



R Package Anatomy

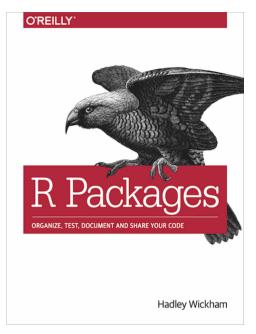
R Foundations for Life Scientists

Sebastian DiLorenzo

Overview



- What is an R package?
- Possible package states
- Package structure:
 - ∘ Code | r/
 - Metadata | DESCRIPTION
 - Documentation | man/
 - Vignettes
 - Import & Export | NAMESPACE
 - o Data data/
 - Compiled code | src/
- git, Github, Rstudio and you!
- CRAN and R CMD check



http://r-pkgs.had.co.nz/

What is an R package?



```
typicalr
DESCRIPTION
NAMESPACE
R
typicalr.Rproj

directory, 3 files
```

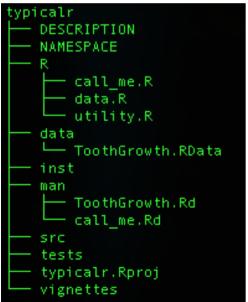
A strict and connected folder and file structure

What is an R package?



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```



A strict and connected folder and file structure

What is an R package?



```
typicalr
DESCRIPTION
NAMESPACE
R
typicalr.Rproj

1 directory, 3 files
```

```
typicalr
DESCRIPTION
NAMESPACE
R
Call_me.R
data.R
utility.R
data
ToothGrowth.RData
inst
man
Call_me.Rd
call_me.Rd
src
tests
typicalr.Rproj
vignettes
```

- A strict and connected folder and file structure
- Sharing code
- Improved quality and rigor
 - Documentation
 - Tests
 - Examples
- Efficiency
- Improvability
- Reproducibility

Package naming



- A name that describes your packages function
 - Letters, numbers and periods
 - Must start with letter
 - Cannot end with period
- Make it googleable
- Check that it doesn't already exist!
 - CRAN
 - o github
 - o Bioconductor

Possible package states



There are five states a package can exist in:

- Source
- Bundled
- Binary
- Installed
- In-memory

Source



The development version of your package. The collection of files on your computer.

Bundled

- A compressed, tar.gz, source package with vignettes built
- .Rbuildignore files are excluded
 - Useful for data for example

Binary

- A bundle that is built for a certain architecture
- Parsed format, skipping the development tools needed to take the package between source and being interpretable by R

Installed



- A binary package decompressed into a package library for R
 - The package library is the directory or directories where library(packagename) searches
 - .libPaths()

In-memory

When you use a package, it is in memory. When developing, a package does not have to be installed to be in memory.

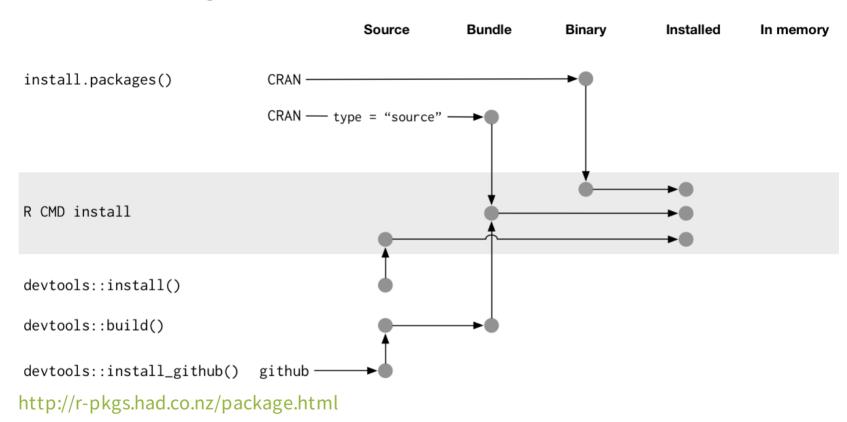
- packagename::function()
 - loads packagename

Note:

- library(packagename)
 - loads and attaches packagename

Possible package states





10/30

R/



```
typicalr
   DESCRIPTION
   NAMESPACE
       call_me.R
       data.R
       utility.R
   data
   └─ ToothGrowth.RData
   inst
   man

    ToothGrowth.Rd

     — call_me.Rd
   src
   tests
   typicalr.Rproj
   vignettes
```

R/



```
typicalr

DESCRIPTION

NAMESPACE

R

call_me.R

data.R

utility.R

data

ToothGrowth.RData

inst

man

call_me.Rd

src

tests

typicalr.Rproj

vignettes
```

```
typicalr/R

— call_me.R

— data.R

utility.R
```

• Code

- Large functions in their own R files
- Utility functions, that your package uses, in one R file
- Bad code

```
o library(), require(), source()
o options(), par()
```

DESCRIPTION



- Title
 - 65 characters, no punctuation
- Version
 - The version of the package
- Description
 - One paragraph

- Authors@R
 - Roles
 - cre*: Creator or maintainer.
 - aut*: Author or authors, that have made significant contributions
 - **ctb**: Contributors, have made smaller contributions.
 - **cph**: Copyright holder. Used if copyright is held by someone other than author, typically company.

