# Table of Contents

1 Introduction ................................................. 1  
  1.1 Legalese .................................................. 1  
  1.2 Obtaining this document .................................. 1  
  1.3 Citing this document ...................................... 1  
  1.4 Notation .................................................. 1  
  1.5 Feedback .................................................. 2  

2 R Basics ....................................................... 3  
  2.1 What is R? .................................................. 3  
  2.2 What machines does R run on? ............................ 3  
  2.3 What is the current version of R? ......................... 4  
  2.4 How can R be obtained? .................................... 4  
  2.5 How can R be installed? .................................... 4  
    2.5.1 How can R be installed (Unix) ....................... 4  
    2.5.2 How can R be installed (Windows) .................. 5  
    2.5.3 How can R be installed (Macintosh) ............... 5  
  2.6 Are there Unix binaries for R? .......................... 6  
  2.7 What documentation exists for R? ....................... 7  
  2.8 Citing R .................................................. 8  
  2.9 What mailing lists exist for R? .......................... 9  
  2.10 What is CRAN? ........................................... 10  
  2.11 Can I use R for commercial purposes? .................. 11  
  2.12 Why is R named R? ..................................... 11  
  2.13 What is the R Foundation? ............................... 11  

3 R and S ....................................................... 13  
  3.1 What is S? ................................................ 13  
  3.2 What is S-PLUS? .......................................... 13  
  3.3 What are the differences between R and S? .............. 13  
    3.3.1 Lexical scoping ..................................... 14  
    3.3.2 Models ................................................. 17  
    3.3.3 Others .................................................. 17  
  3.4 Is there anything R can do that S-PLUS cannot? ........ 19  
  3.5 What is R-plus? .......................................... 20  

4 R Web Interfaces ............................................. 21
5 R Add-On Packages ............................................ 23
  5.1 Which add-on packages exist for R? ...................... 23
    5.1.1 Add-on packages in R .................................. 23
    5.1.2 Add-on packages from CRAN .......................... 23
    5.1.3 Add-on packages from Omegahat ...................... 81
    5.1.4 Add-on packages from Bioconductor .................. 83
    5.1.5 Other add-on packages ............................... 93
  5.2 How can add-on packages be installed? ................. 94
  5.3 How can add-on packages be used? ...................... 94
  5.4 How can add-on packages be removed? ................... 95
  5.5 How can I create an R package? ....................... 96
  5.6 How can I contribute to R? ........................... 96

6 R and Emacs ....................................................... 97
  6.1 Is there Emacs support for R? ......................... 97
  6.2 Should I run R from within Emacs? ................... 97
  6.3 Debugging R from within Emacs ......................... 98

7 R Miscellanea ...................................................... 99
  7.1 How can I set components of a list to NULL? ......... 99
  7.2 How can I save my workspace? ........................ 99
  7.3 How can I clean up my workspace? ................... 99
  7.4 How can I get eval() and D() to work? ............... 99
  7.5 Why do my matrices lose dimensions? ................ 100
  7.6 How does autoloading work? .......................... 100
  7.7 How should I set options? .......................... 100
  7.8 How do file names work in Windows? ................. 101
  7.9 Why does plotting give a color allocation error? .. 101
  7.10 How do I convert factors to numeric? ............... 101
  7.11 Are Trellis displays implemented in R? ............. 101
  7.12 What are the enclosing and parent environments? ... 102
  7.13 How can I substitute into a plot label? ............ 102
  7.14 What are valid names? .............................. 103
  7.15 Are GAMs implemented in R? ......................... 103
  7.16 Why is the output not printed when I source() a file? 104
  7.17 Why does outer() behave strangely with my function? 104
  7.18 Why does the output from anova() depend on the order of factors in the model? ................. 105
  7.19 How do I produce PNG graphics in batch mode? .... 105
  7.20 How can I get command line editing to work? ..... 105
  7.21 How can I turn a string into a variable? .......... 106
  7.22 Why do lattice/trellis graphics not work? ........ 106
  7.23 How can I sort the rows of a data frame? .......... 106
  7.24 Why does the help.start() search engine not work? 106
  7.25 Why did my .Rprofile stop working when I updated R? 107
  7.26 Where have all the methods gone? .................. 107
  7.27 How can I create rotated axis labels? ............. 107
1 Introduction

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

1.1 Legalese

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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/


You can also obtain the R FAQ from the ‘doc/FAQ’ subdirectory of a CRAN site (see ⟨undefined⟩ [What is CRAN?], page ⟨undefined⟩).

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 http://CRAN.R-project.org/bin/windows/base/rw-FAQ.html, ‘‘R for Windows FAQ’’ and the http://CRAN.R-project.org/bin/macosx/RMacOSX-FAQ.html, ‘‘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.
Chapter 2: R Basics

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 [What is S?], page [undefined]) and Sussman’s [What are the differences between R and S?], page [undefined], 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 [R Add-On Packages], page [undefined]).

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.


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 2.7.0. 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 ⟨undefined⟩ [What is CRAN?], page ⟨undefined⟩).

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 ⟨undefined⟩ [Are there Unix binaries for R?], page ⟨undefined⟩), 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 ⟨undefined⟩ [What machines does R run on?], page ⟨undefined⟩). The file ‘INSTALL’ that comes with the R distribution contains a brief introduction, and the “R Installation and Administration” guide (see ⟨undefined⟩ [What documentation exists for R?], page ⟨undefined⟩) 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 versions of the documentation are built.
Use `make dvi` to create DVI versions of the R manuals, such as `refman.dvi` (an R object reference index) and `R-exts.dvi`, the “R Extension Writers Guide”, in the ‘doc/manual’ subdirectory. These files can be previewed and printed using standard programs such as `xdvi` and `dvips`. You can also use `make pdf` to build PDF (Portable Document Format) version of the manuals, and view these using e.g. Acrobat. Manuals written in the GNU Texinfo system can also be converted to info files suitable for reading online with Emacs or stand-alone GNU Info; use `make info` to create these versions (note that this requires Makeinfo version 4.5).

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

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

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

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

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

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

```
$ ./configure --prefix=/where/you/want/R/to/go
```
(E.g., the R executable will then be installed into ‘/where/you/want/R/to/go/bin’.)

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

### 2.5.2 How can R be installed (Windows)

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

For most installations the Windows installer program will be the easiest tool to use. See the http://CRAN.R-project.org/bin/windows/baserw-FAQ.html, ‘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 http://CRAN.R-project.org/bin/macosx/RMacOSX-FAQ.html, ‘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.

<table>
<thead>
<tr>
<th>CPU</th>
<th>Versions</th>
<th>Provider</th>
</tr>
</thead>
<tbody>
<tr>
<td>Debian</td>
<td>i386/amd64</td>
<td>stable/oldstable</td>
</tr>
<tr>
<td>Red Hat</td>
<td>i386/x86_64</td>
<td>fedora7/fedora8</td>
</tr>
<tr>
<td></td>
<td>i386/x86_64</td>
<td>el4/el5</td>
</tr>
<tr>
<td>SuSE</td>
<td>i586/x86_64</td>
<td>10.0/10.1/10.2/10.3</td>
</tr>
<tr>
<td>Ubuntu</td>
<td>i386</td>
<td>dapper/feisty/gutsy</td>
</tr>
<tr>
<td></td>
<td>amd64</td>
<td>dapper/feisty/gutsy</td>
</tr>
</tbody>
</table>

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 the stable distribution of Debian are provided by Johannes Ranke, and available from CRAN. Simply add the line

```
deb http://CRAN.R-project.org/bin/linux/debian stable/
(feel free to use a cran mirror instead of the master) to the file ‘/etc/apt/sources.list’, and install as usual. More details on installing and administering R on Debian Linux can be found at http://CRAN.R-project.org/bin/linux/debian/README. These backports 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:/dsteuer/openSUSE_10.2/
```

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

No other binary distributions are currently publicly 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 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, see (undefined) [How can R be installed?], page (undefined). 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 (undefined) [What is the R Foundation?], page (undefined)).

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.)

Books on R include


The book

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


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

In addition to material written specifically or explicitly for R, documentation for S/S-PLUS (see ⟨undefined⟩ [R and S], page ⟨undefined⟩) can be used in combination with this FAQ (see ⟨undefined⟩ [What are the differences between R and S?], page ⟨undefined⟩). Introductory books include


The book


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

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


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


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

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

### 2.8 Citing R

To cite R in publications, use
Citation strings (or BibTeX entries) for R and R packages can also be obtained by 
citation().

2.9 What mailing lists exist for R?

Thanks to Martin Maechler, there are four mailing lists devoted to R.

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

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

R-help
The ‘main' R mailing list, for discussion about problems and solutions using 
R, announcements (not covered by ‘R-announce' and ‘R-packages') about the 
development of R and the availability of new code.

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

Please read the http://www.R-project.org/posting-guide.html, 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 sub-
scribe 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 (undefined) [R Bugs], page (undefined) 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 http://gmane.org, 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 http://www.gnu.org/copyleft/gpl.html, 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 http://www.opensource.org/docs/definition.html, 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 undefined) [What is S?], page (undefined)).

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.
Chapter 3: R and S

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.

  This is also referred to as the “Brown Book”, and of historical interest only.
  This book is often called the “Blue Book”, and introduced what is now known as S version 2.
  This is also called the “White Book”, and introduced S version 3, which added structures to facilitate statistical modeling in S.
  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 http://lib.stat.cmu.edu/S/, 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.

