R News

The Newsletter of the R Project

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Editorial

by Douglas Bates

This edition of R News is the work of a new editorial team and I would particularly like to recognize my associate editors, Paul Murrell and Torsten Hothorn, who stepped up and did a superb job of handling most of the submissions whilst I was otherwise occupied.

This issue accompanies the release of R 2.1.0 and we begin with three articles describing new facilities in this release. For many users the most notable change with this release is the addition of internationalization and localization capabilities, described in our feature article by Brian Ripley, who did most of the work in adding these facilities to R. The next article, also written by Brian Ripley, describes the new package management structure in R 2.1.0 then Paul Murrell updates us on changes in the standard package `grid`.

Following these articles are three articles on contributed packages beginning with Alessandra Brazzale's description of the `hoa` bundle for statistical inference using higher-order asymptotics. By contributing the hoa bundle to CRAN Alessandra has extended to five years the association of R with winners of the Chambers Award for outstanding work on statistical software by a student. She received the 2001 Chambers Award for her work on this software. The 2002 Chambers Award winner, Simon Urbanek, is now a member of the R Development Core Team. The work of the 2003 winner, Daniel Adler for RGL, the 2004 winner, Deepayan Sarkar for Lattice, and the recently-announced 2005 winner, Markus Helbig for JGR, are all intimately connected with R.

The next section of this newsletter is three articles on tools for working with R. We follow these with an article on experiences using R within a large pharmaceutical company. This article is part of a continuing series on the use of R in various settings. We welcome contributions to this series. Finally, an article on magic squares and John Fox's guest appearance in the Programmer's Niche column, where he discusses a short but elegant function for producing textual representations of numbers, put the focus on programming in R, which is where the focus should be, shouldn't it?

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Contents of this issue:

Internationalization Features of R 2.1.0

by Brian D. Ripley

R 2.1.0 introduces a range of features to make it possible or easier to use R in languages other than English or American English: this process is known as *internationalization*, often abbreviated to *i18n* (since 18 letters are omitted). The process of adapting to a particular language, currency and so on is known as *localization* (abbreviated to *l10n*), and R 2.1.0 ships with several localizations and the ability to add others.

What is involved in supporting non-English languages? The basic elements are

1. The ability to represent words in the language. This needs support for the *encoding* used for the language (which might be OS-specific) as well as support for displaying the characters, both at the console and on graphical devices.

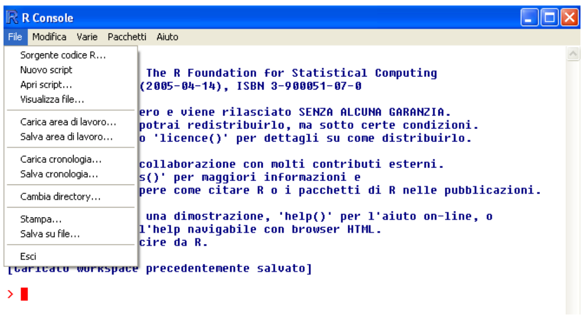
2. Manipulation of text in the language, by for example `grep()`. This may sound straightforward, but earlier versions of R worked with bytes and not characters: at least two bytes are needed to represent Chinese characters.

3. Translation of key components from English to the user's own language. Currently R supports the translation of diagnostic messages and the menus and dialogs of the Windows and MacOS X GUIs.

There are other aspects to internationalization, for example the support of international standard paper sizes rather than just those used in North America, different ways to represent dates and times,[1] monetary amounts and the representation of numbers.[2]

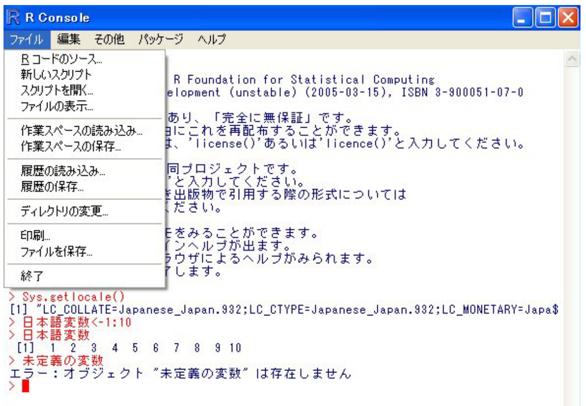
R has 'for ever' had some support for Western European languages, since several early members of the core team had native languages other than English. We have been discussing more comprehensive internationalization for a couple of years, and a group of users in Japan have been producing a modified version of R with support for Japanese. During those couple of years OS support for internationalization has become much more widespread and reliable, and the increasing prevalence of UTF-8[3] locales as standard in Linux distributions made greater internationalization support more pressing.

How successfully your R will support non-English languages depends on the level of operating system support, although as always the core team tries hard to make facilities available across all platforms. Windows NT took internationalization seriously from the mid 1990s, but took a different route (16-bit characters) from most later internationalization efforts. (We still have R users running the obsolete Windows 95/98/ME OSes, which had language-specific versions.) MacOS X is a hybrid of components which approach internationalization in different ways but the R maintainers for that platform have managed to smooth over many of its quirks. Recent Linux and other systems using `glibc` have extensive support. Commercial Unixes have varying amounts of support, although Solaris was a pioneer and often the model for Open Source implementations.



```
 The R Foundation for Statistical Computing
(2005-04-14), ISBN 3-900051-07-0

ero e viene rilasciato SENZA ALCUNA GARANZIA.
potrai redistribuirlo, ma sotto certe condizioni.
o 'licence()' per dettagli su come distribuirlo.

collaborazione con molti contributi esterni.
s()' per maggiori informazioni e
pere come citare R o i pacchetti di R nelle pubblicazioni.

 una dimostrazione, 'help()' per l'aiuto on-line, o
l'help navigabile con browser HTML.
cire da R.

[Caricato workspace precedentemente salvato]

> 
```

Figure 1: Part of the Windows console in an Italian locale.



```
 R Foundation for Statistical Computing
elopment (unstable) (2005-03-15), ISBN 3-900051-07-0

あり、「完全に無保証」です。
目にこれを再配布することができます。
は、'license()'あるいは'licence()'と入力してください。

同プロジェクトです。
'と入力してください。
を出版物で引用する際の形式については
ください。

Eをみることができます。
インヘルプが出ます。
ラウザによるヘルプがみられます。
了します。
> Sys.getlocale()
[1] "LC_COLLATE=Japanese_Japan.932;LC_CTYPE=Japanese_Japan.932;LC_MONETARY=Japa$
> 日本語変数<-1:10
> 日本語変数
 [1]  1  2  3  4  5  6  7  8  9 10
> 未定義の変数
エラー：オブジェクト "未定義の変数" は存在しません
> 
```

Figure 2: Part of the Windows console in Japanese. Note the use of Japanese variable names, that the last line is an error message in Japanese, as well as the difference in width between English and Japanese characters.

Hopefully, if your OS has enough support to allow you to work comfortably in your preferred language, it will have enough support to allow you to use R in that language. Figures 1 and 2 show examples of internationalization for the Windows GUI: note how the menus are translated, variable names are accepted in the preferred language, and error

[1]e.g. the use of 12-hour or 24-hour clock.

[2]for example, the use of `,` for the decimal point, and the use of `,` or `.` or nothing as the thousands separator.

[3]see below.

messages are translated too. The Japanese screenshot shows another difference: the Japanese characters are displayed at twice the width of the English ones, and cursor movement has to take this into account.

The rest of this article expands on the concepts and then some of the issues they raise for R users and R programmers. Quite a lot of background is needed to appreciate what users of very different languages need from the internationalization of R.

Locales

A *locale* is a specification of the user-specific environment within which an operating system is running an application program such as R. What exactly this covers is OS-specific, but key components are

- The set of 'legal' characters the user might input: this includes which characters are alphabetic and which are numeric. This is the C locale category `LC_CTYPE`.
- How characters are sorted: the C locale category `LC_COLLATE`. Even where languages share a character set they may sort words differently: it comes as a surprise to English-speaking visitors to Denmark to find 'Aa' sorted at the end of the alphabet.
- How to represent dates and times (C locale category `LC_TIME`). The meaning of times also depends on the timezone which is sometimes regarded as part of the locale (and sometimes not).
- Monetary formatting (C locale category `LC_MONETARY`).
- Number formatting (C locale category `LC_NUMERIC`).
- The preferred language in which to communicate with the user (for some systems, C locale category `LC_MESSAGES`).
- How characters in that language are encoded.

How these are specified is (once again) OS-specific. The first four categories can be set by `Sys.setlocale()`: the initial settings are taken from the OS and can be queried by calling `Sys.getlocale()` (see Figure 2). On Unix-like OSes the settings are taken from environment variables with the names given, defaulting to the value of `LC_ALL` and then of `LANG`. If none of these are set, the value is likely to be `C` which is usually implemented as the settings appropriate in the USA. Other aspects of the locale are reported by `Sys.localeconv()`.

Other OSes have other ways of specifying the locale: for example both Windows and MacOS X have listboxes in their user settings. This is becoming more common: when I select a 'Language' at the login screen for a session in Fedora Core 3 Linux I am actually selecting a locale, not just my preferred language.

R does not fully support `LC_NUMERIC`, and is unlikely ever to. Because the comma is used as the separator in argument lists, it would be impossible to parse expressions if it were also allowed as the decimal point. We do allow the decimal point to be specified in `scan()`, `read.table()` and `write.table()`. `Sys.setlocale()` does allow `LC_NUMERIC` to be set, with a warning and with inconsistent behaviour.

For the R user

The most important piece of advice is to specify your locale when asking questions, since R will behave differently in different locales. We have already seen experienced R users insisting on R-help that R has been broken when it seems they had changed locales. To be sure, quote the output of `Sys.getlocale()` and `localeToCharset()`.

For the package writer

Try not to write language-specific code. A package which was submitted to CRAN with variables named `años` worked for the author and the CRAN testers, but not on my Solaris systems. Use only ASCII characters[4] for your variable names, and as far as possible for your documentation.

Languages and character sets

What precisely do we mean by 'the preferred language'? Once again, there are many aspects to consider.

- The language, such as 'Chinese' or 'Spanish'. There is an international standard ISO 639[5] for two-letter abbreviations for languages, as well as some three-letter ones. These are pretty standard, except that for Hebrew which has been changed.
- Is this Spanish as spoken in Spain or in Latin America?
- ISO 639 specifies `no` as 'Norwegian', but Norway has two official languages, Bokmål and Nynorsk. Which is this?[6]

[4]Digits and upper- and lower-case A–Z, without accents.

[5]`http://www.w3.org/WAI/ER/IG/ert/iso639.htm` or `http://www.loc.gov/standards/iso639-2/englangn.html`

[6]Bokmål, usually, with `nn` for Nynorsk and `nb` for Bokmål specifically.

- The same language can be written in different ways. The most prominent example is Chinese, which has Simplified and Traditional orthography, and most readers can understand only one of them.
- Spelling. The Unix `spell` program has the following comment in the BUGS section of its `man` page:

  > 'British spelling was done by an American.'

  but that of itself is an example of cultural imperialism. The nations living on the British Isles do not consider themselves to speak 'British English' and do not agree on spelling: for example in general Chambers' dictionary (published in Scotland) prefers '-ise' and the Oxford English Dictionary prefers '-ize'.

To attempt to make the description more precise, the two-letter language code is often supplemented by a two-letter 'country or territory' code from ISO 3166[7]. So, for example

pt_BR is Portuguese as written in Brazil.

zh_CN is (simplified) Chinese as written in most of mainland China, and **zh_TW** is (traditional) Chinese as written in Taiwan (which is written in the same way as **zh_HK** used in Hong Kong).

en_US is American.

en_GB is English as written somewhere (unspecified) in the UK.

We need to specify the language for at least three purposes:

1. To delimit the set of characters which can be used, and which of those are 'legal' in object names.
2. To know the sorting order.
3. To decide what language to respond in.

In addition, we might need to know the direction of the language, but currently R only supports left-to-right processing of character strings.

The first two are part of the locale specification. Specifying the language to be used for messages is a little more complicated: a Nynorsk speaker might prefer Nynorsk then Bokmål then generic Norwegian then English, which can be expressed by setting `LANGUAGE=nn:nb:no` (since generic 'English' is the default).

Encodings

Computers work with bits and bytes, and *encoding* is the act of representing characters in the language as bytes, and *vice versa*. The earliest encodings (e.g. for Telex) just represented capital letters and numbers but this expanded to ASCII, which has 92 printable characters (upper- and lower-case letters, digits and punctuation) plus control codes, represented as bytes with the topmost bit as `0`. This is also the ISO 646 international standard and those characters are included in most[8] other encodings.

Bytes allow 256 rather than 128 different characters, and ISO 646 has been extended into the bytes with topmost bit as `1`, in many different ways. There is a series of standards ISO 8859-1 to ISO 8859-15 for such extensions, as well as many vendor-specific ones (such as the 'WinAnsi' and other code pages). Most languages have less than the 186 or more characters[9] that an 8-bit encoding provides. The problem is that given a sequence of bytes there is no way to know that it is in an 8-bit encoding let alone which one.

The CJK[10] languages have tens of thousands of characters. There have been many ways to represent such character sets, for example using shift sequences (like the shift, control, alt and altgr keys on your keyboard) to shift between 'pages' of characters. Windows uses a two-byte encoding for the ideographs, with the 'lead byte' with topmost bit `1` followed by a 'trail byte'. So the character sets used for CJK languages on Windows occupy one or two bytes.

A problem with such schemes is their lack of extensibility. What should we do when a new character comes along, notably the Euro? Most commonly, replace something which is thought to be uncommon (the generic currency symbol in ISO 8859-1 was replaced by the Euro in ISO 8859-15, amongst other changes).

Unicode

Being able to represent one language may not be enough: if for example we want to represent personal names we would like to be able to do so equally for American, Chinese, Greek, Arabic and Maori[11] speakers. So the idea emerged of a universal encoding, to represent all the characters we might like to

[7] `http://www.iso.org/iso/en/prods-services/iso3166ma/index.html`.

[8] In a common Japanese encoding, backslash is replaced by Yen. As this is the encoding used for Windows Japanese fonts, file paths look rather peculiar in a Japanese version of Windows.

[9] the rest are normally allocated to 'space' and control bytes

[10] Chinese, Japanese, Korean: known to Windows as 'East Asian'. The CJK ideographs were also used for Vietnamese until the early twentieth century.

[11] language code `mi`. Maori is usually encoded in ISO 8859-13, along with Lithuanian and Latvian!

print—all human languages, mathematical and musical notation and so on.

This is the purpose of *Unicode*[12], which allows up to 2^{32} different characters, although it is now agreed that only 2^{21} will ever be prescribed. The human languages are represented in the 'basic multilingual plane' (BMP), the first 2^{16} characters, and so most characters you will encounter have a 4-hex-digit representation. Thus `U+03B1` is alpha, `U+05D0` is aleph (the first letter of the Hebrew alphabet) and `U+30C2` is the Katakana letter 'di'.

If we all used Unicode, would everyone be happy? Unfortunately not, as sometimes the same character can be written in various ways. The Unicode standard allows 'only' 20992 slots for CJK ideographs, whereas the Taiwanese national standard defines 48711. The result is that different fonts have different variants for e.g. `U+8FCE` and a variant may be recognizable to only some of the users.

Nevertheless, Unicode is the best we have, and a decade ago Windows NT adopted the BMP of Unicode as its native encoding, using 16-bit characters. However, Unix-alike OSes expect `nul` (the zero byte) to terminate a string such as a file path, and people looked for ways to represent Unicode characters as sequences of a variable number of bytes. By far the most successful such scheme is *UTF-8*, which has over the last couple of years become the *de facto* standard for Linux distributions. So when I select

English (UK)   British English

as my language at the login screen for a session in Fedora Core 3 Linux, I am also selecting UTF-8 as my encoding.

In UTF-8, the 7-bit ASCII characters are represented as a single byte. All other characters are represented as two or more bytes all with topmost bit `1`. This introduces a number of implementation issues:

- Each character is represented by a variable number of bytes, from one up to six (although it is likely at most four will ever be used).
- Some bytes can never occur in UTF-8.
- Many byte sequences are not valid in UTF-8.

The major implementation issue in internationalizing R has been to support such *multi-byte character sets* (MBCSs). There are other examples, including EUC-JP used for Japanese on Unix-alikes and the one- or two-byte encodings used for CJK on older versions of Windows.

As UTF-8 locales can support multiple languages, which are allowed for the 'legal' characters in R object names? This may depend on the OS, but in all the examples we know of all characters which would be alphanumeric in at least one human language are allowed. So for example `ñ` and `ü` are allowed in locale `en_US.utf8` on Linux, just as they were in the Latin-1 locale `en_US` (whereas on Windows the different Latin-1 locales have different sets of 'legal' characters, indeed different in different versions of Windows for some languages). We have decided that only the ASCII numbers will be regarded as numeric in R.

Sorting orders in Unicode are handled by an OS service: this is a very intricate subject so do not expect too much consistency between different implementations (which includes the same language in different encodings).

Fonts

Being able to represent alpha, aleph and the Katakana letter 'di' is one thing: being able to display them is another, and we want to be able to display them both at the console and in graphical output. Effectively all fonts available cover quite small subsets of Unicode, although they may be usable in combinations to extend the range.

R consoles normally work in monospaced fonts. That means that all printable ASCII characters have the same width. Once we move to Unicode, characters are normally categorized into three widths, one (ASCII, Greek, Arabic, ...), two (most CJK ideographs) and zero (the 'combining characters' of languages such as Thai). Unfortunately there are two conventions for CJK characters, with some fonts having e.g. Katakana single-width and some (including that used in Figure 2) double-width.

Which characters are available in a font can seem capricious: for example the one I originally used to test translations had directional single quotes but not directional double quotes.

If displaying another language is not working in a UTF-8 locale the most likely explanation is that the font used is incomplete, and you may need to install extra OS components to overcome this.

Font support for R graphics devices is equally difficult and has currently only been achieved on Windows and on comprehensively equipped X servers. In particular, `postscript()` and `pdf()` are restricted to Western and Eastern European languages as the commonly-available fonts are (and some are restricted to ISO 8859-1).

For the R user

Now that R is able to accept input in different encodings, we need a way to specify the encoding. Connections allow you to specify the encoding via the `encoding` argument, and the encoding for `stdin` can be set when reading from a file by the command-

[12]There is a more formal definition in the ISO 10646 standard, but for our purposes Unicode is a more precisely constrained version of the same encoding. There are various versions of Unicode, currently 4.0.1—see `http://www.unicode.org`.

line argument `--encoding`. Also, `source()` has an `encoding` argument.

It is important to make sure the encoding is correct: in particular a UTF-8 file will be valid input in most locales, but will only be interpreted properly in a UTF-8 locale or if the encoding is specified. So to read a data file produced on Windows containing the names of Swiss students in a UTF-8 locale you will need one of

```
A <- read.table(file("students",
                     encoding="latin1"))
A <- read.table(file("students",
                     encoding="UCS-2LE"))
```

the second if this is a 'Unicode' Windows file.[13]

In a UTF-8 locale, characters can be entered as e.g. `\u8fce` or `\u{8fce}` and non-printable characters will be displayed by `print()` in the first of these forms. Further, `\U` can be used with up to 8 hex digits for characters not in the BMP.

For the R programmer

There is a common assumption that one byte = one character = one display column. As from R 2.1.0 a character can use more than one byte and extend over more than one column when printed. The function `nchar()` now has a `type` argument allowing the number of bytes, characters or columns to be found—note that this defaults to bytes for backwards compatibility.

Switching between encodings

R is able to support input in different encodings by using on-the-fly translation between encodings. This should be an OS service, and for modern `glibc`-based systems it is. Even with such systems it can be frustratingly difficult to find out what encodings they support, and although most systems accept aliases such as `ISO_8859-1`, `ISO8859-1`, `ISO_8859_1`, `8859_1` and `LATIN-1`, it is quite possible to find that with three systems there is no name that they all accept. One solution is to install GNU `libiconv`: we have done so for the Windows port of R, and Apple have done so for MacOS X.

We have provided R-level support for changing encoding via the function `iconv()`, and `iconvlist()` will (if possible) list the supported encodings.

Quote symbols

ASCII has a quotation mark `"`, apostrophe `'` and grave accent `` ` ``, although some fonts[14] represent the latter two as right and left quotes respectively. Unicode provides a wide variety of quote symbols, include left and right single (U+2018, U+2019) and double (U+201C, U+201D) quotation marks. R makes use of these for `sQuote()` and `dQuote()` in UTF-8 locales.

Other languages use other conventions for quotations, for example low and mirrored versions of the right quotation mark (U+201A, U+201B), as well as guillemets (U+00AB, U+00BB; something like ≪, ≫). Looking at translations of error messages in other GNU projects shows little consistency between native writers of the same language, so we have made no attempt to define language-specific versions of `sQuote()` and `dQuote()`.

Translations

R comes with a lot of documentation in English. There is a Spanish translation of *An Introduction to R* available from CRAN, and an Italian introduction based on it as well as links to Japanese translations of *An Introduction to R*, other manuals and some help pages.

R 2.1.0 facilitates the translation of messages from 'English' into other languages: it will ship with a complete translation into Japanese and of many of the messages into Brazilian Portuguese, Chinese, German and Italian. Updates of these translations and others can be added at a later date by translation packages.

Which these 'messages' are was determined by those (mainly me) who marked up the code for possible translation. We aimed to make all but the most esoteric warning and error messages available for translation, together with informational messages such as the welcome message and the menus and dialogs of the Windows and MacOS X consoles. There are about 4200 unique messages in command-line R plus a few hundred in the GUIs.

One beneficial side-effect even for English readers has been much improvement in the consistency of the messages, as well as some re-writing where translators found the messages unclear.

For the R user

All the end user needs to do is to ensure that the desired translations are installed and that the language is set correctly. To test the latter, try it and see: very likely the internal code will be able to figure out the correct language from the locale name, and the welcome message (and menus if appropriate) will appear in the correct language. If not, try setting the environment variable `LANGUAGE` and if that does not

[13]This will probably not work unless the first two bytes are removed from the file. Windows is inclined to write a 'Unicode' file starting with a Byte Order Mark `0xFEFE`, whereas most Unix-alikes do not recognize a BOM. It would be technically easy to do so but apparently politically impossible.

[14]most likely including the one used to display this document.

help, read the appropriate section of the *R Installation and Administration* manual.

Unix-alike versions of R can be built without support for translation, and it is possible that some OSes will provide too impoverished an environment to determine the language from the locale or even for the translation support to be compiled in.

There is a pseudo-language `en@quot` for which translations are supplied. This is intended for use in UTF-8 locales, and makes use of the Unicode directional single and double quotation marks. This should be selected *via* the `LANGUAGE` environment variable.

For package writers

Any package can have messages marked for translation: see *Writing R Extensions*. Traditionally messages have been `paste`-d together, and such messages can be awkward or impossible to translate into languages with other word orders. We have added support for specifying messages *via* C-like format strings, using the R function `gettextf`. A typical usage is

```
stop(gettextf(
  "autoloader did not find '%s' in '%s'",
              name, package),
     domain = NA)
```

I chose this example as the Chinese translation reverses[15] the order of the two variables. Using `gettextf()` marks the format (the first argument) for translation and then passes the arguments to `sprintf()` for C-like formatting. The argument `domain = NA` is passed to `stop()` as the message returned by `gettextf()` will already be translated (if possible) and so needs no further translation. As the quotation marks are included in the format, translators can use other conventions (and the pseudo-language `en@quot` will).

Plurals are another source of difficulties for translators. Some languages have no plural forms, others have 'singular' and 'plural' as in English, and others have up to four forms. Even for those languages with just 'singular' and 'plural' there is the question of whether zero is singular or plural, which differs by language. There is quite general support for plurals in the R and C functions `ngettextf` and a small number[16] of examples in the R sources.

See *Writing R Extensions* for more details.

For would-be translators

Additional translations and help completing the current ones would be most welcome. Experience has shown that it is helpful to have a small translation team to cross-check each other's work, discuss idiomatic usage and to share the load. Translation will be an ongoing process as R continues to grow.

Please see the documents linked from
`http://developer.r-project.org`.

Future directions

At this point we need to gain more experience with internationalization infrastructure. We know it works with the main R platforms (recent Linux, Windows, MacOS X) and Solaris and for a small set of quite diverse languages.

We currently have no way to allow Windows users to use many languages in one session, as Windows' implementation of Unicode is not UTF-8 and the standard C interface on Windows does not allow UTF-8 as an encoding. We plan on making a 'Unicode' (in the Windows sense) implementation of R 2.2.0 that uses UTF-8 internally and 16-bit characters to interface with Windows. It is likely that such a version will only be available for NT-based versions of Windows.

It is hoped to support a wider range of encodings on the `postscript()` and `pdf()` devices.

The use of encodings in documentation remains problematic, including in this article. `Texinfo` is used for the R manuals but does not currently support even ISO 8859-1 correctly. We have started with some modest support for encodings in `.Rd` files, and may be able to do more.

Acknowledgements

The work of the Japanese group (especially Ei-ji Nakama and Masafumi Okada) supplied valuable early experience in internationalization.

The translations have been made available by translation teams and in particular some enthusiastic individuals. The infrastructure for translation is provided by GNU `gettext`, suitably bent to our needs (for R is a large and complex project, and in particular extensible).

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[15]using `'%2$s'` and `'%1$s'` in the translation to refer to the second and first argument respectively.
[16]currently 22, about 0.5% of the messages.

Packages and their Management in R 2.1.0

by Brian D. Ripley

R 2.1.0 introduces changes that make packages and their management considerably more flexible and less tied to CRAN.

What is a package?

The idea of an R *package* was based quite closely on that of an S *library section*: a collection of R functions with associated documentation and perhaps compiled code that is loaded from a *library*[1] by the `library()` command. The Help Desk article (Ligges, 2003) provides more background.

Such packages still exist, but as from R 2.1.0 there are other types of R extensions, distinguished by the `Type:` field in the 'DESCRIPTION' file: the classic package has `Type: Package` or no `Type:` field. The `Type:` field tells `R CMD INSTALL` and `install.packages()` what to do with the extension, which is still distributed as a tarball or `zip` file containing a directory of the same name as the package.

This allows new types of extensions to be added in the future, but R 2.1.0 knows what to do with two other types.

Translation packages

with `Type: Translation`. These are used to add or update translations of the diagnostic messages produced by R and the standard packages. The convention is that languages are known by their ISO 639 two-letter (or less commonly three-letter) codes, possibly with a 'country or territory' modifier. So package **Translation-sl** should contain translations into Slovenian, and **Translation-zhTW** translations into traditional Chinese as used in Taiwan. *Writing R Extensions* describes how to prepare such a package: it contains compiled translations and so all `R CMD INSTALL` and `install.packages()` need to do is to create the appropriate subdirectories and copy the compiled translations into place.

Frontend packages

with `Type: Frontend`. These are only supported as source packages on Unix, and are used to install alternative front-ends such as the GNOME console, previously part of the R distribution and now in CRAN package **gnomeGUI**. For this type of package the installation runs `configure` and the `make` and so allows maximal flexibility for the package writer.

[1] a directory containing subdirectories of installed packages

Source *vs* binary

Initially R packages were distributed in source form as tarballs. Then the Windows binary packages came along (distributed as Zip files) and later Classic MacOS and MacOS X packages. As from R 2.1.0 the package management functions all have a `type` argument defaulting to the value of `getOption("pkgType")`, with known values `"source"`, `"win.binary"` and `"mac.binary"`. These distributions have different file extensions: `.tar.gz`, `.zip` and `.tgz` respectively.

This allows packages of each type to be manipulated on any platform: for example, whereas one cannot install Windows binary packages on Linux, one can download them on Linux or Solaris, or find out if a MacOS X binary distribution is available.

Note that `install.packages` on MacOS X can now install either `"source"` or `"mac.binary"` package files, the latter being the default. Similarly, `install.packages` on Windows can now install either `"source"` or `"win.binary"` package files. The only difference between the platforms is the default for `getOption("pkgType")`.

Repositories

The package management functions such as `install.packages`, `update.packages` and `packageStatus` need to know where to look for packages. Function `install.packages` was originally written to access a CRAN mirror, but other *repositories* of packages have been created, notably that of Bioconductor. Function `packageStatus` was the first design to allow multiple repositories.

We encourage people with collections of packages to set up a repository. Apart from the CRAN mirrors and Bioconductor there is an Omegahat repository, and I have a repository of hard-to-compile Windows packages to supplement those made automatically. We anticipate university departments setting up repositories of support software for their courses. A repository is just a tree of files based at a URL: details of the format are in *Writing R Extensions*. It can include one, some or all of `"source"`, `"win.binary"` and `"mac.binary"` types in separate subtrees.

Specifying repositories

Specifying repositories has become quite complicated: the (sometimes conflicting) aims were to be intuitive to new users, very flexible and as far as possible backwards compatible.

As before, the place(s) to look for files are specified by the `contriburl` argument. This is a character vector of URLs, and can include `file://` URLs if packages are stored locally, for example on a distribution CD-ROM. Different URLs in the vector can be of different types, so one can mix a distribution CD-ROM with a CRAN mirror.

However, as before, most people will not specify `contriburl` directly but rather the `repos` argument that replaces the `CRAN` argument.[2] The function `contrib.url` is called to convert the base URLs in `repos` into URLs pointing to the correct subtrees of the repositories. For example

```
> contrib.url("http://base.url",
              type = "source")
[1] "http://base.url/src/contrib"
> contrib.url("http://base.url",
              type = "win.binary")
[1] "http://base.url/bin/windows/contrib/2.1"
> contrib.url("http://base.url",
              type = "mac.binary")
[1] "http://base.url/bin/macosx/2.1"
```

This is of course hidden from the average user.

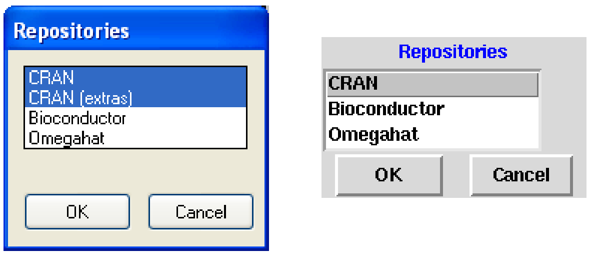

Figure 1: The listboxes from `setRepositories()` on Windows (left) and Unix (right).

The `repos` argument of the package management functions defaults to `getOption("repos")`. This has a platform-specific default, and can be set by calling `setRepositories`. On most systems this uses a listbox widget, as shown in figure 1. Where no GUI is available, a text list is used such as

```
> setRepositories()
--- Please select repositories for use
    in this session ---


1: + CRAN
2: + CRAN (extras)
3:   Bioconductor
4:   Omegahat

Enter one or more numbers separated by spaces
1: 1 4
```

The list of repositories and which are selected by default can be customized for a user or for a site: see `?setRepositories`. We envisaged people distributing a CD-ROM containing R and a repository, with `setRepositories()` customized to include the local repository by default.

Suppose a package exists on more than one repository?

Since multiple repositories are allowed, how is this resolved? The rule is to select the latest version of the package, from the first repository on the list that is offering it. So if a user had

```
> getOption("repos")
[1] "file://d:/R/local"
[2] "http://cran.us.r-project.org"
```

packages would be fetched from the local repository if they were current there, and from a US CRAN mirror if there is an update available there.

