

# What is Bioconductor?

• • •

Maria Doyle  
Bioconductor Community Manager  
[maria.doyle@ul.ie](mailto:maria.doyle@ul.ie)

Slides: Lori Shepherd, Bioconductor Core Team

# 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 annually.

- Community Advisory Board (CAB)

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

- Core Team

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

- Global Bioconductor Community !!

## Note:

Bioconductor Foundation is being dissolved as we now have NumFocus as fiscal sponsor.



# Technical Advisory Board

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



Vince Carey



Charlotte Soneson



Levi Waldron



Henrik Bengtsson



Helena Crowell



Sean Davis



Laurent Gatto



Ludwig Geistlinger



Kasper Daniel Hansen



Stephanie Hicks



Wolfgang Huber



Rafael Irizarry



Lori (Shepherd) Kern



Michael Love



Davide Risso



Kevin Rue-Albrecht



Mike Smith



Leo Lahti



Luyi Tian



Kozo Nishida



Nicole Ortogero



Daniela Cassol



Aedin Culhane



Johannes Rainer



Maria Doyle



Lori (Shepherd) Kern



Enis Afgan



Hedia Tnani



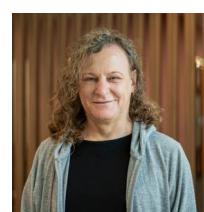
Estefania Mancini



Umar Ahmad



Xueyi Dong



Stevie Pederson



Mengbo Li



Jiefei Wang



Jordana Muqanguzi



Janani Ravi

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

# Core Team

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



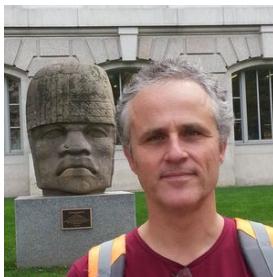
Lori (Shepherd) Kern



Vince Carey



Alexandru Mahmoud



Herve Pages



Marcel Ramos



Robert Shear



Nikhil Mane



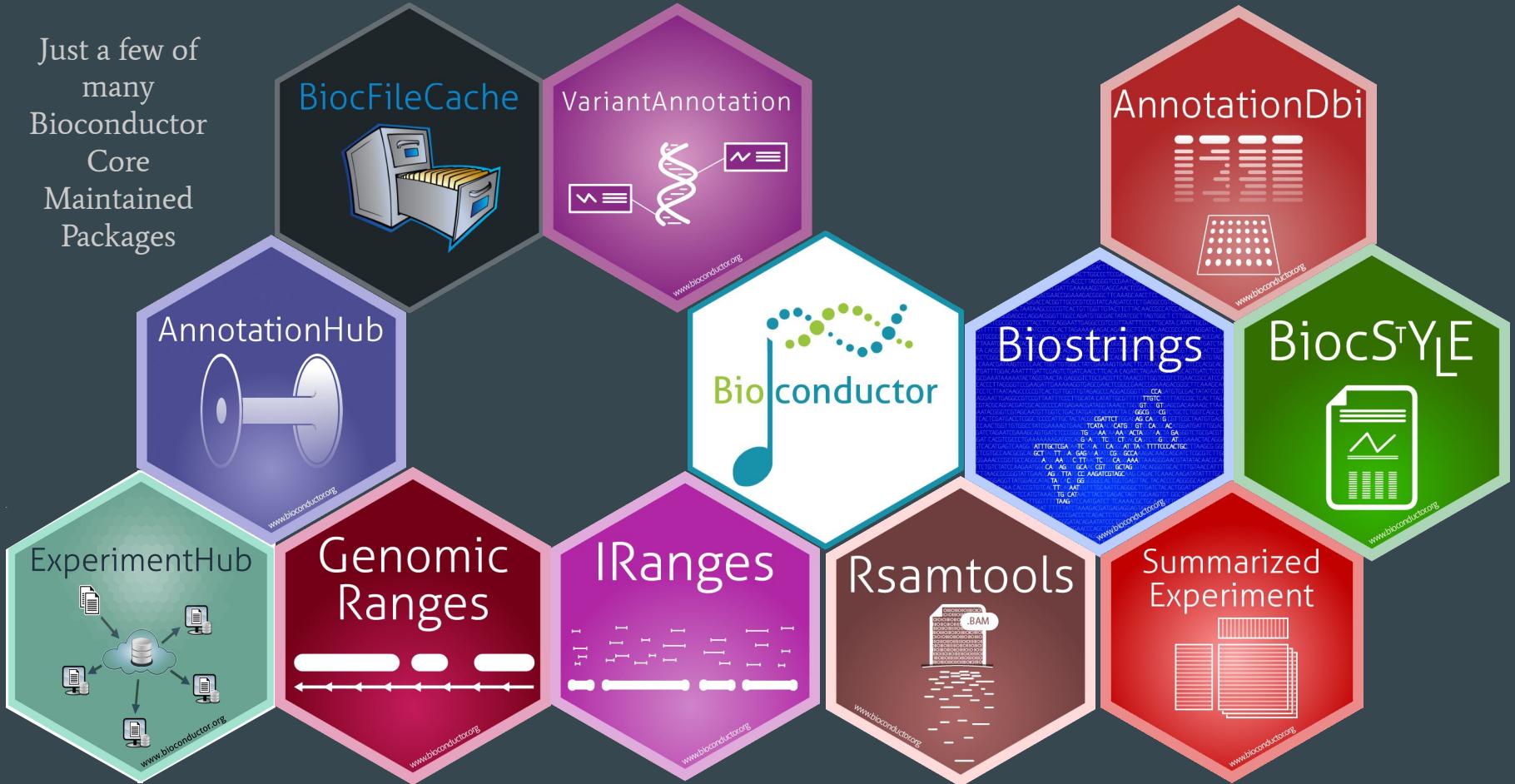
Jennifer Wokaty



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 connect experienced package maintainers, developers and users with those who are less experienced, fostering a collaborative and welcoming community of R Bioconductor users.

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

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

This screenshot shows the Bioconductor Forum support site at https://support.bioconductor.org/. The page displays a list of posts from users like James W. MacDonald, Hervé Pages, and Peter Hickey. Posts are categorized by tags such as Bioconductor, Transcriptomics, DifferentialExpression, DESeq2, RUVNormData, MergingData, Imma, Bioconductor, Recognition, Awards, Bioconductor Community Engagement, Outreach, and Diversity Award, and Bioconductor Long-term Contribution Award.

