# 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
5. Set of Functions + Documentation + Data + Versions
6. Set of Functions + Documentation + Data + Versions + Dependencies

# The resource with All the information

https://cran.r-project.org/doc/manuals/r-release/R-exts.html

**Writing R Extensions**

**Table of Contents**

# What's in a Name?

Package Names:

- must start with letter
- no underscores
- periods allowable or use CamelCase
- can have numbers
- should be Google-able

# What's in a Name?

If you have a package name in mind before you start, use the `available` package:

```
install.packages("available")
available::available("packageName")
```

Checks CRAN/Bioconductor/GitHub for potentially similar package names.

# Starting Up

- This will use GitHub for packages, sign up for an account if you don't have one.

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

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

In RStudio, File -> New Project -> New Directory -> R Package using devtools (scroll down).

# Trying our first build

In RStudio, click `Build → Clean and Rebuild`.

Boom! You have a package installed.

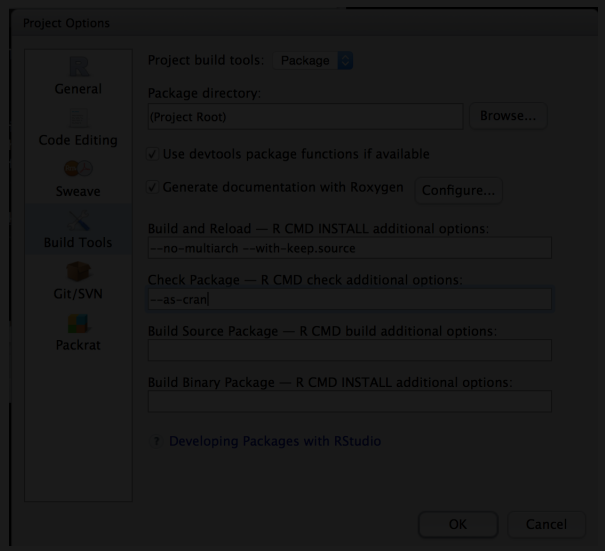
In RStudio, click `Build → Check Package`.

This checks our package.

# Setting Up RStudio

Go to Build -> Configure Build Tools

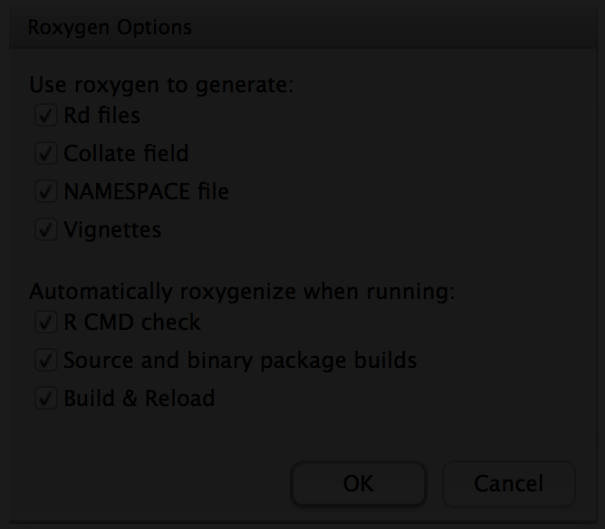
Add `--as-cran` to "Check Package" (may not be necessary anymore)



# Setting Up: Documentation

In RStudio, click `Build → Configure Build Tools → Generate Documentation with Roxygen`. If that is gray, install `roxygen2`.

