

# Building R Packages

**What are R Packages?**

# R Packages

1. Sets of Functions
2. Set of Functions + Documentation
3. Set of Functions + Documentation + Data
4. Set of Functions + Documentation + Data + Vignettes
5. Set of Functions + Documentation + Data + Vignettes + Versions
6. Set of Functions + Documentation + Data + Vignettes + Versions + Dependencies

# Windows and RTools

If you have a Windows machine, you need to install RTools from <https://cran.r-project.org/bin/windows/Rtools/> (choose the frozen one).

---

## Using Rtools40 on Windows

Starting with R 4.0.0 (released April 2020), R for Windows uses a brand new toolchain bundle called **rtools40**.

This version of Rtools upgrades the mingw-w64 gcc toolchains to version 8.3.0, and introduces a new build system based on [msys2](#), which makes easier to build and maintain R itself as well as the system libraries needed by R packages on Windows. For more information about the latter, follow the links at the bottom of this document.

*This documentation is about rtools40, the current version used for R 4.0.0 and newer. For information about previous versions of Rtools that can be used with R 3.6.3 or older, please visit [this page](#).*

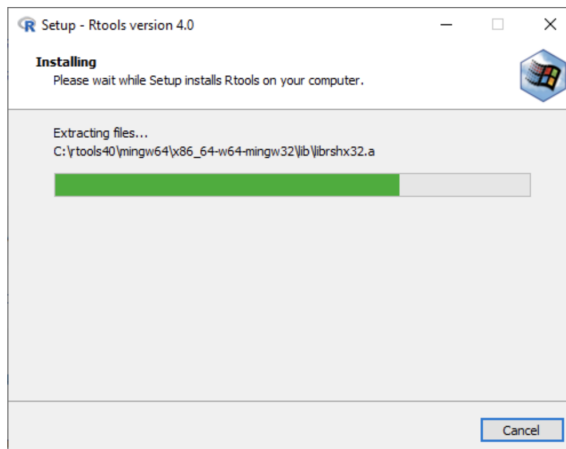
## Installing Rtools40

Note that rtools40 is only needed build R packages with C/C++/Fortran code from source. By default, R for Windows installs the precompiled “binary packages” from CRAN, for which you do not need rtools!

To use rtools40, download the installer from CRAN:

- On Windows 64-bit: [rtools40-x86\\_64.exe](#) (recommended: includes both i386 and x64 compilers)
- On Windows 32-bit: [rtools40-i686.exe](#) (i386 compilers only)

**Note for RStudio users:** please check you are using the latest version of RStudio (at least 1.2.5042) to work with rtools40.



Building Rtools on the RVM

# Starting Up

Use RStudio and the `devtools` and `usethis` packages. It's easier.

```
install.packages(c("devtools", "usethis"))
```

In RStudio, File -> New Project -> New Directory -> R Package with devtools (scroll down), with a name:

- must start with letter
- no underscores
- periods allowable or use CamelCase
- can have numbers

# Checking Package Names

Try the `available::available` function:

