

R FAQ

Frequently Asked Questions on R
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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., 51 Franklin Street, Fifth Floor, Boston, MA 02110-1301, U.S.A.

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 9).

1.3 Citing this document

In publications, please refer to this FAQ as Hornik (2008), “The R FAQ”, and give the above, *official* URL and the ISBN 3-900051-08-9:

```
@Misc{,
  author      = {Kurt Hornik},
  title       = {The {R} {FAQ}},
  year        = {2008},
  note        = {{{ISBN} 3-900051-08-9}},
  url         = {http://CRAN.R-project.org/doc/FAQ/R-FAQ.html}
}
```

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 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 12) 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 13, 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 22).

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, Luke Tierney, and Simon Urbanek.

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, powerpc-apple-darwin, mips-sgi-irix, rs6000-ibm-aix, 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 2.8.1. 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 9).

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 6), 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 3). 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 6) 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 2000 and later (including 64-bit versions of Windows) on ix86 and x86_64 chips. 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 inside a disk image named `‘R.dmg’`. Once downloaded 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 a R.app Mac OS X GUI. Inside `‘bin/macosx/powerpc/contrib/x.y’` there are prebuilt binary packages (for powerpc version of Mac OS X) 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 R.app 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 the following packages.

	CPU	Versions	Provider
Debian	i386/amd64	etch-cran/sarge	Johannes Ranke
Red Hat	i386/x86_64	fedora7/fedora8/fedora9	Martyn Plummer
	i386/x86_64	el4/el5	Bob Kinney
SuSE	i586/x86_64	10.2/10.3/11.0	Detlef Steuer
Ubuntu	i386	dapper/gutsy/hardy/intrepid	Vincent Goulet
	amd64	dapper/gutsy/hardy/intrepid	Michael Rutter

Debian packages, maintained by Dirk Eddelbuettel and Doug Bates, have long been part of the Debian distribution, and can be accessed through APT, the Debian package maintenance tool. Use e.g. `apt-get install r-base r-recommended` to install the R environment and recommended packages. If you also want to build R packages from source, also run `apt-get install r-base-dev` to obtain the additional tools required for this. So-called “backports” of the current R packages for at least the *stable* distribution of Debian are provided by Johannes Ranke, and available from CRAN. See <http://CRAN.R-project.org/bin/linux/debian/README> for details on R Debian packages and installing the backports, which should also be suitable for other Debian derivatives. Native backports for Ubuntu are provided by Vincent Goulet and Michael Rutter.

On SUSE, you can set up an installation source for R within Yast by setting (e.g.)

```
Protocol: HTTP
Server name: software.opensuse.org
Directory: /download/home:/dststeuer/opensuse_10.2/
```

With this setting, online updates will check for new versions of R.

The ‘bin/solaris’ directory of a CRAN site contains binary packages for Solaris on the SPARC and x64 platforms, provided by Mithun Sridharan.

No other binary distributions are currently publically available via CRAN.

A “live” Linux distribution with a particular focus on R is *Quantian*, which provides a directly bootable and self-configuring “Live DVD” containing numerous applications of interests to scientists and researchers, including several hundred CRAN and Bioconductor packages, the “ESS” extensions for Emacs, the “JGR” Java GUI for R, the Ggobi visualization tool as well as several other R interfaces. The *Quantian* website at <http://dirk.eddelbuettel.com/quantian/> contains more details as well download information.

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 L^AT_EX, see [Section 2.5](#) [How can

R be installed?], page 4. 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 10).

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`).
- “R Internals” (`R-ints`) is a guide to R’s internal structures. (Added in R 2.4.0.)

An annotated bibliography (BibTeX format) of R-related publications can be found at

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

Books on R by R Core Team members include

John M. Chambers (2008), “Software for Data Analysis: Programming with R”. Springer, New York, ISBN 978-0-387-75935-7, <http://stat.stanford.edu/~jmc4/Rbook/>.

Peter Dalgaard (2008), “Introductory Statistics with R”, 2nd edition. Springer, ISBN 978-0-387-79053-4, <http://www.biostat.ku.dk/~pd/ISwR.html>.

Robert Gentleman (2008), “R Programming for Bioinformatics”. Chapman & Hall/CRC, Boca Raton, FL, ISBN 978-1-420-06367-7, <http://www.bioconductor.org/pub/RBioinf/>.

Stefano M. Iacus (2008), “Simulation and Inference for Stochastic Differential Equations: With R Examples”. Springer, New York, ISBN 978-0-387-75838-1.

Deepayan Sarkar (2007), “Lattice: Multivariate Data Visualization with R”. Springer, New York, ISBN 978-0-387-75968-5.

W. John Braun and Duncan J. Murdoch (2007), “A First Course in Statistical Programming with R”. Cambridge University Press, Cambridge, ISBN 978-0521872652.

P. Murrell (2005), “R Graphics”, Chapman & Hall/CRC, ISBN: 1-584-88486-X, <http://www.stat.auckland.ac.nz/~paul/RGraphics/rgraphics.html>.

William N. Venables and Brian D. Ripley (2002), “Modern Applied Statistics with S” (4th edition). Springer, ISBN 0-387-95457-0, <http://www.stats.ox.ac.uk/pub/MASS4/>.

Jose C. Pinheiro and Douglas M. Bates (2000), “Mixed-Effects Models in S and S-Plus”. Springer, ISBN 0-387-98957-0.

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.