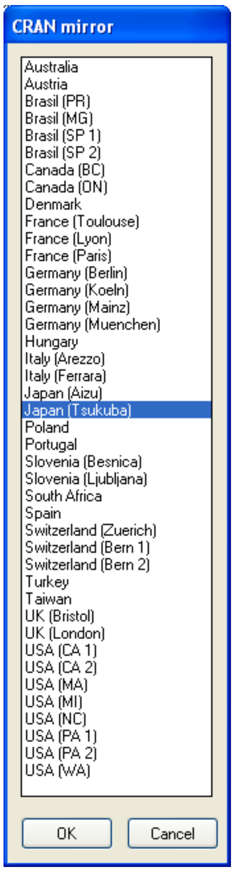

Figure 2: Selecting a CRAN mirror on Windows.

No default CRAN

Windows users are already used to selecting a CRAN mirror. Now 'factory-fresh' R does not come with a default CRAN mirror. On Unix the default is in fact

```
> getOption("repos")
    CRAN
"@CRAN@"
```

[2]This still exists but has been deprecated and will be removed in R 2.2.0.

Whenever `@CRAN@` is encountered in a repository specification, the function `chooseCRANmirror` is called to ask for a mirror (and can also be called directly and from a menu item on the Windows GUI). The Windows version is shown in Figure 2: there are MacOS X and Tcl/Tk versions, as well as a text-based version using `menu`.[3]

Experienced users can avoid being asked for a mirror by setting `options("repos")` in their '.Rprofile' files: examples might be

```
options(repos=
   c(CRAN="http://cran.xx.r-project.org"))
```

on Unix-alikes and

```
options(repos=
   c(CRAN="http://cran.xx.r-project.org",
     CRANextra=
       "http://www.stats.ox.ac.uk/pub/RWin"))
```

on Windows.

Although not essential, it is helpful to have a *named* vector of repositories as in this example: for example `setRepositories` looks at the names when setting its initial selection.

Installing packages

Users of the Windows GUI will be used to selecting packages to be installed from a scrollable list box. This now works on all platforms from the command line if `install.packages` is called with no `pkgs` (first) argument. Packages from all the selected repositories are listed in alphabetical order, and the packages from bundles are listed[4] individually in the form `MASS (VR)`.

The `dependencies` argument introduced in `R 2.0.0` can be used to install a package and its dependencies (and their dependencies ...), and R will arrange to install the packages in a suitable order. The `dependencies` argument can be used to select only those dependencies that are essential, or to include those which are suggested (and might only be needed to run some of the examples).

Installing all packages

System administrators often want to install 'all' packages, or at least as many as can be installed on their system: a standard Linux system lacks the additional software needed to install about 20 and a handful can only be installed on Windows or on Linux.

The new function `new.packages()` is a helpful way to find out which packages are *not* installed of those offered by the repositories selected. If called as `new.packages(ask = "graphics")` a list box is used to allow the user to select packages to be installed.

[3] `menu` has been much enhanced for `R 2.1.0`.

[4] provided the repository has been set up to supply the information.

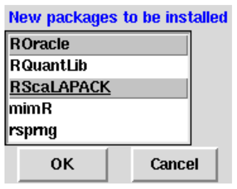

Figure 3: Selecting amongst uninstalled packages on Linux.

Updating packages

The only real change in `update.packages` is the `ask` argument. This defaults to `ask = TRUE` where as before the user is asked about each package (but with a little more information and the option to quit). Other options are `ask = FALSE` to install all updates, and `ask = "graphics"` to use a listbox (similar to figure 3) to de-select packages (as by default all the updates are selected).

Looking at repositories

The function `CRAN.packages` was (as it name implies) designed to look at a single CRAN mirror. It has been superseded by `available.packages` which can look at one or more repositories and by default looks at those specified by `getOption("repos")` for package type (source/binary) specified by `getOption("pkgType")`. This returns a matrix with rather more columns than before, including `"Repository"`, the dependencies and the contents of bundles.

Function `packageStatus` is still available but has been re-implemented on top of functions such as `available.packages`. Its `summary` method allows a quick comparison of the installed packages with those offered by the selected repositories. However, its `print` method is concise: see figure 4.

Bibliography

U. Ligges. R help desk: Package management. *R News*, 3(3):37–39, December 2003. URL `http://CRAN.R-project.org/doc/Rnews/`. 8

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```
> (ps <- packageStatus())
--- Please select a CRAN mirror for use in this session ---
Number of installed packages:

                      ok upgrade unavailable
  c:/R/library        34       1           0
  c:/R/rw2010/library 12       0          13

Number of available packages (each package/bundle counted only once):

                                                            installed
  http://www.sourcekeg.co.uk/cran/bin/windows/contrib/2.1          31
  http://www.stats.ox.ac.uk/pub/RWin/bin/windows/contrib/2.1        4

                                                            not installed
  http://www.sourcekeg.co.uk/cran/bin/windows/contrib/2.1             421
  http://www.stats.ox.ac.uk/pub/RWin/bin/windows/contrib/2.1            8

> summary(ps)

Installed packages:
-------------------
*** Library c:/R/library
$ok
 [1] "abind"       "acepack"     "akima"       "ash"         "car"
...
$upgrade
[1] "XML"

$unavailable
NULL

*** Library c:/R/rw2010/library
$ok
 [1] "base"      "datasets"  "graphics"  "grDevices" "grid"    "methods"  "splines"   "stats"    "stats4"
[10] "tcltk"     "tools"     "utils"

$upgrade
NULL

$unavailable
 [1] "boot"       "cluster"    "foreign"    "KernSmooth"  "lattice"
...

Available packages:
-------------------
(each package appears only once)

*** Repository http://www.sourcekeg.co.uk/cran/bin/windows/contrib/2.1
$installed
 [1] "abind"       "acepack"     "akima"       "ash"         "car"
...

$"not installed"
  [1] "accuracy"          "adapt"             "ade4"
...
[421] "zicounts"

*** Repository http://www.stats.ox.ac.uk/pub/RWin/bin/windows/contrib/2.1
$installed
[1] "GLMMGibbs" "xgobi"     "XML"       "yags"

$"not installed"
[1] "gsl"         "hdf5"        "ncdf"        "RDCOMClient"      "rgdal"  "RNetCDF"     "survnnet"    "udunits"

> upgrade(ps)
XML :
0.97-0 at c:/R/library
0.97-3 at http://www.stats.ox.ac.uk/pub/RWin/bin/windows/contrib/2.1
Update (y/N)?  y
```

Figure 4: packageStatus on a Windows machine. The voluminous summary has been edited to save space.

Recent Changes in grid Graphics

by Paul Murrell

Introduction

The **grid** graphics package provides an alternative graphics system to the "traditional" S graphics system that is provided by the **graphics** package.

The majority of high-level plotting functions (functions that produce whole plots) that are currently available in the base packages and in add-on packages are built on the **graphics** package, but the **lattice** package (Sarkar, 2002), which provides high-level Trellis plots, is built on **grid**.

The **grid** graphics package can be useful for customising **lattice** plots, creating complex arrangements of several **lattice** plots, or for producing graphical scenes from scratch.

The basic features of **grid** were described in an R News article in June 2002 (Murrell, 2002). This article provides an update on the main features that have been added to **grid** since then. This article assumes a familiarity with the basic **grid** ideas of units and viewports.

Changes to grid

The most important organisational change is that **grid** is now a "base" package, so it is installed as part of the standard R installation. In other words, package writers can assume that **grid** is available.

The two main areas where the largest changes have been made to **grid** are viewports and graphical objects. The changes to viewports are described in the next section and summarised in Table 1 at the end of the article. A separate section describes the changes to graphical objects with a summary in Table 2 at the end of the article.

Changes to viewports

grid provides great flexibility for creating regions on the page to draw in (viewports). This is good for being able to locate and size graphical output on the page in very sophisticated ways (e.g., **lattice** plots), but it is bad because it creates a complex environment when it comes to adding further output (e.g., annotating a **lattice** plot).

The first change to viewports is that they are now much more persistent; it is possible to have any number of viewports defined at the same time.

There are also several new functions that provide a consistent and straightforward mechanism for navigating to a particular viewport when several viewports are currently defined.

A viewport is just a rectangular region that provides a geometric and graphical context for drawing. The viewport provides several coordinate systems for locating and sizing output, and it can have graphical parameters associated with it to affect the appearance of any output produced within the viewport. The following code describes a viewport that occupies the right half of the graphics device and within which, unless otherwise specified, all output will be drawn using thick green lines. A new feature is that a viewport can be given a name. In this case the viewport is called `"rightvp"`. The name will be important later when we want to navigate back to this viewport.

```
> vp1 <- viewport(x=0.5, width=0.5,
                  just="left",
                  gp=gpar(col="green", lwd=3),
                  name="rightvp")
```

The above code only creates a description of a viewport; a corresponding region is created on a graphics device by *pushing* the viewport on the device, as shown below.[1]

```
> pushViewport(vp1)
```

Now, all drawing occurs within the context defined by this viewport until we change to another viewport. For example, the following code draws some basic shapes, all of which appear in the right half of the device, with thick green lines (see the right half of Figure 1). Another new feature is that a name can be associated with a piece of graphical output. In this case, the rectangle is called `"rect1"`, the line is called `"line1"`, and the set of circles are called `"circles1"`. These names will be used later in the section on "Changes to graphical objects".

```
> grid.rect(name="rect1")
> r <- seq(0, 2*pi, length=5)[-5]
> x <- 0.5 + 0.4*cos(r + pi/4)
> y <- 0.5 + 0.4*sin(r + pi/4)
> grid.circle(x, y, r=0.05,
```

[1]The function used to be called `push.viewport()`.

```
                 name="circles1")
> grid.lines(x[c(2, 1, 3, 4)],
             y[c(2, 1, 3, 4)],
             name="line1")
```

There are two ways to change the viewport. You can *pop* the viewport, in which case the region is permanently removed from the device, or you can navigate *up* from the viewport and leave the region on the device. The following code demonstrates the second option, using the upViewport() function to revert to using the entire graphics device for output, but leaving a viewport called "rightvp" still defined on the device.

```
> upViewport()
```

Next, a second viewport is defined to occupy the left half of the device, this viewport is pushed, and some output is drawn within it. This viewport is called "leftvp" and the graphical output is associated with the names "rect2", "lines2", and "circles2". The output from the code examples so far is shown in Figure 1.

```
> vp2 <- viewport(x=0, width=0.5,
                  just="left",
                  gp=gpar(col="blue", lwd=3),
                  name="leftvp")
> pushViewport(vp2)
> grid.rect(name="rect2")
> grid.circle(x, y, r=0.05,
              name="circles2")
> grid.lines(x[c(3, 2, 4, 1)],
             y[c(3, 2, 4, 1)],
             name="line2")
```

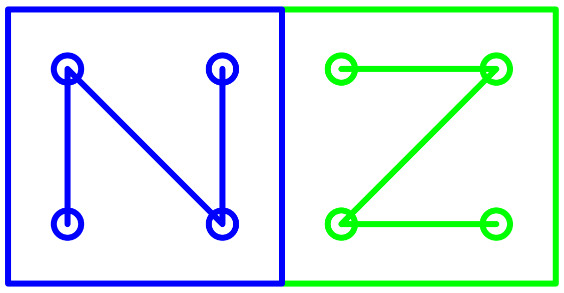

Figure 1: Some simple shapes drawn in some simple viewports.

There are now three viewports defined on the device; the function current.vpTree() shows all viewports that are currently defined.[2]

```
> current.vpTree()
```

```
viewport[ROOT]->(
  viewport[leftvp],
  viewport[rightvp])
```

There is always a ROOT viewport representing the entire device and the two viewports we have created are both direct children of the ROOT viewport. We now have a tree structure of viewports that we can navigate around. As before, we can navigate up from the viewport we just pushed and, in addition, we can navigate *down* to the previous viewport. The function downViewport() performs the navigation to a viewport lower down the viewport tree. It requires the name of the viewport to navigate to. In this case, we navigate down to the viewport called "rightvp".

```
> upViewport()
> downViewport("rightvp")
```

It is now possible to add further output within the context of the viewport called "rightvp". The following code draws some more circles, this time explicitly grey (but still with thick lines; see Figure 2). The name "circles3" is associated with these extra circles.

```
> x2 <- 0.5 + 0.4*cos(c(r, r+pi/8, r-pi/8))
> y2 <- 0.5 + 0.4*sin(c(r, r+pi/8, r-pi/8))
> grid.circle(x2, y2, r=0.05,
              gp=gpar(col="grey"),
              name="circles3")
> upViewport()
```

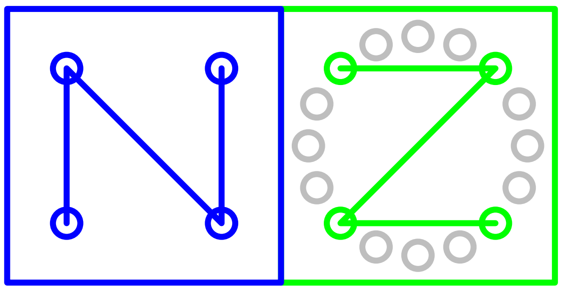

Figure 2: Navigating between viewports and annotating.

What this simple demonstration shows is that it is possible to define a number of viewports during drawing and leave them in place for others to add

[2]The output of current.vpTree() has been reformatted to make the structure more obvious; the natural output is all just on a single line.

further output. A more sophisticated example is now presented using a **lattice** plot.[3]

The following code creates a simple **lattice** plot. The "trellis" object created by the histogram() function is stored in a variable, hist1, so that we can use it again later; printing hist1 produces the plot shown in Figure 3.[4]

```
> hist1 <- histogram(
    par.settings=list(fontsize=list(text=8)),
    rnorm(500), type = "density",
    panel=
      function(x, ...) {
        panel.histogram(x, ...)
        panel.densityplot(x,
                          col="brown",
                          plot.points=FALSE)
      })
> trellis.par.set(canonical.theme("pdf"))
> print(hist1)
```

The **lattice** package uses **grid** to produce output and it defines lots of viewports to draw in. In this case, there are six viewports created, as shown below.

```
> current.vpTree()
```

```
viewport[ROOT]->(
  viewport[plot1.toplevel.vp]->(
    viewport[plot1.],
    viewport[plot1.panel.1.1.off.vp],
    viewport[plot1.panel.1.1.vp],
    viewport[plot1.strip.1.1.off.vp],
    viewport[plot1.xlab.vp],
    viewport[plot1.ylab.vp]))
```

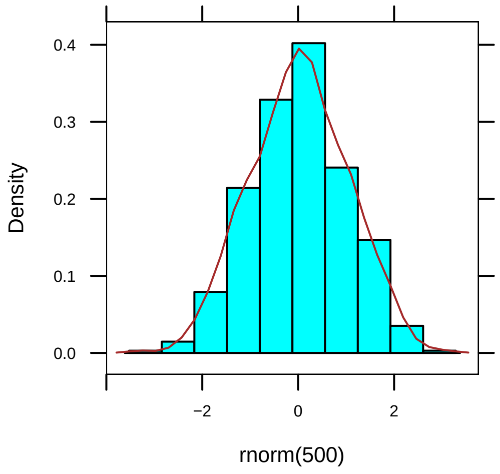

Figure 3: A simple **lattice** plot.

What we are going to do is add output to the **lattice** plot by navigating to a couple of the viewports that **lattice** set up and draw a border around the viewport to show where it is. We will use the frame() function defined below to draw a thick grey rectangle around the viewport, then a filled grey rectangle at the top-left corner, and the name of the viewport in white within that.

```
> frame <- function(name) {
    grid.rect(gp=gpar(lwd=3, col="grey"))
    grid.rect(x=0, y=1,
              height=unit(1, "lines"),
              width=1.2*stringWidth(name),
              just=c("left", "top"),
              gp=gpar(col=NA, fill="grey"))
    grid.text(name,
              x=unit(2, "mm"),
              y=unit(1, "npc") -
                unit(0.5, "lines"),
              just="left",
              gp=gpar(col="white"))
  }
```

The viewports used to draw the **lattice** plot consist of a single main viewport called (in this case) "plot1.toplevel.vp", and a number of other viewports within that for drawing the various components of the plot. This means that the viewport tree has three levels (including the top-most ROOT viewport). With a multipanel **lattice** plot, there can be many more viewports created, but the naming scheme for the viewports uses a simple pattern and

[3]This low-level **grid** mechanism is general and available for any graphics output produced using **grid** including **lattice** output. An additional higher-level interface has also been provided specifically for **lattice** plots (e.g., the trellis.focus() function).

[4]The call to trellis.par.set() sets **lattice** graphical parameters so that the colours used in drawing the histogram are those used on a PDF device. This explicit control of the **lattice** "theme" makes it easier to exactly reproduce the histogram output in a later example.

there are **lattice** functions provided to generate the appropriate names (e.g., `trellis.vpname()`).

When there are more than two levels, there are two ways to specify a particular low-level viewport. By default, `downViewport()` will search within the children of a viewport, so a single viewport name will work as before. For example, the following code annotates the **lattice** plot by navigating to the viewport `"plot1.panel.1.1.off.vp"` and drawing a frame to show where it is. This example also demonstrates the fact that `downViewport()` returns a value indicating how many viewports were descended. This "'depth" can be passed to `upViewport()` to ensure that the correct number of viewports are ascended after the annotation.

```
> depth <-
    downViewport("plot1.panel.1.1.off.vp")
> frame("plot1.panel.1.1.off.vp")
> upViewport(depth)
```

Just using the final destination viewport name can be ambiguous if more than one viewport in the viewport tree has the same name, so it is also possible to specify a *viewport path*. A viewport path is a list of viewport names that must be matched in order from parent to child. For example, this next code uses an explicit viewport path to frame the viewport `"plot1.xlab.vp"` that is a child of the viewport `"plot1.toplevel.vp"`.

```
> depth <-
    downViewport(vpPath("plot1.toplevel.vp",
                        "plot1.xlab.vp"))
> frame("plot1.xlab.vp")
> upViewport(depth)
```

It is also possible to use a viewport name or viewport path in the `vp` argument to drawing functions, in which case the output will occur in the named viewport. In this case, the viewport path is strict, which means that the full path must be matched starting from the context in which the `grob` was drawn. The following code adds a dashed white line to the borders of the frames. This example also demonstrates that viewport paths can be specified as explicit strings, with a `"::"` path separator.

The final output after all of these annotations is shown in Figure 4.

```
> grid.rect(
    gp=gpar(col="white", lty="dashed"),
    vp="plot1.toplevel.vp::plot1.panel.1.1.off.vp")
> grid.rect(
    gp=gpar(col="white", lty="dashed"),
    vp="plot1.toplevel.vp::plot1.xlab.vp")
```

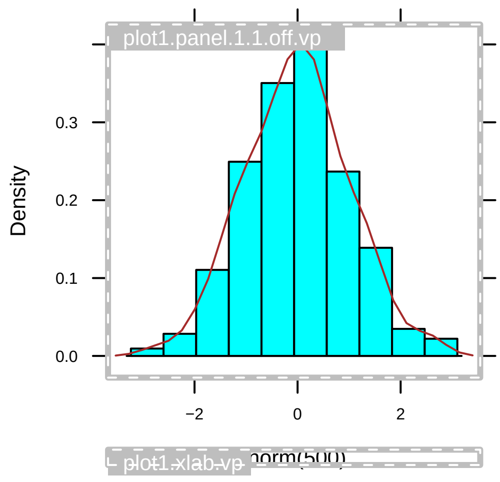

Figure 4: Annotating the simple **lattice** plot.

Changes to graphical objects

All **grid** drawing functions create graphical objects representing the graphical output. This is good because it makes it possible to manipulate these objects to modify the current scene, but there needs to be a coherent mechanism for working with these objects.

There are several new functions, and some existing functions have been made more flexible, to provide a consistent and straightforward mechanism for accessing, modifying, and removing graphical objects.

All **grid** functions that produce graphical output, also create a graphical object, or `grob`, that represents the output, and there are functions to access, modify, and remove these graphical objects. This can be used as an alternative to modifying and rerunning the R code to modify a plot. In some situations, it will be the only way to modify a low-level feature of a plot.

Consider the output from the simple viewport example (shown in Figure 2). There are seven pieces of output, each with a corresponding `grob`: two rectangles, `"rect1"` and `"rect2"`; two lines, `"line1"` and `"line2"`; and three sets of circles, `"circles1"`, `"circles2"`, and `"circles3"`. A particular piece of output can be modified by modifying the corresponding `grob`; a particular `grob` is identified by its name.

The names of all (top-level) `grobs` in the current scene can be obtained using the `getNames()` function.[5]

[5]Only introduced in R version 2.1.0; a less efficient equivalent for version 2.0.0 is to use `grid.get()`.

```
> getNames()
```

```
[1] "rect1"    "circles1" "line1"    "rect2"
[5] "circles2" "line2"    "circles3"
```

The following code uses the `grid.get()` function to obtain a copy of all of the `grobs`. The first argument specifies the names(s) of the `grob`(s) that should be selected; the `grep` argument indicates whether the name should be interpreted as a regular expression; the `global` argument indicates whether to select just the first match or all possible matches.

```
> grid.get(".*", grep=TRUE, global=TRUE)
```

```
(rect[rect1], circle[circles1], lines[line1],
 rect[rect2], circle[circles2], lines[line2],
 circle[circles3])
```

The value returned is a `gList`; a list of one or more `grobs`. This is a useful way to obtain copies of one or two objects representing some portion of a scene, but it does not return any information about the context in which the `grobs` were drawn, so, for example, just drawing the `gList` is unlikely to reproduce the original output (for that, see the `grid.grab()` function below).

The following code makes use of the `grid.edit()` function to change the colour of the grey circles to black (see Figure 5). In general, most arguments provided in the creation of the output are available for editing (see the documentation for individual functions). It should be possible to modify the `gp` argument for all `grobs`.

```
> grid.edit("circles3", gp=gpar(col="black"))
```

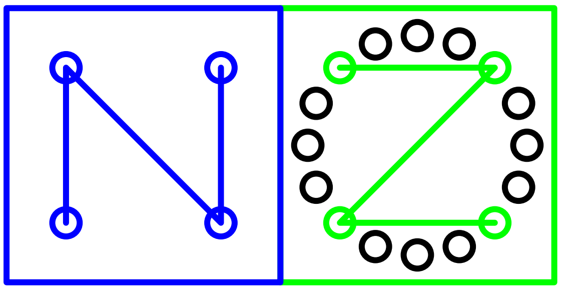

Figure 5: Editing **grid** output.

The following code uses `grid.remove()` to delete all of the `grobs` whose names end with a `"2"` – all of the blue output (see Figure 6).

```
> grid.remove(".+2$", grep=TRUE, global=TRUE)
```

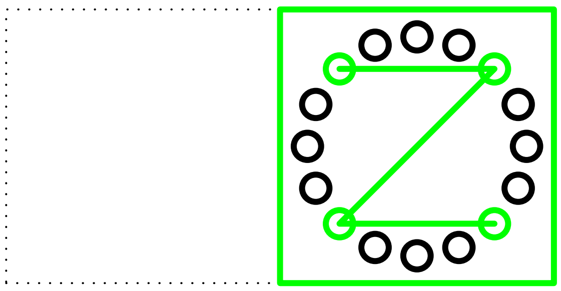

Figure 6: Deleting **grid** output.

These manipulations are possible with any **grid** output. For example, in addition to lots of viewports, a **lattice** plot creates a large number of `grobs` and all of these can be accessed, modified, and deleted using the **grid** functions (an example is given at the end of the article).

Hierarchical graphical objects

Basic `grobs` simply consist of a description of something to draw. As shown above, it is possible to get a copy of a `grob`, modify the description in a `grob`, and/or remove a `grob`.

It is also possible to create and work with more complicated graphical objects that have a tree structure, where one graphical object is the parent of one or more others. Such a graphical object is called a `gTree`. The functions described so far all work with `gTrees` as well, but there are some additional functions just for creating and working with `gTrees`.

In simple usage, a `gTree` just groups several `grobs` together. The following code uses the `grid.grab()` function to create a `gTree` from the output in Figure 6.

```
> nzgrab <- grid.grab(name="nz")
```

If we draw this `gTree` on a new page, the output is exactly the same as Figure 6, but there is now only one graphical object in the scene: the `gTree` called `"nz"`.

```
> grid.newpage()
```

```
> grid.draw(nzgrab)
```

```
> getNames()
```

```
[1] "nz"
```

This gTree has four children; the four original grobs that were "grabbed". The function childNames() prints out the names of all of the child grobs of a gTree.

```
> childNames(grid.get("nz"))
```

```
[1] "rect1"    "circles1" "line1"
[4] "circles3"
```

A gTree contains viewports used to draw its child grobs as well as the grobs themselves, so the original viewports are also available.

```
> current.vpTree()
```

```
viewport[ROOT]->(
  viewport[leftvp],
  viewport[rightvp])
```

The grid.grab() function works with any output produced using **grid**, including **lattice** plots, and there is a similar function grid.grabExpr(), which will capture the output from an expression.[6] The following code creates a gTree by capturing an expression to draw the histogram in Figure 3.

```
> histgrab <- grid.grabExpr(
    { trellis.par.set(canonical.theme("pdf"));
      print(hist1) },
    name="hist", vp="leftvp")
```

The grid.add() function can be used to add further child grobs to a gTree. The following code adds the histogram gTree as a child of the gTree called "nz". An important detail is that the histogram gTree was created with vp="leftvp"; this means that the histogram gets drawn in the viewport called "leftvp" (i.e., in the left half of the scene). The output now looks like Figure 7.

```
> grid.add("nz", histgrab)
```

There is still only one graphical object in the scene, the gTree called "nz", but this gTree now has five children: two lots of circles, one line, one rectangle, and a **lattice** histogram (as a gTree).

```
> childNames(grid.get("nz"))
```

```
[1] "rect1"    "circles1" "line1"
[4] "circles3" "hist"
```

The functions for accessing, modifying, and removing graphical objects all work with hierarchical graphical objects like this. For example, it is possible to remove a specific child from a gTree using grid.remove().

When dealing with a scene that includes gTrees, a simple grob name can be ambiguous because, by default, grid.get() and the like will search within the children of a gTree to find a match.

Just as you can provide a viewport path in downViewport() to unambiguously specify a particular viewport, it is possible to provide a grob path in grid.get(), grid.edit(), or grid.remove() to unambiguously specify a particular grob.

A grob path is a list of grob names that must be matched in order from parent to child. The following code demonstrates the use of the gPath() function to create a grob path. In this example, we are going to modify one of the grobs that were created by **lattice** when drawing the histogram. In particular, we are going to modify the grob called "plot1.xlab" which represents the x-axis label of the histogram.

In order to specify the x-axis label unambiguously, we construct a grob path that identifies the grob "plot1.xlab", which is a child of the grob called "hist", which itself is a child of the grob called "nz". That path is used to modify the grob which represents the xaxis label on the histogram. The xaxis label is moved to the far right end of its viewport and is drawn using a bold-italic font face (see Figure 8).

