

What is Bioconductor?

• • •

Lori Ann Shepherd Kern
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Bioconductor is not a package; it's a package repository

Bioconductor provides tools for the analysis, comprehension, and visualization of genetic and genomic data as an R package repository system. It is open source and open development, relying on community contributed R packages.

- Website: <https://bioconductor.org/>
- Support Site: <https://support.bioconductor.org/>
- Contributors Resource: <https://contributions.bioconductor.org/>



Just some of the many
Bioconductor available packages!!



Bioconductor is an organization

Advisory Boards Help Shape the direction of the project and ensure technological relevance:

- Bioconductor Foundation / European Bioconductor Society

501(c)(3) organization , handles money regarding conference organization, donation, and sponsorship

- Scientific Advisory Board (SAB)

Provides external guidance and oversight of scientific direction of the project. Invitation Only Board.

- Technical Advisory Board (TAB)

Advises on Project and Package level infrastructure for the project. Open Call to anyone; elections held annual in Spring

- Community Advisory Board (CAB)

Dedicated to developing, enhancing, and diversifying the Bioconductor community. Open Call to anyone; elections held annual in Spring

- Core Team

Developers that maintain, enhance, and develop core packages and project level infrastructure

- International Bioconductor Community !!

Note:

Bioconductor Foundation will likely dissolve as we explore a collaboration with NumFocus.



