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* 3.7 was released on 1 May, 2018. It is compatible with R 3.5.1 and consists of 1560 software packages, 342 experiment data packages, and 919 up-to-date annotation packages. The release announcement includes descriptions of 98 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

```
source("https://bioconductor.org/biocLite.R")
biocLite()
```

Install additional packages and dependencies, e.g., **SingleCellExperiment**, with

```
BiocInstaller::biocLite("SingleCellExperiment")
```

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.

Our annual conference will be on July 25 ('Developer Day'), 26, and 27, 2018, in Toronto, Canada, and features an exceptional line-up of morning scientific talks and afternoon hands-on workshops.

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