R Package Development

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Plan

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References

- R Installation and Administration [R-admin], R Core team
- Writing R Extensions [R-ext], R Core team

Use `help.start()` to access them from your local installation, or `http://cran.r-project.org/manuals.html` from the web.

Terminology

A **package** is loaded from a **library** by the function `library()`. Thus a library is a directory containing installed packages.

Calling `library("foo", lib.loc = "/path/to/bar")` loads the package (book) *foo* from the library `bar` located at `/path/to/bar`.

Packages

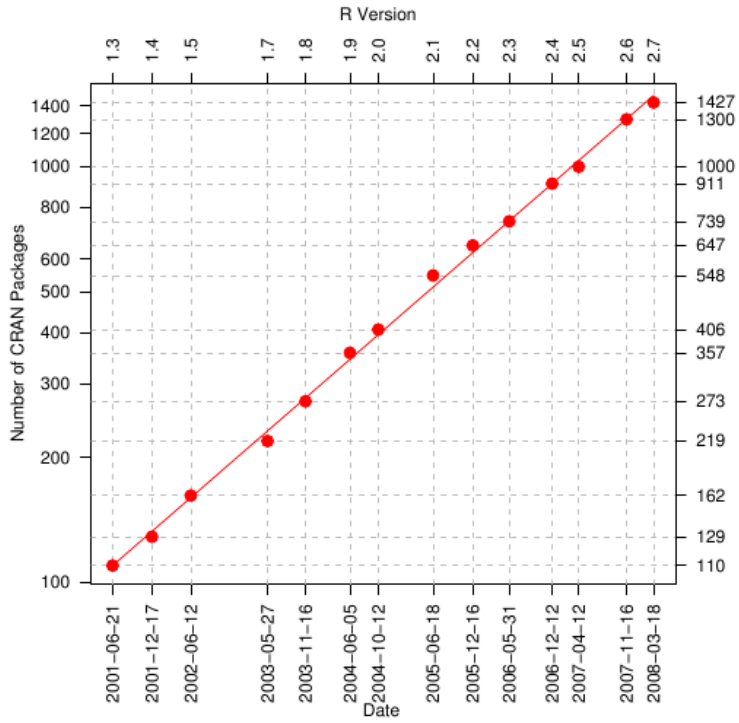
One of the aspects that make R appealing:

CRAN package repository features 5986 available packages.

R-forge 1800 hosted projects.

Bioconductor 934 reviewed packages in latest release (version 3.0).

Numbers checked in October 2014



Why packages

Packages provide a mechanism for loading optional code and attached documentation as needed.

There is more to it – packages are a means to

- logically group your own functions
- keep code and documentation together and consistent
- keep code and data together
- keep track of changes in code
- summarise all packages used for a analysis (see `sessionInfo()`)
- make a reproducible research compendium (container for code, text, data as a means for distributing, managing and updating)
- optionally test your code
- . . . project managment

even if you do not plan to distribute them.

Package creation workflow

Workflow

1. Prepare your code as .R file(s)
2. Use function `package.skeleton()` to place them in the "package layout"
3. Create the .tar.gz file using **R CMD build myRpackage**
4. (Optional, but recommended) Check the .tar.gz for errors using **R CMD check myRpackage_1.0.tar.gz**
5. Install the package using **R CMD INSTALL myRpackage_1.0.tar.gz** or `install.packages()`

Notes

- Use steps 1-5 to create the initial version of the package, and steps 3-5 to update the package.
- Text in **bold** is executed **outside R** (i.e. from the console).

