

Laboratório de Biologia Computacional e Molecular

Centro de Biotecnologia da UFRGS Universidade Federal do Rio Grande do Sul



R para Ciências da Vida (BCM13065) Aula 4

PPGBCM - UFRGS

Diego Bonatto 2024/2

1. CRAN (Comprehensive R Archive Network)

Descrição: O principal repositório oficial para pacotes R. Ele garante que os pacotes estejam bem documentados e sejam amplamente testados antes de serem disponibilizados.

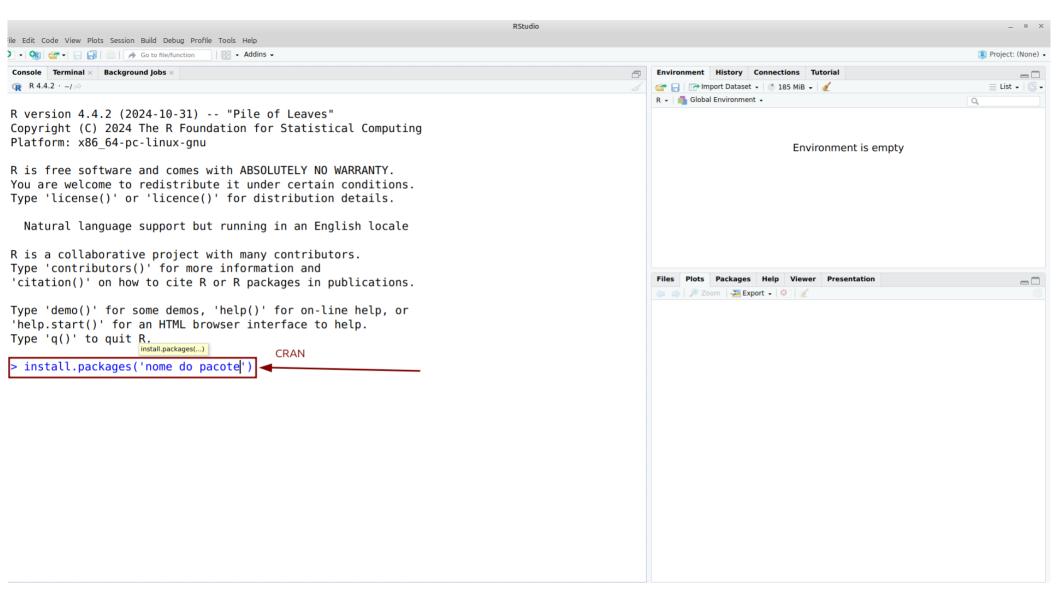
URL: https://cran.r-project.org

Características:

Extensa biblioteca de pacotes para diferentes áreas (estatística, biologia, machine learning, etc.).

Atualizado regularmente.

Suporte para pacotes compatíveis com múltiplas plataformas (Windows, Mac, Linux).



2. Bioconductor

Descrição: Focado em pacotes para análise de dados genômicos e biológicos.

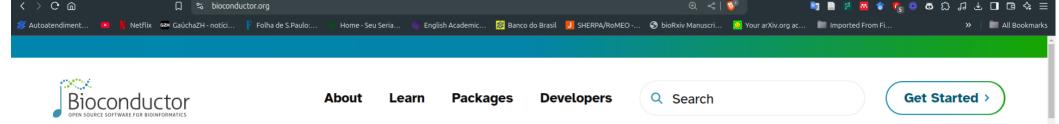
URL: https://www.bioconductor.org

Características:

Grande suporte para bioinformática e ciências da vida.

Inclui pacotes para análise de sequenciamento de RNA, genomas e estudos de associação genômica.

Requer instalação especial usando o R.



Open source software for Bioinformatics

The Bioconductor project aims to develop and share open source software for precise and repeatable analysis of biological data.

We foster an inclusive and collaborative community of developers and data scientists.

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Get started

1. Install R

The current release of Bioconductor is version 3.20; it works with R version 4.4.0. Users of older R and Bioconductor must update their installation to take advantage of new features and to access packages that have been added to Bioconductor since the last release.

The development version of Bioconductor is version 3.21; it works with R version 4.5.0. More recent 'devel' versions of R (if available) will be supported during the next Bioconductor release cycle.

- Download the most recent version of R. The R FAQs and the R Installation and Administration Manual contain detailed instructions for installing R on various platforms (Linux, OS X, and Windows being the main ones).
- Start the R program; on Windows and OS X, this will usually mean double-clicking on the R application, on UNIX-like systems, type "R" at a shell prompt.