Key posts include:

- A user asks if the Imma package can be applied to Log2 RUV-normalized data, with a reply from Hervé Pages.
- A post about the "News: Last Week to Nominate for BioC2023 Awards!" with 12 views.
- A post about the "Junior Developer or New Package Developer Award" with 52 views.
- A post about the "Bioconductor Community Engagement, Outreach, and Diversity Award" with 76 views.
- A post about the "Bioconductor Long-term Contribution Award" with 73 views.
- A post about "Nominations for Bioconductor 2023 Awards!" with 94 views.
- A post about "DESeq2 about comparision of gene expression change on two-time points between two group samples." with 22 views.
- A post about "Could not find function "read\_block\_OLD"" with 94 views.
- A post about "News: course - single-cell RNAseq data analysis with R and Bioconductor" with 33 views.
- A post about "Installing denvins on a Singularity container" with 142 views.
- A post about "Keep getting this error "Warning: unable to access index for repository?"" with 258 views.

The footer of the page includes a note about a warning related to the "read\_block" namespace conflict.

This screenshot shows the Bioconductor Community support site at https://support.bioconductor.org/user/list/order=reputation. The page displays a grid of member profiles, each with a small profile picture, name, reputation score, and last visit information. The members listed include James W. MacDonald, Gordon Singh, Michael Linn, Aaron Lin, Martin Morgan, Sean Davis, Ryan C. Thompson, Wolfgang Huber, Steve Langmead, Guest User, Michael Lawrence, Dan Tenenbaum, Naomi Altman, Seth Falcon, Marc Carlson, Valerie Oberndorfer, Vincent J. Carey, Kasper Daniel Hansen, 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: slack.bioconductor.org

The screenshot shows the Slack application window for the 'community-bioc' team. The left sidebar lists various channels, with '# general' currently selected. The main pane displays the '# general' channel, which has 2,397 members. A pinned message from Friday, May 19th, discusses the compilation of Bioconductor packages under Windows and Linux. Another message from Maria Doyle on May 22nd announces a training course. Michael Kesling and others joined the channel. PN joined on May 20th. A message input field at the bottom is ready for a new post.