Technical Advisory Board

<https://bioconductor.org/about/technical-advisory-board/>



Vince Carey



Charlotte Soneson



Levi Waldron



Aedin Culhane



Sean Davis



Laurent Gatto



Robert Gentleman



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Davide Risso



Kevin Rue-Albrecht



Mike Smith



Leo Lahti



Luyi Tian



Kozo Nishida



Nicole Ortogero



Daniela Cassol



Aedin Culhane



Johannes Rainer



Hedia Tnani



<https://bioconductor.org/about/community-advisory-board/>



Maria Doyle



Lori (Shepherd) Kern



Enis Afgan



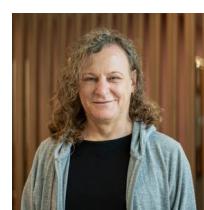
Estefania Mancini



Umar Ahmad



Xueyi Dong



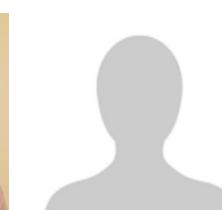
Stevie Pederson



Mengbo Li



Jiefei Wang



Jordana Muqanguzi



Janani Ravi

Core Team

<https://bioconductor.org/about/core-team/>



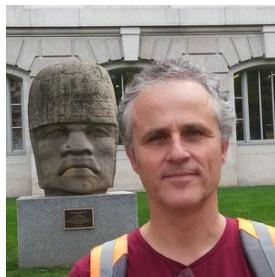
Lori (Shepherd) Kern



Vince Carey



Alexandru Mahmoud



Herve Pages



Marcel Ramos



Robert Shear



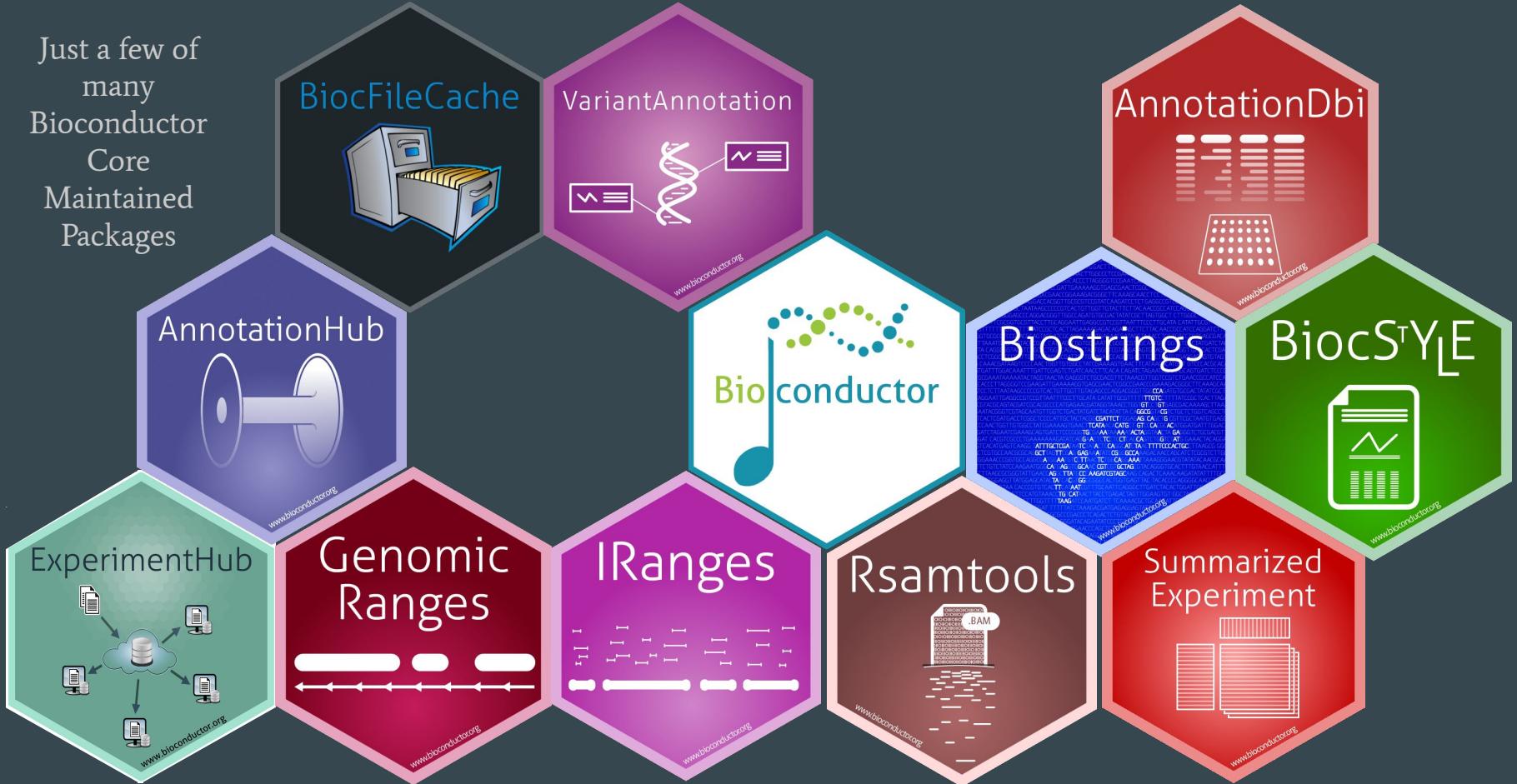
Jennifer Wokaty



Kayla Interdonato

Core Team: It's Not Just the Packages

Just a few of
many
Bioconductor
Core
Maintained
Packages



Core Team: Infrastructure Development and Maintenance

- Develop and maintain Bioconductor infrastructure packages
- Bioconductor.org maintenance
- Support.bioconductor.org maintenance
- Answering questions on all outlets
- Bioconductor Build System (BBS) for daily builds and reporting
- Docker Image generation
- Binary Package generation (AnVIL/Docker)
- New Package Submission (SPB) process and review
- AWS infrastructure
- Azure infrastructure
- OSN infrastructure
- Jetstream2 processes
- Maintaining the git ecosystem
- Package download stats
- BiocManager maintenance
- Bioconductor ExperimentHub and AnnotationHub integration
- Outreachy projects
- And more So if we don't get to your question right away please be kind!

Bioconductor is a community!

Bioconductor provides resources and infrastructure to link experienced package maintainers, developers and users with the inexperienced to foster a collaborative and welcoming community of R Bioconductor users.

- Support Site: <https://support.bioconductor.org/>
- Community Slack channel: community-bioc.slack.com
- Conferences / Workshops / Events: <https://bioconductor.org/help/events/>
- Mentoring Program: [#developers-mentorship](https://community-bioc.slack.com) channel

Support Site: <https://support.bioconductor.org/>

This screenshot shows the Bioconductor Forum support site. At the top, there's a navigation bar with links for Import bookmarks, Bioconductor Home, Trello, Mail, RoswellLinks, SupportSites, Bioconductor, RunningNotes, SharedWithMe, and Management. Below the navigation is a search bar and a user profile for shepherd (3.4k). The main content area displays a list of posts. The first post is from shepherd about a problem with retrieving genes using p value and log2fc as conditions. It has 10 views and 1 reply. The reply is from James W. MacDonald, asking if the user has part of their code. The second post is from shepherd about a KEGO error, with 8 views and 1 reply from Hervé Pages. The third post is from shepherd about a Bioconductor New Package Developer Award, with 12 views and 1 reply from Gordon Smyth. The fourth post is from shepherd about a junior developer award, with 52 views and 1 reply from Michael Love. The fifth post is from shepherd about Bioconductor Community Engagement, Outreach, and Diversity Award, with 76 views and 1 reply from Aaron Lun. The sixth post is from shepherd about a Bioconductor Long-term Contribution Award, with 73 views and 1 reply from Martin Morgan. The seventh post is from shepherd about Bioconductor 2023 Awards!, with 94 views and 1 reply from Sean Davis. The eighth post is from shepherd about a DESeq2 comparison of gene expression change, with 22 views and 1 reply from Dan Tenenbaum. The ninth post is from shepherd about a "read_block" error, with 94 views and 1 reply from Kasper Daniel Hansen. The tenth post is from shepherd about a course on single-cell RNAseq data analysis with R and Bioconductor, with 33 views and 1 reply from Vincent J. Carey, Jr. The eleventh post is from shepherd about installing denvirs on Singularity, with 142 views and 1 reply from Julie Zhu. The twelfth post is from shepherd about a namespace conflict, with 258 views and 1 reply from Peter Hickey.

This screenshot shows the Bioconductor Community support site. At the top, there's a navigation bar with links for Import bookmarks, Bioconductor Home, Trello, Mail, RoswellLinks, SupportSites, Bioconductor, RunningNotes, SharedWithMe, and Management. Below the navigation is a search bar and a user profile for shepherd (3.4k). The main content area displays a grid of member profiles. Each profile includes a small icon, the member's name, their reputation score, the number of visits, and the last time they visited. The members shown include James W. MacDonald, Gordon Smyth, Michael Love, Aaron Lun, Martin Morgan, Sean Davis, Hervé Pages, Wolfgang Huber, Steve Langmead, Guest User, Michael Lawrence, Dan Tenenbaum, Ryan C. Thompson, Seth Falcon, Marc Carlson, Valerie Oberndorfer, Vincent J. Carey, Jr., Kasper Daniel Hansen, Naomi Altman, Mike Smith, igentlemen, Rory Stark, Benton Carvalho, and Julie Zhu.

Ask questions about packages or data analysis
Thousands of Bioconductor users and maintainers are members

Community Slack channel: community-bioc.slack.com

The screenshot shows the Slack interface for the 'community-bioc' channel. The left sidebar lists various channels under the 'community-bioc' category, with '# general' selected. The main pane displays the '# general' channel, which has 2,397 members. A pinned message from Friday, May 19th, discusses compilation times and executables for Windows. Another message from Maria Doyle on May 22nd promotes a training course. Michael Kesling joined the channel on May 22nd. PN joined on May 20th. A message from Michael Kesling on May 22nd asks about querying genes by tissue-specific expression. A message from PN on May 20th indicates that Anna Powell joined. The bottom of the screen shows the message input field for '# general'.

general - community-bioc - Slack

File Edit View Go History Window Help

← → ⌂ Search community-bioc

general Link to join the slack team - <https://slack.bioconductor.org/>

4 Pinned + Code of Conduct +

installation or many development suites (cuda devtools, ktools, MSVC, compilers, tools) under windows and that the compilation time under windows is important (15 minutes or more). I am afraid that this discourages many... I'd like to be able to provide the Windows executables directly in the package... Under linux, the compilation seems to me unavoidable because of the risk of incompatibility with the libc library... Is it possible to indicate a compilation under linux and no compilation under windows in the DESCRIPTION file or should I make two different packages?