```
> grid.edit(gPath("nz", "hist", "plot1.xlab"),
            x=unit(1, "npc"), just="right",
            gp=gpar(fontface="bold.italic"))
```

Summary

When a scene is created using the **grid** graphics system, a tree of viewport objects is created to represent the drawing regions used in the construction of the scene and a list of graphical objects is created to represent the actual graphical output.

Functions are provided to view the viewport tree and navigate within it in order to add further output to a scene.

Other functions are provided to view the graphical objects in a scene, to modify those objects, and/or remove graphical objects from the scene. If graphical objects are modified or removed, the scene is redrawn to reflect the changes. Graphical objects can also be grouped together in a tree structure and dealt

[6]The function grid.grabExpr() is only available in R version 2.1.0; the grid.grab() function could be used instead by explicitly opening a new device, drawing the histogram, and then capturing it.

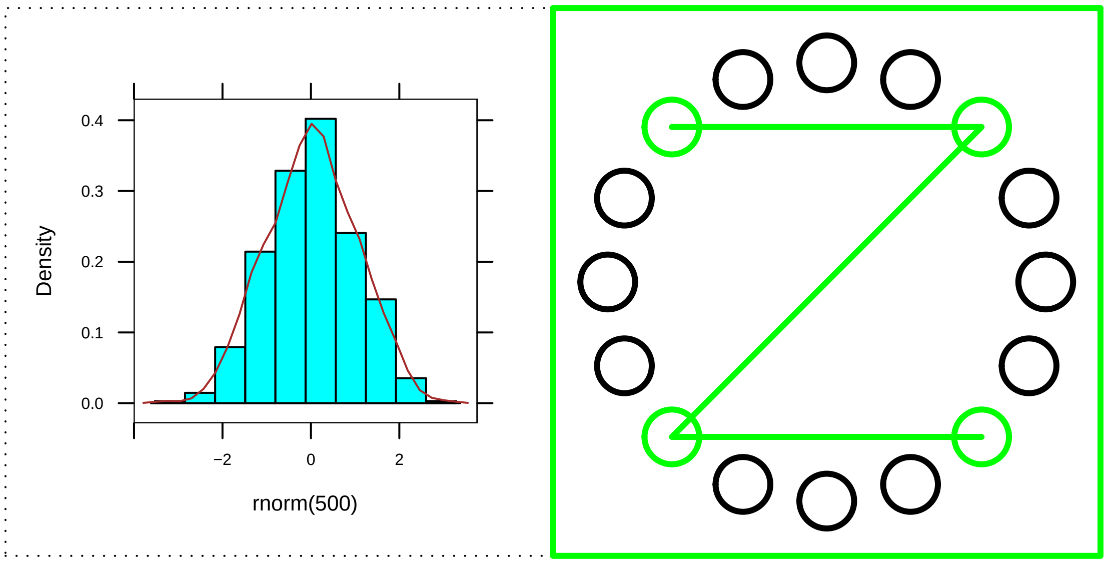

Figure 7: Grabbing **grid** output.

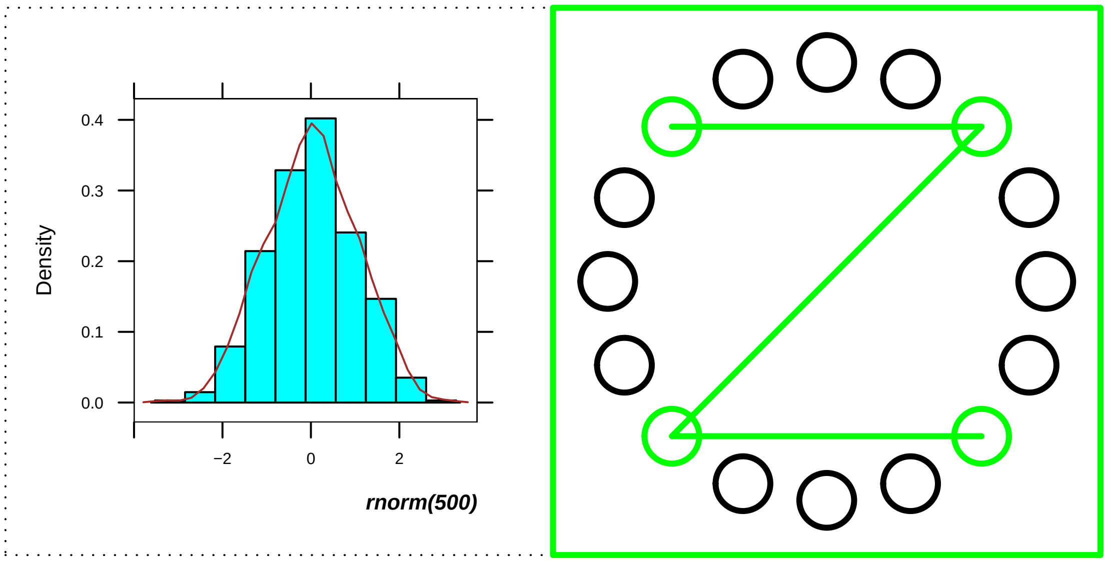

Figure 8: Editing a `gTree`.

Table 1: Summary of the new and changed functions in R 2.0.0 relating to viewports.

Function	Description
`pushViewport()`	Create a region for drawing on the current graphics device.
`popViewport()`	Remove the current drawing region (does not delete any output).
`upViewport()`	Navigate to parent drawing region (but do not remove current region).
`downViewport()`	Navigate down to named drawing region.
`current.viewport()`	Return the current viewport.
`current.vpTree()`	Return the current tree of viewports that have been created on the current device.
`vpPath()`	Create a viewport path; a concatenated list of viewport names.
`viewport(..., name=)`	A viewport can have a name associated with it.

Table 2: Summary of the new and changed functions since R 2.0.0 relating to graphical objects (some functions only available since R 2.1.0).

Function	Description
`grid.get()`	Return a single `grob` or a `gList` of `grobs`.
`grid.edit()`	Modify one or more `grobs` and (optionally) redraw.
`grid.remove()`	Remove one or more `grobs` and (optionally) redraw.
`grid.add()`	Add a `grob` to a `gTree`.
`grid.grab()`	Create a `gTree` from the current scene.
`grid.grabExpr()`	Create a `gTree` from an R expression (only available since R 2.1.0).
`gPath()`	Create a `grob` path; a concatenated list of `grob` names.
`getNames()`	List the names of the top-level `grobs` in the current scene (only available since R 2.1.0).
`childNames()`	List the names of the children of a `gTree`.
`grid.rect(..., name=)`	Grid drawing functions can associate a name with their output.

with as a single unit.

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hoa: An R package bundle for higher order likelihood inference

by Alessandra R. Brazzale

Introduction

The likelihood function represents the basic ingredient of many commonly used statistical methods for estimation, testing and the calculation of confidence intervals. In practice, much application of likelihood inference relies on first order asymptotic results such as the central limit theorem. The approximations can, however, be rather poor if the sample size is small or, generally, when the average information available per parameter is limited. Thanks to the great progress made over the past twenty-five years or so in the theory of likelihood inference, very accurate approximations to the distribution of statistics such as the likelihood ratio have been developed. These not only provide modifications to well-established approaches, which result in more accurate inferences, but also give insight on when to rely upon first order methods. We refer to these developments as *higher order asymptotics*.

One intriguing feature of the theory of higher order likelihood asymptotics is that relatively simple and familiar quantities play an essential role. The higher order approximations discussed in this paper are for the significance function, which we will use to set confidence limits or to calculate the p-value associated with a particular hypothesis of interest. We start with a concise overview of the approximations used in the remainder of the paper. Our first example is an elementary one-parameter model where one can perform the calculations easily, chosen to illustrate the potential accuracy of the procedures. Two more elaborate examples, an application of binary logistic regression and a nonlinear growth curve model, follow. All examples are carried out using the R code of the `hoa` package bundle.

Basic ideas

Assume we observed n realizations $y_1, \ldots, y_n$ of independently distributed random variables $Y_1, \ldots, Y_n$ whose density function $f(y_i;\theta)$ depends on an unknown parameter θ. Let $\ell(\theta) = \sum_{i=1}^n \log f(y_i;\theta)$ denote the corresponding log likelihood and $\hat\theta = \text{argmax}_\theta \ell(\theta)$ the maximum likelihood estimator. In almost all applications the parameter θ is not scalar but a vector of length d. Furthermore, we may re-express it as $\theta = (\psi, \lambda)$, where ψ is the d_0-dimensional *parameter of interest*, about which we wish to make inference, and λ is a so-called *nuisance parameter*, which is only included to make the model more realistic.

Confidence intervals and p-values can be computed using the *significance function* $p(\psi;\hat\psi) = \Pr(\hat\Psi \le \hat\psi;\psi)$ which records the probability left of the observed "data point" $\hat\psi$ for varying values of the unknown parameter ψ (Fraser, 1991). Exact elimination of λ, however, is possible only in few special cases (Severini, 2000, Sections 8.2 and 8.3). A commonly used approach is to base inference about ψ on the *profile log likelihood* $\ell_\mathrm{p}(\psi) = \ell(\psi, \hat\lambda_\psi)$, which we obtain from the log likelihood function by replacing the nuisance parameter with its constrained estimate $\hat\lambda_\psi$ obtained by maximising $\ell(\theta) = \ell(\psi, \lambda)$ with respect to λ for fixed ψ. Let $j_\mathrm{p}(\psi) = -\partial^2 \ell_\mathrm{p}(\psi)/\partial\psi\partial\psi^\top$ denote the observed information from the profile log likelihood. Likelihood inference for scalar ψ is typically based on the

- Wald statistic, $w(\psi) = j_\mathrm{p}(\hat\psi)^{1/2}(\hat\psi - \psi)$;
- likelihood root,
  $$r(\psi) = \text{sign}(\hat\psi - \psi)\left[2\{\ell_\mathrm{p}(\hat\psi) - \ell_\mathrm{p}(\psi)\}\right]^{1/2};$$
  or
- score statistic, $s(\psi) = j_\mathrm{p}(\hat\psi)^{-1/2} d\ell_\mathrm{p}(\psi)/d\psi$.

Under suitable regularity conditions on $f(y;\theta)$, all of these have asymptotic standard normal distribution up to the first order. Using any of the above statistics we can approximate the significance function by $\Phi\{w(\psi)\}$, $\Phi\{r(\psi)\}$ or $\Phi\{s(\psi)\}$. When $d_0 > 1$, we may use the quadratic forms of the Wald, likelihood root and score statistics whose finite sample distribution is $\chi^2_{d_0}$ with d_0 degrees of freedom up to the second order. We refer the reader to Chapters 3 and 4 of Severini (2000) for a review of first order likelihood inference.

Although it is common to treat $\ell_{\mathrm{p}}(\psi)$ as if it were an ordinary log likelihood, first order approximations can give poor results, particularly if the dimension of λ is high and the sample size small. An important variant of the likelihood root is the *modified likelihood root*

$$r^*(\psi) = r(\psi) + \frac{1}{r(\psi)} \log\{q(\psi)/r(\psi)\}, \qquad (1)$$

where $q(\psi)$ is a suitable correction term. Expression (1) is a higher order pivot whose finite sample distribution is standard normal up to the third order. As it was the case for its first order counterpart r, the significance function is approximated by $\Phi\{r^*(\psi)\}$, and there is a version of r^* for multidimensional ψ (Skovgaard, 2001, Section 3.1). More details about the computation of the $q(\psi)$ correction term are given in the Appendix.

It is sometimes useful to decompose the modified likelihood root as

$$r^*(\psi) = r(\psi) + r_{\mathrm{inf}}(\psi) + r_{\mathrm{np}}(\psi),$$

where r_{inf} is the *information adjustment* and r_{np} is the *nuisance parameter adjustment*. The first term accounts for non normality of r, while the second compensates r for the presence of the nuisance parameter λ. Pierce and Peters (1992, Section 3) discuss the behaviour of these two terms in the multiparameter exponential family context. They find that while r_{np} is often appreciable, the information adjustment r_{inf} has typically a minor effect, provided the ψ-specific information $j_{\mathrm{p}}(\hat{\psi})$ is not too small relative to the dimension of λ.

A simple example

Suppose that a sample $y_1, \ldots, y_n$ is available from the Cauchy density

$$f(y;\theta) = \frac{1}{\pi\{1 + (y-\theta)^2\}}. \qquad (2)$$

The maximum likelihood estimate $\hat{\theta}$ of the unknown location parameter θ is the value which maximises the log likelihood function

$$\ell(\theta; y) = -\sum_{i=1}^{n} \log\{1 + (y_i - \theta)^2\}.$$

For $n = 1$, we obtain the exact distribution of $\hat{\theta} = y$ from (2) as $F(\hat{\theta};\theta) = F(y;\theta) = \pi^{-1}\arctan(y-\theta)$.

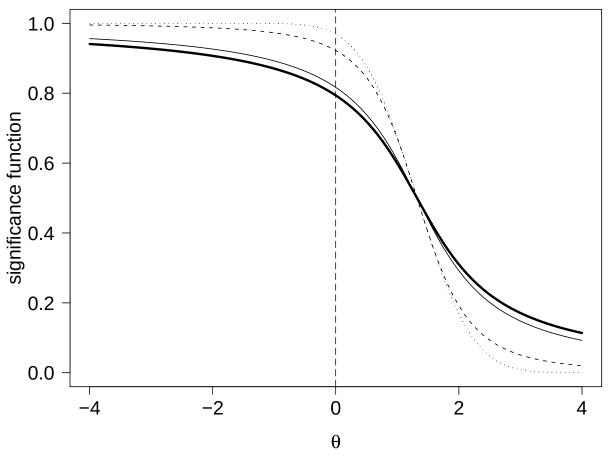

Figure 1: Significance functions for the location parameter of a Cauchy distribution when $y = 1.32$: exact (bold), Wald pivot (dotted), r (dashed) and r^* (solid). The vertical dashed line corresponds to the null hypothesis $\theta = 0$.

Assume that $y = 1.32$ was observed. In Figure 1 we compare the exact significance function $p(\theta; y) = \Pr(Y \leq y; \theta)$ (bold line) to the two first order approximations obtained from the Wald statistic

$$w(\theta) = \sqrt{2}(y - \theta),$$

(dotted line), and from the likelihood root

$$r(\theta) = \mathrm{sign}(\hat{\theta} - \theta)\left[2\log\{1 + (y-\theta)^2\}\right]^{1/2},$$

(dashed line). We also show the third order approximation $\Phi\{r^*(\theta)\}$ (solid line). Since this is a location model and there is no nuisance parameter, the statistic $q(\theta)$ in (1) is the score statistic

$$s(\theta) = \sqrt{2}(y-\theta)/\{1 + (y-\theta)^2\}$$

(see formula (6) in the Appendix). The vertical dashed line corresponds to the null hypothesis that $\theta = 0$. The exact p-value is 0.413, while the first and third order approximations yield 0.0619 (Wald), 0.155 (r) and 0.367 (r^*). The r^* statistic is strikingly accurate, while the first order approximations are very poor. This is surprising if we consider that the score function is not monotonic in y and that only one observation is available. Figure 2 summarises the R code used to generate Figure 1 and obtain the above p-values.

Suppose now that we observed a sample of size $n = 15$ from the Student t distribution with 3 degrees of freedom. It is no longer possible to derive the exact distribution of the maximum likelihood estimator $\hat{\theta}$, but we may use the code provided in the `marg` package of the `hoa` package bundle to compute the p-values for testing the significance of the location parameter.

```
## likelihood pivots
> wald.stat <- function(theta, y) {
+    sqrt(2) * (y - theta) }
> lik.root <- function(theta, y) {
+    sign(y - theta) * sqrt( 2 * log(1 + (y - theta)^2) ) }
> score.stat <- function(theta, y) {
+    ( sqrt(2) * (y - theta) )/( 1 + (y - theta)^2 ) }
> rstar <- function(theta, y) {
+    lik.root(theta, y) + 1/lik.root(theta, y) * log( score.stat(theta, y)/lik.root(theta, y) ) }

## significance functions : Figure 1
> theta.seq <- seq(-4, 4, length = 100)
> par( las = 1, mai = c(0.9, 0.9, 0.2, 0.2) )
> plot( theta.seq, pcauchy( q = 1.32 - theta.seq ), type = "l", lwd = 2, ylim = c(0,1),
+    xlab = expression(theta), ylab = "significance function", cex.lab = 1.5, cex.axis = 1.5 )
> lines( theta.seq, pnorm( wald.stat(theta.seq, 1.32) ), lty = "dotted" )
> lines( theta.seq, pnorm( lik.root(theta.seq, 1.32) ), lty = "dashed" )
> lines( theta.seq, pnorm( rstar(theta.seq, 1.32) ), lty = "solid" )
> abline( v = 0, lty = "longdash" )

## p-values
> 2 * ( min( tp <- pt(1.32, df = 1), 1 - tp ) )
> 2 * ( min( tp <- pnorm( wald.stat(0, 1.32) ), 1 - tp ) )
> 2 * ( min( tp <- pnorm( lik.root(0, 1.32) ), 1 - tp ) )
> 2 * ( min( tp <- pnorm( rstar(0, 1.32) ), 1 - tp ) )
```

Figure 2: R code for drawing Figure 1 and calculating the p-values for testing the significance of the location parameter θ of a Cauchy distribution when $y = 1.32$.

```
## simulated data
> library(marg)
> set.seed(321)
> y <- rt(n = 15, df = 3)
> y.rsm <- rsm(y ~ 1, family = student(3))
> y.cond <- cond(y.rsm, offset = 1)
> summary(y.cond, test = 0)
```

The previous set of instructions yields the p-values 0.282 (Wald), 0.306 (r) and 0.354 (r^*). The difference between first order and higher order approximations is slightly smaller than it was the case before. For this particular model a sample size of $n = 15$ still does not provide enough information on the scalar parameter θ to wipe out completely the effect of higher order corrections.

Higher order asymptotics in R

`hoa` is an R package bundle which implements higher order inference for three widely used model classes: logistic regression, linear non normal models and nonlinear regression with possibly non homogeneous variance. The corresponding code is organised in three packages, namely `cond`, `marg` and `nlreg`. We already saw a (very elementary) application of the `marg` code. The two examples which follow will give a glimpse of the use of the routines in `cond` and `nlreg`. Attention is restricted to the calculation of p-values and confidence intervals, although several routines for accurate point estimation and model checking are also available. The `hoa` bundle includes a fourth package, called `sampling`, which we will not discuss here. It implements a Metropolis-Hastings sampler which can be used to simulate from the conditional distribution of the higher order statistics considered in `marg`.

The `hoa` package bundle will soon be available on CRAN. More examples of applications, and generally of the use of likelihood asymptotics, are given in Brazzale et al. (to appear).

Example 1: Binary data

Collet (1998) gives a set of binary data on the presence of a sore throat in a sample of 35 patients undergoing surgery during which either of two devices was used to secure the airway. In addition to the variable of interest, device `type` (1=tracheal tube or 0=laryngeal mask), there are four further explanatory variables: the `age` of the patient in years, an indicator variable for `sex` (1=male, 0=female), an indicator variable for `lubricant` use (1=yes, 0=no) and the `duration` of the surgery in minutes. The observations form the data frame `airway` which is part of the `hoa` bundle.

A natural starting point for the analysis is a logistic regression model with success probability of the form

$$\Pr(Y = 1; \beta) = \frac{\exp(x^\top \beta)}{1 + \exp(x^\top \beta)},$$

where x represents the explanatory variables associated with the binary `response` Y (1=sore throat and 0=no sore throat). The following set of instructions fits this model to the data with all five explanatory variables included.

```
## binomial model fit
> airway.glm <- glm( formula(airway),
+    family = binomial, data = airway )
> summary( airway.glm )

[omitted]

Coefficients:
            Estimate Std. Error z value Pr(>|z
(Intercept) -2.75035    2.08914  -1.316   0.18
age          0.02245    0.03763   0.597   0.55
sex1         0.32076    1.01901   0.315   0.75
lubricant1   0.08448    0.97365   0.087   0.93
duration     0.07183    0.02956   2.430   0.01
type1       -1.62968    0.94737  -1.720   0.08

[omitted]
```

The coefficient of device `type` is only marginally significant.

As in the previous example we may wonder whether the sample size is large enough to allow us to rely upon first order inference. For the airway data we have $n = 35$ and $p = 5$, so we might expect higher order corrections to the usual approximations to have little effect. We can check this using the routines in the `cond` package.

```
## higher order inference
> library(cond)
> airway.cond <- cond( airway.glm,
+    offset = type1 )
> summary( airway.cond )
#    produces 95% confidence intervals
```

As our model is a canonical exponential family, the correction term $q(\psi)$ in (1) involves the Wald statistic $w(\psi)$ plus parts of the observed information matrix (see formula (5) in the Appendix). The 95% confidence intervals obtained from the Wald pivot and from the likelihood root are respectively $(-3.486, 0.227)$ and $(-3.682, 0.154)$. The third order statistic r^* yields a 95% confidence interval of $(-3.130, 0.256)$. First and third order results are rather different, especially with respect to the lower bound.

[1]Technical details are omitted from the output.

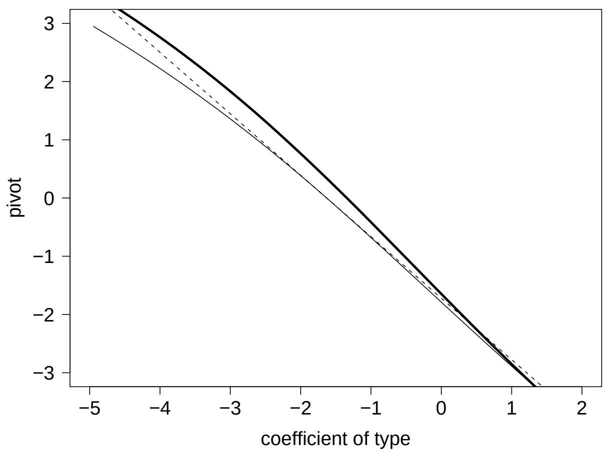

Figure 3: `airway` data analysis: profile plots of the pivots $w(\psi)$ (dashed line), $r(\psi)$ (solid line) and $r^*(\psi)$ (bold line), where ψ is the coefficient of the covariate device `type`.

Figure 3 plots the profiles of the first and third order pivots $w(\psi)$ (dashed line), $r(\psi)$ (solid line) and $r^*(\psi)$ (bold line). The correction term $q(\psi)$ is particularly significant for values of ψ belonging to the lower half of the confidence interval. The nuisance parameter correction is $r_{\text{np}} = 0.51$, while $r_{\text{inf}} = 0.059$ is about ten times smaller.

Example 2: Nonlinear regression

A simple illustration of nonlinear regression is Example 7.7 of Davison and Hinkley (1997), which refers to the `calcium` data of package `boot`. This data set records the calcium uptake (in nmoles/mg) of cells y as a function of time x (in minutes), after being suspended in a solution of radioactive calcium. There are 27 observations in all. The model is

$$y_i = \beta_0\{1 - \exp(-\beta_1 x_i)\} + \sigma_i \varepsilon_i, \qquad (3)$$

where β_0 and β_1 are unknown regression coefficients and the error term $\varepsilon_i \sim N(0, 1)$ is standard normal. We complete the definition of model (3) by allowing the response variance $\sigma_i^2 = \sigma^2(1 + x_i)^\gamma$ to depend nonlinearly on the time covariate through the two variance parameters γ and σ^2.

Figure 4 gives the R code for the analysis. The variables `cal` and `time` represent respectively the calcium uptake and suspension time. Model (3) is fitted by maximum likelihood using the `nlreg` routine of package `nlreg`, which yields $\hat{\beta}_0 = 4.317$ (s.e. 0.323), $\hat{\beta}_1 = 0.207$ (s.e. 0.036), $\hat{\gamma} = 0.536$ (s.e. 0.320), and $\log \hat{\sigma}^2 = -2.343$ (s.e. 0.634). Note that the baseline variance σ^2 is fitted on the logarithmic scale. This does not affect inference based on the r and r^* statistics, which are parametrisation invariant, and ensures positive values for σ^2 when the Wald statistic

```
> library(boot)
> library(nlreg)

## maximum likelihood fit
> calcium.nl <- nlreg( cal ~ b0 * (1 - exp(-b1 * time)), weights = ~ (1 + time)^g,
+    data = calcium, start = c(b0 = 4, b1 = 0.1, g = 0) )
> summary( calcium.nl )    # yields estimates and standard errors

## pivot profiling for \gamma
> calcium.prof <- profile( calcium.nl, offset = g )
> summary( calcium.prof )

 Two-sided confidence intervals for g
                  lower upper
r* - Fr (0.95) -0.14340 1.191
r* - Sk (0.95) -0.14320 1.190
r (0.95)       -0.12441 1.154
Wald (0.95)    -0.08991 1.163

  Estimate Std. Error
g   0.5364     0.3196

[omitted]

## inference on proportion of maximum
> calcium.nl <- nlreg( cal ~ b0 * (1 - exp(- log(1 + exp(psi)) * time / 15)),
+    data = calcium, start = c(b0 =4.3, psi =2) )
> calcium.prof <- profile( calcium.nl, offset = psi )
> calcium.sum <- summary( calcium.prof )
> exp(calcium.sum$CI) / (1 + exp(calcium.sum$CI))    # 95% confidence intervals for \pi

## profile and contour plots : Figure 5
> calcium.prof <- profile( calcium.nl )
> par( las = 1, mai = c(0.5, 0.5, 0.2, 0.2) )
> contour( calcium.prof, alpha = 0.05, cl1 = "black", cl2 = "black", lwd2 = 2 )
```

Figure 4: `calcium` uptake data analysis: R code for model fitting and pivot profiling for different parameters of interest (variance parameter γ and "proportion of maximum" π).

is used. Figure 4 shows also how to use the `profile` method of the `nlreg` package to set various first and higher order 95% confidence intervals for the variance parameter γ.[1] A difficulty we had not to face in the previous two examples is that it is no longer possible to calculate the correction term in (1) exactly. The `profile` function implements two slightly different versions of the higher order pivot r^* which we obtain by using the two approximations of $q(\psi)$ discussed in the Appendix. The four statistics agree in letting us question the heterogeneity of the response variance.

Davison and Hinkley (1997, p. 356) consider not only inference on the nonlinear mean function, but also on other aspects of the model such as the "proportion of maximum", $\pi = 1 - \exp(-\beta_1 x)$. For $x = 15$ minutes they give the estimate $\hat{\pi} = 0.956$ and the associated 95% bootstrap confidence interval $(0.83, 0.98)$. We may obtain the corresponding first and higher order likelihood analogues by reparametrizing the mean response curve into (π, β_0) and re-running the whole analysis. This time we assume that the response variance is homogeneous. Because of the constraint that π must lie in the interval $(0, 1)$, we actually fit the model for $\psi = \log\{\pi/(1-\pi)\}$ and back-transform to the original scale by $\pi = \exp(\psi)/\{1 + \exp(\psi)\}$. This yields the intervals $(0.87, 0.99)$ and $(0.88, 0.99)$ for respectively the Wald and likelihood root statistics and $(0.87, 0.99)$ for both versions of r^*, which is in agreement with the bootstrap simulation.

The `profile` method of the `nlreg` package provides also all elements needed to display graphically a fitted nonlinear model, as done for instance in Figure 5 with respect to the second model fit. The `contour` method of the `nlreg` package represents, in fact, an enhanced version of the original algorithm by Bates and Watts (1988, Chapter 6), to which we refer the reader for the interpretation of these plots. The dashed, solid and bold lines represent respectively the Wald pivot, the likelihood root r and Skovgaard's (1996) approximation to the r^* statistic

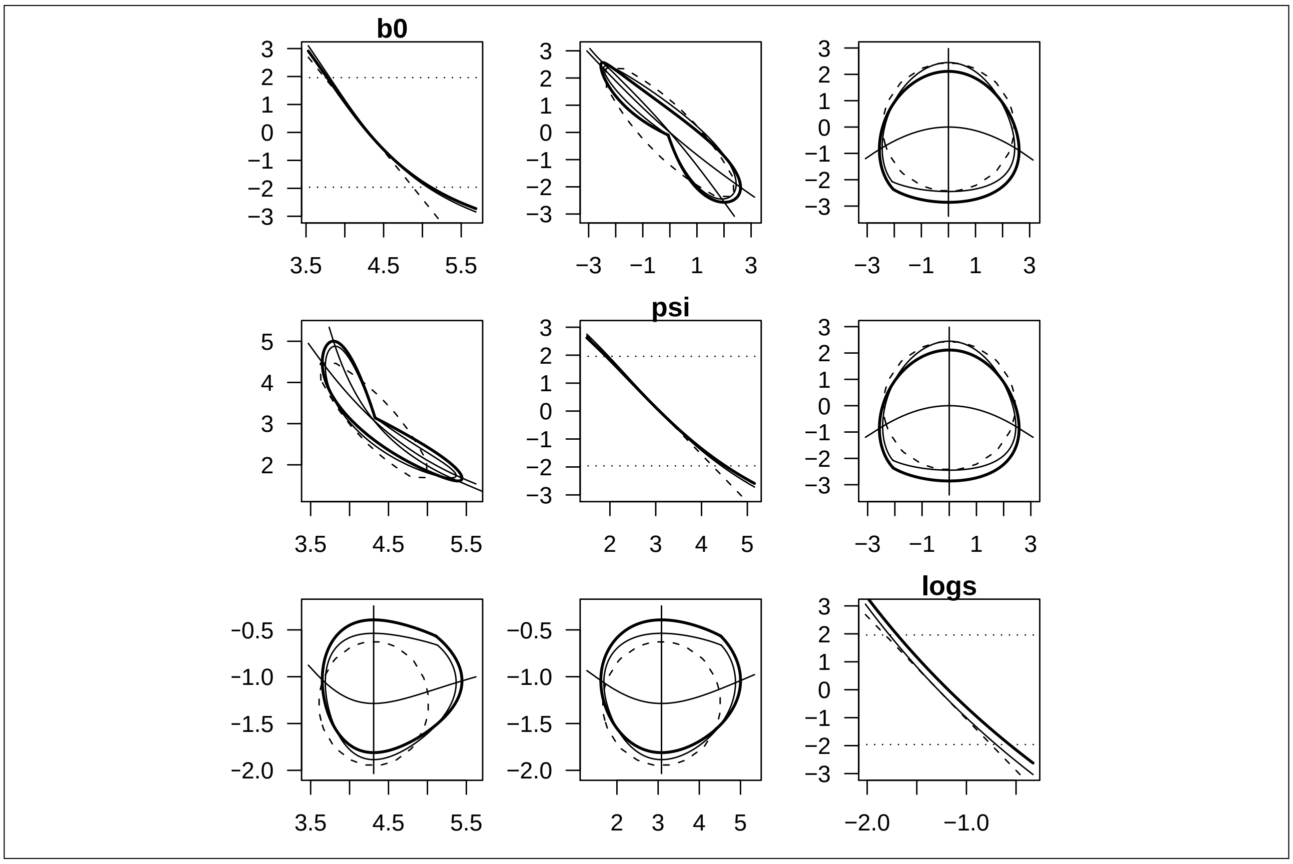

Figure 5: `calcium` uptake data analysis: profile plots and profile pair sketches for the parameters β_0, ψ and $\log \sigma^2$ using the Wald statistic (dashed), the likelihood root r (solid) and Skovgaard's (1996) approximation to r^* (bold).

(see the Appendix). The bivariate contour plots in the lower triangle are plotted on the original scale, whereas the ones in the upper triangle are on the r scale. Figure 5 highlights different aspects of the model fit. First, the maximum likelihood estimate of $\log \sigma^2$ is biased downwards, which we can tell from the fact the corresponding r^* profile is shifted to the right of r. Otherwise, there does not seem to be a huge difference between first and higher order methods as the corresponding profiles and contours are not too different. The finite sample estimates of β_0 and ψ are strongly correlated, while they are almost independent of $\log \hat{\sigma}^2$. The contours of $r(\psi)$ and $r^*(\psi)$ are close to elliptic which indicates that the log likelihood function is not too far from being quadratic. A further indication for a small curvature effect due to parametrisation is that the contours on the original and on the r scale look similar.

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Appendix: $q(\psi)$ correction term

In this appendix we give the general expression of the correction term $q(\psi)$ in (1) and the explicit formulae for two special model classes, that is, linear exponential families and regression-scale models. We will furthermore discuss two ways of approximating $q(\psi)$ in case we cannot calculate it explicitly.

Basic expression

Let $\ell(\theta) = \ell(\psi, \lambda)$ be the log likelihood function, $\hat{\theta} = (\hat{\psi}, \hat{\lambda})$ the maximum likelihood estimator of the d-dimensional parameter $\theta = (\psi, \lambda)$, and $j(\theta) = -\partial^2 \ell(\theta)/\partial\theta\partial\theta^\top$ the $d \times d$ observed information matrix. Denote $\hat{\lambda}_\psi$ the constrained maximum likelihood estimator of the nuisance parameter λ given the value of the scalar parameter of interest ψ. Write $j_{\lambda\lambda}(\theta)$ the corner of $j(\theta) = j(\psi, \lambda)$ which corresponds to λ, and $\hat{\theta}_\psi = (\psi, \hat{\lambda}_\psi)$.

The basic expression for $q(\psi)$ is

$$q(\psi) = \frac{|\ell_{;\hat\theta}(\hat\theta) - \ell_{;\hat\theta}(\hat\theta_\psi) \quad \ell_{\lambda^\top;\hat\theta}(\hat\theta_\psi)|}{\{|j_{\lambda\lambda}(\hat\theta_\psi)||j(\hat\theta)|\}^{1/2}}, \qquad (4)$$

where $|\cdot|$ indicates determinant (Severini, 2000, Section 7.4.1). The $d \times d$ matrix appearing in the numerator of $q(\psi)$ consists of a column vector formed using so-called *sample space derivatives*

$$\ell_{;\hat\theta}(\theta) = \frac{\partial \ell(\theta; \hat\theta|a)}{\partial \hat\theta},$$

and a $d \times (d-1)$ matrix of *mixed derivatives*

$$\ell_{\lambda^\top;\hat\theta} = \frac{\partial^2 \ell(\psi, \lambda; \hat\theta|a)}{\partial \lambda^\top \partial \hat\theta}.$$

The former are defined as the derivatives of the log likelihood function $\ell(\psi, \lambda; \hat\theta|a)$ with respect to the maximum likelihood estimator $\hat\theta$; mixed derivatives furthermore involve differentiation with respect to the whole parameter θ or parts of it (Severini, 2000, Section 6.2.1). Note that to do so, the data vector has to be re-expressed as $y = (\hat\theta, a)$, where a represents the observed value of an ancillary statistic upon which we condition.

Approximations

Exact computation of the sample space derivatives involved in expression (4) requires that we are able to write the data vector y as a function of the maximum likelihood estimator $\hat\theta$ and of an ancillary statistic a. This is, with few exceptions, only feasible for linear exponential families and transformation models, in which cases the $q(\psi)$ term involves familiar likelihood quantities. If the reference model is a full rank exponential family with ψ and λ taken as canonical parameters, the correction term

$$q(\psi) = w(\psi)\,\{|j_{\lambda\lambda}(\hat\theta)|/|j_{\lambda\lambda}(\hat\theta_\psi)|\}^{1/2} \qquad (5)$$

depends upon the Wald statistic. In case of a regression-scale model, that is, of a linear regression model with non necessarily normal errors,

$$q(\psi) = s(\psi)\,\{|j_{\lambda\lambda}(\hat\theta_\psi)|/|j_{\lambda\lambda}(\hat\theta)|\}^{1/2} \qquad (6)$$

involves the score statistic. Here, ψ is linear in (β, σ) and the nuisance parameter λ is taken linear in β and $\xi = \log\sigma$, where β and σ represent respectively the regression coefficients and the scale parameter.

In general, the calculation of the sample space derivatives $\ell_{;\hat\theta}(\theta)$ and mixed derivatives $\ell_{\lambda^\top;\hat\theta}(\theta)$ may be difficult or impossible. To deal with this difficulty, several approximations were proposed. For a comprehensive review we refer the reader to Section 6.7 of Severini (2000). Here we will mention two of them. A first approximation, due to Fraser et al. (1999), is based upon the idea that in order to differentiate the likelihood function $\ell(\theta; \hat\theta|a)$ on the surface in the n-dimensional sample space defined by conditioning on a we need not know exactly the transformation from y to $(\hat\theta, a)$, but only the d vectors which are tangent to this surface (Severini, 2000, Section 6.7.2). Skovgaard (1996) on the other hand suggests to approximate the sample space and mixed derivatives by suitable covariances of the log likelihood and of the score vector (Severini, 2000, Section 6.7.3). While the first approximation maintains the third order accuracy of r^*, we lose one degree when following Skovgaard's (1996) approach. See Sections 7.5.3 and 7.5.4 of Severini (2000) for the details.

The `hoa` package

The expressions of $q(\psi)$ implemented in the `hoa` package bundle are: i) (5) and (6) for respectively the `cond` and `marg` packages (logistic and linear non normal regression), and ii) the two approximations discussed above for the `nlreg` package (nonlinear heteroscedastic regression). The formulae are given in Brazzale et al. (to appear). The `nlreg` package also implements Skovgaard's (2001, Section 3.1) multiparameter extension of the modified likelihood root. The implementation of the `cond` and `nlreg` packages is discussed in Brazzale (1999) and Bellio and Brazzale (2003).

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Fitting linear mixed models in R

Using the lme4 package

by Douglas Bates

The lme function, which fits linear mixed models of the form described in Pinheiro and Bates (2000), has been available in the required R package nlme for several years. Recently my colleagues and I have been developing another R package, called lme4, and its lmer function which provides more flexible fitting of linear mixed models and also provides extensions to generalized linear mixed models.

The good news for lme users is that the lmer function fits a greater range of models, is more reliable, and is faster than the lme function. The bad news is that the model specification has been changed slightly. The purpose of this article is to introduce lmer, to describe how it can be used to fit linear mixed models and to highlight some of the differences between lmer and lme.

Linear mixed models

Before describing how to fit linear mixed models I will describe what they are. In building a statistical model for experimental or observational data we often want to characterize the dependence of a response, such as a patient's heart rate, on one or more covariates, such as the patient identifier, whether the patient is in the treatment group or the control group, and the time under treatment. We also want to characterize the "unexplained" variation in the response. Empirical models (i.e., models that are derived from the data itself, not from external assumptions on the mechanism generating the data) are generally chosen to be linear in the parameters as these are much simpler to use than are nonlinear models.

Some of the available covariates may be repeatable in the sense that (conceptually, at least) we can obtain new observations with the same values of the covariate as in the current study. For example, we can recruit a new patient to the study and assign this patient to the treatment group or to the control group. We can then observe this patient's heart rate at one minute, five minutes, etc. after treatment. Hence we would regard both the treatment factor and the time after treatment covariate as repeatable.

A factor is repeatable if the set of possible levels of the factor is fixed and each of these levels is itself repeatable. In most studies we would not regard the patient identifier factor (or, more generally, the "subject" factor or any other factor representing an experimental unit) as being repeatable. Instead we regard the subjects in the study as a random sample from the population of interest.

Our goals in modeling repeatable covariates and non-repeatable covariates are different. With a repeatable covariate we want to characterize the change in the response between different levels and for this we use *fixed-effects* terms that represent, say, the typical rate of change of the response with respect to time under treatment or the difference between a typical response in the treatment and the control groups. For a non-repeatable covariate we want to characterize the variation induced in the response by the different levels of the covariate and for this we use *random-effects* terms.

A statistical model that incorporates both fixed-effects terms and random-effects terms is called a *mixed-effects model* or, more simply, a *mixed model*.

Single grouping factor

As indicated above, a random effect is associated with a *grouping factor*, which would be the patient identifier in our example, and possibly with other covariates. We specify a random-effects term in lmer by a linear model term and a grouping factor separated by '|', which we would read as "given" or "conditional on". That is, a random effect is a linear model term conditional on the level of the grouping factor.

Because the precedence of '|' as an operator is lower than most other operators used in linear model formulae, the entire random-effects expression should be enclosed in parentheses.

Many models for longitudinal data (repeated measurements over time on each of several subjects) incorporate random effects associated with a single grouping factor. Consider the `HR` (heart rate) data from the `SASmixed` package

```
> data("HR", package = "SASmixed")
> names(HR)

[1] "Patient" "Drug"    "baseHR"
[4] "HR"      "Time"
```

Initially we fit a linear mixed model with fixed-effects terms for the base heart rate, the time since administration of the medication, the type of drug and the time/drug interaction. The random effect associated with the patient is a simple additive shift.

