

rOpenSci Packages: Development, Maintenance, and Peer Review

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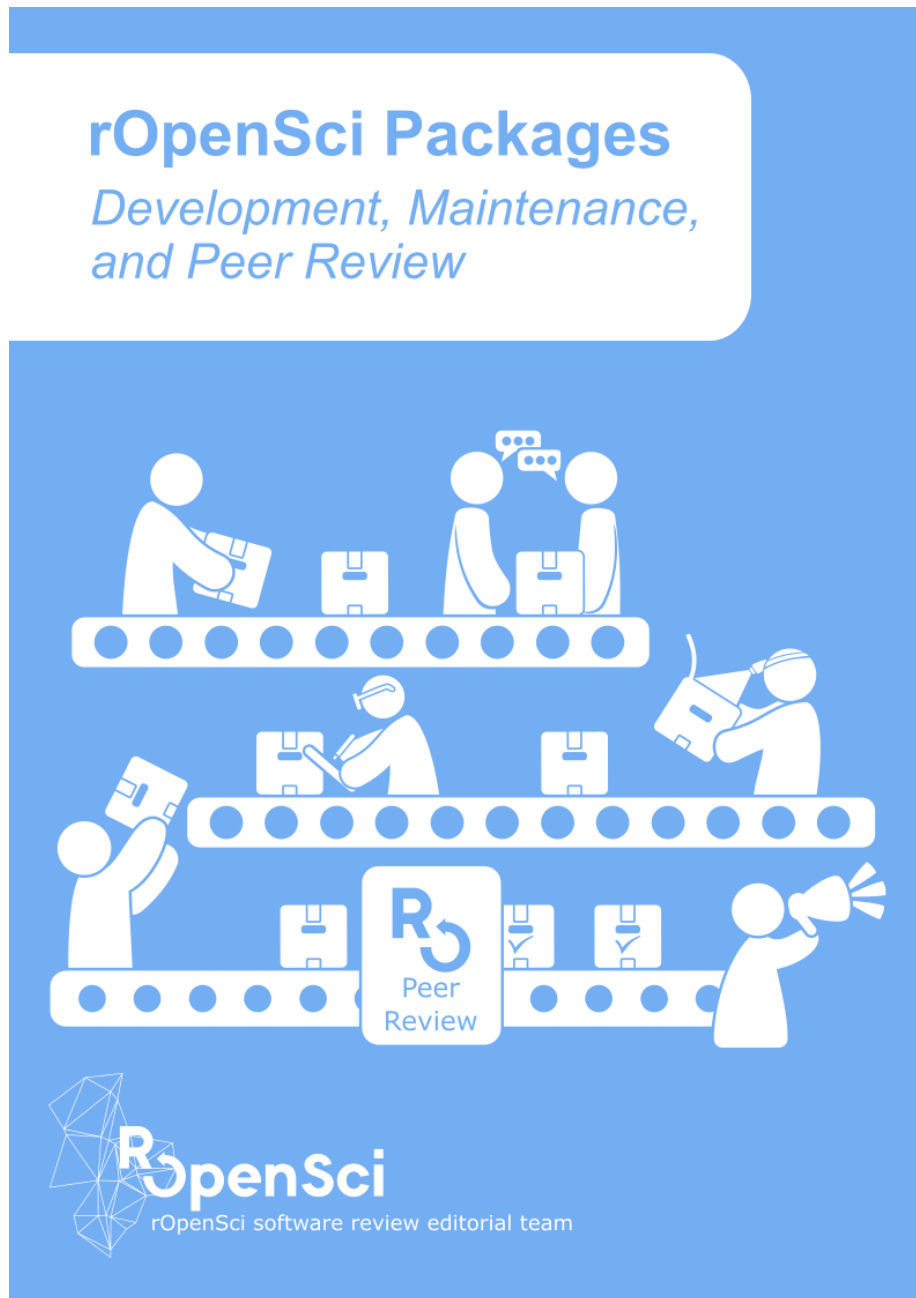


Figure 1: cover image

Preface

Welcome! This book is a guide for authors, maintainers, reviewers and editors of rOpenSci.

The [first section of the book](#) contains our guidelines for creating and testing R packages.

The [second section](#) is dedicated to rOpenSci's software peer review process: what it is, our policies, and specific guides for authors, editors and reviewers throughout the process.

The [third and last section](#) features our best practice for nurturing your package once it has been onboarded: how to collaborate with other developers, how to document releases, how to promote your package and how to leverage GitHub as a development platform. The third section also features a [chapter for anyone wishing to start contributing to rOpenSci packages](#).

We hope that you'll find the guide useful and clear, and welcome your suggestions in the [issue tracker of the book](#). Happy R packaging!

The rOpenSci editorial team.

This book is a living document. You can view updates to our best practices and policies via the [release notes](#).

You can cite this book using [its Zenodo metadata and DOI](#).

If you want to contribute to this book (suggestions, corrections) please refer to [the GitHub repository](#) in particular [the contributing guidelines](#). Thanks!

We are thankful for all authors, reviewers and guest editors for helping us improve the system and this guide over the years. Thanks also to the following persons who made contributions to this guide and its previous incarnations: [Katrin Leinweber](#), [John Baumgartner](#), [François Michonneau](#), [Christophe Dervieux](#), [Lorenzo Busetto](#), [Ben Marwick](#), [Nicholas Horton](#), [Chris Kennedy](#), [Mark Padgham](#), [Jeroen Ooms](#), [Sean Hughes](#), [Jan Gorecki](#), [Joseph Stachelek](#), [Dean Attali](#), [Julia Gustavsen](#), [Nicholas Tierney](#), [Rich FitzJohn](#), [Tiffany Timbers](#), [Hilmar Lapp](#), [Miles McBain](#), [Bryce Mecum](#), [Jonathan Carroll](#), [Carl Boettiger](#), [Florian Privé](#), [Stefanie Butland](#), [Daniel Possenriede](#), [Hadley Wickham](#), [Hugo Gruson](#), [Mauro Lepore](#). [Matthew Fidler](#) Please tell us if we forgot to acknowledge your contribution!

Part I

Building Your Package

Chapter 1

Packaging Guide

rOpenSci accepts packages that meet our guidelines via a streamlined [Software Peer Review process](#). To ensure a consistent style across all of our tools we have written this chapter highlighting our guidelines for package development. Please also read and apply our [chapter about continuous integration \(CI\)](#). Further guidance for after the review process is provided in the third section of this book starting with [a chapter about collaboration](#).

We strongly recommend that package developers read Hadley Wickham's concise but thorough book on package development which is available for [free online](#) (and [print](#)). Our guide is partially redundant with other resources but highlights rOpenSci's guidelines.

To read why submitting a package to rOpenSci is worth the effort to meet guidelines, have a look at [reasons to submit](#).

1.1 Package name and metadata

1.1.1 Naming your package

- We strongly recommend short, descriptive names in lower case. If your package deals with one or more commercial services, please make sure the name does not violate branding guidelines. You can check if your package name is available, informative and not offensive by using the [available package](#). In particular, do *not* choose a package name that's already used on CRAN or Bioconductor.
- A more unique package name might be easier to track (for you and us to assess package use) and search (for users to find it and to google their questions). Ob-

viously a *too* unique package name might make the package less discoverable (e.g. it might be an argument for naming your package [geojson](#)).

- Find other interesting aspects of naming your package [in this blog post by Nick Tierney](#), and in case you change your mind, find out [how to rename your package in this other blog post of Nick's](#).

1.1.2 Creating metadata for your package

We recommend you to use the [codemeta package](#) for creating and updating a JSON [CodeMeta](#) metadata file for your package via `codemeta::write_codemeta()`. It will automatically include all useful information, including [GitHub topics](#). CodeMeta uses [Schema.org terms](#) so as it gains popularity the JSON metadata of your package might be used by third-party services, maybe even search engines.

1.2 Platforms

- Packages should run on all major platforms (Windows, macOS, Linux). Exceptions may be granted packages that interact with system-specific functions, or wrappers for utilities that only operate on limited platforms, but authors should make every effort for cross-platform compatibility, including system-specific compilation, or containerization of external utilities.

1.3 Package API

1.3.1 Function and argument naming

- Functions and arguments naming should be chosen to work together to form a common, logical programming API that is easy to read, and auto-complete.
 - Consider an `object_verb()` naming scheme for functions in your package that take a common data type or interact with a common API. `object` refers to the data/API and `verb` the primary action. This scheme helps avoid namespace conflicts with packages that may have similar verbs, and makes code readable and easy to auto-complete. For instance, in **stringi**, functions starting with `stri_` manipulate strings (`stri_join()`, `stri_sort()`), and in **googlesheets** functions starting with `gs_` are calls to the Google Sheets API (`gs_auth()`, `gs_user()`, `gs_download()`).
- For functions that manipulate an object/data and return an object/data of the same type, make the object/data the first argument of the function so as to enhance compatibility with the pipe operator (`%>%`)

- We strongly recommend `snake_case` over all other styles unless you are porting over a package that is already in wide use.
- Avoid function name conflicts with base packages or other popular ones (e.g. `ggplot2`, `dplyr`, `magrittr`, `data.table`)
 - Argument naming and order should be consistent across functions that use similar inputs.
- Package functions importing data should not import data to the global environment, but instead must return objects. Assignments to the global environment are to be avoided in general.

1.3.2 Console messages

- Use `message()` and `warning()` to communicate with the user in your functions. Please do not use `print()` or `cat()` unless it's for a `print.*()` or `str.*()` methods, as these methods of printing messages are harder for the user to suppress.

1.3.3 Interactive/Graphical Interfaces

If providing graphical user interface (GUI) (such as a Shiny app), to facilitate workflow, include a mechanism to automatically reproduce steps taken in the GUI. This could include auto-generation of code to reproduce the same outcomes, output of intermediate values produced in the interactive tool, or simply clear and well-documented mapping between GUI actions and scripted functions. (See also “Testing” below.)

The `tabulizer` package e.g. has an interactive workflow to extract tables, but can also only extract coordinates so one can re-run things as a script. Besides, two examples of shiny apps that do code generation are <https://gdancik.shinyapps.io/shinyGEO/>, and <https://github.com/wallaceEcoMod/wallace/>

1.4 Code Style

- For more information on how to style your code, name functions, and R scripts inside the `R/` folder, we recommend reading the [code chapter in Hadley's book](#). We recommend the `styler` package for automating part of the code styling.
- You can choose to use `=` over `<-` as long you are consistent with one choice within your package. We recommend avoiding the use of `->` for assignment

within a package. If you do use `<-` throughout your package, and you also use R6 in that package, you'll be forced to use `=` for assignment within your `R6Class` construction - this is not considered an inconsistency because you can't use `<-` in this case.

1.5 README

- All packages should have a README file, named `README.md`, in the root of the repository. The README should include, from top to bottom:
 - The package name
 - Badges for continuous integration and test coverage, the badge for rOpenSci peer-review once it has started (see below), a [repostatus.org](#) badge, and any other badges. If the README has many more badges, you might want to consider using a table for badges, see [this example](#), [that one](#) and [that one](#). Such a table should be more wide than high.
 - Short description of goals of package, with descriptive links to all vignettes (rendered, i.e. readable, cf [the documentation website section](#)) unless the package is small and there's only one vignette repeating the README.
 - Installation instructions
 - Any additional setup required (authentication tokens, etc)
 - Brief demonstration usage
 - If applicable, how the package compares to other similar packages and/or how it relates to other packages
 - Citation information

If you use another repo status badge such as a [lifecycle](#) badge, please also add a [repostatus.org](#) badge. [Example of a repo README with two repo status badges](#).

In all cases, for adding [repostatus.org](#) badges you can use the `rodev::use_repostatus_badge()` function.

- Once you have submitted a package and it has passed editor checks, add a peer-review badge via

```
[! [] (https://badges.ropensci.org/<issue_id>_status.svg)] (https://github.com/ropensci/s
```

where `issue_id` is the number of the issue in the software-review repository. For instance, the badge for [rtimicropem](#) review uses the number 126 since it's the [review issue number](#). The badge will first indicated “under review” and then “peer-reviewed” once your package has been onboarded (issue labelled “approved” and closed), and will link to the review issue.

- If your README has many badges consider ordering them in an html table to make it easier for newcomers to gather information at a glance. See examples in [drake repo](#) and in [qualtRics repo](#). Possible sections are
 - Development (CI statuses cf [CI chapter](#), Slack channel for discussion, re-postatus)
 - Release/Published ([CRAN version and release date badges from METACRAN](#), [CRAN checks API badge](#), Zenodo badge)
 - Stats/Usage (downloads e.g. [download badges from METACRAN](#)) The table should be more wide than it is long in order to mask the rest of the README.
- If your package connects to a data source or online service, or wraps other software, consider that your package README may be the first point of entry for users. It should provide enough information for users to understand the nature of the data, service, or software, and provide links to other relevant data and documentation. For instance, a README should not merely read, “Provides access to GooberDB,” but also include, “..., an online repository of Goober sightings in South America. More information about GooberDB, and documentation of database structure and metadata can be found at *link*”.
- We recommend not creating README.md directly, but from a README.Rmd file (an R Markdown file) if you have any demonstration code. The advantage of the .Rmd file is you can combine text with code that can be easily updated whenever your package is updated.
- Extensive examples should be kept for a vignette. If you want to make the vignettes more accessible before installing the package, we suggest [creating a website for your package](#)
- Consider using `usethis::use_readme_rmd()` to get a template for a README.Rmd file and to automatically set up a pre-commit hook to ensure that README.md is always newer than README.Rmd.
- *After* a package is accepted but before transfer, the rOpenSci footer should be added to the bottom of the README file with the following markdown line:

```
[![ropensci_footer](https://ropensci.org/public_images/github_footer.png)](https://ropensci.org)
```

- Add a code of conduct and contribution guidelines, cf [this section of the book](#).
- See the [gistr README](#) for a good example README to follow for a small package, and [bowerbird README](#) for a good example README for a larger package.

1.6 Documentation

- All exported package functions should be fully documented with examples.
- We request all submissions to use `roxygen2` for documentation. `roxygen2` is an R package that automatically compiles `.Rd` files to your `man` folder in your package from simple tags written above each function.
- More information on using `roxygen2` [documentation](#) is available in the R packages book.
- One key advantage of using `roxygen2` is that your `NAMESPACE` will always be automatically generated and up to date.
- All functions should document the type of object returned under the `@return` heading.
- We recommend using the `@family` tag in the documentation of functions to allow their grouping in the documentation of the installed package and potentially in the package’s website, see [this section of Hadley Wickham’s book](#) and [this section of the present chapter](#) for more details.
- The package should contain top-level documentation for `?foobar`, (or `?`foobar-package`` if there is a naming conflict). Optionally, you can use both `?foobar` and `?`foobar-package`` for the package level manual file, using `@aliases roxygen` tag. `usethis::use_package_doc()` adds the template for the top-level documentation.
- The package should contain at least one vignette providing a substantial coverage of package functions, illustrating realistic use cases and how functions are intended to interact. If the package is small, the vignette and the README may have very similar content.
- You could re-use documentation pieces (e.g. details about authentication, related packages) across the vignettes/README/man pages. A possible approach for that is the use of [R Markdown fragments, relying on knitr use of child documents so you can store the re-used parts in a folder in man/, and call them from both the README and the vignette as well as in man pages by using the @includeRmd tag available from roxygen 0.7.0](#).
- As is the case for a README, top-level documentation or vignettes may be the first point of entry for users. If your package connects to a data source or online service, or wraps other software, it should provide enough information for users to understand the nature of the data, service, or software, and provide links to other relevant data and documentation. For instance, a vignette intro or documentation should not merely read, “Provides access to GooberDB,” but also include, “..., an online repository of Goober sightings in South America. More information about GooberDB, and documentation of database structure

and metadata can be found at *link*". Any vignette should outline prerequisite knowledge to be able to understand the vignette upfront.

The general vignette should present a series of examples progressing in complexity from basic to advanced usage.

