twang Functions for propensity score estimating and weighting, nonresponse weighting, and diagnosis of the weights. By Greg Ridgeway, Dan McCaffrey, Andrew Morral.

untb Utilities for biodiversity data. Includes the simulation of ecological drift under Hubbell's Unified Neutral Theory of Biodiversity, and the calculation of various diagnostics such as Preston curves. By Robin K. S. Hankin.

wccsom SOM networks for comparing patterns with peak shifts. By Ron Wehrens.

Other changes

- Packages **fdim** and **sound** were resurrected from the Archive.

- Packages **Malmig**, **nlrq** and **nprq** were moved from the main CRAN section to the Archive.

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R Foundation News

by Kurt Hornik

Donations and new members

Donations

Christof Schramm (Germany)
Gordon Blunt (UK)
BC Cancer Agency (Canada)
David Kinniburgh (UK)
Richard Leeuw (USA)

New benefactors

Numbers Internation Pty Ltd, Australia
Institute of Mathematical Statistics, USA

New supporting institutions

Department of Statistics, University of California at Los Angeles, USA

Department of Statistics, Brigham Young University, USA

Max-Planck-Institut für demographische Forschung (MPI), Rostock, Germany

Center für digitale Systeme, Freie Universität Berlin, Germany

New supporting members

Axel Benner (Germany)
Gordon Blunt (UK)
Christopher Brown (USA)
Seth Falcon (USA)
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Matthew Wilkes (UK)
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News from the Bioconductor Project

by Seth Falcon

On April 27, 2006 the Bioconductor project released version 1.8 designed for the 2.3 release series of R. This release brings 35 newly contributed packages for a total of 173 packages. The sustained increase in the number of contributed packages demonstrates that the ideas of "publishing software, not just papers about software" and "reproducible research" have been adopted by many bioinformaticians around the world.

To help navigate the growing collection of packages, we've implemented a categorization system, inspired by Achim Zeileis' and Kurt Hornik's **ctv** package, called **biocViews**. The views generated by **biocViews** integrate Bioconductor's three main

package repositories (software, annotation data, and experiment data) and provide users with assistance in finding packages appropriate for their analysis needs. You can see the views for yourself by browsing to http://bioconductor.org/packages/1.8/BiocViews.html. The views that a given package appears in are determined through the **biocViews** field in the package's 'DESCRIPTION' file. Developers can control the categorization of their packages by setting the values of this field.

Another new addition with the 1.8 release is a collection of microarray annotation support packages for Affymetrix GeneChips. These cdf and probe packages are produced by the Molecular and Behavioral Neuroscience Institute (MBNI) at the University of Michigan. These new packages are fundamentally different from standard packages based on the Affymetrix probe set designations; each probe sequence is blasted against the current UniGene build and then filtered using a particular annotation source such as GenBank, Entrez Gene, ENSEMBL, or Tigr. Only those probes that blast to a unique genomic sequence are retained, so each probe set interrogates only one transcript. There are also packages designed for special situations such as analyzing chimpanzee samples with human chips, and packages with 3' biased probe sets for analyzing samples that may contain degraded mRNA. A word of caution is perhaps in order. The results obtained using the new packages will be different from those obtained with the standard packages; despite the advantage of more up-to-date annotation source data, it is not clear that the results based upon the new cdf packages should be preferred. For more information, visit the MBNI web page http://brainarray.mhri.med.umich.edu/Brainarray/

Database/CustomCDF/genomic_curated_CDF.asp.

Looking towards the 1.9 release, the core team will be working on improvements to allow Bioconductor to work with larger datasets and focusing on integrating new core classes that will allow representation of data from array-based technologies such as SNP and tiling arrays.

To this end, we have begun a redesign of our annotation data packages to allow them to use SQLite rather than R environments as the underlying data storage mechanism. This will provide additional flexibility, a slight decrease in disk use, and a significantly smaller memory footprint. The SQLite-based annotation packages will have a compatibility layer that will allow most programs that work with the current annotation packages to continue to function without change. However, we recommend interested users to familiarize themselves with the **RSQLite** package.

Many of our users are unable to process their microarray data on their current hardware due to memory limitations and we anticipate these problems to increase as more investigators attempt to process larger numbers of arrays simultaneously and as high-throughput technologies like SNP chips and tiling arrays become more popular. To address these issues, we will be working on bounded memory algorithms. As a starting point, we will implement a microarray normalization routine that will allow processing of an arbitrary number of arrays while requiring memory for just three arrays.

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Forthcoming Events: DSC 2007

The fifth conference on Directions in Statistical Computing will take place in Auckland, New Zealand, on February 15 and 16, 2007. This conference will deal with future directions in (open source) statistical computing and graphics.

Call for Papers

We invite abstracts on topics presenting innovations or exciting applications of statistical computing.

A web page offering more information on DSC 2007 and on-line registration is available at http://www.stat.auckland.ac.nz/dsc-2007/ Please send all abstracts to dsc-2007@stat.auckland.ac.nz.

We hope to see you in Auckland!

The organizing committee:
Paul Murrell, Ross Ihaka, David Scott, and Thomas Yee.
dsc-2007@stat.auckland.ac.nz