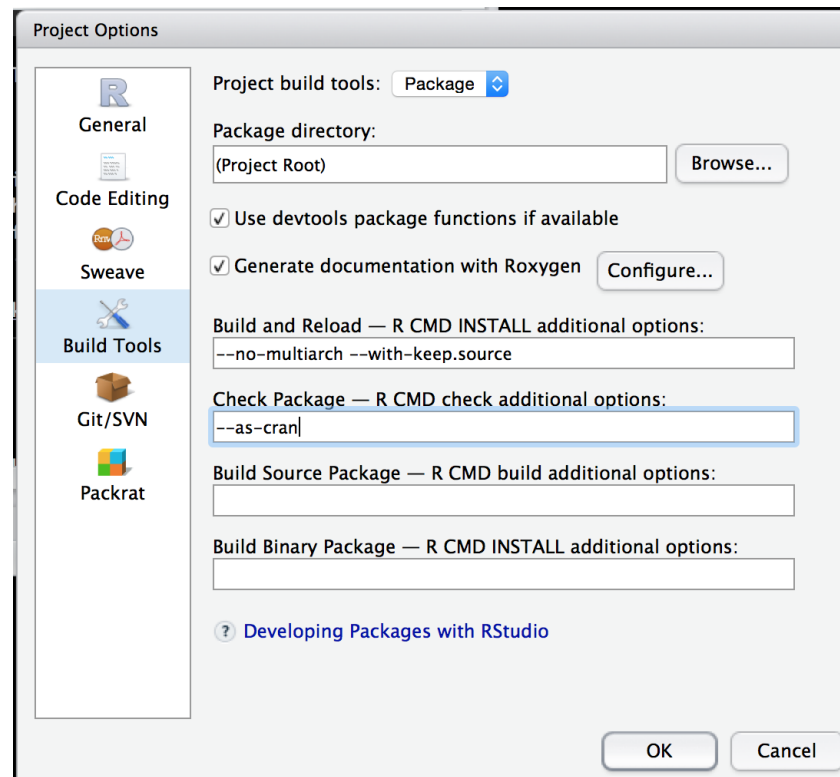
```
available::available("ggplot")
```

```
## — ggplot —————  
## Name valid: ✓  
## Available on CRAN: ✕  
## Available on Bioconductor: ✓  
## Available on GitHub: ✓  
## Abbreviations: http://www.abbreviations.com/ggplot  
## Wikipedia: https://en.wikipedia.org/wiki/ggplot  
## Wiktionary: https://en.wiktionary.org/wiki/ggplot  
## Urban Dictionary:  
##   Not found.  
## Sentiment:???
```

# Setting Up

Go to Build -> Configure Build Tools

Add `--as-cran` to “Check Package” (useful later)



# Documentation is a pain

...but it's worthwhile. Writing out argument definitions makes it easier to identify if argument names make sense.



From <https://imgflip.com/i/4mvkhl>



# Documentation is a pain



**Karen Cranston**  
@kcranstn



@mtholder motivating git: You mostly collaborate with yourself, and me-from-two-months-ago never responds to email. @swcarpentry

10:23 AM · Aug 23, 2013 · TweetDeck

**29** Retweets   **7** Quote Tweets   **22** Likes

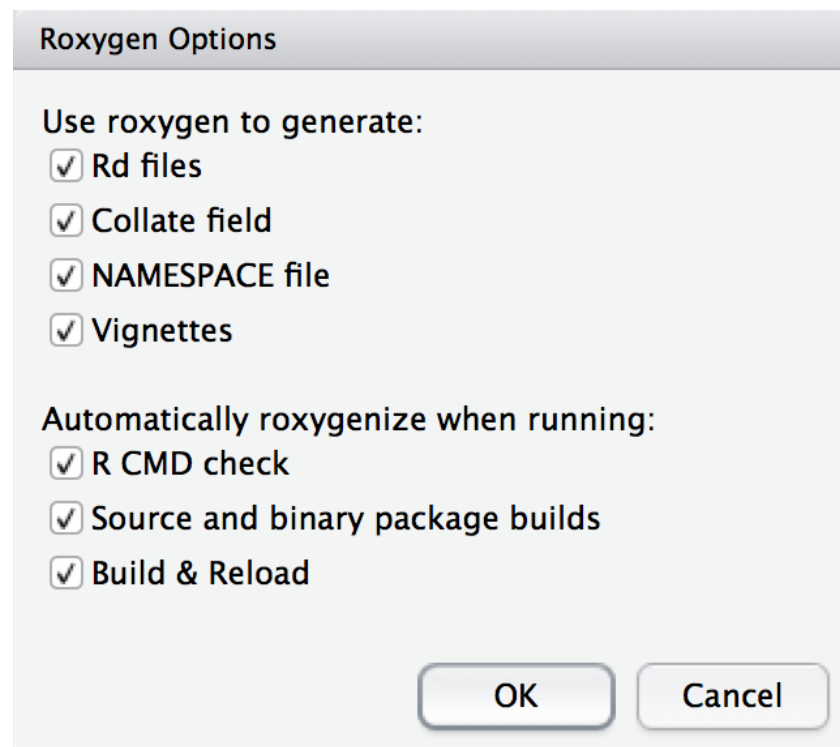


<https://twitter.com/kcranstn/status/370914072511791104>

# Use Roxygen2

Click Generate documents with Roxygen. If that is gray, install `roxygen2`:

```
install.packages("roxygen2")
```



Click "Configure" - click all the boxes.