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



# DESCRIPTION file

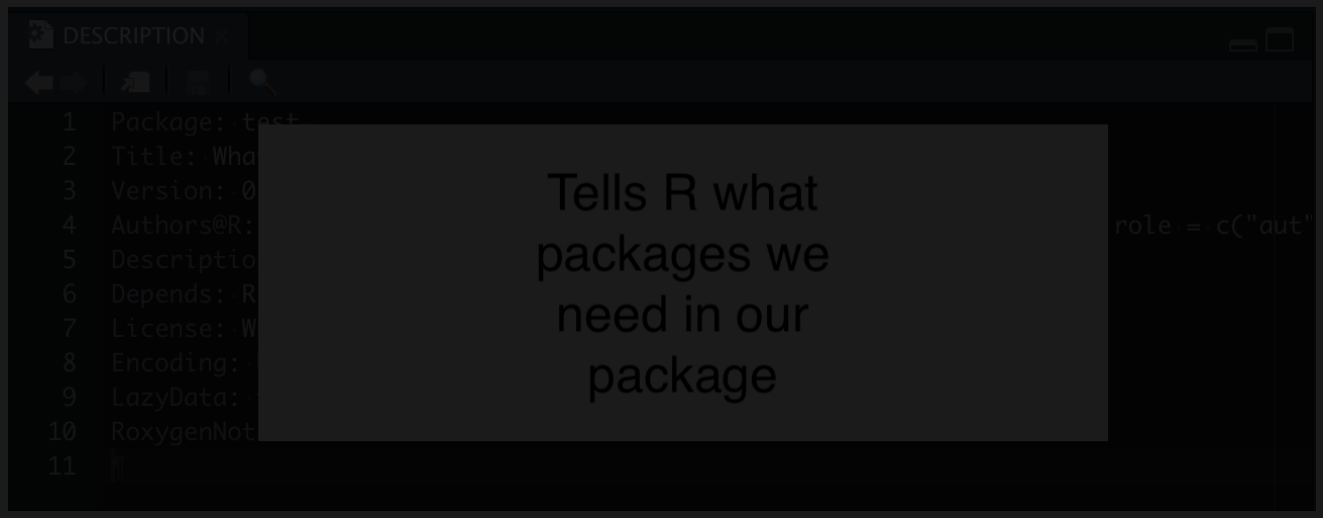
In the RStudio project, go to "Go to file/function" search bar on the menu bar. Also `Ctrl + .` on Mac.

- 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

```
Package: test
Title: What the Package Does (one line, title case)
Version: 0.0.0.9000
Authors@R: person("First", "Last", email = "first.last@example.com", role = c("aut"
Description: What the package does (one paragraph).
Depends: R (>= 3.5.3)
License: What license is it under?
Encoding: UTF-8
LazyData: true
RoxygenNote: 6.1.1
```


DESCRIPTION
1 Package: test
2 Title: Wha
3 Version: 0
4 Authors@R:
5 Descriptio
6 Depends: R
7 License: W
8 Encoding:
9 LazyData:
10 RoxygenNot
11
role = c("aut"
Tells R what packages we need in our package

# DESCRIPTION

- "Title - What the Package Does (Title Case)
- “Author: YOURNAME”
- “Maintainer: YOURNAME <your@email.com>”
- “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

# DESCRIPTION: additional fields

- **Imports:** package1, package2
  - packages with functions we need **in code**
- **Depends:** package3, package5
  - **ALL** functions loaded from package, but **loaded in user library** before your package
  - Similar to `library(package3); library(yourpackage)` - not recommended
- **Suggests:** package4, package6: used in **examples** or **vignettes**

# DESCRIPTION: not so fun default

In the RStudio build, it may add something like:

```
Depends: R (>= 3.5.3)
```

This is not great because anyone with a lower R version (like 3.4) cannot install your package. Unless you need the newest R functionality, delete this line.

Additional Changes to DESCRIPTION

# Authors

I add this to the `DESCRIPTION` file:

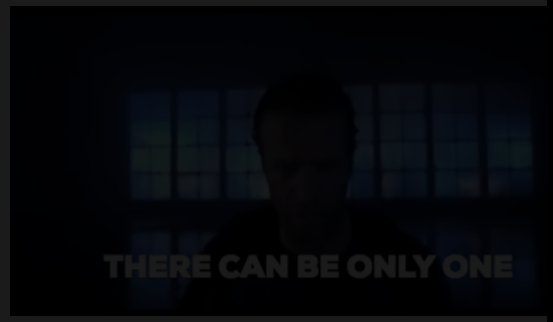
```
Authors@R: person(given = "John",
           family = "Muschelli",
           role = c("aut", "cre"),
           email = "muschellij2@gmail.com",
           comment = c(ORCID = "0000-0001-6469-1750"))
```

# Authors

I use `Authors@R` even if there is only one author because of the `desc` package issue and that package is relied upon for site building and stuff later.