# 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.

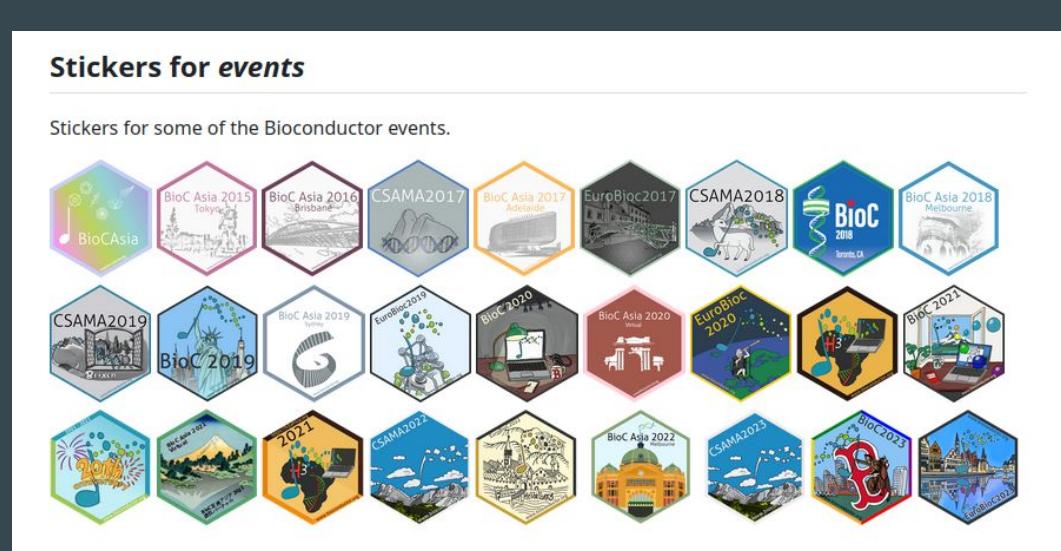
The calendar highlights several events:

- May 1: Bioconductor 16
- May 2-3: 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 workshops, such as:

- bioinformatics 2023 - Free, Global, Online Weeks of Training
- bioinformatics 2023 - Bioconductor Analysis Methods for Genome-Scale Biology
- 11-16 June 2023 - Bioconductor Berlin, Germany
- 12-13 July 2023 - Bioconductor Boston, USA
- CSAM/CB 2023 hybrid, Distributional Latent-Scale Single-Cell Analytics with Bioconductor
- 2023 Big Data Science Bioinformatics Conference
- 21 July - 04 August 2023 — Boston
- bioinformatics 2023 - Bioconductor Analysis Methods for Genome-Scale Biology
- 22-26 August 2023 — Hybrid In-Person and Virtual Conference
- EuropBioC2023: European Bioconductor Conference
- EuropBioC2023: European Bioconductor Conference

At the bottom, there is a "Previous (recent)" section and a note about the bioconductor-trainee committee meeting.





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: [slack.bioconductor.org](https://slack.bioconductor.org)
- Mastodon: <https://genomic.social/@bioconductor>
- LinkedIn: <https://www.linkedin.com/company/bioconductor>

# Website: <https://bioconductor.org>

The screenshot shows the Bioconductor website homepage. At the top, there is a green banner with the text "⚠ Registration Open for Bioc2024 July 24-26". Below the banner, the Bioconductor logo is displayed, followed by navigation links for "About", "Learn", "Packages", and "Developers". A search bar and a "Get Started >" button are also present. The main title "Open source software for Bioinformatics" is prominently displayed in large, bold, dark blue and green letters. Below the title, a subtitle states: "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." A "Get started >" button is located below this subtitle. At the bottom, there are two buttons: "For Users" (which is highlighted) and "For Developers". A call-to-action section titled "Create bioinformatic solutions with Bioconductor" contains two items: "Software, Annotation and Experiment Packages" and "Docker Containers for Bioconductor".

## Note:

The Bioconductor website got a new look in 2024!

# Bioconductor Basics

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How do I get started?

# How does a user interact with Bioconductor?

R version 4.1.1 Patched (2021-09-10 r88888) -- "Kick Things"  
Copyright (C) 2021 The R Foundation for Statistical Computing  
Platform: x86\_64-pc-linux-gnu (64-bit)

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

Bioconductor version 3.14 (BioManager: 1.30.16), R 4.1.1 Patched (2021-09-10  
r88888)

↑  
R and  
Rstudio

File Edit View Search Terminal Help  
(base) shepherd@jbcj433:~ R

R version 4.1.1 Patched (2021-09-10 r88888) -- "Kick Things"  
Copyright (C) 2021 The R Foundation for Statistical Computing  
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Bioconductor version 3.14 (BioManager 1.30.16), R 4.1.1 Patched (2021-09-10  
r88888)

## Migrate Your Genomic Research to the Cloud

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

Launch Terra, AnVIL's cloud computing environment.

