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-oriente hands-on workshops, as well as a developer day, starting to take shape.

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