Roles, see `?person`

- `cre` - creator/maintainer, can only have one
- `aut` = author, can have multiple



# Maintainer

If you use `Authors@R`, you should be able to remove the Maintainer field, but I don't. I am explicit about `Maintainer` because some people use that field as some parsers use `Author` and not `Authors@R`.

```
Maintainer: John Muschelli <muschellij2@gmail.com>
```

# License

I use `License: GPL-3` or `GPL-2`.

- For GPL-3:

```
usethis::use_gpl3_license()
```

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

https://kbroman.org/pkg_primer/pages/licenses.html

# DESCRIPTION: Package Title

Change the `Title` so that it's Title Case and make sure to put single quotes around weird words (like science-specific).

```
Title: How to Analyze Data and Images
```

- do **not** start with R package or Package

# DESCRIPTION: Description

Change the `Description` so that it's a sentence (prose) and it ends with a period.

Also I keep putting single quotes around weird words (like science-specific). Make sure to put links in angle brackets (`<http...>`).

Use DOIs if you can (`<doi...>`). If you go too long on a line, indent it with 4 spaces "" and go to the next.

- Look at some of favorite package descriptions

# 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). Delete `hello.R` file if present.

Function names should likely be verbs

# Adding a package to DESCRIPTION field

Say you want to use `dplyr` functions for your code:

```
usethis::use_package("dplyr")
```

but what if you did this instead? (Function masking)

```
usethis::use_package("dplyr", type = "Depends")
```

# Roxygen2

Highlight the following code:

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

Go to `Code -> Insert Roxygen Skeleton`

# Roxygen Skeleton

Roxygen header (what turns into a help file):

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

# Roxygen Skeleton

- `@param` stands for a parameter/argument for that function.
- `@return` denotes what the function returns. This is required.

# Roxygen Skeleton

- `@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 and `\donttest{}` for not testing
    - make sure `\dontrun{}` not `\dontrun {}` (spaces fail)

# Roxygen Skeleton:

```
#' Print the top of a matrix
#' @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)
#' }
```

# Roxygen Skeleton

Instead of `Title`, you can use separate `@title` and `@description` tags if you want them to be different. For example:

```
#' @title Print the top of a matrix
#' @description \code{top} is a small function to not just present the first rows
```