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

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

(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

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

(lexical scope!), a version for S is

```r
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 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 [How can I save my workspace?], page (undefined)) 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 [R and Emacs], page (undefined)), 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 $y \sim x + 0$ is an alternative to $y \sim x - 1$ for specifying a model with no intercept. Models with no parameters at all can be specified by $y \sim 0$.

### 3.3.3 Others

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

Some known differences are the following.

- In R, if `x` is a list, then `x[i] <- NULL` and `x[[i]] <- NULL` remove the specified elements from `x`. The first of these is incompatible with S, where it is a no-op. (Note that you can set elements to NULL using `x[i] <- list(NULL).`)

- In S, the functions named `.First` and `.Last` in the ‘.Data’ directory can be used for customizing, as they are executed at the very beginning and end of a session, respectively.

In R, the startup mechanism is as follows. R first sources the system startup file `$R_HOME/library/base/R/Rprofile`]. Then, it searches for a site-wide startup profile
unless the command line option ‘--no-site-file’ was given. The name of this file is
taken from the value of the R_PROFILE environment variable. If that variable is unset,
the default is ‘$R_HOME/etc/Rprofile.site’. This code is loaded in package base.
Then, unless ‘--no-init-file’ was given, R searches for a file called ‘.Rprofile’ in
the current directory or in the user’s home directory (in that order) and sources it into
the user workspace. It then loads a saved image of the user workspace from ‘.RData’
in case there is one (unless ‘--no-restore’ was specified). If needed, the functions
.First() and .Last() should be defined in the appropriate startup profiles.

• In R, T and F are just variables being set to TRUE and FALSE, respectively, but are not
reserved words as in S and hence can be overwritten by the user. (This helps e.g. when
you have factors with levels "T" or "F".) Hence, when writing code you should always
use TRUE and FALSE.

• In R, dyn.load() can only load shared objects, as created for example by R CMD SHLIB.

• In R, attach() currently only works for lists and data frames, but not for directories.
(In fact, attach() also works for R data files created with save(), which is analogous
to attaching directories in S.) Also, you cannot attach at position 1.

• Categories do not exist in R, and never will as they are deprecated now in S. Use factors
instead.

• In R, For() loops are not necessary and hence not supported.

• In R, assign() uses the argument ‘envir=’ rather than ‘where=’ as in S.

• The random number generators are different, and the seeds have different length.

• R passes integer objects to C as int * rather than long * as in S.

• R has no single precision storage mode. However, as of version 0.65.1, there is a single
precision interface to C/FORTRAN subroutines.

• By default, ls() returns the names of the objects in the current (under R) and global
(under S) environment, respectively. For example, given

\[
x <- 1; \text{fun} <- \text{function()} \{ y <- 1; \text{ls()} \}
\]

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., \( f(a) \leftarrow b \) is evaluated as \( a \leftarrow "f\leftarrow"(a, value = b) \). 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”, http://www.amstat.org/publications/jcgs/, 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.

http://www.xlsolutions-corp.com/, XLSolutions Corporation is currently beta testing a commercially supported version of R named R+ (read R plus).


Chapter 4: R Web Interfaces

4 R Web Interfaces

Rweb is developed and maintained by Jeff Banfield. The http://www.math.montana.edu/Rweb/, 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.

http://www.warwick.ac.uk/go/dfirth, 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/.

http://www.rpad.org/Rpad, 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.
http://stats.math.uni-augsburg.de/Rserve/, 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).

http://openstatserver.org/index.html, 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. http://steve-chen.net/R_PHP/, 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. http://dssm.unipa.it/R-php/?cmd=home, 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.

http://www.bioconductor.org/, 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, http://rwui.cryst.bbk.ac.uk, Rwui is a web application to 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.
- **AIS**: Tools to look at the data (“Ad Inidicia Spectata”).
- **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,
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.
BMA  Bayesian Model Averaging for linear models, generalizable linear models and survival models (Cox regression).
BPHO  Bayesian Prediction with High-order Interactions.
BRugs  OpenBUGS and its R interface BRugs.
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 biodemographic analysis.
BiodiversityR  GUI for biodiversity and community ecology analysis.
BootCL  Bootstrapping test for chromosomal localization.
**BradleyTerry**  
Specify and fit the Bradley-Terry model and structured versions.

**Brobdingnag**  
Very large numbers in R.

**BSDA**  

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

**CCA**  
Canonical correlation analysis.

**CDNmoney**  
Components of Canadian monetary aggregates.

**CGIwithR**  
Facilities for the use of R to write CGI scripts.

**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.

**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**  

**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.

**CoxBoost**  
Cox survival models by likelihood based boosting.
Chapter 5: R Add-On Packages

**CreditMetrics**
Functions for calculating the CreditMetrics risk model.

**DAAG**

**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**

**Devore6**

**Devore7**
**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.

**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.

**FKBL**
Fuzzy Knowledge Base Learning.

**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**

**FitAR**
Subset AR model fitting.

**Flury**
Data sets 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.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>FunCluster</td>
<td>Functional profiling of cDNA microarray expression data.</td>
</tr>
<tr>
<td>FunNet</td>
<td>Functional analysis of gene co-expression networks.</td>
</tr>
<tr>
<td>G1DBN</td>
<td>Dynamic Bayesian Network inference using 1st order conditional dependencies.</td>
</tr>
<tr>
<td>GAMBoost</td>
<td>Generalized additive models by likelihood based boosting.</td>
</tr>
<tr>
<td>GDD</td>
<td>Platform and X11 independent device for creating bitmaps (png, gif and jpeg) using the GD graphics library.</td>
</tr>
<tr>
<td>GEOmap</td>
<td>Topographic and geologic mapping.</td>
</tr>
<tr>
<td>GLDEX</td>
<td>Fit RS and FMKL generalised lambda distributions using discretized and maximum likelihood methods.</td>
</tr>
<tr>
<td>GOSim</td>
<td>Computation of functional similarities between GO terms and gene products.</td>
</tr>
<tr>
<td>GPArotation</td>
<td>Gradient Projection Algorithm rotation for factor analysis.</td>
</tr>
<tr>
<td>GRASS</td>
<td>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.</td>
</tr>
<tr>
<td>GSA</td>
<td>Gene set analysis.</td>
</tr>
<tr>
<td>GSM</td>
<td>Gamma Shape Mixture.</td>
</tr>
<tr>
<td>GenABEL</td>
<td>Genome-wide SNP association analysis.</td>
</tr>
<tr>
<td>GenKern</td>
<td>Functions for generating and manipulating generalised binned kernel density estimates.</td>
</tr>
<tr>
<td>GeneCycle</td>
<td>Identification of periodically expressed genes.</td>
</tr>
<tr>
<td>GeneF</td>
<td>Generalized $F$-statistics.</td>
</tr>
<tr>
<td>GeneNT</td>
<td>Relevance or Dependency network and signaling pathway discovery.</td>
</tr>
<tr>
<td>GeneTS</td>
<td>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.</td>
</tr>
<tr>
<td>Geneland</td>
<td>MCMC inference from individual genetic data based on a spatial statistical model.</td>
</tr>
<tr>
<td>GeoXp</td>
<td>Interactive exploratory spatial data analysis.</td>
</tr>
<tr>
<td>GillespieSSA</td>
<td>Gillespie’s Stochastic Simulation Algorithm (SSA).</td>
</tr>
<tr>
<td>GroupSeq</td>
<td>Computations related to group-sequential boundaries.</td>
</tr>
<tr>
<td>Package</td>
<td>Description</td>
</tr>
<tr>
<td>-----------</td>
<td>-----------------------------------------------------------------------------</td>
</tr>
<tr>
<td>HH</td>
<td>Support software for “Statistical Analysis and Data Display” by Richard M.</td>
</tr>
<tr>
<td>HI</td>
<td>Simulation from distributions supported by nested hyperplanes.</td>
</tr>
<tr>
<td>HSAUR</td>
<td>Functions, data sets, analyses and examples from the book “A Handbook of</td>
</tr>
<tr>
<td></td>
<td>Statistical Analyses Using R” by Brian S. Everitt and Torsten Hothorn (2006),</td>
</tr>
<tr>
<td></td>
<td>Chapman &amp; Hall/CRC.</td>
</tr>
<tr>
<td>HTMLapplets</td>
<td>Functions inserting dynamic scatterplots and grids in documents generated by</td>
</tr>
<tr>
<td></td>
<td>R2HTML.</td>
</tr>
<tr>
<td>HFWutils</td>
<td>Utilities by H. Felix Wittmann: Excel connections, string matching, and passing by reference.</td>
</tr>
<tr>
<td>HardyWeinberg</td>
<td>Graphical tests for Hardy-Weinberg equilibrium.</td>
</tr>
<tr>
<td>HiddenMarkov</td>
<td>Hidden Markov Models.</td>
</tr>
<tr>
<td>HighProbability</td>
<td>Estimation of the alternative hypotheses having frequentist or Bayesian probabilities at least as great as a specified threshold, given a list of $p$-values.</td>
</tr>
<tr>
<td>Hmisc</td>
<td>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 code, recoding variables, and bootstrap repeated measures analysis.</td>
</tr>
<tr>
<td>HydroMe</td>
<td>Estimation of soil hydraulic parameters from experimental data.</td>
</tr>
<tr>
<td>HyperbolicDist</td>
<td>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.</td>
</tr>
<tr>
<td>IBrokers</td>
<td>R API to Interactive Brokers Trader Workstation.</td>
</tr>
<tr>
<td>ICE</td>
<td>Iterated Conditional Expectation: kernel estimators for interval-censored data.</td>
</tr>
<tr>
<td>ICEinfer</td>
<td>Incremental Cost-Effectiveness (ICE) statistical inference (from two unbiased samples).</td>
</tr>
<tr>
<td>ICS</td>
<td>ICS/ICA computation based on two scatter matrices.</td>
</tr>
<tr>
<td>ICSP</td>
<td>Tools for multivariate nonparametrics.</td>
</tr>
<tr>
<td>IDPmisc</td>
<td>Utilities from the Institute of Data Analyses and Process Design, IDP/ZHW.</td>
</tr>
<tr>
<td>Package</td>
<td>Description</td>
</tr>
<tr>
<td>--------------</td>
<td>-----------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Icens</td>
<td>Functions for computing the NPMLE for censored and truncated data.</td>
</tr>
<tr>
<td>Iso</td>
<td>Functions to perform isotonic regression.</td>
</tr>
<tr>
<td>JADE</td>
<td>JADE and ICA performance criteria.</td>
</tr>
<tr>
<td>JLLprod</td>
<td>Nonparametric estimation of homothetic and generalized homothetic production functions.</td>
</tr>
<tr>
<td>JGR</td>
<td>Java Gui for R.</td>
</tr>
<tr>
<td>JM</td>
<td>Joint Modeling of longitudinal and survival data.</td>
</tr>
<tr>
<td>JavaGD</td>
<td>Java Graphics Device.</td>
</tr>
<tr>
<td>JointGLM</td>
<td>Joint modeling of mean and dispersion through two interlinked GLM’s.</td>
</tr>
<tr>
<td>JointModeling</td>
<td>Joint modeling of mean and dispersion.</td>
</tr>
<tr>
<td>JudgeIt</td>
<td>Calculates bias, responsiveness, and other characteristics of two-party electoral systems, with district-level electoral and other data.</td>
</tr>
<tr>
<td>Kendall</td>
<td>Kendall rank correlation and Mann-Kendall trend test.</td>
</tr>
<tr>
<td>LDheatmap</td>
<td>Heat maps of linkage disequilibrium measures.</td>
</tr>
<tr>
<td>LLAhclust</td>
<td>Hierarchical clustering of variables or objects based on the likelihood linkage analysis method.</td>
</tr>
<tr>
<td>LLN</td>
<td>Learning with latent networks.</td>
</tr>
<tr>
<td>LMGene</td>
<td>Date transformation and identification of differentially expressed genes in gene expression arrays.</td>
</tr>
<tr>
<td>LearnBayes</td>
<td>Functions for Learning Bayesian Inference.</td>
</tr>
<tr>
<td>Lmoments</td>
<td>Estimation of L-moments and the parameters of normal and Cauchy polynomial quantile mixtures.</td>
</tr>
<tr>