Creating a package - package.skeleton()

A minimal package

We prepared a file read.R that containt the function `readFasta()`. Function package.skeleton() automates some of the setup for a new package:

```
> package.skeleton(name="myRpackage", code_files="read.R")

Creating directories ...
Creating DESCRIPTION ...
Creating NAMESPACE ...
Creating Read-and-delete-me ...
Copying code files ...
Making help files ...
Done.
Further steps are described in
'./myRpackage/Read-and-delete-me'.
```

```
> package.skeleton(name="myRpackage", code_files="read.R")
```

produces

```
myRpackage/
|-- DESCRIPTION
|-- NAMESPACE
|-- man
|   `-- myRpackage-package.Rd
|   `-- readFasta.Rd
|-- R
|   `-- read.R
`-- Read-and-delete-me

2 directories, 6 files
```

Building the package

Note

To build the package we will first delete the documentation templates (we will revisit this later).

```
# delete documentation templates
$ rm -rf myRpackage/man/*
$ R CMD build myRpackage
* checking for file myRpackage/DESCRIPTION ... OK
* preparing myRpackage:
* checking DESCRIPTION meta-information ... OK
* checking for LF line-endings in source and make files
* checking for empty or unneeded directories
* building myRpackage_1.0.tar.gz
```

Installing and using the package

```
$ R CMD INSTALL myRpackage_1.0.tar.gz
* installing to library /ext/home/R/x86_64-pc-linux-gnu-library/3.1
* installing *source* package myRpackage ...
** R
** preparing package for lazy loading
** help
No man pages found in package  myRpackage
*** installing help indices
** building package indices
** testing if installed package can be loaded
* DONE (myRpackage)
```

Use package

We can verify the new package is now available (although still not fully functional!) from R:

```
> library("myRpackage")
>
> readFasta("aDnaSeq.fasta")

Error:  "DnaSeq" is not a defined class
```

Exercise 1: Create a package

Follow the steps from the previous slides to create the example package containing the `readFasta()` function.

Exercise 2: Complete the package functionality

Add the `GenericSeq` class to the package by adding a new file `DataClasses.R` to your package. Copy this file to the package `R/` directory and then rebuild the package following steps 3-5.

Using `devtools`

Rebuilding and reloading packages can be a bit cumbersome. Package `devtools` has many great tools for package development, such as `load_all()` that mimics the rebuild/reload process.

```
> library(devtools)
> load_all("myRpackage/")
>
> readFasta("aDnaSeq.fasta")
```

... and many more!

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Package commands

Building packages

`R CMD build myRpackage` – the `R` package builder builds R package (and vignettes if available).

Checking packages

`R CMD check myRpackage_1.0.tar.gz` or `R CMD check myRpackage` – the `R` package checker tests whether the package or source work correctly.

- The package is installed (checks missing cross-references and duplicate aliases in help files).
- File names validity, permissions.
- Package DESCRIPTION file is checked for completeness, and some of its entries for correctness.
- `R` and `.Rd` files are checked for syntax errors.
- A check is made for missing documentation entries.
- Codoc checking
- Examples provided by the package's documentation are run.
- If available, package tests are run and vignettes are executed and compiled.

Package commands

Installing packages

`R CMD INSTALL myRpackage_1.0.tar.gz` or `install.packages("myRpackage_1.0.tar.gz")` – installs the package in the default library. Other libraries can be specified with the `-l` option or `lib` argument.

Loading

Use `library()` or `require()`.

On Windows

`R` is very much Unix centric. To build from source on Windows, you will need `Rtools`[a]. See the *The Windows toolset* in R-Admin for more details.

[a] http://cran.r-project.org/bin/windows/Rtools/

DESCRIPTION

```
Package: myRpackage ## mandatory (*)
Type: Package ## optional, 'Package' is default type
Title: What the package does (short line) ## *
Version: 1.0 ##  *
Date: 2013-05-10 ## release date of the current version
Author: Who wrote it ## *
Maintainer: Who to complain to <yourfault@somewhere.net> ## *
Description: More about what it does (maybe more than one line) ## *
License: What license is it under? ## *
Depends: methods, Biostrings ## for e.g.
Imports: evd ## for e.g.
Suggests: BSgenome.Hsapiens.UCSC.hg19 ## for e.g.
Collate: 'DataClasses.R' 'read.R' ## for e.g.
```

Lazy loading

A mechanism used to defer initialization of an object until the point at which it is needed. The individual objects in the package's environment are indirect references to the actual objects until, for example a function is called or an object loaded.

