## Document and share

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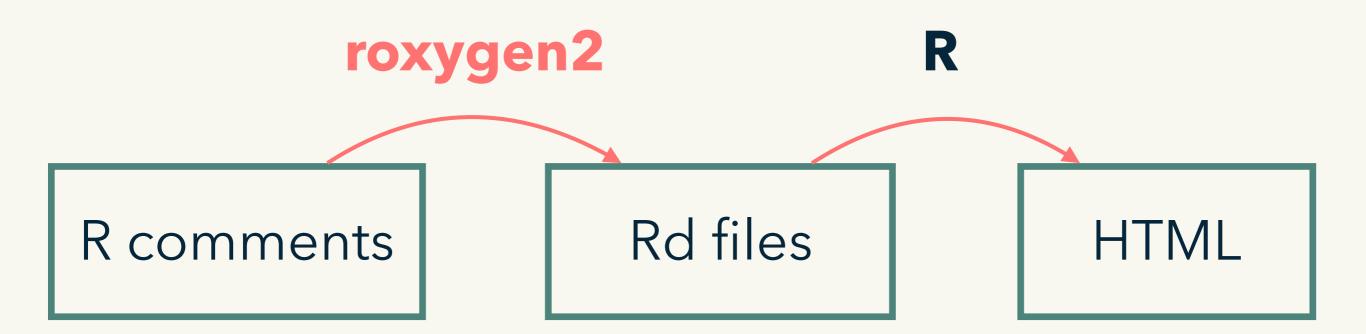


### Overview

- 1. Function docs
- 2. Other docs
- 3. R CMD check
- 4. Continuous integration
- 5. CRAN submission

# Function docs with roxygen2

## Roxygen2



## You write specially formatted comments in .R

```
In R/add_col.R
#' Add a column to a data frame
#'
#' Allows you to specify the position. Will replace existing variable
  with the same name if present.
# '
  @param x A data frame
  @param name Name of variable to create. If a variable of that name
#'
     already exists it will be replaced
  @param value Values to insert.
  @param where Position to insert. Use 1 to insert on LHS, or −1 to insert on
# '
     RHS.
  @examples
\#' df <- data.frame(x = 1:5)
#' add_col(df, "y", runif(5))
  add_{col}(df, "y", runif(5), where = 1)
# '
  add_col(df, "x", 5:1)
```

## You write specially formatted comments in .R

Roxygen comment

```
Add a column to a data frame
#'
                           the position. Will replace existing variable
   Allov
          Roxygen tag
                           bresent.
   with
# '
   @param x A data frame
# '
#'
   @param name Name of variable to create. If a variable of that name
#'
     already exists it will be replaced
   @param value Values to insert.
#'
   @param where Position to insert. Use 1 to insert on LHS.
#'
   @examples
   df \leftarrow data.frame(x = 1:5)
   add_col(df, "y", runif(5))
# '
   add_{col}(df, "y", runif(5), where = 1)
#'
   add_col(df, "x", 5:1)
```

## Roxygen translates to .Rd

```
In man/add_col.Rd
% Generated by roxygen2: do not edit by hand
% Please edit documentation in R/add_col.R
\name{add_col}
\alias{add_col}
\title{Add a column to a data frame}
\usage{
add_{col}(x, name, value, ncol(x) + 1)
\arguments{
\item{x}{A data frame}
\item{name}{Name of variable to create. If a variable of that name
already exists it will be replaced}
\item{value}{Values to insert.}
\item{where}{Position to insert. Use 1 to insert on LHS.}
}
\description{
Allows you to specify the position. Will replace existing variable
with the same name if present.
}
```

In almost all cases

you can ignore
these files

#### Add a colum to a data frame

## R translates to .html for viewing

#### **Description**

Similar to cbind, but allows you to specify the position. Will replac existing variable with the same name if present.