# Modifying the Skeleton

Things to do:

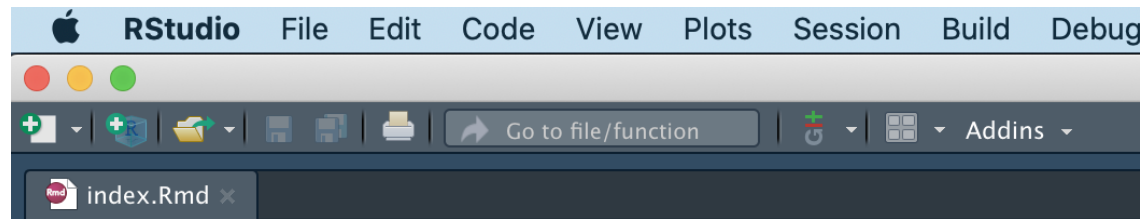
1. Delete `R/hello.R` (skip if used devtools)
2. Delete `man/hello.Rd` (skip if used devtools)
3. In RStudio, Build → Configure Build Tools → Generate Documentation with Roxygen, make sure that's clicked. I click Vignettes and Build and Reload.
4. In RStudio, add `--as-cran` under the "Check options" in Build → Configure Build Tools.
5. Delete the `NAMESPACE` file (skip devtools). If building fails, add an empty file with `# Generated by roxygen2: do not edit by hand` at the top and rerun.

# DESCRIPTION file

In the RStudio project, go to “Go to file/function” search bar on the menu bar.

- This searches through the files in the package.
  - Also searches for **function names** and can go to that function in the file

Type “DESCRIPTION” and open that file.



# DESCRIPTION file

- "Title - What the Package Does (Title Case)
- "Author: YOURNAME"
- "Maintainer: YOURNAME [your@email.com](#)" -> we will remove this
- "Description: Use paragraph prose here. Don't start with word package" Use four spaces when indenting paragraphs within the Description.
- "License:", one of GPL-2 GPL-3 LGPL-2 LGPL-2.1 LGPL-3 AGPL-3 Artistic-2.0 BSD\_2\_clause BSD\_3\_clause MIT

# Authors

I add this to the DESCRIPTION file:

```
Authors@R: c(person(given = "John",  
                    family = "Muschelli",  
                    email = "muschellij2@gmail.com",  
                    role = c("aut", "cre"),  
                    comment = c(ORCID = "0000-0001-6469-1750")))
```

Use `Authors@R` even if there is only one author.

# License

```
usethis::use_gpl3_license("John Muschelli")
```

- <https://www.r-project.org/Licenses/>

# DESCRIPTION file: additional fields

- You do not use `library` or `require` in functions in a package
- Imports: package1, package2
  - packages with specific functions called in package
  - Anything other than base package needs to be imported (`stats`, `methods`)
- Depends: package3, package5
  - packages with **ALL** functions loaded from package
- Suggests: package4, package6
  - used in **examples** or **vignettes**

```
usethis::use_package("tidyr", type = "Imports")  
usethis::use_package("dplyr", type = "Suggests")
```



# Description

- Change the `Description` so that it's a sentence and it ends with a period.
- Put single quotes around weird words (like science-specific).
- Make sure to put links in angle brackets (`<http...>`). Use DOIs if you can.
- If you go too long on a line, indent it with 4 spaces " ".

```
Type: Package
Package: SummarizedActigraphy
Title: Coerce 'Actigraphy' to Summarized Experiments
Version: 0.3.0
Authors@R: c(
  person(given = "John",
    family = "Muschelli",
    role = c("aut", "cre"),
    email = "muschellij2@gmail.com",
    comment = c(ORCID = "0000-0001-6469-1750"))
)
Description: Provides functions for coercing 'actigraphy' data into
  'SummarizedExperiment' objects used for genomic analysis. This
  conversion enables the use of functions that work on the
  'SummarizedExperiment' class.
License: GPL-3
```

# Roxygen2

Roxygen allows for functions and documentation in the same file. Let's make a function:

```
top = function(x, n) {  
  xx = x[1:n, 1:n]  
  hist(xx)  
  print(xx)  
}
```

Save this to `top.R` file in `R/` (where R functions are).