Thanks for your help!

Maria Doyle 10:16 AM 3 days until the annual (and 1st Bioconductor) Smörgåsbord training course starts! There is still time to register if you want to participate.

Join us for a week of free, online, self-paced #Bioconductor and #UseGalaxy #bioinformatics learning!

May 22-26 <https://gallantries.github.io/video-library/modules/bioconductor>

Ajda Prstavec 11:07 AM joined #general. Also, Michael Kesling and Yuka Takemon joined.

Michael Kesling 2:28 PM Hi everyone. I'm new here. I'm wondering if there's a package or function in bioconductor for querying genes that have a tissue-specific pattern. For most of what I've found on the web, I need to start with a single gene and then browse its attributes. At NCBI Gene, I can see tissue-specific expression for that particular gene. I'd rather perform a query for tissue-specific expression and then get a list of genes back. Is there a way to do that? Thanks very much!

PN 6:58 PM joined #general. Also, Anna Powell joined.

Message #general

+ Aa 😊 @ | ⌂ 🔍

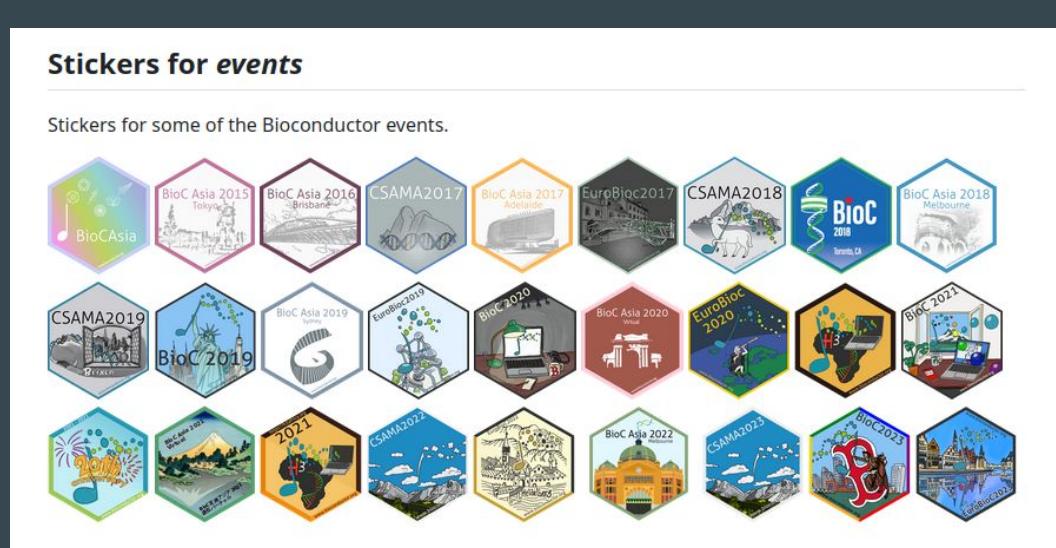
Bioconductor Conferences / Workshops / Events

Screenshot of the Bioconductor Events page (<https://bioconductor.org/help/events/>) showing a calendar view for May 2023.

The calendar highlights several events:

- May 1: Bioconductor 16
- May 2-4: Ann Arbor Pitchathon: Big Data Developers Picnic
- May 23-26: Bioinformatics 2023 - Free, Global, Online Weeks of Training

Below the calendar, there is a "Course material" section listing various training programs and a "Upcoming" section listing conferences like Bioinformatics 2023 and EuroBioC 2023.





BioC2019 - New York City, USA



Brixen, Italy 2019

Developing Packages

While the Core Team maintains many ‘core infrastructure packages’, Bioconductor is largely community contributed.

Anyone can contribute a Bioconductor package.

Bioconductor has certain, specific package requirements that must be met and every package undergoes a review process. Once accepted, a package is added to the daily builder and available through BiocManager.



Just some of the many
Bioconductor available packages!!



Working Groups and Committees

<https://workinggroups.bioconductor.org/>

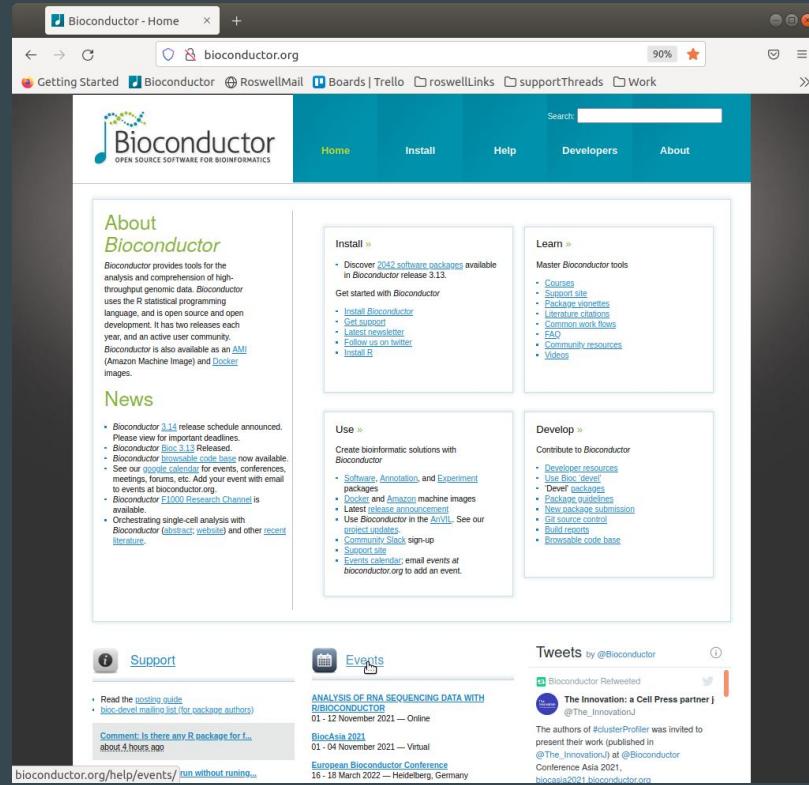
- Code of Conduct
- Conference Planning
- Cloud Methods
- Developers Training
- Education
- Mass Spectrometry for Proteomics and Metabolomics
- Multilingual
- Package Review
- Industry
- Website
- Social Media
- Package Failure Notifications
- Your new working group.....?

