

PACKAGES I

LECTURE 20

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STAT 430: Data Science Programming Methods (Fall 2019)

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Rough Plan

- Why packages?
- Basic package structure
- Package building
- Package documentation (roxygen2)
- Resources:
 - Lander, *R for Everyone*, 2017, Chapter 30
 - Wickham, *R Packages*, 2015
 - R Core, *Writing R Extensions*

PACKAGES

Key Features

- Basic unit of code organisation for R
- Entire infrastructure for code
 - Building
 - Testing
 - Documenting
 - Distributing
 - Deploying
 - Versioning
- Even when you do not plan to submit to CRAN or alike
- Excellent model to organize code at work or in a lab

Key Resources

- Definite treatment is the [Writing R Extensions](#) manual
 - Included with every copy of R
 - Also on the [web](#)
 - Admittedly a little “dense” – but authoritative
- Many on-line tutorials and posts plus short coverage
- We will look at at Lander (2017), [R for Everyone, Chapter 30](#)
- The book [R Packages](#) (Wickham, 2015) is also popular ([website](#))

So What is a Package?

- Typically a collection of several R functions
- Usually with documentation
 - manual pages (also called help pages)
 - optional vignettes in html or pdf
- Help pages frequently contain examples
- Packages may contain compiled code (not our focus today)
- Packages may contain tests (more next lecture)

Essential Structure

- **DESCRIPTION** *required* file defining the package name, license, description and dependencies
- **NAMESPACE** to declare what is imported and exported
- **R/** very common directory with R functions
- **man/** very common directory with documentation
- **src/** *optional* directory with C or C++ or Fortran or ... source code which R will automatically compile and make loadable
- **data/** *optional* directory with data sets
- **inst/** *optional* directory for *other directories to be included*
- **tests/** *optional* tests starting point (more next lecture)

DESCRIPTION

- A simple collection of 'key: value' pairs
- The format follows the [Debian Control File](#) specs
 - So there are existing parsers
 - R itself has functions should you need them
- There are a number of important mandatory fields
 - See next few slides
- As well as additional optional fields

DESCRIPTION

- **Package**, **Title**, **Version**, **Type** supply important meta-data
- **Author** and **Maintainer** state authorship and copyright, as well as a person to contact for questions and issues
- **Description** is used for a brief synopsis including references
- **Depends**, **Imports**, **Suggests** delineate dependencies
 - **Depends** used to be standard, attaches the named packages
 - **Imports** now preferred in conjunction with the **NAMESPACE** file
 - **Suggests** lists *optional* packages that are used if present but are not essential for the package to be functional
- **License** should list a known open source license (see manual)

DESCRIPTION Example

Package: pkgKitten

Type: Package

Title: Create Simple Packages Which Do not Upset R Package Checks

Version: 0.1.4

Date: 2016-11-13

Author: Dirk Eddelbuettel

Maintainer: Dirk Eddelbuettel <edd@debian.org>

Description: Provides a function kitten() which creates cute little packages which pass R package checks. This sets it apart from package.skeleton() which it calls, and which leaves imperfect files behind. As this is not exactly helpful for beginners, kitten() offers an alternative.

License: GPL (>= 2)

Suggests: whoami (>= 1.1.0)

NeedsCompilation: no

Packaged: 2016-11-13 14:52:34.898805 UTC; edd

Repository: CRAN

Date/Publication: 2016-11-13 16:50:45

NAMESPACE

- Lists which packages are imported from
 - These must be listed in **DESCRIPTION** and its **Imports** field
 - Can import packages 'whole' or just particular identifiers
- Similarly states what is exported from a package
 - Default value is a regular expression for all visible identifiers
 - (Allowing invisible one starting with a dot)
 - You can also selected exports explicitly naming functions
- For packages with compiled code
 - Lists the dynamic library containing the code

Package Creation Helpers

- There are several
- The official one is `package.skeleton()` in base R
 - leaves suboptimal package that does not pass `R CMD check`
- So I once wrote `pkgKitten` and its `kitten()` to postprocess
- There is also RStudio's File -> New Project -> New Directory -> R Package (but sadly not with RStudio Cloud :-/)
- (And also `devtools` / `usethis` which I am less familiar with ...)

