

# Developing Your First R Package

## A Case Study with `esvis`

*Daniel Anderson*  
04-10-2018



# Want to follow along?

If you'd like to follow along, please make sure you have the following packages installed

```
install.packages(c("tidyverse", "esvis",
                   "devtools", "roxygen2",
                   "usethis"))
```

# #whomi



- Research Assistant Professor (newly) in the College of Education
- Work a lot in growth modeling and measurement
- Preacher of the R gospel
- Dad of two amazing girls



the fam



# Some review

- What is an R function?

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- What is an R function?
  - Anything that carries out an operation in R, including `+` and `<-`
- What are the components of a function?
  - **Formals** (arguments), **Body** (everything between the braces), and **Environment** (where the function lives)

```
poly <- function(x, power) {  
  z <- x^power  
  return(z)  
}
```

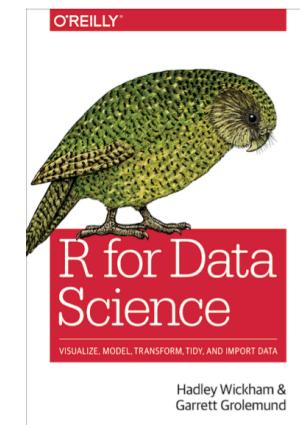
The diagram shows the R code for the `poly` function. A green curly brace on the right side groups the two lines of code: `z <- x^power` and `return(z)`. An arrow points from the label "Body" to this brace. Another arrow points from the label "Formals" to the parameter `x` in the first argument of the `function` call.

# When should you write a function?

*Hadley's rule*

You should consider writing a function whenever you've copied and pasted a block of code more than twice (i.e. you now have three copies of the same code).

r4ds





**Hadley Wickham** ✅

@hadleywickham

## Time to write a function



**Fluff Society** @FluffSociety

"Ctr+C, Ctr+V, Ctr+V, Ctr+V."

7:29 PM - 16 Sep 2017

# Bundle your functions

Once you've written more than one function, you may want to bundle them. There are two general ways to do this:

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source?

Write a package

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source?

Write a package



# Reasons to avoid sourcing

- Documentation is generally more sparse
- Directory issues
  - Which leads to reproducibility issues

# More importantly

Bundling functions into a package is not that hard!



# my journey with esvis

# Background

## *Effect sizes*

Standardized mean differences

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## *Effect sizes*

### Standardized mean differences

- Assumes reasonably normally distributed distributions (mean is a good indicator of central tendency)
- Differences in means may not reflect differences at all points in scale if variances are different
- Substantive interest may also lie with differences at other points in the distribution.

# Varying differences

*Quick simulated example*

```
library(tidyverse)
common_var <- tibble(low = rnorm(1000, 10, 1),
                      high = rnorm(1000, 12, 1),
                      var = "common")
diff_var <- tibble(low = rnorm(1000, 10, 1),
                     high = rnorm(1000, 12, 2),
                     var = "diff")
d <- bind_rows(common_var, diff_var)
head(d)
```

```
## # A tibble: 6 x 3
##       low   high var
##   <dbl> <dbl> <chr>
## 1 11.6   11.3 common
## 2 10.6   11.5 common
## 3 10.2   13.9 common
## 4 9.23   12.5 common
## 5 9.44   12.0 common
## 6 11.4   10.8 common
```

