

termstrc Term Structure and Credit Spread Estimation. Offers several widely-used term structure estimation procedures, i.e., the parametric Nelson and Siegel approach, Svensson approach and cubic splines. By Robert Ferstl and Josef Hayden.

tframe Time Frame coding kernel. Functions for writing code that is independent of the way time is represented. By Paul Gilbert.

timsac TIME Series Analysis and Control package. By The Institute of Statistical Mathematics.

trackObjs Track Objects. Stores objects in files on disk so that files are automatically rewritten when objects are changed, and so that objects are accessible but do not occupy memory until they are accessed. Also tracks times when objects are created and modified, and cache some basic characteristics of objects to allow for fast summaries of objects. By Tony Plate.

tradeCosts Post-trade analysis of transaction costs. By Aaron Schwartz and Luyi Zhao.

tripEstimation Metropolis sampler and supporting functions for estimating animal movement from archival tags and satellite fixes. By Michael Sumner and Simon Wotherspoon.

twslm A two-way semilinear model for normalization and analysis of cDNA microarray data. Huber's and Tukey's bisquare weight functions are available for robust estimation of the two-way semilinear models. By Deli Wang and Jian Huang.

vbmp Variational Bayesian multinomial probit regression with Gaussian process priors. By Nicola Lama and Mark Girolami.

vrtest Variance ratio tests for weak-form market efficiency. By Jae H. Kim.

waved The WaveD Transform in R. Makes available code necessary to reproduce figures and tables in recent papers on the WaveD method for wavelet deconvolution of noisy signals. By Marc Raimondo and Michael Stewart.

wikibooks Functions and datasets of the german WikiBook "GNU R" which introduces R to new users. By Joerg Schlarmann.

wmtsa Insightful Wavelet Methods for Time Series Analysis. Software to book "Wavelet Methods for Time Series Analysis" by Donald B. Percival and Andrew T. Walden, Cambridge University Press, 2000. By William Constantine and Donald Percival.

wordnet An interface to WordNet using the Jawbone Java API to WordNet. By Ingo Feinerer.

yest Model selection and variance estimation in Gaussian independence models. By Petr Simecek.

Other changes

- CRAN's Devel area is gone.
- Package **write.snns** was moved up from Devel.
- Package **anm** was resurrected from the Archive.
- Package **Rcmdr.HH** was renamed to **Rcmdr-Plugin.HH**.
- Package **msgcop** was renamed to **sbgcop**.
- Package **grasper** was moved to the Archive.
- Package **tapiR** was removed from CRAN.

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R Foundation News

by Kurt Hornik

Donations and new members

Donations

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News from the Bioconductor Project

by *Hervé Pagès and Martin Morgan*

Bioconductor 2.1 was released on October 8, 2007 and is designed to be compatible with R 2.6.0, released five days before Bioconductor. This release contains 23 new software packages, 97 new annotation (or metadata) packages, and many improvements and bug fixes to existing packages.

New packages

The 23 new software packages provide exciting analytic and interactive tools. Packages address Affymetrix array quality assessment (e.g., **arrayQualityMetrics**, **AffyExpress**), error assessment (e.g., **OutlierD**, **MCRestimate**), particular application domains (e.g., comparative genomic hybridization, **CGHcall**, **SMAP**; SNP arrays, **oligoClasses**, **RLMM**, **VanillaICE**; SAGE, **sagenhaft**; gene set enrichment, **GSEABase**; protein interaction, **Rintact**) and sophisticated modeling tools (e.g., **timecourse**, **vbmp**, **maigesPack**). **exploRase** uses the GTK toolkit to provide an integrated user interface for systems biology applications.

Several packages benefit from important infrastructure developments in R. Recent changes allow consolidation of C code common to several packages into a single location (**preprocessCore**), greatly simplifying code maintenance and improving reliability. Many new packages use the S4 class system. A number of these extend classes provided in **Biobase**, facilitating more seamless interoperability. The ability to access web resources, including convenient XML parsing, allow Bioconductor packages such as **GSEABase** to access important curated resources.

SQLite-based annotations

This release provides SQLite-based annotations in addition to the traditional environment-based ones. Annotations contain *maps* between information from microarray manufactures, standard naming conventions (e.g., Entrez gene identifiers) and re-

sources such as the Gene Ontology consortium. Eighty-six SQLite-based annotation packages are currently available. The name of these packages end with ".db" (e.g., **hgu95av2.db**). For an example of different metadata packages related to specific chips, view the annotations available for the hgu95av2 chip: <http://bioconductor.org/packages/2.1/hgu95av2.html>

New *genome wide* metadata packages provide a more complete set of maps, similar to those provided in the chip-based annotation packages. Genome wide annotations have an "org." prefix in their name, and are available as SQLite-based packages only. Five organisms are currently supported: human (**org.Hs.eg.db**), mouse (**org.Mm.eg.db**), rat (**org.Rn.eg.db**), fly (**org.Dm.eg.db**) and yeast (**org.Sc.sgd.db**). The ***LLMappings** packages will be deprecated in Bioconductor 2.2.

Environment-based (e.g., **hgu95av2**) and SQLite-based (e.g., **hgu95av2.db**) packages contain the same data. For the end user, moving from **hgu95av2** to **hgu95av2.db** is transparent because the objects (or *maps*) in **hgu95av2.db** can be manipulated as if they were environments (i.e., functions `ls`, `mget`, `get`, etc... still work on them). Using SQLite allows considerable flexibility in querying maps and in performing complex joins between tables, in addition to placing the burden of memory management and optimized query construction in `sqlite`. As with the implementation of operations like `ls` and `mget`, the intention is to recognize common use cases and to code these so that R users do not need to know the underlying SQL query.

Looking ahead

For the next release (BioC 2.2, April 2008) all our annotations will be SQLite-based and we will deprecate the environment-based versions.

We anticipate increasing emphasis on sequence-based technologies like Solexa (<http://www.illumina.com>) and 454 (<http://www.454.com>). The volume of data these technologies generate is very large (a three day Solexa run produces almost a terabyte of raw data, with 10's of gigabytes appropriate