Create a virtual cohort in AnVIL's Gen3 Data Explorer.

Discover and launch repeatable workflows with Dockstore.

Explore emerging support for cross-platform data sharing and analysis via the NIH Cloud Platform Interoperability effort.

9 CONSORTIA  
254 COHORTS  
291K SUBJECTS  
314K SAMPLES  
3.9PB SIZE

← AnVIL

Docker

Home > Help > Docker for Bioconductor

## Docker containers for Bioconductor

Docker packages software into self-contained environments, called containers, that include necessary dependencies to run. Containers can run on any operating system including Windows and Mac (using modern Linux kernels) via the Docker engine.

Containers can also be deployed in the cloud using [Amazon Elastic Container Service](#), [Google Kubernetes Engine](#) or [Microsoft Azure Container Instances](#).

### Quick start

- Install Docker
- Run container with Bioconductor and RStudio

```
docker run -e RASSWORD=bio \ -p 8787:8787 \ bioconductor/bioconductor_docker:devel
```

# 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

# 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 >

For Users

For Developers

## Create bioinformatic solutions with Bioconductor

⊕ [Software, Annotation and Experiment Packages](#)

⊕ [Docker Containers for Bioconductor](#)



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# Bioconductor Packages (biocViews) Page

 Bioconductor  
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

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

Home > BiocViews

**Bioconductor version 3.19 (Release)**

Find biocViews:

▼ **Software (2300)**

- ▶ AssayDomain (915)
- ▶ BiologicalQuestion (978)
- ▶ Infrastructure (570)
- ▶ ResearchField (1103)
- ShinyApps (30)
- ▶ StatisticalMethod (841)
- ▶ Technology (1493)
- WorkflowManagement (1)
- ▶ WorkflowStep (1240)
- ▶ AnnotationData (926)
- ▶ ExperimentData (430)
- ▶ Workflow (30)

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

Home &gt; BiocViews

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- ▶ AnnotationData (926)
- ▶ ExperimentData (430) Books coming soon!
- ▶ Workflow (30)

## Packages found under Software:

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The screenshot shows the Bioconductor website interface. At the top, there is a navigation bar with links for About, Learn, Packages (which is underlined), Developers, a search bar, and a 'Get Started' button. Below the navigation bar, the page title is 'Home > BiocViews'. On the left side, there is a sidebar titled 'Search for biocViews Terms' with a red box and arrow around it. The main content area has a heading 'Biocconductor version 3.19 (Release)' and a search bar for 'Find biocViews:'. A list of categories is shown, with 'Software (2300)' highlighted in a blue box and a red arrow pointing to it. Below this list is another sidebar titled 'Search for package name' with a red box and arrow around it. The main content area also features a heading 'Packages found under Software:' and a table listing five packages: BiocVersion, GenomeInfoDb, BiocGenerics, S4Vectors, and IRanges. Each row in the table contains information about the package, its maintainer (Hervé Pagès), and its purpose.

**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
<u>BiocVersion</u>	Bioconductor Package Maintainer	Set the appropriate version of Bioconductor packages	1
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Search for  
biocViews  
Terms

Search for  
package  
name

[Home](#) > [BiocViews](#)**Bioconductor version 3.19 (Release)**

Find biocViews:

**Software (2300)**

- ▶ AssayDomain (915)
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## Packages found under Software:

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

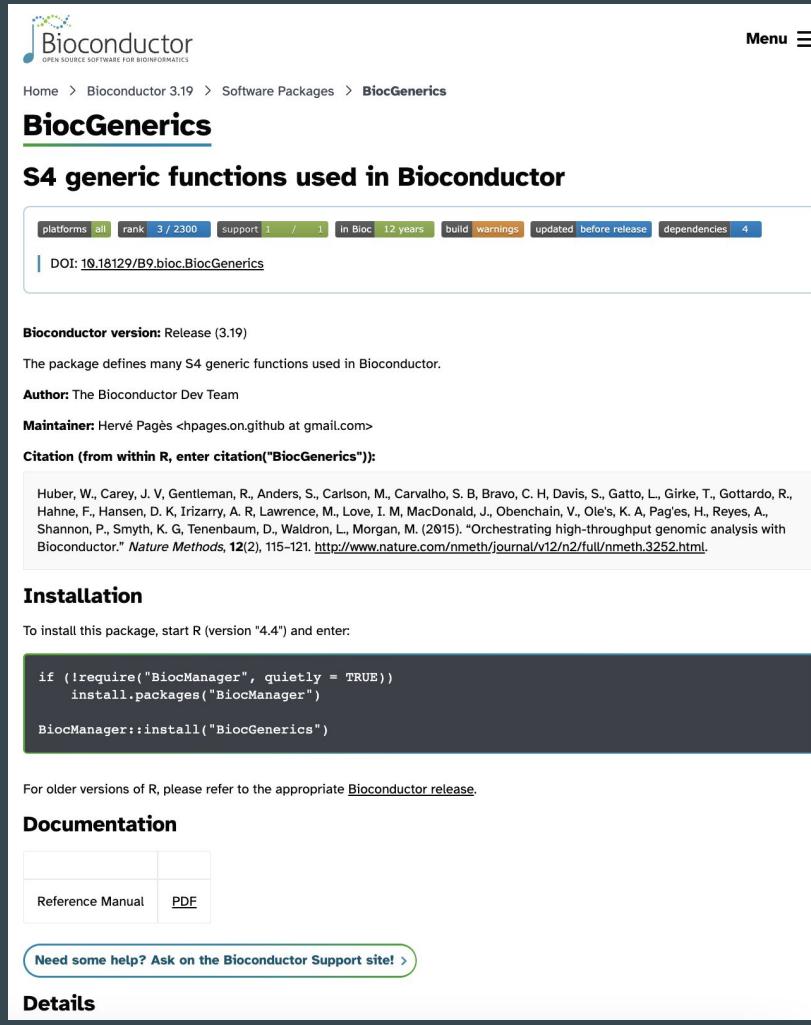
Show All entries

Search table:

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# Bioconductor Package Landing Page



The image shows a screenshot of the Bioconductor package landing page for `BiocGenerics`. The page has a dark header with the Bioconductor logo and a "Menu" button. The main navigation bar includes "Home", "Bioconductor 3.19", "Software Packages", and the current page, "BiocGenerics". Below the header, the package name "BiocGenerics" is displayed in large, bold, black font. A sub-section title "S4 generic functions used in Bioconductor" follows. A horizontal bar at the top of the content area contains various metrics: platforms (all), rank (3 / 2300), support (1 / 1), in BioC (12 years), build (warnings), updated (before release), and dependencies (4). A DOI link ([10.18129/B9.bioc.BiocGenerics](https://doi.org/10.18129/B9.bioc.BiocGenerics)) is also present. The content area starts with a "Bioconductor version: Release (3.19)" section, followed by a brief description of the package's purpose. It then lists the "Author: The Bioconductor Dev Team", "Maintainer: Hervé Pagès <[hpages.on.github@gmail.com](mailto:hpages.on.github@gmail.com)>", and the "Citation (from within R, enter citation("BiocGenerics")):" which is a reference to a Nature Methods paper. Below this is the "Installation" section with R code for installation, and a note for older R versions. The "Documentation" section includes links to the "Reference Manual" and "PDF". A "Need some help? Ask on the Bioconductor Support site! >" button is at the bottom, and a "Details" section is at the very bottom.

**BiocGenerics**

## S4 generic functions used in Bioconductor

platforms all | rank 3 / 2300 | support 1 / 1 | in BioC 12 years | build warnings | updated before release | dependencies 4

DOI: [10.18129/B9.bioc.BiocGenerics](https://doi.org/10.18129/B9.bioc.BiocGenerics)

**Bioconductor version:** Release (3.19)

The package defines many S4 generic functions used in Bioconductor.

**Author:** The Bioconductor Dev Team

**Maintainer:** Hervé Pagès <[hpages.on.github@gmail.com](mailto:hpages.on.github@gmail.com)>

**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., Pag'es, 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/nmeth.3252.html>.

