions for handling multiple processes: simple wrappers around the Unix process management API calls.

**fortunes**

R fortunes.

**forward**

Forward search approach to robust analysis in linear and generalized linear regression models.

**fpc**

Fixed point clusters, clusterwise regression and discriminant plots.

**fracdiff**

Maximum likelihood estimation of the parameters of a fractionally differenced ARIMA( $p, d, q$ ) model (Haslett and Raftery, Applied Statistics, 1989).

**ftnonpar**

Features and strings for nonparametric regression.

**g.data**

Create and maintain delayed-data packages (DDP's).

**gRbase**

A package for graphical modelling in R. Defines S4 classes for graphical meta data and graphical models, and illustrates how hierarchical log-linear models may be implemented and combined with **dynamicGraph**.

**gafit**

Genetic algorithm for curve fitting.



<b>gam</b>	Functions for fitting and working with Generalized Additive Models, as described in chapter 7 of the White Book, and in “Generalized Additive Models” by T. Hastie and R. Tibshirani (1990).
<b>gap</b>	Genetic analysis package for both population and family data.
<b>gbm</b>	Generalized Boosted Regression Models: implements extensions to Freund and Schapire’s AdaBoost algorithm and J. Friedman’s gradient boosting machine. Includes regression methods for least squares, absolute loss, logistic, Poisson, Cox proportional hazards partial likelihood, and AdaBoost exponential loss.
<b>gclus</b>	Clustering Graphics. Orders panels in scatterplot matrices and parallel coordinate displays by some merit index.
<b>gee</b>	An implementation of the Liang/Zeger generalized estimating equation approach to GLMs for dependent data.
<b>geepack</b>	Generalized estimating equations solver for parameters in mean, scale, and correlation structures, through mean link, scale link, and correlation link. Can also handle clustered categorical responses.
<b>genetics</b>	Classes and methods for handling genetic data. Includes classes to represent genotypes and haplotypes at single markers up to multiple markers on multiple chromosomes, and functions for allele frequencies, flagging homo/heterozygotes, flagging carriers of certain alleles, computing disequilibrium, testing Hardy-Weinberg equilibrium, . . .
<b>geoR</b>	Functions to perform geostatistical data analysis including model-based methods.
<b>geoRglm</b>	Functions for inference in generalised linear spatial models.
<b>ggm</b>	Functions for defining directed acyclic graphs and undirected graphs, finding induced graphs and fitting Gaussian Markov models.
<b>gld</b>	Basic functions for the generalised (Tukey) lambda distribution.
<b>gllm</b>	Routines for log-linear models of incomplete contingency tables, including some latent class models via EM and Fisher scoring approaches.
<b>glmmML</b>	A Maximum Likelihood approach to generalized linear models with random intercept.
<b>gmp</b>	Arithmetic “without limitations” using the GNU Multiple Precision library.
<b>gpclib</b>	General polygon clipping routines for R based on Alan Murta’s C library.
<b>grasper</b>	Generalized Regression Analysis and Spatial Predictions for R.
<b>gregmisc</b>	Miscellaneous functions written/maintained by Gregory R. Warnes.
<b>gridBase</b>	Integration of base and grid graphics.
<b>gss</b>	A comprehensive package for structural multivariate function estimation using smoothing splines.

<b>gstat</b>	multivariable geostatistical modelling, prediction and simulation. Includes code for variogram modelling; simple, ordinary and universal point or block (co)kriging, sequential Gaussian or indicator (co)simulation, and map plotting functions.
<b>gtkDevice</b>	GTK graphics device driver that may be used independently of the R-GNOME interface and can be used to create R devices as embedded components in a GUI using a Gtk drawing area widget, e.g., using RGtk.
<b>hapassoc</b>	Likelihood inference of trait associations with SNP haplotypes and other attributes using the EM Algorithm.
<b>haplo.score</b>	Score tests for association of traits with haplotypes when linkage phase is ambiguous.
<b>haplo.stats</b>	Statistical analysis of haplotypes with traits and covariates when linkage phase is ambiguous.
<b>hdf5</b>	Interface to the NCSA HDF5 library.
<b>hett</b>	Functions for the fitting and summarizing of heteroscedastic t-regression.
<b>hier.part</b>	Hierarchical Partitioning: variance partition of a multivariate data set.
<b>hierfstat</b>	Estimation of hierarchical F-statistics from haploid or diploid genetic data with any numbers of levels in the hierarchy, and tests for the significance of each F and variance components.
<b>homals</b>	Homogeneity Analysis (HOMALS) package with optional Tcl/Tk interface.
<b>hopach</b>	Hierarchical Ordered Partitioning and Collapsing Hybrid (HOPACH).
<b>httpRequest</b>	Implements HTTP Request protocols (GET, POST, and multipart POST requests).
<b>hwde</b>	Models and tests for departure from Hardy-Weinberg equilibrium and independence between loci.
<b>ifs</b>	Iterated Function Systems distribution function estimator.
<b>impute</b>	Imputation for microarray data (currently KNN only).
<b>ineq</b>	Inequality, concentration and poverty measures, and Lorenz curves (empirical and theoretic).
<b>intcox</b>	Implementation of the Iterated Convex Minorant Algorithm for the Cox proportional hazard model for interval censored event data.
<b>ipred</b>	Improved predictive models by direct and indirect bootstrap aggregation in classification and regression as well as resampling based estimators of prediction error.
<b>ismev</b>	Functions to support the computations carried out in “An Introduction to Statistical Modeling of Extreme Values;” by S. Coles, 2001, Springer. The functions

	may be divided into the following groups; maxima/minima, order statistics, peaks over thresholds and point processes.
<b>its</b>	An S4 class for handling irregular time series.
<b>kernlab</b>	Kernel-based machine learning methods including support vector machines.
<b>kinship</b>	Mixed-effects Cox models, sparse matrices, and modeling data from large pedigrees.
<b>klaR</b>	Miscellaneous functions for classification and visualization developed at the Department of Statistics, University of Dortmund.
<b>knnTree</b>	Construct or predict with $k$ -nearest-neighbor classifiers, using cross-validation to select $k$ , choose variables (by forward or backwards selection), and choose scaling (from among no scaling, scaling each column by its SD, or scaling each column by its MAD). The finished classifier will consist of a classification tree with one such $k$ -nn classifier in each leaf.
<b>knncat</b>	Nearest-neighbor classification with categorical variables.
<b>kza</b>	Kolmogorov-Zurbenko Adaptive filter for locating change points in a time series.
<b>labstatR</b>	Functions for the book “Laboratorio di statistica con R” by S. M. Iacus and G. Masarotto, 2002, McGraw-Hill. Function names and documentation in Italian.
<b>lars</b>	Least Angle Regression, Lasso and Forward Stagewise: efficient procedures for fitting an entire lasso sequence with the cost of a single least squares fit.
<b>lasso2</b>	Routines and documentation for solving regression problems while imposing an L1 constraint on the estimates, based on the algorithm of Osborne et al. (1998).
<b>lattice</b>	Lattice graphics, an implementation of Trellis Graphics functions. <i>Recommended.</i>
<b>lazy</b>	Lazy learning for local regression.
<b>ldDesign</b>	Design of experiments for detection of linkage disequilibrium,
<b>leaps</b>	A package which performs an exhaustive search for the best subsets of a given set of potential regressors, using a branch-and-bound algorithm, and also performs searches using a number of less time-consuming techniques.
<b>lgtdl</b>	A set of methods for longitudinal data objects.
<b>limma</b>	LInear Models for MicroArray data.
<b>linprog</b>	Solve linear programming/linear optimization problems by using the simplex algorithm.
<b>lme4</b>	Fit linear and generalized linear mixed-effects models.
<b>lmeSplines</b>	Fit smoothing spline terms in Gaussian linear and nonlinear mixed-effects models.
<b>lmm</b>	Linear mixed models.

<b>lmtest</b>	A collection of tests on the assumptions of linear regression models from the book “The linear regression model under test” by W. Kraemer and H. Sonnberger, 1986, Physica.
<b>locfdr</b>	Computation of local false discovery rates.
<b>locfit</b>	Local Regression, likelihood and density estimation.
<b>logistf</b>	Firth’s bias reduced logistic regression approach with penalized profile likelihood based confidence intervals for parameter estimates.
<b>logspline</b>	Logspline density estimation.
<b>lokern</b>	Kernel regression smoothing with adaptive local or global plug-in bandwidth selection.
<b>lpSolve</b>	Functions that solve general linear/integer problems, assignment problems, and transportation problems via interfacing Lp_solve.
<b>lpbridge</b>	Local polynomial (ridge) regression.
<b>mAr</b>	Estimation of multivariate AR models through a computationally efficient step-wise least-squares algorithm.
<b>magic</b>	A variety of methods for creating magic squares of any order greater than 2, and various magic hypercubes.
<b>mapdata</b>	Supplement to package <b>maps</b> , providing the larger and/or higher-resolution databases.
<b>mapproj</b>	Map Projections: converts latitude/longitude into projected coordinates.
<b>maps</b>	Draw geographical maps. Projection code and larger maps are in separate packages.
<b>maptools</b>	Set of tools for manipulating and reading geographic data, in particular ESRI shapefiles.
<b>maptree</b>	Functions with example data for graphing and mapping models from hierarchical clustering and classification and regression trees.
<b>mathgraph</b>	Tools for constructing and manipulating objects from a class of directed and undirected graphs.
<b>maxstat</b>	Maximally selected rank and Gauss statistics with several p-value approximations.
<b>mcgibbsit</b>	Warnes and Raftery’s MCGibbsit MCMC diagnostic.
<b>mclust</b>	Model-based cluster analysis: the 2002 version of MCLUST.
<b>mda</b>	Code for mixture discriminant analysis (MDA), flexible discriminant analysis (FDA), penalized discriminant analysis (PDA), multivariate additive regression splines (MARS), adaptive back-fitting splines (BRUTO), and penalized regression.
<b>meanscore</b>	Mean Score method for missing covariate data in logistic regression models.