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      = 2008,
  note      = {{ISBN} 3-900051-07-0},
  url       = {http://www.R-project.org}
}
```

Citation strings (or Bib_TE_X 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.

R-devel

This list is for questions and discussion about code development in R.

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

Note in particular that R-help is intended to be comprehensible to people who want to use R to solve problems but who are not necessarily interested in or knowledgeable about programming. Questions likely to prompt discussion unintelligible to non-programmers (e.g., questions involving C or C++) should go to R-devel.

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.

Send email to 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 122 for more details.

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 for comments and reports.

Many of the R project’s mailing lists are also available via [Gmane](#), from which they can be read with a web browser, using an NNTP news reader, or via RSS feeds. See <http://dir.gmane.org/index.php?prefix=gmane.comp.lang.r> for the available mailing lists, and <http://www.gmane.org/rss.php> for details on RSS feeds.

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 Wirtschaftsuniversität Wien, Austria, can be found at the URL

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

Daily mirrors are available at URLs including

http://cran.at.R-project.org/	(WU Wien, Austria)
http://cran.au.R-project.org/	(PlanetMirror, Australia)
http://cran.br.R-project.org/	(Universidade Federal do Paraná, Brazil)
http://cran.ch.R-project.org/	(ETH Zürich, Switzerland)
http://cran.dk.R-project.org/	(SunSITE, Denmark)
http://cran.es.R-project.org/	(Spanish National Research Network, Madrid, Spain)
http://cran.fr.R-project.org/	(INRA, Toulouse, France)
http://cran.pt.R-project.org/	(Universidade do Porto, Portugal)
http://cran.uk.R-project.org/	(U of Bristol, United Kingdom)
http://cran.za.R-project.org/	(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 bzipped 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. 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-2, GPL-3, 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 12).

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 6) 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 109) 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 107), 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. Unless `‘--no-environ’` was given on the command line, R searches for site and user files to process for setting environment variables. Then, R searches for a site-wide startup profile unless the command line

option ‘`--no-site-file`’ was given. This code is loaded in package **base**. Then, unless ‘`--no-init-file`’ was given, R searches for a user profile file, 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-data`’ or ‘`--no-restore`’ were specified). Next, a function `.First()` is run if found on the search path. Finally, function `.First.sys` in the **base** package is run. When terminating an R session, by default a function `.Last` is run if found on the search path, followed by `.Last.sys`. If needed, the functions `.First()` and `.Last()` should be defined in the appropriate startup profiles. See the help pages for `.First` and `.Last` for more details.

- 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.
- In R, indexing a vector, matrix, array or data frame with `[]` using a character vector index looks only for exact matches (whereas `[[` and `$` allow partial matches). In S, `[]` allows partial matches.
- S has a two-argument version of `atan` and no `atan2`. A call in S such as `atan(x1, x2)` is equivalent to R’s `atan2(x1, x2)`. However, beware of named arguments since S’s `atan(x = a, y = b)` is equivalent to R’s `atan2(y = a, x = b)` with the meanings of `x` and `y` interchanged. (R used to have undocumented support for a two-argument `atan` with positional arguments, but this has been withdrawn to avoid further confusion.)
- Numeric constants with no fractional and exponent (i.e., only integer) part are taken as integer in S-PLUS 6.x or later, but as double in R.

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 \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?

For a very long time, there was no such thing.

XL Solutions Corporation is currently beta testing a commercially supported version of R named R+ (read R plus).

In addition, **REvolution Computing** has released **RPro**, an enterprise-class statistical analysis system based on R, suitable for deployment in professional, commercial and regulated environments.

Random Technologies offers **RStat**, an enterprise-strength statistical computing environment which combines R with enterprise-level validation, documentation, software support, and consulting services, as well as related R-based products.

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.jstatsoft.org/v04/i01/>).

[Ulf Bartel](#) has developed **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.

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/>.

CGI-based web access to R is also provided at <http://hermes.sdu.dk/cgi-bin/go/>. There are many additional examples of web interfaces to R which basically allow to submit R code to a remote server, see for example the collection of links available from <http://biostat.mc.vanderbilt.edu/twiki/bin/view/Main/StatCompCourse>.

[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, and allows submission of data using both GET and POST methods. 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. David’s paper “CGIwithR: Facilities for Processing Web Forms Using R” was published in the Journal of Statistical Software (<http://www.jstatsoft.org/v08/i10/>). The package is now maintained by [Duncan Temple Lang](#) and has a web page at <http://www.omegahat.org/CGIwithR/>.

Rpad, developed and actively maintained by Tom Short, provides a sophisticated environment which combines some of the features of the previous approaches with quite a bit of Javascript, allowing for a GUI-like behavior (with sortable tables, clickable graphics, editable output), etc.

Jeff Horner is working on the R/Apache Integration Project which embeds the R interpreter inside Apache 2 (and beyond). A tutorial and presentation are available from the project web page at <http://biostat.mc.vanderbilt.edu/twiki/bin/view/Main/RApacheProject>.

Rserve is a project actively developed by Simon Urbanek. It implements a TCP/IP server which allows other programs to use facilities of R. Clients are available from the web site for Java and C++ (and could be written for other languages that support TCP/IP sockets).

OpenStatServer is being developed by a team lead by Greg Warnes; it aims “to provide clean access to computational modules defined in a variety of computational environments (R, SAS, Matlab, etc) via a single well-defined client interface” and to turn computational services into web services.

Two projects use PHP to provide a web interface to R. **R_PHP_Online** by Steve Chen (though it is unclear if this project is still active) is somewhat similar to the above Rcgi and Rweb. **R-php** is actively developed by Alfredo Pontillo and Angelo Mineo and provides both a web interface to R and a set of pre-specified analyses that need no R code input.

webbioc is “an integrated web interface for doing microarray analysis using several of the Bioconductor packages” and is designed to be installed at local sites as a shared computing resource.

Finally, **Rwui** is a web application to create user-friendly web interfaces for R scripts. All code for the web interface is created automatically. There is no need for the user to do any extra scripting or learn any new scripting techniques.

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:

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

ADaCGH	Analysis of data from aCGH experiments.
AER	Functions, data sets, examples and vignettes for the book “Applied Econometrics with R” by Christian Kleiber and Achim Zeileis, 2008, Springer-Verlag, New York.
AIS	Tools to look at the data (“Ad Inidicia Spectata”).
ALS	Multivariate curve resolution alternating least squares (MCR-ALS).
AMORE	A MORE flexible neural network package, providing the TAO robust neural network algorithm.
ARES	Allelic richness estimation, with extrapolation beyond the sample size.

- AcceptanceSampling** Creation and evaluation of acceptance sampling plans,
- AdMit** Adaptive mixture of Student t distributions.
- AdaptFit** Adaptive semiparametric regression.
- AlgDesign** Algorithmic experimental designs. Calculates exact and approximate theory experimental designs for D, A, and I criteria.
- Amelia** Amelia II: a program for missing data.
- AnalyzefMRI** Functions for I/O, visualisation and analysis of functional Magnetic Resonance Imaging (fMRI) datasets stored in the ANALYZE format.
- ArDec** Time series autoregressive decomposition.
- BACCO** Bayesian Analysis of Computer Code Output. Contains **approximator**, **calibrator**, and **emulator**, for Bayesian prediction of complex computer codes, calibration of computer models, and emulation of computer programs, respectively.
- BARD** Better Automated ReDistricting.
- BAYSTAR** Bayesian analysis of threshold autoregressive models.
- BB** Barzilai-Borwein spectral methods for solving nonlinear system of equations, and for optimizing nonlinear objective functions subject to simple constraints.
- BCE** Bayesian Composition Estimator for sample (taxonomic) composition from biomarker data.
- BHH2** Functions and data sets reproducing some examples in “Statistics for Experimenters II” by G. E. P. Box, J. S. Hunter, and W. C. Hunter, 2005, John Wiley and Sons.
- BLCOP** Black-Litterman and copula-opinion pooling frameworks.
- BMA** Bayesian Model Averaging for linear models, generalizable linear models and survival models (Cox regression).
- BPHO** Bayesian Prediction with High-order Interactions.
- BaM** Functions and datasets for “Bayesian Methods: A Social and Behavioral Sciences Approach” (2nd edition) by Jeff Gill, 2007, CRC Press.
- BayHaz** Functions for Bayesian Hazard rate estimation.
- BayesTree** Bayesian methods for tree based models.
- BayesValidate** Bayesian software validation using posterior quantiles.
- Bchron** Create chronologies based on radiocarbon and non-radiocarbon dated depths.
- Bhat** Functions for general likelihood exploration (MLE, MCMC, CIs).
- BiasedUrn** Biased urn model distributions.

- BioIDMapper** Mapping between BioIDs.
- Biodem** A number of functions for biodemographycal analysis.
- BiodiversityR** GUI for biodiversity and community ecology analysis.
- BiplotGUI** Interactive biplots in R.
- Bolstad** Functions and data sets for the book “Introduction to Bayesian Statistics” by W. M. Bolstad, 2004, John Wiley and Sons.
- BootCL** Bootstrapping test for chromosomal localization.
- BootPR** Bootstrap prediction intervals and bias-corrected forecasting.
- BradleyTerry** Specify and fit the Bradley-Terry model and structured versions.
- Brobdingnag** Very large numbers in R.
- BSDA** Data sets for the book “Basic Statistics and Data Analysis” by L. J. Kitchens, 2003, Duxbury.
- BSagri** Statistical methods for safety assessment in agricultural field trials.
- BsMD** Bayes screening and model discrimination follow-up designs.
- CADStat** A GUI to several statistical methods for biological inferences.
- CCA** Canonical correlation analysis.
- CDNmoney** Components of Canadian monetary aggregates.
- CGIwithR** Facilities for the use of R to write CGI scripts.
- CHsharp** Choi and Hall clustering in 3d.
- CORREP** Multivariate correlation estimation.
- COZIGAM** Constrained Zero-Inflated Generalized Additive Model.
- CPE** Concordance probability estimates in survival analysis.
- CTFS** The CTFS large plot forest dynamics analyses.
- CTT** Classical Test Theory functions.
- CVThresh** Level-dependent Cross-Validation Thresholding.
- Cairo** Graphics device using cairographics library for creating high-quality PNG, PDF, SVG, PostScript output and interactive display devices such as X11.
- CarbonEL** Carbon Event Loop.

- CellularAutomaton**
One-dimensional cellular automata.
- ChainLadder**
Mack- and Munich-chain-ladder methods for insurance claims reserving.
- CircStats** Circular Statistics, from “Topics in Circular Statistics” by S. Rao Jammalamadaka and A. SenGupta, 2001, World Scientific.
- CoCo** Graphical modeling for contingency tables using CoCo.
- ComPairWise**
Compare phylogenetic or population genetic data alignments.
- CombMSC**
Combined Model Selection Criteria.
- CompetingRiskFrailty**
Competing risk model with frailties for right censored survival data.
- Containers**
Object-oriented data structures including stack, queue, and binary search tree.
- ConvergenceConcepts**
Seeing convergence concepts in action.
- CoxBoost** Cox survival models by likelihood based boosting.
- CreditMetrics**
Functions for calculating the CreditMetrics risk model.
- CvM2SL2Test**
Cramer-von Mises two sample tests.
- DAAG** Various data sets used in examples and exercises in “Data Analysis and Graphics Using R” by John H. Maindonald and W. John Brown, 2003.
- DAAGbio** Data sets and functions, for demonstrations with expression arrays.
- DAAGxtras**
Data sets and functions additional to **DAAG**.
- DBI** 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.
- DCluster** A set of functions for the detection of spatial clusters of diseases using count data.
- DDHFm** Variance stabilization by Data-Driven Haar-Fisz (for microarrays).
- DEA** Data Envelopment Analysis.
- DEoptim** Differential Evolution Optimization.
- DICOM** Import and manipulate medical imaging data using the Digital Imaging and Communications in Medicine (DICOM) Standard.

DPpackage

Semiparametric Bayesian analysis using Dirichlet process priors.

Davies Functions for the Davies quantile function and the Generalized Lambda distribution.

Defaults Create global function defaults.

DescribeDisplay

R interface to the DescribeDisplay GGobi plugin.

Design 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.

Devore5 Data sets and sample analyses from “Probability and Statistics for Engineering and the Sciences (5th ed)” by Jay L. Devore, 2000, Duxbury.

Devore6 Data sets and sample analyses from “Probability and Statistics for Engineering and the Sciences (6th ed)” by Jay L. Devore, 2003, Duxbury.

Devore7 Data sets and sample analyses from “Probability and Statistics for Engineering and the Sciences (7th ed)” by Jay L. Devore, 2008, Thomson.

DiagnosisMed

Diagnostic test accuracy evaluation for medical professionals.

DierckxSpline

R companion to “Curve and Surface Fitting with Splines” by Paul Dierckx, 1993, Oxford University Press.

EDR Estimation of the effective dimension reduction (EDR) space.

EMC Evolutionary Monte Carlo (EMC) algorithm.

EMCC Evolutionary Monte Carlo (EMC) methods for clustering.

EMD Empirical mode decomposition and Hilbert spectral analysis.

EMV Estimation of missing values in a matrix by a k -th nearest neighbors algorithm.

ETC Tests and simultaneous confidence intervals for equivalence to control.

EVER Estimation of Variance by Efficient Replication.

EbayesThresh

Empirical Bayes thresholding and related methods.

Ecdat Data sets from econometrics textbooks.

EffectiveDose

Estimate the effective dose level for quantal bioassay data by nonparametric techniques.

ElemStatLearn

Data sets, functions and examples from the book “The Elements of Statistical Learning: Data Mining, Inference, and Prediction” by Trevor Hastie, Robert Tibshirani and Jerome Friedman (2001), Springer.

Epi

Statistical analysis in epidemiology, with functions for demographic and epidemiological analysis in the Lexis diagram.

FAiR

Factor Analysis in R, using genetic algorithms.

FGN

Fractional Gaussian Noise model fitting.

FITSio

FITS (Flexible Image Transport System) utilities.

FKBL

Fuzzy Knowledge Base Learning.

FTICRMS

Analysis of Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry data.

FactoClass

Combination of factorial methods and cluster analysis.

FactoMineR

Factor analysis and data mining with R.

Fahrmeir

Data from the book “Multivariate Statistical Modelling Based on Generalized Linear Models” by Ludwig Fahrmeir and Gerhard Tutz (1994), Springer.

FieldSim

Random fields simulations.

FinTS

Companion to the book “Analysis of Financial Time Series” (2nd edition) by Ruey Tsay (2005), Wiley.

FitAR

Subset AR model fitting.

Flury

Data sets from from “A First Course in Multivariate Statistics” by Bernard Flury (1997), Springer.

FrF2

Analysis of fractional factorial designs with 2-level factors.

FracSim

Simulation of one- and two-dimensional fractional and multifractional Levy motions.

FunCluster

Functional profiling of cDNA microarray expression data.

FunNet

Functional analysis of gene co-expression networks.

G1DBN

Dynamic Bayesian Network inference using 1st order conditional dependencies.

GAMBoost

Generalized additive models by likelihood based boosting.

- GDD** Platform and X11 independent device for creating bitmaps (png, gif and jpeg) using the GD graphics library.
- GEOmap** Topographic and geologic mapping.
- GExMap** Functions for the analysis of genomic distribution of genes lists produced by transcriptomic studies.
- GLDEX** Fit RS and FMKL generalised lambda distributions using discretized and maximum likelihood methods.
- GOSim** Computation of functional similarities between GO terms and gene products.
- GPArotation**
Gradient Projection Algorithm rotation for factor analysis.
- GRASS** 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.
- GSA** Gene set analysis.
- GSM** Gamma Shape Mixture.
- GenABEL** Genome-wide SNP association analysis.
- GenKern** Functions for generating and manipulating generalised binned kernel density estimates.
- GeneCycle**
Identification of periodically expressed genes.
- GeneF** Generalized F -statistics.
- GeneNT** Relevance or Dependency network and signaling pathway discovery.
- GeneNet** Modeling and inferring gene networks.
- GeneTS** 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.
- Geneland** MCMC inference from individual genetic data based on a spatial statistical model.
- GeoXp** Interactive exploratory spatial data analysis.
- GillespieSSA**
Gillespie's Stochastic Simulation Algorithm (SSA).
- GridR** Executes functions on remote hosts, clusters or grids.
- GroupSeq** Computations related to group-sequential boundaries.
- HAPim** Methods for QTL detection and fine mapping.
- HH** Support software for "Statistical Analysis and Data Display" by Richard M. Heiberger and Burt Holland, Springer, 2005.

- HI** Simulation from distributions supported by nested hyperplanes.
- HSAUR** Functions, data sets, analyses and examples from the book “A Handbook of Statistical Analyses Using R” by Brian S. Everitt and Torsten Hothorn (2006), Chapman & Hall/CRC.
- HTMLapplets**
Functions inserting dynamic scatterplots and grids in documents generated by **R2HTML**.
- HFWutils** Utilities by H. Felix Wittmann: Excel connections, string matching, and passing by reference.
- HardyWeinberg**
Graphical tests for Hardy-Weinberg equilibrium.
- HiddenMarkov**
Hidden Markov Models.
- 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.
- HydroMe** Estimation of soil hydraulic parameters from experimental data.
- 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.
- IBrokers** R API to Interactive Brokers Trader Workstation.
- ICE** Iterated Conditional Expectation: kernel estimators for interval-censored data.
- ICEinfer** Incremental Cost-Effectiveness (ICE) statistical inference (from two unbiased samples).
- ICS** ICS/ICA computation based on two scatter matrices.
- ICSNP** Tools for multivariate nonparametrics.
- IDPmisc** Utilities from the Institute of Data Analyses and Process Design, IDP/ZHW.
- ISA** Functions to support “Introduzione alla Statistica Applicata con esempi in R” by Federico M. Stefanini, Pearson Education Milano, 2007.
- ISOcodes** ISO language, territory, currency, script and character codes.
- ISwR** Data sets for “Introductory Statistics with R” by Peter Dalgaard, 2002, Springer.
- Icens** Functions for computing the NPMLE for censored and truncated data.
- Iso** Functions to perform isotonic regression.

- JADE** JADE and ICA performance criteria.
- JGR** Java Gui for R.
- JM** Joint Modeling of longitudinal and survival data.
- JavaGD** Java Graphics Device.
- JointGLM** Joint modeling of mean and dispersion through two interlinked GLM's. *Defunct* in favor of **JointModeling**.
- JointModeling**
Joint modeling of mean and dispersion.
- JudgeIt** Calculates bias, responsiveness, and other characteristics of two-party electoral systems, with district-level electoral and other data.
- KMsurv** Data sets and functions for “Survival Analysis, Techniques for Censored and Truncated Data” by Klein and Moeschberger, 1997, Springer.
- Kendall** Kendall rank correlation and Mann-Kendall trend test.
- KernSmooth**
Functions for kernel smoothing (and density estimation) corresponding to the book “Kernel Smoothing” by M. P. Wand and M. C. Jones, 1995. *Recommended*.
- LDheatmap**
Heat maps of linkage disequilibrium measures.
- LDtests** Exact tests for linkage disequilibrium and Hardy-Weinberg equilibrium.
- LIM** Linear Inverse Model examples and solution methods.
- LIStest** Longest increasing subsequence independence test.
- LLAhclust** Hierarchical clustering of variables or objects based on the likelihood linkage analysis method.
- LLN** Learning with latent networks.
- LMGene** Date transformation and identification of differentially expressed genes in gene expression arrays.
- LearnBayes**
Functions for Learning Bayesian Inference.
- Lmoments** Estimation of L-moments and the parameters of normal and Cauchy polynomial quantile mixtures.
- LogConcDEAD**
Maximum likelihood estimation of a log-concave density.
- LogicReg** Routines for Logic Regression.
- LoopAnalyst**
A collection of tools to conduct Levins' Loop Analysis.

LowRankQP

Low Rank Quadratic Programming: QP problems where the hessian is represented as the product of two matrices.

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

MAclinical

Class prediction based on microarray data and clinical parameters.

MBA Multilevel B -spline Approximation.

MBESS Methods for the Behavioral, Educational, and Social Sciences.

MCAPS Weather and air pollution data, risk estimates, and other information from the Medicare Air Pollution Study (MCAPS) of 204 U.S. counties, 1999–2002.

MCE Tools for evaluating Monte Carlo Error.

MCMCpack

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

MCPAN Multiple comparisons using normal approximation.

MCPMod Design and analysis of dose-finding studies.

MChtest Monte Carlo hypothesis tests.

MDD Minimum Detectable Difference calculations for several continuous and binary endpoints.

MEMSS Data sets and sample analyses from “Mixed-effects Models in S and S-PLUS” by J. Pinheiro and D. Bates, 2000, Springer.

MFDA Model Based Functional Data Analysis.

Mifuns Pharmacometric tools for data preparation, analysis, simulation, and reporting.

MKLE Maximum kernel likelihood estimation.

MKmisc Miscellaneous Functions from M. Kohl.

MLDA Methylation Linear Discriminant Analysis (MLDA).

MLDS Maximum Likelihood Difference Scaling.

MLEcens Computation of the MLE for bivariate (interval) censored data.

MMG Mixture Model on Graphs.

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.

MSBVAR Bayesian vector autoregression models, impulse responses and forecasting.

- MSVAR** Markov Switching VAR.
- MarkedPointProcess**
Non-parametric analysis of the marks of marked point processes.
- MasterBayes**
Maximum likelihood and Markov chain Monte Carlo methods for pedigree reconstruction, analysis and simulation.
- MatchIt** Select matched samples of the original treated and control groups with similar covariate distributions.
- Matching** Multivariate and propensity score matching with formal tests of balance.
- Matrix** A Matrix package.
- Metabonomic**
GUI for metabonomic analysis.
- MiscPsycho**
Miscellaneous Psychometrics.
- MultEq** Equivalence tests and simultaneous confidence intervals for multiple endpoints.
- 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.
- NMMAPlite**
U.S. National Morbidity, Mortality, and Air Pollution Study data lite.
- NORMT3** Evaluates complex erf, erfc and density of sum of Gaussian and Student’s t .
- NRAIA** Data sets with sample code from “Nonlinear Regression Analysis and Its Applications” by Doug Bates and Donald Watts, 1988, Wiley.
- NestedCohort**
Survival analysis for cohorts with missing covariate information.
- NetIndices**
Estimates network indices, including trophic structure of foodwebs.
- OPE** Fit an outer-product emulator to the multivariate evaluations of a computer model.
- ORMDR** Odds ratio based multivector-dimensionality reduction method for detecting gene-gene interactions.
- Oarray** Arrays with arbitrary offsets.
- PASWR** Data and functions for the book “Probability and Statistics with R” by M. D. Ugarte, A. F. Militino and A. T. Arnholt, 2008, Chapman & Hall/CRC.
- PBSddesolve**
Solver for delay differential equations.

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.

PBSmodelling

Software to facilitate the design, testing, and operation of computer models.

PET

Simulation and reconstruction of PET images.

PHYLOGR

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

PK

Estimation of pharmacokinetic parameters.

PKfit

A nonlinear regression (including a genetic algorithm) program designed to deal with curve fitting for pharmacokinetics.

Unified computational interfaces for pop PK.

POT

Generalized Pareto distribution and Peaks Over Threshold.

PSAgraphics

Propensity Score Analysis Graphics.

PSM

Non-linear mixed-effects modeling using stochastic differential equations.

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.

PairViz

Visualization using Eulerian tours and Hamiltonian decompositions.

Peaks

Spectrum manipulation: background estimation, Markov smoothing, deconvolution and peaks search functions.

PearsonICA

Independent component analysis using score functions from the Pearson system.

PerformanceAnalytics

Econometric tools for performance and risk analysis.

PhySim

Phylogenetic tree simulation.

PolynomF

Univariate polynomials.

Pomic

Pattern oriented modeling information criterion.

PredictiveRegression

Prediction intervals for three basic statistical models.

PresenceAbsence

Presence-absence model evaluation.

ProbForecastGOP

Probabilistic weather field forecasts using the Geostatistical Output Perturbation method introduced by Gel, Raftery and Gneiting (2004).

- ProbeR** Reliability for gene expression from Affymetrix chip.
- ProfessR** Programs to determine student grades and create examinations from question banks.
- PtProcess** Time dependent point process modeling.
- PwrGSD** Power in a Group Sequential Design.
- QCA** Qualitative Comparative Analysis for crisp sets.
- QCAGUI** QCA Graphical User Interface.
- QRMLib** Code to examine Quantitative Risk Management concepts.
- QuantPsyc**
Quantitative Psychology tools.
- R.cache** Fast and light-weight caching of objects.
- R.huge** Methods for accessing huge amounts of data.
- R.matlab** Read and write of MAT files together with R-to-Matlab connectivity.
- R.methodsS3**
Utility functions for defining S3 methods.
- R.oo** R object-oriented programming with or without references.
- R.rsp** R server pages.
- R.utils** Utility classes and methods useful when programming in R and developing R packages.
- 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.
- R2jags** Call JAGS from R.
- RArcInfo** Functions to import Arc/Info V7.x coverages and data.
- RBGL** Interface to the boost C++ graph library.
- RBloomberg**
Fetch data from a Bloomberg API using COM.
- RColorBrewer**
ColorBrewer palettes for drawing nice maps shaded according to a variable.
- RDieHarder**
R interface to the dieharder random number generator test suite.
- REQS** R/EQS interface.
- RExcelInstaller**
Integration of R and Excel under MS Windows.

RFA	Regional Frequency Analysis.
RFOC	Graphics for spherical distributions and earthquake focal mechanisms.
RFreak	An R interface to a modified version of the Free Evolutionary Algorithm Kit FrEAK.g
RGtk2	Facilities for programming graphical interfaces using Gtk (the Gimp Tool Kit) version 2.
RGrace	Mouse/menu driven interactive plotting application.
RGraphics	Data and functions from the book “R Graphics” by Paul Murrell, 2005, Chapman & Hall/CRC.
RHRV	Heart rate variability analysis of ECG data.
RHmm	Hidden Markov Model simulations and estimations.
RII	Estimation of the relative index of inequality for interval-censored data using natural cubic splines.
RIttools	Randomization inference tools.
RJDBC	Access to databases through the JDBC interface.
RJaCGH	Reversible Jump MCMC for the analysis of CGH arrays.
RKEA	R/KEA interface for extracting keyphrases from text documents.
RLMM	A genotype calling algorithm for Affymetrix SNP arrays.
RLRsim	Exact (Restricted) Likelihood Ratio tests for mixed and additive models.
RLadyBug	Analysis of infectious diseases using stochastic epidemic models.
RM2	Revenue management and pricing.
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.
ROCR	Visualizing the performance of scoring classifiers.
RODBC	An ODBC database interface.
ROptEst	Optimally robust estimation.
ROptEstTS	Optimally robust estimation for regression-type models.