<td>LogConcDEAD</td>
<td>Maximum likelihood estimation of a log-concave density.</td>
</tr>
<tr>
<td>LogicReg</td>
<td>Routines for Logic Regression.</td>
</tr>
<tr>
<td>LoopAnalyst</td>
<td>A collection of tools to conduct Levins’ Loop Analysis.</td>
</tr>
</tbody>
</table>
LowRankQP

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

MASS


MBA

Multilevel B-spline Approximation.

MBESS

Methods for the Behavioral, Educational, and Social Sciences.

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.

MChitest

Monte Carlo hypothesis tests.

MEMSS


MFDA

Model Based Functional Data Analysis.

MKLE

Maximum kernel likelihood estimation.

MLDS

Maximum Likelihood Difference Scaling.

MLEcens

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

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


MSBVAR

Bayesian vector autoregression models, impulse responses and forecasting.

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.

MiscPsycho

Miscellaneous Psychometrics.
<table>
<thead>
<tr>
<th>Package</th>
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<tr>
<td>MultEq</td>
<td>Equivalence tests and simultaneous confidence intervals for multiple endpoints.</td>
</tr>
<tr>
<td>NADA</td>
<td>Methods described in “Nondetects And Data Analysis: Statistics for Censored Environmental Data” by Dennis R. Helsel, 2004, John Wiley and Sons.</td>
</tr>
<tr>
<td>NISTnls</td>
<td>A set of test nonlinear least squares examples from nist, the U.S. National Institute for Standards and Technology.</td>
</tr>
<tr>
<td>NMMAPSlite</td>
<td>U.S. National Morbidity, Mortality, and Air Pollution Study data lite.</td>
</tr>
<tr>
<td>NORMT3</td>
<td>Evaluates complex erf, erfc and density of sum of Gaussian and Student’s t.</td>
</tr>
<tr>
<td>NRAIA</td>
<td>Data sets with sample code from “Nonlinear Regression Analysis and Its Applications” by Doug Bates and Donald Watts, 1988, Wiley.</td>
</tr>
<tr>
<td>NestedCohort</td>
<td>Survival analysis for cohorts with missing covariate information.</td>
</tr>
<tr>
<td>ORMDR</td>
<td>Odds ratio based multivector-dimensionality reduction method for detecting gene-gene interactions.</td>
</tr>
<tr>
<td>Oarray</td>
<td>Arrays with arbitrary offsets.</td>
</tr>
<tr>
<td>PBSmapping</td>
<td>Software evolved from fisheries research conducted at the Pacific Biological Station (PBS) in Nanaimo, British Columbia, Canada. Draws maps and implements other GIS procedures.</td>
</tr>
<tr>
<td>PBSmodelling</td>
<td>Software to facilitate the design, testing, and operation of computer models.</td>
</tr>
<tr>
<td>PET</td>
<td>Simulation and reconstruction of PET images.</td>
</tr>
<tr>
<td>PHYLOGR</td>
<td>Manipulation and analysis of phylogenetically simulated data sets (as obtained from PDSIMUL in package PDAP) and phylogenetically-based analyses using GLS.</td>
</tr>
<tr>
<td>PK</td>
<td>Estimation of pharmacokinetic parameters.</td>
</tr>
<tr>
<td>PKfit</td>
<td>A nonlinear regression (including a genetic algorithm) program designed to deal with curve fitting for pharmacokinetics.</td>
</tr>
<tr>
<td>POT</td>
<td>Generalized Pareto distribution and Peaks Over Threshold.</td>
</tr>
<tr>
<td>PSAgraphics</td>
<td>Propensity Score Analysis Graphics.</td>
</tr>
<tr>
<td>PTAk</td>
<td>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.</td>
</tr>
</tbody>
</table>
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.

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.

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.

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.

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 Gtik (the Gimp Tool Kit) version 2.

RGrace
Mouse/menu driven interactive plotting application.

RGraphics

RHmm
Hidden Markov Model simulations and estimations.

RII
Estimation of the relative index of inequality for interval-censored data using natural cubic splines.

RJDBC
Access to databases through the JDBC interface.

RJaCGH
Reversible Jump MCMC for the analysis of CGH arrays.

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.

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.

**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.
**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 or HTML.


**RcmdrPlugin.HH**  Rcmdr support for the introductory course at Temple University.

**RcmdrPlugin.IPSUR**  Rcmdr plugin for “Introduction to Probability and Statistics Using R”.

**RcmdrPlugin.TeachingDemos**  Rcmdr Teaching Demos plug-in.

**RcmdrPlugin.epack**  Rcmdr epack demos plug-in.

**Rcplex**  R interface to CPLEX solvers for linear, quadratic, and (linear and quadratic) mixed integer programs.

**Reliability**  Functions for estimating parameters in software reliability models.

**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.

**Rlsf**  Interface to the LSF queuing system.

**Rmldr**  R-Multifactor Dimensionality Reduction.

**Rmetrics**  Financial engineering and computational finance.

**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.

**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.
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.


Ryacas  An R interfaces to the yacas computer algebra system.


SASxport  Read and write SAS XPORT files.

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.


SNPassoc  SNP-based whole genome association studies.

SNPmaxsel  Maximally selected statistics for SNP data.

SRPM  Shared Reproducibility Package Management.

SQLiteDF  Stores data frames and matrices in SQLite tables.

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).


SensoMineR  
Sensory data analysis.

SeqKnn  
Sequential KNN imputation.

SharedHT2  
Shared Hotelling $T^2$ test for small sample microarray experiments.

SimHap  
A comprehensive modeling framework for epidemiological outcomes and a multiple-imputation approach to haplotypic analysis of population-based data.

Snowball  
Snowball stemmers.

SoDA  

SoPhy  

SparseLogReg  
Sparse logistic regression.

SparseM  
Basic linear algebra for sparse matrices.

SpatialNP  
Multivariate nonparametric methods based on spatial signs and ranks.

SpherWave  
Spherical Wavelets and SW-based spatially adaptive methods.

StatDA  

StatDataML  
Read and write StatDataML.

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

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

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  

TSHRC  
Two Stage Hazard Rate Comparison.

TSMMySQL  
Time Series Database Interface extensions for MySQL.
TSP  Traveling Salesperson Problem (TSP).
TSSQLite  Time Series Database Interface extensions for SQLite.
TSdbi  Time Series Database Interface.
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.
TwslmSpikeWeight  Normalization of cDNA microarray data with the two-way semilinear model (TW-SLM).
TwoWaySurvival  Additive two-way hazards modeling of right censored survival data.
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.
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).
WINRPACK  Reads in WIN pickfile and waveform files.
WeedMap  Map of weed intensity.
WhatIf  Software for evaluating counterfactuals.
XML  Tools for reading XML documents and DTDs.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>XReg</td>
<td>Extreme regression.</td>
</tr>
<tr>
<td>YaleToolkit</td>
<td>Data exploration tools from Yale University.</td>
</tr>
<tr>
<td>ZIGP</td>
<td>Zero Inflated Generalized Poisson (ZIGP) regression models.</td>
</tr>
<tr>
<td>Zelig</td>
<td>Everyone’s statistical software: an easy-to-use program that can estimate, and help interpret the results of, an enormous range of statistical models.</td>
</tr>
<tr>
<td>aaMI</td>
<td>Mutual information for protein sequence alignments.</td>
</tr>
<tr>
<td>abind</td>
<td>Combine multi-dimensional arrays.</td>
</tr>
<tr>
<td>accuracy</td>
<td>A suite of tools designed to test and improve the accuracy of statistical computation.</td>
</tr>
<tr>
<td>acepack</td>
<td>ACE (Alternating Conditional Expectations) and AVAS (Additivity and VAriance Stabilization for regression) methods for selecting regression transformations.</td>
</tr>
<tr>
<td>actuar</td>
<td>Functions related to actuarial science applications.</td>
</tr>
<tr>
<td>ada</td>
<td>Performs boosting algorithms for a binary response.</td>
</tr>
<tr>
<td>adabag</td>
<td>Adaboost.M1 and Bagging.</td>
</tr>
<tr>
<td>adapt</td>
<td>Adaptive quadrature in up to 20 dimensions.</td>
</tr>
<tr>
<td>ade4</td>
<td>Multivariate data analysis and graphical display.</td>
</tr>
<tr>
<td>ade4TkGUI</td>
<td>Tcl/Tk Graphical User Interface for ade4.</td>
</tr>
<tr>
<td>adegenet</td>
<td>Genetic data handling for multivariate analysis using ade4.</td>
</tr>
<tr>
<td>adehabitat</td>
<td>A collection of tools for the analysis of habitat selection by animals.</td>
</tr>
<tr>
<td>adimpro</td>
<td>Adaptive smoothing of digital images.</td>
</tr>
<tr>
<td>adk</td>
<td>Anderson-Darling K-sample test and combinations of such tests.</td>
</tr>
<tr>
<td>adlift</td>
<td>Adaptive Wavelet transforms for signal denoising.</td>
</tr>
<tr>
<td>ads</td>
<td>Spatial point patterns analysis.</td>
</tr>
<tr>
<td>agece</td>
<td>Analysis of growth curve experiments.</td>
</tr>
<tr>
<td>agricolae</td>
<td>Statistical procedures for agricultural research.</td>
</tr>
<tr>
<td>agsemisc</td>
<td>Miscellaneous plotting and utility functions.</td>
</tr>
<tr>
<td>akima</td>
<td>Linear or cubic spline interpolation for irregularly gridded data.</td>
</tr>
<tr>
<td>allelic</td>
<td>A fast, unbiased and exact allelic exact test.</td>
</tr>
<tr>
<td>alr3</td>
<td>Methods and data to accompany the textbook “Applied Linear Regression” by S. Weisberg, 2005, Wiley.</td>
</tr>
<tr>
<td>amap</td>
<td>Another Multidimensional Analysis Package.</td>
</tr>
</tbody>
</table>
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.
aple 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, . . .
argosfilter Argos locations filter.
arq 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).
asypow A set of routines that calculate power and related quantities utilizing asymptotic likelihood ratio methods.
asuR Functions and data sets for a lecture in “Advanced Statistics using R”.
aws Functions to perform adaptive weights smoothing.
backfitRichards
Backfitted independent values of Richards curves.

backtest
Exploring portfolio-based hypotheses about financial instruments.

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.

benchden
28 benchmark densities from Berlinet/Devroye (1994).

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.

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.

bitops
Functions for Bitwise operations on integer vectors.

bivpois
Bivariate Poisson models using the EM algorithm.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>blighty</td>
<td>Function for drawing the coastline of the United Kingdom.</td>
</tr>
<tr>
<td>blockTools</td>
<td>Block, randomly assign, and diagnose potential problems between units in randomized experiments.</td>
</tr>
<tr>
<td>blockrand</td>
<td>Randomization for block random clinical trials.</td>
</tr>
<tr>
<td>bnlearn</td>
<td>Bayesian network structure learning.</td>
</tr>
<tr>
<td>boa</td>
<td>Bayesian Output Analysis Program for MCMC.</td>
</tr>
<tr>
<td>boolean</td>
<td>Boolean logit and probit: a procedure for testing Boolean hypotheses.</td>
</tr>
<tr>
<td>bootStepAIC</td>
<td>Model selection by bootstrapping the <code>stepAIC()</code> procedure.</td>
</tr>
<tr>
<td>bqtl</td>
<td>QTL mapping toolkit for inbred crosses and recombinant inbred lines. Includes maximum likelihood and Bayesian tools.</td>
</tr>
<tr>
<td>brainwaver</td>
<td>Basic wavelet analysis of multivariate time series with a visualisation and parametrization using graph theory.</td>
</tr>
<tr>
<td>brew</td>
<td>Templating framework for report generation.</td>
</tr>
<tr>
<td>brglm</td>
<td>Bias-reduction in binomial-response GLMs.</td>
</tr>
<tr>
<td>brlr</td>
<td>Bias-reduced logistic regression: fits logistic regression models by maximum penalized likelihood.</td>
</tr>
<tr>
<td>butler</td>
<td>Unit testing, profiling and benchmarking for R.</td>
</tr>
<tr>
<td>bvls</td>
<td>The Stark-Parker algorithm for bounded-variable least squares.</td>
</tr>
<tr>
<td>ca</td>
<td>Simple, multiple and joint Correspondence Analysis.</td>
</tr>
<tr>
<td>caMassClass</td>
<td>Processing and Classification of protein mass spectra (SELDI) data.</td>
</tr>
<tr>
<td>caTools</td>
<td>Miscellaneous utility functions, including reading/writing ENVI binary files, a LogitBoost classifier, and a base64 encoder/decoder.</td>
</tr>
<tr>
<td>cacheSweave</td>
<td>Tools for caching Sweave computations.</td>
</tr>
<tr>
<td>cacher</td>
