NBIS

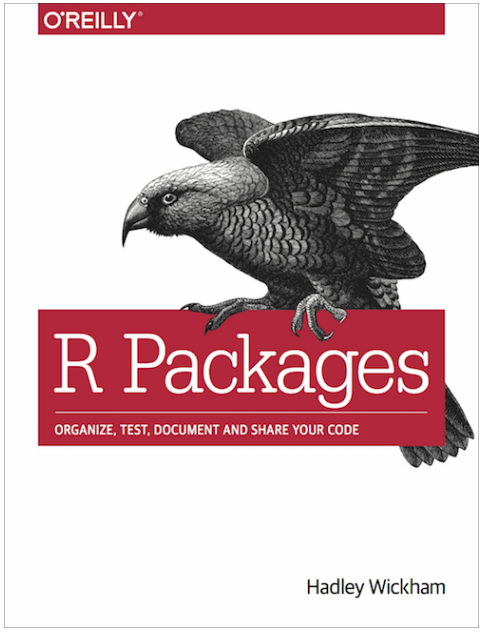
# R Package Anatomy

## R Foundations for Life Scientists

Sebastian DiLorenzo

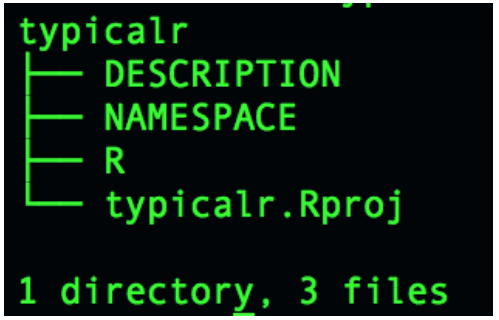
# Overview

- What is an R package?
- Possible package states
- Package structure:
  - Code | `r/`
  - Metadata | `DESCRIPTION`
  - Documentation | `man/`
  - Vignettes
  - Import & Export | `NAMESPACE`
  - 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?




- 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
│   ├── ToothGrowth.Rd
│   └── call_me.Rd
├── src
├── tests
├── typicalr.Rproj
└── vignettes
```

- 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
│   ├── ToothGrowth.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
    - github
    - 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

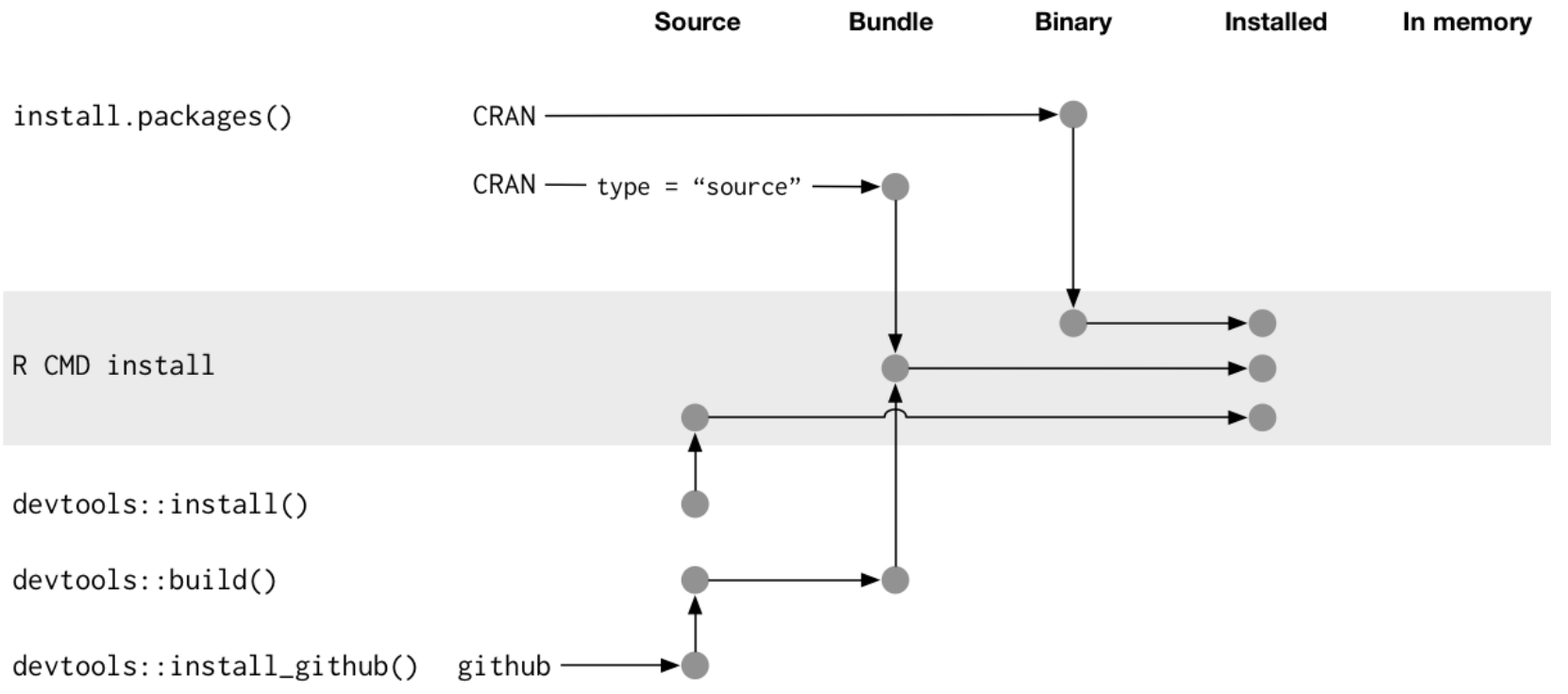
When you use a package, it is in memory. When developing, a package does not have to be installed to be in memory.

- `packagename::function()`
  - loads packagename

Note:

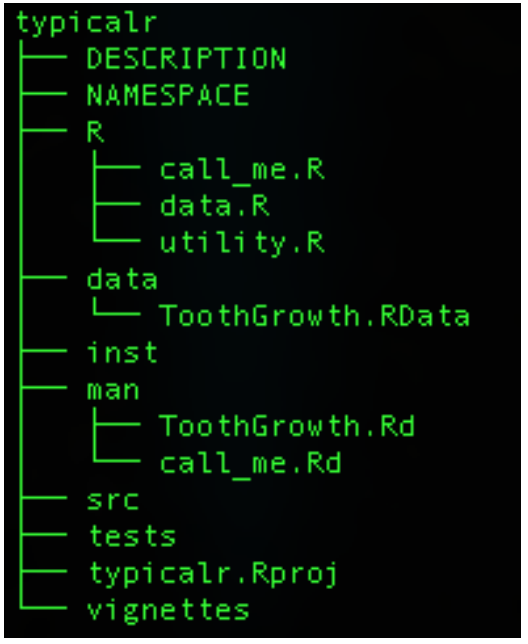
- `library(packagename)`
  - loads and attaches packagename

# Possible package states




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

# R/


typicalr
DESCRIPTION
NAMESPACE
R
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
│   ├── ToothGrowth.Rd
│   └── 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
  - `library()`, `require()`, `source()`
  - `options()`, `par()`

# DESCRIPTION

