News from the Bioconductor Project

by Bioconductor Core Team

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor 3.13 was released on 20 May, 2021. It is compatible with R 4.1.0 and consists of 2042 software packages, 406 experiment data packages, 965 up-to-date annotation packages, and 29 workflows.

Books were introduced in Bioconductor 3.12 and production continues in this release. These are built regularly from source and therefore fully reproducible; an example is the community-developed Orchestrating Single-Cell Analysis with Bioconductor.

The Bioconductor 3.13 release announcement includes descriptions of 133 new software packages, and updates to 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 images provides a very effective on-ramp for power users to rapidly obtain access to standardized and scalable computing environments.

Key learning resources include:

- bioconductor.org 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.

- The Bioconductor YouTube channel includes recordings of keynote and talks from recent conferences including Bioc2020 and BiocAsia2020, in addition to video recordings of training courses.

- Our package submission repository for open technical review of new packages.

The 2021 Bioconductor conference will be virtual, August 4-6, 2021.

In conjunction with the Mexican Bioinformatics Network and the Nodo Nacional de Bioinformática CCG UNAM, the Comunidad de Desarrolladores de Software en Bioinformática have arranged two week-long online workshops addressing development of workflows with RStudio and shiny and analysis of single-cell RNA-seq experiments, August 9-13, 2021.

BiocAsia 2021 will be held November 1-4 2021 as a virtual event The website and call for contributed talks are not open yet. Keep an eye on the events page for updates. The Biopackathon project has many points of contact with Bioconductor and recurs monthly.

The National Human Genome Research Institute's Analysis and Visualization Laboratory (AnVIL) is developing with contributions from Bioconductor core team members. A series of recorded workshops on the use of Bioconductor to explore this cloud computing system is available; additional workshops will be presented in the Fall of 2021.

The Bioconductor project continues to mature as a community. The Technical and Community Advisory Boards provide guidance to ensure that the project addresses leading-edge biological problems with advanced technical approaches, and adopts practices (such

as a project-wide Code of Conduct) that encourages all to participate. We look forward to welcoming you!

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