

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 3.10 was released on 30 October, 2019. It is compatible with R 3.6.1 and consists of 1823 software packages, 384 experiment data packages, 953 up-to-date annotation packages, and 27 workflows. The [release announcement](#) includes descriptions of 94 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", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install()
```

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

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

[Docker](#) and [Amazon](#) images provides a very 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 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.
- Our [package submission](#) repository for open technical review of new packages.

Our [annual conference](#) will be on July 29 - 31, 2020 in Boston, USA.

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