News from the Bioconductor Project

Bioconductor Team
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Bioconductor 2.13 was released on 15 October 2013. It is compatible with R 3.0.2, and consists of 749 software packages, 179 experiment data packages, and more than 690 up-to-date annotation packages. The release includes 84 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_13_release/.

Start using Bioconductor and R version 3.0.2 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()
```

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 Bioconductor packages

GenomicRanges and related packages continue to provide an extensive, mature and extensible framework for interacting with high throughput sequence data. Many contributed packages rely on this infrastructure for interoperable, re-usable analysis; Lawrence et al. (2013) provide an introduction.

Our large collection of microarray, transcriptome and organism-specific annotation packages have also been updated to include current information. Most of these packages now provide access to the 'select' interface (keys, columns, keytypes and select) which enable programmatic access to the databases they contain. This uniform interface simplifies the user experience; one illustration of this is in packages such as **Homo.sapiens**, which coordinate access to model organism gene, transcript, and pathway data bases. The **AnnotationHub**, now with more than 10,000 entries, complements our traditional offerings with diverse whole genome annotations from Ensembl, ENCODE, dbSNP, UCSC, and elsewhere.

This release includes the **PSICQUIC** package, an R interface to a powerful and standardized query language from the HUPO Proteomics Standard Initiative. More than two dozen well-known interaction databases are include, of which BioGrid, BIND, Reactome, STRING, IntAct, UniProt, DIP, and ChEMBL may be the best known. The query language uses a controlled vocabulary honed over several years by an active community, which returns documented and annotated interactions. One can now curate a detailed and up-to-date network illuminating functional relationships between genes and proteins of interest.

Other activities

In a change from the routine, our next Annual Meeting is in Boston, 30 July–1 August 2014, making it easier for east coast and European attendees. The 2013 Annual Meeting was in Seattle, 17–19 July, with our European developer community meeting in Cambridge, UK, 9–10 December. Our very active training and community events are advertised at http://bioconductor.org/help/events/. The Bioconductor mailing lists (http://bioconductor.org/help/mailing-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.

The past year marked our first participation in the Google Summer of Code project. We had many excellent applicants, and sponsored two projects to completion. GSoC participant Shawn Balcome, under Marc Carlson's mentoring, produced the **interactiveDisplay** package for Bioconductor / **shiny** integration. Michel Lang, mentored by Michael Lawrence, added very useful batch job and error recovery functionality to the **BiocParallel** package. This was a very successful experience!

Bibliography

M. Lawrence, W. Huber, H. Pagès, P. Aboyoun, M. Carlson, R. Gentleman, M. T. Morgan, and V. J. Carey. Software for computing and annotating genomic ranges. *PLoS Computational Biology*, 9(8):e1003118, 2013. doi: 10.1371/journal.pcbi.1003118. [p162]