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 3.5 was released on 25 April, 2017. It is compatible with R 3.4 and consists of 1383 software packages, 316 experiment data packages, and 911 up-to-date annotation packages. The release announcement includes descriptions of 88 new 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., AnnotationHub, with

BiocInstaller::biocLite("AnnotationHub")

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:

- bioconductor.org to install, learn, use, and develop Bioconductor packages.
- A listing of available software, linked 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, BioC 2017: Where Software and Biology Connect, will be on June 26 (‘developer day’), 27 and 28, in Boston, MA.

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