# Roxygen2

Highlight the following code:

```
top = function(x, n) {
```

Go to Code -> Insert Roxygen Skeleton

# Roxygen Skeleton Output

```
#' Title
#'  
#' @param x  
#' @param n  
#'  
#' @return  
#' @export  
#' @examples
```

- `@param` stands for a parameter/argument for that function.
- `@return` denotes what the function returns. This is required.
- `@export` - when people install your package, can they use this function
  - non-exported functions are usually helpers, really small, or not fully formed yet
- `@examples` - code to show how the function works. Wrap functions in `\dontrun{ }` if not wanted to run

## Roxygen Skeleton:

You can add @title and @description tags:

```
#' @title
#' @description
#'
#' @param x
#' @param n
#'
#' @return
#' @export
#'
#' @examples
```

# Roxygen Skeleton:

```
#' @title Print the top of a matrix
#' @description \code{top} is a small function to not just present the first rows
#' of a matrix, but also the first number of columns
#'
#' @param x a \code{matrix}
#' @param n Number of rows and columns to display of the matrix
#'
#' @return A \code{NULL}
#' @export
#'
#' @examples
#' mat = matrix(rnorm(100), nrow = 10)
#' top(mat, n = 4)
#' \dontrun{
#'   top(mat, n = 10)
#' }
```

# Functions: a little style

1. Create a file for each function (preference) or at least group. Name file function name.
2. Optional arguments: Set to `NULL` and use `is.null()` to test
3. Put functions together: use `#' @rdname`.
4. See `#' @inheritParams` for different functions with the same arguments.
5. Add logical `verbose` argument for printing
6. Use `message` (not `cat`) for printing. Someone can use `suppressMessages` to stop the printing.
7. Pass `...` to a main function for additional options for the user.
8. Have examples (vignette too)
9. Learn `do.call(FUNCTION, args = list_of_arguments)`
10. Notify/warn/message whenever you have to.

# NAMESPACE

The `NAMESPACE` file tells the R package what to import and export. In Roxygen:

- `@export` - adds this to the `NAMESPACE` file
  - when package is installed, users can call this function
- `@import` - in roxygen, if you want to import a **package**, you say `@import PACKAGENAME`
  - imports **ALL** functions from that package
  - if package is listed under Depends in DESCRIPTION, then the **whole package** is loaded when you load your package
  - otherwise it simply exposes them for your package to use them, but not the user, users still have to do `library(PACKAGENAME)`



# NAMESPACE

- `@importFrom` - in roxygen, if you want to import a **function**, you say `@import PACKAGE_NAME func1 func2`
  - only imports these functions. Better way of doing things.
  - if `pkgA` has function `A` and `pkgB` has functions `A` and `B`, if `@import pkgA A`, `@import pkgB B`, then if you call `A()`, R knows it's from `pkgA`
  - you must import anything explicitly other than from the base package, including anything from `stats` (e.g. `quantile`) or `graphics` (e.g. `hist`)

Add `@importFrom graphics hist` to your `top.R` file

# NAMESPACE - alternative

```
> usethis::use_package("devtools")  
✓ Adding 'devtools' to Imports field in DESCRIPTION  
• Refer to functions with `devtools::fun()`  
|
```

For every function you're using from a package, use `package::function()`

- Preferred way, especially only using infrequently
- Don't need an `@import` or `@importFrom` tag
- Annoying with frequent functions (e.g. `dplyr`), so you can use `import`

```
usethis::use_pipe()
```

# Build and Reload

- Go to Build -> Build and Reload the package
  - First time you may see some warnings (no NAMESPACE file!)
  - Rerunning should get rid of these
  - look in the folders
- Then try Build -> Check Package

# Using Data

The `data/` directory is where data goes, it **must** be named `.RData` or `rda`. The `use_data` function can do this for you:

```
usethis::use_data(DATAOBJECT, compress = "xz")
```

The output will be `DATAOBJECT.rda` in the `data` folder. You can use this in your package

# Making Data

That's not reproducible!

The `data-raw` directory can be data you want to create (such as simulated data).