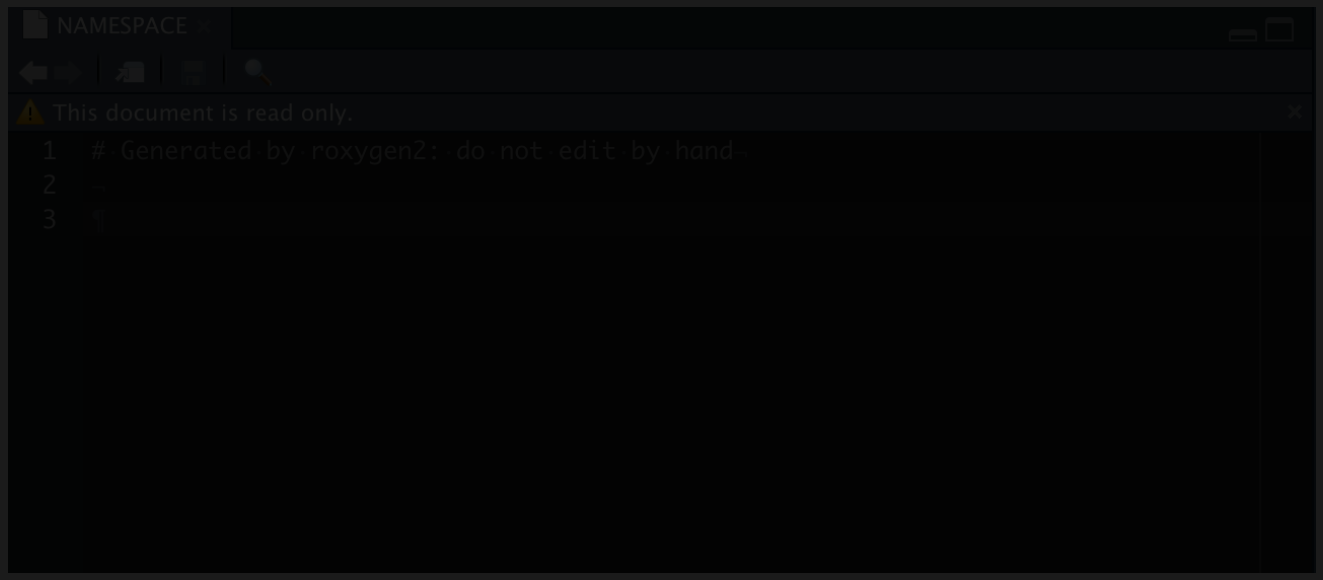
# Roxygen and Markdown

If you want to use `markdown` with `roxygen2`, then you can use

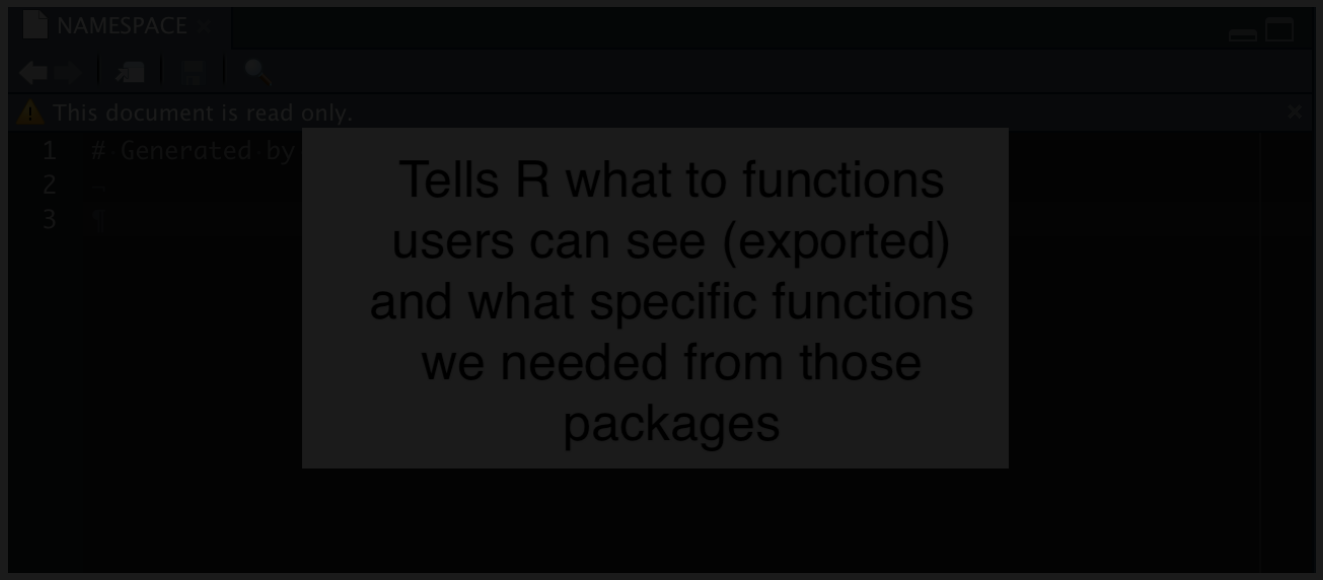
```
usethis::use_roxygen_md()
```

so instead of `\code{top}` you can write `` `top` `` from the previous slide.