<td>Tools for caching and distributing statistical analyses.</td>
</tr>
<tr>
<td>cairoDevice</td>
<td>Loadable CAIRO/GTK device driver.</td>
</tr>
<tr>
<td>Package</td>
<td>Description</td>
</tr>
<tr>
<td>-----------</td>
<td>---------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>calib</td>
<td>Statistical tool for calibration of plate based bioassays.</td>
</tr>
<tr>
<td>calibrate</td>
<td>Calibration of biplot axes.</td>
</tr>
<tr>
<td>candisc</td>
<td>Generalized canonical discriminant analysis.</td>
</tr>
<tr>
<td>car</td>
<td>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.</td>
</tr>
<tr>
<td>caret</td>
<td>Classification and REgression Training.</td>
</tr>
<tr>
<td>caretLSF</td>
<td>Classification and REgression Training, LSF style.</td>
</tr>
<tr>
<td>caretNWS</td>
<td>Classification and REgression Training in parallel using NetworkSpaces.</td>
</tr>
<tr>
<td>cat</td>
<td>Analysis of categorical-variable datasets with missing values.</td>
</tr>
<tr>
<td>catmap</td>
<td>Case-control and TDT meta-analysis package.</td>
</tr>
<tr>
<td>catspec</td>
<td>Special models for categorical variables.</td>
</tr>
<tr>
<td>cba</td>
<td>Clustering for Business Analytics, including implementations of Proximus and Rock.</td>
</tr>
<tr>
<td>cclust</td>
<td>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.</td>
</tr>
<tr>
<td>celsius</td>
<td>Retrieve Affymetrix microarray measurements and metadata from Celsius.</td>
</tr>
<tr>
<td>cfa</td>
<td>Analysis of configuration frequencies.</td>
</tr>
<tr>
<td>cggd</td>
<td>Continuous Generalized Gradient Descent.</td>
</tr>
<tr>
<td>cgh</td>
<td>Analysis of microarray comparative genome hybridisation data using the Smith-Waterman algorithm.</td>
</tr>
<tr>
<td>cghFLasso</td>
<td>Hot spot detecting for CGH array data with fused lasso regression.</td>
</tr>
<tr>
<td>chplot</td>
<td>Augmented convex hull plots: informative and nice plots for grouped bivariate data.</td>
</tr>
<tr>
<td>changeLOS</td>
<td>Change in length of hospital stay (LOS).</td>
</tr>
<tr>
<td>cheb</td>
<td>Discrete linear Chebyshev approximation.</td>
</tr>
<tr>
<td>chemCal</td>
<td>Calibration functions for analytical chemistry.</td>
</tr>
<tr>
<td>choplump</td>
<td>Choplump tests (permutation tests for comparing two groups with some positive but many zero responses).</td>
</tr>
<tr>
<td>chron</td>
<td>A package for working with chronological objects (times and dates).</td>
</tr>
</tbody>
</table>
cir  Nonparametric estimation of monotone functions via isotonic regression and centered isotonic regression.


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.


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.

**colors**  
Mapping between assorted color spaces.

**combinat**  
Combinatorics utilities.

**compHclust**  
Complementary hierarchical clustering.

**compOverlapCorr**  
Comparing overlapping correlation coefficients.

**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.

**contrast**  
A collection of contrast methods.

**copula**  
Classes of commonly used copulas (including elliptical and Archimedean), and methods for density, distribution, random number generators, and plotting.

**corpora**  
Utility functions for the statistical analysis of corpus frequency data.

**corpcor**  
Efficient estimation of covariance and (partial) correlation.

**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.

**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.
**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.

**cwhmisc**  Miscellaneous functions by Christian W. Hoffmann.

**cyclones**  Cyclone identification.

**date**  Functions for dealing with dates. The most useful of them accepts a vector of input dates in any of the forms '8/30/53', '30Aug53', '30 August 1953', . . . , 'August 30 53', or any mixture of these.

**dblcens**  Calculates the NPMLE of the survival distribution for doubly censored data.

**ddesolve**  Solver for Delay Differential Equations.

**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 tesselation (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.

**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.

**desirability**  Desirability function optimization and ranking.

**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.

**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.

**diptest**  Compute Hartigan’s dip test statistic for unimodality.

**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.

**distrSim**  Simulation classes based on package distr.

**distrTEst**  Estimation and Testing classes based on package distr.

**distributions**  Probability distributions based on TI-83 Plus.

**diveMove**  Dive analysis and calibration.

**dlm**  Maximum likelihood and Bayesian analysis of Dynamic Linear Models.

**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).

**dtt**  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.

**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.

**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.

**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.
epiR          Functions for analyzing epidemiological data.
epibasix      Elementary functions for epidemiological analysis.
epicalc       Epidemiological calculator.
epitools      Basic tools for applied epidemiology.
epsi          Edge Preserving Smoothing for Images.
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).
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.
experiment    Designing and analyzing randomized experiments.
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.

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.

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.
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. Recommended.
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.
fpc  Fixed point clusters, clusterwise regression and discriminant plots.
fpca  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.
fsa  Fuzzy set ordination.
ftnonpar  Features and strings for nonparametric regression.
fuzzyFDR  Exact calculation of fuzzy decision rules for multiple testing.
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 metadata 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**.

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

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

**gafit** Genetic algorithm for curve fitting.


**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.


**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.
<table>
<thead>
<tr>
<th>Package</th>
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<tbody>
<tr>
<td>gcmrec</td>
<td>Parameters estimation of the general semiparametric model for recurrent event data proposed by Peña and Hollander.</td>
</tr>
<tr>
<td>gdata</td>
<td>Various functions to manipulate data.</td>
</tr>
<tr>
<td>gee</td>
<td>An implementation of the Liang/Zeger generalized estimating equation approach to GLMs for dependent data.</td>
</tr>
<tr>
<td>geepack</td>
<td>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.</td>
</tr>
<tr>
<td>geiger</td>
<td>Analysis of evolutionary diversification.</td>
</tr>
<tr>
<td>genalg</td>
<td>R based genetic algorithm for binary and floating point chromosomes.</td>
</tr>
<tr>
<td>genetics</td>
<td>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, . . .</td>
</tr>
<tr>
<td>geoR</td>
<td>Functions to perform geostatistical data analysis including model-based methods.</td>
</tr>
<tr>
<td>geoRglm</td>
<td>Functions for inference in generalised linear spatial models.</td>
</tr>
<tr>
<td>geomapdata</td>
<td>Data for topographic and geologic mapping.</td>
</tr>
<tr>
<td>geometry</td>
<td>Mesh generation and surface tesselation, based on the Qhull library.</td>
</tr>
<tr>
<td>geozoo</td>
<td>Definition of geometric objects and display via rggobi.</td>
</tr>
<tr>
<td>getopt</td>
<td>C-like getopt behavior for R scripts.</td>
</tr>
<tr>
<td>ggm</td>
<td>Functions for defining directed acyclic graphs and undirected graphs, finding induced graphs and fitting Gaussian Markov models.</td>
</tr>
<tr>
<td>ggplot</td>
<td>Grammar of graphics based plots for R.</td>
</tr>
<tr>
<td>ggplot2</td>
<td>An implementation of the Grammar of Graphics in R.</td>
</tr>
<tr>
<td>ghyp</td>
<td>Univariate and multivariate generalized hyperbolic distributions.</td>
</tr>
<tr>
<td>giRaph</td>
<td>Data structures and algorithms for computations on graphs.</td>
</tr>
<tr>
<td>gibbs.met</td>
<td>Naive Gibbs sampling with Metropolis steps.</td>
</tr>
<tr>
<td>glasso</td>
<td>Graphical lasso.</td>
</tr>
<tr>
<td>gld</td>
<td>Basic functions for the generalised (Tukey) lambda distribution.</td>
</tr>
<tr>
<td>gllm</td>
<td>Routines for log-linear models of incomplete contingency tables, including some latent class models via EM and Fisher scoring approaches.</td>
</tr>
<tr>
<td>glmc</td>
<td>Fitting Generalized Linear Models subject to Constraints.</td>
</tr>
<tr>
<td>glmmAK</td>
<td>Generalized Linear Mixed Models.</td>
</tr>
<tr>
<td>Package</td>
<td>Description</td>
</tr>
<tr>
<td>-----------</td>
<td>---------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>glmmML</td>
<td>A Maximum Likelihood approach to generalized linear models with random intercept.</td>
</tr>
<tr>
<td>glmpath</td>
<td>L1 regularization path for Generalized Linear Models.</td>
</tr>
<tr>
<td>glpk</td>
<td>Interface to the GNU Linear Programming Kit (GLPK).</td>
</tr>
<tr>
<td>gmaps</td>
<td>Wrapper and auxiliary functions for the maps package to work with the grid graphics system.</td>
</tr>
<tr>
<td>gmodels</td>
<td>Various functions to manipulate models.</td>
</tr>
<tr>
<td>gmp</td>
<td>Arithmetic “without limitations” using the GNU Multiple Precision library.</td>
</tr>
<tr>
<td>gmt</td>
<td>Interface between the GMT 4.0 map-making software and R.</td>
</tr>
<tr>
<td>gum</td>
<td>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.</td>
</tr>
<tr>
<td>goalprog</td>
<td>Weighted and lexicographical goal programming and optimization.</td>
</tr>
<tr>
<td>gpclib</td>
<td>General polygon clipping routines for R based on Alan Murta’s C library.</td>
</tr>
<tr>
<td>gpls</td>
<td>Classification using generalized partial least squares for two-group and multi-group (more than 2 group) classification.</td>
</tr>
<tr>
<td>gplots</td>
<td>Various functions to draw plots.</td>
</tr>
<tr>
<td>grImport</td>
<td>Importing vector graphics.</td>
</tr>
<tr>
<td>granova</td>
<td>Graphical Analysis of Variance.</td>
</tr>
<tr>
<td>graph</td>
<td>Handling of graph data structures.</td>
</tr>
<tr>
<td>grasp</td>
<td>Generalized Regression Analysis and Spatial Predictions for R.</td>
</tr>
<tr>
<td>gregmisc</td>
<td>Miscellaneous functions written/maintained by Gregory R. Warnes.</td>
</tr>
<tr>
<td>gridBase</td>
<td>Integration of base and grid graphics.</td>
</tr>
<tr>
<td>grunR</td>
<td>A Generalized Regression Neural Network.</td>
</tr>
<tr>
<td>grouped</td>
<td>Regression models for grouped and coarse data, under the Coarsened At Random assumption.</td>
</tr>
<tr>
<td>grplasso</td>
<td>Fit user specified models with group lasso penalty.</td>
</tr>
<tr>
<td>gsl</td>
<td>Wrapper for special functions of the Gnu Scientific Library (GSL).</td>
</tr>
<tr>
<td>gss</td>
<td>A comprehensive package for structural multivariate function estimation using smoothing splines.</td>
</tr>
<tr>
<td>gstat</td>
<td>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.</td>
</tr>
<tr>
<td>gsubfn</td>
<td>Miscellaneous string utilities.</td>
</tr>
<tr>
<td>gtools</td>
<td>Various functions to help manipulate data.</td>
</tr>
</tbody>
</table>
gvlima  Global Validation of Linear Models Assumptions.

gvlima  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.

hdrcde  Highest Density Regions and Conditional Density Estimation.

heatmap.plus  Heatmap with sensible behavior.

heplots  Visualizing tests in multivariate linear models.

hett  Functions for the fitting and summarizing of heteroscedastic t-regression.

hexView  Viewing binary files.

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.

hmms.dicnp  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.

hybridHclust
   Hybrid hierarchical clustering via mutual clusters.

hydrogeo
   Groundwater data presentation and interpretation.

hydrosanity
   Graphical user interface for exploring hydrological time series.

ibdreg
   Regression methods for IBD linkage with covariates.

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.

impute
   Imputation for microarray data (currently KNN only).

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.

iplots
   Interactive graphics for R.

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.

ismev
   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.