<b>merror</b>	Accuracy and precision of measurements.
<b>mfp</b>	Multiple Fractional Polynomials.
<b>mgcv</b>	Routines for GAMs and other generalized ridge regression problems with multiple smoothing parameter selection by GCV or UBRE. <i>Recommended.</i>
<b>mimR</b>	An R interface to MIM for graphical modeling in R.
<b>minpack.lm</b>	R interface for two functions from the MINPACK least squares optimization library, solving the nonlinear least squares problem by a modification of the Levenberg-Marquardt algorithm.
<b>mitools</b>	Tools to perform analyses and combine results from multiple-imputation datasets.
<b>mix</b>	Estimation/multiple imputation programs for mixed categorical and continuous data.
<b>mixreg</b>	Functions to fit mixtures of regressions.
<b>mlbench</b>	A collection of artificial and real-world machine learning benchmark problems, including the Boston housing data.
<b>mmlcr</b>	Mixed-mode latent class regression (also known as mixed-mode mixture model regression or mixed-mode mixture regression models) which can handle both longitudinal and one-time responses.
<b>mscalib</b>	Calibration and filtering of MALDI-TOF Peptide Mass Fingerprint data.
<b>msm</b>	Functions for fitting continuous-time Markov multi-state models to categorical processes observed at arbitrary times, optionally with misclassified responses, and covariates on transition or misclassification rates.
<b>muhaz</b>	Hazard function estimation in survival analysis.
<b>multcomp</b>	Multiple comparison procedures for the one-way layout.
<b>multinomRob</b>	Overdispersed multinomial regression using robust (LQD and tanh) estimation.
<b>mvbutils</b>	Utilities by Mark V. Bravington for project organization, editing and backup, sourcing, documentation (formal and informal), package preparation, macro functions, and more.
<b>mvnmle</b>	ML estimation for multivariate normal data with missing values.
<b>mvnormtest</b>	Generalization of the Shapiro-Wilk test for multivariate variables.
<b>mvoutlier</b>	Multivariate outlier detection based on robust estimates of location and covariance structure.
<b>mvpart</b>	Multivariate partitioning.
<b>mvtnorm</b>	Multivariate normal and $t$ distributions.
<b>ncdf</b>	Interface to Unidata netCDF data files.

<b>ncomplete</b>	Functions to perform the regression depth method (RDM) to binary regression to approximate the minimum number of observations that can be removed such that the reduced data set has complete separation.
<b>ncvar</b>	High-level R interface to netCDF datasets.
<b>negenes</b>	Estimating the number of essential genes in a genome on the basis of data from a random transposon mutagenesis experiment, through the use of a Gibbs sampler.
<b>nlme</b>	Fit and compare Gaussian linear and nonlinear mixed-effects models. <i>Recommended.</i>
<b>nlmeODE</b>	Combine the <b>nlme</b> and <b>odesolve</b> packages for mixed-effects modelling using differential equations.
<b>nlrq</b>	Nonlinear quantile regression routines. <i>Defunct.</i>
<b>nnet</b>	Software for single hidden layer perceptrons (“feed-forward neural networks”), and for multinomial log-linear models. Contained in the ‘VR’ bundle. <i>Recommended.</i>
<b>nor1mix</b>	One-dimensional normal mixture models classes, for, e.g., density estimation or clustering algorithms research and teaching; providing the widely used Marron-Wand densities.
<b>norm</b>	Analysis of multivariate normal datasets with missing values.
<b>normalp</b>	A collection of utilities for normal of order $p$ distributions (General Error Distributions).
<b>nortest</b>	Five omnibus tests for the composite hypothesis of normality.
<b>noverlap</b>	Functions to perform the regression depth method (RDM) to binary regression to approximate the amount of overlap, i.e., the minimal number of observations that need to be removed such that the reduced data set has no longer overlap.
<b>npmc</b>	Nonparametric Multiple Comparisons: provides simultaneous rank test procedures for the one-way layout without presuming a certain distribution.
<b>nprq</b>	Nonparametric quantile regression. <i>Defunct.</i>
<b>odesolve</b>	An interface for the Ordinary Differential Equation (ODE) solver lsoda. ODEs are expressed as R functions.
<b>orientlib</b>	Representations, conversions and display of orientation SO(3) data.
<b>ouch</b>	Ornstein-Uhlenbeck models for phylogenetic comparative hypotheses.
<b>oz</b>	Functions for plotting Australia’s coastline and state boundaries.
<b>pamr</b>	Pam: Prediction Analysis for Microarrays.
<b>pan</b>	Multiple imputation for multivariate panel or clustered data.
<b>panel</b>	Functions and datasets for fitting models to Panel data.
<b>pastecs</b>	Package for Analysis of Space-Time Ecological Series.

<b>pcurve</b>	Fits a principal curve to a numeric multivariate dataset in arbitrary dimensions. Produces diagnostic plots. Also calculates Bray-Curtis and other distance matrices and performs multi-dimensional scaling and principal component analyses.
<b>pear</b>	Periodic Autoregression Analysis.
<b>permax</b>	Functions intended to facilitate certain basic analyses of DNA array data, especially with regard to comparing expression levels between two types of tissue.
<b>pgam</b>	Poisson-Gamma Additive Models.
<b>pheno</b>	Some easy-to-use functions for time series analyses of (plant-) phenological data sets.
<b>phyloarray</b>	Software to process data from phylogenetic or identification microarrays.
<b>pinktoe</b>	Converts S trees to HTML/Perl files for interactive tree traversal.
<b>pixmap</b>	Functions for import, export, plotting and other manipulations of bitmapped images.
<b>plotrix</b>	Various useful functions for enhancing plots.
<b>plugdensity</b>	Kernel density estimation with global bandwidth selection via “plug-in”.
<b>pls.pcr</b>	Multivariate regression by PLS and PCR.
<b>polspline</b>	Routines for the polynomial spline fitting routines hazard regression, hazard estimation with flexible tails, logspline, lspec, polyclass, and polymars, by C. Kooperberg and co-authors.
<b>polynom</b>	A collection of functions to implement a class for univariate polynomial manipulations.
<b>ppc</b>	Sample classification of protein mass spectra by peak probability contrasts.
<b>pps</b>	Functions to select samples using PPS (probability proportional to size) sampling, for stratified simple random sampling, and to compute joint inclusion probabilities for Sampford’s method of PPS sampling.
<b>prabclus</b>	Distance based parametric bootstrap tests for clustering, mainly thought for presence-absence data (clustering of species distribution maps). Jaccard and Kulczynski distance measures, clustering of MDS scores, and nearest neighbor based noise detection.
<b>princurve</b>	Fits a principal curve to a matrix of points in arbitrary dimension.
<b>pspline</b>	Smoothing splines with penalties on order $m$ derivatives.
<b>psy</b>	Various procedures used in psychometry: Kappa, ICC, Cronbach alpha, screeplot, PCA and related methods.
<b>pwt</b>	The Penn World Table providing purchasing power parity and national income accounts converted to international prices for 168 countries for some or all of the years 1950–2000.

<b>qcc</b>	Quality Control Charts. Shewhart quality control charts for continuous, attribute and count data. Cusum and EWMA charts. Operating characteristic curves. Process capability analysis. Pareto chart and cause-and-effect chart.
<b>qtl</b>	Analysis of experimental crosses to identify QTLs.
<b>quadprog</b>	For solving quadratic programming problems.
<b>quantreg</b>	Quantile regression and related methods.
<b>qvalue</b>	Q-value estimation for false discovery rate control.
<b>qvcalc</b>	Functions to compute quasi-variances and associated measures of approximation error.
<b>race</b>	Implementation of some racing methods for the empirical selection of the best.
<b>randomForest</b>	Breiman's random forest classifier.
<b>rbugs</b>	Functions to prepare files needed for running BUGS in batch mode, and running BUGS from R. Support for Linux systems with Wine is emphasized.
<b>ref</b>	Functions for creating references, reading from and writing to references and a memory efficient refdata type that transparently encapsulates matrices and data frames.
<b>regress</b>	Fitting Gaussian linear models where the covariance structure is a linear combination of known matrices by maximising the residual log likelihood. Can be used for multivariate models and random effects models.
<b>reldist</b>	Functions for the comparison of distributions, including nonparametric estimation of the relative distribution PDF and CDF and numerical summaries as described in "Relative Distribution Methods in the Social Sciences" by Mark S. Handcock and Martina Morris, 1999, Springer.
<b>relimp</b>	Functions to facilitate inference on the relative importance of predictors in a linear or generalized linear model.
<b>rgdal</b>	Provides bindings to Frank Warmerdam's Geospatial Data Abstraction Library (GDAL).
<b>rgenoud</b>	R version of GENetic Optimization Using Derivatives.
<b>rgl</b>	3D visualization device system (OpenGL).
<b>rimage</b>	Functions for image processing, including Sobel filter, rank filters, fft, histogram equalization, and reading JPEG files.
<b>rlecuyer</b>	R interface to RNG with multiple streams.
<b>rmeta</b>	Functions for simple fixed and random effects meta-analysis for two-sample comparison of binary outcomes.
<b>rmetasim</b>	An interface between R and the metasim simulation engine. Facilitates the use of the metasim engine to build and run individual based population genetics simulations.