ROracle	Oracle Database Interface driver for R. Uses the ProC/C++ embedded SQL.
RPMG	Poor Man’s Gui: create interactive R analysis sessions.
RPostgreSQL	R interface to the PostgreSQL database system.

- RPyGeo** ArcGIS Geoprocessing in R via Python.
- 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.
- RSAGA** SAGA geoprocessing and terrain analysis in R.
- RSEIS** Seismic time series analysis tools.
- RSQLite** Database Interface R driver for SQLite. Embeds the SQLite database engine in R.
- RScaLAPACK**
An interface to ScaLAPACK functions from R.
- RSVGTipsDevice**
An R SVG graphics device with dynamic tips and hyperlinks.
- RSeqMeth**
analysis of Sequenom EpiTYPER data.
- RSvgDevice**
A graphics device for R that uses the new w3.org XML standard for Scalable Vector Graphics.
- RTOMO** Visualization for seismic tomography.
- RTisean** R interface to Tisean algorithms.
- RUnit** Functions implementing a standard Unit Testing framework, with additional code inspection and report generation tools.
- RWeka** An R interface to Weka, a rich collection of machine learning algorithms for data mining tasks.
- RWinEdt** A plug in for using WinEdt as an editor for R.
- RXshrink** Maximum Likelihood Shrinkage via Ridge or Least Angle Regression.
- 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).
- RandVar** Implementation of random variables by means of S4 classes and methods.
- RandomFields**
Creating random fields using various methods.
- RankAggreg**
Weighted rank aggregation.
- RaschSampler**
Sampling binary matrices with fixed margins.
- Ratings** Model-based ratings figures.

- Rcapture** Loglinear models in capture-recapture experiments.
- Rcmdr** A platform-independent basic-statistics GUI (graphical user interface) for R, based on the **tcltk** package.
- RcmdrPlugin.Export**
Graphically export objects to L^AT_EX or HTML.
- RcmdrPlugin.FactoMineR**
Rcmdr plug-in for the **FactoMineR** package.
- RcmdrPlugin.HH**
Rcmdr support for the introductory course at Temple University.
- RcmdrPlugin.IPSUR**
Rcmdr plugin for “Introduction to Probability and Statistics Using R”.
- RcmdrPlugin.SurvivalT**
Rcmdr survival plug-in.
- RcmdrPlugin.TeachingDemos**
Rcmdr Teaching Demos plug-in.
- RcmdrPlugin.epack**
Rcmdr epack demos plug-in.
- RcmdrPlugin.orloca**
Rcmdr orloca plug-in.
- Rcplex** R interface to CPLEX solvers for linear, quadratic, and (linear and quadratic) mixed integer programs.
- Rcpp** R/C++ interface library and package template.
- Read.isi** Access old data saved in fixed-width format based on ISI-formatted codebooks.
- Reliability** Functions for estimating parameters in software reliability models.
- ResearchMethods**
Using GUIs to help teach statistics to non-statistics students.
- ResistorArray**
Electrical properties of resistor networks.
- Rfwdmv** Forward Search for Multivariate Data.
- Rglpk** R/GNU Linear Programming Kit interface.
- RiboSort** Classification and analysis of microbial community profiles.
- Rigroup** Provides small integer group functions.
- Rlab** Functions and data sets for the NCSU ST370 class.
- Rlabkey** Data retrieval from a Labkey database.
- Rlsf** Interface to the LSF queuing system.
- Rmdr** R-Multifactor Dimensionality Reduction.

- 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.
- RobAStBase** Base classes and functions for robust asymptotic statistics.
- RobLox** Optimally robust influence curves for location and scale.
- RobRex** Optimally robust influence curves for regression and scale.
- Rpad** Utility functions for the Rpad workbook-style interface.
- Rsac** Seismic tools for R.
- Rserve** A socket server (TCP/IP or local sockets) which allows binary requests to be sent to R.
- Rsgc** Interface to the SGE cluster/grid queuing system.
- Rsundials** SUite of Nonlinear DIfferential ALgebraic equations Solvers in R.
- Rsymphony** An R interface to the SYMPHONY mixed integer linear program (MILP) solver.
- Runuran** Interface to the UNU.RAN library for Universal Non-Uniform RANdom variate generators.
- Rvelslant** Downhole seismic analysis.
- 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.
- Ryacac** An R interfaces to the yacas computer algebra system.
- SASPECT** Significant AnalysiS of PEptide CounTs.
- 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.
- SASxport** Read and write SAS XPORT files.
- SDaA** Functions and data sets from “Sampling: Design and Analysis” by S. Lohr, 1999, Duxbury.
- SDDA** Stepwise Diagonal Discriminant Analysis.
- SGP** Student growth percentile and percentile growth projection/trajectory functions.
- SIN** A SINful approach to selection of Gaussian Graphical Markov Models.
- SLmisc** Miscellaneous Functions for analysis of gene expression data at SIRS-Lab GmbH.

- SMC** Sequential Monte Carlo (SMC) Algorithm.
- SMPracticals** Data sets and a few functions for use with the practicals outlined in Appendix A of the book “Statistical Models” by Anthony Davison, 2003, Cambridge University Press.
- SMVar** Structural Model for Variances to detect differentially expressed genes.
- SNPMaP** SNP Microarrays and Pooling in R.
- SNPMaP.cdm** Annotation for SNP microarrays and pooling in R.
- SNPassoc** SNP-based whole genome association studies.
- SNPmaxsel** Maximally selected statistics for SNP data.
- SQLiteMap** Manage vector graphical maps using SQLite.
- SQLiteDF** Stores data frames and matrices in SQLite tables.
- SRPM** Shared Reproducibility Package Management.
- STAR** Spike Train Analysis with R.
- SciViews** A bundle of packages to implement a full reusable GUI API for R. Contains **svGUI** with the main GUI features, **svDialogs** for the dialog boxes, **svIO** for data import/export, **svMisc** with miscellaneous supporting functions, and **svViews** providing views and report features (views are HTML presentations of the content of R objects, combining text, tables and graphs in the same document).
- SemiPar** Functions for semiparametric regression analysis, to complement the book “Semiparametric Regression” by R. Ruppert, M. P. Wand, and R. J. Carroll, 2003, Cambridge University Press.
- SenSrivastava** Collection of datasets from “Regression Analysis, Theory, Methods and Applications” by A. Sen and M. Srivastava, 1990, Springer.
- SensoMineR** Sensory data analysis.
- SeqKnn** Sequential KNN imputation.
- SharedHT2** Shared Hotelling T^2 test for small sample microarray experiments.
- SiZer** Significant Zero crossings.
- SimComp** Simultaneous Comparisons for multiple endpoints.
- SimHap** A comprehensive modeling framework for epidemiological outcomes and a multiple-imputation approach to haplotypic analysis of population-based data.

SimpleTable

Bayesian inference and sensitivity analysis for causal effects from 2×2 and $2 \times 2 \times K$ tables in the presence of unmeasured confounding.

Snowball Snowball stemmers.

SoDA Utilities and examples from the book “Software for Data Analysis: Programming with R” by John Chambers, Springer, 2008.

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

SparseLogReg

Sparse logistic regression.

SparseM Basic linear algebra for sparse matrices.

SpatialExtremes

Modeling spatial extremes.

SpatialNP Multivariate nonparametric methods based on spatial signs and ranks.

SpherWave

Spherical Wavelets and SW-based spatially adaptive methods.

StatDA Statistical analysis for environmental data, a companion to the book “Statistical Data Analysis Explained: Applied Environmental Statistics with R” by C. Reimann, P. Filzmoser, R. G. Garrett, and R. Dutter, 2008, John Wiley and Sons.

StatDataML

Read and write StatDataML.

StatFingerprints

Processing and statistical analysis of molecular fingerprint profiles.

StatMatch

Functions to perform statistical matching between two data sources.

StreamMetabolism

Calculation of single station metabolism from diurnal oxygen curves.

SubpathwayMiner

Annotation and identification of metabolic sub-pathways and pathways.

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).

SweaveListingUtils

Utilities for Sweave together with T_EX listings package.

SwissAir Air quality data of Switzerland for one year in 30 min resolution.

SyNet Inference and analysis of sympatry networks.

Synth Causal inference using the synthetic control group method.

- TIMP** A problem solving environment for fitting superposition models.
- TRAMPR** Terminal Restriction Fragment Length Polymorphism (TRFLP) Analysis and Matching Package for R.
- TSA** Functions and datasets detailed in the book “Time Series Analysis With Applications in R” (3rd edition) by Jonathan Cryer and Kung-Sik Chan, 2008, Springer.
- TSHRC** Two Stage Hazard Rate Comparison.
- TSMYSQL**
Time Series Database Interface extensions for MySQL.
- TSP** Traveling Salesperson Problem (TSP).
- TSPostgreSQL**
Time Series Database Interface extensions for PostgreSQL.
- TSSQLite** Time Series Database Interface extensions for SQLite.
- TSdbi** Time Series Database Interface.
- TSfame** Time Series Database Interface extensions for fame.
- TShistQuote**
Time Series Database Interface interface for get.hist.quote.
- TSodbc** Time Series Database Interface extensions for ODBC.
- TSpadi** Connect to a time series database (e.g., Fame) via PADI (Protocol for Application Database Interface), using the **TSdbi** infrastructure.
- TTR** Technical Trading Rules.
- TWIX** Trees With eXtra splits.
- TeachingDemos**
A set of demonstration functions that can be used in a classroom to demonstrate statistical concepts, or on your own to better understand the concepts or the programming.
- TinnR** Resources for the Tinn-R GUI/Editor for R.
- TraMineR** Sequences and trajectories mining for social scientists.
- TwoWaySurvival**
Additive two-way hazards modeling of right censored survival data.
- TwslmSpikeWeight**
Normalization of cDNA microarray data with the two-way semilinear model (TW-SLM).
- UNF** Tools for creating universal numeric fingerprints for data.
- USPS** Unsupervised and Supervised methods of Propensity Score adjustment for bias.
- Umacs** Universal MArkov Chain Sampler.

UsingR	Data sets to accompany the textbook “Using R for Introductory Statistics” by J. Verzani, 2005, Chapman & Hall/CRC.
VDCutil	Utilities supporting VDC, an open source digital library system for quantitative data.
VGAM	Vector Generalized Linear and Additive Models.
VIM	Visualization and Imputation of Missing Values.
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).
VhayuR	R interface to the Vhayu Velocity high volume fast financial market data archival and analysis products.
WINRPACK	Reads in WIN pickfile and waveform files.
WWGbook	Functions and datasets for the book “Linear Mixed Models: A Practical Guide Using Statistical Software” by B. West, K. Welch, and A. Galecki, 2006, Chapman & Hall/CRC.
WaveCGH	Wavelet changepoint detection for array CGH.
WeedMap	Map of weed intensity.
WhatIf	Software for evaluating counterfactuals.
XML	Tools for reading XML documents and DTDs.
XReg	Extreme regression.
YaleToolkit	Data exploration tools from Yale University.
ZIGP	Zero Inflated Generalized Poisson (ZIGP) regression models.
Zelig	Everyone’s statistical software: an easy-to-use program that can estimate, and help interpret the results of, an enormous range of statistical models.
aaMI	Mutual information for protein sequence alignments.
abind	Combine multi-dimensional arrays.
accuracy	A suite of tools designed to test and improve the accuracy of statistical computation.
acepack	ACE (Alternating Conditional Expectations) and AVAS (Additivity and Variance Stabilization for regression) methods for selecting regression transformations.
actuar	Functions related to actuarial science applications.
ada	Performs boosting algorithms for a binary response.

- adabag** Adaboost.M1 and Bagging.
- adapt** Adaptive quadrature in up to 20 dimensions.
- ade4** Multivariate data analysis and graphical display.
- ade4TkGUI**
Tcl/Tk Graphical User Interface for **ade4**.
- adegenet** Genetic data handling for multivariate analysis using **ade4**.
- adehabitat**
A collection of tools for the analysis of habitat selection by animals.
- adimpro** Adaptive smoothing of digital images.
- adk** Anderson-Darling K -sample test and combinations of such tests.
- adlift** Adaptive Wavelet transforms for signal denoising.
- ads** Spatial point patterns analysis.
- agce** Analysis of growth curve experiments.
- agreement** Analyze the agreement between two measurement methods.
- agricolae** Statistical procedures for agricultural research.
- agsemisc** Miscellaneous plotting and utility functions.
- akima** Linear or cubic spline interpolation for irregularly gridded data.
- allelic** A fast, unbiased and exact allelic exact test.
- alr3** Methods and data to accompany the textbook “Applied Linear Regression” by S. Weisberg, 2005, Wiley.
- amap** Another Multidimensional Analysis Package.
- amei** Adaptive Management of Epidemiological Interventions.
- anacor** Simple and Canonical Correspondence Analysis.
- analogue** Analogue methods for palaeoecology.
- anapuce** Tools for microarray data analysis.
- animation** Demonstrate animations in statistics.
- anm** Analog model for statistical/empirical downscaling.
- aod** Analysis of Overdispersed Data.
- apTreeshape**
Analyses of phylogenetic treeshape.
- ape** 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.

- aplpack** Another PLOt PACKAge: stem.leaf, bagplot, faces, spin3R, . . .
- apstable** American Political Science Review style table formatting.
- archetypes**
Archetypal analysis.
- argosfilter** Argos locations filter.
- arm** Data Analysis using Regression and Multilevel/hierarchical models.
- arrayImpute**
Missing imputation for microarray data.
- arrayMissPattern**
Exploratory analysis of missing patterns for microarray data.
- ars** Adaptive Rejection Sampling.
- arules** Mining association rules and frequent itemsets with R.
- arulesSequences**
Mining frequent sequences.
- ash** David Scott's ASH routines for 1D and 2D density estimation.
- aspace** Estimating centrographic statistics and computational geometries from spatial point patterns.
- assist** A suite of functions implementing smoothing splines.
- aster** Functions and datasets for Aster modeling (forest graph exponential family conditional or unconditional canonical statistic models for life history trait modeling).
- asymptTest**
Asymptotic testing.
- asypow** A set of routines that calculate power and related quantities utilizing asymptotic likelihood ratio methods.
- audio** Audio interface for R.
- asuR** Functions and data sets for a lecture in "Advanced Statistics using R".
- aws** Functions to perform adaptive weights smoothing.
- aylmer** A generalization of Fisher's exact test.
- backfitRichards**
Backfitted independent values of Richards curves.
- backtest** Exploring portfolio-based hypotheses about financial instruments.
- bark** Bayesian Additive Regression Kernels.
- bayesGARCH**
Bayesian estimation of the GARCH(1,1) model with Student's t innovations.
- bayesSurv** Bayesian survival regression with flexible error and (later on also random effects) distributions.

bayescount	Bayesian analysis of count distributions with JAGS.
bayesm	Bayes Inference for Marketing/Micro-econometrics.
bayesmix	Bayesian mixture models of univariate Gaussian distributions using JAGS.
bbmle	Modifications and extensions of stats4 MLE code.
bcp	Bayesian Change Point based on the Barry and Hartigan product partition model.
beanplot	Visualization via beanplots.
bear	Bioavailability and bioequivalence data analysis with crossover design.
benchden	28 benchmark densities from Berlinet/Devroye (1994).
bentcableAR	Bent-cable regression for independent data or autoregressive time series.
betaper	Distance decay of similarity among biological inventories in the face of taxonomic uncertainty.
betareg	Beta regression for modeling rates and proportions.
bs	Utilities for the Birnbaum-Saunders distribution.
biOps	Basic image operations and image processing.
biOpsGUI	GUI for Basic image operations.
biclust	BiCluster algorithms.
bicreduc	Reduction algorithm for the NPMLE for the distribution function of bivariate interval-censored data.
bifactorial	Inferences for bi- and trifactorial trial designs.
biglm	Linear regression for data too large to fit in memory.
bigmemory	Manage massive matrices in R using C++, with UNIX support for shared memory.
bim	Bayesian interval mapping diagnostics: functions to interpret QTLCart and Bmapqtl samples.
binGroup	Evaluation and experimental design for binomial group testing.
binMto	Asymptotic simultaneous confidence intervals for many-to-one comparisons of proportions.
bindata	Generation of correlated artificial binary data.
binom	Binomial confidence intervals for several parameterizations.
bio.infer	Compute biological inferences.
biopara	Self-contained parallel system for R.

- bipartite** Visualises bipartite networks and calculates some ecological indices.
- birch** Dealing with very large datasets using BIRCH.
- bise** Auxiliary functions for phenological data analysis.
- bit** A class for vectors of 1-bit booleans.
- bitops** Functions for Bitwise operations on integer vectors.
- bivpois** Bivariate Poisson models using the EM algorithm.
- blighty** Function for drawing the coastline of the United Kingdom.
- blockTools** Block, randomly assign, and diagnose potential problems between units in randomized experiments.
- blockmodeling**
Generalized and classical blockmodeling of valued networks.
- blockrand** Randomization for block random clinical trials.
- bmd** Benchmark dose analysis for dose-response data.
- bnlearn** Bayesian network structure learning.
- boa** Bayesian Output Analysis Program for MCMC.
- boolean** Boolean logit and probit: a procedure for testing Boolean hypotheses.
- boost** Boosting methods for real and simulated data, featuring ‘BagBoost’, ‘Logit-Boost’, ‘AdaBoost’, and ‘L2Boost’.
- boot** 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. *Recommended.*
- bootStepAIC**
Model selection by bootstrapping the `stepAIC()` procedure.
- bootstrap** Software (bootstrap, cross-validation, jackknife), data and errata for the book “An Introduction to the Bootstrap” by B. Efron and R. Tibshirani, 1993, Chapman and Hall.
- bpca** Biplot of multivariate data based on Principal Components Analysis.
- bqtl** QTL mapping toolkit for inbred crosses and recombinant inbred lines. Includes maximum likelihood and Bayesian tools.
- brainwaver**
Basic wavelet analysis of multivariate time series with a visualization and parametrization using graph theory.
- brew** Templating framework for report generation.
- brglm** Bias-reduction in binomial-response GLMs.
- bspec** Bayesian inference on the (discrete) power spectrum of time series.
- bvls** The Stark-Parker algorithm for bounded-variable least squares.

ca	Simple, multiple and joint Correspondence Analysis.
caMassClass	Processing and Classification of protein mass spectra (SELDI) data.
caTools	Miscellaneous utility functions, including reading/writing ENVI binary files, a LogitBoost classifier, and a base64 encoder/decoder.
cacheSweave	Tools for caching Sweave computations.
acher	Tools for caching and distributing statistical analyses.
cairoDevice	Loadable CAIRO/GTK device driver.
calib	Statistical tool for calibration of plate based bioassays.
calibrate	Calibration of biplot axes.
candisc	Generalized canonical discriminant analysis.
car	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.
caret	Classification and REgression Training.
caretLSF	Classification and REgression Training, LSF style.
caretNWS	Classification and REgression Training in parallel using NetworkSpaces.
cat	Analysis of categorical-variable datasets with missing values.
catmap	Case-control and TDT meta-analysis package.
catspec	Special models for categorical variables.
cba	Clustering for Business Analytics, including implementations of Proximus and Rock.
ccgarch	Conditional Correlation GARCH models.
cclust	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.
celsius	Retrieve Affymetrix microarray measurements and metadata from Celsius.
cem	The coarsened exact matching algorithm (and many extensions).
cfa	Analysis of configuration frequencies.
cggd	Continuous Generalized Gradient Descent.
cgh	Analysis of microarray comparative genome hybridisation data using the Smith-Waterman algorithm.
cghFLasso	Hot spot detecting for CGH array data with fused lasso regression.

- chplot** Augmented convex hull plots: informative and nice plots for grouped bivariate data.
- changeLOS** Change in length of hospital stay (LOS).
- cheb** Discrete linear Chebyshev approximation.
- chemCal** Calibration functions for analytical chemistry.
- chemometrics** Companion to the book “Introduction to Multivariate Statistical Analysis in Chemometrics” by K. Varmuza and P. Filzmoser, CRC Press, to appear.
- choplump** Choplump tests (permutation tests for comparing two groups with some positive but many zero responses).
- chron** A package for working with chronological objects (times and dates).
- cir** Nonparametric estimation of monotone functions via isotonic regression and centered isotonic regression.
- circular** Circular statistics, from “Topics in Circular Statistics” by Rao Jammalamadaka and A. SenGupta, 2001, World Scientific.
- clValid** Statistical and biological validation of clustering results.
- clac** Clust Along Chromosomes, a method to call gains/losses in CGH array data.
- class** Functions for classification (k -nearest neighbor and LVQ). Contained in the ‘VR’ bundle. *Recommended*.
- classGraph** Construct graph of S4 class hierarchies.
- classInt** Choose univariate class intervals for mapping or other graphics purposes.
- classPP** Projection Pursuit for supervised classification.
- classify** Explore classification models in high dimensions.
- clim.pact** Climate analysis and downscaling for monthly and daily data.
- climatol** Functions to fill missing data in climatological (monthly) series and to test their homogeneity, plus functions to draw wind-rose and Walter&Lieth diagrams.
- clinfun** Utilities for clinical study design and data analyses.
- clue** CLUster Ensembles.
- clustTool** GUI for clustering data with spatial information.
- cluster** Functions for cluster analysis. *Recommended*.
- clusterGeneration** Random cluster generation (with specified degree of separation).
- clusterRepro** Reproducibility of gene expression clusters.

- clusterSim** Searching for optimal clustering procedure for a data set.
- clusterfly** Explore clustering interactively using R and GGobi.
- clustvarsel** Variable selection for model-based clustering.
- clv** Cluster validation techniques.
- cmprsk** Estimation, testing and regression modeling of subdistribution functions in competing risks.
- cobs99** Constrained B-splines: outdated 1999 version.
- cobs** Constrained B-splines: qualitatively constrained (regression) smoothing via linear programming and sparse matrices.
- cocorresp** Co-correspondence analysis ordination methods for community ecology.
- coda** Output analysis and diagnostics for Markov Chain Monte Carlo (MCMC) simulations.
- codetools** Code analysis tools. *Recommended* for R 2.5.0 or later.
- coin** COnditional INference procedures for the general independence problem including two-sample, K -sample, correlation, censored, ordered and multivariate problems.
- colorRamp** Builds single and double gradient color maps.
- colorspace** Mapping between assorted color spaces.
- combinat** Combinatorics utilities.
- compHclust** Complementary hierarchical clustering.
- compOverlapCorr** Comparing overlapping correlation coefficients.
- compare** Comparing objects for differences.
- compoisson** Conway-Maxwell-Poisson distribution.
- compositions** Functions for the consistent analysis of compositional data (e.g., portions of substances) and positive numbers (e.g., concentrations).
- concor** Concordance, providing “SVD by blocks”.
- concord** Measures of concordance and reliability.
- conf.design** A series of simple tools for constructing and manipulating confounded and fractional factorial designs.
- connectedness** Find disconnected sets for two-way classification.

confrac	Continued fractions.
contrast	A collection of contrast methods.
convexHaz	Nonparametric MLE/LSE of convex hazard.
copas	Statistical methods to model and adjust for bias in meta-analysis.
copula	Classes of commonly used copulas (including elliptical and Archimedean), and methods for density, distribution, random number generators, and plotting.
corcounts	Generate correlated count random variables.
corpcor	Efficient estimation of covariance and (partial) correlation.
corpora	Utility functions for the statistical analysis of corpus frequency data.
corrgram	Plot a correlogram.
corrperm	Permutation tests of correlation with repeated measurements.
covRobust	Robust covariance estimation via nearest neighbor cleaning.
coxphf	Cox regression with Firth's penalized likelihood.
coxphw	Weighted estimation for Cox regression.
coxrobust	Robust Estimation in the Cox proportional hazards regression model.
cramer	Routine for the multivariate nonparametric Cramer test.
crank	Functions for completing and recalculating rankings.
crawl	(C)orrelated (RA)ndom (W)alk (L)ibrary for fitting continuous-time correlated random walk models for animal movement data.
crossdes	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.
crosshybDetector	Detection of cross-hybridization events in microarray experiments.
crq	Quantile regression for randomly censored data.
cslogistic	Likelihood and posterior analysis of conditionally specified logistic regression models.
cts	Continuous time autoregressive models and the Kalman filter.
ctv	Server-side and client-side tools for CRAN task views.
curvetest	Test the equality of two curves, or one curve with 0.
cwhmisc	Miscellaneous functions by Christian W. Hoffmann.
cyclones	Cyclone identification.
data.table	Extension of data frames to allow subscripting by expressions evaluated within the frame.

dataframes2xls	Write data frames to <code>‘.xls’</code> files.
date	Functions for dealing with dates. The most useful of them accepts a vector of input dates in any of the forms <code>‘8/30/53’</code> , <code>‘30Aug53’</code> , <code>‘30 August 1953’</code> , . . . , <code>‘August 30 53’</code> , or any mixture of these.
dblcens	Calculates the NPMLE of the survival distribution for doubly censored data.
ddesolve	Solver for Delay Differential Equations.
ddst	Data driven smooth Neyman test.
deSolve	General solvers for ordinary differential equations (ODE) and for differential algebraic equations (DAE).
deal	Bayesian networks with continuous and/or discrete variables can be learned and compared from data.
debug	Debugger for R functions, with code display, graceful error recovery, line-numbered conditional breakpoints, access to exit code, flow control, and full keyboard input.
degreenet	Models for skewed count distributions relevant to networks.
deldir	Calculates the Delaunay triangulation and the Dirichlet or Voronoi tessellation (with respect to the entire plane) of a planar point set.
delt	Estimation of multivariate densities with adaptive histograms.
demogR	Analysis of age-structured demographic models.
denpro	Visualization of multivariate density functions and estimates with level set trees and shape trees, and visualization of multivariate data with tail trees.
denstrip	Density strips and other methods for compactly illustrating distributions.
depmix	Dependent Mixture Models: fit (multi-group) mixtures of latent Markov models on mixed categorical and continuous (time series) data.
depmixS4	Dependent Mixture Models: fit latent (hidden) Markov models on mixed categorical and continuous (time series) data.
depth	Depth functions tools for multivariate analysis.
desirability	Desirability function optimization and ranking.
dfcrm	Dose-finding by the continual reassessment method.
dglm	Double generalized linear models.
diagram	Functions for visualising simple graphs (networks) and plotting flow diagrams.
diamonds	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.
dice	Calculate probabilities of various dice-rolling events.

- dichromat** Color schemes for dichromats: collapse red-green distinctions to simulate the effects of colour-blindness.
- diffractionmetry** Baseline identification and peak decomposition for x-ray diffractograms.
- digest** 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.
- dipetest** Compute Hartigan’s dip test statistic for unimodality.
- dirichlet** Dirichlet model of consumer buying behavior for marketing research.
- dispmod** Functions for modelling dispersion in GLMs.
- distr** An object orientated implementation of distributions and some additional functionality.
- distrDoc** Documentation for packages **distr**, **distrEx**, **distrSim**, and **distrTEst**.
- distrEx** Extensions of package **distr**.
- distrMod** Object orientated implementation of probability models based on **distr** and **distrEx**.
- distrSim** Simulation classes based on package **distr**.
- distrTEst** Estimation and Testing classes based on package **distr**.
- distrTeach** Extensions of **distr** for teaching stochastics/statistics in secondary school.
- distributions** Probability distributions based on TI-83 Plus.
- divagis** Tools for quality checks of georeferenced plant species accessions.
- diveMove** Dive analysis and calibration.
- dlim** Maximum likelihood and Bayesian analysis of Dynamic Linear Models.
- dlmap** Detection Localization Mapping for QTL.
- doBy** Facilities for groupwise computations.
- dplR** Dendrochronology Program Library in R.
- dprep** Data preprocessing and visualization functions for classification.
