

# 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 3.4 was released on 18 October, 2016. It is compatible with R 3.3 and consists of 1296 software packages, 309 experiment data packages, and 933 up-to-date annotation packages. The [release announcement](#) includes descriptions of 101 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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