<b>rpart</b>	Recursive PARTitioning and regression trees. <i>Recommended.</i>
<b>rpart.permutation</b>	Permutation tests of rpart models.
<b>rpvm</b>	R interface to PVM (Parallel Virtual Machine). Provides interface to PVM APIs, and examples and documentation for its use.
<b>rqmcmb2</b>	Markov chain marginal bootstrap for quantile regression.
<b>rrcov</b>	Functions for robust location and scatter estimation and robust regression with high breakdown point.
<b>rsprng</b>	Provides interface to SPRNG (Scalable Parallel Random Number Generators) APIs, and examples and documentation for its use.
<b>sampling</b>	Implements a modified version of the Sampford sampling algorithm. Given a quantity assigned to each unit in the population, samples are drawn with probability proportional to the product of the quantities of the units included in the sample.
<b>sandwich</b>	Model-robust standard error estimators for time series and longitudinal data.
<b>sca</b>	Simple Component Analysis.
<b>scatterplot3d</b>	Plots a three dimensional (3D) point cloud perspective.
<b>seacarb</b>	Calculates parameters of the seawater carbonate system.
<b>seao</b>	Simple Evolutionary Algorithm Optimization.
<b>seao.gui</b>	Simple Evolutionary Algorithm Optimization: graphical user interface.
<b>segmented</b>	Functions to estimate break-points of segmented relationships in regression models (GLMs).
<b>sem</b>	Functions for fitting general linear Structural Equation Models (with observed and unobserved variables) by the method of maximum likelihood using the RAM approach.
<b>seqinr</b>	Exploratory data analysis and data visualization for biological sequence (DNA and protein) data.
<b>seqmon</b>	Sequential monitoring of clinical trials.
<b>session</b>	Functions for interacting with, saving and restoring R sessions.
<b>setRNG</b>	Set (normal) random number generator and seed.
<b>sfsmisc</b>	Utilities from Seminar fuer Statistik ETH Zurich.
<b>sgeostat</b>	An object-oriented framework for geostatistical modeling.
<b>shapefiles</b>	Functions to read and write ESRI shapefiles.
<b>shapes</b>	Routines for the statistical analysis of shapes, including procrustes analysis, displaying shapes and principal components, testing for mean shape difference, thin-plate spline transformation grids and edge superimposition methods.

**simpleboot**

Simple bootstrap routines.

**skewt**

Density, distribution function, quantile function and random generation for the skewed  $t$  distribution of Fernandez and Steel.

**sm**

Software linked to the book “Applied Smoothing Techniques for Data Analysis: The Kernel Approach with S-PLUS Illustrations” by A. W. Bowman and A. Azzalini, 1997, Oxford University Press.

**sma**

Functions for exploratory (statistical) microarray analysis.

**smoothSurv**

Survival regression with smoothed error distribution.

**sn**

Functions for manipulating skew-normal probability distributions and for fitting them to data, in the scalar and the multivariate case.

**sna**

A range of tools for social network analysis, including node and graph-level indices, structural distance and covariance methods, structural equivalence detection,  $p^*$  modeling, and network visualization.

**snow**

Simple Network of Workstations: support for simple parallel computing in R.

**snowFT**

Fault Tolerant Simple Network of Workstations.

**som**

Self-Organizing Maps (with application in gene clustering).

**sound**

A sound interface for R: Basic functions for dealing with ‘.wav’ files and sound samples.

**spatial**

Functions for kriging and point pattern analysis from “Modern Applied Statistics with S” by W. Venables and B. Ripley. Contained in the ‘VR’ bundle. *Recommended.*

**spatialCovariance**

Computation of spatial covariance matrices for data on rectangles using one dimensional numerical integration and analytic results.

**spatstat**

Data analysis and modelling of two-dimensional point patterns, including multi-type points and spatial covariates.

**spc**

Statistical Process Control: evaluation of control charts by means of the zero-state, steady-state ARL (Average Run Length), setting up control charts for given in-control ARL, and plotting of the related figures.

**spdep**

A collection of functions to create spatial weights matrix objects from polygon contiguities, from point patterns by distance and tessellations, for summarising these objects, and for permitting their use in spatial data analysis; a collection of tests for spatial autocorrelation, including global Moran’s  $I$  and Geary’s  $C$ , local Moran’s  $I$ , saddlepoint approximations for global and local Moran’s  $I$ ; and functions for estimating spatial simultaneous autoregressive (SAR) models. (Was formerly the three packages: **spweights**, **sptestests**, and **spsarlm**.)

**spe**

Stochastic Proximity Embedding.

**splancs**

Spatial and space-time point pattern analysis functions.

<b>statmod</b>	Miscellaneous biostatistical modelling functions.
<b>strucchange</b>	Various tests on structural change in linear regression models.
<b>subselect</b>	A collection of functions which assess the quality of variable subsets as surrogates for a full data set, and search for subsets which are optimal under various criteria.
<b>supclust</b>	Methodology for supervised grouping of predictor variables.
<b>superpc</b>	Supervised principal components.
<b>survey</b>	Summary statistics, generalized linear models, and general maximum likelihood estimation for stratified, cluster-sampled, unequally weighted survey samples.
<b>survival</b>	Functions for survival analysis, including penalised likelihood. <i>Recommended.</i>
<b>survrec</b>	Survival analysis for recurrent event data.
<b>svmpath</b>	Computes the entire regularization path for the two-class svm classifier with essentially the same cost as a single SVM fit.
<b>systemfit</b>	Contains functions for fitting simultaneous systems of equations using Ordinary Least Squares (OLS), Two-Stage Least Squares (2SLS), and Three-Stage Least Squares (3SLS).
<b>tapiR</b>	Tools for accessing (UK) parliamentary information in R.
<b>taskPR</b>	Task-Parallel R package.
<b>tensor</b>	Tensor product of arrays.
<b>tkrplot</b>	Simple mechanism for placing R graphics in a Tk widget.
<b>tree</b>	Classification and regression trees.
<b>treeglia</b>	Stem analysis functions for volume increment and carbon uptake assessment from tree-rings.
<b>tripack</b>	A constrained two-dimensional Delaunay triangulation package.
<b>tseries</b>	Package for time series analysis with emphasis on non-linear modelling.
<b>tuneR</b>	Collection of tools to analyze music, handle wave files, transcription, etc.
<b>tweedie</b>	Maximum likelihood computations for Tweedie exponential family models.
<b>twostage</b>	Functions for optimal design of two-stage-studies using the Mean Score method.
<b>udunits</b>	Interface to Unidata's routines to convert units.
<b>urn</b>	Functions for sampling without replacement (simulated urns).
<b>urca</b>	Unit root and cointegration tests for time series data.
<b>vabayelMix</b>	Variational Bayesian mixture model.
<b>vardiag</b>	Interactive variogram diagnostics.

<b>vcd</b>	Functions and data sets based on the book “Visualizing Categorical Data” by Michael Friendly.
<b>vegan</b>	Various help functions for vegetation scientists and community ecologists.
<b>verification</b>	Utilities for verification of discrete and probabilistic forecasts.
<b>verify</b>	Construction of test suites using verify objects.
<b>vioplot</b>	Violin plots, which are a combination of a box plot and a kernel density plot.
<b>waveslim</b>	Basic wavelet routines for time series analysis.
<b>wavethresh</b>	Software to perform 1-d and 2-d wavelet statistics and transforms.
<b>wle</b>	Robust statistical inference via a weighted likelihood approach.
<b>xgobi</b>	Interface to the XGobi and XGvis programs for graphical data analysis.
<b>xtable</b>	Export data to LaTeX and HTML tables.
<b>zoo</b>	A class with methods for totally ordered indexed observations such as irregular time series.

See CRAN ‘[src/contrib/PACKAGES](#)’ for more information.

There is also a CRAN ‘[src/contrib/Devel](#)’ directory which contains packages still “under development” or depending on features only present in the current development versions of R. Volunteers are invited to give these a try, of course. This area of CRAN currently contains

<b>Dopt</b>	Finding D-optimal experimental designs.
<b>GLMMGibbs</b>	Generalised Linear Mixed Models by Gibbs sampling.
<b>RPgSQL</b>	Provides methods for accessing data stored in PostgreSQL tables.
<b>dseplus</b>	Extensions to <b>dse</b> , the Dynamic Systems Estimation multivariate time series package. Contains PADI, juice and monitoring extensions.
<b>ensemble</b>	Ensembles of tree classifiers.
<b>rcom</b>	R COM Client Interface and internal COM Server.
<b>runStat</b>	Running median and mean.
<b>write.snns</b>	Function for writing a SNNS pattern file from a data frame or matrix.