ivivc  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.
kmc.ci  Confidence intervals for the Kaplan-Meier estimator.
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.
knnncat  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 Adpative filter for locating change points in a time series.
kzft  Kolmogorov-Zurbenko Fourier Transform and application.
kzs  Kolmogorov-Zurbenko Spline.
labdsrv  Laboratory for Dynamic Synthetic Vegephenomenology.
lancet.iraqmortality  Surveys of Iraq mortality published in The Lancet.
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.
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,
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.
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.
lmomco  L-moments and L-comoments.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lnMLE</td>
<td>Marginally specified logistic normal models for longitudinal binary data.</td>
</tr>
<tr>
<td>locfdr</td>
<td>Computation of local false discovery rates.</td>
</tr>
<tr>
<td>locfit</td>
<td>Local Regression, likelihood and density estimation.</td>
</tr>
<tr>
<td>locpol</td>
<td>Kernel local polynomial regression.</td>
</tr>
<tr>
<td>lodplot</td>
<td>Assorted plots of location score versus genetic map position.</td>
</tr>
<tr>
<td>logcondens</td>
<td>Estimate a log-concave probability density from i.i.d. observations.</td>
</tr>
<tr>
<td>logilasso</td>
<td>Analysis of sparse contingency tables with penalization approaches.</td>
</tr>
<tr>
<td>logistf</td>
<td>Firth’s bias reduced logistic regression approach with penalized profile likelihood based confidence intervals for parameter estimates.</td>
</tr>
<tr>
<td>logspline</td>
<td>Logspline density estimation.</td>
</tr>
<tr>
<td>lokern</td>
<td>Kernel regression smoothing with adaptive local or global plug-in bandwidth selection.</td>
</tr>
<tr>
<td>lpSolve</td>
<td>Functions that solve general linear/integer problems, assignment problems, and transportation problems via interfacing Lp.solve.</td>
</tr>
<tr>
<td>lpridge</td>
<td>Local polynomial (ridge) regression.</td>
</tr>
<tr>
<td>lsa</td>
<td>Latent Semantic Analysis.</td>
</tr>
<tr>
<td>lspls</td>
<td>LS-PLS (least squares — partial least squares) models.</td>
</tr>
<tr>
<td>lss</td>
<td>Accelerated failure time model to right censored data based on least-squares principle.</td>
</tr>
<tr>
<td>ltm</td>
<td>Analysis of multivariate Bernoulli data using latent trait models (including the Rasch model) under the Item Response Theory approach.</td>
</tr>
<tr>
<td>ltsa</td>
<td>Linear Time Series Analysis.</td>
</tr>
<tr>
<td>luca</td>
<td>Likelihood Under Covariate Assumptions (LUCA).</td>
</tr>
<tr>
<td>lvplot</td>
<td>Letter-value box plots.</td>
</tr>
<tr>
<td>mAr</td>
<td>Estimation of multivariate AR models through a computationally efficient step-wise least-squares algorithm.</td>
</tr>
<tr>
<td>mFilter</td>
<td>Miscellaneous time series filters.</td>
</tr>
<tr>
<td>maanova</td>
<td>Analysis of N-dye Micro Array experiments using mixed model effect. Contains analysis of variance, permutation and bootstrap, cluster and consensus tree.</td>
</tr>
<tr>
<td>magic</td>
<td>A variety of methods for creating magic squares of any order greater than 2, and various magic hypercubes.</td>
</tr>
<tr>
<td>mapLD</td>
<td>Linkage Disequilibrium mapping.</td>
</tr>
<tr>
<td>Package</td>
<td>Description</td>
</tr>
<tr>
<td>-----------</td>
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</tr>
<tr>
<td>mapdata</td>
<td>Supplement to package maps, providing the larger and/or higher-resolution databases.</td>
</tr>
<tr>
<td>mapproj</td>
<td>Map Projections: converts latitude/longitude into projected coordinates.</td>
</tr>
<tr>
<td>maps</td>
<td>Draw geographical maps. Projection code and larger maps are in separate packages.</td>
</tr>
<tr>
<td>maptools</td>
<td>Set of tools for manipulating and reading geographic data, in particular ESRI shapefiles.</td>
</tr>
<tr>
<td>maptree</td>
<td>Functions with example data for graphing and mapping models from hierarchical clustering and classification and regression trees.</td>
</tr>
<tr>
<td>marginTree</td>
<td>Margin trees for high-dimensional classification.</td>
</tr>
<tr>
<td>mathgraph</td>
<td>Tools for constructing and manipulating objects from a class of directed and undirected graphs.</td>
</tr>
<tr>
<td>matlab</td>
<td>Emulate MATLAB code using R.</td>
</tr>
<tr>
<td>matrixcalc</td>
<td>Collection of functions for matrix differential calculus.</td>
</tr>
<tr>
<td>maxLik</td>
<td>Tools for Maximum Likelihood Estimation.</td>
</tr>
<tr>
<td>maxstat</td>
<td>Maximally selected rank and Gauss statistics with several p-value approximations.</td>
</tr>
<tr>
<td>mblm</td>
<td>Median-based Linear models, using Theil-Sen single or Siegel repeated medians.</td>
</tr>
<tr>
<td>mboost</td>
<td>Gradient boosting for fitting generalized linear, additive and interaction models.</td>
</tr>
<tr>
<td>mcgibbsit</td>
<td>Warnes and Raftery’s MCGibbsit MCMC diagnostic.</td>
</tr>
<tr>
<td>mclust</td>
<td>Model-based clustering and normal mixture modeling including Bayesian regularization.</td>
</tr>
<tr>
<td>mclust02</td>
<td>Model-based cluster analysis: the 2002 version of MCLUST.</td>
</tr>
<tr>
<td>mcmc</td>
<td>Functions for Markov Chain Monte Carlo (MCMC).</td>
</tr>
<tr>
<td>mda</td>
<td>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.</td>
</tr>
<tr>
<td>meboot</td>
<td>Maximum entropy bootstrap for time series.</td>
</tr>
<tr>
<td>mefa</td>
<td>Faunistic count data handling and reporting.</td>
</tr>
<tr>
<td>meifly</td>
<td>Interactive model exploration using GGobi.</td>
</tr>
<tr>
<td>memisc</td>
<td>Miscellaneous Tools for data management, simulation, and presentation of estimates.</td>
</tr>
<tr>
<td>merror</td>
<td>Accuracy and precision of measurements.</td>
</tr>
</tbody>
</table>
meta  Fixed and random effects meta-analysis, with functions for tests of bias, forest and funnel plot.

mfpl  Multiple Fractional Polynomials.

mgcv  Routines for GAMs and other generalized ridge regression problems with multiple smoothing parameter selection by GCV or UBRE. Recommended.

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.

misc3d  A collection of miscellaneous 3d plots, including rgl-based isosurfaces.

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.

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.

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.

mmnormt  The multivariate normal and t distributions.

moc  Fits a variety of mixtures models for multivariate observations with user-defined distributions and curves.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>modeest</td>
<td>Mode estimation and Chernoff distribution.</td>
</tr>
<tr>
<td>modehunt</td>
<td>Multiscale analysis for density functions.</td>
</tr>
<tr>
<td>modeltools</td>
<td>A collection of tools to deal with statistical models.</td>
</tr>
<tr>
<td>moduleColor</td>
<td>Methods for color labeling, calculation of eigengenes, and merging of closely related modules.</td>
</tr>
<tr>
<td>mokken</td>
<td>Mokken Scale Analysis for test and questionnaire data.</td>
</tr>
<tr>
<td>mombf</td>
<td>Moment and inverse moment Bayes factors.</td>
</tr>
<tr>
<td>moments</td>
<td>Moments, skewness, kurtosis and related tests.</td>
</tr>
<tr>
<td>monomvnm</td>
<td>Estimation for multivariate normal data with monotone missingness.</td>
</tr>
<tr>
<td>monreg</td>
<td>Estimation of monotone regression and variance functions in nonparametric models.</td>
</tr>
<tr>
<td>monoProc</td>
<td>Strictly monotone smoothing procedure.</td>
</tr>
<tr>
<td>moonsun</td>
<td>Basic astronomical calculations.</td>
</tr>
<tr>
<td>mota</td>
<td>Mean Optimal Transformation Approach.</td>
</tr>
<tr>
<td>mprobit</td>
<td>Multivariate probit model for binary/ordinal response.</td>
</tr>
<tr>
<td>mra</td>
<td>Analysis of capture-recapture data.</td>
</tr>
<tr>
<td>mratios</td>
<td>Inferences for ratios of coefficients in the general linear model.</td>
</tr>
<tr>
<td>msm</td>
<td>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.</td>
</tr>
<tr>
<td>muS2RC</td>
<td>S-plus to R Compatibility for package muStat.</td>
</tr>
<tr>
<td>muStat</td>
<td>Prentice rank sum test and McNemar test.</td>
</tr>
<tr>
<td>muhaz</td>
<td>Hazard function estimation in survival analysis.</td>
</tr>
<tr>
<td>multcomp</td>
<td>Multiple comparison procedures for the one-way layout.</td>
</tr>
<tr>
<td>multcompView</td>
<td>Visualizations of paired comparisons.</td>
</tr>
<tr>
<td>multic</td>
<td>Quantitative linkage analysis tools using the variance components approach.</td>
</tr>
<tr>
<td>multilevel</td>
<td>Analysis of multilevel data by organizational and social psychologists.</td>
</tr>
<tr>
<td>multinomRob</td>
<td>Overdispersed multinomial regression using robust (LQD and tanh) estimation.</td>
</tr>
<tr>
<td>multtest</td>
<td>Resampling-based multiple hypothesis testing.</td>
</tr>
</tbody>
</table>
**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.

**mvnmle**
ML estimation for multivariate normal data with missing values.

**mvnormtest**
Generalization of the Shapiro-Wilk test for multivariate variables.

**mvtnormpcs**

**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.

**ncvar**
High-level R interface to netCDF datasets.

**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. *Recommended.*

**nlmeODE**
Combine the **nlme** and **odesolve** packages for mixed-effects modelling using differential equations.

**nlrwr**
Non-linear regression with R.
<table>
<thead>
<tr>
<th>Package</th>
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</tr>
</thead>
<tbody>
<tr>
<td>nls2</td>
<td>Non-linear regression with brute force.</td>
</tr>
<tr>
<td>nlstools</td>
<td>Tools for nonlinear regression diagnostics.</td>
</tr>
<tr>
<td>nlt</td>
<td>A nondecimated lifting transform for signal denoising.</td>
</tr>
<tr>
<td>nlts</td>
<td>(Non)linear time series analysis.</td>
</tr>
<tr>
<td>nltsm</td>
<td>NonLinear Transformation Models for survival analysis.</td>
</tr>
<tr>
<td>nnls</td>
<td>The Lawson-Hanson NNLS algorithm for non-negative least squares.</td>
</tr>
<tr>
<td>nonbinROC</td>
<td>ROC-type analysis for non-binary gold standards.</td>
</tr>
<tr>
<td>nor1mix</td>
<td>One-dimensional normal mixture models classes, for, e.g., density estimation or clustering algorithms research and teaching; providing the widely used Marron-Wand densities.</td>
</tr>
<tr>
<td>norm</td>
<td>Analysis of multivariate normal datasets with missing values.</td>
</tr>
<tr>
<td>normwm.test</td>
<td>Normality and white noise testing.</td>
</tr>
<tr>
<td>normalp</td>
<td>A collection of utilities for normal of order $p$ distributions (General Error Distributions).</td>
</tr>
<tr>
<td>nortest</td>
<td>Five omnibus tests for the composite hypothesis of normality.</td>
</tr>
<tr>
<td>noverlap</td>
<td>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.</td>
</tr>
<tr>
<td>np</td>
<td>Nonparametric kernel smoothing methods for mixed datatypes.</td>
</tr>
<tr>
<td>npde</td>
<td>Normalized prediction distribution errors for nonlinear mixed-effect models.</td>
</tr>
<tr>
<td>npplot</td>
<td>Plotting non-parametric LOD scores from multiple input files.</td>
</tr>
<tr>
<td>npmc</td>
<td>Nonparametric Multiple Comparisons: provides simultaneous rank test procedures for the one-way layout without presuming a certain distribution.</td>
</tr>
<tr>
<td>nsRFA</td>
<td>Non-supervised Regional Frequency Analysis.</td>
</tr>
<tr>
<td>numDeriv</td>
<td>Accurate numerical derivatives.</td>
</tr>
<tr>
<td>nws</td>
<td>Functions for NetWorkSpaces and Sleigh.</td>
</tr>
<tr>
<td>obsSens</td>
<td>Sensitivity analysis for observational studies.</td>
</tr>
<tr>
<td>oc</td>
<td>Optimal Classification roll call analysis.</td>
</tr>
<tr>
<td>oce</td>
<td>Analysis of oceanographic data.</td>
</tr>
<tr>
<td>odesolve</td>
<td>An interface for the Ordinary Differential Equation (ODE) solver lsoda. ODEs are expressed as R functions.</td>
</tr>
</tbody>
</table>
odfWeave  Swave processing of Open Document Format (ODF) files.
ofw         Optimal Feature Weighting algorithm.
onion        A collection of routines to manipulate and visualize quaternions and octonions.
openNLP      An interface to http://opennlp.sourceforge.net/, 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
             http://maxent.sourceforge.net/, Maxent Java package for training and us-
             ing maximum entropy models.
openNLPmodels English and spanish models for openNLP.
opmatch      Functions to perform optimal matching, particularly full matching.
orientlib    Representations, conversions and display of orientation SO(3) data.
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.
