

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

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2024/2

Principais repositórios de pacotes - R

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).

Console Terminal Background Jobs

R 4.4.2 · ~/

R version 4.4.2 (2024-10-31) -- "Pile of Leaves"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

install.packages(...)

CRAN

```
> install.packages('nome do pacote')
```

Environment History Connections Tutorial

Import Dataset 185 MiB

R Global Environment

Environment is empty

Files Plots Packages Help Viewer Presentation

Zoom Export

Principais repositórios de pacotes - R

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.

[About](#)[Learn](#)[Packages](#)[Developers](#)[Get Started >](#)

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.

[Get started >](#)

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.

↙ Step 1
Install R

1. 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).
2. 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 install additional packages and to update, find, and troubleshoot are provided below. A devel version of Bioconductor is available. There are good reasons for using **BiocManager::install()** 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 required 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.

Console Terminal Background Jobs

R 4.4.2 ~/

> BiocManager::install('nome do pacote')



Comando para instalar
pacotes do Bioconductor

Environment History Connections Tutorial

Import Dataset 212 MiB

R Global Environment

Environment is empty

Files Plots Packages Help Viewer Presentation

Aesthetic specifications Find in Topic

It's trickier to include a system font on a plot because text drawing is done differently by each graphics device (GD). There are five GDs in common use (`png()`, `pdf()`), on screen devices for Windows, Mac and Linux), so to have a font work everywhere you need to configure five devices in five different ways. Two packages simplify the quandary a bit:


- `showtext` makes GD-independent plots by rendering all text as polygons.
- `extrafont` converts fonts to a standard format that all devices can use.

Both approaches have pros and cons, so you will need to try both of them and see which works best for your needs.

Font face

```
df <- data.frame(x = 1:4, fontface = c("plain", "bold", "italic", "bold.italic"))
ggplot(df, aes(1, x)) +
  geom_text(aes(label = fontface, fontface = fontface))
```

4 - ***bold.italic***



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

Marcel Ramos¹ and Martin Morgan¹

¹Roswell Park Comprehensive Cancer Center, Buffalo, NY

27 August 2024

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Principais repositórios de pacotes - R

3. GitHub







Descrição: Embora não seja um repositório oficial, muitos desenvolvedores disponibilizam pacotes no GitHub antes de submetê-los 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

`{ggstatsplot}` is an extension of `{ggplot2}` 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 `ggstatsplot` is simple: combine these two phases into one in the form of graphics with statistical details, which makes data exploration simpler and faster.



Installation

Type	Command
------	---------

Principais repositórios de pacotes - R

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.

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 repository 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**

Registered 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](#)
- 02/10 [arbR - An R interface to Arbib](#)
- 12/08 [R6Nomograms](#)
- 10/07 [Chapman & Rodden, Quant UX Research](#)