### 5.1.3 Add-on packages from Omegahat

The ‘[src/contrib/Omegahat](#)’ Directory of a CRAN site contains yet unreleased packages from the [Omegahat Project for Statistical Computing](#). Currently, there are

<b>CORBA</b>	Dynamic CORBA client/server facilities for R. Connects to other CORBA-aware applications developed in arbitrary languages, on different machines and allows R functionality to be exported in the same way to other applications.
--------------	---

- OOP** OOP style classes and methods for R and S-PLUS. Object references and class-based method definition are supported in the style of languages such as Java and C++.
- REmbeddedPostgres**  
Allows R functions and objects to be used to implement SQL functions — per-record, aggregate and trigger functions.
- REventLoop**  
An abstract event loop mechanism that is toolkit independent and can be used to replace the R event loop.
- RGdkPixbuf**  
S language functions to access the facilities in the GdkPixbuf library for manipulating images.
- RGnumeric**  
A plugin for the Gnumeric spreadsheet that allows R functions to be called from cells within the sheet, automatic recalculation, etc.
- RGtk** Facilities in the S language for programming graphical interfaces using Gtk, the Gnome GUI toolkit.
- RGtkBindingGenerator**  
A meta-package which generates C and R code to provide bindings to a Gtk-based library.
- RGtkExtra**  
A collection of S functions that provide an interface to the widgets in the gtk+extra library such as the GtkSheet data-grid display, icon list, file list and directory tree.
- RGtkGlade**  
S language bindings providing an interface to Glade, the interactive Gnome GUI creator.
- RGtkHTML**  
A collection of S functions that provide an interface to creating and controlling an HTML widget which can be used to display HTML documents from files or content generated dynamically in S.
- RGtkViewers**  
A collection of tools for viewing different S objects, databases, class and widget hierarchies, S source file contents, etc.
- RJavaDevice**  
A graphics device for R that uses Java components and graphics. APIs.
- RObjectTables**  
The C and S code allows one to define R objects to be used as elements of the search path with their own semantics and facilities for reading and writing variables. The objects implement a simple interface via R functions (either methods or closures) and can access external data, e.g., in other applications, languages, formats, . . .

**RSMMethods**

An implementation of S version 4 methods and classes for R, consistent with the basic material in “Programming with Data” by John M. Chambers, 1998, Springer NY.

**RSPerl**

An interface from R to an embedded, persistent Perl interpreter, allowing one to call arbitrary Perl subroutines, classes and methods.

**RSPython**

Allows Python programs to invoke S functions, methods, etc., and S code to call Python functionality.

**RXLisp**

An interface to call XLisp-Stat functions from within R.

**SASXML**

Example for reading XML files in SAS 8.2 manner.

**SJava**

An interface from R to Java to create and call Java objects and methods.

**SLanguage**

Functions and C support utilities to support S language programming that can work in both R and S-PLUS.

**SNetscape** Plugin for Netscape and JavaScript.

**SWinRegistry**

Provides access from within R to read and write the Windows registry.

**SWinTypeLibs**

Provides ways to extract type information from type libraries and/or DCOM objects that describes the methods, properties, etc. of an interface.

**SXalan**

Process XML documents using XSL functions implemented in R and dynamically substituting output from R.

**Slcc**

Parses C source code, allowing one to analyze and automatically generate interfaces from S to that code, including the table of S-accessible native symbols, parameter count and type information, S constructors from C objects, call graphs, etc.

**Sxslt**

An extension module for libxslt, the XML-XSL document translator, that allows XSL functions to be implemented via R functions.

**5.1.4 Add-on packages from Bioconductor**

The **Bioconductor Project** produces an open source software framework that will assist biologists and statisticians working in bioinformatics, with primary emphasis on inference using DNA microarrays. The following R packages are contained in the current release of Bioconductor, with more packages under development.

**AnnBuilder**

Assemble and process genomic annotation data, from databases such as GenBank, the Gene Ontology Consortium, LocusLink, UniGene, the UCSC Human Genome Project.

**Biobase**

Object-oriented representation and manipulation of genomic data (S4 class structure).

<b>Biostrings</b>	Class definitions and generics for biological sequences along with pattern matching algorithms.
<b>DNAcopy</b>	Segments DNA copy number data using circular binary segmentation to detect regions with abnormal copy number.
<b>DynDoc</b>	Functionality to create and interact with dynamic documents, vignettes, and other navigable documents.
<b>EBarrays</b>	Empirical Bayes tools for the analysis of replicated microarray data across multiple conditions.
<b>GOstats</b>	Tools for manipulating GO and microarrays.
<b>GeneSpring</b>	Functions and class definitions to be able to read and write GeneSpring specific data objects and convert them to Bioconductor objects.
<b>GeneTS</b>	A package for analysing multiple gene expression time series data. Currently, implements methods for cell cycle analysis and for inferring large sparse graphical Gaussian models.
<b>Icens</b>	Functions for computing the NPMLE for censored and truncated data.
<b>LPE</b>	Significance analysis of microarray data with small number of replicates using the Local Pooled Error (LPE) method.
<b>MeasurementError.cor</b>	Two-stage measurement error model for correlation estimation with smaller bias than the usual sample correlation.
<b>PROcess</b>	Ciphergen SELDI-TOF processing.
<b>RBGL</b>	An interface between the graph package and the Boost graph libraries, allowing for fast manipulation of graph objects in R.
<b>RMAGEML</b>	Functionality to handle MAGEML documents.
<b>ROC</b>	Receiver Operating Characteristic (ROC) approach for identifying genes that are differentially expressed in two types of samples.
<b>RSNPper</b>	Interface to chip.org::SNPper for SNP-related data.
<b>RdbiPgSQL</b>	Methods for accessing data stored in PostgreSQL tables.
<b>Rdbi</b>	Generic framework for database access in R.
<b>Resourcerer</b>	Read annotation data from TIGR Resourcerer or convert the annotation data into Bioconductor data package.
<b>Rgraphviz</b>	An interface with Graphviz for plotting graph objects in R.
<b>Ruuid</b>	Creates Universally Unique ID values (UUIDs) in R.
<b>SAGElyzer</b>	Locates genes based on SAGE tags.

<b>SNADData</b>	Data from the book “Social Network Analysis” by Wasserman & Faust, 1999.
<b>aCGH</b>	Classes and functions for Array Comparative Genomic Hybridization data.
<b>affy</b>	Methods for Affymetrix Oligonucleotide Arrays.
<b>affyPLM</b>	For fitting Probe Level Models.
<b>affycomp</b>	Graphics toolbox for assessment of Affymetrix expression measures.
<b>affydata</b>	Affymetrix data for demonstration purposes.
<b>affylmGUI</b>	Graphical User Interface for affy analysis using package <b>limma</b> .
<b>affypdnn</b>	Probe Dependent Nearest Neighbors (PDNN) for the affy package.
<b>altcdfenvs</b>	Utilities to handle cdfenvs.
<b>annaffy</b>	Functions for handling data from Bioconductor Affymetrix annotation data packages.
<b>annotate</b>	Associate experimental data in real time to biological metadata from web databases such as GenBank, LocusLink and PubMed. Process and store query results. Generate HTML reports of analyses.
<b>arrayMagic</b>	Utilities for quality control and processing for two-color cDNA microarray data.
<b>arrayQuality</b>	Performing print-run and array level quality assessment.
<b>bim</b>	Bayesian interval mapping diagnostics: functions to interpret QTLCart and Bmapqtl samples.
<b>convert</b>	Convert Microarray Data Objects.
<b>ctc</b>	Tools to export and import Tree and Cluster to other programs.
<b>daMA</b>	Functions for the efficient design of factorial two-color microarray experiments and for the statistical analysis of factorial microarray data.
<b>ecolitk</b>	Metadata and tools to work with E. coli.
<b>edd</b>	Expression density diagnostics: graphical methods and pattern recognition algorithms for distribution shape classification.
<b>exprExternal</b>	Implementation of exprSet using externalVectors.
<b>externalVector</b>	Basic class definitions and generics for external pointer based vector objects for R.
<b>factDesign</b>	A set of tools for analyzing data from factorial designed microarray experiments. The functions can be used to evaluate appropriate tests of contrast and perform single outlier detection.
<b>gcrma</b>	Background adjustment using sequence information.



- genefilter** Tools for sequentially filtering genes using a wide variety of filtering functions. Example of filters include: number of missing value, coefficient of variation of expression measures, ANOVA  $p$ -value, Cox model  $p$ -values. Sequential application of filtering functions to genes.
- geneplotter** Graphical tools for genomic data, for example for plotting expression data along a chromosome or producing color images of expression data matrices.
- globaltest** Testing globally whether a group of genes is significantly related to some clinical variable of interest.
- goTools** Functions for description/comparison of oligo ID list using the Gene Ontology database.
- gpls** Classification using generalized partial least squares for two-group and multi-group classification.
- graph** Classes and tools for creating and manipulating graphs within R.
- hexbin** Binning functions, in particular hexagonal bins for graphing.
- impute** Imputation for microarray data (currently KNN only).
- limma** Linear models for microarray data.
- limmaGUI** Graphical User Interface for package **limma**.
- makecdfenv** Two functions. One reads a Affymetrix chip description file (CDF) and creates a hash table environment containing the location/probe set membership mapping. The other creates a package that automatically loads that environment.
- marray** Exploratory analysis for two-color spotted microarray data.
- marrayClasses** Class definitions for pre-normalized and normalized cDNA microarray data. Basic methods for accessing/replacing, printing, and subsetting.
- marrayInput** Functions for reading microarray data into R from different image analysis output files, and probe and target description files. Widgets are supplied to facilitate and automate data input and the creation of microarray specific R objects for storing these data.
- marrayNorm** Functions for location and scale normalization procedures based on robust local regression.
- marrayPlots** Functions for diagnostic plots for pre- and post-normalization cDNA microarray intensity data: boxplots, scatter-plots, color images.
- marrayTools** Miscellaneous functions used in the functional genomics core facility in UCB and UCSF.