```
> (fm1 <- lmer(HR ~ baseHR + Time *
+     Drug + (1 | Patient), HR))

Linear mixed-effects model fit by REML
Formula: HR ~ baseHR+Time*Drug+(1|Patient)
   Data: HR
   AIC   BIC logLik MLdeviance REMLdeviance
 790.7 815.8 -386.3      791.9        772.7
Random effects:
 Groups   Name        Variance Std.Dev.
 Patient  (Intercept) 44.5     6.67
 Residual             29.8     5.46
# of obs: 120, groups: Patient, 24

Fixed effects:
            Estimate Std. Error  DF
(Intercept)   33.962      9.931 113
baseHR         0.588      0.118 113
Time         -10.698      2.421 113
Drugb          3.380      3.784 113
Drugp         -3.778      3.802 113
Time:Drugb     3.512      3.424 113
Time:Drugp     7.501      3.424 113
            t value Pr(>|t|)
(Intercept)    3.42  0.00087
baseHR         4.97  2.5e-06
Time          -4.42  2.3e-05
Drugb          0.89  0.37358
Drugp         -0.99  0.32244
Time:Drugb     1.03  0.30717
Time:Drugp     2.19  0.03050
```

The first few lines of the output state that the model has been fit using the REML (restricted or residual maximum likelihood) criterion and indicate the formula and the data set used. The next line provides several measures of the quality of the fit including Akaike's Information Criterion, Schwartz's Bayesian Information Criterion, the log-likelihood (actually the log-restricted likelihood because REML is being used) and the ML and REML versions of the deviance.

The estimates of the variance components are given next. Note that the column headed *Std.Dev.* is **not** the standard error of the estimate of the variance component. It is simply the square root of the estimated variance and is included because many people (and I am one) find it easier to interpret an estimated standard deviation instead of an estimated variance.

Finally the estimates for the fixed-effects coefficients are summarized. If we wish to consider the significance of terms rather than individual coefficients we can use a single-argument call to the `anova` generic which provides the sequential sums of squares and the corresponding F tests.

```
> anova(fm1)

Analysis of Variance Table
          Df Sum Sq Mean Sq Denom
baseHR     1    746     746   113
Time       1    753     753   113
Drug       2     87      43   113
Time:Drug  2    143      72   113
          F value  Pr(>F)
baseHR      25.05 2.1e-06
Time        25.28 1.9e-06
Drug         1.46   0.237
Time:Drug    2.40   0.095
```

At present the denominator degrees of freedom shown in the coefficient table and in the analysis of variance table are upper bounds. In a sense there is no "correct" denominator degrees of freedom because the F test is always an approximation for these models. But, even taking this into account, it is still the case that the denominator degrees of freedom for the `Drug` term should be lower than shown. The reason that these degrees of freedom are not more accurately approximated at present is because it is difficult to decide exactly how this should be done for the general models described below.

Before changing the fixed effects terms in the model we may wish to examine models with more general specifications of the random effects, such as both a random intercept and a random slope (with respect to time) for each patient.

```
> VarCorr(fm2 <- lmer(HR ~ baseHR +
+     Time * Drug + (Time | Patient),
+     HR))

 Groups   Name        Variance Std.Dev.
 Patient  (Intercept) 60.6     7.79
          Time        37.8     6.15
 Residual             24.4     4.94
 Corr


 -0.563
```

```
> head(model.matrix(~Time, HR), n = 3)

  (Intercept)    Time
1           1 0.01667
2           1 0.08333
3           1 0.25000

> head(ranef(fm2)$Patient, n = 3)

    (Intercept)     Time
201       0.871  4.04733
202      -9.341  6.79574
203       5.005 -0.07822

> anova(fm1, fm2)

Data: HR
Models:
fm1:HR ~ baseHR+Time*Drug+(1|Patient)
fm2:HR ~ baseHR+Time*Drug+(Time|Patient)
    Df  AIC  BIC logLik Chisq Chi Df
fm1  9  810  835   -396
fm2 11  810  841   -394  3.77      2
    Pr(>Chisq)
fm1
fm2       0.15
```

To save space I summarized this fitted model using VarCorr which describes only the estimates of the variance components. Notice that the expression Time generates a model matrix (model.matrix) with two columns, (Intercept) and Time, so there are two random effects associated with each patient. The distribution of the random effects is a bivariate normal distribution with mean zero and a positive-definite 2×2 variance-covariance matrix. The estimates of the two variances and the estimated correlation are given in the output.

The ranef generic function returns the BLUPs (Best Linear Unbiased Predictors) of the random effects and anova provides a likelihood ratio test when given multiple model fits to the same data set. As described in Pinheiro and Bates (2000), the p-value calculated for this test will be conservative (i.e. it is an upper bound on the true p-value) because the parameter space is bounded and in the null hypothesis one of the parameters is at the boundary.

Multiple random-effects expressions

As shown above, the estimated variance-covariance matrix from a random-effects expression, such as (Time|Patient), for which the model matrix has multiple columns is a general, positive-definite, symmetric matrix. ("General" in the sense that there are no constraints imposed on this matrix other than its being positive-definite.)

Occasionally we wish to impose further constraints such as independence of random effects associated with the same grouping factor. For example we can fit a model with an intercept and slope for each patient but assuming independence of these random effects with

```
> VarCorr(fm3 <- lmer(HR ~ baseHR +
+     Time * Drug + (1 | Patient) +
+     (Time - 1 | Patient), HR))

 Groups   Name        Variance Std.Dev.
 Patient  (Intercept) 47.9     6.92
 Patient  Time        25.0     5.00
 Residual             25.6     5.06

> anova(fm1, fm3, fm2)

Data: HR
Models:
fm1: HR~baseHR+Time*Drug+(1|Patient)
fm3: HR~baseHR+Time*Drug+(1|Patient)
      +(Time-1|Patient)
fm2: HR~baseHR+Time*Drug+(Time|Patient)
    Df  AIC  BIC logLik Chisq Chi Df
fm1  9  810  835   -396
fm3 10  811  839   -396  0.84      1
fm2 11  810  841   -394  2.93      1
    Pr(>Chisq)
fm1
fm3      0.358
fm2      0.087
```

The fitted model fm3 has a random intercept and a random slope for each patient, as does fm2, but in fm3 these random effects are assumed to be independent within patient. Hence fm3 uses one fewer degree of freedom than does fm2.

In general the random effects from each expression are modeled as independent. If the model matrix from the ith random-effects expression has q_i columns and the grouping factor has k_i levels (this number is well-defined because unused levels are dropped during construction of the model frame) the corresponding random effects vector has length $k_i q_i$ and could be arranged as a $k_i \times q_i$ matrix as shown in the ranef output above. The rows share a common $k_i \times k_i$ variance-covariance matrix. Different rows are independent.

Nested and non-nested grouping factors

We have seen an example of multiple random-effects expressions for the same grouping factor. It is more common to create random-effects expressions associated with different grouping factors. For example in a multicenter trial we may have observations over time on each of several patients at each of several institutions and it could be appropriate to use random effects for both patient and institution.

If each patient is observed at only one institution we say that the levels of patient are *nested* within the levels of institution; otherwise the factors are non-nested. Notice that it only takes one patient migrating between institutions to cause the grouping factors to lose the nesting property. This may not be a primary concern in the analysis of multicenter trials but it is an important issue in the analysis of student test scores over time where it is quite common to have some portion of the students observed at multiple schools. In these cases analysis of the data as if students were nested within schools is at best an approximation and at worst quite inappropriate.

A major distinction between `lme` and `lmer` is that `lme` is optimized for nested grouping factors whereas `lmer` handles nested and non-nested grouping factors equally easily. In `lmer` one simply provides multiple random-effects expressions and the determination of nested or non-nested is done in the code.

Consider the `star` data (Student Teacher Achievement Ratio) from the `mlmRev` package. These data are from a large study - 26,796 observations on a total of 11,598 students in 80 schools. We inferred teacher ids from characteristics of the teacher and classroom, resulting in 1387 distinct teacher ids. (This teacher count is not entirely accurate but it is a reasonable approximation.)

We fit an initial model to the math test scores.

```
> VarCorr(fm4 <- lmer(math ~ gr +
+     sx + eth + cltype + (yrs |
+     id) + (yrs | sch), star))

 Groups   Name        Variance Std.Dev.Corr
 id       (Intercept) 1079.2   32.85
          yrs           22.9    4.78   -0.315
 sch      (Intercept)  292.8   17.11
          yrs           56.8    7.53   -0.777
 Residual              584.1   24.17

> anova(fm4)

Analysis of Variance Table
       Df  Sum Sq Mean Sq   Denom
gr      3 1622511  540837   24566
sx      1    9641    9641   24566
eth     5  192909   38582   24566
cltype  2   63848   31924   24566
       F value  Pr(>F)
gr       925.9 < 2e-16
sx        16.5 4.9e-05
eth       66.0 < 2e-16
cltype    54.6 < 2e-16
```

It happens in this case that the grouping factors `id` and `sch` are not nested but if they were nested there would be no change in the model specification. It is likely that the `lmer` function would converge more rapidly if the grouping factors were nested but even with the nonnested grouping factors in this large study convergence is reasonably fast.

Specifying levels

Because nested and non-nested grouping factors are expressed in exactly the same way, it is not possible to use implicit nesting when specifying the levels of the grouping factors. Implicit nesting occurs when the levels of the "inner" grouping factor are reused for different levels of the "outer" grouping factor. For example, if the patients are numbered starting at patient 1 for each institution then patient 1 at institution 1 is distinguished from patient 1 at institution 2 only if it is assumed that patient is nested within institution.

For `lmer` each distinct experimental unit must correspond to a distinct level in the corresponding grouping factor. It is easy to create a new grouping factor with this property from implicitly nested factors using the interaction operator '`:`'. The `Pixel` data set in the `MEMSS` package has one grouping factor `Dog` and another factor `Side`. If we wish to fit a model with random effects for "side within dog" we must first create a `dog/side` factor as

```
> Pixel$DS <- with(Pixel,Dog:Side)[drop=TRUE]
```

In this case the subset expression `[drop=TRUE]` is not needed but it is a good practice to use it whenever creating such a factor. The expression results in any combinations of levels that does not occur in the data being dropped from the list of levels in the newly created factor.

Summary

The `lmer` function in the `lme4` package fits linear mixed models. There are vast changes in the internals of `lmer` relative to the earlier `lme` function and we hope they will ensure that `lmer` is faster, more reliable, and easier to use than was `lme`. The biggest impact on the user is the change in model specification, which was made so as to clarify the model being fit. The `lmer` function uses a single model formula including random-effects expressions that specify both a linear model term and a grouping factor and can be used to fit models based on multiple nested or non-nested grouping factors. It can also be used to fit generalized linear mixed models but that is a topic for another day.

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Using R for Statistical Seismology

by Ray Brownrigg & David Harte

Statistical Seismology is a relatively new term used to describe the application of statistical methodology to earthquake data. The purpose is to raise new questions about the physical earthquake process, and to describe stochastic components not explained by physical models. Such stochastic quantification allows one to test the validity of various physical hypotheses, and also makes probability forecasts more feasible.

We describe here a suite of R packages, known as the "Statistical Seismology Library" (SSLib). This paper firstly introduces SSLib, providing a little history, and a description of its structure. Then the various components of SSLib are described in more detail and some examples are given. While the packages were developed primarily to analyse earthquake data, two of the packages (Fractal and PtProcess) have more general applicability.

For a general text on seismology, see Lay and Wallace (1995). Further, a large collection of seismological software can be found at `http://orfeus.knmi.nl/other.services/software.links.shtml`.

Introduction to SSLib

The Statistical Seismology Library (SSLib) is a collection of earthquake hypocentral catalogues (3D location of the rupture initiation point, time and magnitude) and R functions to manipulate, describe and model event data contained in the catalogues. At this stage, analyses include graphical data displays, fitting of point process models, estimation of fractal dimensions, and routines to apply the M8 Algorithm. While we have named it the "Statistical Seismology Library", the type of analyses that are performed really only reflect the research interests of the authors. Part of the rationale was to require our students and collaborators to formally document their programs so that others could determine what they were supposed to do, and to be able to use them after they have possibly moved on. Another aim was to make some of our statistical methods and models more directly available to our seismologist and geophysicist colleagues.

The library is divided into a number of R packages. Details of these and source code can all be found on the Statistical Seismology Library web page (`http://homepages.paradise.net.nz/david.harte/SSLib/`). Package names with a specifically seismological character are prefixed by "ss" (e.g. the New Zealand catalogue is named ssNZ), whereas those with a more general statistical interest are not (e.g. PtProcess and Fractal). A reference manual (standard R format) for each package can also be found on the web page, along with a Users Guide that contains examples and shows how the different packages relate to each other (Harte, 2005e).

SSLib was started in 1996 as an S-PLUS library (Harte, 1998). After being ported to the R language in 1999, development of SSLib switched to using the R implementation. At this time, SSLib was only available on the Unix and Linux platforms, but in 2004 a Windows version was released.

Earthquake Catalogues

Generally, users will want to use their own earthquake catalogues. However SSLib does contain various earthquake catalogues including the New Zealand catalogue and the PDE catalogue (Preliminary Determinations of Epicentres) which is a worldwide catalogue collated by the US Geological Survey. Further details of the catalogues available in SSLib can be found on the SSLib web page (see `http://homepages.paradise.net.nz/david.harte/SSLib/`).

The earthquake catalogues are based on raw data available from the World Wide Web. These data are generally collected by national seismological observatories. The raw data appears in many different formats, but the SSLib input routines coerce these different formats into a single common structure. This allows for both a uniformity in analysis, and the ability to make comparisons between the different catalogues. Nevertheless, the data structure within the catalogue packages allows for the inclusion of any number of extra data fields; see Harte (2005e) for further details.

Catalogue Manipulation Utilities

The **ssBase** package (Harte, 2005b) provides catalogue preparation and data manipulation functions. These include functions for date/time formatting, data summaries, printing and data subsetting. This package also contains other functions of a general nature used by the other packages.

A catalogue can be subsetted on any combination of location, time range, depth range or magnitude range, with the location being rectangular (in the latitude/longitude sense), circular (actually cylindrical in 3 dimensions), spherical, or based on an arbitrary polygon on the surface of the earth. Many of the analysis functions will work directly with a subset 'object'.

Exploratory Data Analyses

The **ssEDA** package (Harte, 2005c) consists of functions for exploratory data analysis. In particular these can provide histograms of event depth or event frequency (monthly or yearly), line plots of magnitude over time, maps of the locations of the epicentres, and frequency-magnitude plots to determine a *b*-value (see Figure 2) or to check the completeness of a catalogue. Further, the epicentre maps can identify different magnitudes and depths. Interactive graphics can be used to identify individual events on epicentral plots, and dynamic graphics can be used to show 3-dimensional views with rotation and linked plots.

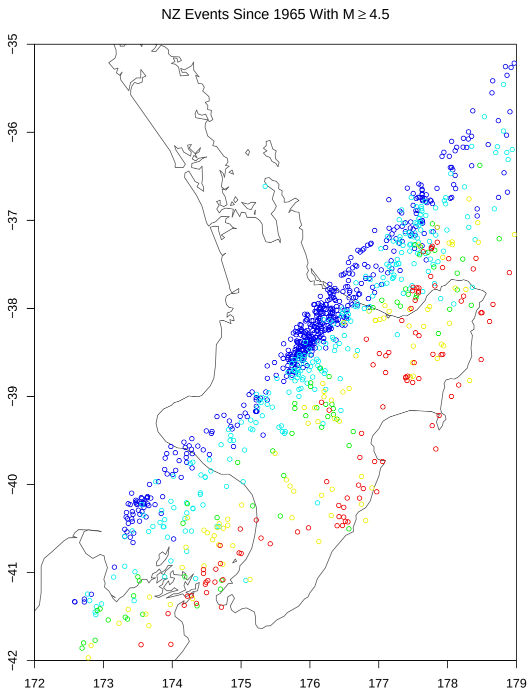

Figure 1: Epicentral plot of events from the NZ catalogue since 1965 with magnitude ≥ 4.5 (1777 events). The Pacific tectonic plate to the east is subducting the Australian plate to the west.

Figure 1 shows a map of the epicentres of a subset of events from the New Zealand catalogue. The colour of the point depicts the depth of the event, with the most shallow events at the red end of the spectrum and the deep events at the blue end of the spectrum. The R commands required to display this plot follow.

```
library(ssNZ)
library(ssEDA)
b <- subset.rect(NZ, minday=julian(1, 1, 1965),
                 minmag=4.5, minlat=-42,
                 maxlat=-35, minlong=172,
                 maxlong=179, mindepth=40)
epicentres(b, depth=c(40, 60, 80, 100, 150,
           200, Inf), mapname="nz",
           criteria=FALSE, cex=0.8,
           usr=c(172, 179, -42, -35))
title(expression(paste("NZ Events Since 1965
      With ", M >= 4.5)))
```

Figure 2 is a frequency-magnitude plot for the same subset as used in Figure 1 and displays the Gutenberg-Richter law (Lay and Wallace, 1995). This law says that the logarithm of the cumulative number of events with magnitude greater than m is linear as a function of m. The R commands required to present this graph (given the call to `subset.rect` from the previous figure) follow.

```
freq.magnitude(b)
title("Frequency Magnitude Power-Law
      Relationship")
```

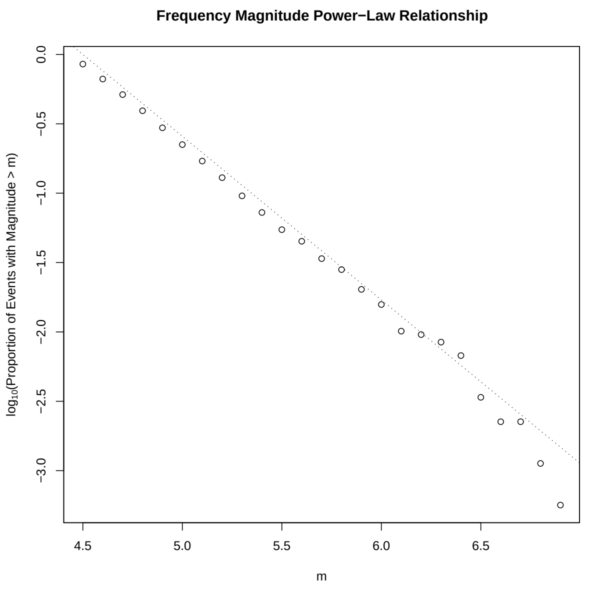

Figure 2: Plot of events from the NZ catalogue since 1965 with magnitude ≥ 4.5 showing the Gutenberg-Richter law. The absolute value of the slope is referred to as the *b*-value and is typically about one.

The interactive graphics is provided by the `epicentres.identify` function through use of the `identify` R function. The dynamic graphics is provided through the `threeD` function, which links to an external viewer provided by the `xgobi` software (Swayne et al., 1998) via the `xgobi` R function. Unfortunately `xgobi` is not easily usable on a Windows system, so work is in progress to use `ggobi` (GGobi) instead.

Point Process Modelling

The **PtProcess** package (Harte, 2004), which can be used independently of the other packages, provides a framework for point process modelling. This includes parameter estimation, model evaluation and simulation. This package is likely to be of most interest to a general statistical audience.

Our **PtProcess** package has a slightly different emphasis to the point process packages **spatstat** (available on CRAN) and **ptproc** (`http://sandybox.typepad.com/software/ptproc/index.html`). Our point process models are for *events* strictly ordered by time, and are conditional on the history of the process up to time t. This could be thought of as the *ground process* (Daley and Vere-Jones, 2003). Other event characteristics could be added as *marks*, e.g. earthquake event magnitude. The **spatstat** package (Baddeley and Turner, 2005) has an emphasis on the spatial location of items, presumably at the same point in time, e.g. tree locations or animals in a forest, etc. Emphasis is then on modelling the spatial intensity. Here marks can be added, e.g. the particular species of tree. The **ptproc** package (Peng, 2003) is derived from our package, and has extended the procedure into multidimensional processes. However, these additional variables are not treated as marks, and hence provides an alternative direction to our intended direction.

While the conditional intensity functions provided within the package have a distinctly seismological flavour, the general methodology and structure of the package is probably applicable to a reasonably large class of point process models. The models fitted are essentially marked point processes (Daley and Vere-Jones, 2003), where the mark distribution has been explicitly built into the conditional intensity function. Our next task is to separate the mark distribution and ground intensity function, and further generalise the framework so that any number of mark distributions can be attached to a given ground intensity function.

Currently the conditional intensity function is the most basic "building block". The conditional intensity function, $\lambda(t|\mathcal{H}_t)$, can be thought of as an instantaneous value of the Poisson rate parameter at time t and is conditional on the history of the process up to but not including t. We have given each conditional intensity function a suffix "`.cif`". There are a number of "generic"-like functions which perform some operation given an intensity function, for example, simulate a process, perform a goodness of fit evaluation, etc.

As an example, consider the ETAS (Epidemic Type Aftershock Sequence) model. This assumes that earthquake events behave in a similar way to an epidemic, where each event reproduces a number of aftershocks. The larger the event, the more aftershocks that will be reproduced. If various criticality conditions are satisfied, the aftershock sequence will eventually die out. See Harte (2004) and Utsu and Ogata (1997) for further technical details about the ETAS model.

The package contains an example dataset provided by Yosihiko Ogata. These data were simulated over the time interval $(0, 800)$. Using these data and approximate maximum likelihood solutions for the parameters contained in `p` (the ETAS model contains 5 parameters), the conditional intensity function can be plotted as follows (see Figure 3).

```
library(PtProcess)
data(Ogata)

p <- c(0.02, 70.77, 0.47, 0.002, 1.25)
ti <- seq(0, 800, 0.5)

plot(ti, log(etas.cif(Ogata, ti, p)),
     ylab=expression(paste("log ", lambda(t))),
     xlab="Time", type="l", xlim=c(0, 800),
     main="Conditional Intensity Function")
```

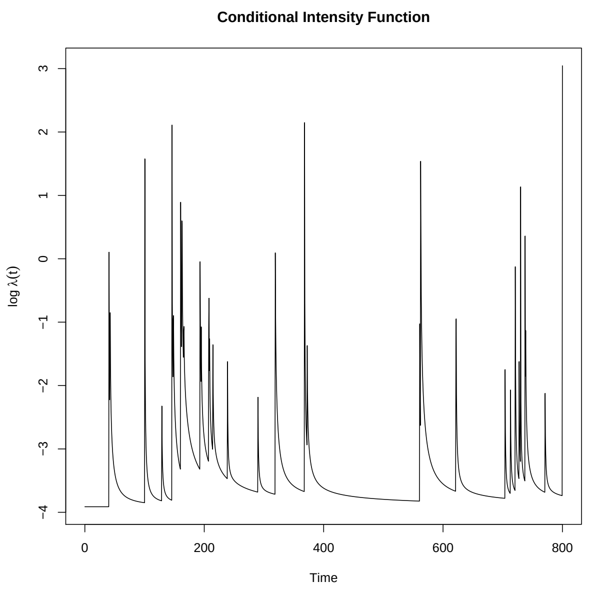

Figure 3: The spikes occur at event times and their heights are proportional to the event magnitudes, with an "Omori" decay (Lay and Wallace, 1995) in the rate after each event.

Further, the log-likelihood can be calculated as follows.

```
pp.LL(Ogata, etas.cif, p, c(0, 800))
```

Using the vector `p` as initial values, maximum likelihood parameter estimates can be calculated as follows.

```
posterior <- make.posterior(Ogata, etas.cif,
                            c(0, 800))
neg.posterior <- function(params)
                     (-posterior(params))
p <- c(0.02, 70.77, 0.47, 0.002, 1.25)
z <- nlm(neg.posterior, p, hessian=TRUE,
         iterlim=1000, typsize=p)
```

The function `make.posterior` creates a log-likelihood function to be evaluated on the time interval $(0, 800)$, and also gives one the option of enforcing constraints on the parameters (none here). We then create a negative posterior function because the function `nlm` is a minimiser. The maximum likelihood parameter estimates are contained within the object `z`.

The creation of the `posterior` function was partly done so that the function to be "optimised" within S-PLUS had only one argument. This is not necessary in R. Further, the use of priors has not been as useful as was initially thought. Consequently, it is probably best to revise the package so that the optimisation works more directly on the `pp.LL` function.

One way to test for the goodness of fit is to calculate the transformed residual process. This effectively creates a new time variable which magnifies or contracts the original process, assuming that the fitted model is correct, in such a manner that the resultant process is a homogeneous Poisson process with rate parameter one. A plot of the transformed event times versus the event number should roughly follow the line $x = y$. Large deviations from this line indicate a poorly fitting model. This can be achieved with the following code.

```
tau <- pp.resid(Ogata, z$estimate, etas.cif)
n <- nrow(Ogata)
plot(1:n, tau, type="l", xlab="Event Number",
     ylab="Transformed Time",
     xlim=c(0, n), ylim=c(0, n))
abline(a=0, b=1, lty=2, col="red")
```

Using the maximum likelihood parameter estimates, one can simulate the process over the subsequent interval $(800, 1200)$, say. This is achieved as follows.

```
x <- pp.sim(Ogata, z$estimate, etas.cif,
           TT=c(800, 1200))
```

The object `x` contains the original `Ogata` data, with the new simulated events appended. One may be interested in forecasting the time taken for an event with magnitude ≥ 6, say, to occur after time 800. One would then perform many such simulations, and determine the empirically simulated distribution for the given event of interest.

As can be seen, the conditional intensity function is the essential ingredient in each of the above analyses, and hence an entity like this is an essential component in a more object oriented setup for these models. It is a relatively simple step to set this up in a more object oriented manner, however, we have held off with this until we have disentangled the conditional intensity into its ground process and a general number of mark distributions.

Other Analyses

The **ssM8** package (Harte, 2005d) implements the Keilis-Borok & Kossobokov M8 algorithm (Keilis-Borok and Kossobokov, 1990). It is an empirically based algorithm that attempts to deduce "times of increased probability". We have been involved in projects that have attempted to test the efficacy of this algorithm.

The **Fractal** package (Harte, 2005a) has been used to calculate various fractal dimensions based on earthquake hypocentral locations, for example, see Harte (2001).

Problems and Future Development

We have already mentioned a number of extensions to the Point Process package: separating the conditional intensity into a ground intensity and a general number of mark distributions, writing more object oriented code, and determining if there is still a need for the `make.posterior` function. To implement more object oriented code, the naming conventions would clearly need to be changed.

There is a difference with the functions contained in the **chron** package (Ripley and Hornik, 2001; Grothendieck and Petzoldt, 2004) and our "datetimes" format in **ssBase** (Harte, 2005b). We would prefer to use the **chron** functions, however, we would like the `format.times` function within **chron** to have greater flexibility, including fractional numbers of seconds. For example, we would like the ability to specify a times format as `hh:mm:ss.s`, or `hh:mm:ss.ss`. Further, many historical earthquake events do not have all date-time components available, and our "datetimes" format has a mechanism to deal with this. Note that the `POSIX` functions are inappropriate, as the event times are generally stored as UTC times.

A feature that we have included in all of our packages is a "changes" manual page. This documents all recent changes made to the package with the date. We have found this particularly useful when old analyses have been repeated and different answers are produced!

As noted earlier, the type of analyses included in SSLib largely reflects our own research interests. This also means that it is continually being changed and augmented.

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Literate programming for creating and maintaining packages

Jonathan Rougier

Outline

I describe a strategy I have found useful for developing large packages with lots of not-obvious mathematics that needs careful documentation. The basic idea is to combine the 'noweb' literate programming tool with the Unix 'make' utility. The source of the package itself has the usual structure, but with the addition of a `noweb` directory alongside the `R` and `man` directories. For further reference below, the general directory tree structure I adopt is

$$\begin{tikzcd}
 & \text{pkgName} \arrow[dl] \arrow[d] \arrow[dr] \arrow[drr] & & \\
\text{R} & \text{man}, \ldots & \text{inst} \arrow[d] & \text{noweb} \arrow[d] \\
 & & \text{doc} & \text{doc}
\end{tikzcd}$$

where '...' denotes other optional directories such as `src` and `data`.

The files in the `noweb` directory are the entry-point for *all* of the documented code in the package, including `*.R` files, `*.Rd` files, low-level source code, datasets, and so on. The `noweb` tool, under the control of the file 'Makefile' and the Unix `make` utility, is used to strip the files in the `noweb` directory into the appropriate places in the other directories. Other targets in 'Makefile' also handle things like building the package, installing it to a specific location, cleaning up and creating various types of documentation.

A complete example R package is available at http://maths.dur.ac.uk/stats/people/jcr/myPkg.tar.gz containing the code below, and a bit more to make 'myPkg' into a proper R package.

Literate programming and `noweb`

The basic idea of *literate programming* is that when writing complicated programs, it makes a lot of sense to keep the code and the documentation of the code together, in one file. This requires a mechanism for treating the file one way to strip out and assemble the code, and another way to create the documentation. With such a mechanism in place, the functionality of the code can be made much more transparent—and the documentation much more informative—because the code itself can be written in a modular or 'bottom-up' fashion, and then assembled in the correct order automatically.

I use the `noweb` literate programming tool. A `noweb` file looks like a LaTeX file with additional environments delimited by `<<name of environment>>=` and `@`. These define code chunks that appear specially-formatted in the documentation, and which get stripped out and assembled into the actual code. Here is an example of a minimal `noweb` file, called, say, 'myDoc1.nw'.