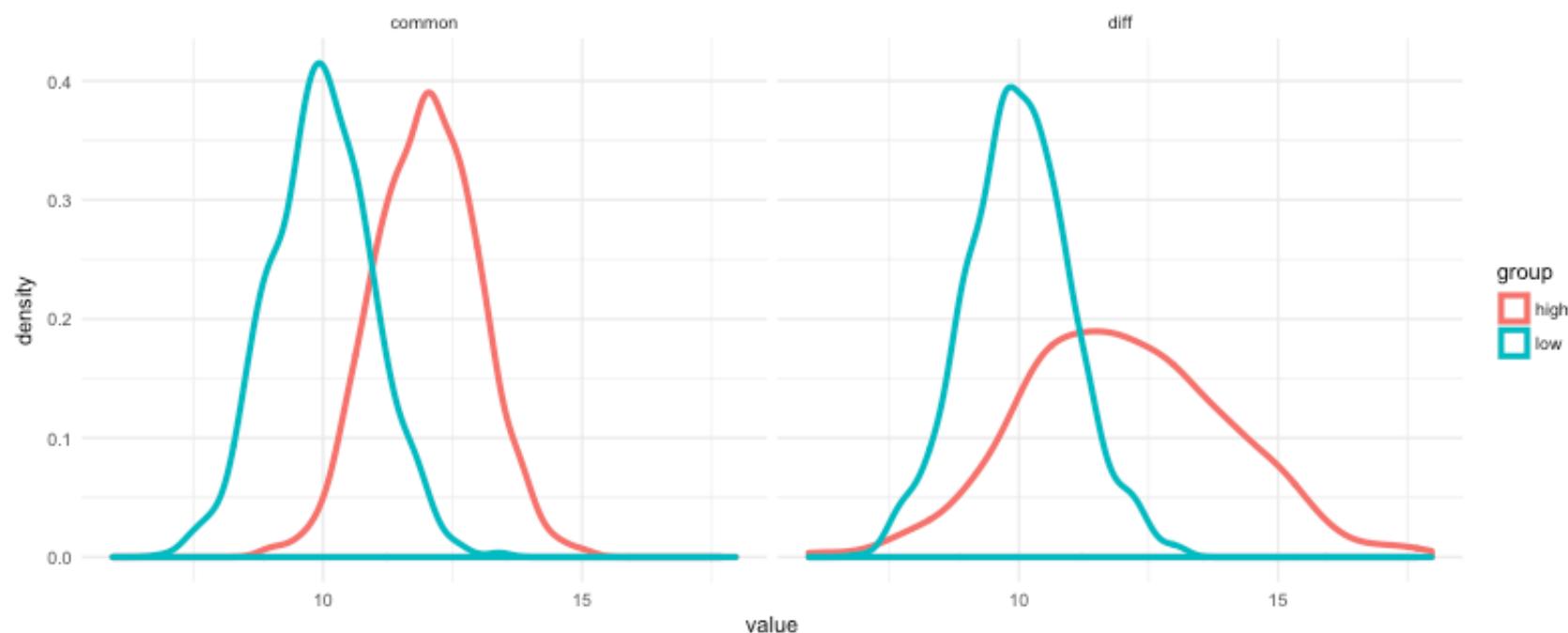
# Restructure the data for plotting

```
d <- d %>%
  gather(group, value, -var)
d
```

```
## # A tibble: 4,000 x 3
##   var     group value
##   <chr>  <chr>  <dbl>
## 1 common low    11.6
## 2 common low    10.6
## 3 common low    10.2
## 4 common low    9.23
## 5 common low    9.44
## 6 common low    11.4
## 7 common low    10.6
## 8 common low    8.81
## 9 common low    9.21
## 10 common low   9.80
## # ... with 3,990 more rows
```

# Plot the distributions

```
theme_set(theme_minimal())  
  
ggplot(d, aes(value, color = group)) +  
  geom_density(lwd = 1.5) +  
  facet_wrap(~var)
```



# Binned effect sizes

1. Cut the distributions into  $n$  bins (based on percentiles)
2. Calculate the mean difference between paired bins
3. Divide each mean difference by the overall pooled standard deviation

$$d_{[i]} = \frac{\bar{X}_{foc[i]} - \bar{X}_{ref[i]}}{\sqrt{\frac{(n_{foc}-1)Var_{foc} + (n_{ref}-1)Var_{ref}}{n_{foc}+n_{ref}-2}}}$$

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*visualize it!*

# Back to the simulated example

```
common <- filter(d, var == "common")
diff   <- filter(d, var == "diff")
```

```
library(esvis)
qtile_es(value ~ group, common)
```

```
##   ref_group foc_group low_qtile high_qtile midpoint      es      se
## 1     high       low      0.00      0.33     0.165 -2.029997 0.09597083
## 2     high       low      0.33      0.66     0.495 -2.060516 0.09631753
## 3     high       low      0.66      0.99     0.825 -2.065950 0.09640567
```