- dr** Functions, methods, and datasets for fitting dimension reduction regression, including pHD and inverse regression methods SIR and SAVE.
- drc** Non-linear regression analysis for multiple curves with focus on concentration-response, dose-response and time-response curves.
- drm** Regression and association models for clustered categorical responses.
- drfit** Dose-response data evaluation.
- dse** Dynamic System Estimation, a multivariate time series package bundle. Contains **dse1** (the base system, including multivariate ARMA and state space models) and **dse2** (extensions for evaluating estimation techniques, forecasting, and for evaluating forecasting model).

dti	DTI (Diffusion Tensor Image) analysis.
dtf	Discrete Trigonometric Transforms.
dtw	Dynamic Time Warping algorithms.
dyn	Time series regression.
dynamicGraph	Interactive graphical tool for manipulating graphs.
dynamicTreeCut	Methods for detection of clusters in hierarchical clustering dendrograms.
dynamo	Estimation, simulation, regularization and prediction of univariate dynamic models including ARMA, ARMA-GARCH, ACD, and MEM.
dynlm	Dynamic linear models and time series regression.
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.
eRm	Estimating extended Rasch models.
earth	Earth: multivariate adaptive regression spline models.
eba	Fitting and testing probabilistic choice models, especially the BTL, elimination-by-aspects (EBA), and preference tree (Pretree) models.
ecespa	Functions and data for spatial point pattern analysis.
eco	Fitting Bayesian models of ecological inference in 2 by 2 tables.
ecodist	Dissimilarity-based functions for ecological analysis.
ecolMod	Figures, data sets and examples from the book “A Practical Guide to Ecological Modelling — Using R as a Simulation Platform” by Karline Soetaert and Peter M. J. Herman, 2008, Springer.
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.
eiPack	Ecological inference and higher-dimension data management.
eigenmodel	Semiparametric factor and regression models for symmetric relational data.
elasticnet	Elastic net regularization and variable selection.
ellipse	Package for drawing ellipses and ellipse-like confidence regions.
elliptic	A suite of elliptic and related functions including Weierstrass and Jacobi forms.
elrm	Exact Logistic Regression via MCMC.
emdbook	Data sets and auxiliary functions for “Ecological Models and Data” by Ben Bolker (work in progress).

- emme2** Functions to read from and write to an EMME/2 databank.
- empiricalBayes**
A bundle for dealing with extreme multiple testing problems by estimating local false discovery rates. Contains packages **localFDR** and **HighProbability**.
- emplik** Empirical likelihood ratio for means/quantiles/hazards from possibly right censored data.
- emu** Interface to the Emu speech database system.
- energy** E-statistics (energy) tests for comparing distributions: multivariate normality, Poisson test, multivariate k -sample test for equal distributions, hierarchical clustering by e-distances.
- ensembleBMA**
Probabilistic forecasting using Bayesian Model Averaging of ensembles using a mixture of normal distributions.
- entropy** Entropy estimation.
- epiR** Functions for analyzing epidemiological data.
- epibasix** Elementary functions for epidemiological analysis.
- epicalc** Epidemiological calculator.
- epitools** Basic tools for applied epidemiology.
- eqtl** Tools for analyzing eQTL experiments.
- equivalence**
Tests and graphics for assessing tests of equivalence.
- ergm** An integrated set of tools to analyze and simulate networks based on exponential-family random graph models (ERGM).
- etm** Empirical Transition Matrix.
- 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.

- exactmaxsel** Exact methods for maximally selected statistics for binary response variables.
- exams** Automatic generation of simple (statistical) exams.
- experiment** Designing and analyzing randomized experiments.
- expert** Modeling of data using expert opinion.
- extRemes** Extreme value toolkit.
- fArma** The Rmetrics module for “ARMA Time Series Modelling”.
- fAsianOptions** The Rmetrics module for “Option Valuation”.
- fAssets** The Rmetrics module for “Assets Selection and Modelling”.
- fBasics** The Rmetrics module for “Markets and Basic Statistics”.
- fBonds** The Rmetrics module for “Bonds and Interest Rate Models”.
- fCalendar** The Rmetrics module for “Chronological and Calendarical Objects”.
- fCopulae** The Rmetrics module for “Dependence Structures with Copulas”.
- fEcofin** The Rmetrics module for “Economic and Financial Data Sets”.
- fExoticOptions** The Rmetrics module for “Option Valuation”.
- fExtremes** The Rmetrics module for “Extreme Financial Market Data”.
- fGarch** The Rmetrics module for “Autoregressive Conditional Heteroskedastic Modelling”.
- fImport** The Rmetrics module for “Chronological and Calendarical Objects”.
- fMultivar** The Rmetrics module for “Multivariate Market Analysis”.
- fNonlinear** The Rmetrics module for “Nonlinear and Chaotic Time Series Modelling”.
- fOptions** The Rmetrics module for “Basics of Option Valuation”.
- fPortfolio** The Rmetrics module for “Portfolio Selection and Optimization”.
- fRegression** The Rmetrics module for “Regression Based Decision and Prediction”.
- fSeries** The Rmetrics module for “Financial Time Series Objects”.
- fTrading** The Rmetrics module for “Technical Trading Analysis”.
- fUnitRoots** The Rmetrics module for “The Dynamical Process Behind Markets”.
- fUtilities** The Rmetrics module for “Rmetrics Function Utilities”.
- fame** Interface for FAME time series database.

far	Modelization for Functional AutoRegressive processes.
faraway	Functions and datasets for books by Julian Faraway.
fastICA	Implementation of FastICA algorithm to perform Independent Component Analysis (ICA) and Projection Pursuit.
fbati	Gene by environment interaction tests.
fda	Functional Data Analysis: analysis of data where the basic observation is a function of some sort.
fdim	Functions for calculating fractal dimension.
fdrtool	Estimation and control of (local) False Discovery Rates.
feature	Feature significance for multivariate kernel density estimation.
femmeR	Output analysis of FEMME model results.
ff	Flat file database designed for large vectors and multi-dimensional arrays.
ffmanova	Fifty-fifty MANOVA.
fgac	Families of Generalized Archimedean Copulas.
fgui	Function GUI.
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.
filehash	Simple file-based hash table.
filehashSQLite	Simple key-value database using SQLite as the backend.
financial	Solving financial problems in R.
fingerprint	Functions to operate on binary fingerprint data.
flexclust	Flexible cluster algorithms.
flexmix	Flexible Mixture Modeling: a general framework for finite mixtures of regression models using the EM algorithm.
fmri	Functions for the analysis of fMRI experiments.
foba	Forward, backward, and foba sparse learning algorithms for ridge regression.
forecasting	A bundle with functions and datasets for forecasting. Contains forecast (time series forecasting), fma (data sets from the book “Forecasting: Methods and Applications” by Makridakis, Wheelwright & Hyndman, 1998), and Mcomp (data from the M-competitions).
foreign	Functions for reading and writing data stored by statistical software like Minitab, S, SAS, SPSS, Stata, Systat, etc. <i>Recommended.</i>

forensic	Statistical methods in forensic genetics.
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.
fossil	Palaeoecological and palaeogeographical analysis tools.
fpc	Fixed point clusters, clusterwise regression and discriminant plots.
fzca	Restricted MLE for Functional Principal Components Analysis.
fracdiff	Maximum likelihood estimation of the parameters of a fractionally differenced ARIMA(p, d, q) model (Haslett and Raftery, Applied Statistics, 1989).
fractal	Insightful fractal time series modeling and analysis.
frailtypack	Fit a shared gamma frailty model and Cox proportional hazards model using a Penalized Likelihood on the hazard function.
frontier	Maximum likelihood estimation of stochastic frontier production and cost functions.
fso	Fuzzy set ordination.
ftnonpar	Features and strings for nonparametric regression.
fts	Fast operations for time series objects via an interface to tslib (a C++ time series library).
fuzzyFDR	Exact calculation of fuzzy decision rules for multiple testing.
fuzzyOP	Fuzzy numbers and the main mathematical operations on these.
fuzzyRankTests	Fuzzy rank tests and confidence intervals.
fxregime	Frankel-Wei regression and structural change tools for estimating, testing, dating and monitoring (de facto) exchange rate regimes.
g.data	Create and maintain delayed-data packages (DDP's).
gRain	Probability propagation in graphical independence networks.
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 .
gRc	Inference in graphical Gaussian models with edge and vertex symmetries.
gWidgets	gWidgets API for building toolkit-independent, interactive GUIs.
gWidgetsRGtk2	Toolkit implementation of gWidgets for RGtk2 .

gWidgetsWWW

Toolkit implementation of gWidgets for `www`.

gWidgetsRJava

Toolkit implementation of **gWidgets** for **rJava**.

gWidgetstcltk

Toolkit implementation of **gWidgets** for **tcltk**.

gafit

Genetic algorithm for curve fitting.

gam

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).

gamair

Data sets used in the book “Generalized Additive Models: An Introduction with R” by S. Wood (2006).

gamlss

Functions to fit Generalized Additive Models for Location Scale and Shape.

gamlss.cens

A GAMLSS add on package for censored data.

gamlss.dist

Extra distributions for GAMLSS modeling.

gamlss.mx

A GAMLSS add on package for fitting mixture distributions.

gamlss.nl

A GAMLSS add on package for fitting non linear parametric models.

gamlss.tr

A GAMLSS add on for generating and fitting truncated (`gamlss.family`) distributions.

gap

Genetic analysis package for both population and family data.

gbev

Gradient Boosted regression trees with Errors-in-Variables.

gbm

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.

gbs

Generalized Birnbaum-Saunders distributions.

gcl

Compute a fuzzy rules or tree classifier from data.

gclus

Clustering Graphics. Orders panels in scatterplot matrices and parallel coordinate displays by some merit index.

gcmrec

Parameters estimation of the general semiparametric model for recurrent event data proposed by Peña and Hollander.

gdata

Various functions to manipulate data.

gee

An implementation of the Liang/Zeger generalized estimating equation approach to GLMs for dependent data.

geepack

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.

- geiger** Analysis of evolutionary diversification.
- genalg** R based genetic algorithm for binary and floating point chromosomes.
- gene2pathway**
Prediction of KEGG pathway membership for individual genes based on Inter-Pro domain signatures.
- genetics** 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, . . .
- geoR** Functions to perform geostatistical data analysis including model-based methods.
- geoRglm** Functions for inference in generalised linear spatial models.
- geomapdata**
Data for topographic and geologic mapping.
- geometry** Mesh generation and surface tessellation, based on the Qhull library.
- geonames** Interface to www.geonames.org web service.
- geozoo** Definition of geometric objects and display via **rggobi**.
- getopt** C-like getopt behavior for R scripts.
- ggm** Functions for defining directed acyclic graphs and undirected graphs, finding induced graphs and fitting Gaussian Markov models.
- ggplot** Grammar of graphics based plots for R.
- ggplot2** An implementation of the Grammar of Graphics in R.
- ghyp** Univariate and multivariate generalized hyperbolic distributions.
- giRaph** Data structures and algorithms for computations on graphs.
- gibbs.met** Naive Gibbs sampling with Metropolis steps.
- glasso** Graphical lasso.
- gld** Basic functions for the generalised (Tukey) lambda distribution.
- gllm** Routines for log-linear models of incomplete contingency tables, including some latent class models via EM and Fisher scoring approaches.
- glmC** Fitting Generalized Linear Models subject to Constraints.
- glmmAK** Generalized Linear Mixed Models.
- glmmBUGS**
Generalised Linear Mixed Models with WinBUGS.
- glmmML** A Maximum Likelihood approach to generalized linear models with random intercept.

glmnet	Lasso and elastic-net regularized generalized linear models.
glmpath	L1 regularization path for Generalized Linear Models.
glpk	Interface to the GNU Linear Programming Kit (GLPK).
gmaps	Wrapper and auxiliary functions for the maps package to work with the grid graphics system.
gmm	Generalized Method of Moments.
gmodels	Various functions to manipulate models.
gmp	Arithmetic “without limitations” using the GNU Multiple Precision library.
gmt	Interface between the GMT 4.0 map-making software and R.
gnm	Functions to specify and fit generalized nonlinear models, including models with multiplicative interaction terms such as the UNIDIFF model from sociology and the AMMI model from crop science.
goalprog	Weighted and lexicographical goal programming and optimization.
gpclip	General polygon clipping routines for R based on Alan Murta’s C library.
gpls	Classification using generalized partial least squares for two-group and multi-group (more than 2 group) classification.
gplots	Various functions to draw plots.
grImport	Importing vector graphics.
grade	Binary grading functions.
granova	Graphical Analysis of Variance.
graph	Handling of graph data structures.
graphicsQC	Quality Control for graphics in R.
grasp	Generalized Regression Analysis and Spatial Predictions for R.
gregmisc	Miscellaneous functions written/maintained by Gregory R. Warnes.
gridBase	Integration of base and grid graphics.
grnnR	A Generalized Regression Neural Network.
grouped	Regression models for grouped and coarse data, under the Coarsened At Random assumption.
grplasso	Fit user specified models with group lasso penalty.
grpreg	Regularization paths for regression models with grouped covariates.
gsarima	functions for Generalized SARIMA time series simulation.
gsl	Wrapper for special functions of the Gnu Scientific Library (GSL).
gss	A comprehensive package for structural multivariate function estimation using smoothing splines.

gstat	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.
gsubfn	Miscellaneous string utilities.
gtm	Generative topographic mapping.
gtools	Various functions to help manipulate data.
gumbel	Functions for the Gumbel-Hougaard copula.
gvlna	Global Validation of Linear Models Assumptions.
hapassoc	Likelihood inference of trait associations with SNP haplotypes and other attributes using the EM Algorithm.
haplo.ccs	Estimate haplotype relative risks in case-control data.
haplo.stats	Statistical analysis of haplotypes with traits and covariates when linkage phase is ambiguous.
hapsim	Haplotype data simulation.
hbim	Hill/Bliss Independence Model for combination vaccines.
hddplot	Use known groups in high-dimensional data to derive scores for plots.
hdeco	Hierarchical DECOMposition of entropy for categorical map comparisons.
hdf5	Interface to the NCSA HDF5 library.
hdrnde	Highest Density Regions and Conditional Density Estimation.
heatmap.plus	Heatmap with sensible behavior.
helloJavaWorld	A demonstration how to interface to a jar file that resides inside an R package.
heplots	Visualizing tests in multivariate linear models.
hett	Functions for the fitting and summarizing of heteroscedastic t-regression.
hexView	Viewing binary files.
hexbin	Hexagonal binning routines.
hier.part	Hierarchical Partitioning: variance partition of a multivariate data set.
hierfstat	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.
hints	Provide hints on what to do next.
hlr	Hidden logistic regression.

- hmm.discnp** Hidden Markov models with discrete non-parametric observation distributions.
- hoa** A bundle of packages for higher order likelihood-based inference. Contains **cond** for approximate conditional inference for logistic and loglinear models, **csampling** for conditional simulation in regression-scale models, **marg** for approximate marginal inference for regression-scale models, and **nlreg** for higher order inference for nonlinear heteroscedastic models.
- homals** Homogeneity Analysis (HOMALS) package with optional Tcl/Tk interface.
- homtest** Homogeneity tests for regional frequency analysis.
- hopach** Hierarchical Ordered Partitioning and Collapsing Hybrid (HOPACH).
- hot** Computation on micro-arrays.
- howmany** A lower bound for the number of correct rejections.
- hsmm** Hidden Semi Markov Models.
- HttpRequest** Implements HTTP Request protocols (GET, POST, and multipart POST requests).
- hwde** Models and tests for departure from Hardy-Weinberg equilibrium and independence between loci.
- hwriter** Easy-to-use and versatile functions to output R objects in HTML format.
- hybridHclust** Hybrid hierarchical clustering via mutual clusters.
- hydrogeo** Groundwater data presentation and interpretation.
- hydrosanity** Graphical user interface for exploring hydrological time series.
- hyperdirichlet** Routines for the hyperdirichlet distribution.
- hypergeo** The hypergeometric function over the whole complex plane.
- ibdreg** Regression methods for IBD linkage with covariates.
- ic.infer** Inequality constrained inference in linear normal situations.
- ic50** Evaluation of compound screens.
- icomp** Calculates the ICOMP criterion and its variations.
- identity** Jacquard condensed coefficients of identity.
- ifa** Independent Factor Analysis.
- ifs** Iterated Function Systems distribution function estimator.
- ifultools** Insightful research tools.
- ig** Robust and classical versions of the inverse Gaussian distribution.

igraph	Routines for simple graphs.
iid.test	Testing whether data is independent and identically distributed.
imprProbEst	Minimum distance estimation in an imprecise probability model.
impute	Imputation for microarray data (currently KNN only).
imputeMDR	Multifactor Dimensionality Reduction (MDR) analysis for incomplete data.
ineq	Inequality, concentration and poverty measures, and Lorenz curves (empirical and theoretic).
inetwork	Network analysis and plotting.
inline	Inline C/C++ function calls from R.
intcox	Implementation of the Iterated Convex Minorant Algorithm for the Cox proportional hazard model for interval censored event data.
intervals	Tools for working with points and intervals.
iplots	Interactive graphics for R.
ipptoolbox	Uncertainty quantification and propagation in the framework of Dempster-Shafer theory and imprecise probabilities.
ipred	Improved predictive models by direct and indirect bootstrap aggregation in classification and regression as well as resampling based estimators of prediction error.
irr	Coefficients of Interrater Reliability and Agreement for quantitative, ordinal and nominal data.
irtoys	Simple interface to the estimation and plotting of IRT models.
isnev	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.
its	An S4 class for handling irregular time series.
ivive	In vitro in vivo correlation (IVIVC) modeling.
jit	Just-in-time compiler.
kappalab	The “laboratory for capacities”, an S4 tool box for capacity (or non-additive measure, fuzzy measure) and integral manipulation on a finite setting.
kerfdr	Semi-parametric kernel-based approach to local fdr estimations.
kernelPop	Spatially explicit population genetic simulations.
kernlab	Kernel-based machine learning methods including support vector machines.
kin.cohort	Analysis of kin-cohort studies.

kinship	Mixed-effects Cox models, sparse matrices, and modeling data from large pedigrees.
kknn	Weighted k -nearest neighbors classification and regression.
klaR	Miscellaneous functions for classification and visualization developed at the Department of Statistics, University of Dortmund.
klin	Linear equations with Kronecker structure.
kml	K -Means for Longitudinal data.
knnFinder	Fast nearest neighbor search.
knnTree	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.
knncat	Nearest-neighbor classification with categorical variables.
knnflex	A more flexible k -NN.
knorm	Microarray data from multiple biologically interrelated experiments.
kohonen	Supervised and unsupervised self-organising maps.
ks	Kernel smoothing: bandwidth matrices for kernel density estimators and kernel discriminant analysis for bivariate data.
kza	Kolmogorov-Zurbenko Adaptive filter for locating change points in a time series.
kzft	Kolmogorov-Zurbenko Fourier Transform and application.
kzs	Kolmogorov-Zurbenko Spline.
labdsv	Laboratory for Dynamic Synthetic Vegetation Phenomenology.
labstatR	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.
laercio	Tests to compare means.
lago	LAGO for rare target detection.
lancet.iraqmortality	Surveys of Iraq mortality published in The Lancet.
languageR	Data sets and functions for the book “Analyzing Linguistic Data: A practical introduction to statistics” by R. H. Baayen, 2007, Cambridge: Cambridge University Press.
lars	Least Angle Regression, Lasso and Forward Stagewise: efficient procedures for fitting an entire lasso sequence with the cost of a single least squares fit.
laser	Likelihood Analysis of Speciation/Extinction Rates from phylogenies.
lasso2	Routines and documentation for solving regression problems while imposing an L1 constraint on the estimates, based on the algorithm of Osborne et al. (1998).

- latentnet** Latent position and cluster models for statistical networks.
- latentnetHRT** Latent position and cluster models for statistical networks, implementing the original specification by Handcock, Raftery and Tantrum.
- lattice** Lattice graphics, an implementation of Trellis Graphics functions. *Recommended.*
- latticeExtra** Generic functions and standard methods for Trellis-based displays.
- latticist** A Lattice-based tool for exploratory visualization.
- lawstat** Statistical tests widely utilized in biostatistics, public policy and law.
- lazy** Lazy learning for local regression.
- ldDesign** Design of experiments for detection of linkage disequilibrium.
- lda.cv** Cross-validation for linear discriminant analysis.
- ldbounds** Lan-DeMets method for group sequential boundaries.
- leaps** 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.
- lga** Tools for Linear Grouping Analysis (LGA).
- lgtdl** A set of methods for longitudinal data objects.
- lhs** Latin Hypercube Samples.
- limSolve** Solving linear inverse models.
- linprog** Solve linear programming/linear optimization problems by using the simplex algorithm.
- ljr** Logistic Joinpoint Regression.
- lme4** Fit linear and generalized linear mixed-effects models.
- lmeSplines** Fit smoothing spline terms in Gaussian linear and nonlinear mixed-effects models.
- lmm** Linear mixed models.
- lmodel2** Model II simple linear regression.
- lmom** *L*-moments.
- lmomco** *L*-moments and *L*-comoments.
- lmtest** 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.
- lnMLE** Marginally specified logistic normal models for longitudinal binary data.

locfdr	Computation of local false discovery rates.
locfit	Local Regression, likelihood and density estimation.
locpol	Kernel local polynomial regression.
lodplot	Assorted plots of location score versus genetic map position.
logcondens	Estimate a log-concave probability density from i.i.d. observations.
logilasso	Analysis of sparse contingency tables with penalization approaches.
logistf	Firth's bias reduced logistic regression approach with penalized profile likelihood based confidence intervals for parameter estimates.
loglognorm	Double log normal distribution functions.
logregperm	Inference in Logistic Regression using permutation tests.
logspline	Logspline density estimation.
lokern	Kernel regression smoothing with adaptive local or global plug-in bandwidth selection.
longRPart	Recursive partitioning of longitudinal data using mixed-effects models.
longitudinal	Analysis of multiple time course data.
longmemo	Datasets and Functionality from the textbook "Statistics for Long-Memory Processes" by J. Beran, 1994, Chapman & Hall.
lpSolve	Functions that solve general linear/integer problems, assignment problems, and transportation problems via interfacing Lp_solve.
lpSolveAPI	An R interface to the lp_solve library API.
lpc	Lassoed principal components for testing significance of features.
lpridge	Local polynomial (ridge) regression.
lsa	Latent Semantic Analysis.
lspls	LS-PLS (least squares — partial least squares) models.
lss	Accelerated failure time model to right censored data based on least-squares principle.
ltm	Analysis of multivariate Bernoulli data using latent trait models (including the Rasch model) under the Item Response Theory approach.
ltsa	Linear Time Series Analysis.
luca	Likelihood Under Covariate Assumptions (LUCA).
lvplot	Letter-value box plots.

mAr	Estimation of multivariate AR models through a computationally efficient step-wise least-squares algorithm.
mFilter	Miscellaneous time series filters.
maanova	Analysis of <i>N</i> -dye Micro Array experiments using mixed model effect. Contains analysis of variance, permutation and bootstrap, cluster and consensus tree.
magic	A variety of methods for creating magic squares of any order greater than 2, and various magic hypercubes.
mapLD	Linkage Disequilibrium mapping.
mapdata	Supplement to package maps , providing the larger and/or higher-resolution databases.
mapproj	Map Projections: converts latitude/longitude into projected coordinates.
maps	Draw geographical maps. Projection code and larger maps are in separate packages.
maptools	Set of tools for manipulating and reading geographic data, in particular ESRI shapefiles.
maptree	Functions with example data for graphing and mapping models from hierarchical clustering and classification and regression trees.
marelac	Datasets, constants, conversion factors, utilities for the marine and lacustrine sciences.
marginTree	Margin trees for high-dimensional classification.
marginalmodelplots	Marginal model plots for linear and generalized linear models.
mathgraph	Tools for constructing and manipulating objects from a class of directed and undirected graphs.
matlab	Emulate MATLAB code using R.
matrixcalc	Collection of functions for matrix differential calculus.
maxLik	Tools for Maximum Likelihood Estimation.
maxstat	Maximally selected rank and Gauss statistics with several p-value approximations.
mblm	Median-based Linear models, using Theil-Sen single or Siegel repeated medians.
mboost	Gradient boosting for fitting generalized linear, additive and interaction models.
mcgibbsit	Warnes and Raftery's MCGibbsit MCMC diagnostic.
mclust	Model-based clustering and normal mixture modeling including Bayesian regularization.
mclust02	Model-based cluster analysis: the 2002 version of MCLUST.

mcmc	Functions for Markov Chain Monte Carlo (MCMC).
mco	Multi criteria optimization algorithms.
mda	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.
meboot	Maximum entropy bootstrap for time series.
mefa	Faunistic count data handling and reporting.
meifly	Interactive model exploration using GGobi.
memisc	Miscellaneous Tools for data management, simulation, and presentation of estimates.
merror	Accuracy and precision of measurements.
meta	Fixed and random effects meta-analysis, with functions for tests of bias, forest and funnel plot.
mfp	Multiple Fractional Polynomials.
mgcv	Routines for GAMs and other generalized ridge regression problems with multiple smoothing parameter selection by GCV or UBRE. <i>Recommended.</i>
mi	Missing-data imputation and model checking.
micEcon	Tools for microeconomic analysis and microeconomic modelling.
mice	Multivariate Imputation by Chained Equations.
mimR	An R interface to MIM for graphical modeling in R.
minet	Mutual Information NETwork.
minpack.lm	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.
minxent	Entropy optimization distribution under constraints.
misc3d	A collection of miscellaneous 3d plots, including rgl-based isosurfaces.
mirf	Multiple Imputation and Random Forests for unobservable phase, high-dimensional data.
mitools	Tools to perform analyses and combine results from multiple-imputation datasets.
mix	Estimation/multiple imputation programs for mixed categorical and continuous data.
mixPHM	Mixtures of proportional hazard models.
mixdist	Finite mixture distribution models.

- mixer** Random graph clustering via estimation of Erdős-Rényi mixtures.
- mixlow** Assessing drug synergism/antagonism.
- mixreg** Functions to fit mixtures of regressions.
- mixstock** Mixed stock analysis functions.
- mixtools** Tools for mixture models.
- mlCopulaSelection**
Copula selection and fitting using maximum likelihood.
- mlbench** A collection of artificial and real-world machine learning benchmark problems, including the Boston housing data.
- mlegp** Maximum Likelihood Estimates of Gaussian Processes.
- mlica** Independent Component Analysis using Maximum Likelihood.
- mlmRev** Examples from Multilevel Modelling Software Review.
- mlmmm** Maximum likelihood estimation under multivariate linear mixed models with missing values.
- mlogit** Estimation of the multinomial logit model with choice specific variables.
- mmlcr** 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.
- mnormt** The multivariate normal and t distributions.
- moc** Fits a variety of mixtures models for multivariate observations with user-defined distributions and curves.
- modeest** Mode estimation and Chernoff distribution.
- modehunt** Multiscale analysis for density functions.
- modeltools**
A collection of tools to deal with statistical models.
- moduleColor**
