

News from the Bioconductor Project

Bioconductor Team

Program in Computational Biology

Fred Hutchinson Cancer Research Center

Bioconductor 2.12 was released on 3 October 2012. It is compatible with R 3.0.1, and consists of 671 software packages and more than 675 up-to-date annotation packages. The release includes 65 new software packages, and enhancements to many others. Descriptions of new packages and updated NEWS files provided by current package maintainers are at http://bioconductor.org/news/bioc_2_12_release/.

Start using Bioconductor and R version 3.0.1 with

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

Install additional packages, e.g., **VariantTools**, with

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("VariantTools")
```

Upgrade installed packages with

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

New this release is `biocValid()`, a companion function to detect R / Bioconductor version mis-matches.

Explore available Bioconductor packages at <http://bioconductor.org/packages/release/>. All packages are grouped by 'BiocViews' to identify coherent groups of packages. Each package has an html page with the descriptions and links to vignettes, reference manuals, and use statistics.

A Bioconductor Amazon Machine Instance is available and updated; see <http://bioconductor.org/help/bioconductor-cloud-ami>.

Core annotation and software packages

This release includes **AnnotationHub**, a resource that enables ready access to large genome-scale resources (e.g., GTF or FASTA files from Ensembl; ENCODE tracks from UCSC) in formats (e.g., GRanges or VCF instances) that allow smooth integration with R work flows. The **AnnotationHub** resource can be queried through simple tab completion, or via metadata about resource provenance. Additional new annotation resources include **ensemblVEP** to query the Ensembl Variant Effect Predictor, and **KEGGREST** and **UniProt.ws** packages for on-line integration of data from corresponding resources. Our large collection of microarray- and organism-specific annotation packages have been updated to include current information.

GenomicRanges and related packages, e.g., **VariantAnnotation**, **IRanges**, **Biostrings**, **Rsamtools**, **GenomicFeatures** provide an extensive, mature and extensible framework for interacting with high throughput sequence data, either as a user or package developer. Many contributed packages rely on this infrastructure for interoperable, re-usable analysis.

Other activities

Bioconductor's Annual Meeting is in Seattle, 17-19 July 2013, see <http://bioconductor.org/bioc2013>; our European developer community meets in December, with final arrangements

pending. Additional training and community activities advertised at <http://bioconductor.org/help/events/>. The active Bioconductor mailing lists (<http://bioconductor.org/help/mailling-list/>) connect users with each other, to domain experts, and to maintainers eager to ensure that their packages satisfy the needs of leading edge approaches. Keep abreast of packages added to the 'devel' branch and other activities by following Bioconductor on Twitter.

Package developers will be interested in ongoing efforts planned for our next release. Activities include better integration of parallel evaluation, graphical interfaces to Bioconductor objects (e.g., via [shiny](#), elaboration of **AnnotationHub** to support user-contributed and locally curated data, a repository for workflow and other packages that change infrequently but require significant computational resources to build, and efforts to ease integrate with github and other social coding resources. Our Google Summer of Code participants are enabling progress on some of these topics.