This will have scripts with `use_data` at the end to make the data.

```
usethis::usethis::use_data_raw()
```

# Documenting Data

Note how DATAOBJECT is the name of the object/rda. Now we can document the data as follows:

```
#' @title Some object to document
# '
#' @description A list containing things
# '
#' @format A list with 7 elements, which are:
#' \describe{
#' \item{x}{first thing}
#' \item{y}{second thing}
#' }
"DATAOBJECT"
```

# Different kinds of data

The `inst/` directory will copy any of the contents to the installed directory path. So if `blah.csv` was in `inst/` then it will be in the directory.

Most times, however, people put data in `inst/extdata` to separate folders out.

You can use `find.package` to find the installed directory:

```
find.package("readr")
```

```
## [1] "/Users/johnmuscchelli/Library/R/4.0/library/readr"
```

To get files, though, you should use `system.file`:

```
system.file("extdata", package = "readr")
```

```
## [1] "/Users/johnmuscchelli/Library/R/4.0/library/readr/extdata"
```

# Different kinds of data

If you pass in multiple characters, it assumes you put it together with `file.path`:

```
system.file("extdata", "challenge.csv", package = "readr")
```

```
## [1] "/Users/johnmuschelli/Library/R/4.0/library/readr/extdata/challenge.csv"
```

The `mustWork` argument is useful for making sure the file exists:

```
system.file("extdata", "asdfsdf.csv", package = "readr", mustWork = TRUE)
```

```
## Error in system.file("extdata", "asdfsdf.csv", package = "readr", mustWork = TRUE): no file
```



# Using the file system

1. `file.path` > paste for paths (or `fs` package)
2. Use `file.exists`. Use `any` and `all`
3. `file.remove` if you need to delete things
4. Make temporary (empty, non-existent) files, with extension:  
`tempfile(fileext = ".csv")`.
5. `dir.create` to create and `unlink` to destroy directories.
6. Using `tempdir()` for stuff that's intermediate.
7. Tempdir sub-directory: `tdir = tempfile(); dir.create(tdir);`  
`on.exit({ unlink(tdir) })`
8. `file.copy` and `file.rename`
9. `download.file` or `curl::curl_download`

# Vignettes

- <http://r-pkgs.had.co.nz/vignettes.html>

A package has data + code + dependencies. A vignette can tie this together to tell you **how** to use the package. Typically it is an analysis.

- **THIS IS EXACTLY WHAT A REPRODUCIBLE PAPER IS!**

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

- Can make private packages that are the workflow for your paper

# Unit tests

The `testthat` package is great for unit testing. Put test scripts in `tests/testthat`, always named `test-DESCRIPTOR.R`. To set up `testthat`:

```
usethis::use_testthat()
```