Other Social Media

Bioconductor has other social media outlets to connect the community!

- Community Slack channel: community-bioc.slack.com
- Twitter: <https://twitter.com/Bioconductor>
- Mastodon: <https://genomic.social/@bioconductor>
- LinkedIn: <https://www.linkedin.com/company/bioconductor>
- Facebook: <https://www.facebook.com/bioconductor> (Rarely Used except for announcements)

Website: <https://bioconductor.org>



Note:

The Bioconductor website is getting a new look!

We are looking for feedback from all types of users (beginner to advanced). If you are willing to be involved please let me know!!

Bioconductor Basics

• • •

How do I get started?

How does a user interact with Bioconductor?

RStudio interface showing R code and package management. The terminal window displays the R startup message and package details. The environment pane shows an empty global environment.

R and
Rstudio

Terminal window showing R code and Docker container output. The terminal displays the R startup message and package details. The Docker container output shows the same information, indicating a successful build and run of the Docker image.

AnVIL web application interface. The main page features a title "Migrate Your Genomic Research to the Cloud" and a subtitle "Analyze large, open & controlled-access genomic datasets with familiar tools and reproducible workflows in a secure cloud-based computing environment." It includes sections for Terra, Gen3, Dockstore, and NIH Cloud Platform. Key statistics are displayed in colored circles: 9 CONSORTIA, 254 COHORTS, 291K SUBJECTS, 314K SAMPLES, and 3.9PB SIZE.

AnVIL

Bioconductor Docker documentation page. It provides instructions for running Docker containers for Bioconductor. It covers topics like Quick start, Dockerfiles, Current Containers, Docker Compose, Using docker-compose, Modifying image Container, and Microsoft Azure Container Instances. It also includes links for GitHub, Docker Hub, and Docker Registry.

Docker

Installing Bioconductor Packages: BiocManager

- Bioconductor provides a function for installing packages from the Bioconductor repository and CRAN repository through the `BiocManager` package on CRAN
- To install any Bioconductor package (or CRAN package) in R terminal or Rstudio:

```
# download and install BiocManager  
> install.packages("BiocManager")  
  
# usage  
> library(BiocManager)  
> install( <name of package[s]> )  
  
# list all CRAN/Biocondutor packages available or search for name  
> BiocManager::available() / BiocManager::available("Genomic")
```

Bioconductor Package: AnVIL

AnVIL (NHGRI Analysis Visualization and Informatics Lab-space)

- Analyze large, open & controlled-access genomic datasets with familiar tools and reproducible workflows in a secure cloud-based computing environment.

<https://anvilproject.org/>

AnVIL users can perform data analysis with Bioconductor in Jupyter Notebooks or Rstudio.

- The Bioconductor AnVIL package provides an `AnVIL::install()` to download Bioconductor package binaries.

Bioconductor Packages: Docker

<https://bioconductor.org/help/docker/>

- Release and devel docker containers available
 - `bioconductor/bioconductor_docker:devel`
 - `bioconductor/bioconductor_docker:RELEASE_X_Y`
- Install docker
- Pull the desired bioconductor docker version
- Run
 - Rstudio Server
 - command line (directly into R or as a bash shell)
- Packages available as binary package install using `BiocManager::install`
- Ability to modify base image as needed
- Available on Singularity
- Available on Microsoft Container Registry and Azure

Finding Bioconductor Packages

Bioconductor Home Page

The screenshot shows the Bioconductor Home page (https://www.bioconductor.org) displayed in a web browser window. The page has a dark blue header with the Bioconductor logo and navigation links for Home, Install, Help, Developers, and About. A search bar is located in the top right corner. The main content area features several sections: 'About Bioconductor' with a detailed description of the project; 'BioC 2021' with a message about the conference; 'Install >' with links to software packages and R installation; 'Learn >' with links to courses, support, and documentation; 'News' with a list of recent developments; 'Use >' with links to software, annotation, and experiment packages; and 'Develop >' with links to developer resources and package submission guidelines.

About Bioconductor

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community.

Bioconductor is also available as an [AMI](#) (Amazon Machine Image) and [Docker](#) images.

News

- Bioconductor [BioC 3.13](#) Released.
- Bioconductor [Browsable code base](#) now available.
- See our [google calendar](#) for events, conferences, meetings, forums, etc. Add your event with email to events at bioconductor.org.
- Bioconductor [F1000 Research Channel](#) is available.
- Orchestrating single-cell analysis with Bioconductor ([abstract](#); [website](#)) and other [recent literature](#).
- Bioconductor [3.13](#) release schedule announced. Please view for important deadlines.

BioC 2021

Thanks for a great conference. We appreciate all participants. Look for materials and videos to be posted over the next several weeks on the courses page and on the Bioconductor YouTube channel.

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- Discover [2042 software packages](#) available in Bioconductor release 3.13.

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Use >

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- [Docker](#) and [Amazon machine images](#)
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- Use Bioconductor in the [AnVIL](#). See our [project updates](#).
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- [Use BioC 'devrel'](#)
- ['Devel' packages](#)
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https://www.bioconductor.org

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Bioconductor biocViews Page

Bioconductor - BioViews X +

https://bioconductor.org/packages/release/BiocViews.html#Software 120% ⭐

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All Packages

Bioconductor version 3.13 (Release)

Autocomplete biocViews search:

Packages found under Software:

Rank based on number of downloads: lower numbers are more frequently downloaded.