Methods for color labeling, calculation of eigengenes, and merging of closely related modules.
- mokken** Mokken Scale Analysis for test and questionnaire data.
- mombf** Moment and inverse moment Bayes factors.
- moments** Moments, skewness, kurtosis and related tests.
- monomvn** Estimation for multivariate normal data with monotone missingness.
- monreg** Estimation of monotone regression and variance functions in nonparametric models.
- monoProc** Strictly monotone smoothing procedure.
- moonsun** Basic astronomical calculations.

mota	Mean Optimal Transformation Approach.
mpm	Spectral map analysis.
mprobit	Multivariate probit model for binary/ordinal response.
mra	Analysis of capture-recapture data.
mratios	Inferences for ratios of coefficients in the general linear model.
mrdr	Model-robust concentration-response analysis.
msBreast	Protein mass spectra dataset from a breast cancer study.
msDilution	Protein mass spectra dataset from a dilution experiment.
msProcess	Tools for protein mass spectra processing including data preparation, denoising, noise estimation, baseline correction, intensity normalization, peak detection, peak alignment, peak quantification, and various functionalities for data ingestion/conversion, mass calibration, data quality assessment, and protein mass spectra simulation.
msProstate	Protein mass spectra dataset from a prostate cancer study.
msm	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.
muS2RC	S-plus to R Compatibility for package muStat .
muStat	Prentice rank sum test and McNemar test.
muUtil	Utility functions for package muStat .
muhaz	Hazard function estimation in survival analysis.
multcomp	Multiple comparison procedures for the one-way layout.
multcompView	Visualizations of paired comparisons.
multic	Quantitative linkage analysis tools using the variance components approach.
multilevel	Analysis of multilevel data by organizational and social psychologists.
multinomRob	Overdispersed multinomial regression using robust (LQD and tanh) estimation.
multipol	Utilities to manipulate multivariate polynomials.
multtest	Resampling-based multiple hypothesis testing.
muscor	Multi-stage Convex Relaxation.
mvbutils	Utilities by Mark V. Bravington for project organization, editing and backup, sourcing, documentation (formal and informal), package preparation, macro functions, and more.

mvna	Nelson-Aalen estimator of the cumulative hazard in multistate models.
mvnml	ML estimation for multivariate normal data with missing values.
mvnormtest	Generalization of the Shapiro-Wilk test for multivariate variables.
mvtnormp	Multivariate Normal and T Distribution functions of Dunnett (1989).
mvoutlier	Multivariate outlier detection based on robust estimates of location and covariance structure.
mvpart	Multivariate partitioning.
mvtnorm	Multivariate normal and t distributions.
nFDR	Nonparametric Estimate of FDR Based on Bernstein polynomials.
nFactors	Non-graphical solution to the Cattell Scree Test.
ncdf	Interface to Unidata netCDF data files.
ncf	Spatial nonparametric covariance functions.
ncomplete	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.
negenes	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.
netmodels	Tools for the study of scale free and small world networks.
network	Tools to create and modify network objects, which can represent a range of relational data types.
networksis	Simulate bipartite graphs with fixed marginals through sequential importance sampling.
neural	RBF and MLP neural networks with graphical user interface.
neuralnet	Training of neural networks.
nice	Get or set UNIX priority (niceness) of running R process.
nlme	Fit and compare Gaussian linear and nonlinear mixed-effects models. <i>Recommended.</i>
nlmeODE	Combine the nlme and odesolve packages for mixed-effects modelling using differential equations.
nlrwr	Non-linear regression with R.
nls2	Non-linear regression with brute force.
nlstools	Tools for nonlinear regression diagnostics.
nlt	A nondecimated lifting transform for signal denoising.

nltts	(Non)linear time series analysis.
nltm	NonLinear Transformation Models for survival analysis.
nnet	Software for single hidden layer perceptrons (“feed-forward neural networks”), and for multinomial log-linear models. Contained in the ‘VR’ bundle. <i>Recommended.</i>
npls	The Lawson-Hanson NNLS algorithm for non-negative least squares.
noia	Implementation of the Natural and Orthogonal InterAction (NOIA) model.
nonbinROC	ROC-type analysis for non-binary gold standards.
nor1mix	One-dimensional normal mixture models classes, for, e.g., density estimation or clustering algorithms research and teaching; providing the widely used Marron-Wand densities.
norm	Analysis of multivariate normal datasets with missing values.
normwm.test	Normality and white noise testing.
normalp	A collection of utilities for normal of order p distributions (General Error Distributions).
nortest	Five omnibus tests for the composite hypothesis of normality.
noverlap	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.
np	Nonparametric kernel smoothing methods for mixed datatypes.
nparmacomp	Nonparametric relative contrast effects.
npde	Normalized prediction distribution errors for nonlinear mixed-effect models.
npplot	Plotting non-parametric LOD scores from multiple input files.
npmc	Nonparametric Multiple Comparisons: provides simultaneous rank test procedures for the one-way layout without presuming a certain distribution.
nsRFA	Non-supervised Regional Frequency Analysis.
numDeriv	Accurate numerical derivatives.
nws	Functions for NetWorkSpaces and Sleigh.
obsSens	Sensitivity analysis for observational studies.
oc	Optimal Classification roll call analysis.
oce	Analysis of oceanographic data.
odesolve	An interface for the Ordinary Differential Equation (ODE) solver lsoda. ODEs are expressed as R functions.
odfWeave	Sweave processing of Open Document Format (ODF) files.

ofw	Optimal Feature Weighting algorithm.
onemap	Analysis of molecular marker data from non-model systems to simultaneously estimate linkage and linkage phases (genetic map construction).
onion	A collection of routines to manipulate and visualize quaternions and octonions.
openNLP	An interface to openNLP , a collection of natural language processing tools including a sentence detector, tokenizer, pos-tagger, shallow and full syntactic parser, and named-entity detector, using the Maxent Java package for training and using maximum entropy models.
openNLPmodels	English and spanish models for openNLP .
opentick	Interface to opentick real time and historical market data.
optmatch	Functions to perform optimal matching, particularly full matching.
orientlib	Representations, conversions and display of orientation SO(3) data.
orloca	Operations Research LOCational Analysis models.
orloca.es	Spanish version of orloca package.
orth	Multivariate logistic regressions using orthogonalized residuals.
orthopolynom	Functions for orthogonal and orthonormal polynomials.
ouch	Ornstein-Uhlenbeck models for phylogenetic comparative hypotheses.
outliers	A collection of some tests commonly used for identifying outliers.
oz	Functions for plotting Australia's coastline and state boundaries.
pARccs	Estimation of partial attributable risks from case-control data.
pARtial	(Partial) attributable risk estimates, corresponding variance estimates and confidence intervals.
pack	Create and manipulate raw vectors.
packClassic	Illustrate the tutorial "S4: From Idea To Package".
pairwiseCI	Calculate and plot unadjusted confidence intervals for two sample comparisons.
paleoTS	Modeling evolution in paleontological time-series.
paltran	Functions for paleolimnology.
pamr	Pam: Prediction Analysis for Microarrays.
pan	Multiple imputation for multivariate panel or clustered data.
panel	Functions and datasets for fitting models to Panel data.
papply	Parallel apply function using MPI.

paran	Horn's test of principal components/factors.
partitions	Additive partitions of integers.
partsm	Periodic AutoRegressive Time Series Models.
party	Unbiased recursive partitioning in a conditional inference framework.
pastecs	Package for Analysis of Space-Time Ecological Series.
pbatR	Frontend to PBAT to run within R.
pcaPP	Robust PCA by Projection Pursuit.
pcalg	Standard and robust estimation of the skeleton (ugraph) of a Directed Acyclic Graph (DAG) via the PC algorithm.
pcse	Panel-Corrected Standard Error estimation.
pcurve	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.
pear	Periodic Autoregression Analysis.
pec	Prediction Error Curves for survival models.
penalized	Penalized estimation in generalized linear models.
peperr	Parallellised Estimation of Prediction ERRor.
permax	Functions intended to facilitate certain basic analyses of DNA array data, especially with regard to comparing expression levels between two types of tissue.
permtest	Permutation test to compare variability within and distance between two groups.
perturb	Perturbation analysis for evaluating collinearity.
pga	An ensemble method for variable selection by carrying out Darwinian evolution in parallel universes.
pgam	Poisson-Gamma Additive Models.
pgirmess	Functions for analysis and display of ecological and spatial data.
phangorn	Phylogenetic analysis in R.
pheno	Some easy-to-use functions for time series analyses of (plant-) phenological data sets.
phpSerialize	Serialize R to PHP associative array.
picante	Tools for integrating phylogenies and ecology.
pinktoe	Converts S trees to HTML/Perl files for interactive tree traversal.
pixmap	Functions for import, export, plotting and other manipulations of bitmapped images.

plRasch	Log linear by linear association models.
playwith	A GUI for interactive plots using GTK+.
plink	Separate calibration linking methods.
plm	Linear models for panel data.
plotSEMM	Graphing nonlinear latent variable interactions in SEMM.
plotrix	Various useful functions for enhancing plots.
plugdensity	Kernel density estimation with global bandwidth selection via “plug-in”.
pls	Partial Least Squares Regression (PLSR) and Principal Component Regression (PCR).
plsgenomics	PLS analyses for genomics.
plyr	Tools for splitting, applying and combining data.
pmg	Poor Man’s GUI.
pmml	Generate Predictive Modelling Markup Language (PMML) for various models.
poLCA	POLytomous variable Latent Class Analysis.
poilog	Poisson lognormal and bivariate Poisson lognormal distribution.
polspline	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.
polyapost	Simulating from the Polya posterior.
polycor	Polychoric and polyserial correlations.
polynom	A collection of functions to implement a class for univariate polynomial manipulations.
pomp	Partially-observed Markov processes.
popbio	Construction and analysis of matrix population models.
popgen	Statistical and POPulation GENetics.
poplab	Population Lab, a tool for constructing a virtual electronic population evolving over time.
portfolio	Classes for analyzing and implementing portfolios.
portfolioSim	Framework for simulating equity portfolio strategies.
powell	Optimizes a function using Powell’s UObyQA algorithm.
powerGWASinteraction	Power calculations for interactions for GWAS.

- powerpkg** Power analyses for the affected sib pair and the TDT design.
- ppc** Sample classification of protein mass spectra by peak probability contrasts.
- ppls** Penalized Partial Least Squares.
- pps** 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.
- prabclus** 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.
- predbayescor**
Classification rule based on Bayesian naive Bayes models with feature selection bias corrected.
- predmixcor**
Classification rule based on Bayesian mixture models with feature selection bias corrected.
- prefmod** Utilities to fit paired comparison models for preferences.
- prettyR** Pretty descriptive stats.
- prim** Patient Rule Induction Method (PRIM).
- princurve** Fits a principal curve to a matrix of points in arbitrary dimension.
- prob** Elementary probability on finite sample spaces.
- prodlim** Product limit estimation.
- profileModel**
Tools for profiling inference functions for various model classes.
- profr** Alternative display for profiling information.
- proftools** Profile output processing tools for R.
- proj4** A simple interface to the PROJ.4 cartographic projections library.
- proptest** Tests of the proportional hazards assumption in the Cox model.
- proto** An object oriented system using prototype or object-based (rather than class-based) object oriented ideas.
- proxy** Distance and similarity measures.
- pscl** R in the Political Science Computational Laboratory, Stanford University.
- pseudo** Pseudo-observations.
- pspline** Smoothing splines with penalties on order m derivatives.
- psy** Various procedures used in psychometry: Kappa, ICC, Cronbach alpha, screeplot, PCA and related methods.

psych	Procedures for personality and psychological research.
psychometric	Applied psychometric theory: functions useful for correlation theory, meta-analysis (validity-generalization), reliability, item analysis, inter-rater reliability, and classical utility.
psyphy	Functions for analyzing psychophysical data in R.
pwr	Basic functions for power analysis.
pwt	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.
pvclust	Hierarchical clustering with p -value.
qAnalyst	Variables and attributes control charts.
qcc	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.
qdg	Infer QTL-directed Dependency Graphs for phenotype networks.
qgen	Quantitative Genetics using R.
qlspack	Quasi least squares package.
qp	q -order partial correlation graph search algorithm.
qpcR	Modelling and analysis of real-time PCR data.
qtl	Analysis of experimental crosses to identify QTLs.
qtlDesign	Tools for the design of QTL experiments.
qtlbim	QTL Bayesian Interval Mapping.
quadprog	For solving quadratic programming problems.
qualV	Qualitative methods for the validation of models.
quantchem	Quantitative chemical analysis: calibration and evaluation of results.
quantmod	Quantitative financial modelling framework.
quantreg	Quantile regression and related methods.
quantregForest	Quantile Regression Forests, a tree-based ensemble method for estimation of conditional quantiles.
qvalue	Q-value estimation for false discovery rate control.
qvcalc	Functions to compute quasi-variances and associated measures of approximation error.
r2lUniv	R to \LaTeX Univariate: perform basic analysis and generate corresponding \LaTeX code.

rJava	Low-level R to Java interface. Allows creation of objects, calling methods and accessing fields.
rPorta	An R interface to PORTA, a collection of routines for analyzing polytopes and polyhedra.
race	Implementation of some racing methods for the empirical selection of the best.
rake	Raking survey datasets by re-weighting.
ramps	Bayesian geostatistical modeling of Gaussian processes using a reparameterized and marginalized posterior sampling (RAMPS) algorithm.
randaes	Random number generator based on AES cipher.
random	True random numbers using random.org.
randomLCA	Random effects Latent Class Analysis.
randomSurvivalForest	Ishwaran and Kogalur's random survival forest.
randomForest	Breiman's random forest classifier.
randtoolbox	Toolbox for pseudo and quasi random number generation.
rankreg	Rank regression estimator for the AFT model with right censored data.
rateratio.test	Exact rate ratio test.
rattle	A graphical user interface for data mining in R using GTK.
rbounds	Perform Rosenbaum bounds sensitivity tests for matched data.
rbugs	Functions to prepare files needed for running BUGS in batch mode, and running BUGS from R. Support for Linux systems with Wine is emphasized.
rcdd	C Double Description for R, an interface to the CDD computational geometry library.
rcdk	Interface to the CDK libraries, a Java framework for cheminformatics.
rcom	R COM Client Interface and internal COM Server.
rcompgen	Completion generator for R. <i>Recommended</i> for R 2.5.0 or 2.6.0.
rconifers	Interface to the CONIFERS forest growth model.
rda	Shrunk Centroids Regularized Discriminant Analysis.
rdetools	Relevant Dimension Estimation (RDE) in feature spaces.
realized	Realized variance toolkit.
ref	Functions for creating references, reading from and writing to references and a memory efficient refdata type that transparently encapsulates matrices and data frames.

regress	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.
regsubseq	Detect and test regular sequences and subsequences.
regtest	Regression testing.
relaimpo	RELATIVE IMPORTance of regressors in linear models.
relations	Data structures for k -ary relations with arbitrary domains, predicate functions, and fitters for consensus relations.
relax	Functions for report writing, presentation, and programming.
relaxo	Relaxed Lasso.
reldist	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.
relimp	Functions to facilitate inference on the relative importance of predictors in a linear or generalized linear model.
relsurv	Various functions for regression in relative survival.
repolr	Repeated measures proportional odds logistic regression.
reporttools	Generate L ^A T _E X tables of descriptive statistics
reshape	Flexibly reshape data.
resper	Sampling from restricted permutations.
reweight	Adjustment of survey respondent weights.
rgcvtack	R interface for GCVPACK Fortran package.
rgdal	Provides bindings to Frank Warmerdam’s Geospatial Data Abstraction Library (GDAL).
rgenoud	R version of GENetic Optimization Using Derivatives.
rggm	Robustified methods for Gaussian Graphical Models.
rggobi	Interface between R and GGobi.
rgl	3D visualization device system (OpenGL).
rgr	The GSC (Geological Survey of Canada) applied geochemistry EDA package.
rhosp	Side effect risks in hospital: simulation and estimation.
richards	Richards curves.
rimage	Functions for image processing, including Sobel filter, rank filters, fft, histogram equalization, and reading JPEG files.
rindex	Indexing for R.

risksetROC	Riskset ROC curve estimation from censored survival data.
rjacobi	Jacobi polynomials and Gauss-Jacobi quadrature related operations.
rjags	Bayesian graphical models via an interface to the JAGS MCMC library.
rjson	JSON (JavaScript Object Notation) for R.
rlecuyer	R interface to RNG with multiple streams.
rmeta	Functions for simple fixed and random effects meta-analysis for two-sample comparison of binary outcomes.
rmetasim	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.
robfilter	Robust time series filters.
robust	Insightful robust package.
robustbase	Basic Robust Statistics.
rootSolve	Nonlinear root finding, equilibrium and steady-state analysis of ordinary differential equations.
roxygen	A Doxygen-like in-source documentation system for Rd, collation, namespace and callgraphs.
rpanel	Simple interactive controls for R using the tcltk package.
rpart	Recursive PARTitioning and regression trees. <i>Recommended.</i>
rpubchem	R interface to the PubChem collection.
rpvm	R interface to PVM (Parallel Virtual Machine). Provides interface to PVM APIs, and examples and documentation for its use.
rqmcmb2	Markov chain marginal bootstrap for quantile regression.
rrcov	Functions for robust location and scatter estimation and robust regression with high breakdown point.
rrp	Random Recursive Partitioning.
rscproxy	A portable C-style interface to R (StatConnector).
rsm	Response-Surface Models.
rsprng	Provides interface to SPRNG (Scalable Parallel Random Number Generators) APIs, and examples and documentation for its use.
rstream	Unified object oriented interface for multiple independent streams of random numbers from different sources.
rtiff	Read TIFF format images and return them as pixmap objects.
runjags	Run Bayesian MCMC models in the BUGS syntax using JAGS.

rv	Simulation-based random variable object class.
rwm	R Workspace Manager.
rwt	Rice Wavelet Toolbox wrapper, providing a set of functions for performing digital signal processing.
s20x	Stats 20x functions.
sac	Semiparametric empirical likelihood ratio based test of changepoint with one-change or epidemic alternatives with data-based model diagnostic.
sampfling	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.
sampleSelection	Estimation of sample selection models.
sampling	A set of tools to select and to calibrate samples.
samr	Significance Analysis of Microarrays.
sandwich	Model-robust standard error estimators for time series and longitudinal data.
sapa	Insightful Spectral Analysis for Physical Applications.
sbgcop	Semiparametric Bayesian Gaussian copula estimation.
sca	Simple Component Analysis.
scaleboot	Approximately unbiased p -values via multiscale bootstrap.
scape	functions to import and plot results from statistical catch-at-age models, used in fisheries stock assessments.
scapeMCMC	Markov-chain Monte Carlo diagnostic plots, accompanying the scape package.
scatterplot3d	Plots a three dimensional (3D) point cloud perspective.
schoolmath	Functions and datasets for math used in school.
sciplot	Scientific graphing functions for factorial designs.
scope	Data manipulation using arbitrary row and column criteria.
scout	Scout method for covariance-regularized regression.
scrime	Tools for the analysis of high-dimensional data developed/implemented at the group “Statistical Complexity Reduction In Molecular Epidemiology” (SCRIME), with main focus on SNP data.
scuba	Scuba diving calculations and decompression models.
sda	Shrinkage Discriminant Analysis.

sdcMicro	Statistical Disclosure Control methods for the generation of public and scientific use files.
sde	Simulation and inference for Stochastic Differential Equations.
sdtalt	Signal Detection Theory measures and ALternatives.
seacarb	Calculates parameters of the seawater carbonate system.
seas	Detailed seasonal plots of temperature and precipitation data.
seewave	Time wave analysis and graphical representation.
segclust	Segmentation and segmentation/clustering.
segmented	Functions to estimate break-points of segmented relationships in regression models (GLMs).
selectiongain	Calculate the gain from a model selection.
sem	Functions for fitting general linear Structural Equation Models (with observed and unobserved variables) by the method of maximum likelihood using the RAM approach.
sendplot	Tool for sending interactive plots.
sensR	Thurstonian models for sensory discrimination.
sensitivity	Sensitivity analysis.
seqinr	Exploratory data analysis and data visualization for biological sequence (DNA and protein) data.
seqmon	Sequential monitoring of clinical trials.
seriation	Infrastructure for seriation.
session	Functions for interacting with, saving and restoring R sessions.
setRNG	Set (normal) random number generator and seed.
sets	Data structures and basic operations for ordinary sets, and generalizations such as fuzzy sets, multisets, and fuzzy multisets.
sfsmisc	Utilities from Seminar fuer Statistik ETH Zurich.
sgeostat	An object-oriented framework for geostatistical modeling.
shape	Functions for plotting graphical shapes.
shapefiles	Functions to read and write ESRI shapefiles.
shapes	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.
siar	Stable Isotope Analysis in R.
sigma2tools	Test of hypothesis about sigma2.

- signal** A set of generally Matlab/Octave-compatible signal processing functions.
- signalextraction**
Real-time signal extraction (Direct Filter Approach).
- simba** Functions for similarity calculation of binary data.
- simco** Import Structure files and deduce similarity coefficients from them.
- simecol** SIMulation of ECOLogical (and other) dynamic systems.
- simex** SIMEX and MCSIMEX algorithms for measurement error models.
- similarityRichards**
Similarity of Richards curves.
- simone** Statistical Inference for MODular NETworks (SIMoNe).
- simpleboot**
Simple bootstrap routines.
- singlecase** Tests for single case studies in neuropsychology.
- 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.
- smacof** Multidimensional scaling based on stress minimization by means of majorization (smacof).
- smatr** (Standardized) Major Axis estimation and Testing Routines.
- smoothSurv**
Survival regression with smoothed error distribution.
- smoothtail** Smooth estimation of generalized Pareto distribution shape parameter.
- 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.
- snowfall** Wrapper around **snow** for easier development of parallel R programs.
- snp.plotter**
Plots of p -values using single SNP and/or haplotype data.
- snpXpert** Tools to analyze SNP data.

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.
sp	A package that provides classes and methods for spatial data, including utility functions for plotting data as maps, spatial selection, and much more.
spBayes	Fit Gaussian models with potentially complex hierarchical error structures by Markov chain Monte Carlo (MCMC).
space	Sparse PARTial Correlation Estimation.
spam	SPArse Matrix algebra.
spatclus	Arbitrarily shaped multiple spatial cluster detection for case event data.
spatgraphs	Graphs for 2-d point patterns.
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. <i>Recommended.</i>
spatialCovariance	Computation of spatial covariance matrices for data on rectangles using one dimensional numerical integration and analytic results.
spatialkernel	Nonparameteric estimation of spatial segregation in a multivariate point process.
spatstat	Data analysis and modelling of two-dimensional point patterns, including multitype 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 , sptest , and spsarlm .)
spe	Stochastic Proximity Embedding.
spectralGP	Approximate Gaussian processes using the Fourier basis.
spectrino	Spectra organizer, visualization and data extraction from within R.
spgrass6	Interface between the GRASS 6.0 geographical information system and R.
spgwr	Geographically weighted regression.

splanCS	Spatial and space-time point pattern analysis functions.
spls	Sparse Partial Least Squares (SPLS) regression.
splus2R	Insightful package providing missing S-PLUS functionality in R.
spssDDI	Read SPSS system files and produce valid DDI version 3.0 documents.
spsurvey	Spatial survey design and analysis.
sqldf	Perform SQL selects on R data frames.
ssanv	Sample Size Adjusted for Nonadherence or Variability of input parameters.
ssize.fdr	Sample size calculations for microarray experiments.
sspir	State SPace models In R.
sspline	Smoothing splines on the sphere.
st	Shrinkage t statistic.
staRt	Inferenza classica con TI-83 Plus.
stab	Data analysis of drug stability.
startupmsg	Utilities for start-up messages.
stashR	A Set of Tools for Administering SHared Repositories.
statmod	Miscellaneous biostatistical modelling functions.
statnet	Software tools for the statistical modeling of network data.
stepPlr	L2 penalized logistic regression with a stepwise variable selection.
stepwise	A stepwise approach to identifying recombination breakpoints in a sequence alignment.
stinepack	Stineman interpolation package.
stochasticGEM	Fitting Stochastic General Epidemic Models.
stochmod	Learning and inference algorithms for a variety of probabilistic models.
stream.net	Building and analyzing binary stream networks.
strucchange	Various tests on structural change in linear regression models.
subplex	The subplex algorithm for unconstrained optimization.
subselect	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.
sudoku	Sudoku puzzle solver.
supclust	Methodology for supervised grouping of predictor variables.

superpc	Supervised principal components.
surv2sample	Two-sample tests for survival analysis.
survBayes	Fits a proportional hazards model to time to event data by a Bayesian approach.
surveillance	Outbreak detection algorithms for surveillance data.
survey	Summary statistics, generalized linear models, and general maximum likelihood estimation for stratified, cluster-sampled, unequally weighted survey samples.
surveyNG	Complex survey samples: database interface, sparse matrices.
survival	Functions for survival analysis, including penalised likelihood. <i>Recommended.</i>
survivalROC	Time-dependent ROC curve estimation from censored survival data.
survrec	Survival analysis for recurrent event data.
svcR	A support vector machine technique for clustering.
svcm	2d and 3d Space-Varying Coefficient Models.
svmpath	Computes the entire regularization path for the two-class svm classifier with essentially the same cost as a single SVM fit.
systemfit	Contains functions for fitting simultaneous systems of equations using Ordinary Least Squares (OLS), Two-Stage Least Squares (2SLS), and Three-Stage Least Squares (3SLS).
taskPR	Task-Parallel R package.
tcltk2	A series of widgets and functions to supplement tcltk .
tdist	Computes the distribution of a linear combination of independent Student's t variables.
tdm	A tool for Therapeutic Drug Monitoring.
tdthap	Transmission/disequilibrium tests for extended marker haplotypes.
tensor	Tensor product of arrays.
tensorA	Advanced tensors arithmetic with named indices.
termstrc	Term structure and credit spread estimation.
tframe	Time Frame coding kernel: functions for writing code that is independent of the way time is represented.
tframePlus	Time Frame coding kernel extensions.
tgp	Bayesian regression and adaptive sampling with Treed Gaussian Process models.
tileHMM	Hidden Markov Models for ChIP-on-Chip analysis.

time	Time tracking for developers.
timeDate	The Rmetrics module for “Chronological and Calendarical Objects”.
timeSeries	The Rmetrics module for “Financial Time Series Objects”.
timereg	Code and data sets for the book “Dynamic Regression Models for Survival Data” by T. Martinussen and T. Scheike, 2006, Springer Verlag, plus more recent developments.
timsac	TIME Series Analysis and Control package.
tis	Time indexes and time indexed series.
titan	Titration analysis for mass spectrometry data.
titecrm	TIme-To-Event Continual Reassessment Method and calibration tools.