pARtial      (Partial) attributable risk estimates, corresponding variance estimates and con-
             fidence intervals.
pairwiseCI    Calculate and plot unadjusted confidence intervals for two sample comparisons.
paleoTS      Modeling evolution in paleontological time-series.
paleoTSalt   Modeling evolution in paleontological time-series (alternate parameterization).
pamr         Pan: 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.
partsms      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.
pcaPP        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.

penalized  Penalized estimation in generalized linear models.

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.

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.

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.

plotAndPlayGTK  A GUI for interactive plots using GTK.

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.
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, polyclas, 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.
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.
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.
profileModel Tools for profiling inference functions for various model classes.
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.
qgen Quantitative Genetics using R.
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.
### Chapter 5: R Add-On Packages

<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>qtlbim</td>
<td>QTL Bayesian Interval Mapping.</td>
</tr>
<tr>
<td>quadprog</td>
<td>For solving quadratic programming problems.</td>
</tr>
<tr>
<td>qualV</td>
<td>Qualitative methods for the validation of models.</td>
</tr>
<tr>
<td>quantchem</td>
<td>Quantitative chemical analysis: calibration and evaluation of results.</td>
</tr>
<tr>
<td>quantmod</td>
<td>Quantitative financial modelling framework.</td>
</tr>
<tr>
<td>quantreg</td>
<td>Quantile regression and related methods.</td>
</tr>
<tr>
<td>quantregForest</td>
<td>Quantile Regression Forests, a tree-based ensemble method for estimation of conditional quantiles.</td>
</tr>
<tr>
<td>qvalue</td>
<td>Q-value estimation for false discovery rate control.</td>
</tr>
<tr>
<td>qvcalc</td>
<td>Functions to compute quasi-variances and associated measures of approximation error.</td>
</tr>
<tr>
<td>r2lUniv</td>
<td>R to Univariate: perform basic analysis and generate corresponding code.</td>
</tr>
<tr>
<td>rJava</td>
<td>Low-level R to Java interface. Allows creation of objects, calling methods and accessing fields.</td>
</tr>
<tr>
<td>race</td>
<td>Implementation of some racing methods for the empirical selection of the best.</td>
</tr>
<tr>
<td>rake</td>
<td>Raking survey datasets by re-weighting.</td>
</tr>
<tr>
<td>ramps</td>
<td>Bayesian geostatistical modeling of Gaussian processes using a reparameterized and marginalized posterior sampling (RAMPS) algorithm.</td>
</tr>
<tr>
<td>randaes</td>
<td>Random number generator based on AES cipher.</td>
</tr>
<tr>
<td>random</td>
<td>True random numbers using random.org.</td>
</tr>
<tr>
<td>randomLCA</td>
<td>Random effects Latent Class Analysis.</td>
</tr>
<tr>
<td>randomSurvivalForest</td>
<td>Ishwaran and Kogalur’s random survival forest.</td>
</tr>
<tr>
<td>randomForest</td>
<td>Breiman’s random forest classifier.</td>
</tr>
<tr>
<td>rankreg</td>
<td>Rank regression estimator for the AFT model with right censored data.</td>
</tr>
<tr>
<td>rateratio.test</td>
<td>Exact rate ratio test.</td>
</tr>
<tr>
<td>rattle</td>
<td>A graphical user interface for data mining in R using GTK.</td>
</tr>
<tr>
<td>rbugs</td>
<td>Functions to prepare files needed for running BUGS in batch mode, and running BUGS from R. Support for Linux systems with Wine is emphasized.</td>
</tr>
<tr>
<td>rcdd</td>
<td>C Double Description for R, an interface to the CDD computational geometry library.</td>
</tr>
</tbody>
</table>
rcdk  Interface to the CDK libraries, a Java framework for cheminformatics.
recom  R COM Client Interface and internal COM Server.
recompgen  Completion generator for R. Recommended for R 2.5.0 or 2.6.0.
rda  Shrunken Centroids Regularized Discriminant Analysis.
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.
reshape  Flexibly reshape data.
resper  Sampling from restricted permutations.
reweight  Adjustment of survey respondent weights.
rgcvpack  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.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rhosp</td>
<td>Side effect risks in hospital: simulation and estimation.</td>
</tr>
<tr>
<td>richards</td>
<td>Richards curves.</td>
</tr>
<tr>
<td>rimage</td>
<td>Functions for image processing, including Sobel filter, rank filters, fft, histogram equalization, and reading JPEG files.</td>
</tr>
<tr>
<td>rindex</td>
<td>Indexing for R.</td>
</tr>
<tr>
<td>risksetROC</td>
<td>Riskset ROC curve estimation from censored survival data.</td>
</tr>
<tr>
<td>riv</td>
<td>Robust Instrumental Variables estimators based on high breakpoint point S-estimators of multivariate location and scatter matrices.</td>
</tr>
<tr>
<td>rjacobi</td>
<td>Jacobi polynomials and Gauss-Jacobi quadrature related operations.</td>
</tr>
<tr>
<td>rjson</td>
<td>JSON (JavaScript Object Notation) for R.</td>
</tr>
<tr>
<td>rlecuyer</td>
<td>R interface to RNG with multiple streams.</td>
</tr>
<tr>
<td>rmeta</td>
<td>Functions for simple fixed and random effects meta-analysis for two-sample comparison of binary outcomes.</td>
</tr>
<tr>
<td>rmetsim</td>
<td>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.</td>
</tr>
<tr>
<td>robfilter</td>
<td>Robust time series filters.</td>
</tr>
<tr>
<td>robust</td>
<td>Insightful robust package.</td>
</tr>
<tr>
<td>robustbase</td>
<td>Basic Robust Statistics.</td>
</tr>
<tr>
<td>rpanel</td>
<td>Simple interactive controls for R using the tcltk package.</td>
</tr>
<tr>
<td>rpart</td>
<td>Recursive PARTitioning and regression trees. Recommended.</td>
</tr>
<tr>
<td>rpart.permutation</td>
<td>Permutation tests of rpart models.</td>
</tr>
<tr>
<td>rpubchem</td>
<td>R interface to the PubChem collection.</td>
</tr>
<tr>
<td>rpvm</td>
<td>R interface to PVM (Parallel Virtual Machine). Provides interface to PVM APIs, and examples and documentation for its use.</td>
</tr>
<tr>
<td>rqmcmb2</td>
<td>Markov chain marginal bootstrap for quantile regression.</td>
</tr>
<tr>
<td>rrcov</td>
<td>Functions for robust location and scatter estimation and robust regression with high breakdown point.</td>
</tr>
<tr>
<td>rrp</td>
<td>Random Recursive Partitioning.</td>
</tr>
<tr>
<td>rsprng</td>
<td>Provides interface to SPRNG (Scalable Parallel Random Number Generators) APIs, and examples and documentation for its use.</td>
</tr>
<tr>
<td>rstream</td>
<td>Unified object oriented interface for multiple independent streams of random numbers from different sources.</td>
</tr>
</tbody>
</table>
**rtiff**  Read TIFF format images and return them as pixmap objects.

**rv**  Simulation-based random variable object class.

**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.

**sampling**  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.

**scagnostics**  Compute scagnostics.

**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.

**scrim**  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.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sdcMicro</td>
<td>Statistical Disclosure Control methods for the generation of public and scientific use files.</td>
</tr>
<tr>
<td>sde</td>
<td>Simulation and inference for Stochastic Differential Equations.</td>
</tr>
<tr>
<td>seacarb</td>
<td>Calculates parameters of the seawater carbonate system.</td>
</tr>
<tr>
<td>seas</td>
<td>Detailed seasonal plots of temperature and precipitation data.</td>
</tr>
<tr>
<td>seewave</td>
<td>Time wave analysis and graphical representation.</td>
</tr>
<tr>
<td>segclust</td>
<td>Segmentation and segmentation/clustering.</td>
</tr>
<tr>
<td>segmented</td>
<td>Functions to estimate break-points of segmented relationships in regression models (GLMs).</td>
</tr>
<tr>
<td>sem</td>
<td>Functions for fitting general linear Structural Equation Models (with observed and unobserved variables) by the method of maximum likelihood using the RAM approach.</td>
</tr>
<tr>
<td>sendplot</td>
<td>Tool for sending interactive plots.</td>
</tr>
<tr>
<td>sensitivity</td>
<td>Sensitivity analysis.</td>
</tr>
<tr>
<td>seqinr</td>
<td>Exploratory data analysis and data visualization for biological sequence (DNA and protein) data.</td>
</tr>
<tr>
<td>seqmon</td>
<td>Sequential monitoring of clinical trials.</td>
</tr>
<tr>
<td>seriation</td>
<td>Infrastructure for seriation.</td>
</tr>
<tr>
<td>session</td>
<td>Functions for interacting with, saving and restoring R sessions.</td>
</tr>
<tr>
<td>setRNG</td>
<td>Set (normal) random number generator and seed.</td>
</tr>
<tr>
<td>sets</td>
<td>Data structures and basic operations for ordinary sets, and generalizations such as fuzzy sets, multisets, and fuzzy multisets.</td>
</tr>
<tr>
<td>sfsmisc</td>
<td>Utilities from Seminar fuer Statistik ETH Zurich.</td>
</tr>
<tr>
<td>sgeostat</td>
<td>An object-oriented framework for geostatistical modeling.</td>
</tr>
<tr>
<td>shape</td>
<td>Functions for plotting graphical shapes.</td>
</tr>
<tr>
<td>shapefiles</td>
<td>Functions to read and write ESRI shapefiles.</td>
</tr>
<tr>
<td>shapes</td>
<td>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.</td>
</tr>
<tr>
<td>siar</td>
<td>Stable Isotope Analysis in R.</td>
</tr>
<tr>
<td>sigma2tools</td>
<td>Test of hypothesis about sigma2.</td>
</tr>
<tr>
<td>signal</td>
<td>A set of generally Matlab/Octave-compatible signal processing functions.</td>
</tr>
<tr>
<td>signalextraction</td>
<td>Real-time signal extraction (Direct Filter Approach).</td>
</tr>
<tr>
<td>simba</td>
<td>Functions for similarity calculation of binary data.</td>
</tr>
</tbody>
</table>
**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.

**simpleboot**  Simple bootstrap routines.

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


**sma**  Functions for exploratory (statistical) microarray analysis.

**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.

**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

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

spatkernel
Nonparametric 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, sptests, 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.

plus2R
Insightful package providing missing S-PLUS functionality in R.

spsurvey
Spatial survey design and analysis.

sqldf
Perform SQL selects on R data frames.

ssauv
Sample Size Adjusted for Nonadherence or Variability of input parameters.

sspir
State SPace models In R.

sspline
Smoothing splines on the sphere.

st
Shrinkage t statistic.

staRt
Inferenza classica con TI-83 Plus.
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. Recommended.

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.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>svcm</td>
<td>2d and 3d Space-Varying Coefficient Models.</td>
</tr>
<tr>
<td>svmpath</td>
<td>Computes the entire regularization path for the two-class svm classifier with essentially the same cost as a single SVM fit.</td>
</tr>
<tr>
<td>systemfit</td>
<td>Contains functions for fitting simultaneous systems of equations using Ordinary Least Squares (OLS), Two-Stage Least Squares (2SLS), and Three-Stage Least Squares (3SLS).</td>
</tr>
<tr>
<td>tcltk2</td>
<td>A series of widgets and functions to supplement tcltk.</td>
</tr>
<tr>
<td>tdist</td>
<td>Computes the distribution of a linear combination of independent Student’s $t$ variables.</td>
</tr>
<tr>
<td>tdm</td>
<td>A tool for Therapeutic Drug Monitoring.</td>
</tr>
<tr>
<td>tdthap</td>
<td>Transmission/disequilibrium tests for extended marker haplotypes.</td>
</tr>
<tr>
<td>tensor</td>
<td>Tensor product of arrays.</td>
</tr>
<tr>
<td>tensorA</td>
<td>Advanced tensors arithmetic with named indices.</td>
</tr>
<tr>
<td>termstrc</td>
<td>Term structure and credit spread estimation.</td>
</tr>
<tr>
<td>tframe</td>
<td>Time Frame coding kernel: functions for writing code that is independent of the way time is represented.</td>
</tr>
<tr>
<td>tgp</td>
<td>Bayesian regression and adaptive sampling with Treed Gaussian Process models.</td>
</tr>
<tr>
<td>time</td>
<td>Time tracking for developers.</td>
</tr>
<tr>
<td>timsac</td>
<td>TIMe Series Analysis and Control package.</td>
</tr>
<tr>
<td>titan</td>
<td>Titration analysis for mass spectrometry data.</td>
</tr>
<tr>
<td>titecrm</td>
<td>TIme-To-Event Continual Reassessment Method and calibration tools.</td>
</tr>
<tr>
<td>tkrcl</td>
<td>TK widget tools for rgl package.</td>