## Installation

To install this package, start R (version "4.4") and enter:

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

BiocManager::install("BiocGenerics")
```

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

## Documentation

Reference Manual | [PDF](#)

Need some help? Ask on the Bioconductor Support site! >

## Details

# All Bioconductor packages use git for source control

Home > Developers > How To > [Git](#)

## Source Control

The *Bioconductor* project is maintained in a Git source control system. Package maintainers update their packages by pushing changes to their git repositories.

Please see the [Git Version Control](#) for different scenarios and workflows from setting up remotes, transitioning from svn, syncing github and Bioconductor git.bioconductor.org repositories, and troubleshooting.

## Annotation packages

Traditional Annotation packages are not stored in GIT due to the size of annotation files. To update an existing Annotation package please send an email to [maintainer@bioconductor.org](mailto:maintainer@bioconductor.org). A member of the Bioconductor team will be in contact to receive the updated package.

Newer annotation packages can be stored in GIT as it is a requirement to use the [AnnotationHub](#) or similar server hosted data. The larger sized files are not included directly in the package. To contribute a new Annotation package please contact [hubs@bioconductor.org](mailto:hubs@bioconductor.org) for guidance and read the documentation on [How to Create A Hub package](#).

Currently direct updates to annotation packages, even those stored on git, are not supported. If you wish to update an annotation package, make required changes and push to [git.bioconductor.org](https://git.bioconductor.org). Then send an email to [hubs@bioconductor.org](mailto:hubs@bioconductor.org) or [maintainer@bioconductor.org](mailto:maintainer@bioconductor.org) requesting the package be propagated.

## More help

Need more help? Ask on the [bioc-devel](#) mailing list.

## Package Archives

Follow [Installation](#) instructions to use this package in your R session.

Source Package	<a href="#">BiocGenerics_0.50.0.tar.gz</a>
Windows Binary	<a href="#">BiocGenerics_0.50.0.zip</a>
macOS Binary (x86_64)	<a href="#">BiocGenerics_0.50.0.tgz</a>
macOS Binary (arm64)	<a href="#">BiocGenerics_0.50.0.tgz</a>
Source Repository	<code>git clone https://git.bioconductor.org/packages/BiocGenerics</code>
Source Repository (Developer Access)	<code>git clone git@git.bioconductor.org:packages/BiocGenerics</code>
Bioc Package Browser	<a href="https://code.bioconductor.org/browse/BiocGenerics/">https://code.bioconductor.org/browse/BiocGenerics/</a>
Package Short Url	<a href="https://bioconductor.org/packages/BiocGenerics/">https://bioconductor.org/packages/BiocGenerics/</a>
Package Downloads Report	<a href="#">Download Stats</a>

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](https://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()`



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# Open source software for Bioinformatics

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

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For Developers

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# Bioconductor build/check results

[Build System RSS Feeds](#)

## Bioconductor 3.20 (devel)

Latest results

- **Software builds:** [browse](#), [download](#) (start at 2pm EST, new report Mondays through Saturdays)
- **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:** [browse](#), [download](#) (new report on Saturdays)

## Bioconductor 3.19 (release)

Latest results

- **Software builds:** [browse](#), [download](#) (start on Sundays and Wednesdays at 2pm EST, new report on Wednesdays and Saturdays)
- **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:** [browse](#), [download](#) (new report on Saturdays)

## Archived results for past releases

[Switch to long report](#)

# Multiple platform build/check report for BioC 3.20

This page was generated on 2024-06-20 12:15 -0400 (Thu, 20 Jun 2024).