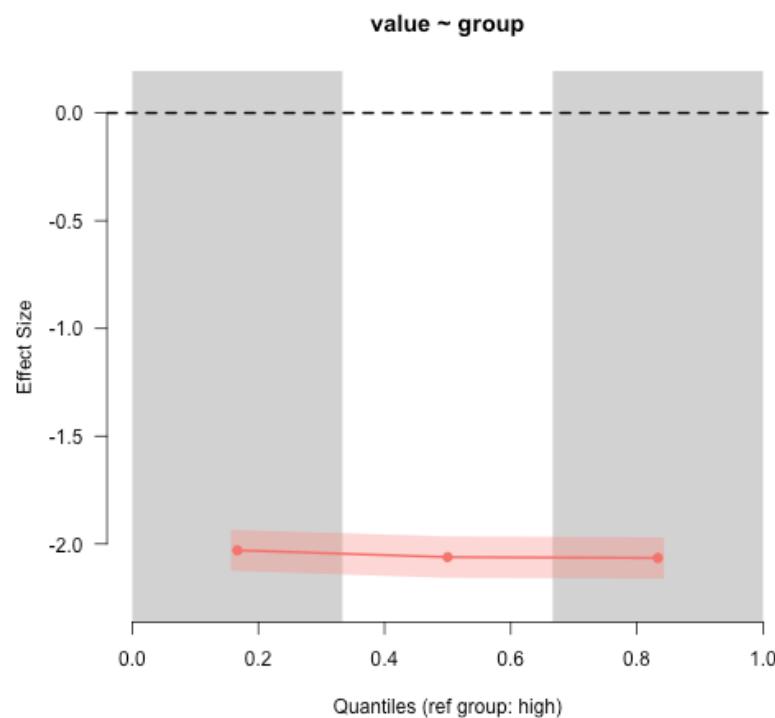
```
qtile_es(value ~ group, diff)
```

```
##   ref_group foc_group low_qtile high_qtile midpoint      es      se
## 1     high       low      0.00      0.33     0.165 -0.6246141 0.07984666
## 2     high       low      0.33      0.66     0.495 -1.2220534 0.08480555
## 3     high       low      0.66      0.99     0.825 -1.9406473 0.09441250
```

# Visualize it

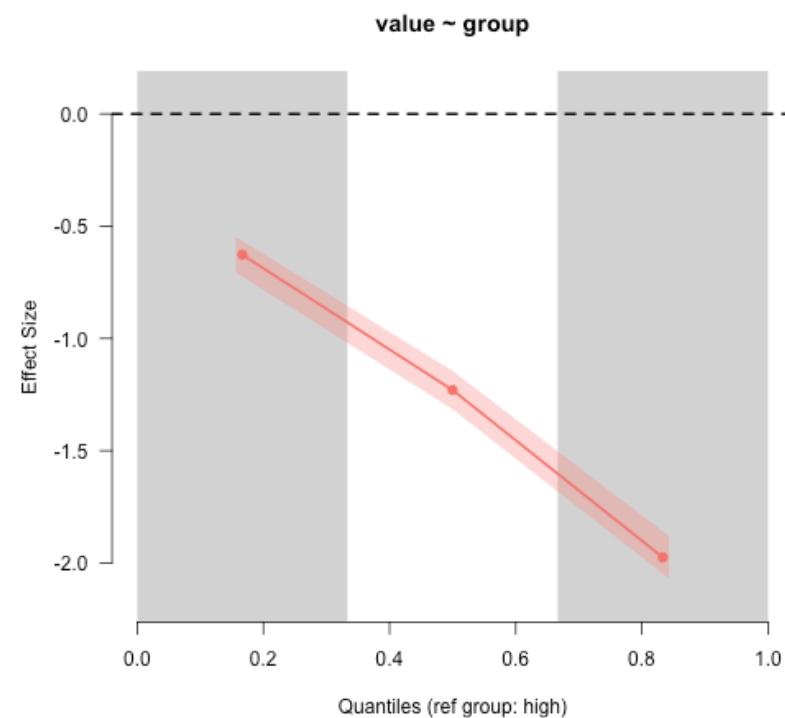
*Common Variance*

```
binned_plot(value ~ group, common)
```