And a specific test:

```
usethis::use_test("name of test")
```

**General Rule:** Any package issue turns into a test.

# Unit tests

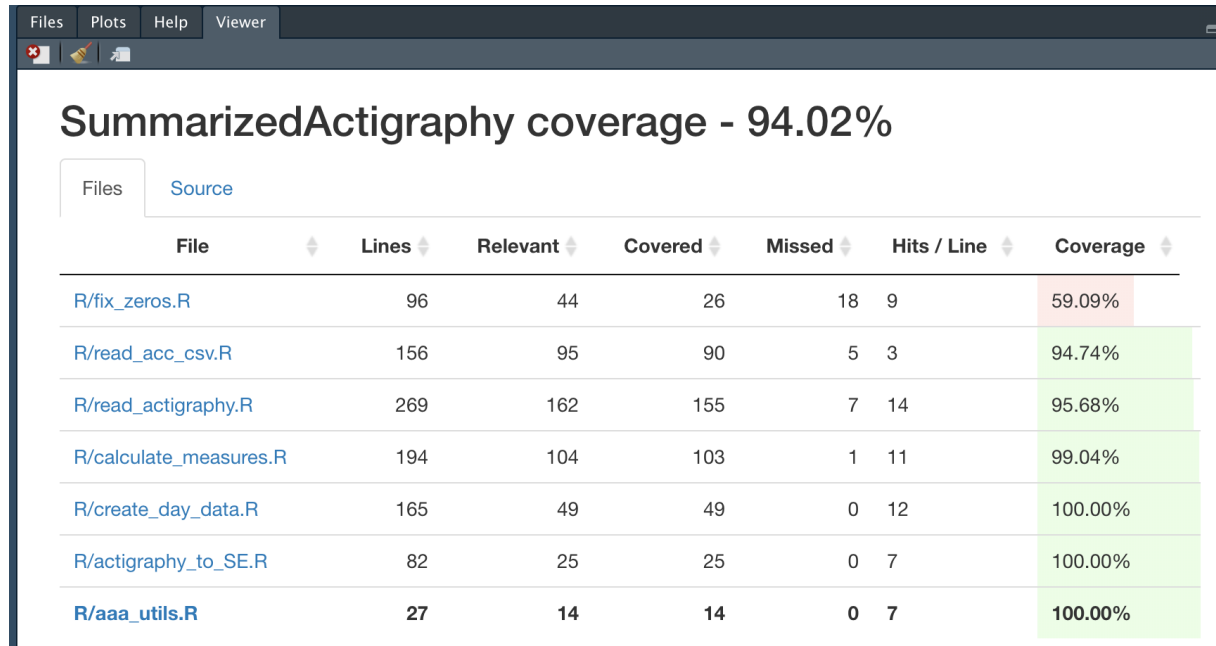
The `testthat` package is great for unit testing. Put test scripts in `tests/testthat`, always named `test-DESCRIPTOR.R`. To set up `testthat`:

```
testthat::context("OVERALL DESCRIPTION OF TESTS IN THIS FILE")
testthat::test_that("Description of this test", { MYCODE })
testthat::expect_equal(OUTPUT, 1234.34535)
testthat::expect_identical(OUTPUT1, OUTPUT2)
testthat::expect_true(SOME_OUTPUT)
testthat::expect_silent({ no_warning_error_code })
testthat::expect_message({ some_warn }, "a[test]regexp")
```

# Code Coverage: % Code covered in tests

Use `covr` package:

```
covr::package_coverage() # run tests
covr::report() # get a report
covr::report(covr::package_coverage(type = "all")) # run them all
```



SummarizedActigraphy coverage - 94.02%

File	Lines	Relevant	Covered	Missed	Hits / Line	Coverage
<a href="#">R/fix_zeros.R</a>	96	44	26	18	9	59.09%
<a href="#">R/read_acc_csv.R</a>	156	95	90	5	3	94.74%
<a href="#">R/read_actigraphy.R</a>	269	162	155	7	14	95.68%
<a href="#">R/calculate_measures.R</a>	194	104	103	1	11	99.04%
<a href="#">R/create_day_data.R</a>	165	49	49	0	12	100.00%
<a href="#">R/actigraphy_to_SE.R</a>	82	25	25	0	7	100.00%
<a href="#">R/aaa_utils.R</a>	27	14	14	0	7	100.00%

# Process

- Go to Build → Load All to load all functions
- Change your code, write functions
- Build → Check Package
- Fix errors/notes
- Make tests
- Check code coverage
- Iterate

That's a lot of it - next slides are  
gravy

# Checking Packages in the Past

“But does it work on someone else’s machine or just mine?”



<https://memegenerator.net/instance/85107524/thinking-stick-man-ask-friend-to-check-my-package-why-arent-they-done-yet>



# Continuous integration (Thoughtworks.com)

Continuous Integration (CI) is a development practice that requires developers to integrate code into a shared repository several times a day. Each check-in is then verified by an automated build, allowing teams to detect problems early.



**Travis CI**



**GitHub**




**AppVeyor**

# Building CI and README

```
usethis::use_git() # make a Git repo
usethis::use_github() # must have GITHUB_PAT set up
usethis::use_github(protocol = "https") # must have GITHUB_PAT set up
usethis::use_readme_rmd() # make a readme
usethis::use_github_action_check_standard()
usethis::use_appveyor() # Windows - or use github action
usethis::use_travis() # Linux/OSX - or use github action
```


# GitHub Actions - Build all 3 OSes

<https://github.com/r-lib/actions>


 github.com/r-lib/actions

README.md

## GitHub Actions for the R language

 R-CMD-check

passing

 Community

github-actions

This repository stores [GitHub Actions](#) for R projects, which can be used to do a variety of CI tasks. It also has a number of [example workflows](#) which use these actions.