- Functionality likely to be used by only more advanced users or developers might be better put in a separate vignette (e.g. programming/NSE with dplyr).
- The vignette(s) should include citations to software and papers where appropriate.
- The README, the top-level package docs, vignettes, websites, etc., should all have enough information at the beginning to get a high-level overview of the package and the services/data it connects to, and provide navigation to other relevant pieces of documentation. This is to follow the principle of *multiple points of entry* i.e. to take into account the fact that any piece of documentation may be the first encounter the user has with the package and/or the tool/data it wraps.
- Add #' @noRd to internal functions.
- Only use package startup messages when necessary (function masking for instance). Avoid package startup messages like "This is foobar 2.4-0" or citation guidance because they can be annoying to the user. Rely on documentation for such guidance.
- You can choose to have a README section about use cases of your package (other packages, blog posts, etc.), [example](#).
- If you prefer not to clutter up code with extensive documentation, you can place further examples outside of the R script and use the @example tag; and you place further documentation in files in a man-roxygen folder in the root of your package, and those will be combined into the manual file by the use of @template <file name>, for example.
 - Put any documentation for an object in a .R file in the man-roxygen folder (at the root of your package). For example, [this file](#). Link to that template file from your function (e.g.) with the @template keyword (e.g.). The contents of the template will be inserted when documentation is built into the resulting .Rd file that users will see when they ask for documentation for the function.
 - Note that if you are using markdown documentation, markdown currently doesn't work in template files, so make sure to use latex formatting.
 - In most cases you can ignore templates and man-roxygen, but there are two cases in which leveraging them will greatly help:

1. When you have a lot of documentation for a function/class/object separating out certain chunks of that documentation can keep your .R source file tidy. This is especially useful when you have a lot of code in that .R file. On the other hand, it means the docs are not readable “in-source” since they’re in another file.
 2. When you have the same documentation parts used across many .R functions it’s helpful to use a template. This reduces duplicated text, and helps prevent mistakenly updating documentation for one function but not the other. Using a template file for a parameter documentation is an alternative to defining the parameter for one function and using `@inheritParams` for other functions using the same parameter.
- Starting from `roxygen2` version 7.0.0, R6 classes are officially supported. See the [roxygen2 docs](#) for details on how to document R6 classes.

1.7 Documentation website

We recommend creating a documentation website for your package using [pkgdown](#). [Here](#) is a good tutorial to get started with `pkgdown`, and unsurprisingly `pkgdown` has [its own documentation website](#).

There are a few elements we’d like to underline here.

1.7.1 Automatic deployment of the documentation website

You only need to worry about automatic deployment of your website until approval and transfer of your package repo to the ropensci organization; indeed, after that a `pkgdown` website will be built for your package after each push to the GitHub repo. You can find the status of these builds at https://dev.ropensci.org/job/package_name, e.g. [for magick](#); and the website at https://docs.ropensci.org/package_name, e.g. [for magick](#). The website build will use your `pkgdown` config file if you have one, except for the styling that will use the [rotemplate package](#). The resulting website will have search enabled by Algolia. Please report bugs, questions and feature requests about the central builds at <https://github.com/ropensci/docs/> and about the template at <https://github.com/ropensci/rotemplate/>.

If your package vignettes need credentials (API keys, tokens, etc.) to knit, you might want to [precompute them](#) since credentials cannot be used on the docs server.

Before submission and before transfer, you could use the [approach documented by pkgdown](#) or the [tic package](#) for automatic deployment of the package’s website. This would save you the hassle of running (and remembering to run) `pkgdown::build_site()` yourself every time the site needs to be updated. First

refer to our [chapter on continuous integration](#) if you're not familiar with continuous integration. In any case, do not forget to update all occurrences of the website URL after transfer to the ropensci organization.

1.7.2 Grouping functions in the reference

When your package has many functions, use grouping in the reference, which you can do more or less automatically.

If you use `roxygen2` above version 6.1.1, you should use the `@family` tag in your functions documentation to indicate grouping. This will give you links between functions in the local documentation of the installed package ("See also" section) *and* allow you to use the `pkgdown::has_concept` function in the config file of your website. Non-rOpenSci example courtesy of [optiRum](#): [family tag](#), [pkgdown config file](#) and [resulting reference section](#).

Less automatically, see the example of [drake website](#) and [associated config file](#).

1.7.3 Branding of authors

You can make the names of (some) authors clickable by adding their URL, and you can even replace their names with a logo (think rOpenSci... or your organisation/company!). See [pkgdown documentation](#) and this example in the wild: [pkgdown config file](#), [resulting website](#).

1.7.4 Tweaking the navbar

You can make your website content easier to browse by tweaking the navbar, refer to [pkgdown documentation](#). In particular, note that if you name the main vignette of your package "pkg-name.Rmd", it'll be accessible from the navbar as a `Get started` link instead of via `Articles > Vignette Title`.

1.7.5 Mathjax

Once your package is transferred and it gets a website using our `pkgdown` template, if you want to use Mathjax you'll need to specify it in the `pkgdown` config file like so:

```
template:
  params:
    mathjax: true
```

1.7.6 Package logo

To use your package logo in the pkgdown homepage, refer to `usethis::use_logo()`. If your package doesn't have any logo, the [rOpenSci docs builder](#) will use rOpenSci logo instead.

1.8 Authorship

The DESCRIPTION file of a package should list package authors and contributors to a package, using the Authors@R syntax to indicate their roles (author/creator/contributor etc.) if there is more than one author, and using the comment field to indicate the ORCID ID of each author, if they have one (cf [this post](#)). See [this section of “Writing R Extensions”](#) for details. If you feel that your reviewers have made a substantial contribution to the development of your package, you may list them in the Authors@R field with a Reviewer contributor type ("rev"), like so:

```
person("Bea", "Hernández", role = "rev",  
comment = "Bea reviewed the package (v. X.X.XX) for rOpenSci, see <https://github.
```

Only include reviewers after asking for their consent. Read more in [this blog post “Thanking Your Reviewers: Gratitude through Semantic Metadata”](#). Note that ‘rev’ will raise a CRAN NOTE unless the package is built using R v3.5. Make sure you use roxygen2’s latest CRAN version.

Please do not list editors as contributors. Your participation in and contribution to rOpenSci is thanks enough!

1.9 Testing

- All packages should pass R CMD check/devtools::check() on all major platforms.
- All packages should have a test suite that covers major functionality of the package. The tests should also cover the behavior of the package in case of errors.
- It is good practice to write unit tests for all functions, and all package code in general, ensuring key functionality is covered. Test coverage below 75% will likely require additional tests or explanation before being sent for review.

- We recommend using `testthat` for writing tests. Strive to write tests as you write each new function. This serves the obvious need to have proper testing for the package, but allows you to think about various ways in which a function can fail, and to *defensively* code against those. [More information](#).
- Packages with shiny apps should use a unit-testing framework such as [shinytest](#) to test that interactive interfaces behave as expected.
- For testing your functions creating plots, we suggest using [vdiff](#), an extension of the `testthat` package.
- Once you've set up CI, use your package's code coverage report (cf [this section of our book](#)) to identify untested lines, and to add further tests.
- `testthat` has a function `skip_on_cran()` that you can use to not run tests on CRAN. We recommend using this on all functions that are API calls since they are quite likely to fail on CRAN. These tests will still run on Travis.
- Even if you use [continuous integration](#), we recommend that you run tests locally prior to submitting your package, as some tests are often skipped (you may need to set `Sys.setenv(NOT_CRAN="true")` in order to ensure all tests are run). In addition, we recommend that prior to submitting your package, you use MangoTheCat's [goodpractice](#) package to check your package for likely sources of errors, and run `spelling::spell_check_package()` to find spelling errors in documentation.

1.10 Examples

- Include extensive examples in the documentation. In addition to demonstrating how to use the package, these can act as an easy way to test package functionality before there are proper tests. However, keep in mind we require tests in contributed packages.
- You can run examples with `devtools::run_examples()`. Note that when you run R CMD CHECK or equivalent (e.g., `devtools::check()`) your examples that are not wrapped in `\dontrun{}` or `\donttest{}` are run.
- In addition to running examples locally on your own computer, we strongly advise that you run examples on one of the CI systems, e.g. Travis-CI. Again, examples that are not wrapped in `\dontrun{}` or `\donttest{}` will be run, but for those that are you can add `r_check_args: "--run-dontrun"` to run examples wrapped in `\dontrun{}` in your `.travis.yml` (and/or `--run-donttest` if you want to run examples wrapped in `\donttest{}`).

1.11 Package dependencies

- Use `Imports` instead of `Depends` for packages providing functions from other packages. Make sure to list packages used for testing (`testthat`), and documentation (`knitr`, `roxygen2`) in your `Suggests` section of package dependencies (if you use `usethis` for adding testing infrastructure via `usethis::use_testthat()` or a vignette via `usethis::use_vignette()`, the necessary packages will be added to `DESCRIPTION`). If you use any package in the examples or tests of your package, make sure to list it in `Suggests`, if not already listed in `Imports`.
- If your (not Bioconductor) package depends on Bioconductor packages, make sure the installation instructions in the `README` and vignette are clear enough even for a user who is not familiar with the Bioconductor release cycle.
 - Should the user use `BiocManager` (recommended)? Document this.
 - Is the automatic installation of Bioconductor packages by `install.packages()` enough? In that case, mention that the user needs to run `setRepositories()` if they haven't set the necessary Bioconductor repositories yet.
 - If your package depends on Bioconductor after a certain version, mention it in `DESCRIPTION` and in the installation instructions.
- Specifying minimum dependencies (e.g. `glue (>= 1.3.0)` instead of just `glue`) should be a conscious choice. If you know for a fact that your package will break below a certain dependency version, specify it explicitly. But if you don't, then no need to specify a minimum dependency. In that case when a user reports a bug which is explicitly related to an older version of a dependency then address it then. An example of bad practice would be for a developer to consider the versions of their current state of dependencies to be the minimal version. That would needlessly force everyone to upgrade (causing issues with other packages) when there is no good reason behind that version choice.
- For most cases where you must expose functions from dependencies to the user, you should import and re-export those individual functions rather than listing them in the `Depends` fields. For instance, if functions in your package produce `raster` objects, you might re-export only printing and plotting functions from the **raster** package.
- If your package uses a *system* dependency, you should
 - indicate it in `DESCRIPTION`
 - Check that it is listed by `sysreqsdb` to allow automatic tools to install it, and `submit a contribution` if not.

- check for it in a `configure` script ([example](#)) and give a helpful error message if it cannot be found ([example](#)). `configure` scripts can be challenging as they often require hacky solutions to make diverse system dependencies work across systems. Use examples ([more here](#)) as a starting point but note that it is common to encounter bugs and edge cases and often violate CRAN policies. Do not hesitate to [ask for help on our forum](#).
- Consider the trade-offs involved in relying on a package as a dependency. On one hand, using dependencies reduces coding effort, and can build on useful functionality developed by others, especially if the dependency performs complex tasks, is high-performance, and/or is well vetted and tested. On the other hand, having many dependencies places a burden on the maintainer to keep up with changes in those packages, at risk to your package's long-term sustainability. It also increases installation time and size, primarily a consideration on your and others' development cycle, and in automated build systems. "Heavy" packages - those with many dependencies themselves, and those with large amounts of compiled code - increase this cost. Here are some approaches to reducing dependencies:
 - Small, simple functions from a dependency package may be better copied into your own package if the dependency if you are using only a few functions in an otherwise large or heavy dependency. On the other hand, complex functions with many edge cases (e.g. parsers) require considerable testing and vetting.
 - * An common example of this is in returning tidyverse-style "tibbles" from package functions that provide data. One can avoid the modestly heavy **tibble** package dependency by returning a tibble created by modifying a data frame like so:


```
class(df) <- c("tbl_df", "tbl", "data.frame")
```

 (Note that this approach is [not universally endorsed](#).)
 - Ensure that you are using the package where the function is defined, rather than one where it is re-exported. For instance many functions in **devtools** can be found in smaller specialty packages such as **sessioninfo**. The `%>%` function should be imported from **magrittr**, where it is defined, rather than the heavier **dplyr**, which re-exports it.
 - Some dependencies are preferred because they provide easier to interpret function names and syntax than base R solutions. If this is the primary reason for using a function in a heavy dependency, consider wrapping the base R approach in a nicely-named internal function in your package.
 - If dependencies have overlapping functionality, see if you can rely on only one.
 - More dependency-management tips can be found [in this post by Scott Chamberlain](#).

1.12 Recommended scaffolding

- For HTTP requests we recommend using [curl](#), [crul](#), or [httr](#) over [RCurl](#). If you like low level clients for HTTP, [curl](#) is best, whereas [crul](#) or [httr](#) are better for higher level access. [crul](#) is maintained by rOpenSci. We recommend the rOpenSci maintained packages [webmockr](#) for mocking HTTP requests, and [vcr](#) for caching HTTP requests in package tests.
- For parsing JSON, use [jsonlite](#) instead of [rjson](#) or [RJSONIO](#).
- For parsing, creating, and manipulating XML, we strongly recommend [xml2](#) for most cases. You can refer to [Daniel Nüst's notes about migration from XML to xml2](#).

1.13 Miscellaneous CRAN gotchas

This is a collection of CRAN gotchas that are worth avoiding at the outset.

- Make sure your package title is in Title Case.
- Do not put a period on the end of your title.
- Do not put 'in R' or 'with R' in your title as this is obvious from packages hosted on CRAN. If you would like this information to be displayed on your website nonetheless, check the [pkgdown documentation](#) to learn how to override this.
- Avoid starting the description with the package name or "This package ...".
- Make sure you include links to websites if you wrap a web API, scrape data from a site, etc. in the Description field of your DESCRIPTION file. URLs should be enclosed in angle brackets, e.g. `<https://www.r-project.org>`.
- In both the Title and Description fields, the names of packages or other external software must be quoted using single quotes (e.g., *'Rcpp' Integration for the 'Armadillo' Templated Linear Algebra Library*).
- Avoid long running tests and examples. Consider `testthat::skip_on_cran` in tests to skip things that take a long time but still test them locally and on Travis.
- Include top-level files such as `paper.md`, `.travis.yml` in your `.Rbuildignore` file.

1.13.1 CRAN checks

Once your package is on CRAN, it will be [regularly checked on different platforms](#). Failures of such checks, when not false positives, can lead to the CRAN team's reaching out. You can monitor the state of the CRAN checks via

- the [foghorn](#) package

- the [CRAN checks API](#) maintained by rOpenSci, that provides [badges](#). You can add one of them to the README of your package via `rodev::use_cchecks_badge()`.

1.14 Bioconductor gotchas

If you intend your package to be submitted to, or if your package is on, Bioconductor, refer to [Bioconductor packaging guidelines](#).

1.15 Further guidance

- *R Packages* by Hadley Wickham and Jenny Bryan is an excellent, readable resource on package development which is available for [free online](#) (and [print – link to former version by Hadley Wickham as the new version is not published yet as of June 2019](#)).
- [Writing R Extensions](#) is the canonical, usually most up-to-date, reference for creating R packages.
- If you are submitting a package to rOpenSci via the [software-review repo](#), you can direct further questions to the rOpenSci team in the issue tracker, or in our [discussion forum](#).
- Before submitting a package use the [goodpractice](#) package (`goodpractice::gp()`) as a guide to improve your package, since most exceptions to it will need to be justified. E.g. the use of `foo` might be generally bad and therefore flagged by `goodpractice` but you had a good reason to use it in your package.

Chapter 2

Continuous Integration Best Practices

This chapter summarizes our guidelines about continuous integration after explaining what continuous integration is.

Along with [last chapter](#), it forms our guidelines for Software Peer Review.

2.1 Why use continuous integration (CI)?

All rOpenSci packages must use one form of continuous integration. This ensures that all commits, pull requests and new branches are run through `R CMD check`. rOpenSci packages' continuous integration must also be linked to a code coverage service, indicating how many lines are covered by unit tests.

Both test status and code coverage should be reported via badges in your package README.

2.2 How to use continuous integration?

The `usethis` package offers a few functions for continuous integration setup, see [the documentation](#).

Details will be provided below for different services.

2.3 Which continuous integration service(s)?

Different continuous integration services will support builds on different operating systems.

