

R Foundation News

by Kurt Hornik

Donations and new members

New supporting institutions

Massachusetts General Hospital Biostatistics Center,
Boston, USA

National Public Health Institute, Helsinki, Finland

New supporting members

Micah Altman (USA)

Robert M. Baskin (USA)

Annette Baumann (Germany)

Abdu Benheddi (Switzerland)

David Booth (USA)

Rafael Borges (USA)

Lance Brannmann (USA)

Romain Francois (France)

John Gavin (UK)

David Henderson (USA)

Paulo Justiniano (Brasil)

Stephen Kaluzny (USA)

John Maindonald (Australia)

Masafumi Okada (Japan)

Friedrich Schuster (Germany)

Klemens Vierlinger (Austria)

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News from the Bioconductor Project

by Seth Falcon

Bioconductor 1.9 was released on October 4, 2006 and is designed to be compatible with R 2.4.0, released one day before Bioconductor. There are 26 new packages in the release and many improvements have been made to existing packages.

One area that has flourished in this release is software for analyzing cell-based assays. Below we summarize these developments. Of particular interest to the R community may be the **EBImage** package which provides an interface to the ImageMagick image processing library.

cellHTS Provides a comprehensive set of tools for the preprocessing, quality assessment and visualization of data from systematic cell-based screens, for example RNAi screens, and for the detection of effectors.

prada, **rflowcyt** Both provide import and management of data from flow cytometry, many visualization functions, and tools that help to do regression modeling on these data.

EBImage Provides an R class for storing 2D and 3D images. It provides an interface to the ImageMagick image processing and analysis library. All R functions that work on numeric vectors and arrays can be applied to the image objects. Other methods focus on detecting objects (cells) in the images and extracting numeric descriptors for the objects, so they can be subjected to regression and machine learning methods.

The *BiocViews* system (see the **biocViews** package), of package categorization introduced last May has been well received and is now the primary web interface for browsing Bioconductor packages. The views for the 1.9 release are available at <http://bioconductor.org/packages/1.9/BiocViews.html>. We are exploring web application frameworks, in particular Django, for providing more flexible query-based package discovery. A link to our prototype package search application is available at <http://bioconductor.org/apptest>.

The 2.0 release of Bioconductor is scheduled for April 2007. Core members are focusing on the following milestones for the 2.0 release:

- A new generation of annotation data packages that use SQLite databases instead of R environment objects.
- Updates to the **annotate** package to provide more flexible interfaces to the SQLite-based annotation packages.
- The release of **oligo** which will replace the **affy** package and provide cross-manufacturer support (presently Affymetrix and Nimblegen) for new high-throughput technologies such as SNP, exon, and tiling arrays.

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