**matchprobes**

Tools for sequence matching of probes on arrays.

**multtest**

Multiple testing procedures for controlling the family-wise error rate (FWER) and the false discovery rate (FDR). Tests can be based on  $t$ - or  $F$ -statistics for one- and two-factor designs, and permutation procedures are available to estimate adjusted  $p$ -values.

**ontoTools**

Graphs and sparse matrices for working with ontologies.

**pairseqsim**

Pairwise sequence alignment and scoring algorithms for global, local and overlap alignment with affine gap penalty.

**pamr**

Pam: Prediction Analysis for Microarrays.

**pickgene**

Adaptive gene picking for microarray expression data analysis.

**prada**

Tools for analyzing and navigating data from high-throughput phenotyping experiments based on cellular assays and fluorescent detection.

**qvalue**

Q-value estimation for false discovery rate control.

**rama**

Robust Analysis of MicroArrays: robust estimation of cDNA microarray intensities with replicates using a Bayesian hierarchical model.

**reposTools**

Tools for dealing with file repositories and allow users to easily install, update, and distribute packages, vignettes, and other files.

**rhdf5**

Storage and retrieval of large datasets using the HDF5 library and file format.

**siggenes**

Identifying differentially expressed genes and estimating the False Discovery Rate (FDR) with both the Significance Analysis of Microarrays (SAM) and the Empirical Bayes Analyses of Microarrays (EBAM).

**simpleaffy**

Very simple high level analysis of Affymetrix data.

**splicegear**

A set of tools to work with alternative splicing.

**tkWidgets**

Widgets in Tcl/Tk that provide functionality for Bioconductor packages.

**vsn**

Calibration and variance stabilizing transformations for both Affymetrix and cDNA array data.

**webbioc**

Integrated web interface for doing microarray analysis using several of the Bioconductor packages.

**widgetTools**

Tools for creating Tcl/Tk widgets, i.e., small-scale graphical user interfaces.

### 5.1.5 Other add-on packages

**Jim Lindsey** has written a collection of R packages for nonlinear regression and repeated measurements, consisting of **event** (event history procedures and models), **gnlm** (generalized nonlinear regression models), **growth** (multivariate normal and elliptically-contoured repeated measurements models), **repeated** (non-normal repeated measurements models),

**rmutil** (utilities for nonlinear regression and repeated measurements), and **stable** (probability functions and generalized regression models for stable distributions). All analyses in the new edition of his book “Models for Repeated Measurements” (1999, Oxford University Press) were carried out using these packages. Jim has also started **dna**, a package with procedures for the analysis of DNA sequences. Jim’s packages can be obtained from <http://www.luc.ac.be/~jlindsey/rcode.html>.

More code has been posted to the R-help mailing list, and can be obtained from the mailing list archive.

## 5.2 How can add-on packages be installed?

(Unix only.) The add-on packages on CRAN come as gzipped tar files named *pkg\_version.tar.gz*, which may in fact be “bundles” containing more than one package. Provided that **tar** and **gzip** are available on your system, type

```
$ R CMD INSTALL /path/to/pkg_version.tar.gz
```

at the shell prompt to install to the library tree rooted at the first directory given in **R\_LIBS** (see below) if this is set and non-null, and to the default library (the ‘**library**’ subdirectory of ‘**R\_HOME**’) otherwise. (Versions of R prior to 1.3.0 installed to the default library by default.)

To install to another tree (e.g., your private one), use

```
$ R CMD INSTALL -l lib /path/to/pkg_version.tar.gz
```

where *lib* gives the path to the library tree to install to.

Even more conveniently, you can install and automatically update packages from within R if you have access to CRAN. See the help page for **CRAN.packages()** for more information.

You can use several library trees of add-on packages. The easiest way to tell R to use these is via the environment variable **R\_LIBS** which should be a colon-separated list of directories at which R library trees are rooted. You do not have to specify the default tree in **R\_LIBS**. E.g., to use a private tree in ‘**\$HOME/lib/R**’ and a public site-wide tree in ‘**/usr/local/lib/R-contrib**’, put

```
R_LIBS="$HOME/lib/R:/usr/local/lib/R-contrib"; export R_LIBS
```

into your (Bourne) shell profile or even preferably, add the line

```
R_LIBS="$HOME/lib/R:/usr/local/lib/R-contrib"
```

your ‘**~/.Renviron**’ file. (Note that no **export** statement is needed or allowed in this file; see the on-line help for **Startup** for more information.)

## 5.3 How can add-on packages be used?

To find out which additional packages are available on your system, type

```
library()
```

at the R prompt.

This produces something like

```

Packages in '/home/me/lib/R':

mystuff      My own R functions, nicely packaged but not documented

Packages in '/usr/local/lib/R/library':

KernSmooth  Functions for kernel smoothing for Wand & Jones (1995)
MASS        Main Package of Venables and Ripley's MASS
base        The R Base package
boot        Bootstrap R (S-Plus) Functions (Canty)
class       Functions for Classification
cluster     Functions for clustering (by Rousseeuw et al.)
datasets    The R datasets Package
foreign     Read data stored by Minitab, S, SAS, SPSS, Stata, ...
grDevices   The R Graphics Devices and Support for Colours and Fonts
graphics    The R Graphics Package
grid        The Grid Graphics Package
lattice     Lattice Graphics
methods     Formal Methods and Classes
mgcv        GAMs with GCV smoothness estimation and GAMMs by REML/PQ
nlme        Linear and nonlinear mixed effects models
nnet        Feed-forward Neural Networks and Multinomial Log-Linear
            Models
rpart       Recursive partitioning
spatial     Functions for Kriging and Point Pattern Analysis
splines     Regression Spline Functions and Classes
stats       The R Stats Package
stats4      Statistical functions using S4 classes
survival    Survival analysis, including penalised likelihood
tcltk       Tcl/Tk Interface
tools       Tools for Package Development
utils       The R Utils Package

```

You can “load” the installed package *pkg* by

```
library(pkg)
```

You can then find out which functions it provides by typing one of

```
library(help = pkg)
help(package = pkg)
```

You can unload the loaded package *pkg* by

```
detach("package:pkg")
```

## 5.4 How can add-on packages be removed?

Use

```
$ R CMD REMOVE pkg_1 ... pkg_n
```

to remove the packages *pkg\_1*, ..., *pkg\_n* from the library tree rooted at the first directory given in `R_LIBS` if this is set and non-null, and from the default library otherwise. (Versions of R prior to 1.3.0 removed from the default library by default.)

To remove from library *lib*, do

```
$ R CMD REMOVE -l lib pkg_1 ... pkg_n
```

## 5.5 How can I create an R package?

A package consists of a subdirectory containing the files ‘DESCRIPTION’ and ‘INDEX’, and the subdirectories ‘R’, ‘data’, ‘demo’, ‘exec’, ‘inst’, ‘man’, ‘src’, and ‘tests’ (some of which can be missing). Optionally the package can also contain script files ‘configure’ and ‘cleanup’ which are executed before and after installation.

See [section “Creating R packages” in \*Writing R Extensions\*](#), for details.

R version 1.3.0 has added the function `package.skeleton()` which will set up directories, save data and code, and create skeleton help files for a set of R functions and datasets.

See [Section 2.10 \[What is CRAN?\]](#), [page 8](#), for information on uploading a package to CRAN.

## 5.6 How can I contribute to R?

R is in active development and there is always a risk of bugs creeping in. Also, the developers do not have access to all possible machines capable of running R. So, simply using it and communicating problems is certainly of great value.

One place where functionality is still missing is the modeling software as described in “Statistical Models in S” (see [Section 3.1 \[What is S?\]](#), [page 10](#)); some of the nonlinear modeling code is not there yet.

The [R Developer Page](#) acts as an intermediate repository for more or less finalized ideas and plans for the R statistical system. It contains (pointers to) TODO lists, RFCs, various other writeups, ideas lists, and CVS miscellanea.

Many (more) of the packages available at the Statlib S Repository might be worth porting to R.

If you are interested in working on any of these projects, please notify [Kurt Hornik](#).

## 6 R and Emacs

### 6.1 Is there Emacs support for R?

There is an Emacs package called ESS (“Emacs Speaks Statistics”) which provides a standard interface between statistical programs and statistical processes. It is intended to provide assistance for interactive statistical programming and data analysis. Languages supported include: S dialects (S 3/4, S-PLUS 3.x/4.x/5.x, and R), LispStat dialects (XLispStat, ViSta) and SAS. Stata and SPSS dialect (SPSS, PSPP) support is being examined for possible future implementation

ESS grew out of the need for bug fixes and extensions to S-mode 4.8 (which was a GNU Emacs interface to S/S-PLUS version 3 only). The current set of developers desired support for XEmacs, R, S4, and MS Windows. In addition, with new modes being developed for R, Stata, and SAS, it was felt that a unifying interface and framework for the user interface would benefit both the user and the developer, by helping both groups conform to standard Emacs usage. The end result is an increase in efficiency for statistical programming and data analysis, over the usual tools.