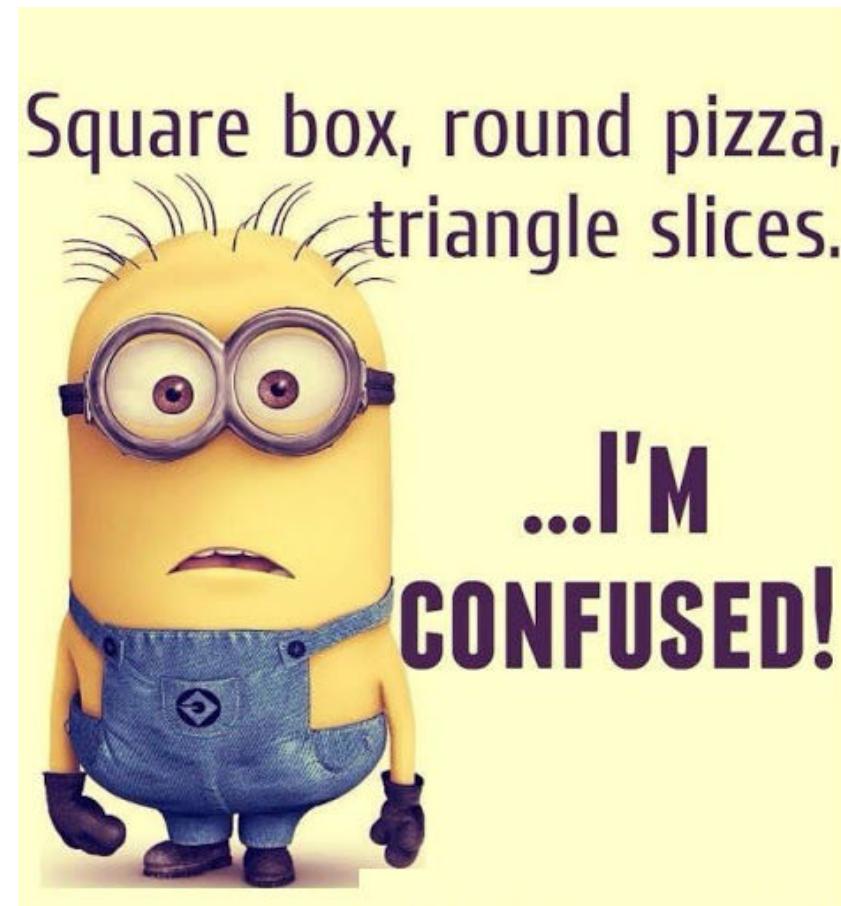
*Different Variance*

```
binned_plot(value ~ group, diff)
```



# Wait a minute...

- The *esvis* package will (among other things) calculate and visually display binned effect sizes.
- But how did we get from an idea, to functions, to a package?



taking a step back

# Package Creation

*The (a) recipe*

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  - can be boring and mundane but just something you do a lot

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4. Document your function

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4. Document your function
5. Install/fiddle/install
6. Write tests for your functions

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7. Host your package somewhere public (GitHub is probably best) and promote it - leverage the power of open source!

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Use tools throughout (which we'll talk about momentarily) to help automate many of the steps, and make the whole thing less painful

# A really good point

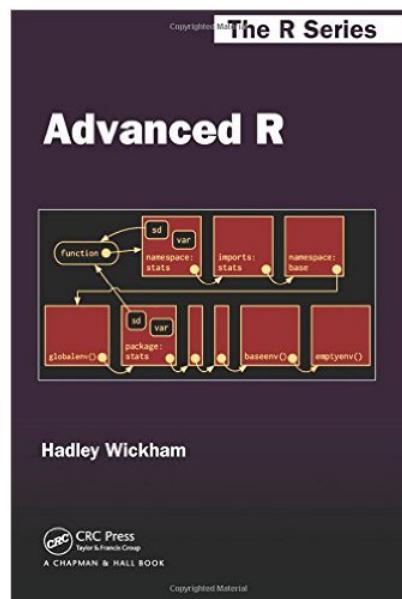
- 1a) check that no one had the same idea 😊
  - Maëlle Salmon  (@ma\_salmon) April 10, 2018

