

News from the Bioconductor Project

by *Bioconductor Core Team*

The *Bioconductor* project provides tools for the analysis and comprehension of high-throughput genomic data. *Bioconductor* 3.8 was released on 31 October, 2018. It is compatible with R 3.5.2 and consists of 1649 software packages, 360 experiment data packages, and 941 up-to-date annotation packages. The [release announcement](#) includes descriptions of 95 new software packages and updated NEWS files for many additional packages.

Start using *Bioconductor* by installing the most recent version of R and evaluating the commands

```
if (!requireNamespace("BiocManager"))
  install.packages("BiocManager")
BiocManager::install()
```

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

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

Additional [installation instructions](#) are available. [Docker](#) and [Amazon](#) images provide an effective on-ramp for power users to rapidly obtain access to standardized and scalable computing environments. Key resources include:

- The bioconductor.org web site to install, learn, use, and develop *Bioconductor* packages.
- A listing of [available software](#), linking to pages describing each package.
- A question-and-answer style [user support site](#) and developer-oriented [mailing list](#).
- The [F1000Research Bioconductor channel](#) for peer-reviewed *Bioconductor* work flows.
- Our [package submission](#) repository for open technical review of new packages.
- The *Bioconductor* [community slack](#) for in-depth conversation about *Bioconductor* software use and development.

Key training resources include [common workflows](#) and last year's conference [workshop booklet](#). Our [annual conference](#) will be on June 24 through 27, 2019 in New York City, with a line-up of morning scientific talks and afternoon user-orientate hands-on workshops, as well as a developer day, starting to take shape.

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