R support contains code for editing R source code (syntactic indentation and highlighting of source code, partial evaluations of code, loading and error-checking of code, and source code revision maintenance) and documentation (syntactic indentation and highlighting of source code, sending examples to running ESS process, and previewing), interacting with an inferior R process from within Emacs (command-line editing, searchable command history, command-line completion of R object and file names, quick access to object and search lists, transcript recording, and an interface to the help system), and transcript manipulation (recording and saving transcript files, manipulating and editing saved transcripts, and re-evaluating commands from transcript files).

The latest stable version of ESS are available via CRAN or the [ESS web page](http://stat.ethz.ch/ESS/). The HTML version of the documentation can be found at <http://stat.ethz.ch/ESS/>.

ESS comes with detailed installation instructions.

For help with ESS, send email to [ESS-help@stat.math.ethz.ch](mailto:ESS-help@stat.math.ethz.ch).

Please send bug reports and suggestions on ESS to [ESS-bugs@stat.math.ethz.ch](mailto:ESS-bugs@stat.math.ethz.ch). The easiest way to do this from is within Emacs by typing `M-x ess-submit-bug-report` or using the [ESS] or [iESS] pulldown menus.

### 6.2 Should I run R from within Emacs?

Yes, *definitely*. Inferior R mode provides a readline/history mechanism, object name completion, and syntax-based highlighting of the interaction buffer using Font Lock mode, as well as a very convenient interface to the R help system.

Of course, it also integrates nicely with the mechanisms for editing R source using Emacs. One can write code in one Emacs buffer and send whole or parts of it for execution to R; this is helpful for both data analysis and programming. One can also seamlessly integrate with a revision control system, in order to maintain a log of changes in your programs and data, as well as to allow for the retrieval of past versions of the code.

In addition, it allows you to keep a record of your session, which can also be used for error recovery through the use of the transcript mode.

To specify command line arguments for the inferior R process, use `C-u M-x R` for starting R.

### 6.3 Debugging R from within Emacs

To debug R “from within Emacs”, there are several possibilities. To use the Emacs GUD (Grand Unified Debugger) library with the recommended debugger GDB, type `M-x gdb` and give the path to the R *binary* as argument. At the `gdb` prompt, set `R_HOME` and other environment variables as needed (using e.g. `set env R_HOME /path/to/R/`, but see also below), and start the binary with the desired arguments (e.g., `run --quiet`).

If you have ESS, you can do `C-u M-x R` `(RET)` `- d` `(SPC)` `g d b` `(RET)` to start an inferior R process with arguments ‘-d gdb’.

A third option is to start an inferior R process via ESS (`M-x R`) and then start GUD (`M-x gdb`) giving the R binary (using its full path name) as the program to debug. Use the program `ps` to find the process number of the currently running R process then use the `attach` command in `gdb` to attach it to that process. One advantage of this method is that you have separate `*R*` and `*gud-gdb*` windows. Within the `*R*` window you have all the ESS facilities, such as object-name completion, that we know and love.

When using GUD mode for debugging from within Emacs, you may find it most convenient to use the directory with your code in it as the current working directory and then make a symbolic link from that directory to the R binary. That way ‘`.gdbinit`’ can stay in the directory with the code and be used to set up the environment and the search paths for the source, e.g. as follows:

```
set env R_HOME /opt/R
set env R_PAPERSIZE letter
set env R_PRINTCMD lpr
dir /opt/R/src/appl
dir /opt/R/src/main
dir /opt/R/src/nmath
dir /opt/R/src/unix
```

## 7 R Miscellanea

### 7.1 How can I set components of a list to NULL?

You can use

```
x[i] <- list(NULL)
```

to set component `i` of the list `x` to `NULL`, similarly for named components. Do not set `x[i]` or `x[[i]]` to `NULL`, because this will remove the corresponding component from the list.

For dropping the row names of a matrix `x`, it may be easier to use `rownames(x) <- NULL`, similarly for column names.

### 7.2 How can I save my workspace?

`save.image()` saves the objects in the user's `.GlobalEnv` to the file `‘.RData’` in the R startup directory. (This is also what happens after `q("yes")`.) Using `save.image(file)` one can save the image under a different name.

### 7.3 How can I clean up my workspace?

To remove all objects in the currently active environment (typically `.GlobalEnv`), you can do

```
rm(list = ls(all = TRUE))
```

(Without `‘all = TRUE’`, only the objects with names not starting with a `‘.’` are removed.)

### 7.4 How can I get `eval()` and `D()` to work?

Strange things will happen if you use `eval(print(x), envir = e)` or `D(x^2, "x")`. The first one will either tell you that `"x"` is not found, or print the value of the wrong `x`. The other one will likely return zero if `x` exists, and an error otherwise.

This is because in both cases, the first argument is evaluated in the calling environment first. The result (which should be an object of mode `"expression"` or `"call"`) is then evaluated or differentiated. What you (most likely) really want is obtained by “quoting” the first argument upon surrounding it with `expression()`. For example,

```
R> D(expression(x^2), "x")
2 * x
```

Although this behavior may initially seem to be rather strange, is perfectly logical. The “intuitive” behavior could easily be implemented, but problems would arise whenever the expression is contained in a variable, passed as a parameter, or is the result of a function call. Consider for instance the semantics in cases like

```
D2 <- function(e, n) D(D(e, n), n)
```

or

```
g <- function(y) eval(substitute(y), sys.frame(sys.parent(n = 2)))
g(a * b)
```

See the help page for `deriv()` for more examples.



## 7.5 Why do my matrices lose dimensions?

When a matrix with a single row or column is created by a subscripting operation, e.g., `row <- mat[2, ]`, it is by default turned into a vector. In a similar way if an array with dimension, say, `2 x 3 x 1 x 4` is created by subscripting it will be coerced into a `2 x 3 x 4` array, losing the unnecessary dimension. After much discussion this has been determined to be a *feature*.

To prevent this happening, add the option `'drop = FALSE'` to the subscripting. For example,

```
rowmatrix <- mat[2, , drop = FALSE] # creates a row matrix
colmatrix <- mat[, 2, drop = FALSE] # creates a column matrix
a <- b[1, 1, 1, drop = FALSE]       # creates a 1 x 1 x 1 array
```

The `'drop = FALSE'` option should be used defensively when programming. For example, the statement

```
somerows <- mat[index, ]
```

will return a vector rather than a matrix if `index` happens to have length 1, causing errors later in the code. It should probably be rewritten as

```
somerows <- mat[index, , drop = FALSE]
```

## 7.6 How does autoloading work?

R has a special environment called `.AutoloadEnv`. Using `autoload(name, pkg)`, where `name` and `pkg` are strings giving the names of an object and the package containing it, stores some information in this environment. When R tries to evaluate `name`, it loads the corresponding package `pkg` and reevaluates `name` in the new package's environment.

Using this mechanism makes R behave as if the package was loaded, but does not occupy memory (yet).

See the help page for `autoload()` for a very nice example.

## 7.7 How should I set options?

The function `options()` allows setting and examining a variety of global “options” which affect the way in which R computes and displays its results. The variable `.Options` holds the current values of these options, but should never directly be assigned to unless you want to drive yourself crazy—simply pretend that it is a “read-only” variable.

For example, given

```
test1 <- function(x = pi, dig = 3) {
  oo <- options(digits = dig); on.exit(options(oo));
  cat(.Options$digits, x, "\n")
}
test2 <- function(x = pi, dig = 3) {
  .Options$digits <- dig
  cat(.Options$digits, x, "\n")
}
```

we obtain:

```
R> test1()
3 3.14
R> test2()
3 3.141593
```

What is really used is the *global* value of `.Options`, and using `options(OPT = VAL)` correctly updates it. Local copies of `.Options`, either in `.GlobalEnv` or in a function environment (frame), are just silently disregarded.

## 7.8 How do file names work in Windows?

As R uses C-style string handling, ‘\’ is treated as an escape character, so that for example one can enter a newline as ‘\n’. When you really need a ‘\’, you have to escape it with another ‘\’.

Thus, in filenames use something like "c:\\data\\money.dat". You can also replace ‘\’ by ‘/’ ("c:/data/money.dat").

## 7.9 Why does plotting give a color allocation error?

On an X11 device, plotting sometimes, e.g., when running `demo("image")`, results in “Error: color allocation error”. This is an X problem, and only indirectly related to R. It occurs when applications started prior to R have used all the available colors. (How many colors are available depends on the X configuration; sometimes only 256 colors can be used.)

One application which is notorious for “eating” colors is Netscape. If the problem occurs when Netscape is running, try (re)starting it with either the ‘`-no-install`’ (to use the default colormap) or the ‘`-install`’ (to install a private colormap) option.

You could also set the `colortype` of `X11()` to “`pseudo.cube`” rather than the default “`pseudo`”. See the help page for `X11()` for more information.

