

News from the Bioconductor Project

by Bioconductor Core Team

[Bioconductor](#) provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor 3.13 was released on 20 May, 2021. It is compatible with R 4.1.0 and consists of 2042 software packages, 406 experiment data packages, 965 up-to-date annotation packages, and 29 workflows.

[Books](#) were introduced in Bioconductor 3.12 and production continues in this release. These are built regularly from source and therefore fully reproducible; an example is the community-developed [Orchestrating Single-Cell Analysis with Bioconductor](#).

The Bioconductor [3.13 release announcement](#) includes descriptions of 133 new software packages, and updates to NEWS files for many additional packages. Start using Bioconductor by installing the most recent version of R and evaluating the commands

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

Install additional packages and dependencies, e.g., [SingleCellExperiment](#), with

```
BiocManager::install("SingleCellExperiment")
```

[Docker](#) images provides a very effective on-ramp for power users to rapidly obtain access to standardized and scalable computing environments.

Key learning resources include:

- [bioconductor.org](#) to install, learn, use, and develop Bioconductor packages.
- A list of [available software](#), linking to pages describing each package.
- A question-and-answer style [user support site](#) and developer-oriented [mailing list](#).
- A community slack ([sign up](#)) for extended technical discussion.
- The [F1000Research Bioconductor channel](#) for peer-reviewed Bioconductor work flows.
- The [Bioconductor YouTube](#) channel includes recordings of keynote and talks from recent conferences including Bioc2020 and BiocAsia2020, in addition to video recordings of training courses.
- Our [package submission](#) repository for open technical review of new packages.

The [2021 Bioconductor conference](#) will be virtual, August 4-6, 2021.

In conjunction with the [Mexican Bioinformatics Network](#) and the [Nodo Nacional de Bioinformática CCG UNAM](#), the Comunidad de Desarrolladores de Software en Bioinformática have arranged two week-long [online workshops](#) addressing development of workflows with RStudio and shiny and analysis of single-cell RNA-seq experiments, August 9-13, 2021.

BiocAsia 2021 will be held November 1-4 2021 as a virtual event The website and call for contributed talks are not open yet. Keep an eye on [the events page](#) for updates. The Biopackathon project has many points of contact with Bioconductor and recurs monthly.

The National Human Genome Research Institute's Analysis and Visualization Laboratory ([AnVIL](#)) is developing with contributions from Bioconductor core team members. A [series of recorded workshops](#) on the use of Bioconductor to explore this cloud computing system is available; additional workshops will be presented in the Fall of 2021.

The Bioconductor project continues to mature as a community. The [Technical](#) and [Community](#) Advisory Boards provide guidance to ensure that the project addresses leading-edge biological problems with advanced technical approaches, and adopts practices (such

as a project-wide [Code of Conduct](#)) that encourages all to participate. We look forward to welcoming you!

Bioconductor Core Team
Biostatistics and Bioinformatics
Roswell Park Comprehensive Cancer Center, Buffalo, NY
USA maintainer@bioconductor.org