tkrgl	TK widget tools for rgl package.
tkrplot	Simple mechanism for placing R graphics in a Tk widget.
tlmise	Two-level normal independent sampling estimation.
tm	A framework for text mining applications within R.
topmodel	An R implementation of TOPMODEL.
tossm	Testing Of Spatial Structure Methods.
tpr	Temporal Process Regression.
trackObjs	Track objects.
tradeCosts	Post-trade analysis of transaction costs.
tree	Classification and regression trees.
treelet	Treelet: a novel construction of multi-scale bases that extends wavelets to non-smooth signals.
triangle	Standard distribution functions for the triangle distribution.
trimcluster	Cluster analysis with trimming.
trip	Spatial analysis of animal track data.
tripEstimation	Metropolis sampler and supporting functions for estimating animal movement from archival tags and satellite fixes.
tripack	A constrained two-dimensional Delaunay triangulation package.
truncgof	Goodness-of-fit tests allowing for left truncated data.
truncnorm	Truncated normal distribution.
trust	Local optimization using two derivatives and trust regions.

tsDyn	Time series analysis based on dynamical systems theory.
tsModel	Time series modeling for air pollution and health.
tseries	Package for time series analysis with emphasis on non-linear modelling.
tseriesChaos	Routines for the analysis of non-linear time series.
tsfa	Time Series Factor Analysis.
tuneR	Collection of tools to analyze music, handle wave files, transcription, etc.
tutoR	Student-friendly package to mask common functions.
twang	Toolkit for Weighting and Analysis of Nonequivalent Groups.
tweedie	Maximum likelihood computations for Tweedie exponential family models.
twslm	A two-way semilinear model for normalization and analysis of cDNA microarray data.
udunits	Interface to Unidata's routines to convert units.
ump	Uniformly Most Powerful tests.
unbalhaar	Function estimation via Unbalanced Haar wavelets.
uncompress	For uncompressing '.Z' files.
untb	Ecological drift under the UNTB (Unified Neutral Theory of Biodiversity).
urca	Unit root and cointegration tests for time series data.
urn	Functions for sampling without replacement (simulated urns).
uroot	Unit root tests and graphics for seasonal time series.
vabayelMix	Variational Bayesian mixture model.
varSelRF	Variable selection using random forests.
varmixt	Mixture model on the variance for the analysis of gene expression data.
vars	VAR modeling.
vbmp	Variational Bayesian Multinomial Probit Regression.
vcd	Functions and data sets based on the book "Visualizing Categorical Data" by Michael Friendly.
vegan	Various help functions for vegetation scientists and community ecologists.
verification	Utilities for verification of discrete and probabilistic forecasts.
verify	Construction of test suites using verify objects.
vioplot	Violin plots, which are a combination of a box plot and a kernel density plot.
vrtest	Variance ratio tests for weak-form market efficiency.

wasim	Tools for data processing and visualization of results of the WASIM-ETH hydrological model.
waveclock	Time-frequency analysis of cycling cell luminescence data.
waved	WaveD transform in R.
wavelets	Functions for computing wavelet filters, wavelet transforms and multiresolution analyses.
waveslim	Basic wavelet routines for time series analysis.
wavethresh	Software to perform 1-d and 2-d wavelet statistics and transforms.
wccsom	SOM networks for comparing patterns with peak shifts.
wgain	Whole Genome Average Interval Mapping for QTL detection using mixed models.
wikibooks	Functions and datasets for the German WikiBook “GNU R”.
wle	Robust statistical inference via a weighted likelihood approach.
wmtsa	Insightful Wavelet Methods for Time Series Analysis.
wnominate	WNOMINATE roll call analysis software.
wombsoft	Wombling computation.
wordnet	WordNet interface.
write.snns	Function for exporting data to SNNS (Stuttgart Neural Network Simulator) pattern files.
xgobi	Interface to the XGobi and XGvis programs for graphical data analysis.
xlsReadWrite	Natively read and write Excel files.
xtable	Export data to \LaTeX and HTML tables.
xts	Extensible time series.
yaImpute	Performs popular nearest neighbor routines.
yacca	Yet Another Canonical Correlation Analysis package.
yaml	Methods to convert R to YAML and back.
yest	Gaussian independence models.
zipfR	Statistical models for word frequency distributions.
zoeppritz	Zoeppritz equations: calculate and plot scattering coefficients of seismic waves when they interact at an interface between two layers.
zoo	A class with methods for totally ordered indexed observations such as irregular time series.

See CRAN ‘`src/contrib/PACKAGES`’ for more information.

Some CRAN packages that do not build out of the box on Windows, require additional software, or are shipping third party libraries for Windows cannot be made available on CRAN in form of a Windows binary packages. Nevertheless, some of these packages are available at the “CRAN extras” repository at <http://www.stats.ox.ac.uk/pub/RWin/> kindly provided by Brian D. Ripley. Note that this repository is a default repository for recent versions of R for Windows.

There used to be a CRAN ‘`src/contrib/Devel`’ directory with packages still “under development” or depending on features only present in the current development versions of R. This area is no longer provided, with packages formerly in this area either in the regular package area or the archive ‘`src/contrib/Archive`’.

5.1.3 Add-on packages from Omegahat

The **Omegahat Project for Statistical Computing** provides a variety of open-source software for statistical applications, with special emphasis on web-based software, Java, the Java virtual machine, and distributed computing. A CRAN style R package repository is available via <http://www.omegahat.org/R/>.

Currently, there are the following packages.

- Aspell** An interface to facilities in the aspell library.
- CGIwithR** Facilities for the use of R to write CGI scripts.
- CORBA** 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.
- Combinations**
 Compute the combinations of choosing r items from n elements.
- IDocs** Infrastructure for interactive documents.
- IDynDocs** Interactive and dynamic Documents with XML/XSL.
- 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++.
- RCurl** Allows one to compose HTTP requests to fetch URIs, post forms, etc., and process the results returned by the Web server.
- RDCOMClient**
 Provides dynamic client-side access to (D)COM applications from within R.
- RDCOMEvents**
 Provides facilities to use R functions and objects as handlers for DCOM events.
- RDCOMServer**
 Facilities for exporting S objects and functions as COM objects.
- 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.

RGoogleDocs

Initial, elementary interface to Google's Document API.

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.

RGtkIPrimitives

A collection of low-level primitives for interactive use with R graphics and the gtkDevice using **RGtk**.

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.

RMatlab A bi-directional interface between R and Matlab.

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, . . .

RSMETHODS

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.

Rcompression

In-memory decompression for GNU zip and bzip2 formats.

REXIF Extract meta-information from JPEG files.

RFLICKR R interface to Flickr API.

Rlibstree Suffix Trees in R via the libstree C library.

Rstem Interface to Snowball implementation of Porter’s word stemming algorithm.

RwxDevice

R graphics device using wxWidgets.

RwxWidgets

Facilities to program GUIs using wxWidgets in 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.

SSOAP A client interface to SOAP (Simple Object Access Protocol) servers from within S.

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.
- XML** Tools for reading XML documents and DTDs.
- Zillow** Simple interface to Zillow.com's house price estimate API.

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. A CRAN style R package repository is available via <http://www.bioconductor.org/>.

The following R packages are contained in the current release of Bioconductor, with more packages under development.

- ABarray** Microarray QA and statistical data analysis for Applied Biosystems Genome Survey Micorarray (AB1700) gene expression data.
- ACME** Algorithms for Calculating Microarray Enrichment (ACME).
- AffyCompatible**
Affymetrix GeneChip software compatibility
- AffyExpress**
Affymetrix quality assessment and analysis tool.
- AnnBuilder**
Processing annotation data from public data repositories and building annoat-
ion data packages or XML data documents using the source data.
- AnnotationDbi**
Annotation DataBase Interface.
- BAC** Bayesian Analysis of Chip-chip experiment.
- BCRANK** Predicting binding site consensus from ranked DNA sequences.
- BGmix** Bayesian models for differential gene expression.
- BSgenome** Infrastructure for Biostrings-based genome data packages.
- BioMVCClass**
Model-View-Controller (MVC) classes that use **Biobase**.
- Biobase** Object-oriented representation and manipulation of genomic data (S4 class structure).
- BiocCaseStudies**
Support for the Bioconductor Case Studies monograph.
- Biostrings** Class definitions and generics for biological sequences along with pattern match-
ing algorithms.
- BufferedMatrix**
Microarray analysis methods that use BufferedMatrix objects.

BufferedMatrixMethods

A matrix data storage object held in temporary files.

CALIB Calibration model for estimating absolute expression levels from microarray data.

CGHcall Calling aberrations for array CGH tumor profiles.

CORREP Multivariate correlation estimation and statistical inference.

Category A collection of tools for performing category analysis.

CoCiteStats

A collection of software tools for dealing with co-citation data.

DEDS Differential Expression via Distance Summary for microarray data.

DNAcopy Segments DNA copy number data using circular binary segmentation to detect regions with abnormal copy number.

DynDoc Functionality to create and interact with dynamic documents, vignettes, and other navigable documents.

EBImage Image processing and image analysis toolkit.

EBarrays Empirical Bayes tools for the analysis of replicated microarray data across multiple conditions.

GEOmetadb

A compilation of metadata from NCBI GEO.

GEOquery

Get data from NCBI Gene Expression Omnibus (GEO).

GGBase Infrastructure for genetics of gene expression.

GGtools Software and data for genetical genomics.

GLAD Gain and Loss Analysis of DNA.

GOstats Tools for manipulating GO and microarrays.

GSEABase

Gene set enrichment data structures and methods.

GSEAlm Linear model toolset for Gene Set Enrichment Analysis.

GeneMeta A collection of meta-analysis tools for analyzing high throughput experimental data.

GeneR Package manipulating nucleotidic sequences (Embl, Fasta, GenBank).

GeneRfold

R for genes and sequences, using viennaRNA package (fold).

GeneSelector

GeneSelector.

GeneSpring

Functions and class definitions to be able to read and write GeneSpring specific data objects and convert them to Bioconductor objects.

- GeneTraffic**
GeneTraffic R integration functions.
- GeneticsBase**
Classes and functions for handling genetic data.
- GeneticsDesign**
Functions for designing genetics studies.
- GeneticsPed**
Pedigree and genetic relationship functions.
- GenomeGraphs**
Plotting genomic information from Ensembl.
- GlobalAncova**
Calculates a global test for differential gene expression between groups.
- GraphAT** Graph theoretic Association Tests.
- GraphAlignment**
GraphAlignment.
- HEM** Heterogeneous Error Model for analysis of microarray data.
- Harshlight**
A “corrective make-up” program for microarray chips.
- Heatplus** A heat map displaying covariates and coloring clusters.
- Icens** Functions for computing the NPMLE for censored and truncated data.
- KEGGSOAP**
Client-side SOAP access KEGG.
- LBE** Estimation of the false discovery rate.
- LMGene** Analysis of microarray data using a linear model and log data transformation.
- LPE** Significance analysis of microarray data with small number of replicates using the Local Pooled Error (LPE) method.
- MANOR** Micro-Array NORmalization.
- MLInterfaces**
Uniform interfaces to machine learning code for the exprSet class from Bioconductor.
- MVCClass**
Model-View-Controller (MVC) classes.
- MantelCorr**
Compute Mantel Cluster Correlations.
- MassSpecWavelet**
Mass spectrum processing by wavelet-based algorithms.
- MeasurementError.cor**
Two-stage measurement error model for correlation estimation with smaller bias than the usual sample correlation.

MergeMaid	Cross-study comparison of gene expression array data.
Mfuzz	Soft clustering of time series gene expression data.
MiPP	Misclassification Penalized Posterior Classification.
OCplus	Operating characteristics plus sample size and local fdr for microarray experiments.
OLIN	Optimized Local Intensity-dependent Normalisation of two-color microarrays.
OLINgui	Graphical user interface for OLIN .
OrderedList	Similarities of ordered gene lists.
OutlierD	Outlier detection using quantile regression on the M-A scatterplots of high-throughput data.
PCpheno	Phenotypes and cellular organizational units.
PGSEA	Parametric Gene Set Enrichment Analysis.
PROcess	Ciphergen SELDI-TOF processing.
RBGL	An interface between the graph package and the Boost graph libraries, allowing for fast manipulation of graph objects in R.
RBioinf	Support for R for Bioinformatics monograph.
RLMM	A genotype calling algorithm for Affymetrix SNP arrays.
RMAGEML	Functionality to handle MAGEML documents.
ROC	Receiver Operating Characteristic (ROC) approach for identifying genes that are differentially expressed in two types of samples.
RSNPper	Interface to chip.org::SNPper for SNP-related data.
RWebServices	Expose R functions as web services through Java/Axis/Apache.
RankProd	Rank Product method for identifying differentially expressed genes.
RbcBook1	Support for Springer monograph on Bioconductor.
Rdbi	Generic framework for database access in R.
RdbiPgSQL	Methods for accessing data stored in PostgreSQL tables.
Rdisop	Decomposition of isotopic patterns.
RefPlus	Functions for pre-processing Affymetrix data using the RMA+ and the RMA++ methods.
Resourcerer	Read annotation data from TIGR Resourcerer or convert the annotation data into Bioconductor data package.

- Rgraphviz** An interface with Graphviz for plotting graph objects in R.
- Ringo** R Investigation of NimbleGen Oligoarrays..
- Rintact** Interface to EBI Intact protein interaction data base.
- Rredland** Interface to redland RDF utilities.
- Rtreemix** Mutagenetic trees mixture models.
- Ruuid** Creates Universally Unique ID values (UUIDs) in R.
- SAGx** Statistical Analysis of the GeneChip.
- SBMLR** Systems Biology Markup Language (SBML) interface and biochemical system analysis tools.
- SLGI** Synthetic Lethal Genetic Interaction.
- SLqPCR** Functions for analysis of real-time quantitative PCR data at SIRS-Lab GmbH.
- SMAP** A Segmental Maximum A Posteriori approach to array-CGH copy number profiling.
- SNPchip** Classes and methods for high throughput SNP chip data.
- ScISI** In Silico Interactome.
- SemSim** Gene ontology-based semantic similarity measures.
- TypeInfo** Optional type specification prototype.
- VanillaICE**
Methods for fitting Hidden Markov Models to SNP chip data.
- XDE** A Bayesian hierarchical model for cross-study analysis of differential gene expression.
- aCGH** Classes and functions for Array Comparative Genomic Hybridization data.
- adSplit** Annotation-driven clustering.
- affxparser** Package for parsing Affymetrix files (CDF, CEL, CHP, BPMAP, BAR).
- affy** Methods for Affymetrix Oligonucleotide Arrays.
- affyPLM** For fitting Probe Level Models.
- affyPara** Parallelized preprocessing methods for Affymetrix Oligonucleotide Arrays.
- affyQCReport**
QC Report Generation for affyBatch objects.
- affycomp** Graphics toolbox for assessment of Affymetrix expression measures.
- affycoretools**
Functions useful for those doing repetitive analyses.
- affyio** Tools for parsing Affymetrix data files.
- affylmGUI**
Graphical User Interface for affy analysis using package **limma**.

- affyPdn** Probe Dependent Nearest Neighbors (PDNN) for the **affy** package.
- altcdfenvs** Utilities to handle cdfenvs.
- annaffy** Functions for handling data from Bioconductor Affymetrix annotation data packages.
- annotate** 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.
- annotationTools**
Annotate microarrays and perform cross-species gene expression analyses using flat file databases.
- apComplex**
Estimate protein complex membership using AP-MS protein data.
- aroma.light**
Light-weight methods for normalization and visualization of microarray data using only basic R data types.
- arrayQuality**
Performing print-run and array level quality assessment.
- arrayQualityMetrics**
Quality metrics on ExpressionSets.
- beadarray** Quality control and low-level analysis of BeadArrays.
- beadarraySNP**
Normalization and reporting of Illumina SNP bead arrays.
- bgafun** A method to identify specificity determining residues in protein families.
- bgx** Bayesian Gene eXpression.
- bioDist** A collection of software tools for calculating distance measures.
- biocGraph** Graph examples and use cases in Bioinformatics.
- biocViews** Categorized views of R package repositories.
- biomaRt** Interface to BioMart databases (e.g., Ensembl)
- bridge** Bayesian Robust Inference for Differential Gene Expression.
- cellHTS** Analysis of cell-based screens.
- cellHTS2** Analysis of cell-based screens — revised version of **cellHTS**.
- cghMCR** Find chromosome regions showing common gains/losses.
- clusterStab**
Compute cluster stability scores for microarray data.
- codelink** Manipulation of Codelink Bioarrays data.
- convert** Convert Microarray Data Objects.

copa	Functions to perform cancer outlier profile analysis.
cosmo	Supervised detection of conserved motifs in DNA sequences.
cosmoGUI	GUI for constructing constraint sets used by the cosmo package.
ctc	Tools to export and import Tree and Cluster to other programs.
daMA	Functions for the efficient design of factorial two-color microarray experiments and for the statistical analysis of factorial microarray data.
diffGeneAnalysis	Performs differential Gene expression Analysis.
ecolitk	Metadata and tools to work with E. coli.
edd	Expression density diagnostics: graphical methods and pattern recognition algorithms for distribution shape classification.
exonmap	High level analysis of Affymetrix exon array data.
explorase	GUI for exploratory data analysis of systems biology data.
externalVector	Vector objects for R with external storage.
factDesign	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.
fbat	Family Based Association Tests for genetic data.
fdrame	FDR Adjustments of Microarray Experiments (FDR-AME).
flowClust	Clustering for flow cytometry.
flowCore	Basic structures for flow cytometry data.
flowQ	Quality control for flow cytometry.
flowUtils	Utilities for flow cytometry.
flowViz	Visualization for flow cytometry.
gaga	GaGa hierarchical model for microarray data analysis.
gaggle	Broadcast data between R and Java bioinformatics programs.
gcrma	Background adjustment using sequence information.
genArise	A tool for dual color microarray data.
geneRecommender	A gene recommender algorithm to identify genes coexpressed with a query set of genes.
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.
- goProfiles** Statistical analysis of functional profiles.
- 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.
- hopach** Hierarchical Ordered Partitioning and Collapsing Hybrid (HOPACH).
- hypergraph** Capabilities for representing and manipulating hypergraphs.
- idiogram** Plotting genomic data by chromosomal location.
- impute** Imputation for microarray data (currently KNN only).
- keggorth** Graph support for KO, KEGG Orthology.
- lapmix** Laplace mixture model in microarray experiments.
- limma** Linear models for microarray data.
- limmaGUI** Graphical User Interface for package **limma**.
- logicFS** Identification of SNP interactions.
- lumi** BeadArray specific methods for Illumina microarrays.
- maCorrPlot** Visualize artificial correlation in microarray data.
- maDB** Microarray database and utility functions for microarray analysis.
- maSigPro** Significant gene expression profile differences in time course microarray data.
- maanova** Tools for analyzing micro array experiments.
- macat** MicroArray Chromosome Analysis Tool.
- made4** Multivariate analysis of microarray data using ADE4.
- maigesPack** Functions to handle cDNA microarray data, including several methods of data analysis.
- makePlatformDesign** Creates the Platform Design environments (PDenvs) required by **oligo**.

- 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.
- matchprobes** Tools for sequence matching of probes on arrays.
- mdqc** Mahalanobis Distance Quality Control for microarrays.
- metaArray** Integration of microarray data for meta-analysis.
- 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.
- nem** Nested Effects Models to reconstruct phenotypic hierarchies.
- nnNorm** Spatial and intensity based normalization of cDNA microarray data based on robust neural nets.
- nudge** Normal Uniform Differential Gene Expression detection.
- occugene** Functions for multinomial occupancy distribution.
- oligo** Oligonucleotide arrays.
- oligoClasses** Classes for high-throughput SNP arrays.
- oneChannelGUI** Extend the capabilities of **affyImGUI**.
- ontoTools** Graphs and sparse matrices for working with ontologies; formal objects for nomenclatures with provenance management.
- pamr** Pam: Prediction Analysis for Microarrays.
- panp** Presence-Absence calls from Negative strand matching Probesets.
- pathRender** Render molecular pathways.
- pcaMethods** A collection of PCA methods.
- pcot2** Principal coordinates and Hotelling's T-square method.
- pdInfoBuilder** Platform design information package builder.
- pdmclass** CLASSification of microarray samples using Penalized Discriminant Methods.
- pgUtils** Utility functions for PostgreSQL databases.

- pickgene** Adaptive gene picking for microarray expression data analysis.
- pkgDepTools**
Package dependency tools.
- plgem** Power Law Global Error Model.
- plier** Implements the Affymetrix PLIER (Probe Logarithmic Error Intensity Estimate) algorithm.
- plw** Probe level Locally moderated Weighted *t*-tests.
- ppiStats** Protein-Protein Interaction Statistical package.
- prada** Tools for analyzing and navigating data from high-throughput phenotyping experiments based on cellular assays and fluorescent detection.
- preprocessCore**
A collection of pre-processing functions.
- puma** Propagating Uncertainty in Microarray Analysis.
- quantsmooth**
Quantile smoothing and genomic visualization of array data.
- qvalue** Q-value estimation for false discovery rate control.
- rHVDM** Hidden Variable Dynamic Modeling.
- rama** Robust Analysis of MicroArrays: robust estimation of cDNA microarray intensities with replicates using a Bayesian hierarchical model.
- rbsurv** Robust likelihood-based survival modeling with microarray data.
- reb** Regional Expression Biases.
- rflowcyt** Statistical tools and data structures for analytic flow cytometry.
- rsbml** R support for SBML, using libsbml.
- rtracklayer**
R interface to genome browsers and their annotation tracks.
- safe** Significance Analysis of Function and Expression.
- sagenhaft** Functions for reading and comparing SAGE (Serial Analysis of Gene Expression) libraries.
- seqLogo** Sequence logos for DNA sequence alignments.
- sigPathway**
Pathway analysis.
- 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.
- simulatorAPMS**
Computationally simulates the AP-MS technology.

- sizepower** Sample size and power calculation in microarray studies.
- snapCGH** Segmentation, normalization and processing of aCGH data.
- snpMatrix** The `snp.matrix` and `X.snp.matrix` classes.
- spikeLI** Affymetrix Spike-in Langmuir Isotherm data analysis tool.
- splicegear** A set of tools to work with alternative splicing.
- plots** Visualization routines for high throughput screens.
- spotSegmentation**
Microarray spot segmentation and gridding for blocks of microarray spots.
- sscore** S-score algorithm for Affymetrix oligonucleotide microarrays.
- ssize** Estimate microarray sample size.
- stam** STructured Analysis of Microarray data.
- stepNorm** Stepwise normalization functions for cDNA microarrays.
- tilingArray**
Analysis of tiling arrays.
- timecourse**
Statistical analysis for developmental microarray time course data.
- tkWidgets** Widgets in Tcl/Tk that provide functionality for Bioconductor packages.
- topGO** Enrichment analysis for Gene Ontology.
- twilight** Estimation of local false discovery rate.
- vbmp** Variational Bayesian Multinomial Probit regression.
- vsn** Calibration and variance stabilizing transformations for both Affymetrix and cDNA array data.
- weaver** Tools and extensions for processing Sweave documents.
- webbioc** Integrated web interface for doing microarray analysis using several of the Bioconductor packages.
- widgetInvoke**
Evaluation widgets for functions.
- widgetTools**
Tools for creating Tcl/Tk widgets, i.e., small-scale graphical user interfaces.
- xcms** LC/MS and GC/MS data analysis: framework for processing and visualization of chromatographically separated mass spectral data.
- xps** Methods for processing and analysis of Affymetrix Oligonucleotide Arrays.
- yaqcaffy** Affymetrix expression data quality control and reproducibility analysis.

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://popgen.unimaas.nl/~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 in your library search path (see the help page for `.libPaths()` for details on how the search path is determined).

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 repositories such as CRAN. See the help page for `available.packages()` 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.)
codetools   Code Analysis Tools for R
datasets    The R Datasets Package
foreign     Read Data Stored by Minitab, S, SAS, SPSS, Stata, Systat,
           dBase, ...

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 9, 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 12); 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 (R, S 3/4, and S-PLUS 3.x/4.x/5.x/6.x/7.x), LispStat dialects (XLispStat, ViSta), SAS, Stata, and BUGS.

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](#). 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.

Please send bug reports and suggestions on ESS to 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 121).

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 a Unix-alike, if your installation supports the `type="cairo"` option to the `png()` device there should be no problems, and the default settings should just work. This option is not available for versions of R prior to 2.7.0, or without support for cairo. From R 2.7.0 `png()` by default uses the Quartz device on Mac OS X, and that too works in batch mode.

Earlier versions of 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 or PDF file then converts it to any bitmap format supported by Ghostscript. On some installations this produces ugly output, on others it is perfectly satisfactory. Many systems now come with Xvfb from X.Org (possibly as an optional install), which is an X11 server that does not require a screen; and there is the **GDD** package from CRAN, which produces PNG, JPEG and GIF bitmaps without X11.

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 `xypplot()` 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()` (e.g., `DF[order(DF$a, DF[["b"]]),]` to sort the data frame `DF` on columns named `a` and `b`).

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”, *R News*, **3/2**, 7–12.

7.28 Why is `read.table()` so inefficient?

By default, `read.table()` needs to read in everything as character data, and then try to figure out which variables to convert to numerics or factors. For a large data set, this takes considerable amounts of time and memory. Performance can substantially be improved by using the `colClasses` argument to specify the classes to be assumed for the columns of the table.

7.29 What is the difference between `package` and `library`?

A *package* is a standardized collection of material extending R, e.g. providing code, data, or documentation. A *library* is a place (directory) where R knows to find packages it can use

(i.e., which were *installed*). R is told to use a package (to “load” it and add it to the search path) via calls to the function `library`. I.e., `library()` is employed to load a package from libraries containing packages.

See Chapter 5 [R Add-On Packages], page 22, for more details. See also Uwe Ligges (2003), “R Help Desk: Package Management”, *R News*, **3/3**, 37–39.

7.30 I installed a package but the functions are not there

To actually *use* the package, it needs to be *loaded* using `library()`.

See Chapter 5 [R Add-On Packages], page 22 and Section 7.29 [What is the difference between package and library?], page 117 for more information.

7.31 Why doesn't R think these numbers are equal?

The only numbers that can be represented exactly in R's numeric type are integers and fractions whose denominator is a power of 2. Other numbers have to be rounded to (typically) 53 binary digits accuracy. As a result, two floating point numbers will not reliably be equal unless they have been computed by the same algorithm, and not always even then. For example