And some further recommendations/good advice

# Some resources

We surely won't get through all the steps tonight. In my mind, the best resources are:

*Advanced R*



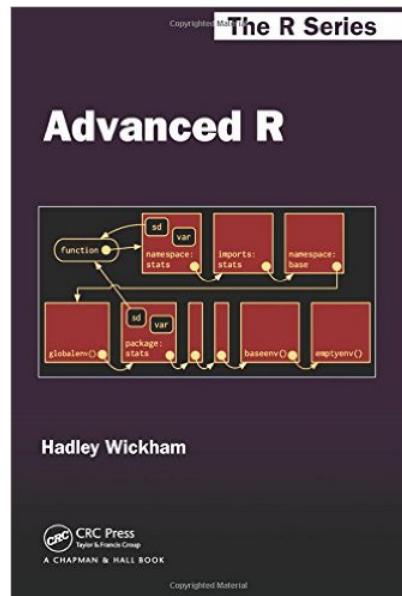
*R Packages*



# Some resources

We surely won't get through all the steps tonight. In my mind, the best resources are:

*Advanced R*



*R Packages*



For a really quick but really good intro, see [Hilary Parker's blog post](#)

# Our package

We're going to write a package today! Let's keep it really simple...

1. Idea: Report basic descriptive statistics for a vector, `x`: `n`, `mean`, and `sd`.  
Let's also have it report on the number of missing observations.

# Our function

- Let's have it return either (a) a named vector, or (b) a dataframe (whichever you prefer is fine)
- What will be the formal arguments?
- What will the body look like?

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*Want to give it a go?*

# The approach I took...

```
describe <- function(x) {  
  n      <- as.integer(length(na.omit(x)))  
  nmiss <- as.integer(sum(is.na(x)))  
  mn     <- mean(x, na.rm = TRUE)  
  stdev <- sd(x, na.rm = TRUE)  
  
  out <- tibble::tibble(n_valid    = n,  
                        n_missing   = nmiss,  
                        mean        = mn,  
                        sd          = stdev)  
  
  out  
}
```

# The approach I took...

```
describe <- function(x) {  
  n      <- as.integer(length(na.omit(x))) # Count number of valid cases  
  nmiss <- as.integer(sum(is.na(x)))  
  mn     <- mean(x, na.rm = TRUE)  
  stdev <- sd(x, na.rm = TRUE)  
  
  out <- tibble::tibble(n_valid    = n,  
                        n_missing   = nmiss,  
                        mean        = mn,  
                        sd          = stdev)  
  
  out  
}
```

# The approach I took...

```
describe <- function(x) {  
  n      <- as.integer(length(na.omit(x)))  
  nmiss <- as.integer(sum(is.na(x))) # Count the number of missing  
  mn     <- mean(x, na.rm = TRUE)  
  stdev <- sd(x, na.rm = TRUE)  
  
  out <- tibble::tibble(n_valid    = n,  
                        n_missing   = nmiss,  
                        mean        = mn,  
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  out  
}
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# The approach I took...

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describe <- function(x) {  
  n      <- as.integer(length(na.omit(x)))  
  nmiss <- as.integer(sum(is.na(x)))  
  mn     <- mean(x, na.rm = TRUE) # Calculate mean  
  stdev <- sd(x, na.rm = TRUE)  
  
  out <- tibble::tibble(n_valid    = n,  
                        n_missing   = nmiss,  
                        mean        = mn,  
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  mn     <- mean(x, na.rm = TRUE)  
  stdev <- sd(x, na.rm = TRUE) # Standard deviation  
  
  out <- tibble::tibble(n_valid    = n,  
                        n_missing   = nmiss,  
                        mean        = mn,  
                        sd          = stdev)  
  out  
}
```

# The approach I took...

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describe <- function(x) {  
  n      <- as.integer(length(na.omit(x)))  
  nmiss <- as.integer(sum(is.na(x)))  
  mn     <- mean(x, na.rm = TRUE)  
  stdev <- sd(x, na.rm = TRUE)  
  
  out <- tibble:::tibble(n_valid    = n,      # Bundle it all  
                         n_missing = nmiss,  
                         mean       = mn,  
                         sd         = stdev)  
  
  out  
}
```

# The approach I took...