1. [r-lib/actions/setup-r](#) - Sets up [R](#)
2. [r-lib/actions/setup-pandoc](#) - Sets up [pandoc](#)
3. [r-lib/actions/setup-tinytex](#) - Sets up LaTeX with [tinytex](#)
4. [r-lib/actions/pr-fetch](#) - Fetches changes of a PR associated with an event
5. [r-lib/actions/pr-push](#) - Pushes changes to a PR associated with an event
6. [r-lib/actions/run-rchk](#) - Runs [rchk](#) tests to detect memory protection errors in C source code.

## Examples

See the [r-lib/actions/examples](#) directory for a variety of example workflows using these actions.

\*\*\*

# GitHub Actions

```
usethis::use_github_action_check_standard()
```

- adds file to `.github/workflows/`

```
usethis::use_github_action_check_standard()  
✓ Setting active project to '/Users/johnmuschelli/Dropbox/Packages/SummarizedActigraphy'  
✓ Creating '.github/'  
✓ Adding '^\\.github$' to '.Rbuildignore'  
✓ Adding '*.html' to '.github/.gitignore'  
✓ Creating '.github/workflows/'  
✓ Writing '.github/workflows/R-CMD-check.yaml'  
● Copy and paste the following lines into '/Users/johnmuschelli/Dropbox/Packages/SummarizedActigraphy/README.Rmd':  
  <!-- badges: start -->  
  [![R build status](https://github.com/muschellij2/SummarizedActigraphy/workflows/R-CMD-check/badge.svg)](https://github.com/muschellij2/SummarizedActigraphy/actions)  
  <!-- badges: end -->
```

# Configuring Travis

In `.travis.yml`, add the following lines:

```
os:  
  - linux  
  - osx  
  
warnings_are_errors: true  
after_success:  
  - Rscript -e 'covr::codecov(type = "all")'
```

# Configuring Appveyor

In `appveyor.yml`, add the following lines:

```
environment:  
  global:  
    WARNINGS_ARE_ERRORS: 1
```

# Adding to the **README.Rmd**

These function adds following lines, changing GITHUB\_USERNAME/REPO to the correct version

```
[![R build status](https://github.com/GITHUB_USERNAME/REPO/workflows/R-CMD-check/badge.svg)](https://github.com/GITHUB_USERNAME/REPO/workflows/R-CMD-check)  
[![Travis-CI Build Status](https://travis-ci.com/GITHUB_USERNAME/REPO.svg?branch=master)](https://travis-ci.com/GITHUB_USERNAME/REPO)  
[![AppVeyor Build Status](https://ci.appveyor.com/api/projects/status/github/GITHUB_USERNAME/REPO)](https://ci.appveyor.com/api/projects/status/github/GITHUB_USERNAME/REPO)
```

or a general badge:

```
usethis::use_badge("Travis-CI Build Status",  
src = "https://travis-ci.com/GITHUB_USERNAME/REPO.svg?branch=master",  
href = "https://travis-ci.com/GITHUB_USERNAME/REPO")
```

to the **README.Rmd**.

# S3, S4, Reference Classes

- S3 - simple - just say `class(x) = "myS3Class"`
  - Usually List of objects
  - <http://adv-r.had.co.nz/S3.html>
- S4 - more complex - see `new`
  - name, representation (slots), and inheritance (does it act like an array/list)
  - <http://adv-r.had.co.nz/S4.html>
- Reference Classes
  - very different, `class$method()`
  - <http://adv-r.had.co.nz/R5.html>



# S3, S4 Methods

- `S3:bar <- function(y) UseMethod("bar", y)`
  - `bar.myS3Class` will allow you to use `bar(x)`
- `S4:setGeneric("myGeneric", function(x)`  
`standardGeneric("myGeneric"))`

```
setMethod("myGeneric", signature(x = "myS3Class"), function(x, y) {  
  x@slot + y  
})
```

# Compiled Code: C and C++

See <http://r-pkgs.had.co.nz/src.html>

- The `src/` folder has compiled code.
- `cleanup` generally deletes intermediate or downloaded files run in `configure`.
- `configure` runs code before `make` is run
- `Makevars` or a `Makefile` gives direction for compiling code
- There are `configure.win` and `Makevars.win` for Windows-specific setup.
- See `.Call` for calling these compiled functions.

Using `Rcpp` is a different framework.

Questions?