```
\documentclass[a4paper]{article}
\usepackage{noweb}\noweboptions{smallcode}
\pagestyle{noweb}

\begin{document}

Here is some \LaTeX\ documentation.  Followed
by the top-level source code.
<<R>>=
# The source of this file is noweb/myDoc1.nw
<<foo function>>
<<bar function>>
@

Now I can describe the [[foo]] function in more
detail, and then give the code.
<<foo function>>=
"foo" <- function(x) 2 * x^2 - 1
@

And here is the [[bar]] function.
<<bar function>>=
"bar" <- function(y) sqrt((1 + y) / 2)
@

% stuff for man page not shown
\end{document}
```

The `[[name]]` syntax is used by `noweb` to highlight variable names. There are many additional features of `noweb` that are useful to programmers. More information can be found at the `noweb` homepage, http://www.eecs.harvard.edu/~nr/noweb/.

Tangle

`noweb` strips out the code chunks and assembles them using the 'notangle' command. One useful feature is that it can strip out chunks with specific identifiers using the `-R` flag. Thus the command `notangle -RR myDoc1.nw` will strip all the code chunks identified directly or indirectly by `<<R>>=`, assembling them in the correct order. The result of this command is the file

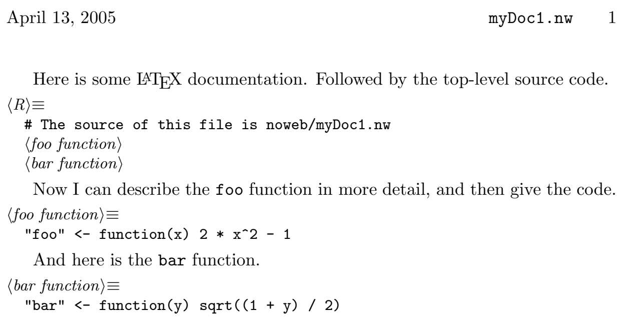
```
# The source of this file is noweb/myDoc1.nw
"foo" <- function(x) 2 * x^2 - 1
"bar" <- function(y) sqrt((1 + y) / 2)
```

which is written to standard output. By redirecting the standard output we can arrange for this file to go in the appropriate place in the package directory tree. So the full command in this case would be `notangle -RR myDoc1.nw > ../R/myDoc1.R`. So as long as we are consistent in always labelling the 'top' chunk of the R code with an `<<R>>=` identifier, we can automate the process of getting the R code out.

If we want, we can do the same thing using `<<man>>=` for the content of `man` pages, `<<src>>=` for low-level code, `<<data>>=` for datasets, and so on. Each of these can be stripped out and saved as a file into the appropriate place in the package directory tree.

Weave

To build the documentation, `noweb` uses the 'noweave' command, where it is useful to set the `-delay` option. Again, this is written to the standard output, and can be redirected to place the resulting LaTeX file at the appropriate place in the package tree. I put the LaTeX versions of the `*.nw` files in the directory `noweb/doc`. Thus the appropriate command is `noweave -delay myDoc1.nw > doc/myDoc1.tex`. This file contains quite a lot of LaTeX commands inserted by `noweb` to help with cross-referencing and indexing, and so is not particularly easy to read. But after using `latex`, the result is a `dvi` file which integrates the LaTeX documentation and the actual code, in a very readable format.


April 13, 2005 myDoc1.nw 1

Here is some LaTeX documentation. Followed by the top-level source code.

⟨*R*⟩≡
```
# The source of this file is noweb/myDoc1.nw
⟨foo function⟩
⟨bar function⟩
```
Now I can describe the `foo` function in more detail, and then give the code.

⟨*foo function*⟩≡
```
"foo" <- function(x) 2 * x^2 - 1
```
And here is the `bar` function.

⟨*bar function*⟩≡
```
"bar" <- function(y) sqrt((1 + y) / 2)
```

Similarity to 'Sweave'

Many users of R will be familiar with Friedrich Leisch's 'Sweave' function, available in the **tools** package. `Sweave` provides a means of embedding R code into a report, such as a LaTeX report, and then automatically replacing this code with its output. It uses the `notangle` functionality of a literate programming tool like `noweb`, because the R code must be stripped out, prior to evaluating it. The difference is that when `Sweave` builds the resulting document it does more than `noweave` would do, because it must actually evaluate R on each code chunk and put the *output* back into the document. In the literate programming described in this article, all that `notangle` does is wrap the code chunk in a LaTeX command to format it differently. `Sweave` can duplicate the simpler behaviour of `notangle` with the arguments `echo=TRUE,eval=FALSE` in each code chunk: see the help file for the function 'RWeaveLatex' for more details.

Using `make`

Our starting point is a collection of `*.nw` files in the `noweb` subdirectory. We could, by hand, issue a series of `notangle` and `noweave` commands, each time we update one or more of these files. Happily, the Unix tool `make` can be used instead. `make` requires a file of specifiers, often called 'Makefile', which describe the kinds of things that can be made, and the commands necessary to make them. Obvious candidates for things we would like to make are the `*.R` and `*.Rd` files that go into the `R` and `man` subdirectories, and the documentation that goes into the `inst/doc` subdirectory.

The `make` utility is very powerful, and complicated. I am not an expert at writing a 'Makefile', but the following approach seems to work well. My `Makefile` lives in the `noweb` directory, and all of the path specifiers take this as their starting point.

Simple `make` targets

Suppose that we have compiled a list of files that ought to be in the `R` subdirectory (say, 'RFILES'), and we want to use the command 'make R' to update these files according to changes that have occurred in the `noweb/*.nw` files; the argument `R` is known as a 'target' of the `make` command. We need the following lines in `Makefile`:

```
# make R files in ../R

R:      $(RFILES)

$(RFILES):      %.R : %.nw
        @echo 'Building R file for $<'
        @notangle -RR $< > ../R/$@
        @if test `egrep '^<<man>>=' $<` ; then \
          notangle -Rman $< > ../man/$*.Rd ; fi
```

After the comment, prefixed by `#`, the first line states that the command 'make R' depends on the files in the list 'RFILES', which we have already compiled. The next set of lines is executed for each component of 'RFILES' in turn, *conditionally on the* `*.R` *file being older than the corresponding* `*.nw` *file*. Where the `*.R` file is out-of-date in this way, a message is printed, `notangle` is called, and the `*.R` file is rebuilt and placed in the `R` subdirectory; if there is a `<<man>>=` entry, the `*.Rd` file is also rebuilt and placed in the `man` subdirectory.

A 'Makefile' has its own syntax. Within a target specification, the tags '$<', '$@' and '$*' indicate the origin file, the result file, and the file stem. Under each initial line the collection of subsequent commands is indented by tabbing, and the backslash at the end of the line indicates that the next line is a continuation. The `@` at the start of each command line suppresses the printing of the command to the standard output.

The attractive feature of `make` is that it only rebuilds files that are out-of-date, and it does this all automatically using information in the file date-stamps. This saves a lot of time with a large package in which there are many `*.nw` files in the `noweb` directory. In my experience, however, one feels a certain loss of control with so much automation. The useful command 'make --dry-run R' will print out the commands that will be performed when the command 'make R' is given, but not actually do them, which is a useful sanity check. The command 'touch myDoc1.nw' will change the date-stamp on 'myDoc1.nw', so that all derived files such as 'myDoc1.R' will automatically be out-of-date, which will force a rebuild even if 'myDoc1.nw' has not been modified: this can be another useful sanity-check.

Suppose instead we want to rebuild the LaTeX documentation in the `noweb/doc` subdirectory, using the command 'make latex'. We need the following lines in 'Makefile':

```
# make latex files in doc

latex:  $(TEXFILES)

$(TEXFILES):    %.tex : %.nw
        @echo 'Building tex file for $<'
        @noweave -delay $< > doc/$@
        @cd doc; \
          latex $@ > /dev/null
```

where ‘TEXFILES’ is a list of files that ought to be in the noweb/doc subdirectory. As before, each *.tex file is only rebuilt if it is out-of-date relative to the corresponding *.nw file. The resulting *.tex file is put into noweb/doc, and then latex is called to create the corresponding *.dvi file (rather lazily, the output from latex is diverted to /dev/null and lost).

Slightly more complicated, suppose we want to put pdf versions of the *.tex files into the subdirectory inst/doc, using the command ‘make pdf’. We need the following lines in ‘Makefile’:

```
# make pdf files in ../inst/doc

pdf:    $(TEXFILES) $(PDFFILES)

$(PDFFILES):    %.pdf : %.tex
        @echo 'Building pdf file for $<'
        @cd doc; \
          pdflatex $< > /dev/null;
        @mv doc/$@ ../inst/doc/
```

where ‘PDFFILES’ is a list of files that ought to be in the inst/doc subdirectory. The new feature here is that the command ‘make pdf’ depends on both ‘TEXFILES’ and ‘PDFFILES’. This means that each component of ‘TEXFILES’ is updated, if necessary, *before* the *.pdf file is rebuilt from the *.tex file. To rebuild the *.pdf file, the pdflatex command is called on the *.tex file in noweb/doc, and then the result is moved to inst/doc.

Additional lines in the ‘Makefile’

The main role of additional lines in ‘Makefile’ is to supply the lists ‘RFILES’, ‘TEXFILES’ and so on. The following commands achieve this, and a little bit else besides, and go at the start of ‘Makefile’:

```
## minimal Makefile

# look in other directories for files
vpath %.R ../R
vpath %.tex doc
vpath %.pdf ../inst/doc

# get lists of files
NWFILES = $(wildcard *.nw)
RFILES = $(NWFILES:.nw=.R)
TEXFILES = $(NWFILES:.nw=.tex)
PDFFILES = $(NWFILES:.nw=.pdf)

# here are the various targets for make

.PHONY: R latex pdf install

# Now insert the lines from above ...
```

The three ‘vpath’ lines are necessary to help make to look in other directories than noweb for certain types of file. Thus the *.R files are to be found in ../R, the *.tex files in doc, and so on (all relative to the noweb directory). The next four lines compile the lists of various types of file: ‘NWFILES’ are found in the noweb directory, ‘RFILES’ are ‘NWFILES’ files with the ‘nw’ suffix replaced with a ‘R’ suffix, and so on. For the final line, the .PHONY command is a bit of defensive programming to identify the targets of the make command.

Example

The file http://maths.dur.ac.uk/stats/people/jcr/myPkg.tar.gz contains a small example of an R package created using noweb and make, where there is only one *.nw file in the noweb directory, namely myDoc1.nw. The following commands illustrate the steps outlined above (‘debreu’ is my computer):

```
debreu% make --dry-run R
make: Nothing to be done for `R'.
debreu% touch myDoc1.nw
debreu% make --dry-run R
echo 'Building R file for myDoc1.nw'
notangle -RR myDoc1.nw > ../R/myDoc1.R
if test `egrep '^<<man>>=' myDoc1.nw` ; then \
  notangle -Rman myDoc1.nw > ../man/myDoc1.Rd ; fi
debreu% make R
Building R file for myDoc1.nw
debreu% make --dry-run pdf
echo 'Building tex file for myDoc1.nw'
noweave -delay myDoc1.nw > doc/myDoc1.tex
cd doc; \
  latex myDoc1.tex > /dev/null
echo 'Building pdf file for myDoc1.tex'
cd doc; \
  pdflatex myDoc1.tex > /dev/null;
mv doc/myDoc1.pdf ../inst/doc/
debreu% make pdf
Building tex file for myDoc1.nw
Building pdf file for myDoc1.tex
```

Initially the source file myDoc1.nw is up-to-date. I touch it to make it more recent than the derived files myDoc1.{R,Rd,tex,pdf}. The dry run shows the commands that will be executed when I type make R: in this case the file myDoc1.R is built and moved to ../R. After issuing the command make R the only output to screen is the comment ‘Building R file for myDoc1.nw’. The dry run for make pdf shows a more complicated set of operations, because before myDoc1.pdf can be built, myDoc1.tex has to be built.

More complicated targets

The make command can also be used to perform more complicated operations. Two that I have found useful are building the package, and installing the package onto my $R_LIBS path. In both cases, these operations must first make sure that the files are all up-to-date. For ‘make install’, for example, we might have:

```
PKGNAME = myPkg
RLIBRARY = /tmp/
R = R

# install

install:        $(RFILES) $(PDFFILES)
     @echo 'Installing $(PKGNAME) at $(RLIBRARY)'
     @cd ../..; \
       $(R) CMD INSTALL -l $(RLIBRARY) $(PKGNAME)
```

where the variables 'PKGNAME', 'RLIBRARY' and 'R' are specified separately, so that it is easy to change them for different packages, different locations on `$R_LIBS` or different versions of R. These are best put at the top of the 'Makefile'. The target `install` should be added to the `.PHONY` line.

Issuing the `make install` command when everything is up-to-date gives:

```
debreu% make --dry-run install
echo 'Installing myPkg at /tmp/'
cd ../..; R CMD INSTALL -l /tmp/ myPkg
debreu% make install
Installing myPkg at /tmp/
* Installing *source* package 'myPkg' ...
** R
** inst
** help
>>> Building/Updating help pgs for package 'myPkg'
     Formats: text html latex example
* DONE (myPkg)
```

If some of the files were not up-to-date then they would have been rebuilt from the original `*.nw` files first.

Conclusion

The great thing about literate programming is that there is no arguing with the documentation, since the documentation actually includes the code itself, presented in a format that is easy to check. For those of us who use LaTeX, `noweb` is a very simple literate programming tool. I have found using `noweb` to be a good discipline when developing code that is moderately complicated. I have also found that it saves a lot of time when providing code for other people, because the programmer's notes and the documentation become one and the same thing: I shudder to think how I used to write the code first, and then document it afterwards.

For large projects, for which the development of an R package is appropriate, it is often possible to break the tasks down into chunks, and assign each chunk to a separate file. At this point the Unix `make` utility is useful both for automating the processing of the individual files, and also for speeding up this process by not bothering with up-to-date files. The 'Makefile' that controls this process is almost completely generic, so that the one described above can be used in any package which conforms to the outline given in the introduction, and which uses the tags 'R', 'man' and so on to identify the type of code chunk in each `*.nw` file.

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CRAN Task Views

by Achim Zeileis

With the fast-growing list of packages on CRAN (currently about 500), the following two problems became more apparent over the last years:

1. When a new user comes to CRAN and is looking for packages that are useful for a certain task (e.g., econometrics, say), which of all the packages should he/she look at as they might contain relevant functionality?

2. If it is clear that a collection of packages is useful for a certain task, it would be nice if the full collection could be installed easily in one go.

The package **ctv** tries to address both problems by providing infrastructure for maintained task views on CRAN-style repositories. The idea is the following: a (group of) maintainer(s) should provide: (a) a list of packages that are relevant for a specific task (which can be used for automatic installation) along with (b) meta-information (from which HTML pages can be generated) giving an overview of what each package is doing. Both aspects of the task views are equally important as is the fact that the views are maintained. This should provide some quality control and also provide the meta-information in the jargon used in the community that the task view addresses.

Using CRAN task views is very simple: the HTML overviews are available at http://CRAN.R-project.org/src/contrib/Views/ and the task view installation tools are very similar to the package installation tools. The list of views can be queried by `CRAN.views()` that returns a list of `"ctv"` objects:

```
R> library(ctv)
R> x <- CRAN.views()
R> x


CRAN Task Views
```

```
---------------
Name: Econometrics
Topic: Computational Econometrics
Maintainer: Achim Zeileis
Repository: http://cran.r-project.org
---------------
Name: Finance
Topic: Empirical Finance
Maintainer: Dirk Eddelbuettel
Repository: http://cran.r-project.org
---------------
Name: MachineLearning
Topic: Machine Learning&Statistical Learning
Maintainer: Torsten Hothorn
Repository: http://cran.r-project.org
---------------
Name: gR
Topic: gRaphical models in R
Maintainer: Claus Dethlefsen
Repository: http://cran.r-project.org



R> x[[1]]


CRAN Task View
--------------
Name:       Econometrics
Topic:      Computational Econometrics
Maintainer: Achim Zeileis
Repository: http://cran.r-project.org
Packages:   bayesm, betareg, car*, Design,
            dse, dynlm, Ecdat, fCalendar,
            Hmisc, ineq, its, lmtest*, Matrix,
            micEcon, MNP, nlme, quantreg,
            sandwich*, segmented, sem,
            SparseM, strucchange, systemfit,
            tseries*, urca*, uroot, VR,
            zicounts, zoo*
            (* = core package)
```

Note that currently each CRAN task view is associated with a single CRAN-style repository (i.e., a repository which has in particular a `src/contrib` structure), future versions of **ctv** should relax this and make it possible to include packages from various repositories into a view, but this is not implemented, yet.

A particular view can be installed subsequently by either passing its name or the corresponding `"ctv"` object to `install.views()`:

```
R> install.views("Econometrics",
+                lib = "/path/to/foo")
R> install.views(x[[1]],
+                lib = "/path/to/foo")
```

An overview of these client-side tools is given on the manual page of these functions.

Writing a CRAN task is also very easy: all information can be provided in a single XML-based format called `.ctv`. The `.ctv` file specifies the name, topic and maintainer of the view, has an information section (essentially in almost plain HTML), a list of the associated packages and further links. For examples see the currently available views in **ctv** and also the vignette contained in the package. All it takes for a maintainer to write a new task view is to write this `.ctv` file, the rest is generated automatically when the view is submitted to us. Currently, there are task views available for econometrics, finance, machine learning and graphical models in R—furthermore, task views for spatial statistic and statistics in the social sciences are under development. But to make these tools more useful, task views for other topics are needed: suggestions for new task views are more than welcome and should be e-mailed to me. Of course, other general comments about the package **ctv** are also appreciated.

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Using Control Structures with Sweave

Damian Betebenner

Sweave is a tool loaded by default with the `utils` package that permits the integration of R/S with LaTeX. In one of its more prominant applications, Sweave enables literate statistical practice—where R/S source code is interwoven with corresponding LaTeX formatted documentation (R Development Core Team, 2005; Leisch, 2002a,b). A particularly elegant implementation of this is the `vignette()` function (Leisch, 2003). Another, more pedestrian, use of Sweave, which is the focus of this article, is the batch processing of reports whose contents, including figures and variable values, are dynamic in nature. Dynamic forms are common on the web where a base `.html` template is populated with user specific data drawn, most often, from a database. The incorporation of repetitive and conditional control structures into the processed files allows for almost limitless possibilities to weave together output from R/S within the confines of a LaTeX document and produce professional quality dynamic output.

Motivation for the current project came as a result of pilot data analyses for a state department of education. Dissemination of the analyses to schools in the state required the production of approximately 3,000 school reports documenting the results using school specific numbers/text, tables, and figures. The R/Sweave/LaTeX combination was deployed in various ways to produce prototype reports. This article provides details of the process so that others with similar document production needs can employ this combination of tools.

Outline of Process

The production process is quite basic in its implementation: Sweave a file using an appropriate dataframe to create a `.tex` that includes appropriate output. Most users of Sweave would have little problem creating such a `.tex` file based upon a given dataframe. Adding the capacity to deal with numerous different dataframes is possible using basic control structures available in R. In general, there are two files necessary for the mass production of reports:

`template.Rnw` A template file that provides the template into which all the relevant R output is placed.

`master.R` A master file that loops over all the recipients of the template file, creates the subset of data to be used within the template file, Sweaves the template and saves the output to a recipient specific `.tex` file.

In the following, the essential parts of each of these files is discussed in detail:

master.R

The `master.R` file implements a control structure *outside* of the Sweave process. This allows one to create a `.tex` file for each recipient. The key to the creation of these files is the creation of a distinct `outfile` for each unique recipient in the list. A basic `master.R` file which performs this looks like:

```
load(the.data.frame)
recip.list <- unique(the.data.frame$recip)
for (name in recip.list){
  subset.data <- subset(the.data.frame,
           the.data.frame$recip==name)
  outfile <- paste(name, "tex", sep=".")
  Sweave("template.Rnw", output=outfile)
}
```

The process starts by sourcing `master.R`. This loads a master data frame that contains the data for all the potential report recipients. A list of recipients is then derived from that dataframe. A looping structure is implemented that subsets the appropriate data file from the master data frame. Crucially, this subsetted data frame contains the recipient specific data that is used to construct the individualized report. Finally, a recipient specific `.tex` file is created by by Sweaving the template, `template.Rnw`.

Depending upon the number of recipients, it is entirely possible for thousands of `.tex` files to be generated. To avoid the files accumulating in the same directory, one can easily modify the code to place the output in other directories. For example, if one wished to create a distinct directory for each recipient, the following additions would suffice:

```
for (name in recip.list){
  subset.data <- subset(the.data.frame,
           the.data.frame$recip==name)
  outfile <- paste(name, "tex", sep=".")
  dir.create(name)
  setwd(name)
  Sweave(file.path("..", "template.Rnw"),
                   output=outfile)
  setwd("..")
}
```

This basic control structure can be tweaked in many ways. For example, a call can be made to a relational database that pulls the relevant data into R for processing. This is particularly attractive for those applications where data storage is cumbersome and better administered with a relational database.

template.Rnw

The template, `template.Rnw`, is a standard Sweave file containing LaTeX markup together with documentation and code chunks. The file, as its name suggests, is a template into which recipient specific numbers/text, tables, and figures can be included. One of the greatest challenges to producing a template is ensuring that it will produce the expected output given the range of possible values it is expected to accept.

One of the easiest ways of providing recipient specific output with the `template.Rnw` file is through the liberal use of the `\Sexpr` function. For the aforementioned school reports, the name of the school was included throughout the text, tables, and figures to provide a customized feel. In particular, the fancyhdr LaTeX package was used and the school name was included in the left header. Because school names, and string expressions in general, vary widely in their length, care must be exercised so that any place that the `\Sexpr` is utilized, the string (or number) resulting from `\Sexpr` will function in the LaTeX document for the range of values of the field that occur in the data set.

The creation of recipient specific tables is a frequently encountered (particularly with `.html`) means of dynamic report generation. There are a number of ways of including tables into the template.Rnw document. Perhaps the simplest way is through the use of the xtable function within David Dahl's xtable package which produces LaTeX output for a variety of R objects. A basic code chunk yielding .tex markup producing a table is given by

```
<<echo=FALSE,results=tex>>=
xtable(object, caption="table:caption",
       label="table:label")
@
```

Though suitable for a variety of tasks, the function xtable is limited in its capacity to produce complex tables (e.g., tables with multicolumn headers). Another frequently encountered difficulty occurs when tables being produced are long and possibly extend over several pages. Such long tables are not a problem with |.html| because the pages can be of nearly infinite length. However, printed pages must have the table broken into pieces according to the space available on the page. The LaTeX code produced by xtable will not yield acceptable results. To circumvent this, one can use the latex.table function provided by Roger Koenker's quantreg package together with the option for using the longtable LaTeX package. The latex.table function accepts matrix objects and outputs results to a specified file. As such, its incorporation into the Sweave document requires a slightly different two part technique than that used with xtable:

1. latex.table is called within a code chunk and produces the required LaTeX markup and saves it to an output file.

```
<<echo=False>>=
latex.table(matrix,
        file=paste(name, ":table.tex",
                   sep=""))
@
```

2. The LaTeX markup for the table is inserted into the document (n.b., outside of a code chunk) at the appropriate place:

```
\begin{center}
\input{\Sexpr{name}:table.tex}
\end{center}
```

As with xtable, there are still limitations to the amount of tabular complexity available with latex.table. Multicolumn headings, multirow headings, colored columns, etc. are all difficult if not impossible to produce. Depending upon ones willingness to program, however, all effects can ultimately be produced. Though tedious, frequent use of Sexpr commands outside of code chunks or cat commands within code chunks allows all LaTeX commands to be incorporated into the final .tex document upon Sweave compilation.

In many instances, particularly with tables and figures, it's necessary to produce multiple tables or figures within a single Sweave document based upon particular attributes of the recipient. For example, with the school project each school's report contained information pertinent to each grade in the school. Thus, a table was produced for each grade within the school. To implement this, a loop is placed *within* template.Rnw. This procedure, given in FAQ A.8 from Friedrich Leisch's Sweave User Manual (Leisch, 2005), is useful is many situations.

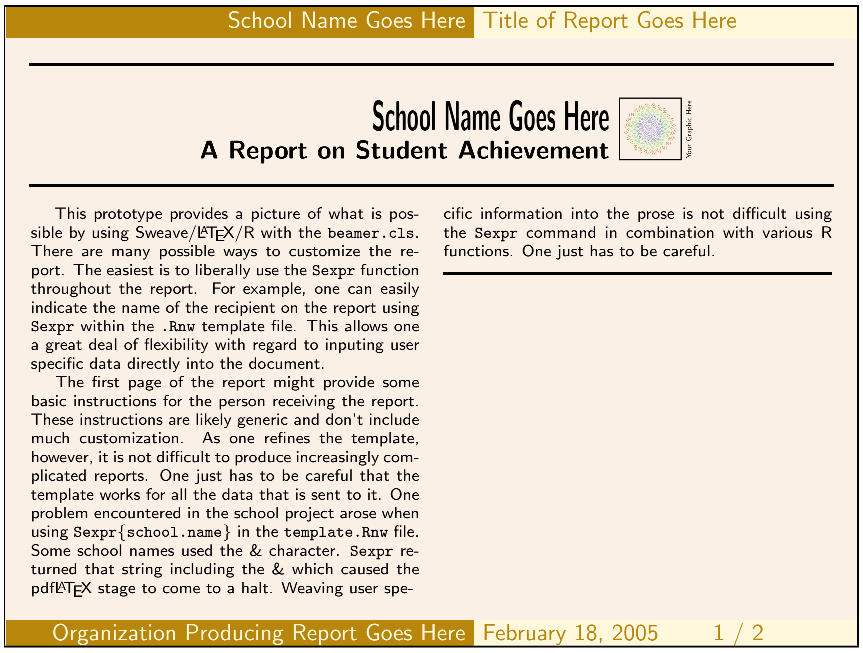
A major difficulty with control structures within the template is the variable nature of the output. In the example with school reports, some rural schools have grades 1 through 12. Thus, if a table or figure is produced for each grade, one must take account of the fact that so many tables or figures will result in the .tex document. The simplest way to accommodate different numbers of loop iterations within the template is to create a \newpage each time the loop completes. Thus, for example, each figure for each grade receives a page to itself. This doesn't always look acceptable for especially parsimonious tables or figures. However, combining multiple tables on a single page can often cause overfull hbox and vbox situations to occur. A workaround to this difficulty is to use the LaTeX \scalebox and \resizebox commands. These commands allow great flexibility in shrinking output to fit a given page. In general, a good deal of planning and experimentation is necessary to produce a template that works well for all situations.

The extent to which one wishes to make the reports specific to a particular recipient can be extended far beyond expressing the recipient specific information in tables and figures. For reports where the recipient is an individual, text within the report can be made gender specific through the use of if else statements based upon values in the subsetted data frame that the template is using to construct the recipient specific report. Supposing the gender code in the subsetted data frame is 1 for males and 2 for females, one could incorporate he/she (or him/her) pronouns into the text using a simple if else statement such as

```
\Sexpr{if (data.frame$gender==1) "he"
          else "she"}
```

The amount of customization is limited only by the amount of work put into constructing the template.

One is not limited to the basic LaTeX classes (e.g., article.cls or report.cls) when producing the template. The beamer.cls (Tantau, 2004) is Sweave compatible and provides extensive functionality to produce rich, full color .pdf output with extensive hyperlink capabilities. Figure 1 presents a two page example demonstrating some possibilities of the R/LaTeX/Sweave combination for dynamic .pdf report generation using the beamer.cls. Other



School Name Goes Here | Title of Report Goes Here

School Name Goes Here
A Report on Student Achievement

This prototype provides a picture of what is possible by using Sweave/LaTeX/R with the `beamer.cls`. There are many possible ways to customize the report. The easiest is to liberally use the `Sexpr` function throughout the report. For example, one can easily indicate the name of the recipient on the report using `Sexpr` within the `.Rnw` template file. This allows one a great deal of flexibility with regard to inputing user specific data directly into the document.

The first page of the report might provide some basic instructions for the person receiving the report. These instructions are likely generic and don't include much customization. As one refines the template, however, it is not difficult to produce increasingly complicated reports. One just has to be careful that the template works for all the data that is sent to it. One problem encountered in the school project arose when using `Sexpr{school.name}` in the `template.Rnw` file. Some school names used the & character. `Sexpr` returned that string including the & which caused the pdfLaTeX stage to come to a halt. Weaving user specific information into the prose is not difficult using the `Sexpr` command in combination with various R functions. One just has to be careful.

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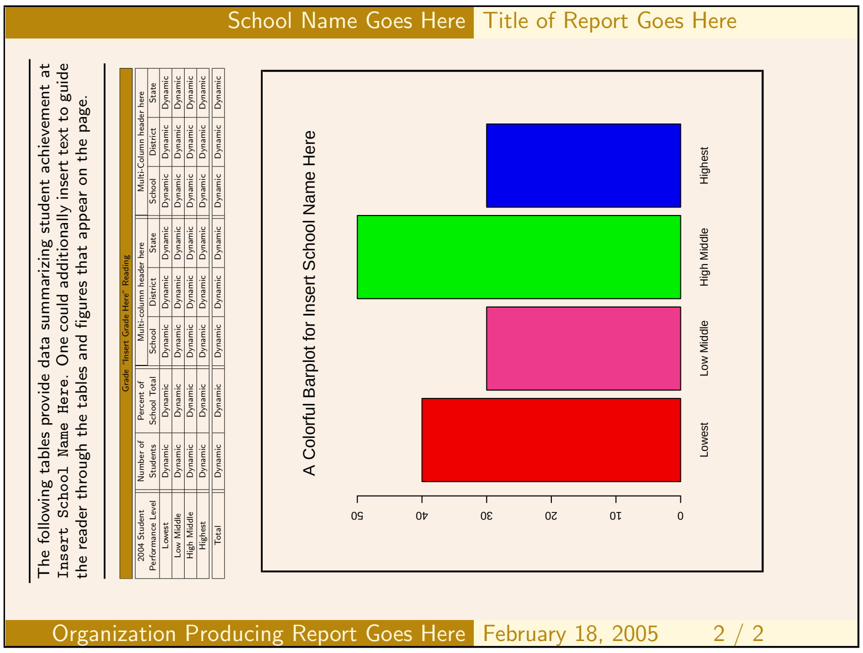

School Name Goes Here | Title of Report Goes Here

The following tables provide data summarizing student achievement at `Insert School Name Here`. One could additionally insert text to guide the reader through the tables and figures that appear on the page.

Grade "Insert Grade Here" Reading								
2004 Student Performance Level	Number of Students	Percent of School Total	Multi-column header here			Multi-Column header here		
			School	District	State	School	District	State
Lowest	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic
Low Middle	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic
High Middle	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic
Highest	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic
Total	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic	Dynamic

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Figure 1: A basic two-page example demonstrating dynamic `.pdf` using the R/LaTeX/Sweave combination.

LaTeX classes, packages and font families are available that can be combined to yield unlimited possibilities.

Final Compilation

Upon Sweave completion, `master.R` yields numerous `.tex` files that need to be compiled. For the school project, approximately 3,000 `.tex` files were created. In addition, there were, in most cases, three `.pdf` figures created for each school. All of these files can be compiled from within R using the `texi2dvi` command available in the `tools` package. The following loop which can be placed into `master.R` accomplishes this task:

```
for (name in recip.list){
     outfile <- paste(name, "tex", sep=".")
     texi2dvi(outfile, pdf=TRUE, clean=TRUE)
}
```

`texi2dvi` will run LaTeX and BibTeX the appropriate number of times to resolve any reference and citation dependencies. The result is compiled versions of all the `.tex` files generated from the earlier loop containing the Sweave process. It is also possible to perform this task outside of R using a script or batch file to perform the same operations.

Conclusions

For batch production of dynamic `.pdf` or `.ps` documentation, the R/Sweave/LaTeX combination is powerful and nearly limitless in its capabilities. A major benefit to producing reports using this combination of tools is how closely Sweave integrates the processing power of R with the typesetting capability of LaTeX. The key to producing dynamic reports for a large number of recipients is the use of iterative control structures in R. This article provides the author's "homebrew" code. Other, more elegant, solutions are likely possible.

A next step after report generation is report distribution. In theory, given the appropriate server configuration, it should be possible to electronically distribute the reports to the appropriate recipient based upon, for example, an email address contained in the database. I would appreciate learning how others have addressed this and similar problems.

Acknowledgments

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The Value of R for Preclinical Statisticians

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Participation on the R-help mailing list has shown R to be widely used across organizations of all types the world over. This article discusses one corner where R has become an indispensable tool for effective statistical practice: a preclinical pharmaceutical environment at the authors' place of employment.

Preclinical is defined here as a portion of the research and development process for prescription medicines. In this article that portion is defined to start with fundamental discovery, and to end up where a potential product is first put into human subjects in clinical trials. There is a wide variety of knowledge sought across this spectrum, including: biological targets believed to be important influences on a given disease; chemical entities that affect such targets; effectiveness and safety in animals; formulation of product itself. This brief listing is only intended to provide a broad overview. In reality, there are many more areas that could be included based on desired granularity. A complementary term of "nonclinical," which is also commonly used, is perhaps more appropriate here; however, we will stay with the phrase preclinical for brevity.

The hallmark diversity of preclinical research presents unlimited opportunities for statisticians. Data are collected everywhere in the process, and in large quantities. We have the liberty to choose methods of processing and analysis. This is a different environment than clinical biostatistics, where SAS is the dominant tool for various reasons. Below we present examples and discussion on how and why we use R and find it invaluable.

Daily operations

Our corporate-issued laptops run Windows XP and we have a small cluster of dual-processor Opterons that run 64-bit Linux for intensive jobs. The client-server configuration of VNC (TightVNC , 2004) provides a very stable way to bridge the two environments onto one monitor. An X-window session appears as just another window on the Windows desktop. Samba (Samba Team , 1992-2005) sets up file sharing so that a /home directory share under Linux appears as a network drive in Windows. The autocutsel (Witrant , 2004) utility eases cut-and-paste operations between the two operating systems.

If we work on data that can be comfortably explored on our laptops, we stay there. Generating reports for our research collaborators is helped by the right-click cutting and default pasting of a Windows metafile from the windows graphics device into a Microsoft Office document. The internal Data Editor (see ?edit) is very useful for browsing a data frame. Once a workspace has been saved in a Windows folder, launching it from Explorer automatically sets the container working directory. The overall R GUI console is thankfully unobtrusive, and we well appreciate the separation of it from graphics device windows in SDI mode. We find it much more pleasant to switch amongst desktop windows where each stands equally on its own, rather than having to search inside a set of windows within the same application.

If an analysis task becomes too large (in memory or time) for the laptops, it is a simple matter to transfer the R workspace image to a Linux box and pick up right where we left off. Through the aforementioned network drive mapping of a Linux share, source code editing can be done in the same Windows editor, and file operations of saving, copying, opening, etc. are transparently done through the standard Windows GUI.

All these task-oriented details add up to increased productivity. More importantly, however, is the content of the environment itself. We point out here that some of what we say in the rest of the article is not necessarily unique to R, and such benefits can be found in the other implementation of the S language, namely S-PLUS. In his "Exegeses on Linear Models" talk (Venables , 2000), one exegesis from Bill Venables that we particularly admire, and paraphrase here, is that "the subject should dictate what the program should do and not the other way around." Our work environment streams a constant wealth of different data structures and types of scientific questions to address, and we can exercise our freedom to choose our strategies of analysis. Comprehensive data analyses are only limited by our own human capabilities, not by R. R enables us to seamlessly move from data management to exploration to formal evaluations to communications of results. No excuse remains to prevent the production of good data graphs for the purposes of valuable study or presentation. The implementation of modern methods allows us to use resampling, resistance/robustness, and dimension reduction methods on a routine basis, to name a few. We work with cutting edge science, which we firmly believe deserves cutting edge data analysis. R promotes this for us, with its virtues of flexibility, stability and efficiency so clearly practiced by its R Core caretakers.

Professor Brian D. Ripley, in "How Computing has Changed Statistics" (Ripley , 2004), aptly states of R that "the only barrier to understanding how it works, precisely, is skill." We interpret the meaning of "how it works" to be on multiple levels, and the level most important for us is that a true, continuous investment to learn its many functions, structures, and features pays off time and again. It helps us bring value to scientific research, gain trust from our collaborators, and stimulates the intellect.

Illustrations

Preclinical statisticians do not get nearly enough opportunities to provide input to design of experiments. When we do get such an opportunity, we are especially eager to make recommendations as quickly as possible. A recent query involved a crossover design with binary responses. An important part of the design plan was to estimate the number of subjects needed to see a meaningful difference between two conditions, where incidence rates were low. Sample size determination tends to be the predominant aspect of such study design requests.

Estimating sample size is a process of several approximations, but with some effort such approximations do not substantially diminish its value. In this example, tracking down software that could be readily used, or finding a literature reference where a recipe could be programmed, was not timely enough. So a simulation-based approach was taken.

```
calcPower <- function(nsubj, pyn, pny, pnnyy,
                      numsim=1000) {
  ## A simple approach to calculate the power of
  ## McNemar's matched-pair test for these inputs:
  ##  nsubj = the number of subjects/pairs of
  ##   measurements (msmts)
  ##   (note that msmt1 comes from condition 1 and
  ##    msmt2 comes from condition 2)
  ##  pyn = p(msmt1 = yes & msmt2 = no)
  ##  pny = p(msmt1 = no & msmt2 = yes)
  ##  pnnyy = p(msmt1 != msmt2)
  ##  numsim = Number of Simulations
  ##   (at least 1000 recommended)
  outcomes <- rmultinom(n=numsim, size=nsubj,
                        prob=c(pnn=pnnyy, pyy=0,
                          pny=pny, pyn=pyn))
  tscompares <-
    apply(outcomes, 2, function(x) {
      ts <- (((x[3] - x[4])^2) / (x[3] + x[4]))
      if (!is.finite(ts)) ts <- 0
      ts
    })
  mean(tscompares > qchisq(0.95, 1), na.rm=FALSE)
}
```

This simple-minded function evaluates how McNemar's test would behave for a given configuration of underlying parameters, thereby providing an estimate of its power to detect that difference. Recall that small occurrence rates were expected. A grid of potential configurations can be evaluated:

```
powerGrid <-
  expand.grid(pyn=seq(0.01, 0.10, by=.01),
              pny=c(0.001, 0.002, 0.005,
                    seq(0.01, 0.09, by=.01)))
powerGrid$pnnyy <- (1 - powerGrid$pyn -
                    powerGrid$pny)
powerGrid <- subset(powerGrid, pyn > pny)
powerGrid <- powerGrid[order(powerGrid$pyn,
                             powerGrid$pny),]
powerGrid$power <-
  apply(powerGrid, 1,
        function(x) calcPower(100, x[1],
                              x[2], x[3]))
```

From the resulting data frame powerGrid, the context of the study objectives and available resources, a variety of alternatives were explored and recommended to the researcher. Ensuing discussions then produced a design that was later successfully implemented.

We realize that potential influences of period and sequence were ignored in the above calculations, as well as perhaps a more suitable parametric model approach to the postulated analysis. But as we mentioned previously, we felt the approximations in the approach were reasonable enough to address the questions at hand.

Similar sample size scenarios we have encountered include (1) survival data with simple Type I censoring; (2) single population binomial parameter estimation; (3) inspection of device performance within its specified tolerances; and (4) comparability of old and new drug formulations. In all these scenarios the principal recipe of simulating power remains the same as the example above; the key differences include the postulated underlying distribution and the methodology of estimation or testing.

One could argue the drawback of computational time that might be needed to generate sufficient grids of sample size and power values. In the above example, a nsim=10000 or 100000 would provide better estimates of power and the computational time is not prohibitive; we are talking minutes and at most hours to get the needed results. Here is where our small cluster of Linux servers, or simply scheduling something to run overnight, takes advantage of what computers are really good at.

Molecular Modeling

As another illustration, one particular area where our group has been involved in is molecular modeling. Specifically, we are referring to the problem of predicting biological activities of small organic molecules from their chemical "descriptors". The biological activities can be quantitative (e.g., percent inhibition against a target enzyme) or qualitative ("active" vs. "inactive"). The chemical descriptors are properties/features of the molecules computed from their structures. There are two possible goals. One is simply prediction: Given a collection of molecules with unknown biological activities, predict which ones are likely to be active. The other possible goal is interpretation: What chemical properties or substructures are biologically relevant?

Our computational chemistry colleagues have traditionally used techniques such as *k*-nearest neighbors, partial least squares, and neural networks, etc. for such problems, mostly using tools written in-house. A couple of years ago, we started to convince our colleagues that more modern, powerful tools such as random forests (Breiman, 2001; Svetnik et. al. , 2003) can be readily accessible through R. We started working on linking Breiman and Cutler's Fortran code to R after we got tired of using the Fortran code alone, since every little change in the data or parameters required recompiling the source code. It would have been impossible to convince our colleagues to use the tool in that form, no matter how powerful the tool may be. As a result of making random forests available in R, it has become an important component of the methodologies utilized by our colleagues.

Currently, R is installed on the main computer system for the computational chemists, who are invariably Unix based. Whatever R functionalities are required, the development group (who are responsible for research and implementation of new methodologies) would wrap them in shell or Perl scripts. These scripts are then used by the applications group to support specific projects.

Delivery of Tools

Merck preclinical statisticians are outnumbered at least ten to one by potential researchers to collaborate with, and we have global sites that we strive to serve since they have no access to local statisticians. As briefly alluded to in the previous section, the availability of R to communicate with other software offers great potential to serve our customers.

We have recently embarked on a COM-driven[1] framework to take advantage of existing infrastruc-

[1]COM stands for Common Object Model, a Microsoft-driven "standard" for communications between software components.

ture. For instance, virtually everyone at Merck runs the same version of Windows XP and the same version of Microsoft Excel. Use of R(D)COM (Baier and Neuwirth , 2004) allows construction of an application where the user interface is entirely in Excel; namely, input data storage, selection of data and choices through Userforms, and formatted output. The underlying work of the R engine is invisible to the user as it provides calculations and the raw output to Excel for the formatting and the organized presentation. This framework leverages Excel strengths of formatting, familiarity, and ubiquity, and R provides numerical reliability and breadth of data analytic functionality. While we are currently in early stages, the framework has demonstrated reliability for widespread distribution.

Summary

There are several specific aspects that make R uniquely suitable for us and our colleagues:

- Availability of modern methodologies;
- Flexibility for implementing new methods;
- Facilities to package added functionalities;
- Seamless integration with other software;
- Liberty to (try to) install on any platform.

The first point is discussed above. We add that colleagues in our department rely on R for their support of genomic and proteomic research, where access to (or the ability to implement) cutting-edge methodologies is crucial. The second through fourth points are important for us as tool developers. The fact that R is a full-featured language enables us to follow the spirit of "turn ideas into software, quickly and faithfully" (Chambers , 1998). The packaging facility in R lets us easily create, maintain, and distribute tools and associated documentation. The same cannot really be said about most other statistical languages or packages. The COM framework discussed above is but one of many options for integration of R with processes or GUIs, etc. The last point is important not because R is free (as in beer), but because we are not limited to run the software on whatever platform a vendor chooses to support. As long as we can get R to compile and pass all its tests, we are comfortable using it. As an example, when we bought our first 64-bit machine (a dual Opteron 244 with 16GB of RAM), the main motivation was to overcome the memory limitation of a 32-bit platform. Because we can build R from source, we readily built a 64-bit version of R on that box.

This article focused on preclinical statistics use of R. Nearly four years ago we organized our first in-house introductory course on R, and about 20 people attended, mostly from preclinical statistics and other basic research departments that provide quantitative analysis support to researchers. As a sign of the increasing acceptance of R at Merck three years later, attendance more than doubled and mostly included clinical statisticians and SAS programmers. Results based on the use of R by preclinical statisticians have been included in regulatory responses and filings, and no issues have arisen. We are not aware of R use in the traditional core workflows of clinical trials production work to date, but we do expect the use of R within Merck to continue to increase in all areas, including clinical.

In our small corner of the world that is preclinical drug research & development, R is a guide towards better statistical practice and helps expands our influence on scientific research. It is indispensable. If R— the software and community — did not exist, we would be wishing that something like it would come along.

Footnote: The first author recently changed employment from Merck to Centocor. The preclinical/nonclinical experiences with researchers there have been quite similar to date.

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Recreational mathematics with R: introducing the “magic” package

Creating and investigating magic squares with R

Robin K. S. Hankin

Preface

The R computer language (R Development Core Team, 2004) has been applied with a great deal of success to a wide variety of statistical, physical, and medical applications. Here, I show that R is an equally superb research tool in the field of recreational mathematics.

Recreational mathematics is easier to recognize than define, but seems to be characterized by requiring a bare minimum of "raw material": complex notation is not needed, and problems are readily communicated to the general public.

This is not to say that all problems of recreational mathematics are trivial: one could argue that much number theory is recreational in nature; yet attempts to prove Fermat's Last Theorem, or the search for ever higher perfect numbers, have been the catalyst for the development of many fruitful new areas of mathematics.

The study of magic squares is also an example of nontrivial recreational mathematics as the basic concept is simple to grasp—yet there remain unsolved problems in the field whose study has revealed deep mathematical truths.

Here, I introduce the "magic" package, and show that R is an excellent environment for the creation and investigation of magic squares. I also show that one's appreciation of magic squares may be enhanced through computer tools such as R, and that the act of translating 'paper' algorithms of the literature into R idiom can lead to new insight.

Magic squares

Magic squares have essentially zero practical use; their fascination—like much of pure mathematics—lies in the appeal of æsthetics and structure rather than immediate usefulness.

The following definitions are almost universal:

- A *semimagic square* is one all of whose row sums equal all its columnwise sums (i.e. the magic constant).
- A *magic square* is a semimagic square with the sum of both unbroken diagonals equal to the magic constant.
- A *panmagic square* is a magic square all of whose broken diagonals sum to the magic constant.

(all squares are understood to be $n \times n$ and to be *normal*, that is, to comprise n^2 consecutive integers[1]). Functions `is.semimagic()`, `is.magic()`, and `is.panmagic()` test for these properties.

A good place to start is the simplest—and by far the most commonly encountered—magic square, *lo zhu*:

```
> magic(3)

     [,1] [,2] [,3]
[1,]    2    7    6
[2,]    9    5    1
[3,]    4    3    8
```

This magic square has been known since antiquity (legend has it that the square was revealed to humanity inscribed upon the shell of a divine turtle). More generally, if consecutive numbers of a magic square are joined by lines, a pleasing image is often obtained (figure 1, for example, shows a magic square of order 7; when viewed in this way, the algorithm for creating such a square should be immediately obvious).

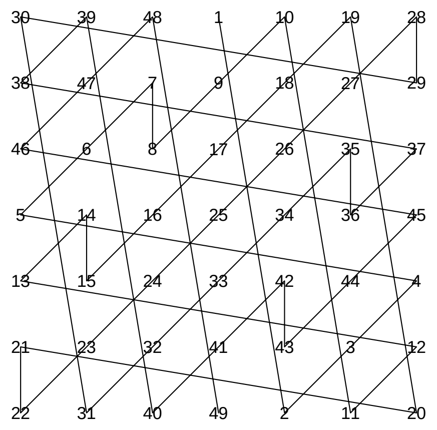


Figure 1: Magic square of order 7 in graphical form (obtained by `magicplot(magic.2np1(3))`)

[1]Most workers require the entries to start at 1, which is the convention here; but there are several instances where starting at 0 is far more convenient. In any case, if `x` is magic, then `x+n` is magic for any integer `n`.

Function `magic()` takes an integer argument n and returns a normal magic square of size $n \times n$. There are eight equivalent forms for *lo zhu* or indeed any magic square, achieved by rotating and reflecting the matrix (Benson and Jacoby, 1976); such equivalence is tested by `eq()` or `%eq%`. Of these eight forms, a magic square `a` is said to be in *Frénicle's standard form* if `a[1,1]`$\leq$`b[1,1]` whenever `a %eq% b`, and `a[1,2]<a[2,1]`. Function `is.standard()` tests for this, and function `as.standard()` places a magic square in standard form. Magic squares returned by `magic()` are always in standard form.

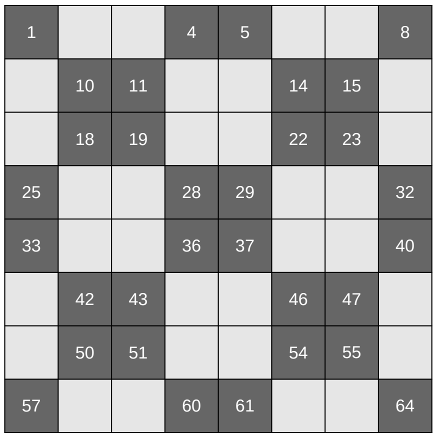
A typical (paper) algorithm for placing magic square `a` in standard form would be "rotate `a` until `a[1,1]<min(a[1,n],a[n,1],a[n,n])` then, if `a[1,2]>a[2,1]`, take the transpose". I shall show later that expressing such an algorithm in R leads to new insight when considering magic hypercubes.

A wide variety of algorithms exists for calculating magic squares. For a given order n, these algorithms generally depend on n modulo 4.

A typical paper algorithm for magic squares of order $n = 4m$ would go as follows.

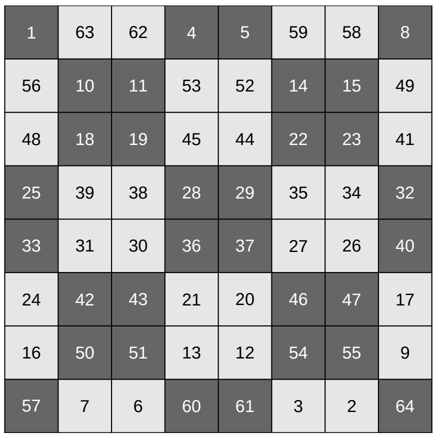
> Algorithm 1: in a square of order $4m$, shade the long major diagonal. Then shade all major diagonals distant by a multiple of 4 cells from the long diagonal. Do the same with the minor diagonals. Then, starting with "1" at the top left corner and proceeding from left to right and top to bottom, count from 1 to n^2, filling in the shaded squares with the appropriate number and omitting the unshaded ones [figure 2]. Fill in the remaining (unshaded) squares in the same way, starting at the lower right corner, moving leftwards and upwards [figure 3].

Such paper algorithms are common in the literature but translating this one into code that uses R's vectorized tools effectively can lead to new insight. The magicness of such squares may be proved by considering the increasing and decreasing sequences separately.



1			4	5			8
	10	11			14	15	
	18	19			22	23	
25			28	29			32
33			36	37			40
	42	43			46	47	
	50	51			54	55	
57			60	61			64

Figure 2: Half-completed magic square of order 8



1	63	62	4	5	59	58	8
56	10	11	53	52	14	15	49
48	18	19	45	44	22	23	41
25	39	38	28	29	35	34	32
33	31	30	36	37	27	26	40
24	42	43	21	20	46	47	17
16	50	51	13	12	54	55	9
57	7	6	60	61	3	2	64

Figure 3: Magic square of order 8

The interesting part of the above paper algorithm lies in determining the pattern of shaded and unshaded squares[2]. As the reader may care to verify, parsing the algorithm into R idiom is not straightforward. An alternative, readily computed in R, would be to recognize that the repeating 4×4 cell `a[2:5,2:5]` is `kronecker(diag(2),matrix(1,2,2)) -> b` say, replicate it with `kronecker(matrix(1,3,3),b) -> g`; then trim off the border by selecting only the middle elements, in this case `g[2:9,2:9]`. Function `magic.4n()` implements the algorithm for general m.

[2]If `a <- matrix(1:(n*n),n,n)`, with `jj` a Boolean vector of length n^2 with `TRUE` corresponding to shaded squares, then with it is clear that `a[jj] <- rev(a[jj])` will return the above magic square.

Magic hypercubes

One of the great strengths of R is its ability to handle arbitrary dimensioned arrays in an efficient and elegant manner.

Generalizing magic squares to magic hypercubes (Hendricks, 1973) is thus natural when working in R. The following definitions represent a general consensus, but are far from universal:

- A *semimagic hypercube* has all "rook's move" sums equal to the magic constant (that is, each $\sum_{i_r=1}^{n} a[i_1, i_2, \ldots, i_{r-1}, i_r, i_{r+1}, \ldots, i_d]$ with $1 \leq r \leq d$ is equal to the magic constant for all values of the other i's).

- A *magic hypercube* is a semimagic hypercube with the additional requirement that all 2^{d-1} long (ie extreme point-to-extreme point) diagonals sum correctly.

- A *perfect magic hypercube* is a magic hypercube with all nonbroken diagonals summing correctly[3].

- A *pandiagonal hypercube* is a perfect magic hypercube with all broken diagonals summing correctly.

(a magic hypercube is understood to be of dimension `rep(n,d)` and normal). Functions `is.semimagichypercube()`, `is.magichypercube()` and `is.perfect(a)` test for the first three properties; the fourth is not yet implemented. Function `is.diagonally.correct()` tests for correct summation of the 2^d (sic) long diagonals.

Magic hypercubes of order $4n$

Consider algorithm 1 generalized to a d-dimensional hypercube. The appropriate generalization of the repeating cell of the 8×8 magic square discussed above is not immediately obvious when considering figure 2, but the R formalism (viz `kronecker(diag(2),matrix(1,2,2))` makes it clear that the appropriate generalization is to replace `matrix(1,2,2)` with `array(1,rep(2,d))`.

The appropriate generalization for `diag(2)` (call it `g`) is not so straightforward, but one might be guided by the following requirements:

- The dimension of `g` must match the first argument to `kronecker()`, viz `rep(2,d)`

- The number of 0s must be equal to the number of 1s: `sum(g==1)==sum(g==0)`

- The observation that `diag(2)` is equal to its transpose would generalize to requiring that `aperm(g,K)` be identical to `g` for any permutation `K`.

These lead to specifying that `g[i1,...,id]` should be zero if $(i_1, \ldots, i_d)$ contains an odd number of 2s and one otherwise.

One appropriate R idiom would be to define a function `dimension(a,p)` to be an integer matrix with the same dimensions as `a`, with element $(n_1, n_2, ..., n_d)$ being n_p, then if `jj` $=$ $\sum_{i=1}^{d}$ `dimension(a,i)`, we can specify `g=jj*0` and then `g[jj%%2==1] <- 1`.

Another application of `kronecker()` gives a hypercube that is of extent $4m + 2$ in each of its `d` dimensions, and this may be trimmed off as above to give an array of dimensions `rep(4m,d)` using `do.call()` and `[<-`. The numbers may be filled in exactly as for the 2d case.

The resulting hypercube is magic, in the sense defined above[4], although it is not perfect; function `magichypercube.4n()` implements the algorithm. The ability to generate magic hypercubes of arbitrary dimension greater than one is apparently novel.

Standard form for hypercubes

Consider again the paper definition for Frénicle's standard form of a magic square `a`: it is rotated so that the smallest number appears at the top left; then if `a[1,2]<a[2,1]`, the transpose is taken.

When coding up such an algorithm in R with an eye to generalizing it to arbitrarily high dimensional hypercubes, it becomes apparent that "rotation" is not a natural operation. The generalization used in the package is directly suggested by R's array capabilities: it is a two-step process in which the first step is to maneuver the smallest possible element to position `[1,1,...,1]` using only operations that reverse the index of some (or all) dimensions. An example would be `a <- a[1:n,n:1,1:n,n:1]`.

The second step is to use function `aperm()` to ensure that the appropriate generalization of `a[1,2]<a[2,1]`, which would be

$$\texttt{a[1,1,...,1,2]} < \texttt{a[1,...,2,1]} < \ldots$$
$$\ldots < \texttt{a[1,2,...,1]} < \texttt{a[2,1,...,1]}$$

holds; the appropriate R idiom is `a <- aperm(a,order(-a[1+diag(d)]))`.

This generalization of Frénicle's standard form to arbitrary dimensional hypercubes appears to be new; it arises directly from the power and elegance of R's array handling techniques.

[3]This condition is quite restrictive; in the case of a tesseract, this would include subsets such as $\sum_{i=1}^{n} a[1, i, n-i+1, n]$ summing correctly.

[4]If I had a rigorous proof of this, the margin might be too narrow for it.

Conclusions

The R language is a natural environment for the investigation of magic squares and hypercubes; and the discipline of translating published algorithms into R idiom can yield new insight. These insights include a new generalization of Frénicle's standard form to hypercubes, and also what appears to be the first algorithm for generating magic hypercubes of any dimension,

Insofar as magic squares and hypercubes are worthy of attention, it is worth creating fast, efficient routines to carry out the "paper" algorithms of the literature. I hope that the `magic` package will continue to facilitate the study of these fascinating objects.

Acknowledgements

I would like to acknowledge the many stimulating and helpful comments made by the R-help list over the years.

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Programmer's Niche

How Do You Spell That Number?

John Fox

Frank Duan recently posted a question to the `r-help` mailing list asking how to translate numbers into words. The program described in this column is a cleaned-up and slightly enhanced version of my response to his question. I found the problem to be an interesting puzzle, and the solution uses several programming techniques that demonstrate the flexibility of R, including its ability to manipulate character-string data and to employ recursive function calls.

One intriguing aspect of the problem is that it required me to raise into consciousness my subconscious knowledge about how numbers are spoken and written in English. I was much more aware of these conventions in the languages (French and Spanish) that I had studied as a non-native speaker. A bit later, I realized that there are variations among English-speaking countries in the manner in which numbers are spoken and written down. Because I was born in the United States and have lived most of my adult life in Canada, I'm terminally confused about English spelling and usage. Canadian conventions are an amalgam of American and British rules.

In any event, it didn't take much time to see that the numbers from *one* to *nineteen* are represented by individual words; the numbers from *twenty-one* to *ninety-nine* are formed as compound words, with components for the tens and units digits — with the exceptions of multiples of ten (*twenty*, *thirty*, etc.), which are single words. The *Chicago Manual of Style* tells me that these compound words should be hyphenated (but offered little additional useful advice about how numbers are to be written out). Numbers from 100 to 999 are written by tacking on (at the left) a phrase like "six hundred" — that is, composed of a number from *one* to *nine* plus the suffix *hundred* (and there is no hyphen). Above this point, additional terms are added at the left, representing multiples of powers of 1000. In American English (and in Canada), the first few powers of 1000 have the following names, to be used as suffixes:

1000^1	*thousand*
1000^2	*million*
1000^3	*billion*
1000^4	*trillion*

Thus, for example, the number 210,363,258 would be rendered "two hundred ten million, three hundred sixty-three thousand, two hundred fifty-eight." There really is no point in going beyond trillions, because double-precision numbers can represent integers exactly only to about 15 decimal digits, or hundreds of trillions. Of course, I could allow numbers to be specified optionally by arbitrarily long character strings of numerals (e.g., `"210363258347237492310"`), but I didn't see a real need to go higher than hundreds of trillions.

One approach to converting numbers to words would be to manipulate the numbers as integers, but it seemed to me simpler to convert numbers to character strings of numerals, which could then be split into individual characters: (1) larger integers can be represented exactly as double-precision floating-point numbers than as integers in R; (2) it is easier to manipulate the individual numerals than to perform repeated integer arithmetic to extract digits; and (3) having the numerals in character form allows me to take advantage of R's ability to index vectors by element names (see below).

I therefore defined the following function to convert a number to a vector of characters containing the numerals composing the number:

```
> makeDigits <- function(x)
+ strsplit(as.character(x), "")[[1]]
```

Here are some examples of the use of this function:

```
> makeDigits(123456)
[1] "1" "2" "3" "4" "5" "6"
> makeDigits(-123456)
[1] "-" "1" "2" "3" "4" "5" "6"
> makeDigits(1000000000)
[1] "1" "e" "+" "0" "9"
```

Notice the problems revealed by the second and third examples: It's necessary to make provision for negative numbers, and R wants to render certain numbers in scientific notation.[1] By setting the `scipen` ("scientific notation penalty") option to a large number, we can avoid the second problem:

```
> options(scipen=100)
> makeDigits(1000000000)
 [1] "1" "0" "0" "0" "0" "0" "0" "0" "0" "0"
```

It also seemed useful to have a function that converts a vector of numerals in character form back into a number:

```
> makeNumber <- function(x)
+ as.numeric(paste(x, collapse=""))
> makeNumber(c("1", "2", "3", "4", "5"))
[1] 12345
```

Finally, by way of preparation, I constructed several vectors of number words:

```
> ones <- c("zero", "one", "two", "three",
+     "four", "five", "six", "seven",
+     "eight", "nine")
> teens <- c("ten", "eleven", "twelve",
+     "thirteen", "fourteen", "fifteen",
+     "sixteen", " seventeen", "eighteen",
+     "nineteen")
> names(ones) <- names(teens) <- 0:9
> tens <- c("twenty", "thirty", "forty",
+     "fifty", "sixty", "seventy", "eighty",
+     "ninety")
> names(tens) <- 2:9
> suffixes <- c("thousand,", "million,",
+     "billion,", "trillion,")
```

Because the names of the elements of the first three vectors are numerals, they can conveniently be indexed; for example:

```
> ones["5"]
     5
"five"
> teens["3"]
         3
"thirteen"
> tens["7"]
        7
"seventy"
```

The vector of suffixes includes a comma after each word.

Figure 1 shows a function for converting a single integer to words; I've added line numbers to make it easier to describe how the function works:

And here are some examples of its use, wrapping long lines of output to fit on the page:

```
> number2words(123456789)
[1] "one hundred twenty-three million,
      four hundred fifty-six thousand,
      seven hundred eighty-nine"
> number2words(-123456789)
[1] "minus one hundred twenty-three million,
      four hundred fifty-six thousand,
      seven hundred eighty-nine"
> number2words(-123456000)
[1] "minus one hundred twenty-three million,
      four hundred fifty-six thousand"
```

I believe that the first five lines of the function are essentially self-explanatory. The rest of the function probably requires some explanation, however:

[6] If the number is composed of a single digit, then we can find the answer by simply indexing into the vector `ones`; the function `as.vector` is used to remove the name of (i.e., the numeral labelling) the selected element.

[7-9] If the number is composed of two digits and is less than or equal to 19, then we can get the answer by indexing into `teens` with the last digit (i.e., the second element of the `digits` vector). If the number is 20 or larger, then we need to attach the tens digit to the ones digit, with a hyphen in between. If,

[1] I don't want to mislead the reader: I discovered these and other problems the hard way, when they surfaced as bugs. The account here is a reconstruction that avoids my missteps. I can honestly say, however, that it took me much longer to write this column explaining how the program works than to write the original program. Moreover, in the process of writing up the program, I saw several ways to improve it, especially in clarity — a useful lesson.