R packages should have CI for all platforms when they contain:

- Compiled code
- Java dependencies
- Dependencies on other languages
- Packages with system calls
- Text munging such as getting people's names (in order to find encoding issues).
- Anything with file system / path calls

In case of any doubt regarding the applicability of these criteria to your package, it's better to add CI for all platforms, and most often not too much hassle.

2.3.1 Travis CI (Linux and Mac OSX)

Travis offers continuous integration for Linux and Mac OSX. Set it up using `rodev::use_ro_travis()` or `usethis::use_travis()`.

R is now a [natively supported language on Travis-CI](#), making it easier than ever to do continuous integration. See [R Packages](#) and Julia Silge's [Beginner's Guide to Travis-CI for R](#) for more help.

To customize your build, have a look at [Travis' docs](#) and at existing Travis config files over rOpenSci's ropensci GitHub organization, e.g. [this one for the spelling package](#).

2.3.1.1 Testing using different versions of R

We require that rOpenSci packages are tested against the latest, previous and development versions of R to ensure both backwards and forwards compatibility with base R. You can enable this on Travis by adding the following to your `.travis.yml` configuration file:

```
r:
- oldrel
- release
- devel
```

Details of how to run tests/checks using different versions of R locally can be found in the R-hub vignette on running [Local Linux checks with Docker](#).

You can fine tune the deployment of tests with each versions by using a testing matrix. See this [more complex example](#) of a Travis configuration where pkgdown documentation is built during the release R version testing only.

For a package depending on Bioconductor packages, or a Bioconductor package, [Travis options allow to test on either Bioconductor release or devel \(or both\)](#).

2.3.1.2 Minimizing build times on Travis

Please use these tips to minimize build time on Travis especially after your package project gets transferred to ropensci Travis account:

- Cache installation of packages. Add `cache: packages` at the beginning of the config file. [Example in the wild](#). It'll already be in the config file if you set Travis up using `usethis::use_travis()`.
- [Enable auto-cancellation of builds](#).
- If you have a matrix to test your package on several Travis systems, place any `after_success` or `before_deploy` commands within one single matrix build to avoid them being executed on every matrix build.

2.3.2 AppVeyor CI (Windows)

For continuous integration on Windows, see [R + AppVeyor](#). Set it up using `usethis::use_appveyor()`.

Here are tips to minimize AppVeyor build time:

- Cache installation of packages. [Example in a config file](#). It'll already be in the config file if you set AppVeyor CI up using `usethis::use_appveyor()`.
- Enable [rolling builds](#).

We no longer transfer AppVeyor projects to ropensci AppVeyor account so after transfer of your repo to rOpenSci's "ropensci" GitHub organization the badge will be `[[AppVeyor Build Status]](https://ci.appveyor.com/api/projects/status/github/ropensci/pkgname?branch=)`

2.3.3 Circle CI (Linux and Mac OSX)

[Circle CI](#) is used, for example, by rOpenSci package [bomrang](#) as an alternative to Travis CI.

2.3.4 GitHub Actions (Linux, Mac OSX, Windows)

GitHub Actions is a new CI service for which there are [examples and actions for R packages](#).

2.4 Test coverage

Continuous integration should also include reporting of test coverage via a testing service such as [Codecov](#) or [Coveralls](#). See the [README for the `covr` package](#) for instructions, as well as `usethis::use_coverage()`.

If you run coverage on several CI services [the results will be merged](#).

2.5 Even more CI: OpenCPU

After transfer to rOpenSci’s “ropensci” GitHub organization, each push to the repo will be built on OpenCPU and the person committing will receive a notification email. This is an additional CI service for package authors that allows for R functions in packages to be called remotely via <https://ropensci.ocpu.io/> using the [opencpu API](#). For more details about this service, consult the OpenCPU [help page](#) that also indicates where to ask questions.

2.6 Even more CI: rOpenSci docs

After transfer to rOpenSci’s “ropensci” GitHub organization, a pkgdown website will be built for your package after each push to the GitHub repo. You can find the status of these builds at https://dev.ropensci.org/job/package_name, e.g. [for magick](#); and the website at https://docs.ropensci.org/package_name, e.g. [for magick](#). The website build will use your pkgdown config file if you have one, except for the styling that will use the [rotemplate package](#). Please report bugs, questions and feature requests about the central builds at <https://github.com/ropensci/docs/> and about the template at <https://github.com/ropensci/rotemplate/>.

Chapter 3

Package Development Security Best Practices

This work-in-progress chapter includes [guidance about managing secrets in packages](#) and [links for further reading](#).

3.1 Miscellaneous

- We recommend you [secure your GitHub account with 2FA](#).
- If the web service your package wraps has either https or http, opt for https.

3.2 Secrets in packages

This section contains guidance for when you develop a package interacting with a web resource requiring credentials (API keys, tokens, etc.). Also refer to [the http vignette about sharing secrets](#).

3.2.1 Secrets in packages and user protection

Say your package needs an API key for making requests on behalf of users of your package.

- In your package documentation, guide the user so the API key doesn't end up in the .Rhistory/script of users of your package.

- Encourage the use of environment variables to store the API key (or even remove the possibility to pass it as an argument to the functions?). You could link [to this intro to startup files](#) and `usethis::edit_r_environ()`.
 - Or your package could depend on, or encourage the use of, [keyring to help user store variables](#) in the specific OS' credential stores (more secure than `.Renviron`): i.e. you'd create a function for setting the key, and have another one for retrieving the key; or the user would write `Sys.setenv(SUPERSECRETKEY = keyring::key_get("myservice"))` at the beginning of their script.
 - Do not print the API key even in verbose mode in any message, warning, error.
- In the GitHub issue template, it should be stated not to share any credentials (it's the case for [rOpenSci issue template](#)). If an user of your package accidentally shares credentials in an issue, make sure they're aware of that so they can revoke the key (i.e. ask them explicitly in an answer whether they realized they shared their key).

3.2.2 Secrets in packages and development

You'll need to protect your secrets as you protect secrets of users, but there's more to take into account and keep in mind.

3.2.2.1 Secrets and recorded requests in tests

If you use `vcr` or `httptest` in tests for caching API responses, you need to make sure the recorded requests / fixtures do not contain secrets. Refer to [vcr security guidance](#) and [httptest guidance](#) “Redacting and Modifying Recorded Requests”, and inspect your recorded requests / fixtures before committing them the first time to be sure you got the setup right.

`vcr` being an `rOpenSci` package, you can post any question you might have to [rOpenSci forum](#)

3.2.2.2 Share secrets with CI services

Now, you might need to share secrets with CI services such as Travis or GitHub Actions.

You could store API keys as environment variables / secrets, referring to the docs of the CI service.

For more details and workflow advice, refer [to the gargle article](#) “Managing tokens securely”.

Document the steps you made in [CONTRIBUTING.md](#) so you, or say a new maintainer, can remember how to do that next time.

3.2.2.3 Secrets and collaborations

What about pull requests from external contributors? Tests using your secrets will fail, so you might want to skip them depending on the context. For instance, in your CI account you could create an environment variable called `THIS_IS_ME` and then skip tests based on the presence of this variable. This obviously means the PR checks by the CI are not exhaustive, so you'll need to check out the PR locally to run all tests.

You could also choose [a more complicated setup](#).

Document the behavior of your package for external PRs in [CONTRIBUTING.md](#) for the sake of people making PRs and of people reviewing them (you in a few weeks, and other authors of the package).

3.2.3 Secrets and CRAN

On CRAN, skip any tests (`skip_on_cran()`) and examples (`dontrun`) requiring credentials.

[Precompute vignettes](#) requiring credentials.

3.3 Further reading

Useful security resources:

- [rOpenSci community call “Security for R”](#) (recording, slides, etc. see in particular [the list of resources](#));
- [the security-related projects of unconf18](#);
- [the notary package](#);
- [gargle article “Managing tokens securely”](#)
- elements outlined in [this bookdown \(repo\)](#) started at the unconf 2017.

Part II

Software Peer Review of Packages

Chapter 4

Software Peer Review, Why? What?

This chapter contains a [general intro](#) to our software peer review system for packages, [reasons to submit a package](#), [reasons to volunteer as a reviewer](#), [why our reviews are open](#), and acknowledgements of [actors of the system](#).

If you use our standards/checklists etc. when reviewing software elsewhere, do tell the recipients (e.g. journal editors, students, internal code review) that they came from rOpenSci, and tell us in [our public forum](#), or [privately by email](#).

4.1 What is rOpenSci Software Peer Review?

rOpenSci's [suite of packages](#) is partly contributed by staff members and partly contributed by community members, which means the suite stems from a great diversity of skills and experience of developers. How to ensure quality for the whole set? That's where software peer review comes into play: packages contributed by the community undergo a transparent, constructive, non adversarial and open review process. For that process relying mostly on volunteer work, [associate editors](#) manage the incoming flow and ensure progress of submissions; authors create, submit and improve their package; [reviewers](#), two per submission, examine the software code and user experience. [This blog post](#) written by rOpenSci editors is a good introduction to rOpenSci software peer review Other blog posts about review itself and reviewed packages can be find [via the "software-peer-review" tag on rOpenSci blog](#).

You can recognize rOpenSci packages that have been peer-reviewed via a green "peer-reviewed" badge in their README, linking to their reviews (cf [this example](#)); and via a blue comment icon near their description on [rOpenSci packages page](#), also linking to the reviews.

Technically, we make the most of [GitHub](#) infrastructure: each package review process is an issue in the [ropensci/software-review GitHub repository](#). For instance, click [here](#) to read the review thread of the `ropenqa` package: the process is an ongoing conversation until acceptance of the package, with two external reviews as important milestones. Furthermore, we use GitHub features such as the use of issue templates (as submission templates), and labelling which we use to track progress of submissions (from editor checks to approval).

4.2 Why submit your package to rOpenSci?

- First, and foremost, we hope you submit your package for review **because you value the feedback**. We aim to provide useful feedback to package authors and for our review process to be open, non-adversarial, and focused on improving software quality.
- Once aboard, your package will continue to receive **support from rOpenSci members**. You'll retain ownership and control of your package, but we can help with ongoing maintenance issues such as those associated with updates to R and dependencies and CRAN policies.
- rOpenSci will **promote your package** through our [webpage](#), [blog](#), and [social media](#). Packages in our suite also get a [documentation website that is automatically built and deployed after each push](#).
- rOpenSci **packages can be cross-listed** with other repositories such as CRAN and BioConductor.
- rOpenSci packages that contain a short accompanying paper can, after review, be automatically submitted to the [Journal of Open-Source Software](#) for fast-tracked publication.
- If you write one, rOpenSci will **promote gitbooks related to your package**: the source of such books can be transferred to the [ropensci-books GitHub organisation](#) for books to be listed [at books.ropensci.org](#).

4.3 Why review packages for rOpenSci?

- As in any peer-review process, we hope you choose to review **to give back to the rOpenSci and scientific communities**. Our mission to expand access to scientific data and promote a culture of reproducible research is only possible through the volunteer efforts of community members like you.
- Review is a two-way conversation. By reviewing packages, you'll have the chance to **continue to learn development practices from authors and other reviewers**.
- The open nature of our review process allows you to **network and meet colleagues and collaborators** through the review process. Our community

is friendly and filled with supportive members expert in R development and many other areas of science and scientific computing.

- To volunteer to be one of our reviewers, fill out [this short form](#) providing your contact information and areas of expertise. We are always looking for more reviewers with both general package-writing experience and domain expertise in the fields where packages are used.

4.4 Why are reviews open?

Our reviewing threads are public. Authors, reviewers, and editors all know each other's identities. The broader community can view or even participate in the conversation as it happens. This provides an incentive to be thorough and provide non-adversarial, constructive reviews. Both authors and [reviewers report](#) that they enjoy and learn more from this open and direct exchange. It also has the benefit of building a community. Participants have the opportunity to meaningfully network with new peers, and new collaborations have emerged via ideas spawned during the review process.

We are aware that open systems can have drawbacks. For instance, in traditional academic review, [double-blind peer review can increase representation of female authors](#), suggesting bias in non-blind reviews. It is also possible reviewers are less critical in open review. However, we posit that the openness of the review conversation provides a check on review quality and bias; it's harder to inject unsupported or subjective comments in public and without the cover of anonymity. Ultimately, we believe that having direct and public communication between authors and reviewers improves quality and fairness of reviews.

Furthermore, authors and reviewers have the ability to contact privately the editors if they have any doubt or question.

4.5 How will users know a package has been reviewed?

- Your package README will feature a peer-review badge linking to the software review thread.
- Your package will get a [docs.ropensci.org docs website](https://docs.ropensci.org/docs-website) that you can link from DESCRIPTION.
- Your package repo will be transferred to the rOpenSci organization.
- If reviewers [agree to be listed in DESCRIPTION](#), their metadata will mention the review.

4.6 Editors and reviewers

4.6.1 Associate editors

rOpenSci's Software Peer Review process is run by:

- [Noam Ross](#), EcoHealth Alliance
- [Scott Chamberlain](#), rOpenSci
- [Karthik Ram](#), rOpenSci
- [Maëlle Salmon](#), rOpenSci
- [Lincoln Mullen](#), George Mason University
- [Anna Krystalli](#), University of Sheffield RSE
- [Melina Vidoni](#), RMIT University (School of Science)
- [Brooke Anderson](#), Colorado State University

4.6.2 Reviewers

We are grateful to the following individuals who have offered up their time and expertise to review packages submitted to rOpenSci.

[Sam Albers](#) · [Toph Allen](#) · [Alison Appling](#) · [Zebulun Arendsee](#) · [Taylor Arnold](#) · [Dean Attali](#) · [Mara Averick](#) · [Suzan Baert](#) · [James Balamuta](#) · [Vikram Baliga](#) · [David Bapst](#) · [Joëlle Barido-Sottani](#) · [Cale Basaraba](#) · [John Baumgartner](#) · [Marcus Beck](#) · [Gabe Becker](#) · [Jason Becker](#) · [Dom Bennett](#) · [Kenneth Benoit](#) · [Aaron Berdanier](#) · [Fred Boehm](#) · [Carl Boettiger](#) · [Ben Bond-Lamberty](#) · [Alison Boyer](#) · [François Briatte](#) · [Eric Brown](#) · [Julien Brun](#) · [Jenny Bryan](#) · [Lorenzo Busetto](#) · [Jennifer Chang](#) · [Jorge Cimentada](#) · [Chase Clark](#) · [Jon Clayden](#) · [Will Cornwell](#) · [Enrico Crema](#) · [Ildiko Czeller](#) · [Laura DeCicco](#) · [Christophe Dervieux](#) · [Amanda Dobbyn](#) · [Jasmine Dumas](#) · [Remko Duursma](#) · [Mark Edmondson](#) · [Paul Egeler](#) · [Evan Eskew](#) · [Manuel Fernandez](#) · [Kim Fitter](#) · [Rich FitzJohn](#) · [Robert Flight](#) · [Zachary Foster](#) · [Auriel Fournier](#) · [Carl Ganz](#) · [Duncan Garmonsway](#) · [Sharla Gelfand](#) · [Monica Gerber](#) · [Duncan Gillespie](#) · [David Gohel](#) · [Laura Graham](#) · [Charles Gray](#) · [Corinna Gries](#) · [Julia Gustavsen](#) · [W Kyle Hamilton](#) · [Ivan Hanigan](#) · [Jeff Hanson](#) · [Rayna Harris](#) · [Ted Hart](#) · [Nujcharee Haswell](#) · [Verena Haunschmid](#) · [Andrew Heiss](#) · [Max Held](#) · [Rafael Pilliard Hellwig](#) · [Bea Hernandez](#) · [Jim Hester](#) · [Peter Hickey](#) · [Roel M. Hogervorst](#) · [Jeff Hollister](#) · [Kelly Hondula](#) · [Sean Hughes](#) · [Brandon Hurr](#) · [Najko Jahn](#) · [Tamora D James](#) · [Max Joseph](#) · [Krunoslav Juraic](#) · [Soumya Kalra](#) · [Zhian N. Kamvar](#) · [Michael Kane](#) · [Andee Kaplan](#) · [Hazel Kavili](#) · [Os Keyes](#) · [Michael Koontz](#) · [Bianca Kramer](#) · [Will Landau](#) · [Erin LeDell](#) · [Thomas Leeper](#) · [Mauro Lepore](#) · [Sam Levin](#) · [Stephanie Locke](#) · [Robin Lovelace](#) · [Julia Stewart Lowndes](#) · [Tim Lucas](#) · [Andrew MacDonald](#) · [Jesse Maegan](#) · [Tristan Mahr](#) · [Ben Marwick](#) · [Miles McBain](#) · [Lucy D'Agostino McGowan](#) · [Amelia McNamara](#) · [Elaine McVey](#) · [Bryce Mecum](#) · [Francois Michonneau](#) · [Helen Rodgers Miller](#) · [Jessica Minnier](#) · [Priscilla Minotti](#) · [Nichole Monhait](#) · [Paula Moraga](#) · [Ross Mounce](#) · [Matt Mulvahill](#) · [Maria Victoria Munafó](#) · [Dillon Niederhut](#) · [Rory Nolan](#) · [Jakub Nowosad](#)