The `LazyLoad` and `LazyData` fields control whether the R objects and the datasets (respectively) use lazy-loading. `LazyLoad` must be set if the *methods* package is used.

`LazyLoad` is now on by default.

Example

R uses *Lazy evaluation*, which delays the evaluation of an expression (here the argument) until its value is actually required [a]:

[a] example from Hadley Wickham's devtools

```
> f <- function(x) { 10 }
> system.time(f(Sys.sleep(3)))

   user  system elapsed
      0       0       0

> f <- function(x) { force(x); 10 }
> system.time(f(Sys.sleep(3)))

   user  system elapsed
  0.000   0.000   3.003
```

Other important fields

Depends A comma-separated list of package names (optionally with versions) which this package depends on.

Suggests Packages that are not necessarily needed: used only in examples, tests or vignettes, packages loaded in the body of functions (see `require()`).

Imports Packages whose name spaces are imported from (as specified in the `NAMESPACE` file) but which do not need to be attached to the search path.

Collate Controls the collation order for the R code files in a package. If filed is present, all source files must be listed.

URL A list of URLs separated by commas or whitespace.

...

The NAMESPACE file

Stored in the package directory. Restrict the symbols that are exported and imports functionality from other packages. Only the exported symbols will have to be documented.
Note: `NAMESPACE` is now required (since R 2.14).

```
export(f, g) ## exports f and g
exportPattern("^[^\\.]")
import(foo) ## imports all symbols from package foo
importFrom(foo, f, g) ## imports f and g from foo
```

It is possible to explicitely use symbol `s` from package *foo* with `foo::s` or `foo:::s` if `s` is not exported.

Attach and load

Packages are attached to the search path with `library` or `require`.

Attach When a package is attached, then all of its dependencies (see `Depends` field in its `DESCRIPTION` file) are also attached. Such packages are part of the evaluation environment and will be searched.

Load One can also use the `Imports` field in the `NAMESPACE` file. Imported packages are loaded but are not attached: they do not appear on the search path and are available only to the package that imported them.

Package subdirectories

R

Contains `source()`able `R` source code to be installed. Files must start with an ASCII (lower or upper case) letter or digit and have one of the extensions `.R` (recommended), `.S`, `.q`, `.r`, or `.s`. File order is important if code relies on *earlier* code – order use `Collate` filed in `DESCRIPTION` file.

Example

```
## works fine without Collate field
AllGenerics.R       DataClasses.R
methods-ClassA.R    methods-ClassB.R
functions-ClassA.R  ...
```

`zzz.R` is generally used to define special functions used to initialize (called after a package is loaded and attached) and clean up (just before the package is detached). See `help(".onLoad"))`, `?.First.Lib` and `?.Last.Lib` for more details.

Package subdirectories

man

Manuals for the objects (package, functions, generics, methods, classes and data sets) in the package in R documentation (`Rd`) format. The filenames must start with an ASCII (lower or upper case) letter or digit and have the extension `.Rd` or `.rd` and should be URL compatible. If you use a NAMESPACE, only exported symbols need to be documented. Without NAMESPACE, internal use only objects should be documented in `pkg-internal.Rd`.

Package subdirectories

data

Contains data files, made available via *lazy-loading* or for loading using `data()`. Data types that are allowed are

R code self-sufficient plain R code (`.R` or `.r`),

Tables possibly compressed tables (`.tab`, `.txt`, or `.csv`, see `?data` for the file formats)

Objects created using `save()` (`.RData` or `.rda`).

Example

There is a `DnaSeq` object in `sequences/data`.

Package subdirectories

inst

Content is copied recursively to the installation directory, for example

CITATION file (see `citation()` function),

doc directory for additional documents (see vignettes[a], later).

extdata directory for other data files, not belonging in `data`.

tests code for unit tests (see later).

[a] It is now also possible to use the `./vignettes` directory for these.

Example

In our *sequences* package, there is a `fasta` sequence in `sequences/inst/extdata` used to illustrate the `readFasta` function.