RStudio Use – and RStudio Cloud workaround

- On a regular RStudio instance on your computer (or lab), try
 - File -> New Project -> New Directory -> R Package
- Using RStudio Cloud, create a new package via
 - Packages menu, select 'Install' and write `pkgKitten`
 - Or at the R prompt do `install.packages("pkgKitten")`
 - Once installed do `library(pkgKitten)`
 - And, say, `kitten("simpleTestPackage")`
- Now we trick RStudio Cloud
 - select `project.Rproj` and 'Rename' to `simpleTestPackage/project.Rproj`
 - then navigate to the directory and open the project file

RStudio

- In the 'Build' menu (top right pane)
 - Click 'Install and Restart'
 - Click 'Check'
- These are the two main access points
- Under 'More' additional options
- Also on command-line
 - R CMD `build` to build
 - R CMD `check` to check

DESCRIPTION file

Auto-generated so some fields need filling in:

Package: simpleTestPackage

Type: Package

Title: What the Package Does Using Title Case

Version: 1.0

Date: 2018-12-28

Author: Your Name

Maintainer: Your Name <your@email.com>

Description: More details about what the package does. See
<[http://cran.r-project.org/doc/manuals/r-release/
R-exts.html#The-DESCRIPTION-file](http://cran.r-project.org/doc/manuals/r-release/R-exts.html#The-DESCRIPTION-file)> for
details on how to write this part.

License: GPL (>= 2)

NAMESPACE file

Very simple for a simple package:

```
exportPattern("^[:alpha:]+")
```


R code

```
## a placeholder  
hello <- function(txt = "world") {  
  cat("Hello, ", txt, "\n")  
}
```

Very simple R/hello.R
with a placeholder
function
Function has one
argument with a default
value

manual / help file

```
\name{hello}
\alias{hello}
\title{
  A simple function doing little
}
\description{
  This function shows a standard text on the
  console. In a time-honoured tradition, it
  defaults to displaying \emph{hello, world}.
}
\examples{
  hello()
  hello("and goodbye")
}
```

Also short and simple. Note that we reindent the `\description` block.

Rd files use a simple markup language.

It is documented in *Writing R Extensions*.

Roxygen2 help files: Start from empty stanza

```
#' Title
#'
#' @param txt
#'
#' @return
#' @export
#'
#' @examples
hello2 <- function(txt = "world") {
  cat("Hello, ", txt, "\n")
}
```

We copy `hello()` over to `hello2()` here.

We then use Code -> Insert Roxygen Skeleton and the file changes to what is shown on the left.

(Of course, the text lines can be added by hand too.)

Roxygen2 help files: Filled-in example

```
#' A simple function doing little
#'
#' @param txt A text argument
#'
#' @return Nothing, side effect of cat()
#' @export
#'
#' @examples
#' hello("world")
hello2 <- function(txt = "world") {
  cat("Hello, ", txt, "\n")
}
```

With **roxygen2** installed, one can edit Tools -> Project Options -> Build Tools and check the box for 'Generate documentatin with Roxygen'.

Generating Rd from the R file is the default, one can also add to **NAMESPACE** following the **@export** tag.

```
% Generated by roxygen2: do not edit by hand
% Please edit documentation in R/hello2.R
\name{hello2}
\alias{hello2}
\title{A simple function doing little}
\usage{
hello2(txt = "world")
}
\arguments{
\item{txt}{A text argument}
}
\value{
Nothing, side effect of cat()
}
\description{
A simple function doing little
}
\examples{
hello("world")
}
```

Here the file on the left gets generated.

Personally, I like **roxygen2** for Rd files. I am less convinced about **@export** tags but many find that useful too.

If you want to do it manually:

```
library(roxygen2)
roxygenize(".", roclets="rd")
```

Roxygen2

Following ‘Help -> Roxygen Quick Reference’ opens a viewer pane with a quick summary shown on the right (and a bit more)

Explains a few commands and contains some further references.

```
#' This is the title.
#'
#' This is the description.
#'
#' These are further details.
#'
#' @section A Custom Section:
#'
#' Text accompanying the custom section.
#'
#' @param x A description of the parameter 'x'. The
#'   description can span multiple lines.
#' @param y A description of the parameter 'y'.
#'
#' @export
#'
#' @examples
#' add_numbers(1, 2) ## returns 3
#' ## don't run this in calls to 'example(add_numbers)'
#' \dontrun{ add_numbers(2, 3) }
#' ## don't test this during 'R CMD check'
#' \donttest{ add_numbers(4, 5) }
add_numbers <- function(x, y) {
  x + y
}
```

Command-line

- As mentioned earlier:
 - R CMD `build .` builds in source directory
 - R CMD `build simpleTestPackage` builds from dir above
 - R CMD `check simpleTestPackage_1.0.tar.gz` checks it
 - R CMD `INSTALL simpleTestPackage_1.0.tar.gz` installs
- All these commands have RStudio IDE equivalents
- While `devtools` / `usethis` helper functions are available, knowing the basic functions is essential