#### **Usage**

```
add col(x, name, value, where = ncol(x) + 1)
```

#### **Arguments**

```
    A data frame
    name
    Name of variabl to create. If variable of that name already exists
    value
    Values to insert.
    where
    position to insert. Use 1 to insert on LHS, or -1 to insert on RHS.
```

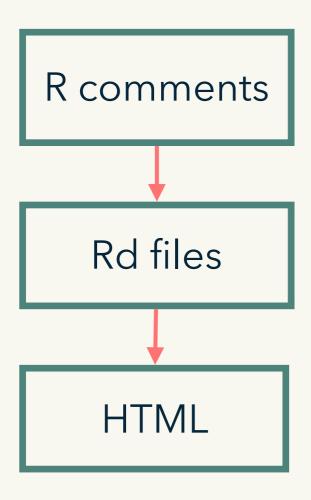
#### **Details**

The columns in

#### **Examples**

```
df <- data.frame(x = 1:5)
add_col(df, "y", runif(5))
add_col(df, "y", runif(5), where = 1)
add_col(df, "x", 5:1)</pre>
```

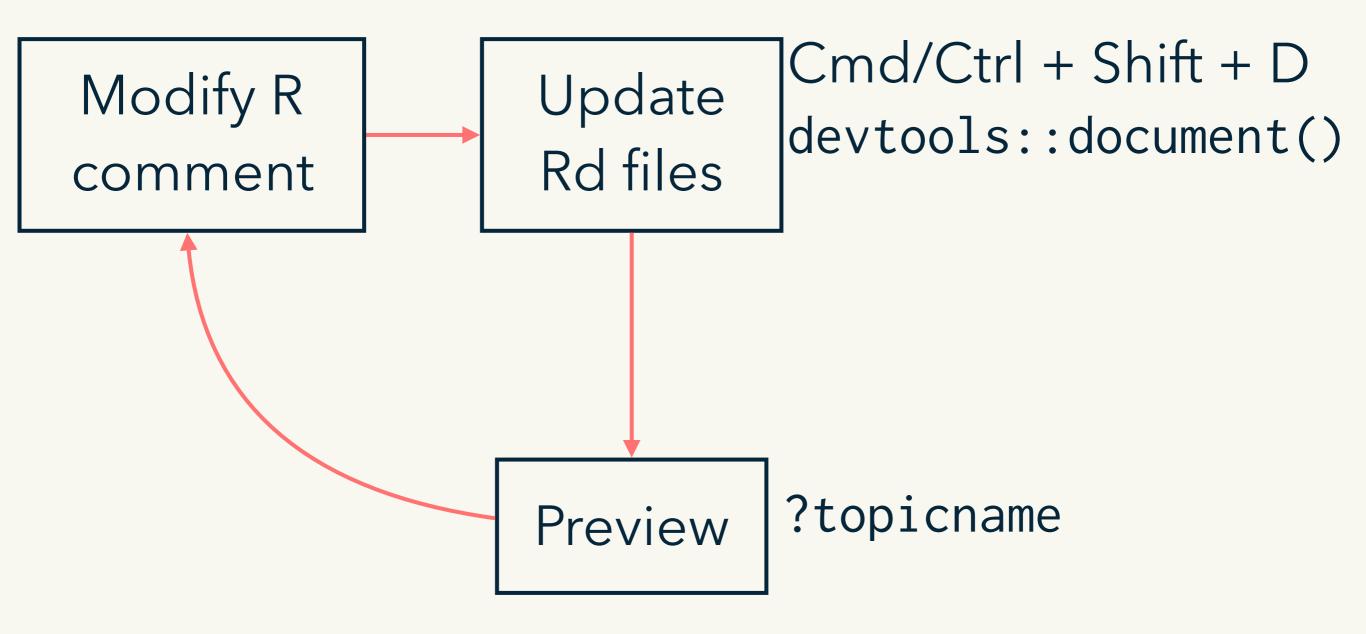
## Easy(er)



### Hard

Writing text that other humans can understand

### Documentation workflow



### Two caveats

- 1. You must have loaded the package with load\_all() at least once.

  Check for message "Using development documentation..."
- 2. This technique only builds individual files so links do not work.

Change project to:

[fordogs]

create\_from\_github("hadley/fordogs", fork = FALSE)

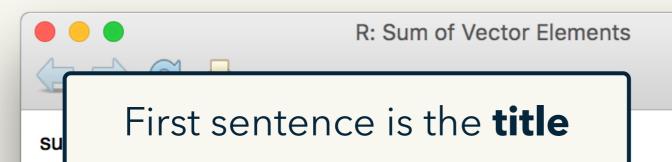
## Your turn

Fix the typos in the documentation for fbind().

Run the documentation workflow to check your work.

Get the package with:

usethis::create\_from\_github("hadley/fordogs", fork = FALSE, protocol = "https")



R Documentation

or

#### Sum of Vector Elements

#### **Description**

sum returns the sum of all the values present in its arguments.