Show All entries Search table:

Package	Maintainer	Title	Rank
BiocGenerics	Bioconductor Package Maintainer	S4 generic functions used in Bioconductor	1
BiocVersion	Bioconductor Package Maintainer	Set the appropriate version of Bioconductor packages	2
S4Vectors	Bioconductor Package Maintainer	Foundation of vector-like and list-like containers in Bioconductor	3
IRanges	Bioconductor Package Maintainer	Foundation of integer range manipulation in Bioconductor	4
Biobase	Bioconductor Package Maintainer	Biobase: Base functions for Bioconductor	5
GenomeInfoDb	Bioconductor Package Maintainer	Utilities for manipulating chromosome names, including modifying them to follow a particular naming style	6
zlibbioc	Bioconductor Package Maintainer	An R packaged zlib-1.2.5	7
XVector	Hervé Pagès	Foundation of external vector representation and manipulation in Bioconductor	8

Bioconductor - BioViews X

https://bioconductor.org/packages/release/BiocViews.html#Software

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Books coming soon!

Software (2041)

- ▶ AssayDomain (819)
- ▶ BiologicalQuestion (866)
- ▶ Infrastructure (480)
- ▶ ResearchField (953)
- ▶ StatisticalMethod (762)
- ▶ Technology (1301)
- ▶ WorkflowStep (1121)
- ▶ AnnotationData (977)
- ▶ ExperimentData (406)
- ▶ Workflow (29)

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Search for
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Bioconductor Package Landing Page

The screenshot shows a web browser window with the title "Bioconductor - BiocGenerics". The URL in the address bar is "bioconductor.org/packages/release/bioc/html/BiocGenerics.html". The page content is as follows:

Bioconductor OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

Home Install Help Developers About

Home » Bioconductor 3.13 » Software Packages » BiocGenerics

BiocGenerics

platforms all rank 1 / 2041 support 0 / 0 in BioC 9.5 years
build warnings updated before release dependencies 5

DOI: [10.1101/129189](https://doi.org/10.1101/129189) [bio:BiocGenerics](#) [f](#) [t](#)

S4 generic functions used in Bioconductor

Bioconductor version: Release (3.13)

The package defines many S4 generic functions used in Bioconductor.

Author: The Bioconductor Dev Team

Maintainer: Bioconductor Package Maintainer <maintainer@bioconductor.org>

Citation (from within R, enter `citation("BiocGenerics")`):

Huber, W., Carey, J. V., Gentleman, R., Anders, S., Carlson, M., Carvalho, S. B., Bravo, C. H., Davis, S., Gatto, L., Girke, T., Gottardo, R., Hahne, F., Hansen, D. K., Irizarry, A. R., Lawrence, M., Love, I. M., MacDonald, J., Obenchain, V., Ole's, K. A., Pages, H., Reyes, A., Shannon, P., Smyth, K. G., Tenenbaum, D., Waldron, L., Morgan, M. (2015). "Orchestrating high-throughput genomic analysis with Bioconductor." *Nature Methods*, **12**(2), 115–121. <http://www.nature.com/nmeth/journal/v12/n2/full/nmeth3252.html>.

Installation

To install this package, start R (version "4.1") and enter:

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("BiocGenerics")
```

For older versions of R, please refer to the appropriate [Bioconductor release](#).

Documentation

[PDF](#) [Reference Manual](#)

Details

Search:

Documentation »

Bioconductor

- Package [vignettes](#) and manuals.
- [Workflows](#) for learning and use.
- Several [online books](#) for comprehensive coverage of a particular research field, biological question, or technology.
- [Course and conference](#) material.
- [Videos](#).
- Community [resources](#) and [tutorials](#).

[R / CRAN](#) packages and [documentation](#)

Support »

Please read the [posting guide](#). Post questions about Bioconductor to one of the following locations:

- [Support site](#) - for questions about Bioconductor packages
- [BioC-devel](#) mailing list - for package developers

All Bioconductor packages use git for source control

The screenshot shows the Bioconductor website with the URL <https://bioconductor.org/developers/how-to/git/>. The page title is "Source Control". It contains a sidebar with links like "C++/Mavericks Best Practices", "Coding Style", "Common Bioconductor Methods and Classes", "Debug C/C++ Code", "Deprecation Guidelines", "Git", "Git Mirrors", "Long Tests", "Querying Web Resources", "Robust and Efficient Code", "Source Control", "Troubleshooting Build Report", "Unit Testing", "Using Bioc Devel", "Using biocViews", "Version Numbering", and "Workflow Vignettes". The main content area discusses Git source control, GitHub workflow, and scenarios for repository creation.

The screenshot shows the Bioconductor website with the URL <https://bioconductor.org/packages/release/bioc/html/GenomicRanges.html>. The page title is "GenomicRanges". It includes sections for "Suggests Me" (listing various Bioconductor packages) and "Links To Me" (listing "Build Report"). Below these are sections for "Package Archives" (listing Source Package, Windows Binary, macOS 10.13 (High Sierra), Source Repository, Package Short Url, and Package Downloads Report) and "Contact us" (support.bioconductor.org). The footer features the Bioconductor logo and links to Home, Install, Help, Developers, About, and Mirrors.

Starting from new package submission and review, a package is moved into the Bioconductor git ecosystem. All changes must be pushed to git.bioconductor.org to propagate to users.

Nightly Builds from git.bioconductor.org

- Packages contributed to Bioconductor have a repository on git.bioconductor.org that should be updated to propagate changes to Bioconductor end users
- Actions performs:
 - Git clone
 - R CMD INSTALL
 - R CMD BUILD
 - R CMD CHECK
- If a package builds and has a valid version bump to indicate a new package version, the package is propagated and available through `BiocManager::install()`

Bioconductor - Home

https://www.bioconductor.org

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About Bioconductor

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community.

Bioconductor is also available as an [AMI](#) (Amazon Machine Image) and [Docker](#) images.

News

- Bioconductor [BioC 3.13 Released](#).
- Bioconductor [Browsable code base](#) now available.
- See our [google calendar](#) for events, conferences, meetings, forums, etc. Add your event with email to events at bioconductor.org.
- Bioconductor [F1000 Research Channel](#) is available.
- Orchestrating single-cell analysis with Bioconductor ([abstract](#); [website](#)) and other [recent literature](#).
- Bioconductor [3.13](#) release schedule announced. Please view for important deadlines.

BioC 2021

Thanks for a great conference. We appreciate all participants. Look for materials and videos to be posted over the next several weeks on the courses page and on the Bioconductor YouTube channel.

Install »

- Discover [2042 software packages](#) available in Bioconductor release 3.13.

Get started with Bioconductor

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Use »

Create bioinformatic solutions with Bioconductor

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- Use Bioconductor in the [AnVIL](#). See our [project updates](#).
- [Community Slack sign-up](#)
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Develop »

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- [Developer resources](#)
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https://bioconductor.org/checkResults/ 110% ☆

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Bioconductor build/check results

[Build System RSS Feeds](#)

Bioconductor 3.18 (devel)

Latest results

- Software builds: [browse](#), [download](#) (new report daily, except on Sundays)
- Mac ARM64 Software builds: [browse](#), [download](#) (new report on Mondays and Thursdays)
- Experiment Data builds: [browse](#), [download](#) (new report on Tuesdays and Thursdays)
- Workflow builds: [browse](#), [download](#) (new report on Tuesdays and Fridays)
- Book builds: [browse](#), [download](#) (new report on Mondays, Wednesdays, and Fridays)
- Long Tests builds: [browse](#), [download](#) (new report on Saturdays)

Bioconductor 3.17 (release)

Latest results

- Software builds: [browse](#), [download](#) (new report daily, except on Sundays)
- Mac ARM64 Software builds: [browse](#), [download](#) (new report on Fridays)
- Annotation Data builds: [browse](#), [download](#) (new report on Wednesdays)
- Experiment Data builds: [browse](#), [download](#) (new report on Tuesdays and Thursdays)
- Workflow builds: [browse](#), [download](#) (new report on Tuesdays and Fridays)
- Book builds: [browse](#), [download](#) (new report on Mondays, Wednesdays, and Fridays)
- Long Tests builds: [browse](#), [download](#) (new report on Saturdays)

Archived results for past releases

Bioconductor 3.16

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Multiple platform build/check report for BioC 3.17

This page was generated on 2023-05-23 11:07:58 -0400 (Tue, 23 May 2023).

Approx. Package Snapshot Date (git pull): **2023-05-22 14:00:16 -0400 (Mon, 22 May 2023)**

Package status is indicated by one of the following glyphs	
TIMEOUT	✓ INSTALL, BUILD, CHECK or BUILD BIN of package took more than 40 minutes
ERROR	✗ Bad DESCRIPTION file, or INSTALL, BUILD or BUILD BIN of package failed, or CHECK produced errors
WARNINGS	✗ CHECK of package produced warnings
OK	✓ INSTALL, BUILD, CHECK and BUILD BIN of package went OK
NA	INSTALL, BUILD, CHECK or BUILD BIN result is not available because of an anomaly in the Build System

Click on any glyph in the report below to access the detailed report.