# NAMESPACE


NAMESPACE
This document is read only.
1 # Generated by roxygen2: do not edit by hand
2
3

# NAMESPACE




Tells R what to functions users can see (exported) and what specific functions we needed from those packages

# NAMESPACE

In Roxygen:

- `@export` - adds this to the NAMESPACE file
    - when package is installed, users can call this function

# NAMESPACE

In Roxygen:

- `@import` - 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)`

You do not have `library()` functions in R package code

# Check

Go to `Build → Check Package`. You should see something like:

```
top: no visible global function definition for 'hist'
Undefined global functions or variables:
  hist
Consider adding
  importFrom("graphics", "hist")
to your NAMESPACE file.
```

The Goal is to have NO Errors/Warnings/Notes on R CMD Check

# Why the Message?

R sees `hist` from `graphics`, but we never told it we needed it

You *should* import anything explicitly other than from the `base` package, includying anything from `stats` (e.g. `quantile`) or `graphics` (e.g. `hist`). Don't import `base`.

# Importing Packages or Functions from Packages

- `@importFrom` - if you want to import a **function**, you say `@import PACKAGENAME func1 func2`
  - only imports these functions (preferred to `@import`)
  - 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`
  - But should use `pkgA::A()` in practice

# Fixing the Message

Add `@importFrom graphics hist` to your `top.R` file (anywhere in the header)

- RStudio: `Build → Check Package` again

# Importing Package Functions

- You only have to import a whole package or a package function, don't mix and match
- You only have to import a function in **one** file.
- For example, `@importFrom graphics hist` can go in any `.R` file.
- Any package you want to import, make sure you use `use_package`, so we'd use:

```
usethis::use_package("graphics")
```

# Build and Reload Again

- RStudio: Go to `Build → Build and Reload` the package
  - First time you may see some warnings (no NAMESPACE file!)
  - Rerunning may get rid of these
- Then try `Build → Check Package`

# Troubleshooting

In case things are not working or seem off

- Delete the `NAMESPACE` file. If building fails, add an empty file with

```
# Generated by roxygen2: do not edit by hand
```

at the top and rerun. - Delete the `man` folder - `roxygen2` will create the documentation automatically

# Including Data

- Data should be small, but good for running examples or vignettes.

Run `use_data_raw()` if you have code to generate data (R data):

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

This will create a `data-raw` folder.

# Including Data

Let's say you want to make a data set `mydata_set`:

Create `data-raw/mydata_set.R` and at the end, run

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

And this will make a `data/mydata_set.rda` file.

# Documenting Data

- You don’t export data.

```
#' My Awesome Data Set
#'
#' A more detailed description
#'
#' @format A `data.frame` with 2 columns elements, which are:
#' \describe{
#' \item{x1}{column of x variables}
#' \item{y2}{column of yvariables}
#' }
"mydata_set"
```

# Including Non-R data

If you want to include other types of data (such as images) put them into the `inst/` folder (or a subfolder of `inst`, I recommend `extdata`). You can access them using `system.file` when installed.

For example, if you have a file `inst/extdata/myimage.nii.gz`:

```
system.file("extdata", "myimage.nii.gz", package = "YOUR_PACKAGE_NAME")
```

will return the filename for you to access it in code.

# Unit Tests

Unit testing packages: `testthat` and `RUnit`.

To use `testthat`, run `usethis::use_testthat()`. All test files must be in `testthat/tests/` and must start with the word `test`.

```
testthat::test_that("Description of test", {
# code for test
testthat::expect_equal(r, 3.5523334)
testthat::expect_true(x)
testthat::expect_is(my_df, "data.frame")
})
```

Good Rule of Thumb: Any issue created/bug found gets a test

If used in a paper, make sure tests check paper results

# What to test

- Object output type (list/data.frame)
- Expected output value (3.233453)
- Multiple inputs give expected output
- Even graphs: https://github.com/r-lib/vdiffr

# Creating Vignettes

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

`title` is on the document, `VignetteIndexEntry` is on the website:

```
---
title: "my-vignette"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{my-vignette}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---
```

95% of what you will be doing is now covered. Mostly it will be documenting and examples

# Creating a README

```
usethis::use_readme_rmd()
```

This will create a `README.Rmd` file for your GitHub/Package.