```
[ 1]  number2words <- function(x){
[ 2]      negative <- x < 0
[ 3]      x <- abs(x)
[ 4]      digits <- makeDigits(x)
[ 5]      nDigits <- length(digits)
[ 6]      result <- if (nDigits == 1) as.vector(ones[digits])
[ 7]      else if (nDigits == 2)
[ 8]          if (x <= 19) as.vector(teens[digits[2]])
[ 9]              else trim(paste(tens[digits[1]], "-", ones[digits[2]], sep=""))
[10]      else if (nDigits == 3) {
[11]          tail <- makeNumber(digits[2:3])
[12]          if (tail == 0) paste(ones[digits[1]], "hundred")
[13]          else trim(paste(ones[digits[1]], "hundred", number2words(tail)))
[14]          }
[15]      else {
[16]          nSuffix <- ((nDigits + 2) %/% 3) - 1
[17]          if (nSuffix > length(suffixes) || nDigits > 15)
[18]              stop(paste(x, "is too large!"))
[19]          pick <- 1:(nDigits - 3*nSuffix)
[20]          trim(paste(number2words(makeNumber(digits[pick])),
[21]              suffixes[nSuffix], number2words(makeNumber(digits[-pick]))))
[22]          }
[23]      if (negative) paste("minus", result) else result
[24]      }
```

Figure 1: A function to convert a single integer into words.

however, the ones digit is 0, `ones["0"]` is `"zero"`, and thus we have an embarrassing result such as `"twenty-zero"`. More generally, the program can produce spurious hyphens, commas, spaces, and the strings `", zero"` and `"-zero"` in appropriate places. My solution was to write a function to trim these off:

```
trim <- function(text){
    gsub("(^\ *)|((\ *|-|,\ zero|-zero)$)",
         "", text)
    }
```

The `trim` function makes use of R's ability to process "regular expressions." See Lumley (2003) for a discussion of the use of regular expressions in R.

`[10-14]` If the number consists of three digits, then the first digit is used for hundreds, and the remaining two digits can be processed as an ordinary two-digit number; this is done by a recursive call to `number2words`[2] — unless the last two digits are 0, in which case, we don't need to convert them into words. The hundreds digit is then pasted onto the representation of the last two digits, and the result is trimmed. Notice that `makeNumber` is used to put the last two digits back into a number (called `tail`).

`[15-22]` Finally, if the number contains more than three digits, we're into the realm of thousands, millions, etc. The computation on line `[16]` determines with which power of 1000 we're dealing. Then, if the number is not too large, the appropriate digits are stripped off from the left of the number and attached to the proper suffix; the remaining digits to the right are recomposed into a number and processed with a recursive call, to be attached at the right.

`[23]` If the original number was negative, the word `"minus"` is pasted onto the front before the result is returned.

The final function, called `numbers2words` (shown in Figure 2), adds some bells and whistles: The various vectors of names are defined locally in the function; the utility functions `makeDigits`, `makeNumbers`, and `trim`, are similarly defined as local functions; and the function `number2words`, renamed `helper`, is also made local. Using a helper function rather than a recursive call permits efficient vectorization, via `sapply`, at the end of `numbers2words`. Were

[2]It's traditional in S to use `Recall` for a recursive function call, but I'm not fond of this convention, and I don't see an argument for it here: It's unlikely that `number2words` will be renamed, and in any event, it will become a local function in the final version of the program (see below).

numbers2words to call itself recursively, the local definitions of objects (such as the vector ones and the function trim) would be needlessly recomputed at each call, rather than only once. Because of R's lexical scoping, objects defined in the environment of numbers2words are visible to helper. For more on recursion in R, see Venables (2001).

numbers2words includes a couple of additional features. First, according to the *Oxford English Dictionary*, the definition of "billion" differs in the U.S. and (traditionally) in Britain: "1. orig. and still commonly in Great Britain: A million millions. (= U.S. trillion.) ... 2. In U.S., and increasingly in Britain: A thousand millions." Thus, if the argument billion is set to "UK", a different vector of suffixes is used. Moreover, provision is made to avoid awkward translations that repeat the word "million," such as "five thousand million, one hundred million, ... ," which is instead, and more properly rendered as "five thousand, one hundred million, ..."

Second, Bill Venables tells me that outside of the U.S., it is common to write or speak a number such 101 as "one hundred and one" rather than as "one hundred one." (Both of these phrases seem correct to me, but as I said, I'm hopelessly confused about international variations in English.) I have therefore included another argument, called and, which is pasted into the number at the appropriate point. By default, this argument set is to "" when billion is "US" and to "and" when billion is "UK".

Some examples, again wrapping long lines of output:

```
> numbers2words(c(1234567890123, -0123, 1000))
[1] "one trillion,
      two hundred thirty-four billion,
      five hundred sixty-seven million,
      eight hundred ninety thousand,
      one hundred twenty-three"

[2] "minus one hundred twenty-three"
[3] "one thousand"
> numbers2words(c(1234567890123, -0123, 1000),
+     billion="UK")

[1] "one billion,
      two hundred and thirty-four thousand,
      five hundred and sixty-seven million,
      eight hundred and ninety thousand,
      one hundred and twenty-three"

[2] "minus one hundred and twenty-three"
[3] "one thousand"

> numbers2words(c(1234567890123, -0123, 1000),
+     and="and")

[1] "one trillion,
      two hundred and thirty-four billion,
      five hundred and sixty-seven million,
      eight hundred and ninety thousand,
      one hundred and twenty-three"

[2] "minus one hundred and twenty-three"
[3] "one thousand"
```

Finally, a challenge to the reader: At present, numbers2words rounds its input to whole numbers. Modify the program so that it takes a digits argument (with default 0), giving the number of places to the right of the decimal point to which numbers are to be rounded, and then make provision for translating such numbers (e.g., 1234567.890) into words.

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```
numbers2words <- function(x, billion=c("US", "UK"),
        and=if (billion == "US") "" else "and"){
    billion <- match.arg(billion)
    trim <- function(text){
        gsub("(^\ *)|((\ *|-|,\ zero|-zero)$)", "", text)
        }
    makeNumber <- function(x) as.numeric(paste(x, collapse=""))
    makeDigits <- function(x) strsplit(as.character(x), "")[[1]]
    helper <- function(x){
        negative <- x < 0
        x <- abs(x)
        digits <- makeDigits(x)
        nDigits <- length(digits)
        result <- if (nDigits == 1) as.vector(ones[digits])
        else if (nDigits == 2)
            if (x <= 19) as.vector(teens[digits[2]])
                else trim(paste(tens[digits[1]], "-", ones[digits[2]], sep=""))
        else if (nDigits == 3) {
            tail <- makeNumber(digits[2:3])
            if (tail == 0) paste(ones[digits[1]], "hundred")
            else trim(paste(ones[digits[1]], trim(paste("hundred", and)),
                helper(tail)))
            }
        else {
            nSuffix <- ((nDigits + 2) %/% 3) - 1
            if (nSuffix > length(suffixes) || nDigits > 15)
                stop(paste(x, "is too large!"))
            pick <- 1:(nDigits - 3*nSuffix)
            trim(paste(helper(makeNumber(digits[pick])),
                suffixes[nSuffix], helper(makeNumber(digits[-pick]))))
            }
        if (billion == "UK"){
            words <- strsplit(result, " ")[[1]]
            if (length(grep("million,", words)) > 1)
                result <- sub(" million, ", ", ", result)
            }
        if (negative) paste("minus", result) else result
        }
    opts <- options(scipen=100)
    on.exit(options(opts))
    ones <- c("zero", "one", "two", "three", "four", "five", "six", "seven",
        "eight", "nine")
    teens <- c("ten", "eleven", "twelve", "thirteen", "fourteen", "fifteen",
        "sixteen", " seventeen", "eighteen", "nineteen")
    names(ones) <- names(teens) <- 0:9
    tens <- c("twenty", "thirty", "forty", "fifty", "sixty", "seventy", "eighty",
        "ninety")
    names(tens) <- 2:9
    suffixes <- if (billion == "US")
                    c("thousand,", "million,", "billion,", "trillion,")
                else
                    c("thousand,", "million,", "thousand million,", "billion,")
    x <- round(x)
    if (length(x) > 1) sapply(x, helper) else helper(x)
    }
```

Figure 2: A function to convert a vector of integers into a vector of strings containing word-equivalents of the integers.

Book Review of Julian J. Faraway: Linear Models with R

Chapman & Hall/CRC, Boca Raton FL, USA, 2005
229 pages, ISBN 1-58488-425-8
http://www.stat.lsa.umich.edu/∼faraway/LMR

This book is useful to serve for the practical aspects of an advanced undergraduate linear regression course. Regarding the potential readership, the Author writes in the preface that the book is "not introductory" and that it "presumes some knowledge of basic statistical theory and practice. Readers are expected to know the essentials of statistical inference such as estimation, hypothesis testing and confidence intervals. A basic knowledge of data analysis is presumed. Some linear algebra and calculus are also required." Thus this book is most suitable for undergraduate statistics majors at least half way through their degrees. The book needs to be accompanied by a theoretical book, such as Seber and Lee (2003). A somewhat similar competitor to the book is Fox (2002).

With a large number (16) of chapters in this smallish book, most of them are short and mention ideas briefly. Of course, some chapters are on core practical topics such as residual diagnostics, transformations, weighted and generalized least squares, ANOVA (factorial designs, block designs), ANCOVA, variable selection techniques, and inference. A good feature of the book is that more 'optional' topics are covered, include missing values, regression splines, robust regression (M-estimation and least trimmed squares), permutation tests, shrinkage methods such as partial least squares, measurement error models including SIMEX, latin squares and iteratively reweighted least squares. Most instructors are unlikely to be familiar with all these topics, and the book does a good job in giving a very gentle introduction to these topics. The reader is usually referred to references at the back for further reading.

The book has two small appendices. The first describes R installation, functions and data, while the second is a quick introduction to R. The examples in the book are based on R 1.9.0. In my copy there were a few font problems, e.g., p.189 has $(\not\beta)_{ij}$ instead of $(\alpha\beta)_{ij}$.

The tone of the book is that of an informal tutorial with some necessary theory interdispersed throughout. Explanations are good overall, and the mathematical notation is quite standard. The Author's website serves as the repository for the book's package, called `faraway`, and includes errata, R commands and data sets (the package is also on CRAN.) The Author writes "Data analysis cannot be learned without actually doing it" and this is facilitated by practical exercises (which are usually short and sharp) at the end of each chapter. Solutions appear unavailable.

The book centers on `lm()` and assumes familiarity with the S language, e.g., I found it referred to "`.`" in a formula without reminding or telling the reader that it means all variables in the data frame other than the response. The book is rather unsuitable as a reference book, for example, summation constraints $\sum_{j=1}^{J} \alpha_j = 0$ is a popular parameterization for a factor with J levels. The function `contr.sum` is alluded to but not mentioned directly in the book, nor how to switch between different parameterizations. Ideally, a handy summary of topics such as the Wilkinson-Rogers operators (e.g., `*`, `/`, `:`) and all the different contrast options available should be put into an appendix for fast and easy reference. This would make Chambers and Hastie (1991) less necessary for students to buy or refer to. The book makes good and frequent use of basic graphics with a liberal sprinkling of plots everywhere, and many examples.

Altogether, there are 27 data sets used in the book; the large majority of these are small. Even though the figures are in black and white, the reader is not encouraged to use colors in the plotting—something very useful on a computer screen. It would be good also that the reader be reminded how to create PDF files of figures (especially if the user uses Linux), which is useful if the user writes reports.

The book has many good points but I picked up a few bad points. For example, the use of extractor functions is not always taken where possible, e.g., `coef(fit)` should be used instead of `fit$coef`. Also, numerous examples use cut-and-paste from previous output rather than extracting quantities from objects, for example, p.20, `60.975` is used rather than `mdls$sigma`. I would have liked the paragraph on additive models expanded to make the reader aware of how to check the linearity assumptions using `lm()` and regression splines.

I thought there were a number of omissions. The prediction problem should be mentioned (in S-PLUS data-dependent terms such as `scale(x)`, `poly(x, 2)` and `bs(x)` give problems, whereas in R, a data-dependent function called inside another function are problematic, e.g., `poly(scale(x), 2)`). Other omissions include not mentioning computational details such as the QR-algorithm and not using more advanced graphics such as those found in the `lattice` package.

Although I agree that the book is "not introductory", neither is it advanced. For example, a broken stick regression model is fitted in

Section 7.2.1. Improvements to this example include using `coef()` instead of `$coef`, and using the `predict` generic function, i.e., `predict(gb, data.frame(pop15=seq(20,48,by=1)))`. The two (dotted) lines described in the text actually do not show up on the plot. Furthermore, although it is instructional to create two basis functions `lhs()` and `rhs()`, the reader is not informed that `bs(pop15, degree=1, df=1, knot=35)` would be equivalent.

In conclusion, the book is quite suitable to serve for the practical component of an advanced undergraduate course in linear models to reasonably prepared students. A sequel on generalized linear models and extensions would be a natural next step!

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R Foundation News

by Bettina Grün

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Changes in R

by the R Core Team

User-visible changes

- box plots by `boxplot()` or `bxp()` now have the median line three times the normal line width in order to distinguish it from the quartile ones.

- Unix-alike versions of R can now be used in UTF-8 locales on suitably equipped OSes. See the internationalization section below.

- The meaning of 'encoding' for a connection has changed: See the internationalization section below.
- There has been some rationalization of the format of warning/error messages, to make them easier to translate. Generally names of functions and arguments are single-quoted, and classes double-quoted.
- Reading text files with embedded `"\"` (as in Windows file names) may now need to use `scan(* , allowEscapes = FALSE)`, see also below.

New features

- %% now warns if its accuracy is likely to be affected by lack of precision (as in 1e18 %% 11, the unrealistic expectation of PR#7409), and tries harder to return a value in range when it is.
- `abbreviate()` now warns if used with non-ASCII chars, as the algorithm is designed for English words.
- The default methods for `add1()` and `drop1()` check for changes in the number of cases in use.

  The "lm" and "glm" methods for `add1()` quoted the <none> model on the original fitted values when using (with a warning) a smaller set of cases for the expanded models.
- Added `alarm()` function to generate a bell or beep or visual alert.
- `all/any()` now attempt to coerce their arguments to logical, as documented in the Blue Book. This means e.g. `any(list())` works.
- New functions for multivariate linear models: `anova.mlm()`, `SSD()`, `estVar()`, `mauchley.test()` (for sphericity).

  `vcov()` now does something more sensible for "mlm" class objects.
- `as.data.frame.table()` has a new argument 'responseName' (contributed by Bill Venables).
- `as.dist()` and `cophenetic()` are now generic, and the latter has a new method for objects of class "dendrogram".
- `as.ts()` is now generic.
- `binomial()` has a new "cauchit" link (suggested by Roger Koenker).
- `chisq.test()` has a new argument 'rescale.p'. It is now possible to simulate (slowly) the P value also in the 1D case (contributed by Rolf Turner).
- `choose(n,k)` and `lchoose(.)` now also work for arbitrary (real) n in accordance with the general binomial theorem. `choose(*,k)` is more accurate (and faster) for small k.
- Added `colorRamp()` and `colorRampPalette()` functions for color interpolation.
- `colSums()/rowSums()` now allow arrays with a zero-length extent (requested by PR#7775).
- `confint()` has stub methods for classes "glm" and "nls" that invoke those in package MASS. This avoids using the "lm" method for "glm" objects if MASS is not attached.

  `confint()` has a default method using asymptotic normality.
- `contr.SAS()` has been moved from the 'nlme' package to the 'stats' package.
- New function `convertColors()` maps between color spaces. `colorRamp()` uses it.
- The `cov()` function in the non-Pearson cases now ranks data after removal of missing values, not before. The pairwise-complete method should now be consistent with cor.test. (Code contributed by Shigenobu Aoki.)
- Added `delayedAssign()` function to replace `delay()`, which is now deprecated.
- `dir.create()` has a new argument 'recursive' serving the same purpose as Unix's `mkdir -p`.
- `do.call()` now takes either a function or a character string as its first argument. The supplied arguments can optionally be quoted.
- `duplicated()` and `unique()` now accept "list" objects, but are fast only for simple list objects.
- `ecdf()` now has jumps of the correct size (a multiple of $1/n$) if there are ties. (Wished by PR#7292).
- `eff.aovlist()` assumed orthogonal contrasts for any term with more than one degree of freedom: this is now documented and checked for. Where each term only occurs in only one stratum the efficiencies are all one: this is detected and orthogonal contrasts are not required.
- New function `encodeString()` to encode character strings in the same way that printing does.

- `file("clipboard")` now work for reading the primary selection on Unix-alikes with an active X11 display. (It has long worked for reading and writing under Windows.) The secondary selection can also be read: see ?file.

  `file()` now allows mode "w+b" as well as "w+".

- `file.append()` has been tuned, including for the case of appending many files to a single file.

- Functions `flush.console()` and `select.list()` are now available on all platforms. There is a Tcl/Tk-based version of `select.list()` called `tk_select.list()` in package tcltk.

- `gc()` now reports maximum as well as current memory use.

- A new function `getGraphicsEvent()` has been added which will allow mouse or keyboard input from a graphics device. (NB: currently only the Windows screen device supports this function. This should improve before the 2.1.0 release.)

- New functions `gray.colors()/grey.colors()` for gray color palettes.

- `grep()`, `gsub()`, `sub()` and `regexpr()` now always attempt to coerce their 'pattern', 'x', 'replacement' and 'text' arguments to character. Previously this was undocumented but done by `[g]sub()` and `regexpr()` for some values of their other arguments. (Wish of PR#7742.)

- `gsub/sub()` have a new 'fixed' method.

- New function `hcl()` for creating colors for a given hue, chroma and luminance (i.e. perceptual hsv).

- `isTRUE()` convenience function to be used for programming.

- `kmeans()` now returns an object of class "kmeans" which has a `print()` method.

  Two alternative algorithms have been implemented.

  If the number of centres is supplied, it has a new option of multiple random starts.

- The limits on the grid size in `layout()` are now documented, and have been raised somewhat by using more efficient internal structures.

- `legend()` now accepts positioning by keyword, e.g. "topleft", and can put a title within the legend. (Suggested by Elizabeth Purdom in PR#7400.)

- `mahalanobis()` now has a '...' argument which is passed to `solve()` for computing the inverse of the covariance matrix, this replaces the former 'tol.inv' argument.

- `menu()` uses a multi-column layout if possible for more than 10 choices.

  `menu(graphics = TRUE)` is implemented on most platforms via `select.list()` or `tk_select.list()`.

- New function `message()` in 'base' for generating "simple" diagnostic messages, replacing such a function in the 'methods' package.

- `na.contiguous()` is now (S3) generic with first argument renamed to 'object'.

- New function `normalizePath()` to find canonical paths (and on Windows, canonical names of components).

- The default in `options("expressions")` has been increased to 5000, and the maximal settable value to 500000.

- `p.adjust()` has a new method "BY".

- `pbeta()` now uses a different algorithm for large values of at least one of the shape parameters, which is much faster and is accurate and reliable for very large values. (This affects `pbinom()`, `pf()`, `qbeta()` and other functions using pbeta at C level.)

- `pch="."` now by default produces a rectangle at least 0.01" per side on high-resolution devices. (It used to be one-pixel square even on high-resolution screens and Windows printers, but 1/72" on `postscript()` and `pdf()` devices.) Additionally, the size is now scalable by 'cex'; see ?points and note that the details are subject to change.

- `pdf()` now responds to the 'paper' and 'pagecentre' arguments. The default value of 'paper' is "special" for backward-compatibility (this is different from the default for `postscript()`).

- `plot.data.frame()` tries harder to produce sensible plots for non-numeric data frames with one or two columns.

- The `predict()` methods for "prcomp" and "princomp" now match the columns of 'newdata' to the original fit using column names if these are available.

- New function `recordGraphics()` to encapsulate calculations and graphics output together on graphics engine display list. To be used with care.

- New function `RSiteSearch()` to query R-related resources on-line (contributed by Jonathan Baron and Andy Liaw).

- `scan()` arranges to share storage of duplicated character strings read in: this can dramatically reduce the memory requirements for large character vectors which will subsequently be turned into factors with relatively few levels. For a million items this halved the time and reduced storage by a factor of 20.

  `scan()` has a new argument 'allowEscapes' (default TRUE) that controls when C-style escapes in the input are interpreted. Previously only `\n` and `\r` were interpreted, and then only within quoted strings when no separator was supplied.

  `scan()` used on an open connection now pushes back on the connection its private 'ungetc' and so is safer to use to read partial lines.

- `scatter.smooth()` and `loess.smooth()` now handle missing values in their inputs.

- `seq.Date()` and `seq.POSIXt()` now allow 'to' to be before 'from' if 'by' is negative.

- `sprintf()` has been enhanced to allow the POSIX/XSI specifiers like "%2$6d", and also accepts "%x" and "%X".

  `sprintf()` does limited coercion of its arguments.

  `sprintf()` accepts vector arguments and operates on them in parallel (after re-cycling if needed).

- New function `strtrim()` to trim character vectors to a display width, allowing for double-width characters in multi-byte character sets.

- `subset()` now has a method for matrices, similar to that for data frames.

- Faster algorithm in `summaryRprof()`.

- `sunflowerplot()` has new arguments 'col' and 'bg'.

- `sys.function()` now has argument 'which' (as has long been presaged on its help page).

- `Sys.setlocale("LC_ALL", )` now only sets the locale categories which R uses, and `Sys.setlocale("LC_NUMERIC", )` now gives a warning (as it can cause R to malfunction).

- `unclass()` is no longer allowed for environments and external pointers (since these cannot be copied and so `unclass()` was destructive of its argument). You can still change the "class" attribute.

- File-name matching is no longer case-insensitive with `unz()` connections, even on Windows.

- New argument 'immediate.' to `warning()` to send an immediate warning.

- New convenience wrappers `write.csv()` and `write.csv2()`.

- There is a new version for `write.table()` which is implemented in C. For simple matrices and data frames this is several times faster than before, and uses negligible memory compared to the object size.

  The old version (which no longer coerces a matrix to a data frame and then back to a matrix) is available for now as `write.table0()`.

- The functions `xinch()`, `yinch()`, and `xyinch()` have been moved from package 'grDevices' into package 'graphics'.

- Plotmath now allows underline in expressions. (PR#7286, contributed by Uwe Ligges.)

- BATCH on Unix no longer sets `--gui="none"` as the X11 module is only loaded if needed.

- The X11 module (and the hence `X11()`, `jpeg()` and `png()` devices and the X-based dataentry editor) is now in principle available under all Unix GUIs except `--gui="none"`, and this is reflected in `capabilities()`.

  `capabilities("X11")` determines if an X server can be accessed, and so is more likely to be accurate.

- Printing of arrays now honours the 'right' argument if there are more than two dimensions.

- Tabular printing of numbers now has headers right-justified, as they were prior to version 1.7.0 (spotted by Rob Baer).

- Lazy-loading databases are now cached in memory at first use: this enables R to run much faster from slow file systems such as USB flash drives. There is a small (less than 2Mb) increase in default memory usage.

- The implicit class structure for numeric vectors has been changed, so that integer/real vectors try first methods for class "integer"/"double" and then those for class "numeric".

  The implicit classes for matrices and arrays have been changed to be "matrix"/"array" followed by the `class(es)` of the underlying vector.

- `splines::splineDesign()` now allows the evaluation of a B-spline basis everywhere instead of just inside the "inner" knots, by setting the new argument 'outer.ok = TRUE'.

- Hashing has been tweaked to use half as much memory as before.

- Readline is not used for tilde expansion when R is run with `--no-readline`, nor from embedded applications. Then " name" is no longer expanded, but " " still is.

- The regular expression code is now based on that in glibc 2.3.3. It has stricter conformance to POSIX, so metachars such as + * may need to be escaped where before they did not (but could have been).

- New encoding 'TeXtext.enc' improves the way `postscript()` works with Computer Modern fonts.

- Replacement in a non-existent column of a data frame tries harder to create a column of the correct length and so avoid a corrupt data frame.

- For Windows and readline-based history, the saved file size is re-read from R_HISTSIZE immediately before saving.

- Collected warnings during start-up are now printed before the initial prompt rather than after the first command.

- Changes to package 'grid':

  - `preDrawDetails()`, `drawDetails()`, and `postDrawDetails()` methods are now recorded on the graphics engine display list. This means that calculations within these methods are now run when a device is resized or when output is copied from one device to another.
  - Fixed bug in `grid.text()` when 'rot' argument has length 0. (privately reported by Emmanuel Paradis)
  - New `getNames()` function to return just the names of all top-level grobs on the display list.
  - Recording on the grid display list is turned off within `preDrawDetails()`, `drawDetails()`, and `postDrawDetails()` methods.
  - Grid should recover better from errors or user-interrupts during drawing (i.e., not leave you in a strange viewport or with strange graphical parameter settings).
  - New function `grid.refresh()` to redraw the grid display list.
  - New function `grid.record()` to capture calculations with grid graphics output.
  - grobWidth and grobHeight ("grobwidth" and "grobheight" units) for primitives (text, rects, etc, ...) are now calculated based on a bounding box for the relevant grob.
    NOTE: this has changed the calculation of the size of a scalar rect (or circle or lines).
  - New arguments 'warn' and 'wrap' for function `grid.grab()`
  - New function `grid.grabExpr()` which captures the output from an expression (i.e., not from the current scene) without doing any drawing (i.e., no impact on the current scene).
  - `upViewport()` now (invisibly) returns the path that it goes up (suggested by Ross Ihaka).
  - The 'gamma' gpar has been deprecated (this is a device property not a property of graphical objects; suggested by Ross Ihaka).
  - New 'lex' gpar; a line width multiplier.
  - `grid.text()` now handles any language object as mathematical annotation (instead of just expressions).
  - `plotViewport()` has default value for 'margins' argument (that match the default value for `par(mar)`).
  - The 'extension' argument to `dataViewport()` can now be vector, in which case the first value is used to extend the xscale and the second value is used to extend the y scale. (suggested by Ross Ihaka).
  - All 'just' arguments (for viewports, layouts, rectangles, text) can now be numeric values (typically between 0 [left] and 1 [right]) as well as character values ("left", "right", ...).
    For rectangles and text, there are additional 'hjust' and 'vjust' arguments which allow numeric vectors of justification in each direction (e.g., so that several pieces of text can have different justifications). (suggested by Ross Ihaka)
  - New 'edits' argument for `grid.xaxis()` and `grid.yaxis()` to allow specification of on-the-fly edits to axis children.
  - `applyEdit(x, edit)` returns x if target of edit (i.e., child specified by a gPath) cannot be found.
  - Fix for calculation of length of max/min/sum unit. Length is now (correctly) reported as 1 (was reported as length of first arg).

  - Viewport names can now be any string (they used to have to be a valid R symbol).
  - The 'label' argument for `grid.xaxis()` and `grid.yaxis()` can now also be a language object or string vector, in which case it specifies custom labels for the tick marks.

Internationalization

- Unix-alike versions of R can now be used in UTF-8 and other multi-byte locales on suitably equipped OSes if configured with option `--enable-mbcs` (which is the default). [The changes to font handling in the X11 module are based on the Japanization patches of Eiji Nakama.]

  Windows versions of R can be used in 'East Asian' locales on suitable versions of Windows.

  See the 'Internationalization' chapter in the 'Installation and Administration' manual.

- New command-line flag `--encoding` to specify the encoding to be assumed for stdin (but not for a console).

- New function `iconv()` to convert character vectors between encodings, on those OSes which support this. See the new `capabilities("iconv")`.

- The meaning of 'encoding' for a connection has changed: it now allows any charset encoding supported by iconv on the platform, and can re-encode output as well as input.

  As the new specification is a character string and the old was numeric, this should not cause incorrect operation.

- New function `localeToCharset()` to find/guess `encoding(s)` from the locale name.

- `nchar()` returns the true number of bytes stored (including any embedded nuls), this being 2 for missing values. It has an optional argument 'type' with possible non-default values "chars" and "width" to give the number of characters or the display width in columns.

- Characters can be entered in hexadecimal as e.g. `\x9c`, and in UTF-8 and other multibyte locales as `\uxxxx`, `\u{xxxx}`, `\Uxxxxxxxx` or `\U{xxxxxxxx}`. Non-printable Unicode characters are displayed C-style as `\uxxxx` or `\Uxxxxxxxx`.

- LC_MONETARY is set to the locale, which affects the result of `Sys.localeconv()`, but nothing else in R itself. (It could affect add-on packages.)

- `source()` now has an 'encoding' argument which can be used to make it try out various possible encodings. This is made use of by `example()` which will convert (non-UTF-8) Latin-1 example files in a UTF-8 locale.

- `read/writeChar()` work in units of characters, not bytes.

- `.C()` now accepts an ENCODING= argument where re-encoding is supported by the OS. See 'Writing R Extensions'.

- delimMatch (tools) now reports match positions and lengths in units of characters, not bytes. The delimiters can be strings, not just single ASCII characters.

- .Rd files can indicate via a `\encoding{}` argument the encoding that should be assumed for non-ASCII characters they contain.

- Phrases in .Rd files can be marked by `\enc{}{}` to show a transliteration to ASCII for use in e.g. text help.

- The use of 'pch' in `points()` now allows for multi-byte character sets: in such a locale a glyph can either be specified as a multi-byte single character or as a number, the Unicode point.

- New function `l10n_info()` reports on aspects of the locale/charset currently in use.

- `scan()` is now aware of double-byte locales such as Shift-JIS in which ASCII characters can occur as the second ('trail') byte.

- Functions `sQuote()` and `dQuote()` use the Unicode directional quotes if in a UTF-8 locale.

- The infrastructure is now in place for C-level error and warning messages to be translated and used on systems with Native Language Support. This has been used for the startup message in English and to translate Americanisms such as 'color' into English: translations to several other languages are under way, and some are included in this release.

  See 'Writing R Extensions' for how to make use of this in a package: all the standard packages have been set up to do translation, and the 'language' 'en@quot' is implemented to allow Unicode directional quotes in a UTF-8 locale.

- R-level `stop()`, `warning()` and `message()` messages can be translated, as can other messages via the new function `gettext()`. Tools `xgettext()` and `xgettext2pot()` are provided in package tools to help manage error messages.