A [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [J](#) [K](#) [L](#) [M](#) [N](#) [O](#) [P](#) [Q](#) [R](#) [S](#) [T](#) [U](#) [V](#) [W](#) [X](#) [Y](#) [Z](#)

Package	Maintainer	INSTALL/BUILD /CHECK
1/2229 a4 1.48.0 (landing page)	Laure Cugnaud	WARNINGS
2/2229 a4Base 1.48.0 (landing page)	Laure Cugnaud	OK
3/2229 a4Classif 1.48.0 (landing page)	Laure Cugnaud	OK
4/2229 a4Core 1.48.0 (landing page)	Laure Cugnaud	OK
5/2229 a4Preproc 1.48.0 (landing page)	Laure Cugnaud	OK
6/2229 a4Reporting 1.48.0 (landing page)	Laure Cugnaud	OK
7/2229 ABarray 1.68.0 (landing page)	Yongming Andrew Sun	OK
8/2229 abseqR 1.18.0 (landing page)	JiaHong Fong	OK
9/2229 ABSSeq 1.54.0 (landing page)	Wentao Yang	OK
10/2229 acde 1.30.0 (landing page)	Juan Pablo Acosta	OK
11/2229 ACE 1.18.0 (landing page)	Jos B Poell	OK
12/2229 aCGH 1.78.0 (landing page)	Peter Dimitrov	OK
13/2229 ACME 2.56.0 (landing page)	Sean Davis	WARNINGS

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Multiple platform build/check report for BioC 3.17

This page was generated on 2023-05-23 11:07:58 -0400 (Tue, 23 May 2023).

Approx. Package Snapshot Date (git pull): 2023-05-22 14:00:16 -0400 (Mon, 22 May 2023)

Hostname	OS	Arch (%)	R version	Installed pkgs
nebbiolo1	Linux (Ubuntu 22.04.2 LTS)	x86_64	4.3.0 RC (2023-04-13 r84269) - "Already Tomorrow"	4817
palomino3	Windows Server 2022 Datacenter	x64	4.3.0 RC (2023-04-13 r84269 u1rt) - "Already Tomorrow"	4168
merida1	macOS 12.6.4 Monterey	x86_64	4.3.0 RC (2023-04-13 r84257) - "Already Tomorrow"	4326

Click on any hostname to see more info about the system (e.g. compliance) (as reported by uname -r, except on Windows and Mac OS X)

Package status is indicated by one of the following glyphs

- TIMEOUT**: INSTALL, BUILD, CHECK or BUILD BIN of package took more than 40 minutes
- ERROR**: Bad DESCRIPTION file, or INSTALL, BUILD or BUILD BIN of package failed, or CHECK of package produced warnings
- WARNINGS**: CHECK of package produced warnings
- OK**: INSTALL, BUILD, CHECK or BUILD BIN of package went OK
- N/A**: INSTALL, BUILD, CHECK or BUILD BIN result is not available because of an anomaly in the Build System
- skipped**: CHECK or BUILD BIN of package was skipped because the BUILD step failed

Click on any glyph in the report below to access the detailed report.

Package propagation status is indicated by one of the following LEDs

- YES**: Package was propagated because it didn't previously exist in the repository
- NO**: Package was not propagated because of a problem (impossible dependencies, or version lower than what is already in the repository)
- UNNEEDED**: Package was not propagated because it is already in the repository with this version. A version bump is required in order to propagate it

A crossed-out package name indicates the package is **deprecated**.

QUICK STATS

nebbiolo1	Linux (Ubuntu 22.04.2 LTS)	x86_64	2028	1	74	2153	4	137	388	1624	
palomino3	Windows Server 2022 Datacenter	x64	2176	1	76	2117	3	45	372	1697	
merida1	macOS 12.6.4 Monterey	x86_64	2367	8	103	2106	15	42	376	1673	
			0	0	0	0	0	0	0	2117	
			50	103	2106	1542	376	1673	0	1	2105

OS / Arch

	INSTALL	BUILD	CHECK	BUILD BIN
Linux (Ubuntu 22.04.2 LTS) / x86_64	0	20	1	74
Windows Server 2022 Datacenter / x64	0	18	1	76
macOS 12.6.4 Monterey / x86_64	0	50	8	103

A crossed-out package name indicates the package is **deprecated**.

A

Package 1/2229	a4 1.48.0 (landing_page)	Laure Cougnaud	git last commit: 8febf4	git last commit date: 2023-04-25 10:19:40 -0400
Package 2/2229	a4Base 1.48.0 (landing_page)	Laure Cougnaud	git last commit: 2ed5793	git last commit date: 2023-04-25 10:19:28 -0400
Package 3/2229	a4Classif 1.48.0 (landing_page)	Laure Cougnaud	git last commit: 1e2f90	git last commit date: 2023-04-25 10:19:33 -0400
Package 4/2229	a4Core 1.48.0 (landing_page)	Laure Cougnaud	git last commit: 5dd09d0	git last commit date: 2023-04-25 10:19:35 -0400
Package 5/2229	a4Preproc 1.48.0 (landing_page)	Laure Cougnaud	git last commit: 23fb08e	git last commit date: 2023-04-25 10:19:30 -0400
Package 6/2229				

Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo1	Linux (Ubuntu 22.04.2 LTS) / x86_64	OK	OK	OK	WARNINGS
palomino3	Windows Server 2022 Datacenter / x64	OK	OK	OK	OK
merida1	macOS 12.6.4 Monterey / x86_64	OK	OK	OK	OK
Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo1	Linux (Ubuntu 22.04.2 LTS) / x86_64	OK	OK	OK	OK
palomino3	Windows Server 2022 Datacenter / x64	OK	OK	OK	OK
merida1	macOS 12.6.4 Monterey / x86_64	OK	OK	OK	OK
Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo1	Linux (Ubuntu 22.04.2 LTS) / x86_64	OK	OK	OK	OK
palomino3	Windows Server 2022 Datacenter / x64	OK	OK	OK	OK
merida1	macOS 12.6.4 Monterey / x86_64	OK	OK	OK	OK
Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo1	Linux (Ubuntu 22.04.2 LTS) / x86_64	OK	OK	OK	OK
palomino3	Windows Server 2022 Datacenter / x64	OK	OK	OK	OK
merida1	macOS 12.6.4 Monterey / x86_64	OK	OK	OK	OK
Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo1	Linux (Ubuntu 22.04.2 LTS) / x86_64	OK	OK	OK	OK
palomino3	Windows Server 2022 Datacenter / x64	OK	OK	OK	OK
merida1	macOS 12.6.4 Monterey / x86_64	OK	OK	OK	OK
Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo1	Linux (Ubuntu 22.04.2 LTS) / x86_64	OK	OK	OK	OK
palomino3	Windows Server 2022 Datacenter / x64	OK	OK	OK	OK
merida1	macOS 12.6.4 Monterey / x86_64	OK	OK	OK	OK

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bioconductor.org/checkResults/3.14/bioc-LATEST/

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Multiple platform build/check report for BioC 3.14

This page was generated on 2021-09-08 12:06:18 +000 (Wed, 08 Sep 2021).

Approx. Package Snapshot Date (git pull): 2021-09-07 14:50:07 -0400 (Tue, 07 Sep 2021)

Timestamp to know what day it was generated

Hostname	OS	Arch (*)	Platform label (**)	R version	Installed pkgs
nebbiolo2	Linux (Ubuntu 20.04.2 LTS)	x86_64	x86_64-linux-gnu	4.1.1 (2021-08-10) -- "Kick Things"	4195
riesling1	Windows Server 2019 Standard	x64	mingw32 / x86_64-w64-mingw32	4.1.1 (2021-08-10) -- "Kick Things"	4003
merida1	macOS 10.14.6 Mojave	x86_64	x86_64-apple-darwin18.7.0	4.1.1 Patched (2021-08-22 r08013) -- "Kick Things"	4039

Click on any hostname to see more info about the system (e.g. compiler). (*) as reported by 'uname -p', except on Windows and Mac OS X. (**) as reported by 'gcc -v'.

Package status is indicated by one of the following glyphs		Package propagation status is indicated by one of the following LEDs	
TIMEOUT	✗ minutes	YES	Package was propagated because it didn't previously exist or version was bumped