^{*:}required

DESCRIPTION



- Depends & Imports
 - Packages and versions that your package needs
 - Versions are optional
 - Depends: Attaches!
 - Imports: Loads!
- Suggests
 - Added functionality

- LazyData
 - Datasets occupy no memory until loaded
- License
 - Can be a file; LICENSE
 - Influences permissions of who can distribute and modify in what way
 - Most common; MIT, GPL-3, CC0.
 - https://tldrlegal.com/
 - CRAN requires a license

Versioning



0.0.0.9000

major.minor.patch.dev

- Major
 - o Large changes, not always backwards compatible
 - o Usually 1 upon first release out of dev
- Minor
 - o Bug fixes & new features. Most common
- Patch
 - Small bugfixes, no new features.
- Dev
 - Only used while under development
 - Always starts at 9000

man/



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```

- Roxygen2
 - ?function
 - Comment block, #', preceding a function
 - Tags, @tags , map values
 - No tag for introduction
 - title*
 - description
 - details
 - Special characters @\%, escape with \

call_me.R

```
#' Output "Call me " followed by input.
#'

#' @param x A character or characters.
#' @return The string "Call me " and \code{x}. I'll write this
#' to display how to section with tags.
#' @examples
#' call_me("Maeby")
call_me <- function(x) {
   paste("Call me ", x, sep="")
}</pre>
```

man/



call_me.R

```
#' Output "Call me " followed by input.
#'
#' @param x A character or characters.
#' @return The string "Call me " and \code{x}. I'll w.
#' to display how to section with tags.
#' @examples
#' call_me("Maeby")
call_me <- function(x) {
   paste("Call me ", x, sep="")
}</pre>
```

call me.Rd

```
% Generated by roxygen2: do not edit by hand
% Please edit documentation in R/call_me.R
\name{call_me}
\alias{call_me}
\title{Output "Call me " followed by input.}
\usage{
call_me(x)
}
\arguments{
\item{x}{A character or characters.}
}
\value{
The string "Call me " and \code{x}. I'll write this
```

> ?call_me
call_me {typicalr}

R Documentation

Output "Call me " followed by input.

Description

Output "Call me " followed by input.

Usage

call me(x)

Arguments

A character or characters.

Value

The string "Call me" and x. I'll write this to display how to section with tags.

Examples

call_me("Maeby")

man/ for datasets



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```

```
head(ToothGrowth)

## len supp dose
## 1 4.2 VC 0.5
## 2 11.5 VC 0.5
## 3 7.3 VC 0.5
## 4 5.8 VC 0.5
## 5 6.4 VC 0.5
## 6 10.0 VC 0.5
```

data.R:

```
#' The Effect of Vitamin C on Tooth Growth in Guinea Pigs
# '
   The response is the length of odontoblasts (cells responsible for tooth growth)
     in 60 guinea pigs. Each animal received one of three dose levels of vitamin C
     (0.5, 1, and 2 mg/day) by one of two delivery methods, orange juice or ascorbic
     acid (a form of vitamin C and coded as VC).
#'
#'
  Qusage ToothGrowth
# '
  Aformat A data frame with 60 observations on 3 variables.
  \describe{
# '
     \item{len}{Tooth length}
     \item{supp}{Supplement type (VC or OJ).}
    \itamsdase\s\Dase in milliarams/dayl
```

vignettes/



- A more complete guide to your package
 - For user/you
 - Examples and use cases
- knitr & rmarkdown
 - knitr: add r code to markdown
- vignettes/package-vignette.Rmd

```
usethis::use_vignette("typicalr-vignette")
```

typicalr-vignette.Rmd

```
title: "Vignette Title"
author: "Vignette Author"
date: "2023-08-14"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{Vignette Title}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---
```

vignettes/



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- knitr & rmarkdown
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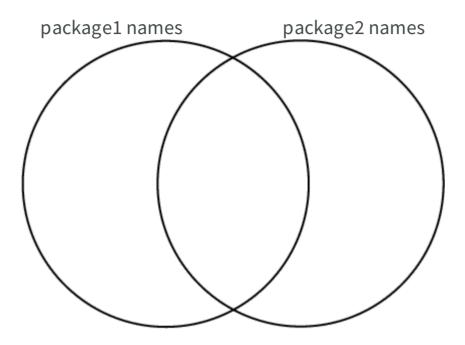
```
usethis::use_vignette("typicalr-vignette")
```

typicalr-vignette.Rmd

```
title: "typicalr"
author: "Sebastian DiLorenzo"
date: "2023-08-14"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{typicalr}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---
```