```
Package: typicalr
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", "cre"))
Description: What the package does (one paragraph). If you want to write lots of things
       be sure to indent so R knows it belongs to the same post.
Depends: R (>= 3.5.0)
License: What license is it under?
Encoding: UTF-8
LazyData: true
RoxygenNote: 6.0.1
Imports: What packages does it need?
URL: package homepage
BugReports: Where to get help
```

- 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

```
Package: typicalr
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", "cre"))
Description: What the package does (one paragraph). If you want to write lots of things
       be sure to indent so R knows it belongs to the same post.
Depends: R (>= 3.5.0)
License: What license is it under?
Encoding: UTF-8
LazyData: true
RoxygenNote: 6.0.1
Imports: What packages does it need?
URL: package homepage
BugReports: Where to get help
```

- 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

NBIS

0.0.0.9000

major.minor.patch.dev

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

# man/

```
typicalr
├── DESCRIPTION
├── NAMESPACE
├── R
│   ├── call_me.R
│   ├── data.R
│   └── utility.R
├── data
│   └── ToothGrowth.RData
├── inst
├── man
│   ├── ToothGrowth.Rd
│   └── call_me.Rd
├── src
├── tests
├── typicalr.Rproj
└── vignettes
```

- `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="")
}
```

# man/

*call_me.R*

```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="")
}
```

*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
   to display how to section with tags.
```

*>?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

| | |
|---|---|
| x | A character or characters. |

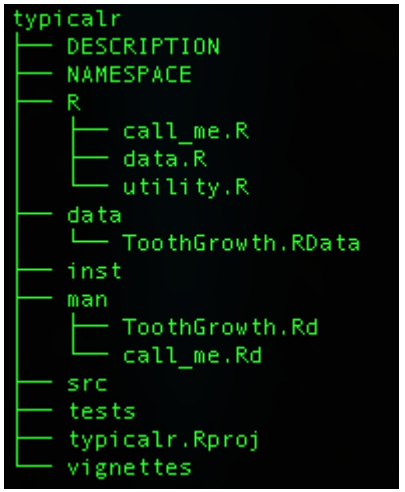
### Value

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

### Examples

```
call_me("Maeby")
```

# man/ for datasets




```
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).
#'
#' @usage ToothGrowth
#'
#' @format A data frame with 60 observations on 3 variables.
#' \describe{
#'   \item{len}{Tooth length}
#'   \item{supp}{Supplement type (VC or OJ).}
#'   \item{dose}{Dose in milligrams/day}
```

# 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: "2021-09-27"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{Vignette Title}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---
```

