



Developing R/Bioconductor packages for bioinformatics

Physalia course 2023

Instructor: Jacques Serizay

Overall goals

Leverage `Bioconductor` principles of interoperability (a.k.a "do-not-reinvent-the-wheel!")

Write sets of interconnected functions for genomic data

Document and test functions

Manage package dependencies

Manage package versions

Manage package continuous integration

Build a dedicated website for your package

Submitting/releasing/maintaining your package

Disseminating your package (publish it!)

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HAVE FUN!

Organizational notes

<https://github.com/js2264/Bioc-workshop>

Ask questions or use chat! Raise hand in Zoom (Participants).

Please use video, and mute microphone when not in use.

Write comments and questions in the dedicated Slack channel.

Please be patient with technical issues (network, Zoom, etc...).

Formal lectures:

Key concepts, theory (~1-2h).

Practical examples / demonstration:

Translate the theory into a real-life `R/Bioconductor` package (~1-2h)

Homeworks:

During the rest of the daily sessions, you will work by yourself, following guided exercises to practice your package development skills. Hints and solution are provided for each exercise. The exercises will mainly focus on specific concepts introduced earlier that day but also build up throughout the week to reach a comprehensive view of package development.

Office hours:

During the last hour of the day, I will be available for 1-to-1 or group meetings to answer questions/give advices.

This is the first edition of this course, and I do appreciate any feedback!!

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2. *Developing R/Bioconductor packages for bioinformatics*
3. *Developing R/Bioconductor packages for bioinformatics*

Why bother developing a package?

Re-usability:

Tired of copying-pasting your functions?



David Robinson

@drob · [Follow](#)



"I wish I'd left this code across scattered .R files instead of combining it into a package" said no one ever [#rstats](#) [r-pkgs.had.co.nz](#)

3:17 PM · Jun 19, 2015



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- Functionalities: Implement new ways of wrangling the data / analyzing it

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BECAUSE IT'S FUN!

Why bother developing a **BIOCONDUCTOR** package?

Why not a CRAN package?

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Who are your friends? Do you like them? Do you want to help them?

Because you are already using Bioconductor ecosystem?