## 7.10 How do I convert factors to numeric?

It may happen that when reading numeric data into R (usually, when reading in a file), they come in as factors. If `f` is such a factor object, you can use

```
as.numeric(as.character(f))
```

to get the numbers back. More efficient, but harder to remember, is

```
as.numeric(levels(f))[as.integer(f)]
```

In any case, do not call `as.numeric()` or their likes directly for the task at hand (as `as.numeric()` or `unclass()` give the internal codes).

## 7.11 Are Trellis displays implemented in R?

The recommended package **lattice** (which is based on another recommended package, **grid**) provides graphical functionality that is compatible with most Trellis commands.

You could also look at `coplot()` and `dotchart()` which might do at least some of what you want. Note also that the R version of `pairs()` is fairly general and provides most of the functionality of `splom()`, and that R’s default plot method has an argument `asp` allowing to specify (and fix against device resizing) the aspect ratio of the plot.

(Because the word “Trellis” has been claimed as a trademark we do not use it in R. The name “lattice” has been chosen for the R equivalent.)

## 7.12 What are the enclosing and parent environments?

Inside a function you may want to access variables in two additional environments: the one that the function was defined in (“enclosing”), and the one it was invoked in (“parent”).

If you create a function at the command line or load it in a package its enclosing environment is the global workspace. If you define a function `f()` inside another function `g()` its enclosing environment is the environment inside `g()`. The enclosing environment for a function is fixed when the function is created. You can find out the enclosing environment for a function `f()` using `environment(f)`.

The “parent” environment, on the other hand, is defined when you invoke a function. If you invoke `lm()` at the command line its parent environment is the global workspace, if you invoke it inside a function `f()` then its parent environment is the environment inside `f()`. You can find out the parent environment for an invocation of a function by using `parent.frame()` or `sys.frame(sys.parent())`.

So for most user-visible functions the enclosing environment will be the global workspace, since that is where most functions are defined. The parent environment will be wherever the function happens to be called from. If a function `f()` is defined inside another function `g()` it will probably be used inside `g()` as well, so its parent environment and enclosing environment will probably be the same.

Parent environments are important because things like model formulas need to be evaluated in the environment the function was called from, since that’s where all the variables will be available. This relies on the parent environment being potentially different with each invocation.

Enclosing environments are important because a function can use variables in the enclosing environment to share information with other functions or with other invocations of itself (see the section on lexical scoping). This relies on the enclosing environment being the same each time the function is invoked. (In C this would be done with static variables.)

Scoping *is* hard. Looking at examples helps. It is particularly instructive to look at examples that work differently in R and S and try to see why they differ. One way to describe the scoping differences between R and S is to say that in S the enclosing environment is *always* the global workspace, but in R the enclosing environment is wherever the function was created.

## 7.13 How can I substitute into a plot label?

Often, it is desired to use the value of an R object in a plot label, e.g., a title. This is easily accomplished using `paste()` if the label is a simple character string, but not always obvious in case the label is an expression (for refined mathematical annotation). In such a case, either use `parse()` on your pasted character string or use `substitute()` on an expression. For example, if `ahat` is an estimator of your parameter  $a$  of interest, use

```
title(substitute(hat(a) == ahat, list(ahat = ahat)))
```

(note that it is ‘==’ and not ‘=’). Sometimes `bquote()` gives a more compact form, e.g.,

```
title(bquote(hat(a) = .(ahat)))
```

where subexpressions enclosed in ‘.(.)’ are replaced by their values.

There are more worked examples in the mailing list archives.

## 7.14 What are valid names?

When creating data frames using `data.frame()` or `read.table()`, R by default ensures that the variable names are syntactically valid. (The argument ‘`check.names`’ to these functions controls whether variable names are checked and adjusted by `make.names()` if needed.)

To understand what names are “valid”, one needs to take into account that the term “name” is used in several different (but related) ways in the language:

1. A *syntactic name* is a string the parser interprets as this type of expression. It consists of letters, numbers, and the dot and (for version of R at least 1.9.0) underscore characters, and starts with either a letter or a dot not followed by a number. Reserved words are not syntactic names.
2. An *object name* is a string associated with an object that is assigned in an expression either by having the object name on the left of an assignment operation or as an argument to the `assign()` function. It is usually a syntactic name as well, but can be any non-empty string if it is quoted (and it is always quoted in the call to `assign()`).
3. An *argument name* is what appears to the left of the equals sign when supplying an argument in a function call (for example, `f(trim=.5)`). Argument names are also usually syntactic names, but again can be anything if they are quoted.
4. An *element name* is a string that identifies a piece of an object (a component of a list, for example.) When it is used on the right of the ‘\$’ operator, it must be a syntactic name, or quoted. Otherwise, element names can be any strings. (When an object is used as a database, as in a call to `eval()` or `attach()`, the element names become object names.)
5. Finally, a *file name* is a string identifying a file in the operating system for reading, writing, etc. It really has nothing much to do with names in the language, but it is traditional to call these strings file “names”.

## 7.15 Are GAMs implemented in R?

Package **gam** from CRAN implements all the Generalized Additive Models (GAM) functionality as described in the GAM chapter of the White Book. In particular, it implements backfitting with both local regression and smoothing splines, and is extendable. There is a `gam()` function for GAMs in package **mgcv**, but it is not an exact clone of what is described in the White Book (no `lo()` for example). Package **gss** can fit spline-based GAMs too. And if you can accept regression splines you can use `glm()`. For gaussian GAMs you can use `bruto()` from package **mda**.

## 7.16 Why is the output not printed when I `source()` a file?

Most R commands do not generate any output. The command

```
1+1
```

computes the value 2 and returns it; the command

```
summary(glm(y~x+z, family=binomial))
```

fits a logistic regression model, computes some summary information and returns an object of class "summary.glm" (see [Section 8.1 \[How should I write summary methods?\]](#), page 61).

If you type '1+1' or 'summary(glm(y~x+z, family=binomial))' at the command line the returned value is automatically printed (unless it is `invisible()`), but in other circumstances, such as in a `source()`d file or inside a function it isn't printed unless you specifically print it.

To print the value use

```
print(1+1)
```

or

```
print(summary(glm(y~x+z, family=binomial)))
```

instead, or use `source(file, echo=TRUE)`.

## 7.17 Why does `outer()` behave strangely with my function?

As the help for `outer()` indicates, it does not work on arbitrary functions the way the `apply()` family does. It requires functions that are vectorized to work elementwise on arrays. As you can see by looking at the code, `outer(x, y, FUN)` creates two large vectors containing every possible combination of elements of `x` and `y` and then passes this to `FUN` all at once. Your function probably cannot handle two large vectors as parameters.

If you have a function that cannot handle two vectors but can handle two scalars, then you can still use `outer()` but you will need to wrap your function up first, to simulate vectorized behavior. Suppose your function is

```
foo <- function(x, y, happy) {
  stopifnot(length(x) == 1, length(y) == 1) # scalars only!
  (x + y) * happy
}
```

If you define the general function

```
wrapper <- function(x, y, my.fun, ...) {
  sapply(seq(along = x), FUN = function(i) my.fun(x[i], y[i], ...))
}
```

then you can use `outer()` by writing, e.g.,

```
outer(1:4, 1:2, FUN = wrapper, my.fun = foo, happy = 10)
```

## 7.18 Why does the output from `anova()` depend on the order of factors in the model?

In a model such as `~A+B+A:B`, R will report the difference in sums of squares between the models `~1`, `~A`, `~A+B` and `~A+B+A:B`. If the model were `~B+A+A:B`, R would report differences between `~1`, `~B`, `~A+B`, and `~A+B+A:B`. In the first case the sum of squares for A is comparing `~1` and `~A`, in the second case it is comparing `~B` and `~B+A`. In a non-orthogonal design (i.e., most unbalanced designs) these comparisons are (conceptually and numerically) different.

Some packages report instead the sums of squares based on comparing the full model to the models with each factor removed one at a time (the famous 'Type III sums of squares')

from SAS, for example). These do not depend on the order of factors in the model. The question of which set of sums of squares is the Right Thing provokes low-level holy wars on R-help from time to time.

There is no need to be agitated about the particular sums of squares that R reports. You can compute your favorite sums of squares quite easily. Any two models can be compared with `anova(model1, model2)`, and `drop1(model1)` will show the sums of squares resulting from dropping single terms.

## 7.19 How do I produce PNG graphics in batch mode?

Under Unix, the `png()` device uses the X11 driver, which is a problem in batch mode or for remote operation. If you have Ghostscript you can use `bitmap()`, which produces a PostScript file then converts it to any bitmap format supported by ghostscript. On some installations this produces ugly output, on others it is perfectly satisfactory. In theory one could also use Xvfb from [X.Org](http://X.Org), which provides an X server with no display.

## 7.20 How can I get command line editing to work?

The Unix command-line interface to R can only provide the inbuilt command line editor which allows recall, editing and re-submission of prior commands provided that the GNU readline library is available at the time R is configured for compilation. Note that the ‘development’ version of readline including the appropriate headers is needed: users of Linux binary distributions will need to install packages such as `libreadline-dev` (Debian) or `readline-devel` (Red Hat).