#### **Usage**

sum(..., na.rm = FALSE)

Next paragraph is the

description

#### **Arguments**

numeric or complex or logical vectors.

na.rm logical. Should missing values (including NaN) be removed?

#### **Details**

This is a generic function: methods can be defined for it directly or via the <u>Summary</u> group generic. For this to work properly, the arguments ... should be unnamed, and dispatch is on the first argument.

If na rm is FALSE an NA

Everything else is the **details** 

## The description block

Everything else is the **details** 

```
First sentence is the title
                                                    Next paragraph is
                                                     the description
   Sum of vector elements
#'
#' 'sum' returns the sum of all the values present in its arguments.
# '
  This is a generic function: methods can be defined for it directly
  or via the [Summary] group generic. For this to work properly,
 the arguments `...` should be unnamed, and dispatch is on the
#' first argument.
```

## There are five tags you'll use for most functions

Tag	Purpose
@param arg	Describe inputs
@examples	Show how the function works. (Usual RStudio shortcuts work)
@seealso	Pointers to related functions
@returns	Describe outputs (value)
@export	Is this a user-visible function?

https://roxygen2.r-lib.org/articles/rd.html

## Your turn

Complete the documentation for fbind().

A good minimum is to describe the types of the input and output (we'll talk a lot more about types tomorrow).

## **Practical Tutorial** How-to **Studying** Working Reference Explanation **Theoretical**

https://www.divio.com/blog/documentation/

#### **Practical**

Learning

Problem

**Studying** 

Working

Understanding

Information

**Theoretical** 

https://www.divio.com/blog/documentation/



Tutorial vignette

How-to vignette

**Studying** 

Working

Explanation vignette

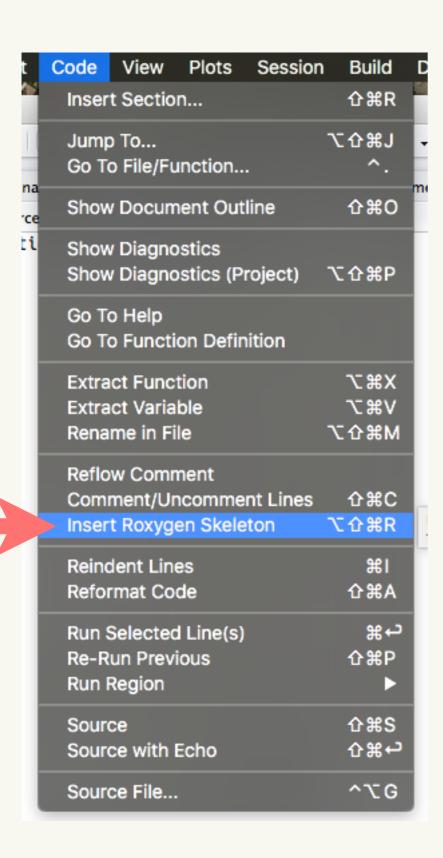
Reference

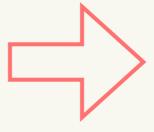
roxygen2

**Theoretical** 

https://www.divio.com/blog/documentation/

## RStudio helps you remember





```
Title
# '
   @param x
   @param y
   @param z
# '
   @return
   @export
# '
#' @examples
fun <- function(x, y, z) {</pre>
```

## Your turn

Document fdist().