· Daniel Nüst · Paul Oldham · Samantha Oliver · Jeroen Ooms · Philipp Ottolinger · Mark Padgham · Marina Papadopoulou · Edzer Pebesma · Thomas Lin Pedersen · Lindsay Platt · Nicholas Potter · Etienne Racine · Nistara Randhawa · David Ranzolin · Neal Richardson · Emily Riederer · tyler rinker · Emily Robinson · Julia Romanowska · Xavier Rotllan-Puig · Bob Rudis · Edgar Ruiz · Kent Russel · Francisco Rodriguez Sanchez · Alicia Schep · Clemens Schmid · Marco Sciaini · Heidi Seibold · Julia Silge · Margaret Siple · Margaret Siple · Peter Slaughter · Mike Smith · Frank Soboczenski · Tuija Sonkkila · Gaurav Sood · Adam Sparks · Joseph Stachelek · Christine Stawitz · Irene Steves · Michael Sumner · Chung-Kai Sun · Sarah Supp · Jason Taylor · Filipe Teixeira · Andy Teucher · Jennifer Thompson · Joe Thorley · Tiffany Timbers · Tim Trice · Ted Underwood · Kevin Ushey · Josef Uyeda · Frans van Dunné · Mauricio Vargas · Remi Vergnon · Claudia Vitolo · Jake Wagner · Ben Ward · Elin Waring · Rachel Warnock · Leah Wasser · Lukas Weber · Karissa Whiting · Stefan Widgren · Anna Willoughby · Luke Winslow · David Winter · Kara Woo · Bruna Wundervald · Lauren Yamane · Taras Zakharko · Hao Zhu · Chava Zibman · Naupaka Zimmerman · Jake Zwart · Lluís · NA · NA · NA

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Laura DeCicco · Ana Laura Diedrichs · Julia Gustavsen · Mauro Lepore

Chapter 5

Software Peer Review policies

This chapter contains the policies of rOpenSci Software Peer Review.

In particular, you'll read our policies regarding software peer review itself: the [review submission process](#) including our [conflict of interest policies](#), and the [aims and scope of the Software Peer Review system](#). This chapter also features our policies regarding [package ownership and maintenance](#).

Last but not least, you'll find the code of conduct of rOpenSci Software Peer Review [here](#).

5.1 Review process

- For a package to be considered for the rOpenSci suite, package authors must initiate a request on the [ropensci/software-review](#) repository.
- Packages are reviewed for quality, fit, documentation, clarity and the review process is quite similar to a manuscript review (see our [packaging guide](#) and [reviewing guide](#) for more details). Unlike a manuscript review, this process will be an ongoing conversation.
- Once all major issues and questions, and those addressable with reasonable effort, are resolved, the editor assigned to a package will make a decision (accept, hold, or reject). Rejections are usually done early (before the review process begins, see [the aims and scope section](#)), but in rare cases a package may also be not onboarded after review & revision. It is ultimately editor's decision on whether or not to reject the package based on how the reviews are addressed.
- Communication between authors, reviewers and editors will first and foremost take place on GitHub, although you can choose to contact the editor by email or Slack for some issues. When submitting a package, please make sure your GitHub notification settings make it unlikely you will miss a comment.

- The author can choose to have their submission put on hold (editor applies the holding label). The holding status will be revisited every 3 months, and after one year the issue will be closed.
- If the author hasn't requested a holding label, but is simply not responding, we should close the issue within one month after the last contact intent. This intent will include a comment tagging the author, but also an email using the email address listed in the DESCRIPTION of the package which is one of the rare cases where the editor will try to contact the author by email.
- If a submission is closed and the author wishes to re-submit, they'll have to start a new submission. If the package is still in scope, the author will have to respond to the initial reviews before the editor starts looking for new reviewers.

5.1.1 Publishing in other Venues

- We strongly suggest submitting your package for review *before* publishing on CRAN or submitting a software paper describing the package to a journal. Review feedback may result in major improvements and updates to your package, including renaming and breaking changes to functions. We do not consider previous publication on CRAN or in other venues sufficient reason to not adopt reviewer or editor recommendations.
- Do not submit your package for review while it or an associated manuscript is also under review at another venue, as this may result on conflicting requests for changes.

5.1.2 Conflict of interest for reviewers/editors

Following criteria are meant to be a guide for what constitutes a conflict of interest for an editor or reviewer. The potential editor or reviewer has a conflict of interest if:

- The authors with a major role are from the potential reviewer/editor's institution or institutional component (e.g., department)
- Within in the past three years, the potential reviewer/editor has been a collaborator or has had any other professional relationship with any person on the package who has a major role
- The potential reviewer/editor serves as a member of the advisory board for the project under review
- The potential reviewer/editor would receive a direct or indirect financial benefit if the package is accepted
- The potential reviewer/editor has significantly contributed to a competitor project.
- There is also a lifetime COI for the family members, business partners, and thesis student/advisor or mentor.

In the case where none of the [associate editors](#) can serve as editor, an external guest editor will be recruited.

5.2 Aims and Scope

rOpenSci aims to support packages that enable reproducible research and managing the data lifecycle for scientists. Packages submitted to rOpenSci should fit into one or more of the categories outlined below. If you are unsure whether your package fits into one of these categories, please open an issue as a pre-submission inquiry ([Examples](#)).

As this is a living document, these categories may change through time and not all previously onboarded packages would be in-scope today. For instance, data visualization packages are no longer in-scope. While we strive to be consistent, we evaluate packages on a case-by-case basis and may make exceptions.

Note that not all rOpenSci projects and packages are in-scope or go through peer review. Projects developed by [staff](#) or at conferences may be experimental, exploratory, address core infrastructure priorities and thus not fall into these categories. Look for the peer-review badge - see below - to identify peer-reviewed packages in the rOpenSci repository.



5.2.1 Package categories

- **data retrieval:** Packages for accessing and downloading data from online sources with scientific applications. Our definition of scientific applications is broad, including data storage services, journals, and other remote servers, as many data sources may be of interest to researchers. However, retrieval packages should be focused on data *sources / topics*, rather than *services*. For example a general client for Amazon Web Services data storage would not be in-scope. (Examples: [rotl](#), [gutenbergr](#))
- **data extraction:** Packages that aid in retrieving data from unstructured sources such as text, images and PDFs, as well as parsing scientific data types and outputs from scientific equipment. Statistical/ML libraries for modeling or prediction are typically not included in this category, but trained models that act as utilities (e.g., for optical character recognition), may qualify. (Examples: [tabulizer](#), [robotstxt](#), [genbankr](#))
- **data munging:** Packages for processing data from formats above. This area does not include broad data manipulations tools such as [reshape2](#) or [tidyr](#), but rather tools for handling data in specific scientific formats. (Example: [plateR](#))

- **data deposition:** Packages that support deposition of data into research repositories, including data formatting and metadata generation. (Example: [EML](#))
- **data validation and testing:** Tools that enable automated validation and checking of data quality and completeness as part of scientific workflows. (Example: [assertr](#))
- **workflow automation:** Tools that automate and link together workflows, such as build systems and tools to manage continuous integration. Does not include general tools for literate programming. (e.g., R markdown extensions not under the previous topics). (Example: [drake](#))
- **version control:** Tools that facilitate the use of version control in scientific workflows. Note that this does not include all tools that interact with online version control services (e.g., GitHub), unless they fit into another category. (Example: [git2rdata](#))
- **citation management and bibliometrics:** Tools that facilitate managing references, such as for writing manuscripts, creating CVs or otherwise attributing scientific contributions, or accessing, manipulating or otherwise working with bibliometric data. (Example: [RefManageR](#))
- **scientific software wrappers:** Packages that wrap non-R utility programs used for scientific research. These programs must be specific to research fields, not general computing utilities. Wrappers must be non-trivial, in that there must be significant added value above simple `system()` call or bindings, whether in parsing inputs and outputs, data handling, etc. Improved installation process, or extension of compatibility to more platforms, may constitute added value if installation is complex. This does not include wrappers of other R packages or C/C++ libraries that can be included in R packages. We strongly encourage wrapping open-source and open-licensed utilities - exceptions will be evaluated case-by-case, considering whether open-source options exist. (Examples: [babette](#), [nlrx](#))
- **field and laboratory reproducibility tools:** Packages that improve reproducibility of real-world workflows through standardization and automation of field and lab protocols, such as sample tracking and tagging, form and data sheet generation, interfacing with laboratory equipment or information systems, and executing experimental designs. (Example: [baRcodeR](#))
- **database software bindings:** Bindings and wrappers for generic database APIs (Example: [rrlite](#))

In addition, we have some *specialty topics* with a slightly broader scope.

- **geospatial data:** We accept packages focused on accessing geospatial data, manipulating geospatial data, and converting between geospatial data formats. (Examples: [osmplotr](#), [tidync](#)).

- **text analysis:** We are currently *piloting* a sub-specialty area for text analysis that includes implementation of statistical/ML methods for analyzing or extracting text data. This does not include packages with new methods, but only implementation or wrapping of previously published methods. As this is a pilot, the scope for this topic is not fully defined and we are still developing a reviewer base and process for this area. Please open a pre-submission inquiry if you are considering submitting a package that falls under this topic. (Example: [textreuse](#))

5.2.2 Other scope considerations

Packages should be *general* in the sense that they should solve a problem as broadly as possible while maintaining a coherent user interface and code base. For instance, if several data sources use an identical API, we prefer a package that provides access to all the data sources, rather than just one.

Packages that include interactive tools to facilitate researcher workflows (e.g., shiny apps) must have a mechanism to make the interactive workflow reproducible, such as code generation or a scriptable API.

Here are some types of packages we are unlikely to accept:

- Packages that wrap or implement statistical or machine learning methods. We are not organized so as to review the correctness of these methods (But see “text analysis”, above).
- Exploratory data analysis packages that visualize or summarize data.
- General workflow or package development support packages.

For packages that are not in the scope of rOpenSci, we encourage submitting them to CRAN, BioConductor, as well as other R package development initiatives (e.g., [cloudyr](#)), and software journals such as JOSS, JSS, or the R journal.

Note that the packages developed internally by rOpenSci, through our events or through collaborations are not all in-scope for our Software Peer Review process.

5.2.3 Package overlap

rOpenSci encourages competition among packages, forking and re-implementation as they improve options of users overall. However, as we want packages in the rOpenSci suite to be our top recommendations for the tasks they perform, we aim to avoid duplication of functionality of existing R packages in any repo without significant improvements. An R package that replicates the functionality of an existing R package may be considered for inclusion in the rOpenSci suite if it significantly improves on alternatives in any repository (RO, CRAN, BioC) by being:

- More open in licensing or development practices
- Broader in functionality (e.g., providing access to more data sets, providing a greater suite of functions), but not only by duplicating additional packages
- Better in usability and performance
- Actively maintained while alternatives are poorly or no longer actively maintained

These factors should be considered *as a whole* to determine if the package is a significant improvement. A new package would not meet this standard only by following our package guidelines while others do not, unless this leads to a significant difference in the areas above.

We recommend that packages highlight differences from and improvements over overlapping packages in their README and/or vignettes.

We encourage developers whose packages are not accepted due to overlap to still consider submittal to other repositories or journals.

5.3 Package ownership and maintenance

5.3.1 Role of the rOpenSci team

Authors of contributed packages essentially maintain the same ownership they had prior to their package joining the rOpenSci suite. Package authors will continue to maintain and develop their software after acceptance into rOpenSci. Unless explicitly added as collaborators, the rOpenSci team will not interfere much with day to day operations. However, this team may intervene with critical bug fixes, or address urgent issues if package authors do not respond in a timely manner (see [the section about maintainer responsiveness](#)).

5.3.2 Maintainer responsiveness

If package maintainers do not respond in a timely manner to requests for package fixes from CRAN or from us, we will remind the maintainer a number of times, but after 3 months (or shorter time frame, depending on how critical the fix is) we will make the changes ourselves.

The above is a bit vague, so the following are a few areas of consideration.

- Examples where we'd want to move quickly:
 - Package `foo` is imported by one or more packages on CRAN, and `foo` is broken, and thus would break its reverse dependencies.

- Package `bar` may not have reverse dependencies on CRAN, but is widely used, thus quickly fixing problems is of greater importance.
- Examples where we can wait longer:
 - Package `hello` is not on CRAN, or on CRAN, but has no reverse dependencies.
 - Package `world` needs some fixes. The maintainer has responded but is simply very busy with a new job, or other reason, and will attend to soon.

We urge package maintainers to make sure they are receiving GitHub notifications, as well as making sure emails from rOpenSci staff and CRAN maintainers are not going to their spam box. Authors of onboarded packages will be invited to the rOpenSci Slack to chat with the rOpenSci team and the greater rOpenSci community. Anyone can also discuss with the rOpenSci community on the [rOpenSci discussion forum](#).

Should authors abandon the maintenance of an actively used package in our suite, we will consider petitioning CRAN to transfer package maintainer status to rOpenSci.

5.3.3 Quality commitment

rOpenSci strives to develop and promote high quality research software. To ensure that your software meets our criteria, we review all of our submissions as part of the Software Peer Review process, and even after acceptance will continue to step in with improvements and bug fixes.

Despite our best efforts to support contributed software, errors are the responsibility of individual maintainers. Buggy, unmaintained software may be removed from our suite at any time.

5.3.4 Package removal

In the unlikely scenario that a contributor of a package requests removal of their package from the suite, we retain the right to maintain a version of the package in our suite for archival purposes.

5.4 Ethics, Data Privacy and Human Subjects Research

rOpenSci packages and other tools are used for a variety of purposes, but our focus is on tools for research. We expect that tools will enable ethical use by research practitioners, who are obligated to adhere to ethical codes such as [Declaration of Helsinki](#) and [The Belmont Report](#). Researchers bear responsibility for their use of software,

but software developers must consider the ethical use of their products, and developers themselves adhere to ethical codes for computer professionals such as those expressed by [IEEE](#) and [ACM](#). rOpenSci contributors often play both the role of both researcher and developer.

We ask that software developers place themselves in researchers' role and consider the requirements of an ethical workflow using authors' software. Given the variation and degree of flux of ethical approaches for Internet-based analyses, judgement calls rather than recipes are required. The [Ethical Guidelines of The Association of Internet Researchers](#) provides a robust framework and we encourage authors, editors, and reviewers to use this in evaluating their work. In general, adherence to legal or regulatory minimum requirements may not be sufficient, though these (e.g., [GDPR](#)), may be relevant. Package authors should direct users to relevant resources for the ethical use of the software.

Some packages, due to the nature of data they handle, may be determined by editors to require enhanced scrutiny. For these, editors may require additional (or reduced) functionality, and robust documentation, defaults, and warnings to direct users to relevant ethical practices. The following topics may merit enhanced scrutiny:

- **Vulnerable populations:** Authors of packages and workflows that deal with information related to vulnerable populations bear responsibility to protect them from likely harms.
- **Personally identifiable or sensitive data:** The release of personally identifiable or sensitive data is potentially harmful. This includes “reasonably re-identifiable” data - which a motivated individual could trace back to the owner or creator even if the data are anonymized. This includes both cases where identifiers (e.g., name, date of birth) are available as part of data, and also if unique pseudonyms/screen names are linked with full-text posts, through which one can link back individuals through cross-reference with other data sets.