```
describe <- function(x) {  
  n      <- as.integer(length(na.omit(x)))  
  nmiss <- as.integer(sum(is.na(x)))  
  mn     <- mean(x, na.rm = TRUE)  
  stdev <- sd(x, na.rm = TRUE)  
  
  out <- tibble::tibble(n_valid    = n,  
                        n_missing   = nmiss,  
                        mean        = mn,  
                        sd          = stdev)  
  
  out # Return the tibble  
}
```

# Informal testing

```
describe(rnorm(100))
```

```
## # A tibble: 1 x 4
##   n_valid n_missing   mean    sd
##       <int>     <int>  <dbl>  <dbl>
## 1      100         0 -0.00975 0.924
```

```
describe(c(rnorm(1000, 10, 4), rep(NA, 27)))
```

```
## # A tibble: 1 x 4
##   n_valid n_missing   mean    sd
##       <int>     <int>  <dbl>  <dbl>
## 1     1000        27  9.76  3.96
```

# Demo

Package skeleton:

- `usethis::create_package`
- `usethis::use_r`
- Use `roxygen2` special comments for documentation
- Run `devtools::document`
- Install and restart, play around

# roxygen2 comments

## Typical arguments

- `@param`: Describe the formal arguments. State argument name and the describe it.
  - | `#' @param x Vector to describe`
- `@return`: What does the function return
  - | `#' @return A tibble with descriptive data`
- `@example` or more commonly `@examples`: Provide examples of the use of your function.
- `@export`: Export your function

If you don't include `@export`, your function will be *internal*, meaning others can't access it easily.

# Other docs

- **.gitignore**: Files to ignore for git commits with some pre-slugged entries
- **NAMESPACE**: Created by `{roxygen2}`. Don't edit it. If you need to, trash it and it will be reproduced.
- **DESCRIPTION**: Describes your package (more on next slide)
- **man/**: The documentation files. Created by `{roxygen2}`. Don't edit.

---

# DESCRIPTION

Metadata about the package. Default fields for our package are

Package: practice

Version: 0.0.0.9000

Title: What the Package Does (One Line, Title Case)

Description: What the package does (one paragraph).

Authors@R: person("First", "Last", email = "first.last@example.com", role = c("aut

License: What license is it under?

Encoding: UTF-8

LazyData: true

ByteCompile: true

RoxygenNote: 6.0.1

---

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This is where the information for `citation(package = "practice")` will come from.

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```

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Some advice - edit within RStudio, or a good text editor like [sublimetext](#). "Fancy" quotes and things can screw this up.

# Description File Fields

The 'Package', 'Version', 'License', 'Description', 'Title', 'Author', and 'Maintainer' fields are mandatory, all other fields are optional.

- Writing R Extensions

Some optional fields include

- Imports and Suggests (we'll do this in a minute).
- URL
- BugReports
- License (we'll have {usethis} create this for us).
- LazyData

# DESCRIPTION for {esvis}

Package: esvis

Type: Package

Title: Visualization and Estimation of Effect Sizes

Version: 0.1.0.9000

Authors@R: person("Daniel", "Anderson", email = "daniela@uoregon.edu",  
role = c("aut", "cre"))

Description: A variety of methods are provided to estimate and visualize distributional differences in terms of effect sizes. Particular emphasis is upon evaluating differences between two or more distributions across the entire scale, rather than at a single point (e.g., differences in means). For example, Probability–Probability (PP) plots display the difference between two or more distributions, matched by their empirical CDFs (see Ho and Reardon, 2012; [doi:10.3102/1076998611411918](https://doi.org/10.3102/1076998611411918)), allowing for examinations of where on the scale distributional differences are largest or smallest. The area under the PP curve (AUC) is an effect-size metric, corresponding to the probability that a randomly selected observation from the x-axis distribution will have a higher value than a randomly selected observation from the y-axis distribution. Binned effect size plots are also available, in which the distributions are split into bins (set by the user) and separate effect sizes (Cohen's d) are produced for each bin – again providing a means to evaluate the consistency (or lack thereof) of the difference between two or more distributions at different points on the scale. Evaluation of empirical CDFs is also provided, with built-in arguments for providing annotations

# DESCRIPTION for {esvis} (continued)

Depends:

R (>= 3.1)

Imports:

sfsmisc

URL: <https://github.com/DJAnderson07/esvis>

BugReports: <https://github.com/DJAnderson07/esvis/issues>

License: MIT + file LICENSE

LazyData: true

RoxygenNote: 6.0.1

Suggests:

testthat,

viridisLite

# Demo

- Change the author name.
  - Add a contributer just for fun.
- Add a license. We'll go for MIT license using