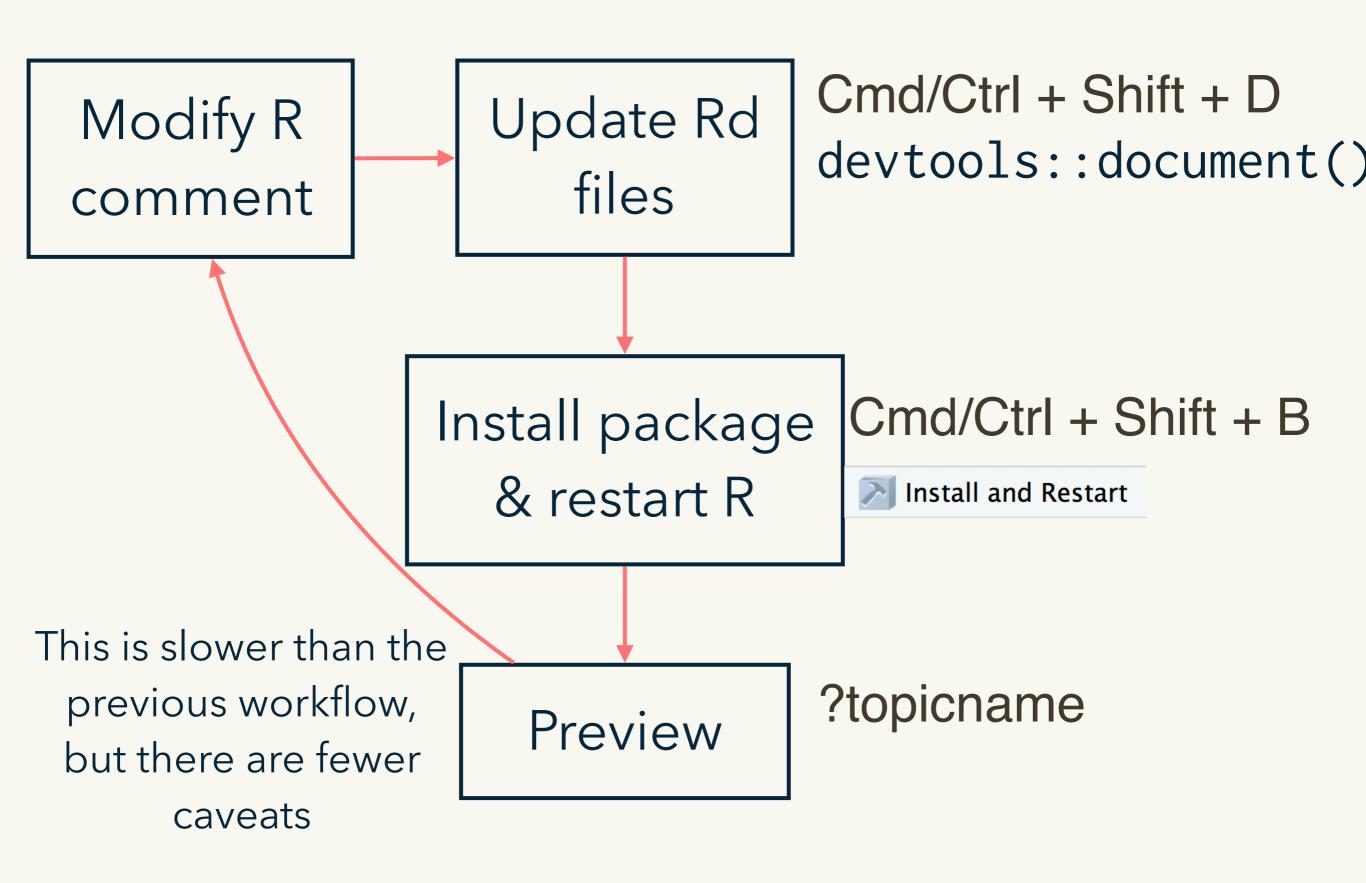
```
fdist(factor(rpois(50, 5)))
fdist(factor(rpois(500, 5)))
fdist(factor(round(rnorm(100, 5))))
```

fdist(ggplot2::diamonds\$cut)
fdist(ggplot2::diamonds\$cut, sort = TRUE)

## Use markdown for formatting

```
# In fordogs package, activate by running
# usethis::use_roxygen_md()
# (Activated by default in new packages)
**bold**, _italic_, `code`
* [func()]
* [pkg::func()]
* [link text][func()]
* [link text][pkg::func()]
```

## Documentation workflow 2



# Package documentation with rmarkdown

## Use vignettes for broader topics

```
usethis::use_vignette("name")
# Adds to DESCRIPTION
Suggests: knitr
VignetteBuilder: knitr
# Creates vignettes/
# Drafts vignettes/name.Rmd
```

## Vignette = Rmarkdown + special metadata

Special output format for vignettes

Special metadata needed by R

Vignettes are long form documentation commonly included in packages. Because they are part of the distribution of the package, they need to be as compact as possible. The 'html\_vignette' output type provides a custom style sheet (and tweaks some options) to ensure that the resulting html is as small as possible. The 'html\_vignette' format:

. . .