While the best response to ethical concerns will be context-specific, these general guidelines should be followed by packages where the challenges above arise:

- Packages should adhere to data source's terms of use, as expressed in website Terms and Conditions, “[robots.txt](#)” files, privacy policies, and other relevant restrictions, and link to them prominently in package documentation. Packages should provide or document functionality to adhere to such restrictions (e.g., scrape from only allowed endpoints, use appropriate rate limiting in code, examples, or vignettes). Note that while Terms and Conditions, Privacy Policies, etc., may not provide sufficient bounds on ethical usage, they can provide an outer bound.
- A key tool in addressing the risks posed in studying vulnerable populations or using personally identifiable data is **informed consent**. Package authors

should support users' acquisition of informed consent when relevant. This may include providing links to data source's preferred method of acquiring consent, contact information of data providers (e.g. forum moderators), documentation of informed consent protocols, or getting pre-approval for general uses of a package.

Note that consent is not implicitly granted just because data are accessible. Accessible data are not necessarily public, as different persons and contexts have different normative expectations of privacy (see work by [Social Data Lab](#)).

- Packages accessing personally identifiable information should take special care to follow [security best practices][Package Development Security Best Practices] (e.g., exclusive use of secure internet protocols, strong mechanisms for storing credentials, etc.).
- Packages that access or handle personally identifiable or sensitive data should enable, document, and demonstrate workflows for de-identification, secure storage, other best practices to minimize risk of harm.

As standards for data privacy and research continue to evolve, we welcome input from authors on considerations specific to their software and supplemental documentation such as approval from university ethics review boards. These may be attached to issue threads of package submissions or pre-submission inquiries, or conveyed directly to editors if needed. General suggestions may be filed as [issues in this book's repository](#).

5.4.1 Resources

The following resources may be helpful for researchers, package authors, editors and reviewers in addressing ethical questions related to privacy and research software.

- The [Declaration of Helsinki](#) and [The Belmont Report](#) provide fundamental principles for ethical practice by researchers.
- Several organizations provide guidance on how to translate these principles into the the context of internet research. These include the [Ethical Guidelines of The Association of Internet Researchers](#), the [NESH Guide to Internet Research Ethics](#), and [BPS' Ethics Guidelines for Internet-Mediated Research](#). [Anabo et al \(2019\)](#) provide a helpful overview of these.
- The Social Media Lab provides a [high-level overview](#) with data on normative expectations of privacy and use on social forums.
- Bechmann A., Kim J.Y. (2019) Big Data: A Focus on Social Media Research Dilemmas. In: Iphofen R. (eds) Handbook of Research Ethics and Scientific Integrity. https://doi.org/10.1007/978-3-319-76040-7_18-1

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5.5 Code of Conduct

rOpenSci’s community is our best asset. Whether you’re a regular contributor or a newcomer, we care about making this a safe place for you and we’ve got your back. We have a Code of Conduct that applies to all people participating in the rOpenSci community, including rOpenSci staff and leadership and to all modes of interaction online or in person. The [Code of Conduct](#) is maintained on the rOpenSci website.

Chapter 6

Guide for Authors

This concise guide presents the software peer review process for you as a package author.

- Consult our [policies](#) see if your package meets our criteria for fitting into our suite and is not overlapping with other packages.
 - If you are unsure whether a package meets our criteria, feel free to open an issue as a pre-submission inquiry to ask if the package is appropriate.
- Read and follow [our packaging style guide](#) and [reviewer's guide](#) to ensure your package meets our style and quality criteria.
 - If you would like your package to also be submitted to [Journal of Open-Source Software](#) (JOSS), it should include a `paper.md` file describing the package. More detail on JOSS's requirements can be found [at their website](#).
 - If you choose this option you should *not* submit your package to JOSS separately. It will be evaluated by JOSS based on the rOpenSci review.
- Please consider the best time in your package's development to submit. Your package should be sufficiently mature so that reviewers are able to review all essential aspects, but keep in mind that review may result in major changes.
 - For any submission or pre-submission inquiry the README of your package should provide enough information about your package (goals, usage, similar packages) for the editors to assess its scope.
 - If you use [repostatus.org badges](#) (which we recommend), submit when you're ready to get an *Active* instead of *WIP* badge. Similarly, if you use [lifecycle badges](#), submission should happen if the package is at least *Maturing*.
 - At the submission stage, all major functions should be stable enough to be fully documented and tested.

- We strongly suggest submitting your package for review *before* publishing on CRAN or submitting a software paper describing the package to a journal. Review feedback may result in major improvements and updates to your package, including renaming and breaking changes to functions.
 - Your package will continue to evolve after review, this book [provides guidance about the topic](#).
- Do not submit your package for review while it or an associated manuscript is also under review at another venue, as this may result on conflicting requests for changes.
- Next, [open a new issue](#) in the software review repository and fill out the template.
- Communication between authors, reviewers and editors will first and foremost take place on GitHub so that the review thread can serve as a full record of the review. You may choose to contact the editor by email or Slack if private consultation is needed (e.g., asking how to respond to a reviewer question). Do not contact reviewers off-thread without asking them in the GitHub thread whether they agree to it.
- *When submitting a package please make sure your GitHub notification settings make it unlikely you will miss a comment.*
- An [editor](#) will review your submission within 5 business days and respond with next steps. The editor may assign the package to reviewers, request that the package be updated to meet minimal criteria before review, or reject the package due to lack of fit or overlap.
- If your package meets minimal criteria, the editor will assign 1-3 reviewers. They will be asked to provide reviews as comments on your issue within 3 weeks.
- We ask that you respond to reviewers' comments within 2 weeks of the last-submitted review, but you may make updates to your package or respond at any time. Here is [an author response example](#). We encourage ongoing conversations between authors and reviewers. See the [reviewing guide](#) for more details.
- Once your package is approved, we will provide further instructions about the transfer of your repository to the rOpenSci repository.

Our [code of conduct](#) is mandatory for everyone involved in our review process.

Chapter 7

Guide for Reviewers

Thanks for accepting to review a package for rOpenSci! This chapter consists of our guidelines to [prepare](#), [submit](#) and [follow up](#) on your review.

You might contact the editor in charge of the submission for any question you might have about the process or your review.

Please strive to complete your review within 3 weeks of accepting a review request. We will aim to remind reviewers of upcoming and past due dates. Editors may assign additional or alternate reviewers if a review is excessively late.

If you use our standards/checklists etc. when reviewing software elsewhere, do tell the recipients (e.g. journal editors, students, internal code review) that they came from rOpenSci, and tell us in [our public forum](#), or [privately by email](#).

7.1 Preparing your review

Note that when installing the package to review it, you should use the `dependencies = TRUE` argument of `devtools::install()` to make sure you have all dependencies available.

7.1.1 General guidelines

To review a package, please begin by copying our [review template](#) and using it as a high-level checklist. In addition to checking off the minimum criteria, we ask that you provide general comments addressing the following:

- Does the code comply with general principles in the [Mozilla reviewing guide](#)?
- Does the package comply with the [rOpenSci packaging guide](#)?

- Are there improvements that could be made to the code style?
- Is there code duplication in the package that should be reduced?
- Are there user interface improvements that could be made?
- Are there performance improvements that could be made?
- Is the documentation (installation instructions/vignettes/examples/demos) clear and sufficient? Does it use the principle of *multiple points of entry* i.e. takes into account the fact that any piece of documentation may be the first encounter the user has with the package and/or the tool/data it wraps?
- Were functions and arguments named to work together to form a common, logical programming API that is easy to read, and autocomplete?
- If you have your own relevant data/problem, work through it with the package. You may find rough edges and use-cases the author didn't think about.

Please be respectful and kind to the authors in your reviews. Our [code of conduct](#) is mandatory for everyone involved in our review process. We expect you to submit your review within 3 weeks, depending on the deadline set by the editor. Please contact the editor directly or in the submission thread to inform them about possible delays.

We encourage you to use automated tools to facilitate your reviewing. These include:

- Checking the package's logs on its continuous integration services (Travis-CI, Codecov, etc.)
- Running `devtools::check()` and `devtools::test()` on the package to find any errors that may be missed on the author's system.
- Using the **covr** package to examine the extent of test coverage.
- Using the **goodpractice** package (`goodpractice::gp()`) to identify likely sources of errors and style issues. Most exceptions will need to be justified by the author in the particular context of their package.
- Using `spelling::spell_check_package()` (and `spelling::spell_check_files("README.Rmd")`) to find spelling errors.

7.1.2 Off-thread interactions

If you interact with the package authors and talked about the review outside a review thread (in chats, DMs, in-person, issues in the project repository), please make sure that your review captures and/or links to elements from these conversations that are relevant to the process.

7.1.3 Experience from past reviewers

First-time reviewers may find it helpful to read (about) some previous reviews. In general you can find submission threads of onboarded packages [here](#). Here are a

few chosen examples of reviews (note that your reviews do not need to be as long as these examples):

- rtika [review 1](#) and [review 2](#)
- NLMR [review 1](#) and [review 2](#)
- bowerbird [pre-review comment](#), [review 1](#), [review 2](#).
- rusda [review](#) (from before we had a review template)

You can read blog posts written by reviewers about their experiences [via this link](#). In particular, in [this blog post by Mara Averick](#) read about the “naive user” role a reviewer can take to provide useful feedback even without being experts of the package’s topic or implementation, by asking themselves “*What did I think this thing would do? Does it do it? What are things that scare me off?*”. In [another blog post](#) Verena Haunschmid explains how she alternated between using the package and checking its code.

As both a former reviewer and package author [Adam Sparks wrote this](#) “[write] a good critique of the package structure and best coding practices. If you know how to do something better, tell me. It’s easy to miss documentation opportunities as a developer, as a reviewer, you have a different view. You’re a user that can give feedback. What’s not clear in the package? How can it be made more clear? If you’re using it for the first time, is it easy? Do you know another R package that maybe I should be using? Or is there one I’m using that perhaps I shouldn’t be? If you can contribute to the package, offer.”

7.1.4 Helper package for reviewers

If working in RStudio, you can streamline your review workflow by using the [pkgreviewr](#) package created by associated editor Anna Krystalli. Say you accepted to review the `refnet` package, you’d write

```
remotes::install_github("ropenscilabs/pkgreviewr")
library(pkgreviewr)
pkgreview_create(pkg_repo = "embruna/refnet",
                 review_parent = "~/Documents/workflows/rOpenSci/reviews/")
```

and

- the GitHub repo of the `refnet` package will be cloned.
- a review project will be created, containing a notebook for you to fill, and the review template.

7.1.5 Feedback on the process

We encourage you to ask questions and provide feedback on the review process on our [forum](#).

7.2 Submitting the Review

- When your review is complete, paste it as a comment into the package software-review issue.
- Additional comments are welcome in the same issue. We hope that package reviews will work as an ongoing conversation with the authors as opposed to a single round of reviews typical of academic manuscripts.
- You may also submit issues or pull requests directly to the package repo if you choose, but if you do, please comment about them and link to them in the software-review repo comment thread so we have a centralized record and text of your review.
- Please include an estimate of how many hours you spent on your review afterwards.

7.3 Review follow-up

Authors should respond within 2 weeks with their changes to the package in response to your review. At this stage, we ask that you respond as to whether the changes sufficiently address any issues raised in your review. We encourage ongoing discussion between package authors and reviewers, and you may ask editors to clarify issues in the review thread as well.

Chapter 8

Guide for Editors

Software Peer Review at rOpenSci is managed by a team of editors. We are piloting a system of a rotating Editor-in-Chief (EIC).

This chapter presents the responsibilities of the [Editor-in-Chief](#), of [any editor in charge of a submission](#), [how to respond to an out-of-scope submission](#) and [how to manage a dev guide release](#).

If you're a guest editor, thanks for helping! Please contact the editor who invited you to handle a submission for any question you might have.

8.1 Handling Editor's Checklist

8.1.1 Upon submission:

- Tag issue with `1/editor-checks` tag and assign a main editor. Please strive to finish the checks and start looking for reviewers within 5 working days.
- Use the [editor template](#) to guide initial checks and record your response to the submission. You can also streamline your editor checks by using the [pkgreviewr package created by associate editor Anna Krystalli](#)
- Check that template has been properly filled out.
- Check against policies for [fit](#) and [overlap](#). Initiate discussion via Slack `#software-review` channel if needed for edge cases that haven't been caught by previous checks by the EIC. If reject, see [this section](#) about how to respond.
- Check that mandatory parts of template are complete. If not, direct authors toward appropriate instructions.
- Run automated tests: `spelling::spell_check_package()`, `goodpractice::gp()` (most exceptions will need to be justified by the author in the particular context of their package.), `devtools::spell_check()`. Run `covr::package_coverage()` using `NOT_CRAN` if needed, as well. Check

that documentation is generated using `roxygen2`, not by hand (this isn't part of automatic tests [yet](#)). Report relevant outputs in the issue thread.

- For packages needing continuous integration on multiple platforms (cf [criteria in this section of the CI chapter](#)) make sure the package gets tested on multiple platforms (having the package built on both Travis and AppVeyor for instance).
- Wherever possible when asking for changes, direct authors to automatic tools such as [usethis](#) and [styler](#), and to online resources (sections of this guide, sections of the [R packages book](#)) to make your feedback easier to use. [Example of editor's checks](#).
- Ideally, the remarks you make should be tackled before reviewers start reviewing.
- If initial checks show major gaps, request changes before assigning reviewers. If the author mentions changes might take time, [apply the holding label](#).
- If the package raises a new issue for rOpenSci policy, start a conversation in Slack or open a discussion on the [rOpenSci forum](#) to discuss it with other editors ([example of policy discussion](#)).

8.1.2 Look for and assign reviewers:

8.1.2.1 Tasks

- Switch numbered tag to 2/seeking-reviewers.
- Ask author to add a rOpenSci review badge to their README, via `rodev::use_review_badge()`, `rodev::use_review_badge(<issue_number>)`. Badge URL is https://badges.ropensci.org/<issue_id>_status.svg. Full link should be:

[! [] (https://badges.ropensci.org/<issue_id>_status.svg)] (<https://github.com/ropensci/s>)

- Use the [email template](#) if needed for inviting reviewers
 - When inviting reviewers, include something like “if I don’t hear from you in a week, I’ll assume you are unable to review,” so as to give a clear deadline when you’ll move on to looking for someone else.
- Assign a due date 3 weeks after all reviewers have been found.
- Once two or more reviewers are found, assign reviewers by tagging in the issue with the following format:

```
Reviewer: @githubname1
Reviewer: @githubname2
Due date: YYYY-MM-DD
```

- Switch numbered tag to 3/reviewers-assigned once reviewers are assigned.
- Update Airtable database: Add one of the review record numbers associated with the package to the Reviews field of each reviewer’s record. Insert new Reviewers record if required.

8.1.2.2 How to look for reviewers

8.1.2.2.1 Where to look for reviewers? As a (guest) editor, use

- the potential suggestions made by the submitter(s), (although submitters may have a narrow view of the types of expertise needed. We suggest not using more than one of suggested reviewers)
- the Airtable database of reviewers and volunteers
- and the authors of [rOpenSci packages](#).

When these sources of information are not enough, * ping other editors in Slack for ideas, * look for users of the package or of the data source/upstream service the package connects to (via their opening issues in the repository, starring it, citing it in papers, talking about it on Twitter). * You can also search for authors of related packages on [r-pkg.org](#). * R-Ladies has a [directory](#) specifying skills and interests of people listed.

8.1.2.3 Criteria for choosing a reviewer

Here are criteria to keep in mind when choosing a reviewer. You might need to piece this information together by searching CRAN and the potential reviewer's GitHub page and general online presence (personal website, Twitter).