  `gettextf()` is a new wrapper to call `sprintf()` using `gettext()` on the format string.

- Function `ngettext()` allows the management of singular and plural forms of messages.

Utilities

- New functions `mirror2html()` and `checkCRAN()`.
- R CMD check has a new option '`--use-valgrind`'.
- R CMD check now checks that Fortran and C++ files have LF line endings, as well as C files. It also checks Makevars[.in] files for portable compilation flags.
- R CMD check will now work on a source tarball and prints out information about the version of R and the package.
- `tools:::.install_package_code_files()` (used to collate R files when installing packages) ensures files are separated by a line feed.
- `vignette()` now returns an object of class "vignette" whose `print()` method opens the corresponding PDF file. The `edit()` method can be used to open the code of the vignette in an editor.
- R CMD INSTALL on Unix has a new option '`--build`' matching that on Windows, to package as tarball the installed package.
- R CMD INSTALL on Unix can now install binary bundles.
- R CMD build now changes src files to LF line endings if necessary.
- R CMD build now behaves consistently between source and binary builds: in each case it prepares a source directory and then either packages that directory as a tarball or calls `R CMD INSTALL -build` on the prepared sources.

  This means that R CMD build `--binary` now respects .Rbuildignore and will rebuild vignettes (unless the option `--no-vignettes` is used). For the latter, it now installs the current sources into a temporary library and uses that version of the package/bundle to rebuild the vignettes.
- R CMD build now reports empty directories in the source tree.
- New function `write_PACKAGES()` in package 'tools' to help with preparing local package repositories. (Based on a contribution by Uwe Ligges.) How to prepare such repositories is documented in the 'R Installation and Administration' manual.
- `package.skeleton()` adds a bit more to DESCRIPTION.
- Sweave changes:
  - `\usepackage[nogin]{Sweave}` in the header of an Sweave file suppresses auto-setting of graphical parameters such as the width of the graphics output.
  - The new `\SweaveInput{}` command works similar to LaTeX's `\input{}` command.
  - Option value `strip.white=all` strips all blank lines from the output of a code chunk.
  - Code chunks with `eval=false` are commented out by `Stangle()` and hence no longer tested by R CMD check.

Documentation

- File doc/html/faq.html no longer exists, and doc/manual/R-FAQ.html (which has active links to other manuals) is used instead. (If makeinfo >= 4.7 is not available, the version on CRAN is linked to.)
- Manual 'Writing R Extensions' has further details on writing new front-ends for R using the new public header files.
- There are no longer any restrictions on characters in the `\name{}` field of a .Rd file: in particular _ is supported.

C-level facilities

- There are new public C/C++ header files Rinterface.h and R_ext/RStartup.h for use with external GUIs.
- Added an `onExit()` function to graphics devices, to be executed upon user break if non-NULL.
- ISNAN now works even in C++ code that undefines the 'isnan' macro.
- R_alloc's limit on 64-bit systems has been raised from just under 2^{31} bytes (2Gb) to just under 2^{34} (16Gb), and is now checked.
- New math utility functions `log1pmx(x)`, `lgamma1p(x)`, `logspace_add(logx, logy)`, and `logspace_sub(logx, logy)`.

Deprecated & defunct

- The aqua module for MacOS X has been removed: `--with-aqua` now refers to the unbundled Cocoa GUI.
- Capabilities "bzip2", "GNOME, "libz" and "PCRE" are defunct.
- The undocumented use of `UseMethod()` with no argument was deprecated in 2.0.1 and is now regarded as an error.
- Capability "IEEE754" is deprecated.
- The 'CRAN' argument to `update.packages()`, `old.packages()`, `new.packages()`, `download.packages()` and `install.packages()` is deprecated in favour of 'repos', which replaces it as a positional argument (so this is only relevant for calls with named args).
- The S3 methods for getting and setting names of "dist" objects have been removed (as they provided names with a different length from the "dist" object itself).
- Option "repositories" is no longer used and so not set.
- `loadURL()` is deprecated in favour of `load(url())`.
- `delay()` is deprecated. Use `delayAssign()` instead.

Installation changes

- New configure option `--enable-utf8` to enable support for UTF-8 locales, on by default.
- R_XTRA_[CF]FLAGS are now used during the configuration tests, and [CF]PICFLAGS if `--enable-R-shlib` was specified. This ensures that features such as inlining are only used if the compilation flags specified support them. (PR#7257)
- Files FAQ, RESOURCES, doc/html/resources.html are no longer in the SVN sources but are made by 'make dist'.
- The GNOME GUI is unbundled, now provided as a package on CRAN.
- Configuring without having the recommended packages is now an error unless `--with-recommended-packages=no` (or equivalent) is used.
- Configuring without having the X11 headers and libraries is now an error unless `--with-x=no` (or equivalent) is used.
- Configure tries harder to find a minimal set of FLIBS. Under some circumstances this may remove from R_LD_LIBRARY_PATH path elements that ought to have specified in LDFLAGS (but were not).
- The C code for most of the graphics device drivers and their afm files are now in package grDevices.
- R is now linked against ncurses/termlib/termcap only if readline is specified (now the default) and that requires it.
- Makeinfo 4.7 or later is now required for building the HTML and Info versions of the manuals.

Installation changes

- There are new types of packages, identified by the Type field in the DESCRIPTION file. For example the GNOME console is now a separate package (on CRAN), and translations can be distributed as packages.
- There is now support of installing from within R both source and binary packages on MacOS X and Windows. Most of the R functions now have a 'type' argument defaulting to `getOption("pkgType")` and with possible values "source", "win.binary" and "mac.binary". The default is "source" except under Windows and the CRAN GUI build for MacOS X.
- `install.packages()` and friends now accept a vector of URLs for 'repos' or 'contriburl' and get the newest available version of a package from the first repository on the list in which it is found. The argument 'CRAN' is still accepted, but deprecated.

  `install.packages()` on Unix can now install from local .tar.gz files via repos = NULL (as has long been done on Windows).

  `install.packages()` no longer asks if downloaded packages should be deleted: they will be deleted at the end of the session anyway (and can be deleted by the user at any time).

  If the repository provides the information, `install.packages()` will now accept the name of a package in a bundle.

  If 'pkgs' is omitted `install.packages()` will use a listbox to display the available packages, on suitable systems.

  'dependencies' can be a character vector to allow only some levels of dependencies (e.g. not "Suggests") to be requested.

- There is a new possible value `update.packages(ask="graphics")` that uses a widget to (de)select packages, on suitable systems.
- The option used is now `getOption("repos")` not `getOption("CRAN")` and it is initially set to a dummy value. Its value can be a character vector (preferably named) giving one or several repositories.

  A new function `chooseCRANmirror()` will select a CRAN mirror. This is called automatically if the `contrib.url()` encounters the initial dummy value of `getOption("repos")`

  A new function `setRepositories()` can be used to create `getOption("repos")` from a (platform-specific) list of known repositories.
- New function `new.packages()` to report uninstalled packages available at the requested repositories. This also reports incomplete bundles. It will optionally install new packages.
- New function `available.packages()`, similar to `CRAN.packages()` but for use with multiple repositories. Both now only report packages whose R version requirements are met.
- `update.packages()` and `old.packages()` have a new option 'checkBuilt' to allow packages installed under earlier versions of R to be updated.
- `remove.packages()` can now remove bundles.
- The Contains: field of the DESCRIPTION file of package bundles is now installed, so later checks can find out if the bundle is complete.
- `packageStatus()` is now built on top of *.packages, and gains a 'method' argument. It defaults to the same repositories as the other tools, those specified by `getOption("repos")`.

Bug fixes

- Configuring for Tcl/Tk makes use of `${TK_LIB_SPEC} ${TK_LIBS}` not `${TK_LIB_SPEC} ${TK_XLIBSW}`, which is correct for recent versions of Tk, but conceivably not for old tkConfig.sh files.
- `detach()` was not recomputing the S4 methods for primitives correctly.
- Methods package now has class "expression" partly fixed in basic classes, so S4 classes can extend these (but "expression" is pretty broken as a vector class in R).
- Collected warnings had messages with unneeded trailing space.
- S4 methods for primitive functions must be exported from namespaces; this is now done automatically. Note that `is.primitive()` is now in 'base', not 'methods'.
- Package grid:
  - Fixed bug in `grid.text()` when "rot" argument has length 0. (reported by Emmanuel Paradis)
- `.install_package_vignette_index()` created an index even in an empty 'doc' directory.
- The `print()` method for factors now escapes characters in the levels in the same way as they are printed.
- `str()` removed any class from environment objects.

  `str()` no longer interprets control characters in character strings and factor levels; also no longer truncates factor levels unless they are longer than 'nchar.max'. Truncation of such long strings is now indicated "outside" the string.

  `str(<S4.object>)` was misleading for the case of a single slot.

  `str()` now also properly displays S4 class definitions (such as returned by `getClass()`.
- `print.factor(quote=TRUE)` was not quoting levels, causing ambiguity when the levels contained spaces or quotes.
- R CMD check was confused by a trailing / on a package name.
- `write.table()` was writing incorrect column names if the data frame contained any matrix-like columns.
- `write.table()` was not quoting row names for a 0-column x.
- `t(x)`'s default method now also preserves `names(dimnames(x))` for 1D arrays 'x'.
- `r <- a %*% b` no longer gives `names(dimnames(r)) == c("", "")` unless one of `a` or `b` has named dimnames.
- Some .Internal functions that were supposed to return invisibly did not. This was behind PR#7397 and PR#7466.
- `eval(expr, NULL, encl)` now looks up variables in encl, as `eval(expr, list(), encl)` always did
- Coercing `as.data.frame(NULL)` to a pairlist caused an error.

- `p.adjust(p, ..)` now correctly works when 'p' contains NAs (or when it is of length 0 or length 2 for method = "hommel").
- 'methods' initialization was calling a function intended for `.Call()` with `.C()`.
- `optim()` needed a check that the objective function returns a value of length 1 (spotted by Ben Bolker).
- `X11()` was only scaling its fonts to pointsize if the dpi was within 0.5 of 100dpi.
- `X11()` font selection was looking for any symbol font, and sometimes got e.g. bold italic if the server has such a font.
- `dpois(*, lambda=Inf)` now returns 0 (or -Inf for log).
- Using pch="" gave a square (pch=0)! Now it is regarded as the same as NA, which was also undocumented but omits the point.
- Base graphics now notices (ab)lines which have a zero coordinate on log scale, and omits them. (PR#7559)
- `stop()` and `warning()` now accept NULL as they are documented to do (although this seems of little use and is equivalent to "").
- `weighted.mean()` now checks the length of the weight vector w.
- `getAnywhere()` was confused by names with leading or trailing dots (spotted by Robert McGehee)
- `eval()` was not handling values from `return()` correctly.
- `par(omd)` is now of the form `c(x1, x2, y1, y2)` to match the documentation and for S-PLUS compatibility.

  [Previously, `par(omd)` was of the form `c(bottom, left, top, right)` like `par(oma)` and `par(omi)`]
- `formatC()` did not check its 'flag' argument, and could segfault if it was incorrect. (PR#7686)
- Contrasts needed to be coerced to numeric (e.g. from integer) inside model.matrix. (PR#7695)
- `socketSelect()` did not check for buffered input.
- Reads on a non-blocking socket with no available data were not handled properly and could result in a segfault.
- The "aovlist" method for `se.contrast()` failed in some very simple cases that were effectively not multistratum designs, e.g. only one treatment occurring in only one stratum.
- `pgamma()` uses completely re-written algorithms, and should work for all (even very extreme) arguments; this is based on Morten Welinder's contribution related to PR#7307.
- `dpois(10, 2e-308, log=TRUE)` and similar cases gave -Inf.
- `x <- 2^(0:1000); plot(x, x^.9, type="l", log="xy")` and `x <- 2^-(1070:170); plot(x, x^.9, type="l", log="xy")` now both work
- `summary.lm()` asked for a report on a reasonable occurrence, but the check failed to take account of NAs.
- `lm()` was miscalculating 'df.residual' for empty models with a matrix response.
- `summary.lm()` now behaves more sensibly for empty models.
- `plot.window()` was using the wrong sign when adjusting xlim/ylim for positive 'asp' and a reversed axis.
- If `malloc()` fails when allocating a large object the allocator now does a gc and tries the `malloc()` again.
- `packageSlot()` and `getGroupMembers()` are now exported from the 'methods' package as they should from documentation and the Green Book.
- `rhyper()` was giving numbers slightly too small, due to a bug in the original algorithm. (PR#7314)
- `gsub()` was sometimes incorrectly matching `^` inside a string, e.g. `gsub("^12", "x", "1212")` was "xx".
- `[g]sub(perl = TRUE)` was giving random results for a 0-length initial match. (PR#7742)
- `[g]sub` was ignoring most 0-length matches, including all initial ones. Note that substitutions such as `gsub("[[:space:]]*", " ", ...)` now work as they do in 'sed' (whereas the effect was previously the same as `gsub("[[:space:]]+", " ", ...)`). (In part PR#7742)
- Promises are now evaluated when extracted from an environment using '`$`' or '`[[ ]]`'.
- `reshape(direction="wide")` had some sorting problems when guessing time points (PR#7669)

- `par()` set 'xaxp' before 'xlog' and 'yaxp' before 'ylog', causing PR#831.
- The logic in `tclRequire()` to check the availability of a Tcl package turned out to be fallible. It now uses a `try()`-and-see mechanism instead.
- Opening a `unz()` connection on a non-existent file left a file handle in use.
- "dist" objects of length 0 failed to print.
- INSTALL and the libR try harder to find a temporary directory (since there might be one left over with the same PID).
- `acf()` could cause a segfault with some datasets. (PR#7771)
- `tan(1+LARGEi)` now gives 0+1i rather than 0+NaNi (PR#7781)
- `summary(data.frame(mat = I(matrix(1:8, 4))))` does not go into infinite recursion anymore.
- `writeBin()` performed byte-swapping incorrectly on complex vectors, also swapping real and imaginary parts. (PR#7778)
- `read.table()` sometimes discarded as blank lines containing only white space, even if `sep=","`.

Changes on CRAN

by Kurt Hornik

New contributed packages

AMORE A MORE flexible neural network package. This package was born to release the TAO robust neural network algorithm to the R users. It has grown and can be of interest for the users wanting to implement their own training algorithms as well as for those others whose needs lie only in the "user space". By Manuel Castejón Limas, Joaquín B. Ordieres Meré, Eliseo P. Vergara González, Francisco Javier Martínez de Pisón Ascacibar, Alpha V. Pernía Espinoza, and Fernando Alba Elías.

BHH2 Functions and data sets reproducing some examples in "Statistics for Experimenters II" by G. E. P. Box, J. S. Hunter, and W. C. Hunter, 2005, John Wiley and Sons. By Ernesto Barrios.

Bolstad Functions and data sets for the book "Introduction to Bayesian Statistics" by W. M. Bolstad, 2004, John Wiley and Sons. By James Curran.

Ecdat Data sets from econometrics textbooks. By Yves Croissant.

GDD Platform and X11 independent device for creating bitmaps (png, gif and jpeg). By Simon Urbanek.

GeneNT The package implements a two-stage algorithm to screen co-expressed gene pairs with controlled FDR and MAS. The packages also constructs relevance networks and clusters co-expressed genes (both similarly co-expressed and transitively co-expressed). By Dongxiao Zhu.

Geneland Detection of spatial structure from genetic data. By Gilles Guillot.

HTMLapplets Functions inserting dynamic scatterplots and grids in documents generated by **R2HTML**. By Gregoire Thomas.

IDPmisc The IDPmisc package contains different high-level graphics functions for displaying large datasets, brewing color ramps, drawing nice arrows, creating figures with differently colored margins and plot regions, and other useful goodies. By Andreas Ruckstuhl, Thomas Unternährer, and Rene Locher.

LDheatmap Produces a graphical display, as a heat map, of measures of pairwise linkage disequilibria between SNPs. Users may optionally include the physical locations or genetic map distances of each SNP on the plot. By Ji-Hyung Shin, Sigal Blay, Jinko Graham, and Brad McNeney.

LogicReg Routines for Logic Regression. By Charles Kooperberg and Ingo Ruczinski.

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

MatchIt Select matched samples of the original treated and control groups with similar covariate distributions—can be used to match exactly on covariates, to match on propensity scores, or perform a variety of other matching procedures. By Daniel Ho, Kosuke Imai, Gary King, and Elizabeth Stuart.

Matching Provides functions for multivariate and propensity score matching and for finding optimal balance based on a genetic search algorithm. A variety of univariate and multivariate tests to determine if balance has been obtained are also provided. By Jasjeet Singh Sekhon.

NORMT3 Evaluates the probability density function of the sum of the Gaussian and Student's *t* density on 3 degrees of freedom. Evaluates the p.d.f. of the sphered Student's *t* density function. Also evaluates the `erf` and `erfc` functions on complex-valued arguments. By Guy Nason.

PK Estimation of pharmacokinetic parameters. By Martin Wolfsegger.

ProbForecastGOP Probabilistic weather field forecasts using the Geostatistical Output Perturbation method introduced by Gel, Raftery and Gneiting (2004). By Yulia Gel, Adrian E. Raftery, Tilmann Gneiting, and Veronica J. Berrocal.

R.matlab Provides methods to read and write MAT files. It also makes it possible to communicate (evaluate code, send and retrieve objects etc.) with Matlab v6 or higher running locally or on a remote host. The auxiliary Java class provides static methods to read and write Java data types. By Henrik Bengtsson.

R.oo Methods and classes for object-oriented programming in R with or without references. By Henrik Bengtsson.

RGrace Mouse/menu driven interactive plotting application. By M. Kondrin.

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

ROCR ROC graphs, sensitivity/specificity curves, lift charts, and precision/recall plots are popular examples of trade-off visualizations for specific pairs of performance measures. ROCR is a flexible tool for creating cutoff-parametrized 2D performance curves by freely combining two from over 25 performance measures (new performance measures can be added using a standard interface). By Tobias Sing, Oliver Sander, Niko Beerenwinkel, and Thomas Lengauer.

ResistorArray Electrical properties of resistor networks. By Robin K. S. Hankin.

Rlab Functions and data sets for the NCSU ST370 class. By Dennis D. Boos, Atina Dunlap Brooks, and Douglas Nychka.

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). By Philippe Grosjean & Eric Lecoutre.

SemiPar Functions for semiparametric regression analysis, to complement the book "Semiparametric Regression" by R. Ruppert, M. P. Wand, and R. J. Carroll, 2003, Cambridge University Press. By Matt Wand.

SeqKnn Estimate missing values sequentially from the gene that had least missing rate in microarray data. By Ki-Yeol Kim and Gwan-Su Yi.

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

Zelig Everyone's statistical software: an easy-to-use program that can estimate, and help interpret the results of, an enormous range of statistical models. By Kosuke Imai, Gary King, and Olivia Lau.

adlift Adaptive Wavelet transforms for signal denoising. By Matt Nunes and Marina Popa.

alr3 Methods and data to accompany the textbook "Applied Linear Regression" by S. Weisberg, 2005, Wiley. By Sanford Weisberg.

arules Provides the basic infrastructure for mining and analyzing association rules and an interface to the C implementations of Apriori and Eclat by Christian Borgelt. By Bettina Gruen, Michael Hahsler and Kurt Hornik.

bayesm Covers many important models used in marketing and micro-econometrics applications. The package includes: Bayes Regression (univariate or multivariate dependent variable), Multinomial Logit (MNL) and Multinomial Probit (MNP), Multivariate Probit, Multivariate Mixtures of Normals, Hierarchical Linear Models with normal prior and covariates, Hierarchical Multinomial Logits with mixture of normals prior and covariates, Bayesian analysis of choice-based conjoint data, Bayesian treatment of linear instrumental variables models, and Analyis of Multivariate Ordinal survey data with scale usage heterogeneity. By Peter Rossi and Rob McCulloch.

bitops Functions for Bitwise operations on integer vectors. S original by Steve Dutky, initial R port and extensions by Martin Maechler. Revised and modified by Steve Dutky.

boost Contains a collection of boosting methods, these are 'BagBoost', 'LogitBoost', 'AdaBoost' and 'L2Boost', along with feature preselection by the Wilcoxon test statistic. Moreover, methods for the simulation of data according to correlation and mean structures of existing real datasets are included. By Marcel Dettling.

changeLOS Change in length of hospital stay (LOS). By Matthias Wangler and Jan Beyersmann.

clac Clust Along Chromosomes, a method to call gains/losses in CGH array data. By Pei Wang, with contributions from Balasubramanian Narasimhan.

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. By José A. Guijarro.

clue CLUster Ensembles. By Kurt Hornik, with contributions from Walter Boehm.

coin Conditional inference procedures for the general independence problem including two-sample, K-sample, correlation, censored, ordered and multivariate problems. By Torsten Hothorn and Kurt Hornik, with contributions by Mark van de Wiel and Achim Zeileis.

colorspace Carries out mapping between assorted color spaces. By Ross Ihaka.

concor Concordance, providing "SVD by blocks". By R. Lafosse.

ctv Server-side and client-side tools for task views to CRAN-style repositories. By Achim Zeileis and Kurt Hornik.

cyclones Functions for locating local minima/maxima. By Rasmus E. Benestad.

eco Fits parametric and nonparametric Bayesian models for ecological inference in 2 by 2 tables. The models are fit using the Markov chain Monte Carlo algorithms that are described in Imai and Lu (2004). By Ying Lu and Kosuke Imai.

edci Detection of edgepoints in images based on the difference of two asymmetric M kernel estimators. Linear and circular regression clustering based on redescending M estimators. Detection of linear edges in images. By Tim Garlipp.

elasticnet Elastic net regularization and variable selection. Also implements the sparse PCA algorithm based on the elastic net/lasso. By Hui Zou and Trevor Hastie.

ensembleBMA Uses Bayesian Model Averaging to create probabilistic forecasts of ensembles using a mixture of normal distributions. By Adrian E. Raftery, J. McLean Sloughter, and Michael Polakowski.

epitools Basic tools for applied epidemiology. By Tomas Aragon.

epsi Smoothing methods for images which are based on a redescending M kernel estimator which preserves edges and corners. By Tim Garlipp.

far Modelizations and previsions functions for Functional AutoRegressive processes using nonparametric methods: functional kernel, estimation of the covariance operator in a subspace, ... By Damon Julien and Guillas Serge.

frailtypack Fit a shared gamma frailty model and Cox proportional hazards model using a Penalized Likelihood on the hazard function. Left truncated, censored data and strata (max=2) are allowed. Original Fortran routines by Virginie Rondeau. Modified Fortran routines, R code and packaging by Juan R Gonzalez.

gcmrec Parameters estimation of the general semiparametric model for recurrent event data proposed by Peña and Hollander. By Juan R. Gonzalez, Elizabeth H. Slate, and Edsel A Peña.

genalg R based genetic algorithm for binary and floating point chromosomes. By Egon Willighagen.

gmp Multiple precision Arithmetic (prime numbers, ...), "arithmetic without limitations" using the C library `gmp`. By Antoine Lucas, Immanuel Scholz, Rainer Boehme, and Sylvain Jasson.

gsl An R wrapper for the special functions and quasi random number generators of the Gnu Scientific Library (`http://www.gnu.org/software/gsl/`). By Robin K. S. Hankin; `qrng` functions by Duncan Murdoch.

hmm.discnp Fits hidden Markov models with discrete non-parametric observation distributions to data sets. Simulates data from such models. By Rolf Turner and Limin Liu..

hopach The Hierarchical Ordered Partitioning and Collapsing Hybrid (HOPACH) clustering algorithm. By Katherine S. Pollard, with Mark J. van der Laan.

intcox Implementation of the Iterated Convex Minorant Algorithm for the Cox proportional hazard model for interval censored event data. By Volkmar Henschel, Christiane Heiss, and Ulrich Mansmann.

irr Coefficients of Interrater Reliability and Agreement for quantitative, ordinal and nominal data: ICC, Finn-Coefficient, Robinson's A, Kendall's W, Cohen's Kappa, ... By Matthias Gamer.

kknn Weighted k-Nearest Neighbors Classification and Regression. By Klaus Schliep & Klaus Hechenbichler.

ks Bandwidth matrices for kernel density estimators and kernel discriminant analysis for bivariate data. By Tarn Duong.

labdsv A variety of ordination and vegetation analyses useful in analysis of datasets in community ecology. Includes many of the common ordination methods, with graphical routines to facilitate their interpretation, as well as several novel analyses. By David W. Roberts.

latticeExtra Generic function and standard methods for Trellis-based displays. By Deepayan Sarkar.

ltm Analysis of multivariate Bernoulli data using latent trait models (including the Rasch model) under the Item Response Theory approach. By Dimitris Rizopoulos.

maanova Analysis of *N*-dye Micro Array experiment using mixed model effect. Containing analysis of variance, permutation and bootstrap, cluster and consensus tree. By Hao Wu, with ideas from Gary Churchill, Katie Kerr and Xiangqin Cui.

matlab Emulate MATLAB code using R. By P. Roebuck.

mcmc Functions for Markov chain Monte Carlo (MCMC). By Charles J. Geyer.

meta Fixed and random effects meta-analysis. Functions for tests of bias, forest and funnel plot. By Guido Schwarzer.

micEcon Tools for microeconomic analysis and microeconomic modelling. By Arne Henningsen.

minpack.lm Provides R interface for two functions from MINPACK library, solving nonlinear least squares problem by modification of the Levenberg-Marquardt algorithm. By Timur V. Elzhov.

mlica An R code implementation of the maximum likelihood (fixed point) algorithm of Hyvaerinen, Karhuna and Oja for independent component analysis. By Andrew Teschendorff.

mlmRev Data and examples from a multilevel modelling software review as well as other well-known data sets from the multilevel modelling literature. By Douglas Bates.

mvoutlier Outlier detection using robust estimations of location and covariance structure. By Moritz Gschwandtner and Peter Filzmoser.

nice Get or set UNIX priority (niceness) of running R process. By Charles J. Geyer.

ouch Fit and compare Ornstein-Uhlenbeck models for evolution along a phylogenetic tree. By Aaron A. King.

outliers A collection of some tests commonly used for identifying outliers. By Lukasz Komsta.

perturb Evaluates collinearity by adding random noise to selected variables. By John Hendrickx.

phpSerialize Serializes R objects for import by PHP into an associative array. Can be used to build interactive web pages with R. By Dieter Menne.

pls Multivariate regression by partial least squares regression (PLSR) and principal components regression (PCR). This package supersedes the **pls.pcr** package. By Ron Wehrens and Bjørn-Helge Mevik.

plsgenomics Provides routines for PLS-based genomic analyses. By Anne-Laure Boulesteix and Korbinian Strimmer.

plugdensity Kernel density estimation with global bandwidth selection via "plug-in"". By Eva Herrmann (C original); R interface et cetera by Martin Maechler.

polycor Computes polychoric and polyserial correlations by quick "two-step" methods or ML, optionally with standard errors; tetrachoric and biserial correlations are special cases. By John Fox.

ppc Sample classification of protein mass spectra by peak probability contrasts. By Balasubramanian Narasimhan, R. Tibshirani, and T. Hastie.

proto An object oriented system using prototype or object-based (rather than class-based) object oriented ideas. By Louis Kates and Thomas Petzoldt.

pvclust Assessing the uncertainty in hierarchical cluster analysis. By Ryota Suzuki and Hidetoshi Shimodaira.

qtlDesign Tools for the design of QTL experiments. By Saunak Sen, Jaya Satagopan, and Gary Churchill.

qvalue Q-value estimation for false discovery rate control. By Alan Dabney and John D. Storey, with assistance from Gregory R. Warnes.

relsurv Various functions for regression in relative survival. By Maja Pohar.

resper Two accept-and-reject algorithms to sample from permutations. By Johannes Hüsing.

rstream Unified object oriented interface for multiple independent streams of random numbers from different sources. By Josef Leydold.

rwt Performing digital signal processing. By P. Roebuck, based on MATLAB extension by Rice University's DSP group.

seqinr Exploratory data analysis and data visualization for biological sequence (DNA and protein) data. By Delphine Charif and Jean Lobry.

spectrino Spectra organizer, visualization and data extraction from within R. By Teodor Krastev.

stepwise A stepwise approach to identifying recombination breakpoints in a sequence alignment. By Jinko Graham, Brad McNeney, and Francoise Seillier-Moiseiwitsch, R interface by Sigal Blay.

survBayes Fits a proportional hazards model to time to event data by a Bayesian approach. Right and interval censored data and a log-normal frailty term can be fitted. By Volkmar Henschel, Christiane Heiss, Ulrich Mansmann.

tdist Computes the distribution of a linear combination of independent Student's t-variables (with small degrees of freedom, dff $\leq$ 100) and/or standard Normal Z random variables. By Viktor Witkovsky and Alexander Savin.

tweedie Maximum likelihood computations for Tweedie families. By Peter Dunn.

uroot Unit root tests (KPSS, ADF, CH and HEGY) and graphics for seasonal time series. By Javier López-de-Lacalle & Ignacio Díaz-Emparanza.

vabayelMix Performs inference of a gaussian mixture model within a bayesian framework using an optimal separable approximation to the posterior density. The optimal posterior approximation is obtained using a variational approach. By Andrew Teschendorff.

verification Contains utilities for verification of discrete and probabilistic forecasts. By the NCAR Research Application Program.

zicounts Fits classical and zero-inflated count data regression model as well as censored count data regression. By S M Mwalili.

Other changes

- Packages **CoCoAn**, **gpls**, and **multiv** were moved from the main CRAN section to the Archive.
- Package **Dopt** was moved from the Devel section of CRAN to the Archive.
- Package **multidim** had to be removed from CRAN.

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Events

Chambers Workshop

A workshop entitled "40 Years of Statistical Computing and Beyond" was held at Bell Laboratories, Murray Hill, NJ, U.S.A. on April 29, 2005 to mark the occasion of John Chambers' retirement from the Labs but not from active research. He is continuing his record of innovation by becoming the first Emeritus Member of Technical Staff in the history of Bell Labs.

R is an implementation of the S language and John is the originator and principal designer of S. Without John's work on S there never would have been an R. His patient responding to questions during early development of R was crucial to its success and, since 2000, he has been a member of the R Development Core Team.

The history and development of the S language and of its implementation in R were featured in many of the presentations at the workshop, especially in those by Rick Becker and Allan Wilks. Naturally, the highlight of the day was John's presentation in which he first looked back on his 40 years of involvement in statistical computing and the development of languages for programming with data and then gave some tantalizing glimpses into the future. The agenda for the workshop can be seen at http://stat.bell-labs.com.

DSC 2005

DSC 2005 – Directions in Statistical Computing – will be held from the evening of August 12 through August 15, in Seattle, Washington. This conference follows on from the successful DSC 1999, 2001, and 2003 conferences at the Vienna University of Technology.

The workshop will focus on, but is not limited to, open source statistical computing.

We are inviting abstracts for contributed presentations on issues related to the development of statistical computing and graphics environments. Abstracts should be sent to dsc2005@u.washington.edu, by May 15 and questions to tlumley@u.washington.edu. More information is available at http://depts.washington.edu/dsc2005/ and online registration will soon open at that website.

Bioconductor User Conference

The 2005 Bioconductor User Conference will be hosted at the Fred Hutchinson Cancer Research Center in Seattle on August 16 and 17, following the DSC. The two day meeting will consist of morning lectures and afternoon laboratories. Scheduled speakers include: Michael Boutros, Eric Schadt, Sridhar Ramaswamy, Rafael Irizarry, and Robert Gentleman. The conference web site can be found at http://www.bioconductor.org/meeting05. For more details contact biocworkshop@fhcrc.org.

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