ERROR	✗ CHECK produced errors	NO	Package was not propagated because of a problem (impossible dependencies, or version lower than what is already propagated)
WARNINGS	✗ CHECK of package produced warnings	UNNEEDED	Package was not propagated because it is already in the repository with this version. A version bump is required in order to propagate it
OK	✗ INSTALL, BUILD, CHECK or BUILD BIN of package was OK		
skipped	✗ CHECK or BUILD BIN of package was skipped because the BUILD step failed		
NA	✗ BUILD, CHECK or BUILD BIN result is not available because of an anomaly in the Build System		

Click on any glyph in the report below to access the detailed report.

A crossed-out package name indicates the package is **deprecated**.

QUICK STATS

nebbiolo2	Linux (Ubuntu 20.04.2 LTS) / x86_64	0	16	2010	0	127	1899	0	46	296	1557
riesling1	Windows Server 2019 Standard / x64	0	23	1977	1	137	1862	1	59	285	1517
merida1	macOS 10.14.6 Mojave / x86_64	0	16	2003	2	127	1890	1	40	283	1566
		0	0	0	0	0	0	0	0	0	1890

OS / Arch

	INSTALL	BUILD	CHECK	BUILD BIN						
Linux (Ubuntu 20.04.2 LTS) / x86_64	0	16	2010	0	127	1899	0	46	296	1557
Windows Server 2019 Standard / x64	0	23	1977	1	137	1862	1	59	285	1517
macOS 10.14.6 Mojave / x86_64	0	16	2003	2	127	1890	1	40	283	1566
	0	0	0	0	0	0	0	0	0	1890

A

a4 1.41.0 (landing page) Laure Cougnaud git_last_commit: 8873a4 git_last_commit_date: 2021-05-19 11:48:29 -0400
Package 2/2027 a4Base 1.41.0 (landing page) Laure Cougnaud git_last_commit: 9a2793c git_last_commit_date: 2021-05-19 11:48:16 -0400
Package 3/2027 a4Classif 1.41.1 (landing page) Laure Cougnaud git_last_commit: 499362f git_last_commit_date: 2021-07-13 05:27:39 -0400
Package 4/2027 a4Core 1.41.0 (landing page) Laure Cougnaud git_last_commit: 5958295 git_last_commit_date: 2021-05-19 11:48:24 -0400

Indicates package version, git commit and commit date that the builders used

Click on any stage for more information

Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo2	Linux (Ubuntu 20.04.2 LTS) / x86_64	OK	OK	OK	OK
riesling1	Windows Server 2019 Standard / x64	OK	OK	OK	OK
merida1	macOS 10.14.6 Mojave / x86_64	OK	OK	OK	OK

Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo2	Linux (Ubuntu 20.04.2 LTS) / x86_64	OK	OK	OK	OK
riesling1	Windows Server 2019 Standard / x64	OK	OK	OK	OK
merida1	macOS 10.14.6 Mojave / x86_64	OK	OK	OK	OK

Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo2	Linux (Ubuntu 20.04.2 LTS) / x86_64	OK	OK	OK	OK
riesling1	Windows Server 2019 Standard / x64	OK	OK	OK	OK
merida1	macOS 10.14.6 Mojave / x86_64	OK	OK	OK	OK

Bioconductor Concepts

- Bioconductor version is closely associated with an R version
- Bioconductor has a release twice a year.
- Bioconductor has a release and devel branch of packages
- Versions of packages have significance

Why is there a release and a devel branch of Bioconductor?

Apr May June July Aug Sept Oct Nov Dec Jan Feb Mar

Spring
Release

Current Stable Release of R (R-patched) on CRAN
used for both Bioconductor Release and Bioconductor
devel branches

Fall
Release

Current Stable Release of R (R-patched) on CRAN
used for Bioconductor release branch
R-devel used for Bioconductor devel branches

Why is there a release and a devel branch of Bioconductor?

- Bioconductor has the concept of a Release and a Devel version of every package.
 - Release is the stable, user centric branch. Changes should only be minimal to fix known issues/bugs
 - Devel is for new features, enhancements, and developments
 - Adapt to changes in base R before an R official release
 - <http://contributions.bioconductor.org/troubleshooting-build-report.html>
 - Adapt to packages enhancement and changes based on package Interoperability. Bioconductor packages can be closely dependent on each other.
- Bioconductor has two releases a year (Spring/Fall).
 - Spring - closely tied to the R release (normally scheduled one week after R release)
 - Fall - Bioconductor devel switches to using R-devel in preparation for spring R release

Versions of packages

- Pre-release < 0.99.0
 - No longer permitted. Only on local, non submitted Bioconductor packages.
- Initial submission into Bioconductor 0.99.0
 - Few exceptions made for x.99.0 on submission for very specific cases (i.e moving from CRAN to Bioconductor)
- On first Bioconductor release a package is generally 1.0.0
- Bioconductor bumps versions at release automatically. Package version x.y.z
 - Y = even = release
 - Y = odd = devel
- BiocManager can validate your installation and package versions with
 - `BiocManager::valid()`
 - `BiocManager::install()`

Other Bioconductor Concepts

interop/endomorphism

- Interoperability
 - How: By reusing common data structures/data classes and existing functions (especially load/read)
 - Why: Users can make workflows easily without worrying about the format of their data
- Endomorphism
 - We encourage developers to practice this when implementing functions so users know what to expect as output “you get what you give”
 - Not always appropriate or implemented but encouraged

Common Classes and Methods

• • •

<https://contributions.bioconductor.org/important-bioconductor-package-development-features.html#reusebioc>

Common Bioconductor Classes and Methods: Importing Data

- GTF, GFF, BED, BigWig, etc., – `rtracklayer ::import()`
- VCF – `VariantAnnotation ::readVcf()`
- SAM / BAM – `Rsamtools ::scanBam()`, `GenomicAlignments ::readGAlignment*`()
- FASTA – `Biostrings ::readDNAStringSet()`
- FASTQ – `ShortRead ::readFastq()`
- MS data (XML-based and mgf formats) – `Spectra ::Spectra()`, `Spectra ::Spectra(source = MsBackendMgf::MsBackendMgf())`

Common Bioconductor Classes and Methods: Classes

- Rectangular feature x sample data – `SummarizedExperiment ::SummarizedExperiment()` (RNAseq count matrix, microarray, ...)
- Genomic coordinates – `GenomicRanges ::GRanges()` (1-based, closed interval)
- Genomic coordinates from multiple samples – `GenomicRanges ::GRangesList()`
- Ragged genomic coordinates – `RaggedExperiment ::RaggedExperiment()`
- DNA / RNA / AA sequences – `Biostrings ::*StringSet()`
- Gene sets – `BiocSet ::BiocSet()`, `GSEABase ::GeneSet()`, `GSEABase ::GeneSetCollection()`
- Multi-omics data – `MultiAssayExperiment ::MultiAssayExperiment()`
- Single cell data – `SingleCellExperiment ::SingleCellExperiment()`
- Mass spec data – `Spectra ::Spectra()`
- File formats – `BiocIO ::`BiocFile-class``

Questions and Comments

I welcome any comments or questions anyone had on the presentation.

- Email
 - lori.shepherd@roswellpark.org
- Community-bioc.slack.com
 - Display name: @lshepherd