- Has not reviewed a package for us within the last 6 months.
- Some package development experience.
- Some domain experience in the field of the package or data source
- No [conflicts of interest](#).
- Try to balance your sense of the potential reviewer's experience against the complexity of the package.
- Diversity - with two reviewers both shouldn't be cis white males.
- Some evidence that they are interested in openness or R community activities, although blind emailing is fine.

Each submission should be reviewed by *two* package reviewers. Although it is fine for one of them to have less package development experience and more domain knowledge, the review should not be split in two. Both reviewers need to review the package comprehensively, though from their particular perspective. In general, at least one reviewer should have prior reviewing experience, and of course inviting one new reviewer expands our pool of reviewers.

8.1.3 During review:

- Check in with reviewers and authors occasionally. Offer clarification and help as needed.

- In general aim for 3 weeks for review, 2 weeks for subsequent changes, and 1 week for reviewer approval of changes.
- Upon all reviews being submitted, change the review status tag to `4/review-in-awaiting-changes` to update the reminder bot.
- Update Airtable database: Add the link to the review comment to the `review_url` field and the number of review hours to the `review_hours` field of each review record.
- If the author stops responding, refer to [the policies](#) and/or ping the other editors in the Slack channel for discussion. Importantly, if a reviewer was assigned to a closed issue, contact them when closing the issue to explain the decision, thank them once again for their work, and make a note in our database to assign them to a submission with high chances of smooth software review next time (e.g. a package author who has already submitted packages to us).
- Upon changes being made, change the review status tag to `5/awaiting-reviewer-response`.

8.1.4 After review:

- Change the status tag to `6/approved`.
- You can use the [comment template](#).
- Add review/er information to the review database.
- If authors intend to submit to CRAN, direct them to the [section about CRAN gotchas](#) and offer to provide support through this process.
- Ask authors to migrate to `ropensci`
 - Create a two-person team in rOpenSci’s “ropensci” GitHub organization, named for the package, with yourself and the package author as members.
 - Have the author transfer the repository to `ropensci`
 - Go to the repository settings in rOpenSci’s “ropensci” GitHub organization and give the author “Admin” access to the repository.
- *If the original repository owner opposes transfer, add a line with its address to [this repos list](#) to ensure the package gets included in rOpenSci package registry.*
- Ask author to:
 - Add a CodeMeta file by running `codemeta::write_codemeta()` ([codemeta GitHub repo](#))
 - Change any needed links, such those for CI badges
 - Re-activate CI services
 - * For Travis, activating the project in the ropensci account should be sufficient
 - * For AppVeyor, tell the author to update the GitHub link in their badge, but do not transfer the project: AppVeyor projects should remain under the authors’ account. The badge is `[! [AppVeyor Build Status](https://ci.appveyor.com/api/projects/status/github/ropensci/`
 - * For Codecov, the webhook may need to be reset by the author.

- Nominate a package to be featured in an rOpenSci blog post or tech note if you think it might be of high interest. Please note in the software review issue one or two things the author could highlight, and tag @ropensci/blog-editors for follow-up.
- If authors maintain a gitbook that is at least partly about their package, contact an rOpenSci staff member so they might contact the authors about transfer to the ropensci-books GitHub organisation.
- Add a “peer-reviewed” topic to the repo.
- Close the software-review issue.

8.1.5 For joint JOSS submissions:

- After repo is transferred to ropensci and admin rights assigned, have author generate a new release with a DOI.
- Ask author to submit package via <https://joss.theoj.org/papers/new>
- Watch for paper to pop up at <https://joss.theoj.org/papers>, then add the following comment to the submission thread:
This submission has been accepted to rOpenSci. The review thread can be found at [LINK TO SOFTWARE REVIEW ISSUE]

8.1.6 Package promotion:

- Alert maintainers of appropriate [task views](#)
- Direct the author to the chapters of the guide about [package releases](#), [marketing](#) and [GitHub grooming](#).

8.2 EiC Responsibilities

The EiC serves for 3 months or a time agreed to by all members of the editorial board. The EiC is entitled to taking scope and overlap decisions as independently as possible (but can still request help/advice). In details, the EiC plays the following roles

- Watches all issues posted to the software-review repo.
- Assigns package submissions to other editors, including self, to handle. Mostly this just rotates among editors, unless the EiC thinks an editor is particularly suited to a package, or an editor declines handling the submission due to being too busy or because of conflicting interests.
- Monitors pace of review process and reminds other editors to move packages along as needed.
- Responds to issues posted to the software-review-meta repo

- Makes decisions on scope/overlap for pre-submission inquiries, referrals from JOSS or other publication partners, and submissions if they see an ambiguous case (This last case may also be done by handling editors (see below)). To initiate discussion, this is posted to the rOpenSci Slack editors-only channel along with a small summary of what the (pre-)submitted/referred submission is about, what doubts the EiC has i.e. digesting information a bit. If after one day or two the EiC feels they haven't received enough answers, they can ping all editors.
- Any editor should feel free to step in on these. See [this section](#) about how to respond to out-of-scope (pre-) submissions.

8.2.1 Inviting a guest editor

After discussion with other editors the EiC might invite a guest editor to handle a submission (e.g. if all editors have a conflict of interest).

When inviting a guest editor,

- Ask about conflicts of interest using the [same phrasing as for reviewers](#),
- Give a link to the [guide for editors](#).

If the person said yes (yay!),

- Make sure they [enabled 2FA for their GitHub account](#),
- Give them write access to the software-review repository,
- Once they've accepted this repo invitation, assign the issue to them,
- Ensure they're (already) invited to rOpenSci Slack workspace,
- Add their name to the Airtable guest-editor table (so their names might appear in this book and in the software-review README).

After the review process is finished (package approved, issue closed),

- Thank the guest editor again,
- Remove their write access from the software-review repository.

8.3 Responding to out-of-scope submissions

Thank authors for their submission, explain the reasons for the decision, and direct them to other publication venues if relevant, and to the rOpenSci discussion forum. Use wording from [Aims and scope](#) in particular regarding the evolution of scope over time, and the overlap and differences between unconf/staff/software-review development.

[Examples of out-of-scope submissions and responses.](#)

8.4 Managing a dev guide release

If you are in charge of managing a release of the very book you are reading, use [the book release guidance](#) as an issue template to be posted [in the dev guide issue tracker](#), and do not hesitate to ask questions to other editors.

8.4.1 Dev guide governance

For very small amendments to the dev guide, no PR review is needed. For larger amendments, request review from at least a few editors (if none participated in the discussion related to the amendment, request a review from all of them on GitHub, and in the absence of any reaction merge after a week).

Two weeks before a dev guide release, once the PR from dev to master **and the release blog post** are ready for review, all editors should be pinged by GitHub (“review request” on the PR from dev to master) and Slack, but the release doesn’t need all of them to explicitly approve the release.

8.4.2 Blog post about a release

The blog post about a release will be reviewed [by editors](#), and one of @ropensci/blog-editors.

8.4.2.1 Content

Refer to the [general rOpenSci blogging guidance](#), and the more specific guidance below.

[First example of such a post](#); [second example](#).

The blog post should mention all important items from the [changelog](#) organized in (sub)sections: e.g. a section about big change A, another one about big change B, and one about smaller changes lumped together. Mention the most important changes first.

For each change made by an external contributor, thank them explicitly using the information from the changelog. E.g. [Matt Fidler] (<https://github.com/mattfidler/>) amended our section on Console messages [ropensci/dev_guide#178] (https://github.com/ropensci/dev_guide/pull/178).

At the end of the post, mention upcoming changes by linking to open issues in the issue tracker, and invite readers to contribute to the dev guide by opening issues and participating in open discussions. Conclusion template:

In this post we summarized the changes incorporated into our book ["rOpenSci Packages: We are grateful for all contributions that made this release possible. We are already working on updates for our next version, such as ISSUE1, ISSUE2. Check out the [the issue tracker](https://github.com/ropensci/dev_guide/issues/) if you

8.4.2.2 Authorship

The editor writing the post is first author, other editors are listed by alphabetical order.

Part III

Maintaining Packages

Chapter 9

Collaboration Guide

Having contributors will improve your package, and if you onboard some of them as package authors with [write permissions to the repo](#), your package will be more sustainably developed.

This chapter contains our guidance for collaboration, in a [section about making your repo contribution- and collaboration-friendly](#) by infrastructure (code of conduct, contribution guidelines, issue labels); and [a section about how to collaborate with new contributors](#), in particular in the context of the rOpenSci’s “ropensci” GitHub organization.

9.1 Make your repo contribution and collaboration friendly

9.1.1 Code of conduct

After transfer to our GitHub organization, [rOpenSci Code of Conduct](#) will apply to your project. Please add this text to the README

```
Please note that this package is released with a [Contributor  
Code of Conduct] (https://ropensci.org/code-of-conduct/).  
By  
contributing to this project, you agree to abide by its terms.
```

And delete the package current code of conduct if there was one.

9.1.2 Contributing guide

We have templates for issue, pull request and contributing guidelines that you can find [in this GitHub repository](#). There is also [a helper function to insert them into your repository](#).

You can tweak them a bit depending on your workflow and package. For example, make sure contributors have instructions in CONTRIBUTING.md for running local tests if not trivial. CONTRIBUTING.md can also contain some details about how you acknowledge contributions (see [this section](#)) and the roadmap of your package (cf [this example](#)).

We encourage you to direct feedback that is not a bug report or a feature request to [rOpenSci forum](#), after making sure you'd see such questions on the forum. Users can use the forum to ask questions about use and report their use cases, and you can subscribe to individual categories and tags to receive notifications about your package. Feel free to mention this in the docs of your package and/or the contributing guidelines/issue template. Please direct your users to tag posts with the package name.

You can use the `lintr` package's own bot, `lintr-bot`, via continuous integration, to get comments if a commit or PR deteriorates the code style of your package. See [this link for guidance](#).

9.1.3 Issue labelling

You can use labels such as “help wanted” and “good first issue” to help potential collaborators, including newbies, find your repo. Cf [GitHub article](#). You can also use the “Beginner” label. See [examples of beginner issues over all ropensci repos](#).

9.2 Working with collaborators

9.2.1 Onboarding collaborators

There's no general rOpenSci rule as to how you should onboard collaborators. You should increase their rights to the repo as you gain trust, and you should definitely acknowledge contributions (see [this section](#)).

You can ask a new collaborator to make PRs (see following section for assessing a PR locally, i.e. beyond CI checks) to dev/master and assess them before merging, and after a while let them push to master, although you might want to keep a system of PR reviews... even for yourself once you have team mates!

A possible model for onboarding collaborators is provided by Jim Hester in [his lintr repo](#).

If your problem is *recruiting* collaborators, you can post an open call like Jim Hester's [on Twitter](#), [GitHub](#), and as an rOpenSci package author, you can ask for help in rOpenSci slack and ask rOpenSci team for ideas for recruiting new collaborators.

9.2.2 Working with collaborators (including yourself)

You could implement the “[gitflow](#)” philosophy as explained by Amanda Dobbyn in [this blog post](#). In a nutshell,

- Keep master shippable as much as possible
- [Branches](#) are cheap. Use them extensively when developing features, testing out new ideas, fixing problems.

One particular aspect of working with collaborators is reviewing pull requests. Even if not adopting gitflow it might make sense for repo collaborators to make PRs and have them reviewed, and in general PRs by external developers will need to be assessed. Sometimes you'll be fine just reading the changes and trusting [Continuous integration](#). Sometimes you'll need more exploration and even extension of the PR in which case we recommend reading “[Explore and extend a pull request](#)” in [happy-gitwithr.com](#).

9.2.3 Be generous with attributions

If someone contributes to your repository consider adding them in DESCRIPTION, as contributor (“ctb”) for small contributions, author (“aut”) for bigger contributions. Traditionally when citing a package in a scientific publication only “aut” authors are listed, not “ctb” contributors; and on pkgdown websites only “aut” names are listed on the homepage, all authors being listed on the authors/ page.

At a minimum consider adding the name of contributors near the feature/bug fix line in [NEWS.md](#).

We recommend your being generous with such acknowledgements, because it is a nice thing to do and because it will make folks more likely to contribute again to your package or other repos of the organization.

As a reminder from [our packaging guidelines](#) if your package was reviewed and you feel that your reviewers have made a substantial contribution to the development of your package, you may list them in the Authors@R field with a Reviewer contributor type (“rev”), like so:

```
person("Bea", "Hernández", role = "rev",
comment = "Bea reviewed the package (v. X.X.XX) for rOpenSci, see <https://github.com/ropensci/
```

Only include reviewers after asking for their consent. Read more in [this blog post “Thanking Your Reviewers: Gratitude through Semantic Metadata”](#). Note that ‘rev’ will raise a CRAN NOTE unless the package is built using R v3.5. Make sure you use `roxygen2`’s latest CRAN version.

Please do not list editors as contributors. Your participation in and contribution to rOpenSci is thanks enough!

9.2.4 Welcoming collaborators to rOpenSci

If you give someone write permissions to the repository,

- please contact one of [the editors](#) so that this new contributor might get **invited to rOpenSci’s “ropensci” GitHub organization** (instead of being [outside collaborators](#))
- please contact rOpenSci community manager [Stefanie Butland](#) so that this new contributor might get **invited to rOpenSci Slack workspace**.

Chapter 10

Changing package maintainers

This chapter presents our guidance for taking over maintenance of a package.

10.1 Do you want to give up maintenance of your package?

We have a call for contributors section in our newsletter that comes out every two weeks. The section is called *Call For Contributors*. In that section we highlight packages looking for new maintainers. If you are looking to leave the role of maintainer of your package, get in touch with us and we can highlight your package in our newsletter. We've been very successful thus far, finding new maintainers for six out of six packages.

10.2 Do you want to take over maintenance of a package?

We have a call for contributors section in our newsletter that comes out every two weeks. The section is called *Call For Contributors*. In that section we highlight packages looking for new maintainers. If you are not subscribed to the newsletter already, it's a good idea to subscribe to get notified when there's a package looking for a new maintainer.

10.3 Taking over maintenance of a package

- Add yourself as the new maintainer in the DESCRIPTION file, with `role = c("aut", "cre")`, and make the former maintainer `aut` only.
- Make sure to change maintainer to your name anywhere else in the package, while retaining the former maintainer as an author (e.g, package level manual file, CONTRIBUTING.md, CITATION, etc.)
- The [Collaboration Guide](#) has guidance about adding new maintainers and collaborators
- Packages that have been archived or [orphaned](#) on CRAN don't need permission of the previous maintainer to be taken over on CRAN. In these cases do get in touch with us so we can offer any help as needed.
- If the package has not been archived by CRAN and there is a maintainer change, have the old maintainer email CRAN and put in writing who the new maintainer is. Make sure to mention that email about the maintainer change when you submit the first new version to CRAN. If the old maintainer is unreachable or will not send this email get in touch with rOpenSci staff.
- If the previous maintainer is reachable, scheduling a meeting will help you get the “lay of the land”

10.3.1 FAQ for new maintainers

- There are a few unresolved issues from the package that I don't know how to fix. Whom may I ask for help?

It depends; here's what to do in different scenarios:

- if the old maintainer can be contacted: reach out to them, and ask for help;
- rOpenSci slack: good for getting help on specific or general problems, the #general room is where many ask questions;
- rOpenSci discussion forum: this forum is a good option, feel free to ask any questions there;
- rOpenSci staff: feel free to get in touch with one of us via slack/email/pinging us on GitHub issues, we'll be happy to help;
- of course there's general R help too if that suits your needs: StackOverflow, Twitter #rstats, etc.

- How much can/should you change in the package?

For general help on changing code in a package, see the [Package evolution](#) section.

When thinking though this, there are many considerations.

How much time do you have to spend on the package? If you have very limited time, it'd be best to focus on the most critical tasks, whatever those are for the

package in question. If you have ample amount of time, your goals can be larger in scope.

How mature is the package? If the package is mature, many people likely have code that depends on the package's API (i.e., the exported functions, and their parameters). In addition, if there are packages that depend on your package on CRAN, then you need to check that whatever changes you make don't break those packages. The more mature the package is, the more careful you need to be about making changes, especially with the names of exported functions, their parameters, and the exact structure of what exported functions return. Changes can be more easily made that only affect internals of the package.

