News from the Bioconductor Project

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The Bioconductor project provides tools for the analysis and comprehension of high-throughput genomic data. The 1104 software packages available in Bioconductor can be viewed at http://bioconductor.org/packages/. Navigate packages using 'biocViews' terms and title search. Each package has an html page with a description, links to vignettes, reference manuals, and usage statistics. Start using Bioconductor version 3.2 by installing R 3.2.3 and evaluating the commands

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

Install additional packages and dependencies, e.g., **AnnotationHub**, with

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

Bioconductor 3.2 Release Highlights

Bioconductor 3.2 was released on 14 October 2015. It is compatible with R 3.2 and consists of 1104 software packages, 257 experiment data packages, and 917 up-to-date annotation packages. There are 80 new software packages and many updates and improvements to existing packages. The release announcement includes descriptions of new packages and updated NEWS files provided by package maintainers.

Our collection of microarray, transcriptome and organism-specific *annotation packages* use the 'select' interface (keys, columns, keytypes) to access static information on gene annotations (**org.*** packages) and gene models (**TxDb.*** packages); these augment packages such as **biomaRt** for interactive querying of web-based resources. The **AnnotationHub** continues to complement our traditional offerings with diverse whole genome annotations from Ensembl, ENCODE, dbSNP, UCSC, and elsewhere; example uses are described in the AnnotationHub How-To vignette.

Other activities

The Bioconductor project has moved from the Fred Hutchinson Cancer Research Center to Roswell Park Cancer Institute, in Buffalo, NY. The transition has brought with it many challenges and opportunities, including the departure of some long-term project personnel and the addition of new team members. In particular, Marc Carlson, Sonali Arora and Paul Shannon were instrumental in the design and implementation of **AnnotationHub** (and annotations in general), tools for biological network analysis, educational material and many other areas. The Bioconductor community is grateful to them for their many valuable contributions.

The Bioconductor F1000 research channel is a recently-launched forum for publication of task-oriented work flows. The channel is peer-reviewed, providing authors with a compelling venue for dissemination of their analysis methods. Users gain fully reproducible descriptions of tasks that cover current, genome-scale analysis problem from start to finish.

The Bioconductor support forum plays an increasing important role in providing with timely, knowledgeable, and accurate answers to user questions. A particularly valuable feature is the opportunity for community members to announce tutorial and other availability, such as Bioconductor for Genomic Data Science offered by long-term contributor Kasper D. Hansen. A highlight of the Bioconductor European Developer Meeting, held in

Cambridge, UK on 7 and 8 December, was recognition of the contributions Aaron Lun and Michael Love make to the success of the Bioconductor support forum through their patient and knowledgeable responses to diverse user questions.

Continued availability of Bioconductor Docker and Amazon images provides a very effective on-ramp for power users to rapidly obtain access to standardized and scalable computing environments. Docker images are available for release and development versions of Bioconductor, with analysis-specific images pre-loaded with packages relevant to common analysis scenarios, e.g., of sequencing, microarray, flow cell, or proteomic data. Both Amazon and Docker images include Rstudio Server for easy web-browser based access.

New Bioconductor package contributors are encouraged to consult the package guidelines and submission sections of the Bioconductor web site, and use the **BiocCheck** package, in addition to R CMD check, for guidance on conforming to Bioconductor package standards. New package submissions are automatically built across Linux, Mac, and Windows platforms, providing an opportunity to address cross-platform issues; many new package contributors take advantage of this facility to refine their package before it is subject to technical preview. Keep abreast of packages added to the 'devel' branch and other activities by following @Bioconductor on Twitter.

The Bioconductor web site advertises training and community events, including the BioC 2016, the Bioconductor annual conference, to be held in Stanford, CA, immediately before the annual *useR!* conference, Friday through Sunday, 24–25 June.