Approx. Package Snapshot Date/Time (git pull): **2024-06-19 14:00 -0400 (Wed, 19 Jun 2024)**

See [this page](#) for all the Bioconductor builds and their schedule.

Package status is indicated by one of the following glyphs

TIMEOUT	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN of package took more than 40 minutes
ERROR	<input checked="" type="checkbox"/> Bad DESCRIPTION file, or INSTALL, BUILD or BUILD BIN of package failed, or CHECK produced errors
WARNINGS	<input checked="" type="checkbox"/> CHECK of package produced warnings
OK	<input checked="" type="checkbox"/> 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

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
1/2242	<a href="#">a4</a> 1.53.0 ( <a href="#">landing.page</a> )	Laure Cougnaud	<span>OK</span>
2/2242	<a href="#">a4Base</a> 1.53.0 ( <a href="#">landing.page</a> )	Laure Cougnaud	<span>OK</span>
3/2242	<a href="#">a4Classif</a> 1.53.0 ( <a href="#">landing.page</a> )	Laure Cougnaud	<span>OK</span>
4/2242	<a href="#">a4Core</a> 1.53.0 ( <a href="#">landing.page</a> )	Laure Cougnaud	<span>OK</span>
5/2242	<a href="#">a4Preproc</a> 1.53.0 ( <a href="#">landing.page</a> )	Laure Cougnaud	<span>OK</span>
6/2242	<a href="#">a4Reporting</a> 1.53.0 ( <a href="#">landing.page</a> )	Laure Cougnaud	<span>OK</span>
7/2242	<a href="#">ABarray</a> 1.73.0 ( <a href="#">landing.page</a> )	Yongming Andrew Sun	<span>OK</span>
8/2242	<a href="#">abseqR</a> 1.23.0 ( <a href="#">landing.page</a> )	JiaHong Fong	<span>OK</span>
9/2242	<a href="#">ABSSeq</a> 1.59.0 ( <a href="#">landing.page</a> )	Wentao Yang	<span>OK</span>
10/2242	<a href="#">acde</a> 1.35.0 ( <a href="#">landing.page</a> )	Juan Pablo Acosta	<span>OK</span>
11/2242	<a href="#">ACE</a> 1.23.0 ( <a href="#">landing.page</a> )	Jos B Poell	<span>OK</span>

[Switch to simplified report](#)

## Multiple platform build/check report for BioC 3.20

This page was generated on 2024-06-20 12:15 -0400 (Thu, 20 Jun 2024).

Approx. Package Snapshot Date/Time (git pull): **2024-06-19 14:00 -0400 (Wed, 19 Jun 2024)**

See [this page](#) for all the Bioconductor builds and their schedule.

Hostname	OS	Arch (*)	R version	Installed pkgs
<a href="#">nebbiolo2</a>	Linux (Ubuntu 22.04.3 LTS)	x86_64	4.4.0 RC (2024-04-16 r86468) -- "Puppy Cup"	<a href="#">4687</a>
<a href="#">Iconway</a>	macOS 12.7.1 Monterey	x86_64	4.4.1 RC (2024-06-06 r86719) -- "Race for Your Life"	<a href="#">4402</a>

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

Package status is indicated by one of the following glyphs	
TIMEOUT	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN of package took more than 40 minutes
ERROR	<input checked="" type="checkbox"/> Bad DESCRIPTION file, or INSTALL, BUILD or BUILD BIN of package failed, or CHECK produced errors
WARNINGS	<input checked="" type="checkbox"/> CHECK of package produced warnings
OK	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or 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
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 or version was bumped
NO	Package was not propagated because of a problem (impossible dependencies, or version lower than what is already propagated)
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 ~~erased-out~~ package name indicates the package is [deprecated](#)

QUICK STATS	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
<a href="#">nebbiolo2</a>	Linux (Ubuntu 22.04.3 LTS) / x86_64	0	9	2233	1 35 2206 1 34 368 1803
<a href="#">Iconway</a>	macOS 12.7.1 Monterey / x86_64	0	54	2176	1 95 2134 2 29 360 1743 0 0 2134

A	Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
Package 1/2242	nebbiolo2	Linux (Ubuntu 22.04.3 LTS) / x86_64	OK	OK	OK	OK
<a href="#">a4 1.53.0</a> ( <a href="#">landing page</a> )	Iconway	macOS 12.7.1 Monterey / x86_64	OK	OK	OK	OK
Laure Cougnaud						
git_last_commit: 181f314						
git_last_commit_date: 2024-04-30 10:24:21 -0400						
Package 2/2242	nebbiolo2	Linux (Ubuntu 22.04.3 LTS) / x86_64	OK	OK	OK	OK
<a href="#">a4Base 1.53.0</a> ( <a href="#">landing page</a> )	Iconway	macOS 12.7.1 Monterey / x86_64	OK	OK	OK	OK
Laure Cougnaud						