10.4 Tasks for rOpenSci staff

As an organization, rOpenSci is interested in making sure packages in our suite are available as long as they are useful to the community. As maintainers need to move on, we will in most cases try to get a new maintainer for each package. To these ends, the following tasks are the responsibility of rOpenSci staff.

- If a repository hasn't seen any activity (commits, issues, pull requests) in quite a long time it may simply be a mature package with little need for changes/etc., so take this into account.
- Current maintainer has not responded to issues/pull requests in many months, via any of emails, GitHub issues, or Slack messages:
 - Make contact and see what the situation is. They may say they'd like to step down as maintainer, in which case look for a new maintainer
- Current maintainer is completely missing/not responding
 - If this happens we will try to contact the maintainer for up to one month. However, if updating the package is urgent, we may use our admin access to make changes on their behalf.
- Put a call out in the "Call for Contributors" section of the rOpenSci newsletter for a new maintainer - get in touch with Scott for this or open an issue in the [newsletter repo](#)

Chapter 11

Releasing a package

Your package should have different versions over time: snapshots of a state of the package that you can release to CRAN for instance. These versions should be properly *numbered, released and described in a NEWS file*. More details below.

Note that you could streamline the process of updating NEWS and versioning your package by using [the fledge package](#).

11.1 Versioning

- We strongly recommend that rOpenSci packages use semantic versioning. A detailed explanation is available in the [description chapter](#).

11.2 Releasing

- Using `devtools::release()` will help you remember about more checks. See [this issue](#) for a more thorough checklist to go through when releasing a new package version.
- Git tag each release after every submission to CRAN. [more info](#)

11.3 News file

A NEWS file describing changes associated with each version makes it easier for users to see what's changing in the package and how it might impact their workflow. You

must add one for your package, and make it easy to read.

- It is mandatory to use a NEWS or NEWS.md file in the root of your package. We recommend using NEWS.md to make the file [more browsable](#).
- Please use our example [NEWS file](#) as a model. You can find a good NEWS file in the wild [in the taxize package repo](#) for instance.
- If you use NEWS, add it to .Rbuildignore, but not if you use NEWS.md
- Update the news file before every CRAN release, with a section with the package name, version and date of release, like (as seen in our example [NEWS file](#)):

```
foobar 0.2.0 (2016-04-01)
=====
```

- Under that header, put in sections as needed, including: NEW FEATURES, MINOR IMPROVEMENTS, BUG FIXES, DEPRECATED AND DEFUNCT, DOCUMENTATION FIXES and any special heading grouping a large number of changes. Under each header, list items as needed (as seen in our example [NEWS file](#)). For each item give a description of the new feature, improvement, bug fix, or deprecated function/feature. Link to any related GitHub issue like (#12). The (#12) will resolve on GitHub in Releases to a link to that issue in the repo.
- After you have added a git tag and pushed up to GitHub, add the news items for that tagged version to the Release notes of a release in your GitHub repo with a title like pkgname v0.1.0. See [GitHub docs about creating a release](#).
- New CRAN releases will be tweeted about automatically by [roknowtifier](#) and written about [in our biweekly newsletter](#) but see [next chapter about marketing](#) about how to inform more potential users about the release.
- For more guidance about the NEWS file we suggest reading the [tidyverse NEWS style guide](#).

Chapter 12

Marketing your package

We will help you promoting your package but here are some more things to keep in mind.

- If you hear of an use case of your package, please encourage its author to post the link to our [discussion forum in the Use Cases category](#), [for a tweet from rOpenSci](#) and [possible inclusion in the rOpenSci biweekly newsletter](#). We also recommend you to add a link to the use case in a “use cases in the wild” section of your README.
- When you release a new version of your package or release it to CRAN for the first time,
 - Make a pull request to [R Weekly](#) with a line about the release under the “New Releases” section (or “New Packages” for the first GitHub/CRAN release).
 - Tweet about it using the “#rstats” hashtag and tag rOpenSci! [Example](#).
 - Consider submitting a short post about the release to [rOpenSci tech notes](#). Contact Stefanie Butland, rOpenSci Community Manager, (e.g. via Slack or stefaniebutland@gmail.com). Refer to [the guidelines about contributing a blog post](#)).
 - Submit your package to lists of packages such as [CRAN Task Views](#), and [rOpenSci non-CRAN Task Views](#).
- If you choose to market your package by giving a talk about it at a meetup or conference (excellent idea!) read [this article of Jenny Bryan’s and Mara Averick’s](#).

Chapter 13

GitHub Grooming

rOpenSci packages are currently in their vast majority developed on GitHub. Here are a few tips to leverage the platform in a section about [making your repo more discoverable](#) and a section about [marketing your own GitHub account after going through peer review](#).

13.1 Make your repository more discoverable

13.1.1 GitHub repo topics

GitHub [repo topics](#) help browsing and searching GitHub repos, and are digested by [codemeta](#) for rOpenSci registry keywords.

We recommend:

- Adding “r”, “r-package” and “rstats” as topics to your package repo.
- Adding any other relevant topics to your package repo.

We might make suggestions to you after your package is onboarded.

13.1.2 GitHub linguist

[GitHub linguist](#) will assign a language for your repo based on the files it contains. Some packages containing a lot of C++ code might get classified as C++ rather than R packages, which is fine and shows the need for the “r”, “r-package” and “rstats” topics.

We recommend overriding GitHub linguist by adding or modifying a `.gitattributes` to your repo in two cases:

- If you store html files in non standard places (not in docs/, e.g. in vignettes/) use the documentation overrides. Add `*.html linguist-documentation=true` to `.gitattributes` ([Example in the wild](#))
- If your repo contains code you haven't authored, e.g. JavaScript code, add `inst/js/* linguist-vendored` to `.gitattributes` ([Example in the wild](#))

This way the language classification and statistics of your repository will more closely reflect the source code it contains, as well as making it more discoverable. Notably, if linguist does not correctly recognize your repo as containing mainly R code, your package won't appear in search results with the `language:R` filter. Similarly, your repo cannot be listed among the [trending R repos](#).

More info about GitHub linguist overrides [here](#).

13.2 Market your own account

- As the author of an onboarded package, you are now a member of rOpenSci's "ropensci" GitHub organization. By default, organization memberships are private; see [how to make it public in GitHub docs](#).
- Even after your package repo has been transferred to rOpenSci, you can [pin it under your own account](#).
- In general we recommend adding at least an avatar (which doesn't need to be your face!) and your name [to your GitHub profile](#).

Chapter 14

Package evolution - changing stuff in your package

This chapter presents our guidance for changing stuff in your package: changing parameter names, changing function names, deprecating functions.

This chapter was initially contributed as a tech note on rOpenSci website by [Scott Chamberlain](#); you can read the original version [here](#).

14.1 Philosophy of changes

Everyone's free to have their own opinion about how freely parameters/functions/etc. are changed in a library - rules about package changes are not enforced by CRAN or otherwise. Generally, as a library gets more mature, changes to user facing methods (i.e., exported functions in an R package) should become very rare. Libraries that are dependencies of many other libraries are likely to be more careful about changes, and should be.

14.2 Parameters: changing parameter names

Sometimes parameter names must be changed for clarity, or some other reason.

A possible approach is check if deprecated arguments are not missing, and stop providing a meaningful message.

```
foo_bar <- function(x, y) {  
  if (!missing(x)) {
```

```

      stop("use 'y' instead of 'x'")
    }
    y^2
  }

foo_bar(x = 5)
#> Error in foo_bar(x = 5) : use 'y' instead of 'x'

```

If you want to be more helpful, you could emit a warning but automatically take the necessary action:

```

foo_bar <- function(x, y) {
  if (!missing(x)) {
    warning("use 'y' instead of 'x'")
    y <- x
  }
  y^2
}

foo_bar(x = 5)
#> 25

```

Be aware of the parameter `...`. If your function has `...`, and you have already removed a parameter (lets call it `z`), a user may have older code that uses `z`. When they pass in `z`, it's not a parameter in the function definition, and will likely be silently ignored – not what you want. Instead, leave the argument around, throwing an error if it used.

14.3 Functions: changing function names

If you must change a function name, do it gradually, as with any other change in your package.

Let's say you have a function `foo`.

```
foo <- function(x) x + 1
```

However, you want to change the function name to `bar`.

Instead of simply changing the function name and `foo` no longer existing straight away, in the first version of the package where `bar` appears, make an alias like:

```
#' foo - add 1 to an input
#' @export
foo <- function(x) x + 1

#' @export
#' @rdname foo
bar <- foo
```

With the above solution, the user can use either `foo()` or `bar()` – either will do the same thing, as they are the same function.

It's also useful to have a message but then you'll only want to throw that message when they use the old function, e.g.,

```
#' foo - add 1 to an input
#' @export
foo <- function(x) {
  warning("please use bar() instead of foo()", call. = FALSE)
  bar(x)
}

#' @export
#' @rdname foo
bar <- function(x) x + 1
```

After users have used the package version for a while (with both `foo` and `bar`), in the next version you can remove the old function name (`foo`), and only have `bar`.

```
#' bar - add 1 to an input
#' @export
bar <- function(x) x + 1
```

14.4 Functions: deprecate & defunct

To remove a function from a package (let's say your package name is `helloworld`), you can use the following protocol:

- Mark the function as deprecated in package version `x` (e.g., `v0.2.0`)

In the function itself, use `.Deprecated()` to point to the replacement function:

```
foo <- function() {
  .Deprecated("bar")
}
```

There's options in `.Deprecated` for specifying a new function name, as well as a new package name, which makes sense when moving functions into different packages.

The message that's given by `.Deprecated` is a warning, so can be suppressed by users with `suppressWarnings()` if desired.

Make a man page for deprecated functions like:

```
#' Deprecated functions in helloworld
#'
#' These functions still work but will be removed (defunct) in the next version.
#'
#' \itemize{
#' \item \code{\link{foo}}: This function is deprecated, and will
#' be removed in the next version of this package.
#' }
#'
#' @name helloworld-deprecated
NULL
```

This creates a man page that users can access like `?`helloworld-deprecated`` and they'll see in the documentation index. Add any functions to this page as needed, and take away as a function moves to defunct (see below).

- In the next version (v0.3.0) you can make the function defunct (that is, completely gone from the package, except for a man page with a note about it).

In the function itself, use `.Defunct()` like:

```
foo <- function() {
  .Defunct("bar")
}
```

Note that the message in `.Defunct` is an error so that the function stops whereas `.Deprecated` uses a warning that let the function proceed.

In addition, it's good to add `...` to all defunct functions so that if users pass in any parameters they'll get the same defunct message instead of a `unused argument` message, so like:


```
foo <- function(...) {  
  .Defunct("bar")  
}
```

Without ... gives:

```
foo(x = 5)  
#> Error in foo(x = 5) : unused argument (x = 5)
```

And with ... gives:

```
foo(x = 5)  
#> Error: 'foo' has been removed from this package
```

Make a man page for defunct functions like:

```
#' Defunct functions in helloworld  
#'  
#' These functions are gone, no longer available.  
#'  
#' \itemize{  
#'   \item \code{\link{foo}}: This function is defunct.  
#' }  
#'  
#' @name helloworld-defunct  
NULL
```

This creates a man page that users can access like `?`helloworld-defunct`` and they'll see in the documentation index. Add any functions to this page as needed. You'll likely want to keep this man page indefinitely.

Chapter 15

Contributing Guide

This chapter outlines how you can contribute to the rOpenSci project as a user or developer.

So you want to contribute to rOpenSci? Fantastic! First of all, maybe contributing code or documentation to a package is not the (only) way you'll want to get involved. Check out our [community page](#) to find out all the ways to participate in the project, from reading about our packages to volunteering to review them.

We strive to make contributing to our suite a constructive and positive experience and we welcome participation that adheres to [our code of conduct](#).

If you wish to contribute to this guide itself, please report any suggestions via [this GitHub repository](#).

15.1 Why contribute to rOpenSci packages?

In general, [as explained by Kara Woo in her talk at the CascadiaR conference](#), contributing to R packages allows you to make things work the way you want (by adding some functionality to your favorite package), can lead to opportunities and allows you to learn about package development.

Specifically at rOpenSci, we strive to make contributing a good experience. This is embedded in [our mission](#): we are creating social infrastructure through a welcoming and diverse community and building capacity of software users and developers and fostering a sense of pride in their work.

15.2 Non code contributions

15.2.1 Reporting use cases for our packages or guidelines

It's valuable to both users and developers of a package to see how it has been used "in the wild". If you see a use case of one of our packages, please add it to our [public forum in the Use Cases category](#). We've created a template to help. We'll tweet about it, and might add it to the [rOpenSci biweekly newsletter](#). You might also let the package author know by opening an issue in the GitHub repository for that package, perhaps suggesting they create a "use cases in the wild" section in the README, and maybe even tag them in a tweet about the use case. This goes a long way to encouraging people to keep up development knowing there are others who appreciate and build on their work. See examples of README's listing use cases in the wild [here](#) and [here](#)

We would also love to hear about examples in which rOpenSci resources or guidelines have been used. Have you implemented better security practices, like signing your commits, based on recommendations in a [Community Call](#), or used our standards/checklists etc. when reviewing software elsewhere? Do tell people (e.g. journal editors, students, internal code review group, users) that they came from rOpenSci, and tell us in our [public forum](#), or [privately by email](#).

15.2.2 Reporting issues or Requesting features

If you already have a package in mind, head to its issue tracker to report a bug or a feature request you might have. E.g. if you have a feature request for `magick`, the place to fill it is <https://github.com/ropensci/magick/issues>

When reporting a bug try to include a reproducible example ("[reprex](#)") to help the package author help you.

15.2.3 Asking other questions

You can use our [discussion forum](#) to ask questions related to the usage of our packages, even when you don't know yet which of our packages could help you.

For more guidance about where to ask questions related to rOpenSci packages, refer to Scott Chamberlain's talk in this [community call](#) or the [corresponding slidedeck](#).

15.3 Code contributions

15.3.1 Prerequisites for package development

Before contributing to one of our packages, you might want to read a bit more about package development in general and our guidelines.

15.3.1.1 Learning about package development

15.3.1.1.1 Tutorials

- Hilary Parker's famous blog post [Writing an R package from scratch](#) or its updated version by Tomas Westlake that shows how to do the same more efficiently using `usethis`.
- [this workflow description](#) by Emil Hvitfeldt
- [This pictorial](#) by Matthew J Denny

15.3.1.1.2 Books

- Hadley Wickham and Jenny Bryan's *R packages* book
- *Writing R extensions*, the official CRAN guide
- *Mastering Software Development in R* by Roger D. Peng, Sean Kross, and Brooke Anderson
- *Advanced R* by Hadley Wickham
- *Testing R code* by Richard Cotton

15.3.1.1.3 MOOCs There is a [Coursera specialization](#) corresponding to the book by Roger Peng, Sean Kross and Brooke Anderson, with a course specifically about R packages.

15.3.1.2 Reading about our guidelines

See the whole first section of this book: [Building Your Package](#)

15.3.2 Finding where to contribute code or documentation

Our packages are developed on GitHub. We have two organizations:

- <https://github.com/ropensci> for more mature packages, including some developed by rOpenSci staff and some developed by community members whose packages have gone through [software peer review](#)
- <https://github.com/ropenscilabs> for experiments and packages that are not ready for release yet.

If you already know what package you'd like to contribute to, have a look at its issue tracker and comment in one of the issues to ask the maintainer whether they'd be interested in your help. E.g. if you like `taxize`, the place to look is <https://github.com/ropensci/taxize/issues>

If you're not sure which package you'd like to contribute to, you can start by browsing [our packages page](#). To browse issues targeted at beginners you could use an advanced GitHub search such as [this one](#) that gets all issues from “ropensci” or “ropenscilabs” organizations that are open and labelled “beginner”.

Still not sure how you can contribute? [Tell us about your expertise and interests](#) and we'll try to match you with a package that could use your help.