2. Get the latest version of Bioconductor

Once R has been installed, get the latest version of Bioconductor by starting R and entering the following commands.

It may be possible to change the Bioconductor version of an existing installation; see the 'Changing version' section of the BiocManager vignette.

Details, including instructions to <u>install additional packages</u> and to <u>update</u>, <u>find</u>, and <u>troubleshoot</u> are provided below. A <u>devel</u> version of Bioconductor is available. There are good <u>reasons for using **BiocManager::install()**</u> for managing Bioconductor resources.

```
if (!require("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(version = "3.20")
```

```
Step 2
Get Bioconductor
```

2.2 Installing *BiocManager*

Use standard R installation procedures to install the BiocManager package. This command is requried only once per R installation.

install.packages("BiocManager", repos = "https://cloud.r-project.org")

2.3 Installing *Bioconductor*, *CRAN*, or GitHub packages

Install Bioconductor (or CRAN) packages with

BiocManager::install(c("GenomicRanges", "Organism.dplyr"))

Installed packages can be updated to their current version with

BiocManager::install()

2.4 Previous releases

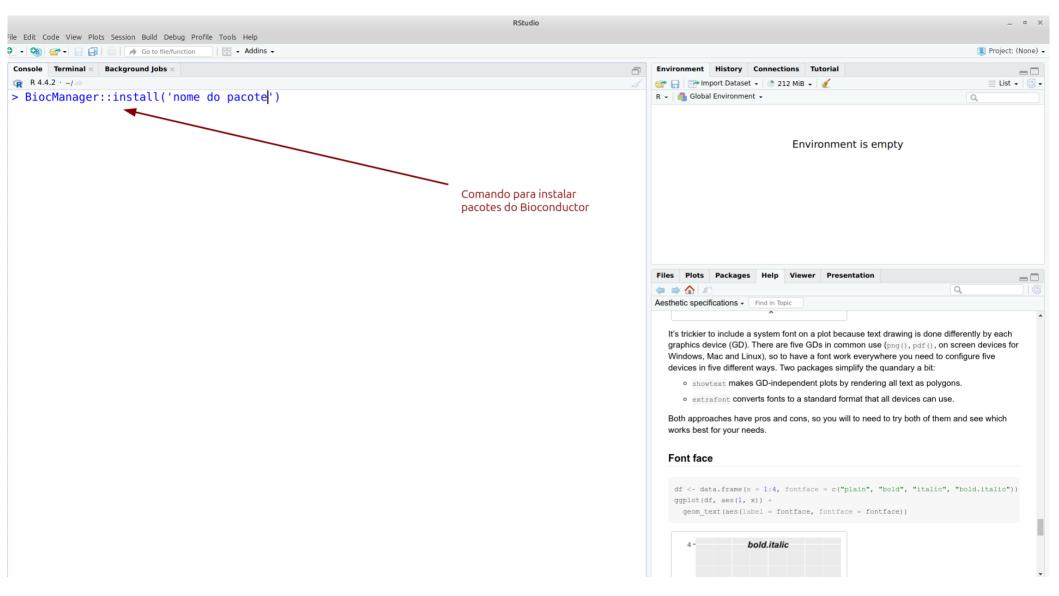
To install CRAN package versions consistent with previous releases of Bioconductor, use the BiocArchive package. BiocArchive enables contemporary installations of CRAN packages with out-of-date *Bioconductor* releases using Posit Public Package Manager.

2.5 Version and validity of installations

Use version() to discover the version of *Bioconductor* currently in use.

BiocManager::version()

Bioconductor packages work best when they are all from the same release. Use valid() to identify packages that are out-of-date or from unexpected versions.



Vinhetas de pacotes do R

As vinhetas do R são documentos incluídos em pacotes que fornecem tutoriais ou exemplos detalhados sobre como usar o pacote e suas funções. Elas servem como guias práticos e são ideais para aprender o propósito e a aplicação de um pacote específico.

Características Principais das Vinhetas:

Formato e Estilo:

- Geralmente escritas em R Markdown ou Sweave (R + LaTeX).
- Combinam explicações teóricas, exemplos de código e saídas dos resultados.

Objetivo:

- Introduzir o usuário às principais funcionalidades de um pacote.
- Explicar aplicações específicas ou fluxos de trabalho.
- Fornecer contextos práticos para as ferramentas oferecidas pelo pacote.