Package subdirectories

tests

Contains additional package-specific test code. We will talk about unit tests later.

demo

R scripts runned via `demo()` that demonstrate some of the functionality of the package. Execution of these scripts is not checked.

src

Contains sources and headers for the compiled code, plus optionally a file Makevars or Makefile.

Adding C/C++ code

Using package `Rcpp`:

Package `Rcpp` makes it easy to call C/C++ code from R. It also has a function:

```
> Rcpp.package.skeleton("myRpackage")
```

that will create a fully functioning R package with C/C++ integration.

Or manually:

1. Add your C/C++ files to directory `src/`
2. Create R wrapper functions for your C/C++ code
3. (Optionally) provide `Makefile` and `Makevars` files in `src/`
4. Add `useDynLib(myRpackage)` to `NAMESPACE` file
5. (For `Rcpp`) also add `LinkingTo: Rcpp` to `DESCRIPTION`

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R documentation format

R objects are documented in files written in *R documentation* (`Rd`) format, a simple markup language much of which closely resembles LaTeX, which can be processed into a variety of formats, including LaTeX, HTML, pdf and plain text.

`man/` directory

The documentation files are in the separate `man/` package directory.

Using roxygen2

Package `roxyxgen2` makes it easier to write documentation using special **in-source** markup (similarly to Doxygen).

Example

```
#' Reads sequences data in fasta and create \code{DnaSeq}
#' and \code{RnaSeq} instances.
#'
#' This funtion reads DNA and RNA fasta files and generates
#' valid \code{"DnaSeq"} and \code{"RnaSeq"} instances.
#'
#' @title Read fasta files.
#' @param infile  the name of the fasta file which the data are to be read from.
#' @return an instance of \code{DnaSeq} or \code{RnaSeq}.
#' @seealso \code{\linkS4class{GenericSeq}}, \code{\linkS4class{DnaSeq}} and \code{\linkS4class{RnaSeq}}.
#' @examples
#' f <- dir(system.file("extdata",package="sequences"),pattern="fasta",full.names=TRUE)
#' f
#' aa <- readFasta(f)
#' aa
#' @author Laurent Gatto \email{lg390@@cam.ac.uk}
#' @export
readFasta <- function(infile){
  lines <- readLines(infile)
  header <- grep("^>", lines)
  if (length(header)>1) {
    warning("Reading first sequence only.")
    lines <- lines[header[1]:(header[2]-1)]
    header <- header[1]
  }
  ##### (code cut for space reasons) #####
  if (validObject(newseq))
    return(newseq)
}
```

Exercise 3: Document readFasta

Use the code from the previous slide to document your own readFasta() function inside your package. When you are finished do the following:

1. To generate the .Rd file for your package run:

```
library(roxygen2)
roxygenise("myRpackage/")
```

2. Rebuild/reload your package
3. Verify that `?readFasta` gives the expected help page.
4. Look at `man/readFasta.Rd` and try to understand the structure.

roxygen2 syntax

For more information on roxygen2: http://cran.r-project.org/web/packages/roxygen2/vignettes/roxygen2.html.

Rd format

An `Rd` file constists of

Header provides basic information about the name of the file, the topics documented, a title, a short textual description and R usage information – mandatory.

Body gives further information defined within *sections* (for example, on the function's arguments and return value, as in the example)

Footer with keyword information – optional.

Every (exported) object must be documented. Package documentation is optional.

Example

```
% File src/library/base/man/load.Rd
\name{load}
\alias{load}
\title{Reload Saved Datasets}
\description{
  Reload the datasets written to a file with the function
  \code{save}.
}
\usage{
load(file, envir = parent.frame())
}
\arguments{
  \item{file}{a connection or a character string giving the
    name of the file to load.}
  \item{envir}{the environment where the data should be
    loaded.}
}
\seealso{
  \code{\link{save}}.
}
\examples{
## save all data
save(list = ls(), file= "all.RData")

## restore the saved values to the current environment
load("all.RData")

## restore the saved values to the workspace
load("all.RData", .GlobalEnv)
}
\keyword{file}
```

Documentation

General comments

- Different objects are documented with different types of `Rd` files, as defined by the `\docType{}` tag.
- Different object documentation require or are advised to contain different sections.
- One `.Rd` file can document several objects by defining multiple `\alias{}`'es.