```
usethis::use_mit_license("First and Last Name")
```
- Install and reload.

# Declare dependencies

- The function **depends** on the `tibble` function within the `{tibble}` package.
- We have to declare this dependency

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## My preferred approach

- Declare package dependencies: `usethis::use_package`
- Create a package documentation page: `usethis::use_package_doc`
  - Declare all dependencies for your package there
  - Only import the functions you need - not the entire package
    - Use `#' importFrom pkg fun_name`
- Generally won't have to worry about namespacing (`tibble::tibble` becomes just plain old `tibble`). The likelihood of conflicts is also reduced, so long as you don't import the full package.

# Demo

# Write tests!

- What does it mean to write tests?
  - ensure your package does what you expect it to

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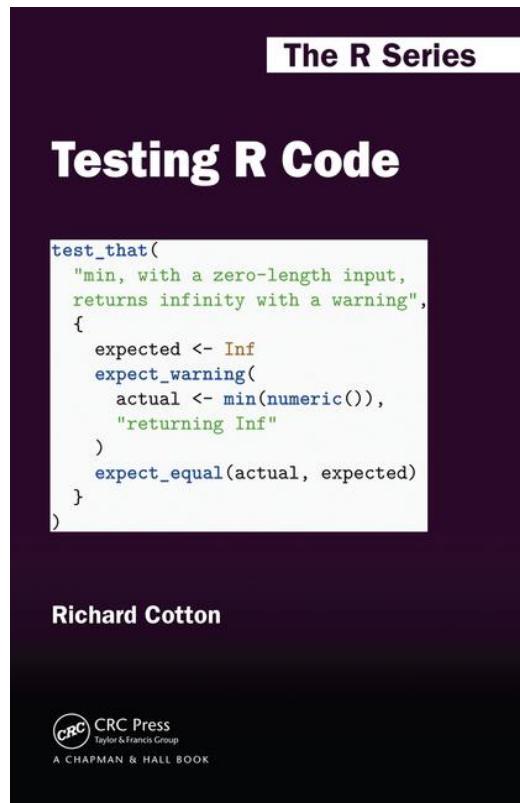
- What does it mean to write tests?
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  - If you write a new function, and it breaks an old one, that's good to know!
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- What does it mean to write tests?
  - ensure your package does what you expect it to
- Why write tests?
  - If you write a new function, and it breaks an old one, that's good to know!
  - Reduces bugs, makes your package code more robust
- How do you write tests?
  - `usethis::use_testthat` sets up the infrastructure
  - make assertions, e.g.: `testthat::expect_equal()`,  
`testthat::expect_warning()`, `testthat::expect_error()`

# Testing

We'll skip over testing for today, because we just don't have time to cover everything. A few good resources:



Richie Cotton's book

r-pkgs Chapter

Karl Broman Blog Post

# Check your R package

- Use `devtools::check()` to run the same checks CRAN will run on your R package.
  - Use `devtools::build_win()` to run the checks on CRAN computers.

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The first time, you'll likely get errors. Be patient. It will probably be **frustrating**, but ultimately worth the effort.



# Let's check now!

🎉 Hooray! 🎉

*You have a package!*



# A few other best practices

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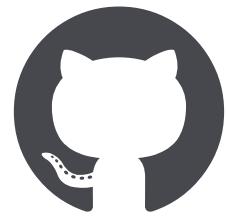
- Create a README with `usethis::use_readme_rmd`.
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- Automate wherever possible (`{devtools}` and `{usethis}` help a lot with this)
- Use the `{goodpractice}` package to help you package code be more robust, specifically with `goodpractice::gp()`. It will give you lots of good ideas

# A few other best practices

- Create a README with `usethis::use_readme_rmd`.
- Try to get your `code coverage` up above 80%.
- Automate wherever possible (`{devtools}` and `{usethis}` help a lot with this)
- Use the `{goodpractice}` package to help you package code be more robust, specifically with `goodpractice::gp()`. It will give you lots of good ideas
- Host on GitHub, and capitalize on integration with other systems (all free, but require registering for an account)
  - `Travis CI`
  - `Appveyor`
  - `codecov`

# Any time left?

*Why you should use git and GitHub*



esvis

# Quickly

- Get started with `usethis::use_git`, followed by `usethis::use_github`.

For this to work, you'll need to set a GITHUB\_PAT environment variable in your `~/.Renvironment`. Follow [Jenny Bryan's](#) instructions, and use `edit_r_environ()` to easily access the right file for editing

Note: I haven't played around with this much. Standard git procedures will work too.

# Create a README

- Use standard R Markdown. Setup the infrastructure with `usethis::use_readme_rmd`.
- Write it just like a normal R Markdown doc and it should all flow into the README.

The screenshot shows a text editor window with the file name "README.md" at the top. The content of the file is as follows:

