

# News from the Bioconductor Project

by *Bioconductor Core Team*

[Bioconductor](#) provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor 3.14 was released on 27 October, 2021. It is compatible with R 4.1.0 and consists of 2083 software packages, 408 experiment data packages, 904 up-to-date annotation packages, and 29 workflows.

The project has developed, over the last several years, the ‘AnnotationHub’ and ‘ExperimentHub’ resources for serving and managing genome-scale annotation data, e.g., from the TCGA, NCBI, and Ensembl. At the time of release there were 60134 records in the AnnotationHub, and 6075 ExperimentHub records. See [the WaldronLab shiny app](#) to get an overview of the AnnotationHub.

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

The Bioconductor 3.14 [release announcement](#) includes descriptions of 89 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 provide 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 Bioc2021 and BiocAsia2021, in addition to video recordings of training courses.
- Our [package submission](#) repository for open technical review of new packages.

The [2021 Bioconductor conference](#) was held in a virtual format 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 held 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](#) was held November 1-4 2021 as a virtual event. 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. Extensive [background material](#) includes a series of recorded workshops.

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!

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