</tr>
<tr>
<td>tkrplot</td>
<td>Simple mechanism for placing R graphics in a Tk widget.</td>
</tr>
<tr>
<td>tlnise</td>
<td>Two-level normal independent sampling estimation.</td>
</tr>
<tr>
<td>tm</td>
<td>A framework for text mining applications within R.</td>
</tr>
<tr>
<td>torus</td>
<td>Torus algorithm for quasi random number generation.</td>
</tr>
<tr>
<td>tpr</td>
<td>Temporal Process Regression.</td>
</tr>
<tr>
<td>trackObjs</td>
<td>Track objects.</td>
</tr>
<tr>
<td>tradeCosts</td>
<td>Post-trade analysis of transaction costs.</td>
</tr>
<tr>
<td>tree</td>
<td>Classification and regression trees.</td>
</tr>
<tr>
<td>treeglia</td>
<td>Stem analysis functions for volume increment and carbon uptake assessment from tree-rings.</td>
</tr>
<tr>
<td>triangle</td>
<td>Standard distribution functions for the triangle distribution.</td>
</tr>
</tbody>
</table>
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.
trust
   Local optimization using two derivatives and trust regions.
tsDyn
   Time series analysis based on dynamical systems theory.
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.
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.
vardia
   Interactive variogram diagnostics.
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.

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.

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 WNOmimate 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 and HTML tables.

xts Extensible time series.

yaImpute Performs popular nearest neighbor routines.

yam Methods to convert R to YAML and back.

yest Gaussian independence models.

zicounts Fit classical, zero-inflated and interval censored count data regression 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.

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 http://www.omegahat.org/, 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.

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.
Chapter 5: R Add-On Packages

**Rexif**  Extract meta-information from JPEG files.

**RGdkPixbuf**  
S language functions to access the facilities in the GdkPixbuf library for manipulating images.

**RGnumeric**  
A plugin for the Gnumeric spreadsheet that allows R functions to be called from cells within the sheet, automatic recalculation, etc.

**RGtk**  
Facilities in the S language for programming graphical interfaces using Gtk, the Gnome GUI toolkit.

**RGtkBindingGenerator**  
A meta-package which generates C and R code to provide bindings to a Gtk-based library.

**RGtkExtra**  
A collection of S functions that provide an interface to the widgets in the gtk-extra library such as the GtkSheet data-grid display, icon list, file list and directory tree.

**RGtkGlade**  
S language bindings providing an interface to Glade, the interactive Gnome GUI creator.

**RGtkHTML**  
A collection of S functions that provide an interface to creating and controlling an HTML widget which can be used to display HTML documents from files or content generated dynamically in S.

**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, . . .

**RSMmethods**  
An implementation of S version 4 methods and classes for R, consistent with the basic material in “Programming with Data” by John M. Chambers, 1998, Springer NY.
RSPerl  An interface from R to an embedded, persistent Perl interpreter, allowing one to call arbitrary Perl subroutines, classes and methods.

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

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

Rcompression  In-memory decompression for GNU zip and bzip2 formats.

Rlibstree  Suffix Trees in R via the libstree C library.

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

RwxWidgets  Facilities to program GUIs using wxWidgets in R.

Ryacas  R interface to yacas.

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.
5.1.4 Add-on packages from Bioconductor

The http://www.bioconductor.org/, 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).

**AffyExpress**  Affymetrix quality assessment and analysis tool.

**AnnBuilder**  Processing annotation date from public data repositories and building annotation data packages or XML data documents using the source data.

**AnnotationDbi**  Annotation DataBase Interface.

**BSgenome**  Infrastructure for Biostrings-based genome data packages.

**BeadExplorer**  QC, normalization, annotation and exploration of Illumina BeadChip data.

**BioMVCClass**  Model-View-Controller (MVC) classes that use Biobase.

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

**Biostrings**  Class definitions and generics for biological sequences along with pattern matching 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.

**ChromoViz**  Draw gene expression profile onto chromosome using SVG.
CoCiteStat
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.

GEOquery
Get data from NCBI Gene Expression Omnibus (GEO).

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.

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

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

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

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.

GeneTraffic
GeneTraffic R integration functions.

GeneticsBase
Classes and functions for handling genetic data.

GeneticsDesign
Functions for designing genetics studies.

GlobalAncova
Calculates a global test for differential gene expression between groups.

GraphAT
Graph theoretic Association Tests.

HEM
Heterogeneous Error Model for analysis of microarray data.

Harshlight
A “corrective make-up” program for microarray chips.
<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heatplus</td>
<td>A heat map displaying covariates and coloring clusters.</td>
</tr>
<tr>
<td>Icens</td>
<td>Functions for computing the NPMLE for censored and truncated data.</td>
</tr>
<tr>
<td>KEGGSOAP</td>
<td>Client-side SOAP access KEGG.</td>
</tr>
<tr>
<td>LBE</td>
<td>Estimation of the false discovery rate.</td>
</tr>
<tr>
<td>LMGene</td>
<td>Analysis of microarray data using a linear model and glog data transformation.</td>
</tr>
<tr>
<td>LPE</td>
<td>Significance analysis of microarray data with small number of replicates using the Local Pooled Error (LPE) method.</td>
</tr>
<tr>
<td>MANOR</td>
<td>Micro-Array NORmalization.</td>
</tr>
<tr>
<td>MCRestimate</td>
<td>Misclassification error estimation with cross-validation.</td>
</tr>
<tr>
<td>MLInterfaces</td>
<td>Uniform interfaces to machine learning code for the exprSet class from Bioconductor.</td>
</tr>
<tr>
<td>MVCClass</td>
<td>Model-View-Controller (MVC) classes.</td>
</tr>
<tr>
<td>MantelCorr</td>
<td>Compute Mantel Cluster Correlations.</td>
</tr>
<tr>
<td>MassSpecWavelet</td>
<td>Mass spectrum processing by wavelet-based algorithms.</td>
</tr>
<tr>
<td>MeasurementError.cor</td>
<td>Two-stage measurement error model for correlation estimation with smaller bias than the usual sample correlation.</td>
</tr>
<tr>
<td>MergeMaid</td>
<td>Cross-study comparison of gene expression array data.</td>
</tr>
<tr>
<td>Mfuzz</td>
<td>Soft clustering of time series gene expression data.</td>
</tr>
<tr>
<td>MiPP</td>
<td>Misclassification Penalized Posterior Classification.</td>
</tr>
<tr>
<td>OCplus</td>
<td>Operating characteristics plus sample size and local fdr for microarray experiments.</td>
</tr>
<tr>
<td>OLIN</td>
<td>Optimized Local Intensity-dependent Normalisation of two-color microarrays.</td>
</tr>
<tr>
<td>OLINgui</td>
<td>Graphical user interface for OLIN.</td>
</tr>
<tr>
<td>OrderedList</td>
<td>Similarities of ordered gene lists.</td>
</tr>
<tr>
<td>OutlierD</td>
<td>Outlier detection using quantile regression on the M-A scatterplots of high-throughput data.</td>
</tr>
<tr>
<td>PGSEA</td>
<td>Parametric Gene Set Enrichment Analysis.</td>
</tr>
<tr>
<td>PROcess</td>
<td>Ciphergen SELDI-TOF processing.</td>
</tr>
</tbody>
</table>
RBGL  An interface between the graph package and the Boost graph libraries, allowing for fast manipulation of graph objects in R.

RLMM  A genotype calling algorithm for Affymetrix SNP arrays.

RMAGEML  Functionality to handle MAGEML documents.

RMAPPER  Interface to mapper.chip.org.

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.

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.

Ruuid  Creates Universally Unique ID values (UUIDs) in R.

SAGElyzer  Locates genes based on SAGE tags.

SAGx  Statistical Analysis of the GeneChip.

SBMLR  Systems Biology Markup Language (SBML) interface and biochemical system analysis tools.

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.
aCGH  Classes and functions for Array Comparative Genomic Hybridization data.
adSplit  Annotation-driven clustering.
affxparser  Package for parsing Affymetrix files (CDF, CEL, CHP, BMAP, BAR).
affy  Methods for Affymetrix Oligonucleotide Arrays.
affyPLM  For fitting Probe Level Models.
affyQCRreport  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.
affypdnn  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.
arrayMagic  Utilities for quality control and processing for two-color cDNA microarray data.
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.
bioGraph  Graph examples and use cases in Bioinformatics.
bioViews  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.
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).
flowCore Basic structures for flow cytometry data.
flowUtils Database interface for flow cytometry.
flowViz Visualization for flow cytometry.
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.
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.
iSNetwork Interactive network plots.
iSPlot Link views that are based on the same data set.
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 an 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.

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.

mnNorm: Spatial and intensity based normalization of cDNA microarray data based on robust neural nets.

oligo: Oligonucleotide arrays.

oligoClasses: Classes for high-throughput SNP arrays.

oneChannelGUI: Extend the capabilities of affylmGUI.

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.

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.

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.
**Pathway analysis.**

**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).**

**Very simple high level analysis of Affymetrix data.**

**Computationally simulates the AP-MS technology.**

**Sample size and power calculation in microarray studies.**

**Segmentation, normalization and processing of aCGH data.**

**Affymetrix Spike-in Langmuir Isotherm data analysis tool.**

**A set of tools to work with alternative splicing.**

**Visualization routines for high throughput screens.**

**Microarray spot segmentation and gridding for blocks of microarray spots.**

**S-score algorithm for Affymetrix oligonucleotide microarrays.**

**Estimate microarray sample size.**

**STructured Analysis of Microarray data.**

**Stepwise normalization functions for cDNA microarrays.**

**Analysis of tiling arrays.**

**Statistical analysis for developmental microarray time course data.**

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

**Enrichment analysis for Gene Ontology.**

**Estimation of local false discovery rate.**

**Variational Bayesian Multinomial Probit regression.**

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

**Tools and extensions for processing Sweave documents.**

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

**Evaluation widgets for functions.**

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

**LC/MS and GC/MS data analysis: framework for processing and visualization of chromatographically separated mass spectral data.**
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 given in R_LIBS (see below) if this is set and non-null, and to the default library (the ‘library’ subdirectory of ‘R_HOME’) otherwise. (Versions of R prior to 1.3.0 installed to the default library by default.)

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

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

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

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

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

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

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

R_LIBS="~lib/R:/usr/local/lib/R-contrib"

your environment (e.g., ‘~/.Renviron’) file. (Note that no export statement is needed or allowed in this file; see the on-line help for Startup for more information.)
5.3 How can add-on packages be used?

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