git_last_commit: 7a868d3						
git_last_commit_date: 2024-04-30 10:24:08 -0400						
Package 3/2242	nebbiolo2	Linux (Ubuntu 22.04.3 LTS) / x86_64	OK	OK	OK	OK
<a href="#">a4Classif 1.53.0</a> ( <a href="#">landing page</a> )	Iconway	macOS 12.7.1 Monterey / x86_64	OK	OK	OK	OK
Laure Cougnaud						
git_last_commit: 7d62634						
git_last_commit_date: 2024-04-30 10:24:14 -0400						

[Switch to simplified report](#)

## Multiple platform build/check report for BioC 3.20

This page was generated on 2024-06-21 13:23:0400 (Fri, 21 Jun 2024).

Approx. Package Snapshot Date/Time (git pull): 2024-06-20 14:00:0400 (Thu, 20 Jun 2024)

Timestamp to know what day it was generated

See [this page](#) for all the Bioconductor builds and their schedule.

Hostname	OS	Arch (*)	R version	Installed pkgs
<a href="#">nebbiolo2</a>	Linux (Ubuntu 22.04.3 LTS)	x86_64	4.4.0 RC (2024-04-16 r86468) -- "Puppy Cup"	4690
<a href="#">Iconway</a>	macOS 12.7.1 Monterey	x86_64	4.4.1 RC (2024-06-06 r86719) -- "Race for Your Life"	4404
<a href="#">kjohnson3</a>	macOS 13.6.5 Ventura	arm64	4.4.1 RC (2024-06-06 r86719) -- "Race for Your Life"	4353

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

Package status is indicated by one of the following glyphs

TIMEOUT	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN of package took more than 40 minutes
ERROR	<input checked="" type="checkbox"/> Bad DESCRIPTION file, or INSTALL, BUILD or BUILD BIN of package failed, or CHECK produced errors
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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 or version was bumped
- NO: Package was not propagated because of a problem (impossible dependencies, or version lower than what is already propagated)
- 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

[nebbiolo2](#)

[Iconway](#)

[kjohnson3](#)

### OS / Arch

	INSTALL	BUILD	CHECK	BUILD BIN
Linux (Ubuntu 22.04.3 LTS) / x86_64	0 9 2233	1 37 2204	2 34 369 1799	
macos 12.7.1 Monterey / x86_64	0 54 2176	1 99 2130	3 28 360 1739	0 1 2129
macos 13.6.5 Ventura / arm64	0 61 2168	3 131 2095	3 63 361 1668	0 0 2095

A

Package 1/2242

[a4Base 1.53.0 \(landing page\)](#)  
Laure Cougnaud  
git last commit: 1a1f1314  
git last commit date: 2024-04-30 10:24:21 -0400

Package 2/2242

[a4Classif 1.53.0 \(landing page\)](#)  
Laure Cougnaud  
git last commit: 7d62634  
git last commit date: 2024-04-30 10:24:08 -0400

Package 3/2242

[a4Core 1.53.0 \(landing page\)](#)  
Laure Cougnaud  
git last commit: 977fb35

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

Click on any stage for more information

Hostname

OS / Arch

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

	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo2	Linux (Ubuntu 22.04.3 LTS) / x86_64	OK	OK	OK
Iconway	macOS 12.7.1 Monterey / x86_64	OK	OK	OK
Kjohnson3	macOS 13.6.5 Ventura / arm64	OK	OK	OK

Hostname

OS / Arch

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

	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo2	Linux (Ubuntu 22.04.3 LTS) / x86_64	OK	OK	OK
Iconway	macOS 12.7.1 Monterey / x86_64	OK	OK	OK
Kjohnson3	macOS 13.6.5 Ventura / arm64	OK	OK	OK

Hostname

OS / Arch

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

	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo2	Linux (Ubuntu 22.04.3 LTS) / x86_64	OK	OK	OK
Iconway	macOS 12.7.1 Monterey / x86_64	OK	OK	OK
Kjohnson3	macOS 13.6.5 Ventura / arm64	OK	OK	OK

Hostname

OS / Arch

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

	INSTALL	BUILD	CHECK	BUILD BIN
nebbiolo2	Linux (Ubuntu 22.04.3 LTS) / x86_64	OK	OK	OK
Iconway	macOS 12.7.1 Monterey / x86_64	OK	OK	OK
Kjohnson3	macOS 13.6.5 Ventura / arm64	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

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

- Email
  - [maria.doyle@ul.ie](mailto:maria.doyle@ul.ie) (Bioconductor Community Manager)
  - [lori.shepherd@roswellpark.org](mailto:lori.shepherd@roswellpark.org) (Bioconductor Project Manager / Core Team)
- [Community-bioc.slack.com](https://Community-bioc.slack.com)
  - Display names: [@Maria Doyle](#), [@lshepherd](#)