## 7.21 How can I turn a string into a variable?

If you have

```
varname <- c("a", "b", "d")
```

you can do

```
get(varname[1]) + 2
```

for

```
a + 2
```

or

```
assign(varname[1], 2 + 2)
```

for

```
a <- 2 + 2
```

or

```
eval(substitute(lm(y ~ x + variable),
               list(variable = as.name(varname[1]))
```

for

```
lm(y ~ x + a)
```

At least in the first two cases it is often easier to just use a list, and then you can easily index it by name

```
vars <- list(a = 1:10, b = rnorm(100), d = LETTERS)
vars[["a"]]
```

without any of this messing about.

## 7.22 Why do lattice/trellis graphics not work?

The most likely reason is that you forgot to tell R to display the graph. Lattice functions such as `xyplot()` create a graph object, but do not display it (the same is true of Trellis graphics in S-PLUS). The `print()` method for the graph object produces the actual display. When you use these functions interactively at the command line, the result is automatically printed, but in `source()` or inside your own functions you will need an explicit `print()` statement.

## 7.23 How can I sort the rows of a data frame?

To sort the rows within a data frame, with respect to the values in one or more of the columns, simply use `order()`.

## 7.24 Why does the `help.start()` search engine not work?

The browser-based search engine in `help.start()` utilizes a Java applet. In order for this to function properly, a compatible version of Java must be installed on your system and linked to your browser, and both Java *and* JavaScript need to be enabled in your browser.

There have been a number of compatibility issues with versions of Java and of browsers. See [section “Enabling search in HTML help” in \*R Installation and Administration\*](#), for further details.

## 7.25 Why did my `.Rprofile` stop working when I updated R?

Did you read the ‘NEWS’ file? For functions that are not in the **base** package you need to specify the correct package namespace, since the code will be run *before* the packages are loaded. E.g.,

```
ps.options(horizontal = FALSE)
help.start()
```

needs to be

```
grDevices::ps.options(horizontal = FALSE)
utils::help.start()
```

(`graphics::ps.options(horizontal = FALSE)` in R 1.9.x).

## 7.26 Where have all the methods gone?

Many functions, particularly S3 methods, are now hidden in namespaces. This has the advantage that they cannot be called inadvertently with arguments of the wrong class, but it makes them harder to view.

To see the code for an S3 method (e.g., `[.terms]`) use

```
getS3method("[", "terms")
```

To see the code for an unexported function `foo()` in the namespace of package "bar" use `bar:::foo`. Don't use these constructions to call unexported functions in your own code—they are probably unexported for a reason and may change without warning.

## 7.27 How can I create rotated axis labels?

To rotate axis labels (using base graphics), you need to use `text()`, rather than `mtext()`, as the latter does not support `par("srt")`.

```
## Increase bottom margin to make room for rotated labels
par(mar = c(7, 4, 4, 2) + 0.1)
## Create plot with no x axis and no x axis label
plot(1 : 8, xaxt = "n", xlab = "")
## Set up x axis with tick marks alone
axis(1, labels = FALSE)
## Create some text labels
labels <- paste("Label", 1:8, sep = " ")
## Plot x axis labels at default tick marks
text(1:8, par("usr")[3] - 0.25, srt = 45, adj = 1,
     labels = labels, xpd = TRUE)
## Plot x axis label at line 6 (of 7)
mtext(1, text = "X Axis Label", line = 6)
```

When plotting the x axis labels, we use `srt = 45` for text rotation angle, `adj = 1` to place the right end of text at the tick marks, and `xpd = TRUE` to allow for text outside the plot region. You can adjust the value of the 0.25 offset as required to move the axis labels up or down relative to the x axis. See `?par` for more information.

Also see Figure 1 and associated code in Paul Murrell (2003), “Integrating grid Graphics Output with Base Graphics Output”, *RNews*, **3/2**, 7–12.



## 8 R Programming

### 8.1 How should I write summary methods?

Suppose you want to provide a summary method for class "foo". Then `summary.foo()` should not print anything, but return an object of class "summary.foo", *and* you should write a method `print.summary.foo()` which nicely prints the summary information and invisibly returns its object. This approach is preferred over having `summary.foo()` print summary information and return something useful, as sometimes you need to grab something computed by `summary()` inside a function or similar. In such cases you don't want anything printed.

### 8.2 How can I debug dynamically loaded code?

Roughly speaking, you need to start R inside the debugger, load the code, send an interrupt, and then set the required breakpoints.

See [section "Finding entry points in dynamically loaded code" in \*Writing R Extensions\*](#).

### 8.3 How can I inspect R objects when debugging?

The most convenient way is to call `R_PV` from the symbolic debugger.

See [section "Inspecting R objects when debugging" in \*Writing R Extensions\*](#).

### 8.4 How can I change compilation flags?

Suppose you have C code file for dynloading into R, but you want to use `R CMD SHLIB` with compilation flags other than the default ones (which were determined when R was built). You could change the file '`R_HOME/etc/Makeconf`' to reflect your preferences, or (at least for systems using GNU Make) override them by the environment variable `MAKEFLAGS`. See [section "Creating shared objects" in \*Writing R Extensions\*](#).

### 8.5 How can I debug S4 methods?

Use the `trace()` function with argument `signature=` to add calls to the browser or any other code to the method that will be dispatched for the corresponding signature. See `?trace` for details.

## 9 R Bugs

### 9.1 What is a bug?

If R executes an illegal instruction, or dies with an operating system error message that indicates a problem in the program (as opposed to something like “disk full”), then it is certainly a bug. If you call `.C()`, `.Fortran()`, `.External()` or `.Call()` (or `.Internal()`) yourself (or in a function you wrote), you can always crash R by using wrong argument types (modes). This is not a bug.

Taking forever to complete a command can be a bug, but you must make certain that it was really R’s fault. Some commands simply take a long time. If the input was such that you *know* it should have been processed quickly, report a bug. If you don’t know whether the command should take a long time, find out by looking in the manual or by asking for assistance.

If a command you are familiar with causes an R error message in a case where its usual definition ought to be reasonable, it is probably a bug. If a command does the wrong thing, that is a bug. But be sure you know for certain what it ought to have done. If you aren’t familiar with the command, or don’t know for certain how the command is supposed to work, then it might actually be working right. Rather than jumping to conclusions, show the problem to someone who knows for certain.

Finally, a command’s intended definition may not be best for statistical analysis. This is a very important sort of problem, but it is also a matter of judgment. Also, it is easy to come to such a conclusion out of ignorance of some of the existing features. It is probably best not to complain about such a problem until you have checked the documentation in the usual ways, feel confident that you understand it, and know for certain that what you want is not available. If you are not sure what the command is supposed to do after a careful reading of the manual this indicates a bug in the manual. The manual’s job is to make everything clear. It is just as important to report documentation bugs as program bugs. However, we know that the introductory documentation is seriously inadequate, so you don’t need to report this.

If the online argument list of a function disagrees with the manual, one of them must be wrong, so report the bug.

### 9.2 How to report a bug

When you decide that there is a bug, it is important to report it and to report it in a way which is useful. What is most useful is an exact description of what commands you type, starting with the shell command to run R, until the problem happens. Always include the version of R, machine, and operating system that you are using; type `version` in R to print this.

The most important principle in reporting a bug is to report *facts*, not hypotheses or categorizations. It is always easier to report the facts, but people seem to prefer to strain to posit explanations and report them instead. If the explanations are based on guesses about how R is implemented, they will be useless; others will have to try to figure out what the facts must have been to lead to such speculations. Sometimes this is impossible. But in any case, it is unnecessary work for the ones trying to fix the problem.

For example, suppose that on a data set which you know to be quite large the command

```
R> data.frame(x, y, z, monday, tuesday)
```

never returns. Do not report that `data.frame()` fails for large data sets. Perhaps it fails when a variable name is a day of the week. If this is so then when others got your report they would try out the `data.frame()` command on a large data set, probably with no day of the week variable name, and not see any problem. There is no way in the world that others could guess that they should try a day of the week variable name.

Or perhaps the command fails because the last command you used was a method for `"["()` that had a bug causing R's internal data structures to be corrupted and making the `data.frame()` command fail from then on. This is why others need to know what other commands you have typed (or read from your startup file).

It is very useful to try and find simple examples that produce apparently the same bug, and somewhat useful to find simple examples that might be expected to produce the bug but actually do not. If you want to debug the problem and find exactly what caused it, that is wonderful. You should still report the facts as well as any explanations or solutions. Please include an example that reproduces the problem, preferably the simplest one you have found.

Invoking R with the `'--vanilla'` option may help in isolating a bug. This ensures that the site profile and saved data files are not read.

On Unix systems a bug report can be generated using the function `bug.report()`. This automatically includes the version information and sends the bug to the correct address. Alternatively the bug report can be emailed to [R-bugs@R-project.org](mailto:R-bugs@R-project.org) or submitted to the Web page at <http://bugs.R-project.org/>.

Bug reports on contributed packages should be sent first to the package maintainer, and only submitted to the R-bugs repository by package maintainers, mentioning the package in the subject line.

There is a section of the bug repository for suggestions for enhancements for R labelled `'wishlist'`. Suggestions can be submitted in the same ways as bugs, but please ensure that the subject line makes clear that this is for the wishlist and not a bug report, for example by starting with `'Wishlist:.'`

Comments on and suggestions for the Windows port of R should be sent to [R-windows@R-project.org](mailto:R-windows@R-project.org).

## 10 Acknowledgments

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More to some soon . . .