```r
library()
```
at the R prompt.

This produces something like

```r
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

```r
library(pkg)
```

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

```r
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 ⟨undefined⟩ [What is CRAN?], page ⟨undefined⟩, 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 ⟨undefined⟩ [What is S?], page ⟨undefined⟩); some of the nonlinear modeling code is not there yet.

The http://developer.R-project.org/, 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 http://ESS.R-project.org/, 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:

```plaintext
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

\[ x[i] <- \text{list(NULL)} \]

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 \( \text{rownames}(x) <- \text{NULL} \), similarly for column names.

7.2 How can I save my workspace?

\( \text{save.image()} \) saves the objects in the user's .GlobalEnv to the file `.RData` in the R startup directory. (This is also what happens after \( \text{q("yes")} \).) Using \( \text{save.image(file)} \) 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

\[ \text{rm(list = ls(all = TRUE))} \]

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

7.4 How can I get \texttt{eval()} and \texttt{D()} to work?

Strange things will happen if you use \( \text{eval(print(x), envir = e)} \) or \( \text{D(x^2, "x")} \). 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 \texttt{expression()}. For example,

\[
\text{R> D(expression(x^2), "x")}
2 * x
\]

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

\[ \text{D2 <- function(e, n) D(D(e, n), n)} \]

or


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

See the help page for \texttt{deriv()} for more examples.

\section*{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., \texttt{row <- mat[2,]}, it is by default turned into a vector. In a similar way if an array with dimension, say, $2 \times 3 \times 1 \times 4$ is created by subscripting it will be coerced into a $2 \times 3 \times 4$ array, losing the unnecessary dimension. After much discussion this has been determined to be a \emph{feature}.

To prevent this happening, add the option \texttt{`drop = FALSE`} to the subscripting. For example,

\begin{verbatim}
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
\end{verbatim}

The \texttt{`drop = FALSE`} option should be used defensively when programming. For example, the statement

\begin{verbatim}
somerows <- mat[index, ]
\end{verbatim}

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

\begin{verbatim}
somerows <- mat[index, , drop = FALSE]
\end{verbatim}

\section*{7.6 How does autoloading work?}

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

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

See the help page for \texttt{autoload()} for a very nice example.

\section*{7.7 How should I set options?}

The function \texttt{options()} allows setting and examining a variety of global “options” which affect the way in which \texttt{R} computes and displays its results. The variable \texttt{.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

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

Chapter 7: R Miscellanea

```r
}  

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

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

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

```r
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 \texttt{lattice} (which is based on another recommended package, \texttt{grid}) provides graphical functionality that is compatible with most Trellis commands.

You could also look at \texttt{coplot()} and \texttt{dotchart()} which might do at least some of what you want. Note also that the R version of \texttt{pairs()} is fairly general and provides most of the functionality of \texttt{splom()}, and that R's default plot method has an argument \texttt{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 \texttt{f()} inside another function \texttt{g()} its enclosing environment is the environment inside \texttt{g()}. The enclosing environment for a function is fixed when the function is created. You can find out the enclosing environment for a function \texttt{f()} using \texttt{environment(f)}.

The “parent” environment, on the other hand, is defined when you invoke a function. If you invoke \texttt{lm()} at the command line its parent environment is the global workspace, if you invoke it inside a function \texttt{f()} then its parent environment is the environment inside \texttt{f()}. You can find out the parent environment for an invocation of a function by using \texttt{parent.frame()} or \texttt{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 \texttt{f()} is defined inside another function \texttt{g()} it will probably be used inside \texttt{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

```r
1+1
```

computes the value 2 and returns it; the command

```r
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 (undefined) [How should I write summary methods?], page (undefined)).

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

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

or

```r
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

```r
foo <- function(x, y, happy) {
  stopifnot(length(x) == 1, length(y) == 1) # scalars only!
  (x + y) * happy
}
```
If you define the general function

```r
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.,

```r
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 [http://www.x.org/Downloads.html](http://www.x.org/Downloads.html), X.Org (possibly as an optional install), which is an X11 server that does not require a screen; and there is the [GDD](http://cran.R-project.org/web/packages/GDD/index.html) 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

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

you can do

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

for

```r
a + 2
```

or

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

for

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

or

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

for

```r
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

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

without any of this messing about.

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

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

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

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

```r
pom options(horizontal = FALSE)
help.start()
```

needs to be

```r
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

```r
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")`.

```r
## 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.


### 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 (undefined) [R Add-On Packages], page (undefined) and (undefined) [What is the difference between package and library?], page (undefined) 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(NaN, 4))

would return the coefficients if the lm() call succeeded and would return c(NaN, NaN, NaN, NaN) 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
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

```r
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 [How do file names work in Windows?], page [undefined]) 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

```r
> str <- "This \"text\" is quoted"
> str
```

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.

```r
> 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

```r
> 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.
Chapter 9: R Bugs

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 \(0.28 \times 100 \neq 28\) or \(0.1 + 0.2 \neq 0.3\), are not a bug. See (undefined) [Why doesn’t R think these numbers are equal?], page (undefined), 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

\[ \text{R> data.frame}(x, y, z, \text{monday, tuesday}) \]

never returns. Do not report that \text{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 \text{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 \text{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 \text{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 \text{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 
10 Acknowledgments

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More to come soon . . .
This is the site for the INLA approach to Bayesian inference within the R project for Statistical Computing. The R-INLA library contains precompiled binaries of the inla-program. To make the program run for all various processors, it is compiled using generic compiler options and 32bit, for Windows, MacOSX and Linux. There is certainly possible to compile the inla-program particularly for your computer/cpu.