```
R> a <- sqrt(2)
R> a * a == 2
[1] FALSE
R> a * a - 2
[1] 4.440892e-16
```

The function `all.equal()` compares two objects using a numeric tolerance of `.Machine$double.eps ^ 0.5`. If you want much greater accuracy than this you will need to consider error propagation carefully.

For more information, see e.g. David Goldberg (1991), “What Every Computer Scientist Should Know About Floating-Point Arithmetic”, *ACM Computing Surveys*, **23/1**, 5–48, also available via http://docs.sun.com/source/806-3568/ncg_goldberg.html.

To quote from “The Elements of Programming Style” by Kernighan and Plauger:

10.0 times 0.1 is hardly ever 1.0.

7.32 How can I capture or ignore errors in a long simulation?

Use `try()`, which returns an object of class “try-error” instead of an error, or preferably `tryCatch()`, where the return value can be configured more flexibly. For example

```
beta[i,] <- tryCatch(coef(lm(formula, data)),
                    error = function(e) rep(NA, 4))
```

would return the coefficients if the `lm()` call succeeded and would return `c(NA, NA, NA, NA)` if it failed (presumably there are supposed to be 4 coefficients in this example).

7.33 Why are powers of negative numbers wrong?

You are probably seeing something like

```
R> -2^2
[1] -4
```

and misunderstanding the precedence rules for expressions in R. Write