NAMESPACE





- @imports and @importsFrom
 - o Defines how/where a function in one package finds a function in another
 - @imports pkg
 - @importsFrom pkg function
- @export
 - Defines which functions are available to user
 - Do not export data

NAMESPACE



call_me.R:

```
#' Output "Call me " followed by input.
#'
#' @param x A character or characters.
#' @return The string "Call me " and \code{x}. I'll write this
#' to display how to section with tags.
#' @examples
#' call_me("Maeby")
#' @export
call_me <- function(x) {
   paste("Call me ",x,sep="")
}</pre>
```

utility.R:

```
#' @import knitr
NULL
```

NAMESPACE:

```
# Generated by roxygen2: do not edit by hand
export(call_me)
import(knitr)
```

NAMESPACE



Import in **DESCRIPTION** and in **NAMESPACE**!?

- DESCRIPTION Imports:
 - "My package needs this package to work"
- NAMESPACE @import
 - "When my package uses this function, use the one from the package in the NAMESPACE"
- Additional effects:
 - NAMESPACE removes need for :::
 - package::function() or function()

data/



Package types:

- Functional
 - Performs a or several functions
 - Contains no or small datasets, <1 MB
- Dataset
 - Contains an interesting dataset
 - Easy to import
 - Few or no functions

```
#Create data in package automatically
usethis::use_data(object, package)

#Manually
save(object, file="path/to/package/data/objec")

#Access raw data
system.file("extdata","filename.csv", package
```

Data types:

- Binary data, .Rdata or .rda
 - o data/ folder
 - A single object with the same name as the data file
- Function data
 - 0 R/sysdata.rda
 - Data that your functions need
- Raw data, .xlsx, .csv etc
 - inst/extdata folder

src/



- Compiled code
 - o Rcpp
 - o rJava
- Scripts
 - o inst/
 - Dependencies

- 1. usethis::use_rcpp()
 - Edit DESCRIPTION
 - #' @useDynLib packagename
 - #' @importFrom Rcpp sourceCpp
- 2. .cpp file in src/

src/filename.cpp:

```
#include <Rcpp.h>
using namespace Rcpp;

// This is a simple example of exporting a C++ function to R. You can
// source this function into an R session using the Rcpp::sourceCpp
// function (or via the Source button on the editor toolbar). Learn
// more about Rcpp at:
//
// http://www.rcpp.org/
// http://adv-r.had.co.nz/Rcpp.html
// http://gallery.rcpp.org/
//
// [[Rcpp::export]]
NumericVector timesTwo(NumericVector x) {
    return x * 2;
}
```

src/



- Compiled code
 - RcpprJava
- Scripts
 - o inst/
 - Dependencies

R/RcppExports.R:

```
# Generated by using Rcpp::compileAttributes(
# Generator token: 10BE3573-1514-4C36-9D1C-5A

timesTwo <- function(x) {
    .Call('_typicalr_timesTwo', PACKAGE = 'ty)
}</pre>
```

- 1. usethis::use_rcpp()
 - Edit DESCRIPTION
 - #' @useDynLib packagename
 - #' @importFrom Rcpp sourceCpp
- 2. .cpp file in src/
- 3. pkgbuild::compile_dll()
- 4. devtools::document()
- 5. Build & Reload
- 6. Add documentation to .cpp

git, Github, Rstudio and you!



- git
 - Version control
 - Working in groups
 - Rstudio integration
- Github
 - Unoffical repository
 - o devtools::install_github()
 - R Package development environment
 - Issues

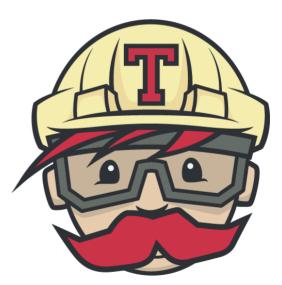


CRAN and R CMD check

NB§S

- Comprehensive R Archive Network
 - R package repository
 - Sign of quality
- R CMD check
 - More than 50 individual checks
 - Three messages:
 - **ERROR**: Always fix.
 - WARNING: Should probably fix. Definitely for CRAN submit.
 - NOTE: Try to solve to CRAN submit, else do not bother.
 - o devtools::check()
- Travis-CI
 - Integrated with your github repository
 - Automates R CMD check
 - Multiple operating systems

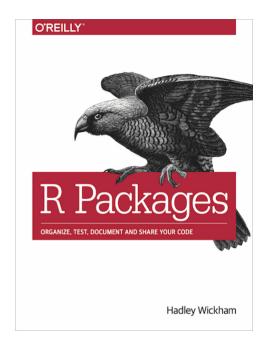




Summary



- What is an R package?
- Possible package states
- Package structure:
 - ∘ Code | r/
 - Metadata | DESCRIPTION
 - Documentation | man/
 - Vignettes
 - Import & Export | NAMESPACE
 - Data | data/
 - Compiled code | src/
- git, Github, Rstudio and you!
- CRAN and R CMD check



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Thank you. Questions?



