

# Creating and Maintaining R Packages

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## Resources

The excellent book *R Packages* by Hadley Wickham:  
[r-pkgs.had.co.nz](http://r-pkgs.had.co.nz)

R Manual - Writing R Extensions:  
[cran.r-project.org/doc/manuals/r-release/R-exts.html](http://cran.r-project.org/doc/manuals/r-release/R-exts.html)

The devtools package

## Steps to create an R package

1. Decide the scope of the package.
2. Collect and clean up all the relevant scripts.
3. Create a new project in R Studio (or use `package.skeleton()` if you don't like R Studio).
4. *Write documentation!*
5. DESCRIPTION and NAMESPACE files (or use roxygen2).
6. *Unit tests!*
7. Deploy the package via Github
8. *Maintain the package!*

## Useful tools

- ▶ R Studio
- ▶ R CMD check
- ▶ The devtools, roxygen2 and testthat packages
- ▶ git and Github
- ▶ Continuous Integration (C.I.)

# How to publish your package

<http://r-pkgs.had.co.nz/release.html>

1. Github (private repo)
2. Github (public repo)
3. CRAN
4. Bioconductor

Which option should I choose?

# CRAN requirements

<https://cran.r-project.org/web/packages/policies.html>

- ▶ R CMD check
- ▶ Maintainers has valid email address
- ▶ License!
- ▶ Works across multiple platforms (Windows, Unix, Mac)

# Bioconductor additional requirements

<https://bioconductor.org/developers/package-guidelines/>

- ▶ R CMD BiocCheck
- ▶ Vignette
- ▶ Reuse existing Bioconductor infrastructure
- ▶ Pass human review