Appendix A

NEWS

A.1 dev

A.2 0.4.0

- 2020-04-02, give less confusing code of conduct guidance: the reviewed packages' COC is rOpenSci COC (@Bisaloo, @cboettig, #240)
- 2020-03-27, add section on Ethics, Data Privacy and Human Subjects Research to Policies chapter
- 2020-03-12, mention GitHub Actions as a CI provider.
- 2020-02-24, add guide for inviting a guest editor.
- 2020-02-14, add mentions of the ropensci-books GitHub organisation and associated subdomain.
- 2020-02-10, add field and laboratory reproducibility tools as a category in scope.
- 2020-02-10, add more guidance about secrets and package development in the security chapter.
- 2020-02-06, add guidance about Bioconductor dependencies (#246).
- 2020-02-06, add package logo guidance (#217).
- 2020-02-06, add one CRAN gotcha: single quoting software names(#245, @aaronwolen)
- 2020-02-06, improve guidance regarding the replacement of “older” pkgdown website links and source (#241, @cboettig)

- 2020-02-06, rephrase the EiC role (#244).
- 2020-02-06, remove the recommendation to add rOpenSci footer (<https://github.com/ropensci/software-review-meta/issues/79>).
- 2020-02-06, remove the recommendation to add a review mention to DESCRIPTION but recommends mentioning the package version when reviewers are added as “rev” authors.
- 2020-01-30, slightly changes the advice on documentation re-use: add a con; mention @includeRmd and @example; correct the location of Rmd fragments (#230).
- 2020-01-30, add more guidance for the editor in charge of a dev guide release (#196, #205).
- 2020-01-22, add guidance in the editor guide about not transferred repositories.
- 2020-01-22, clarify forum guidance (for use cases and in general).
- 2020-01-22, mention an approach for pre-computing vignettes so that the pkg-down website might get build on rOpenSci docs server.
- 2020-01-22, document the use of mathjax with rotemplate (@Bisaloo, #199).
- 2020-01-20, add guidance for off-thread interaction and COIs (@noamross, #197).
- 2020-01-20, add advice on specifying dependency minimum versions (@karthik, @annakrystalli, #185).
- 2020-01-09, start using GitHub actions instead of Travis for deployment.
- -2019-12-11, add note in Documentation sub-section of Packaging Guide section about referencing the new R6 support in roxygen2 (ropensci/dev_guide#189)
- 2019-12-11, add new CRAN gotcha about having ‘in R’ or ‘with R’ in your package title (@bisaloo, ropensci/dev_guide#221)

A.3 0.3.0

- 2019-10-03, include in the approval template that maintainers should include link to the docs.ropensci.org/pkg site (ropensci/dev_guide#191)
- 2019-09-26, add instructions for handling editors to nominate packages for blog posts (ropensci/dev_guide#180)

- 2019-09-26, add chapter on changing package maintainers (ropensci/dev_guide#128) (ropensci/dev_guide#194)
- 2019-09-26, update Slack room to use for editors (ropensci/dev_guide#193)
- 2019-09-11, update instructions in README for rendering the book locally (ropensci/dev_guide#192)
- 2019-08-05, update JOSS submission instructions (ropensci/dev_guide#187)
- 2019-07-22, break “reproducibility” category in policies into component parts. (ropensci/software-review-meta#81)
- 2019-06-18, add link to rOpenSci community call “Security for R” to security chapter.
- 2019-06-17, fix formatting of Appendices B-D in the pdf version of the book (bug report by @IndrajeetPatil, #179)
- 2019-06-17, add suggestion to use R Markdown hunks approach when the README and the vignette share content. (ropensci/dev_guide#161)
- 2019-06-17, add mention of central building of documentation websites.
- 2019-06-13, add explanations of CRAN checks. (ropensci/dev_guide#177)
- 2019-06-13, add mentions of the `rodev` helper functions where relevant.
- 2019-06-13, add recommendation about using `cat` for `str.*()` methods. RStudio assumes that `str` uses `cat`, if not when loading an R object the `str` prints to the console in RStudio and doesn’t show the correct object structure in the properties. ([@mattfidler] (<https://github.com/mattfidler/>) #178)
- 2019-06-12, add more details about git flow.
- 2019-06-12, remove recommendation about `roxygen2` dev version since the latest stable version has what is needed. (@bisaloo, #165)
- 2019-06-11, add mention of `usethis` functions for adding testing or vignette infrastructure in the part about dependencies in the package building guide.
- 2019-06-10, use the new URL for the dev guide, <https://devguide.ropensci.org/>
- 2019-05-27, add more info about the importance of the repo being recognized as a R package by linguist (@bisaloo, #172)
- 2019-05-22, update all links eligible to HTTPS and update links to the latest versions of Hadley Wickham and Jenny Bryan’s books (@bisaloo, #167)
- 2019-05-15, add book release guidance for editors. (ropensci/dev_guide#152)

A.4 0.2.0

- 2019-05-23, add CRAN gotcha: in the Description field of your DESCRIPTION file, enclose URLs in angle brackets.
- 2019-05-13, add more content to the chapter about contributing.
- 2019-05-13, add more precise instructions about blog posts to approval template for editors.
- 2019-05-13, add policies allowing using either <- or = within a package as long as the whole package is consistent.
- 2019-05-13, add request for people to tell us if they use our standards/checklists when reviewing software elsewhere.
- 2019-04-29, add requirement and advice on testing packages using devel and oldrel R versions on Travis.
- 2019-04-23, add a sentence about why being generous with attributions and more info about ctb vs aut.
- 2019-04-23, add link to Daniel Nüst's notes about migration from XML to xml2.
- 2019-04-22, add use of rOpenSci forum to maintenance section.
- 2019-04-22, ask reviewer for consent to be added to DESCRIPTION in review template.
- 2019-04-22, use a darker blue for links (feedback by [@kwstat](#), #138).
- 2019-04-22, add book cover.
- 2019-04-08, improve formatting and link text in README ([@katrinleinweber](#), #137)
- 2019-03-25, add favicon ([@wlandau](#), #136).
- 2019-03-21, improve Travis CI guidance, including link to examples. ([@mpadge](#), #135)
- 2019-02-07, simplify code examples in Package Evolution section (maintenance_evolution.Rmd file) ([@hadley](#), #129).
- 2019-02-07, added a PDF file to export (request by [@IndrajeetPatil](#), #131).

A.5 0.1.5

- 2019-02-01, created a .zenodo.json to explicitly set editors as authors.

A.6 First release 0.1.0

- 2019-01-23, add details about requirements for packages running on all major platforms and added new section to package categories.
- 2019-01-22, add details to the guide for authors about the development stage at which to submit a package.
- 2018-12-21, inclusion of an explicit policy for conflict of interest (for reviewers and editors).
- 2018-12-18, added more guidance for editor on how to look for reviewers.
- 2018-12-04, onboarding was renamed Software Peer Review.

A.7 place-holder 0.0.1

- Added a NEWS.md file to track changes to the book.

Appendix B

Review template

B.1 Package Review

Please check off boxes as applicable, and elaborate in comments below. Your review is not limited to these topics, as described in the reviewer guide

- **Briefly describe any working relationship you have (had) with the package authors.**

☐ As the reviewer I confirm that there are no [conflicts of interest](#) for me to review this work (If you are unsure whether you are in conflict, please speak to your editor *before* starting your review).

B.1.0.1 Documentation

The package includes all the following forms of documentation:

- ☐ **A statement of need** clearly stating problems the software is designed to solve and its target audience in README
- ☐ **Installation instructions:** for the development version of package and any non-standard dependencies in README
- ☐ **Vignette(s)** demonstrating major functionality that runs successfully locally
- ☐ **Function Documentation:** for all exported functions in R help
- ☐ **Examples** for all exported functions in R Help that run successfully locally

- ☐ **Community guidelines** including contribution guidelines in the README or CONTRIBUTING, and DESCRIPTION with URL, BugReports and Maintainer (which may be autogenerated via Authors@R).

B.1.0.1.1 For packages co-submitting to JOSS

- ☐ The package has an **obvious research application** according to [JOSS's definition](#)

The package contains a paper .md matching [JOSS's requirements](#) with:

- ☐ **A short summary** describing the high-level functionality of the software
- ☐ **Authors:** A list of authors with their affiliations
- ☐ **A statement of need** clearly stating problems the software is designed to solve and its target audience.
- ☐ **References:** with DOIs for all those that have one (e.g. papers, datasets, software).

B.1.0.2 Functionality

- ☐ **Installation:** Installation succeeds as documented.
- ☐ **Functionality:** Any functional claims of the software been confirmed.
- ☐ **Performance:** Any performance claims of the software been confirmed.
- ☐ **Automated tests:** Unit tests cover essential functions of the package and a reasonable range of inputs and conditions. All tests pass on the local machine.
- ☐ **Packaging guidelines:** The package conforms to the rOpenSci packaging guidelines

B.1.0.3 Final approval (post-review)

- ☐ **The author has responded to my review and made changes to my satisfaction. I recommend approving this package.**

Estimated hours spent reviewing:

- ☐ Should the author(s) deem it appropriate, I agree to be acknowledged as a package reviewer ("rev" role) in the package DESCRIPTION file.

B.1.1 Review Comments

Appendix C

Editor's template

C.0.1 Editor checks:

- ☐ **Fit:** The package meets criteria for [fit](#) and [overlap](#)
- ☐ **Automated tests:** Package has a testing suite and is tested via Travis-CI or another CI service.
- ☐ **License:** The package has a CRAN or OSI accepted license
- ☐ **Repository:** The repository link resolves correctly
- ☐ **Archive** (JOSS only, may be post-review): The repository DOI resolves correctly
- ☐ **Version** (JOSS only, may be post-review): Does the release version given match the GitHub release (v1.0.0)?

C.0.1.1 Editor comments

Reviewers: Due date:

Appendix D

Review request template

Editors may make use of the e-mail template below in recruiting reviewers.

Dear [REVIEWER]

Hi, this is [EDITOR]. [FRIENDLY BANTER]. I'm writing to ask if you would be willing to review a package for rOpenSci. As you probably know, rOpenSci conducts peer review of R packages contributed to our collection in a manner similar to journals.

The package, [PACKAGE] by [AUTHOR(S)], does [FUNCTION]. You can find it on GitHub here: [REPO LINK]. We conduct our open review process via GitHub as well, here: [ONBOARDING ISSUE]

If you accept, note that we ask reviewers to complete reviews in three weeks. (We've found it takes a similar amount of time to review a package as an academic paper.)

Our [reviewers guide](#) details what we look for in a package review, and includes links to example reviews. Our standards are detailed in our [packaging guide](#), and we provide reviewer [template](#) for you to use. Please make sure you do not have a [conflict of interest](#) preventing you from reviewing this package. If you have questions or feedback, feel free to ask me or post to the [rOpenSci forum](#).

{IF APPLICABLE: The authors have also chosen to jointly submit their package to the Journal of Open Source Software, so this package includes a short paper .md manuscript describing the software that we ask you include in your review.}

Are you able to review? If you can not, suggestions for alternate reviewers are always helpful. If I don't hear from you within a week, I will assume you are unable to review at this time.

Thank you for your time.

Sincerely,

[EDITOR]

Appendix E

Approval comment template

Approved! Thanks <author(s) GitHub username(s)> for submitting and <reviewers' GitHub usernames> for your reviews! <optional: smiling cat emoji à la Scott>

To-dos: - [] Transfer the repo to rOpenSci's "ropensci" GitHub organization under "Settings" in your repo. I have invited you to a team that should allow you to do so. You'll be made admin once you do. - [] Fix all links to the GitHub repo to point to the repo under the ropensci organization. - [] If you already had a pkgdown website **and are ok relying only on rOpenSci central docs building and branding**, * deactivate the automatic deployment you might have set up * remove styling tweaks from your pkgdown config but keep that config file * replace the whole current pkgdown website with a [redirecting page](#) * replace your package docs URL with https://docs.ropensci.org/package_name * In addition, in your DESCRIPTION file, include the docs link in the URL field alongside the link to the GitHub repository, e.g.: URL: <https://docs.ropensci.org/foobar> (website) <https://github.com/ropensci/foobar> - [] Fix any links in badges for CI and coverage to point to the ropensci URL. We no longer transfer Appveyor projects to ropensci Appveyor account so after transfer of your repo to rOpenSci's "ropensci" GitHub organization the badge should be [!AppVeyor Build Status](<https://ci.appveyor.com/api/projects/status/github/ropensci/pkgname?branch=master&svg=true>) - [] We're starting to roll out software metadata files to all ropensci packages via the Codemeta initiative, see <https://github.com/ropensci/codemeta/#codemeta> for how to include it in your package, after installing the package - should be easy as running `codemeta::write_codemeta()` in the root of your package. - [] Activate Zenodo watching the repo - [] Tag and create a release so as to create a Zenodo version and DOI - [] Submit to JOSS at <https://joss.theoj.org/papers/new>, using the rOpenSci GitHub repo URL. When a JOSS "PRE REVIEW" issue is generated for your paper, add the comment: This package has been reviewed by rOpenSci: <https://LINK.TO/THE/REVIEW/ISSUE>, @ropensci/editors

Should you want to acknowledge your reviewers in your package DESCRIPTION, you can do so by making them "rev"-type contributors in the Authors@R field (with their consent). More info on this [here](#).

Welcome aboard! We'd love to host a post about your package - either a [short introduction to it with an example](#) for a technical audience or [a longer post with some narrative about its development or something you learned, and an example of its use](#) for a broader readership. If you are interested, consult [the blog guide](#), and tag ? in your reply. She will get in touch about timing and can answer any questions.

We've put together an online book with our best practice and tips, [this chapter](#) starts the 3d section that's about guidance for after onboarding. Please tell us what could be improved, the corresponding repo is [here](#).

Appendix F

NEWS template

```
foobar 0.2.0 (2016-04-01)
=====

### NEW FEATURES

    * New function added `do_things()` to do things (#5)

### MINOR IMPROVEMENTS

    * Improved documentation for `things()` (#4)

### BUG FIXES

    * Fix parsing bug in `stuff()` (#3)

### DEPRECATED AND DEFUNCT

    * `hello_world()` now deprecated and will be removed in a
      future version, use `hello_mars()`

### DOCUMENTATION FIXES

    * Clarified the role of `hello_mars()` vs. `goodbye_mars()`

### (a special: any heading grouping a large number of changes under one thing)

    * blablabla.
```

```
foobar 0.1.0 (2016-01-01)
```

```
=====
```

```
### NEW FEATURES
```

```
  * released to CRAN
```

Appendix G

Book release guidance

G.1 Release book version

G.1.1 Repo maintenance between releases

- ☐ Look at the issue tracker for [the dev guide](#) and for [software review meta](#) for changes still to be made in the dev guide. Assign dev guide issues to milestones corresponding to versions, either the next one or the one after that, e.g. [version 0.3.0](#). Encourage PRs, have them reviewed.

G.1.2 1 month prior to release

- ☐ Remind editors to open issues/PRs for items they want to see in the next version.
- ☐ Ask editors for any feedback you need from them before release.
- ☐ For each contribution/change make sure the NEWS in Appendix.Rmd were updated.
- ☐ Plan a date for release in communication with @stefaniebutland who will give you a date for publishing a blog post / tech note.

G.1.3 2 weeks prior to release

- ☐ Draft a blog post / tech note about the release with enough advance for editors and then Stef to review it (2 weeks). [Example](#), [General blog post instructions](#), [specific instructions for release posts](#).
- ☐ Make a PR from the dev branch to the master branch, ping editors on GitHub and Slack. Mention the blog post draft in a comment on this PR.

G.1.4 Release

- ☐ Check URLs using [the corresponding script](#).
- ☐ [Spell check](#). Update the [WORDLIST](#) as necessary.
- ☐ Squash and merge the PR from dev to master.
- ☐ Finish your blog post / tech note PR. Underline the most important aspects to be highlighted in tweets as part of the PR discussion.

Appendix H

How to set a redirect

Replace the content of the current website with

```
<html>
<head>
<meta http-equiv="refresh" content="0;URL=https://docs.ropensci.org/<pkgname>/" />
<script language="javascript">
  window.location.href = "https://docs.ropensci.org/<pkgname>"
</script>
</head>
</html>
```


Bibliography