- GitHub renders the README.
- Instructions on how to use the package (examples)
- Instructions on installing 3rd-party dependencies

# Spell Checking

Believe it or not, CRAN will check some spelling.

```
devtools::spell_check()
```

after you have fixed the issues, run

```
spelling::update_wordlist()
```

to make a WORDLIST file. These are correctly spelled but likely jargon.

# Creating NEWS.md

```
usethis::use_news_md()
```

This will create a `NEWS.md` file to update with new versions of the package, discussing changes (CRAN Requires).

```
package 0.2.0
- Added function `get_data`
- Fixed bug in `bad_function` (fixes issue #52).
```

Continuous Integration

# Continuous Integration: Testing on the Cloud

- Travis tests Linux/OSX and Appveyor tests Windows
- Integrate with GitHub, each push tested

```
usethis::use_git()
usethis::use_github() # must have GITHUB_PAT set up
usethis::use_appveyor()
usethis::use_travis()
```

# `appveyor.yml`

Add the following lines:

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

to `appveyor.yml` to make sure warnings are treated as errors.

# Code Coverage

- Code coverage is the percentage of code (without whitespace) which is covered by automated tests.
- Calculated using `covr` package.
- I tend to check coverage by examples, vignettes **and** tests vs. just tests (default).
- You can run `covr::package_coverage(type = "all")` locally.

# Code Coverage with Continuous Integration

- Run `usethis::use_coverage()`, with either `coveralls` or `codecov`.
  - Add lines to `.travis.yml` if necessary

# Releasing to CRAN

- Push all changes to GitHub.
- `usethis::use_cran_comments()`
- Try your package on `rhub` with `devtools::check_rhub()`
- Run on CRAN Windows build `devtools::check_win_devel()`
- Run `devtools::release(check = TRUE)` and go through the steps
- Validate the email from CRAN for submission.

# This is just a starting point

- A lot of additional things we can discuss individually
- https://cran.r-project.org/doc/manuals/r-release/R-exts.html, though huge, should cover "everything"
- Most of the work is documentation (80%) and vignettes and tests (20%)

# Extra Slides

# Making a Website

- `pkgdown` makes nice doc pages for your package
- Run `usethis::use_pkgdown()`. Then run `pkgdown::build_site()`.
- Push everything to GitHub.
- Go to GitHub repo → Settings → Scroll down to "GitHub Pages", set Source to `master branch /docs folder`
- Refresh your webpage.

# No visible binding for global variable issue

If you get `No visible binding for global variable`, you're likely using Non-Standard Evaluation (NSE) or tidy evaluation

# No visible binding for global variable issue

2 options, follow different approaches:

1. Use globalVariables
2. Let's say `col5` is the global variable. At top of function write:

```
col5 = NULL # set to something
rm(list = "col5") # remove it
```

This will remove it but not be a "global" fix. Also, make sure `col5` is **not** an argument in your function

# Skipping tests on CRAN/CI

- Use `testthat::skip_on_cran()` for skipping CRAN tests
- `testthat::skip_on_travis()` and `testthat::skip_on_appveyor()` for CI

# Making a Logo/Hex Sticker

## Install the `hexSticker` package

```
library(hexSticker)
library(desc)
desc = desc::description$new()
fig_dir = file.path("man", "figures")
if (dir.exists(fig_dir)) {
  dir.create(fig_dir, recursive = TRUE)
}
package = desc$get("Package")
hexSticker::sticker(
  package = package,
  # add code here
  filename = file.path(fig_dir, "sticker.png"))
usethis::use_logo(file.path(fig_dir, "sticker.png"))
```