Guidelines for Rd files

These are suggested guidelines for the system help files (in `.Rd` format) that are intended for core developers but may also be useful for package writers. (see `http://developer.r-project.org/Rds.html`)

There are many different sections and marking text (for mathematical notation, tables, cross-references, ...), that will look very familiar to LaTeX users. All are described in *Writing R documentation files* (section 2) of the R-ext manual.
Fortunately, the `prompt(object)` *et. al.* functions will inspect the `object` to be documented and create a specific documentation skeleton for us to be completed.

Package documentation

Provides an short and optional overview of a package.

Example

```
promptPackage("sequences")
```

Demonstration

Let's look at the `sequences-package.Rd` that documents our package.

Data sets documentation

Example

```
\name{rivers}
\docType{data}
\alias{rivers}
\title{Lengths of Major North American Rivers}
\description{
  This data set gives the lengths (in miles) of 141 \dQuote{major}
  rivers in North America, as compiled by the US Geological
  Survey.
}
\usage{rivers}
\format{A vector containing 141 observations.}
\source{World Almanac and Book of Facts, 1975, page 406.}
\references{
  McNeil, D. R. (1977) \emph{Interactive Data Analysis}.
  New York: Wiley.
}
\keyword{datasets}
```

Example

`prompt(myDataFrame)` or `promptData(myDataObject)`

Demonstration

Let's look at the document of the `dnaseq` object.

Function documentation

Many markup command, including `\usage{fun(arg1, arg2, ...)}`, `\arguments{...}`, `\section{Warning}{...}` and `\examples{...}`, which are executed!

Example

`prompt(object=myFunction)` or `prompt(name="myFunction")`

Demonstration

We have written one functions for our package so far, `readFasta`. It's documentation is available in `man/readFasta.Rd`.

Documenting S4 classes and methods

Documentation is 'similar' than for functions. Note that `aliases` are of the form `MyClass-class` or `MyGeneric,signature_list-method`. Additionnal aliases should be added to refer to `MyGeneric`, `MyGeneric-method`, ... and the manuals are accessed with `class?topic` and `method?topic`. Overall documentation for methods should be aliased with `MyGeneric-methods`
See `help("Documentation", package = "methods")` for more details.

Example

`promptClass("MyClass")` and `promptMethods("myMethod")`

Exercise 4: Document GenericSeq using `promptClass()`

Load `GenericSeq` **and** all of its methods into your R session and then run `promptClass("GenericSeq")`. Edit the resulting .Rd file and place it into `man/`.

Compare: `promptClass()` vs roxygen2

Roxygen makes it easy to document individual methods, `promptClass()` makes it easy to document the whole class with all the methods in a single file.

Package vignette

These *executable* documents are in Sweave format (`.Rnw` extension), which is an extended LaTeX document that includes code chunks. These are executed and the output (variable, but also tables and graphs) are displayed in the document. These dynamic reports, are updated automatically if data or analysis change.

The package vignettes are compiled at build time and are the prefered place for more extensive package documentation and use-cases.

Reference: http://www.stat.uni-muenchen.de/~leisch/Sweave/

The `knitr`[a] package is an alternative to the `Sweave` package that provides syntax highlighting, caching, ... and markdown out of the box.

[a] http://yihui.name/knitr/

Vignettes

Demonstration

Let's have a look at the *sequences* package vignette in `sequences/inst/doc`.

sessionInfo()

Prints version information about R and attached or loaded packages.

```
sessionInfo()


## R version 3.1.1 (2014-07-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
##
## locale:
##  [1] LC_CTYPE=en_GB.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8        LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8    LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] knitr_1.6
##
## loaded via a namespace (and not attached):
## [1] evaluate_0.5.5 formatR_1.0    highr_0.3      stringr_0.6.2
## [5] tools_3.1.1
```