# vignettes/

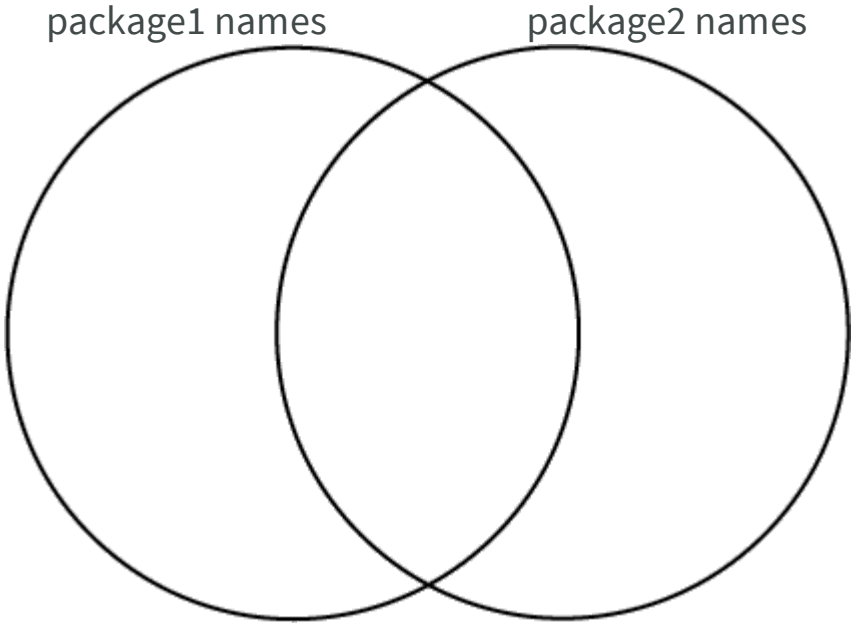
- A more complete guide to your package
  - For user/you
  - Examples and use cases
- `knitr` & `rmarkdown`
  - `knitr`: add r code to markdown
- `vignettes/package-vignette.Rmd`

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

*typicalr-vignette.Rmd*

```
---
title: "typicalr"
author: "Sebastian DiLorenzo"
date: "2021-09-27"
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{typicalr}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---
```

# NAMESPACE




- `@imports` and `@importsFrom`
  - 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="")
}
```

*utility.R:*

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

*NAMESPACE:*

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

export(call_me)
import(knitr)
```

# NAMESPACE

NBIS

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

# src/

- Compiled code
  - `Rcpp`
  - `rJava`
- Scripts
  - `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
  - `Rcpp`
  - `rJava`
- Scripts
  - `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
}
```

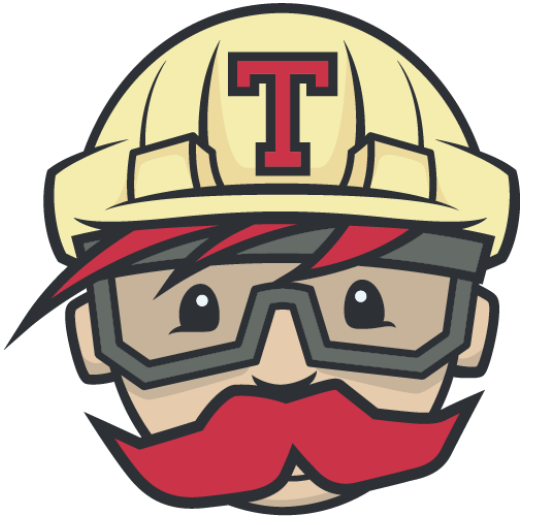
1. `usethis::use_rcpp()`
   - Edit DESCRIPTION
   - `#' @useDynLib packagename`
   - `#' @importFrom Rcpp sourceCpp`
2. `.cpp` file in `src/`
3. `pkgbuild::compile_dll()`
4. `devtools::document()`
5. `Build & Reload`
6. Add documentation to `.cpp`

# git, Github, Rstudio and you!

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

# CRAN and `R CMD check`

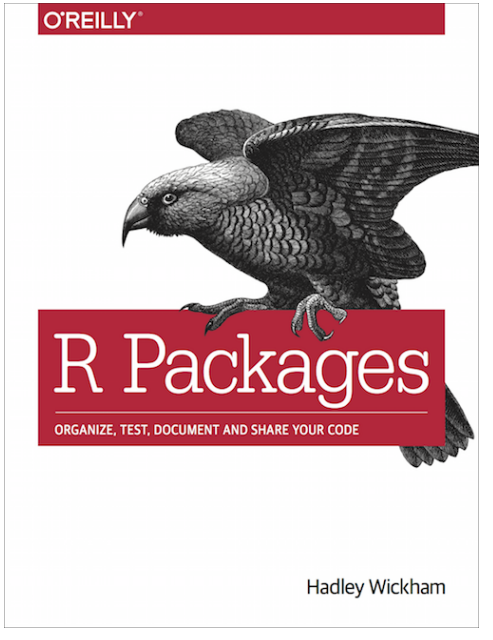
- **C**omprehensive **R** **A**rchive **N**etwork
  - R package repository
  - Sign of quality
- `R CMD check`
  - More than 50 individual checks
  - Three messages:
    - **ERROR**: Always fix.
    - **WARNING**: Should probably fix. Definitely for CRAN submit.
    - **NOTE**: Try to solve to CRAN submit,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



# Summary

NBIS

- 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`




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

# Thank you. Questions?

Graphics from freepik.com

Created: 27-Sep-2021 • Roy Francis • SciLifeLab • NBIS