## Big picture in README

```
usethis::use_readme_rmd()

# * 2-3 paragraph overview

# * Installation instructions

# * Usage example, with pointer to vignettes
```

## If evolving over time, note changes to API

```
usethis::use_news_md()
# * what's new
# * what's changed
# * what's gone away
#
# More info at
# http://style.tidyverse.org/news.html
```

## Turn into a website with pkgdown



use\_pkgdown()
use\_pkgdown\_travis()

# Continuous integration (CI)

```
use_git()
use_github()
use_travis()
use_coverage()
use_pkgdown_travis()
use_github_actions() # dev version
```

## R CMD check

## Automated checking

Runs automated checks for common problems in R packages.

Useful for local packages, even with some false positives.

If you want to submit to CRAN, you must pass R CMD check cleanly.

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



# "If it hurts, do it more often"

- Martin Fowler

#### ==> R CMD build rv2 \* checking for file 'rv2/DESCRIPTION' ... OK \* preparing 'rv2': \* checking DESCRIPTION meta-information ... OK \* installing the package to build vignettes \* creating vignettes ... OK \* checking for LF line-endings in source and make files \* checking for empty or unneeded directories \* building 'rv2\_0.1.tar.gz' ==> R CMD check rv2\_0.1.tar.gz \* using log directory '/Users/hadley/Documents/courses/13-devtools/rv2.Rcheck' \* using R version 3.0.2 (2013-09-25) \* using platform: x86\_64-apple-darwin10.8.0 (64-bit) \* using session charset: UTF-8 \* checking for file 'rv2/DESCRIPTION' ... OK \* this is package 'rv2' version '0.1' \* checking package namespace information ... OK \* checking package dependencies ... OK \* checking if this is a source package ... OK \* checking if there is a namespace ... OK \* checking for executable files ... OK \* checking for hidden files and directories ... OK \* checking for portable file names ... OK

```
* checking for sufficient/correct file permissions ... OK
* checking whether package 'rv2' can be installed ... OK* checking installed package size ... OK
* checking package directory ... OK
* checking DESCRIPTION meta-information ... OK
* checking top-level files ... OK
* checking for left-over files ... OK
* checking index information ... OK
* checking package subdirectories ... OK
* checking R files for non-ASCII characters ... OK
* checking R files for syntax errors ... OK
* checking whether the package can be loaded ... OK
* checking whether the package can be loaded with stated dependencies ... OK
* checking whether the package can be unloaded cleanly ... OK
* checking whether the namespace can be loaded with stated dependencies ... OK
* checking whether the namespace can be unloaded cleanly ... OK
* checking loading without being on the library search path ... OK
* checking dependencies in R code ... OK
* checking S3 generic/method consistency ... OK
* checking replacement functions ... OK
* checking foreign function calls ... OK
* checking R code for possible problems ... OK
* checking Rd files ... OK
* checking Rd metadata ... OK
* checking Rd cross-references ... OK
* checking for missing documentation entries ... OK
* checking for code/documentation mismatches ... OK
```

```
* checking Rd \usage sections ... OK
* checking Rd contents ... OK
* checking for unstated dependencies in examples ... OK
* checking installed files from 'inst/doc' ... OK
* checking files in 'vignettes' ... OK
* checking examples ... OK
* checking for unstated dependencies in tests ... OK
* checking tests ...
 Running 'testthat.R' OK
* checking for unstated dependencies in vignettes ...
OK
* checking package vignettes in 'inst/doc' ... OK
* checking running R code from vignettes ...
   'clt.Rmd' ... OK
OK
* checking re-building of vignette outputs ... OK
* checking PDF version of manual ... OK
```

R CMD check succeeded

# Types of problem

#### **ERROR**

Must fix!