```
esvis

R Package for effect size visualizations.

build passing | build passing | codecov 88% | CRAN 0.1.0

This package is designed to visually compare two or more distributions across the entirety of the scale, rather than only by measures of central tendency (e.g., means). There are also some functions for estimating effect size, including Cohen's  $d$ , Hedges'  $g$ , percentage above a cut, transformed (normalized) percentage above a cut, the area under the curve (conceptually equivalent to the probability that a randomly selected individual from Distribution A has a higher value than a randomly selected individual from Distribution B), and the  $V$  statistic, which essentially transforms the area under the curve to standard deviation units (see Ho, 2009).

Installation

Install directly from CRAN with

install.packages("esvis")

Or the development version from from github with:

# install.packages("devtools")
devtools::install_github("D1Anderson07/esvis")
```

# Use Travis/Appveyor

- Register for a free account
- Run `usethis::use_travis` and `usethis::use_appveyor` to get started.
  - Go to each respective website and "turn on" the repo
  - Copy and paste the code to the badge into your `README`.

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- Now all your code will be automatically tested on Mac/Linux (Travis CI) and Windows (Appveyor)



# codevoc

You can test your code coverage each time you push a new commit by using `codecov`. Initialize with `usethis::use_coverage()`. Overall setup process is pretty similar to Travis CI/Appveyor.

Easily see what is/is not covered by tests!

```
121 2     call <- as.list(match.call())
122
123 2     calcs <- pp_calcs(formula, data, ref_group)
124
125 2     if(!is.null(grid)) {
126         if(grid & !is.null(cut)) {
127             warning(paste("Grid suppressed when cut lines are also provided",
128                           "(plot becomes overly busy otherwise)."))
129         }
130     }
131
132 2     if(!is.null(cut)) grid <- FALSE
133 2     if(is.null(cut) & is.null(grid)) grid <- TRUE
134
135 2     if(!is.null(leg)) {
136         if(leg == "side") n_1 <- TRUE
137     }
138 2     if(ncol(calcs$ps) > 2 & !is.null(shade)) {
139         if(shade == TRUE) {
140             warning(
141                 paste("The area under the curve can only be shaded with two",
142                               "groups. Argument `shade = TRUE` ignored")
143             )
144         }
145     }
146 2     if(ncol(calcs$ps) > 2 & !is.null(text)) {
147         if(text == TRUE) {
148             warning(
149                 paste("The area under the curve can only be shaded with two",
150                               "groups. Argument `text = TRUE` ignored")
151             )
152     }
```

That's all  
*Thanks so much!*