Acessibilidade:

- Disponíveis localmente após a instalação do pacote.
- Frequentemente publicadas online pelos desenvolvedores no CRAN, GitHub ou em outras plataformas.

Installing and Managing *Bioconductor*Packages

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27 August 2024

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3. GitHub

Descrição: Embora não seja um repositório oficial, muitos desenvolvedores disponibilizam pacotes no GitHub antes de submetêlos ao CRAN ou Bioconductor.

URL: https://github.com

Características:

- Acesso a pacotes em desenvolvimento ou experimentais.
- Permite interação direta com os desenvolvedores.
- Instalação por meio do pacote devtools ou remotes.

{ggstatsplot}: {ggplot2} Based Plots with Statistical Details

Status	Usage	Miscellaneous
R-CMD-check passing	downloads 570K	→ codecov 100%
lifecycle maturing	downloads 686/day	JOSS 10.21105/joss.03167

Raison d'être

"What is to be sought in designs for the display of information is the clear portrayal of complexity. Not the complication of the simple; rather ... the revelation of the complex." - Edward R. Tufte

<code>[ggstatsplot]</code> is an extension of <code>[ggplot2]</code> package for creating graphics with details from statistical tests included in the information-rich plots themselves. In a typical exploratory data analysis workflow, data visualization and statistical modeling are two different phases: visualization informs modeling, and modeling in its turn can suggest a different visualization method, and so on and so forth. The central idea of <code>ggstatsplot</code> is simple: combine these two phases into one in the form of graphics with statistical details, which makes data exploration simpler and faster.



Installation

Туре

Command

4. R-Forge

Descrição: Um repositório usado para o desenvolvimento colaborativo de pacotes e projetos R.

URL: https://r-forge.r-project.org

Características:

- Permite o teste e a distribuição de pacotes em desenvolvimento.
- Menos usado atualmente em comparação com o GitHub.

Search

What are R and R-Forge?

R is `GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the R-project homepage for further information.

R-Forge offers a central platform for the development of R packages, R-related software and further projects. It is based on FusionForge offering easy access to the best in SVN, daily built and checked packages, mailing lists, bug tracking, message boards/forums, site hosting, permanent file archival, full backups, and total web-based administration.

A Platform for the Whole R Community

In order to get the most out of R-Forge you'll need to register as a site user and then login. This will allow you to participate fully in all we have to offer, e.g., you may register your project. Of course, you may also browse the site without registration, but will only have limited access to some features. For details see the documentation.

Documentation

- Short Introduction: Stefan Theußl and Achim Zeileis. Collaborative software development using R-Forge. The R Journal, 1(1):9-14, May 2009. URL http://journal.R-project.org/ [bib] [pdf] [local copy](Official R-Forge citation)
- User's Manual: [pdf] (Detailed technical documentation)

If you experience any problems or need help you can submit a support request to the R-Forge team or write an email to R-Forge@R-Project.org.

Thanks... and enjoy the site.

Latest News

ViewVC Repository browsing is back.

Amando Zanderigo - 2023-08-24 12:29 - R-Forge Site Admin

I have fixed the ViewVC respository browsing. If you notice any problems with it, please contact us at R-Forge@R-Project.org.

Maintenance (4-5 April)

Amando Zanderigo - 2023-04-03 12:34 - R-Forge Site Admin

Ongoing maintenance will result in additional downtime on the 4th (and possibly 5th) of April. We apologize for the inconvenience.

Further Maintenance (23-24 March 2023)

R-Forge Statistics

Hosted Projects: **2,146**Reaistered Users: **15,988**

Most Active This Week

- 1 R/exams: Automatic Generation of Exams
- 2 Matrix Methods and Classes
- 3 ctm
- 4 PEMS data analysis tools
- 5 Rmpfr: Multiple Precision Floatingpoint
- 6 Sequence analysis for social scientists
- 7 Curve Estimation etc.
- 8 Optimization and solving packages
- 9 CHNOSZ

All project activities

Recently Registered Projects

12/02 LadderFuelsR

11/13 BATS - Bayesian Adaptive Trial Simulator

10/13 rfnew

06/14 Lindon Precipitation 03/30 ABSTRACT SEARCHER

03/01 my NMR PROJECT

3701 My NMR PROJEC

02/10 arbR - An R interface to Arblib

12/08 R6Nomograms

10/07 Chapman & Rodden, Quant UX Research