	Local	CRAN
ERROR	<b>√</b>	✓
WARNING		
NOTE		<b>√</b>

#### WARNING

Fix if submitting to CRAN

## **NOTE**

Fix if submitting to CRAN

It is possible to submit with a NOTE, but it's best avoided

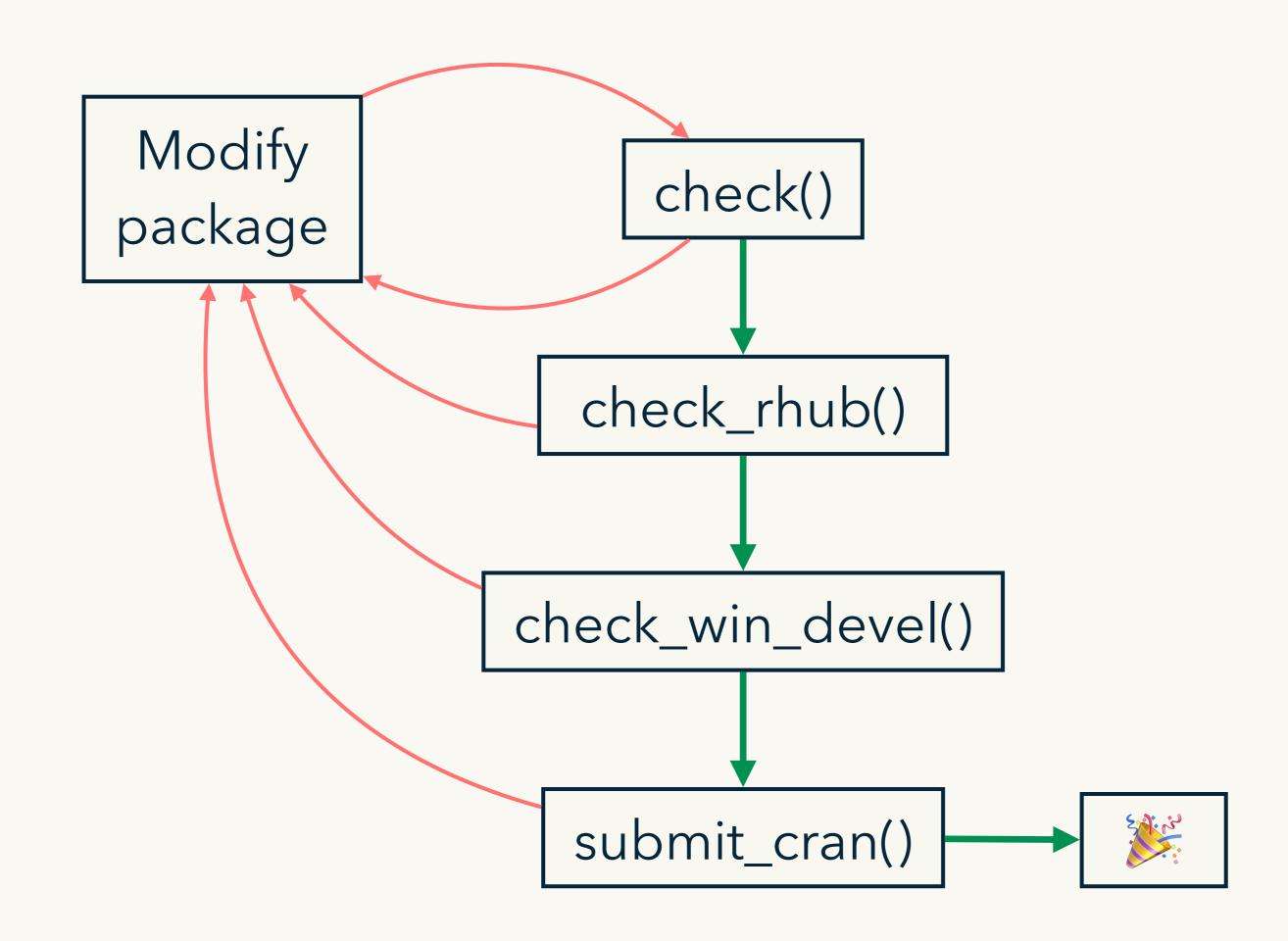
```
# Cmd/Ctrl + Shift + E
devtools::check()
# If you don't understand an error,
```

# google it!

# CRAIT

## Submission to CRAN

```
usethis::use_release_issue()
devtools::release()
# Particularly important for larger packages
# where release process might take weeks.
# But also useful for smaller packages,
# and you should feel free to tweak for your
# needs
```



## cran-comments.md

Goal is to document your process

```
## Test environments
* local OS X install (R-release)
* win-builder (R-release, R-devel)
## R CMD check results
0 errors | 0 warnings | 1 note
* This is a new release. < There's always one note for a new submission
```

# If your submission fails

Do not despair! It happens to everyone, even R-core and tidyverse developers.

If it's from the CRAN robot, just fix the problem & resubmit.

If it's from a human, do not respond to the email and do not argue. Instead update crancomments.md & resubmit.

### For resubmission:

This is a resubmission. Compared to the last submission, I have:

```
* First change.
* Second change.
* Third change
## Test environments
* local OS X install, R 3.2.2
* win-builder (devel and release)
```

## R CMD check results

• • •

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