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 3.6 was released on 31 October, 2017. It is compatible with R 3.4.3 and consists of 1473 software packages, 326 experiment data packages, and 911 up-to-date annotation packages. The release announcement includes descriptions of 100 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

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

Install additional packages and dependencies, e.g., BiocFileCache, with

```r
BiocInstaller::biocLite("BiocFileCache")
```

Docker and Amazon images provide 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 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, still in the planning stages, will be on July 25 (‘Developer Day’), 26, and 27, in Toronto, Canada.

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