```
R> (-2)^2
[1] 4
```

to get the square of -2 .

The precedence rules are documented in `?Syntax`, and to see how R interprets an expression you can look at the parse tree

```
R> as.list(quote(-2^2))
[[1]]
'-'

[[2]]
2^2
```

7.34 How can I save the result of each iteration in a loop into a separate file?

One way is to use `paste()` (or `sprintf()`) to concatenate a stem filename and the iteration number while `file.path()` constructs the path. For example, to save results into files `'result1.rda'`, ..., `'result100.rda'` in the subdirectory `'Results'` of the current working directory, one can use

```
for(i in 1:100) {
  ## Calculations constructing "some_object" ...
  fp <- file.path("Results", paste("result", i, ".rda", sep = ""))
  save(list = "some_object", file = fp)
}
```

7.35 Why are p -values not displayed when using `lmer()`?

Doug Bates has kindly provided an extensive response in a post to the `r-help` list, which can be reviewed at <https://stat.ethz.ch/pipermail/r-help/2006-May/094765.html>.

7.36 Why are there unwanted lines between polygons in PDF output viewed in Adobe Reader?

Output from `polygon()` (and other functions calling `polygon()`) with the argument `border=NA` or `border="transparent"` should suppress border lines between polygons for all graphics devices.

PDF output from R can be made in many ways, both directly, and through for example Postscript or Windows Metafiles converted to PDF in external software. In Adobe Reader, the default setting for line art, such as polygons, is to smooth, which produces the impression of thin borders. Adobe Reader does this both for PDF files written by R or through other software.

This is irritating, especially when using Adobe Reader for presentation. The unwanted effect can be removed by turning off smoothing for line art: use the ‘Edit | Preferences | Page Display | Smooth line art’ menu in Adobe Reader 7.0.

7.37 Why does backslash behave strangely inside strings?

This question most often comes up in relation to file names (see [Section 7.8 \[How do file names work in Windows?\]](#), page 111) but it also happens that people complain that they cannot seem to put a single ‘\’ character into a text string unless it happens to be followed by certain other characters.

To understand this, you have to distinguish between character strings and *representations* of character strings. Mostly, the representation in R is just the string with a single or double quote at either end, but there are strings that cannot be represented that way, e.g., strings that themselves contains the quote character. So

```
> str <- "This \"text\" is quoted"
> str
[1] "This \"text\" is quoted"
> cat(str, "\n")
This "text" is quoted
```

The *escape sequences* ‘\”’ and ‘\n’ represent a double quote and the newline character respectively. Printing text strings, using `print()` or by typing the name at the prompt will use the escape sequences too, but the `cat()` function will display the string as-is. Notice that ‘\n”’ is a one-character string, not two; the backslash is not actually in the string, it is just generated in the printed representation.

```
> nchar("\n")
[1] 1
> substring("\n", 1, 1)
[1] "\n"
```

So how do you put a backslash in a string? For this, you have to escape the escape character. I.e., you have to double the backslash. as in

```
> cat("\\n", "\n")
\n
```

Some functions, particularly those involving regular expression matching, themselves use metacharacters, which may need to be escaped by the backslash mechanism. In those cases you may need a *quadruple* backslash to represent a single literal one.

In versions of R up to 2.4.1 an unknown escape sequence like ‘\p’ was quietly interpreted as just ‘p’. Current versions of R emit a warning.

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).

Starting with R 2.1.0, users can provide personal Makevars configuration files in `‘$HOME/.R’` to override the default flags. See section "Add-on packages" in *R Installation and Administration*.

For earlier versions of R, 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. For example, people sometimes think there is a bug in R’s mathematics because they don’t understand how finite-precision arithmetic works. Rather than jumping to conclusions, show the problem to someone who knows for certain. Unexpected results of comparison of decimal numbers, for example $0.28 * 100 \neq 28$ or $0.1 + 0.2 \neq 0.3$, are not a bug. See [Section 7.31 \[Why doesn’t R think these numbers are equal?\]](#), page 118, for more details.

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.

Before you actually submit a bug report, you should check whether the bug has already been reported and/or fixed. First, try the "Search Existing Reports" facility in the Bug Tracking page at <http://bugs.R-project.org/>. Second, consult <https://svn.R-project.org/R/trunk/NEWS>, which records changes that will appear in the *next* release of R, including some bug fixes that do not appear in Bug Tracking. (Windows users should additionally consult <https://svn.R-project.org/R/trunk/src/gnuwin32/CHANGES>.) Third, if possible try the current r-patched or r-devel version of R. If a bug has already been reported or fixed, please do not submit further bug reports on it. Finally, check carefully whether the bug is with R, or a contributed package. 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.

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 or submitted to the Web page at <http://bugs.R-project.org/>. Please try including results of `sessionInfo()` in your bug report.

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.

Corrections to and comments on message translation should be sent to the last translator (listed at the top of the appropriate ‘.po’ file) or to the translation team as listed at <http://developer.R-project.org/TranslationTeams.html>.

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More to come soon . . .