`sessionInfo()` in vignettes

```
toLatex(sessionInfo())
```

- R version 3.1.1 (2014-07-10), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_GB.UTF-8, LC_NUMERIC=C, LC_TIME=en_GB.UTF-8, LC_COLLATE=en_GB.UTF-8, LC_MONETARY=en_GB.UTF-8, LC_MESSAGES=en_GB.UTF-8, LC_PAPER=en_GB.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_GB.UTF-8, LC_IDENTIFICATION=C
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: knitr 1.6
- Loaded via a namespace (and not attached): evaluate 0.5.5, formatR 1.0, highr 0.3, stringr 0.6.2, tools 3.1.1

Plan

How to test the code in your package?

Or how to make sure that changes in your code do not break existing functionality?

- Implicitely, documentation examples and a vignette do some tests.
- Using `R` 's built-in testing, that runs some code and compares the output to a saved template.
- Specific packages for unit testing: *RUnit*[a] or *testthat*[b].

---

[a] http://cran.r-project.org/web/packages/RUnit/index.html
[b] http://cran.r-project.org/web/packages/testthat/index.html

Using an `.Rout.save` file

In `package/tests/`

Create

- `mytest.R` with code to be tested
- `mytest.Rout.save` with the reference output

When `checking` your package `R` will

1. execute the code in `mytest.R`
2. save the output to `mytest.Rout`
3. compare `mytest.Rout` to `mytest.Rout.save`
4. report any differences

Test individual expression

`expect_that(object_or_expression, condition)` with conditions

equals `expect_that(1+2,equals(3))` or `expect_equal(1+2,3)`

gives_warning `expect_that(warning("a"), gives_warning())`

is_a `expect_that(1, is_a("numeric"))` or `expect_is(1,"numeric")`

is_true `expect_that(2 == 2, is_true())` or `expect_true(2==2)`

matches `expect_that("Testing is fun", matches("fun"))` or `expect_match("Testing is fun", "f.n")`

takes_less_than `expect_that(Sys.sleep(1),takes_less_than(3))`

...

Using testthat

Example

```
library(sequences)

## Loading required package:  Rcpp
## This is package 'sequences'

library(testthat)
a <- new("DnaSeq",sequence="ACGTaa")
test_that("ok test", {
  expect_equal(length(a),6)
  expect_true(seq(a)=="ACGTAA")
  expect_is(a,"DnaSeq")
})
expect_true(seq(a)=="ACGTaa")

## Error:  seq(a) == "ACGTaa" isn't true
```

Plan

Submission

CRAN Read the CRAN Repository Policy[a]. Upload your `--as-cran` checked `myPackage_x.y.z.tar.gz` to `ftp://cran.R-project.org/incoming` or using `http://CRAN.R-project.org/submit.html`. Your package will be installable with `install.packages("myRpackage")`.

R-forge Log in, register a project and wait for acceptance. Then commit you code to the svn repository. Your package will be installable with `install.packages` using `repos="http://R-Forge.R-project.org"`.

[a] `http://cran.r-project.org/web/packages/policies.html`

Submission

Bioconductor Make sure to satisfy submission criteria (pass `check`, have a vignette, use S4 if OO, have a `NAMESPACE`, make use of appropriate existing infrastructure, include a NEWS file, must **not** already be on CRAN, ...) and submit by email. Your package will then be reviewed before acceptance. A svn account will then be created. Package will be installable with `biocLite("myPackage")`.

Other popular un-official repositories are github, bitbucket, ... and packages can be installed with `devtools::install_github`, `devtools::install_bitbucket`.

References

Further reading

- R Installation and Administration, R Core team.
- Writing R Extensions, R Core team.
- Robert Gentleman, R Programming for Bioinformatics, 2008.
- Building packages for Bioconductor: http://www.bioconductor.org/developers/how-to/buildingPackagesForBioc/
- R package development, by Hadley Wickham: http://r-pkgs.had.co.nz/

- This work is licensed under a CC BY-SA 3.0 License
- Slides and other material:
  https://github.com/lgatto/TeachingMaterial

Thank you for you attention.