

Changes on CRAN

by Kurt Hornik

New contributed packages

AER Functions, data sets, examples, demos, and vignettes for the book “Applied Econometrics with R” by C. Kleiber and A. Zeileis (2008, Springer-Verlag, New York, ISBN 978-0-387-77316-2). By Achim Zeileis and Christian Kleiber.

ALS Multivariate curve resolution alternating least squares (MCR-ALS). Alternating least squares is often used to resolve components contributing to data with a bilinear structure; the basic technique may be extended to alternating constrained least squares. Commonly applied constraints include unimodality, non-negativity, and normalization of components. Several data matrices may be decomposed simultaneously by assuming that one of the two matrices in the bilinear decomposition is shared between datasets. By Katharine M. Mullen.

AdMit Performs fitting of an adaptive mixture of Student t distributions to a target density through its kernel function. The mixture approximation can then be used as the importance density in importance sampling or as the candidate density in the Metropolis-Hastings algorithm to obtain quantities of interest for the target density itself. By David Ardia, Lennart F. Hoogerheide and Herman K. van Dijk.

BCE Estimation of taxonomic compositions from biomarker data, using a Bayesian approach. By Karel Van den Meersche and Karline Soetaert.

BLCOP An implementation of the Black-Litterman Model and Atilio Meucci’s copula opinion pooling framework. By Francisco Gochez.

BaM Functions and datasets for “Bayesian Methods: A Social and Behavioral Sciences Approach” by J. Gill (Second Edition, 2007, CRC Press). By Jeff Gill.

BiplotGUI Provides a GUI with which users can construct and interact with biplots. By Anthony la Grange.

CADStat Provides a GUI to several statistical methods useful for causal assessment. Methods include scatterplots, boxplots, linear regression, generalized linear regression, quantile regression, conditional probability calculations, and regression trees. By Lester Yuan, Tom Stockton, Doug Bronson, Pasha Minallah and Mark Fitzgerald.

CHsharp Functions that cluster 3-dimensional data into their local modes. Based on a convergent form of Choi and Hall’s (1999) data sharpening method. By Douglas G. Woolford.

CTT Classical Test Theory Functions. By John T. Willse and Zhan Shu.

ConvergenceConcepts Provides a way to investigate various modes of convergence of random variables. By P. Lafaye de Micheaux and B. Liquet.

CvM2SL2Test Cramer-von Mises Two Sample Tests, featuring functionality to compute the exact p -value(s) for given Cramer-von Mises two-sample test score(s) under the assumption that the populations under comparison have the same probability distribution. By Yuanhui Xiao.

DiagnosisMed Analysis of data from diagnostic test accuracy evaluating health conditions. Designed for use by health professionals. Can estimate sample size for common situations in diagnostic test accuracy, estimate sensitivity and specificity from categorical and continuous test results including some evaluations of indeterminate results, or compare different analysis strategies into measures commonly used by health professionals. By Pedro Brasil.

EVER Estimation of Variance by Efficient Replication, providing delete-a-group jackknife replication. Gives estimates, standard errors and confidence intervals for: totals, means, absolute and relative frequency distributions, contingency tables, ratios, quantiles and regression coefficients, as well as for user-defined estimators (even non-analytic). By Diego Zardetto.

FITSio Utilities to read and write files in the FITS (Flexible Image Transport System) format, a standard format in astronomy. By Andrew Harris.

FTICRMS Programs for Analyzing Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry Data. By Don Barkauskas.

GExMap Analysis of genomic distribution of genes lists produced by transcriptomic studies. By N. Cagnard.

HAPim Provides a set of functions whose aim is to propose 4 methods of QTL detection: HAPimLD (an interval-mapping method designed for unrelated individuals with no family information that makes use of linkage disequilibrium), HAPimLDL (an interval-mapping

method for design of half-sib families, combining linkage analysis and linkage disequilibrium), HaploMax (based on an analysis of variance with a dose haplotype effect), and HaploMaxHS (based on an analysis of variance with a sire effect and a dose haplotype effect in half-sib family design). By S. Dejean, N. Oumouhou, D. Estivals and B. Mangin.

LDtests Exact tests for Linkage Disequilibrium (LD) and Hardy-Weinberg Equilibrium (HWE). By Alex Lewin.

LIStest Compute the p -value for the Longest Increasing Subsequence Independence Test (for continuous random variables). By Jesus Garcia and Veronica Andrea Gonzalez Lopez.

MAclinical Class prediction based on microarray data and clinical parameters. Prediction is performed using a two-step method combining (pre-validated) PLS dimension reduction and random forests. By Anne-Laure Boulesteix.

MCAPS Weather and air pollution data, risk estimates, and other information from the Medicare Air Pollution Study (MCAPS) of 204 U.S. counties, 1999–2002. By Roger D. Peng.

MDD Calculates Minimum Detectable Difference (MDD) for several continuous and binary endpoints. Also contains programs to compare the MDD to the clinically significant difference for most of the same tests. By Don Barkauskas.

Mifuns Pharmacometric tools for common data preparation tasks, stratified bootstrap resampling of data sets, NONMEM control stream creation/editing, NONMEM model execution, creation of standard and user-defined diagnostic plots, execution and summary of bootstrap and predictive check results, implementation of simulations from posterior parameter distributions, reporting of output tables and creation of a detailed analysis log. By Bill Knebel.

MKmisc Miscellaneous Functions from M. Kohl. By Matthias Kohl.

MSVAR Estimation of a 2 state Markov Switching VAR. By James Eustace.

Metabonomic Graphical user interface for metabonomic analysis (baseline, normalization, peak detection, PCA, PLS, nearest neighbor, neural network). By Jose L. Izquierdo.

NetIndices Estimates network indices, including trophic structure of foodwebs. Indices include ascendancy network indices, direct and indirect dependencies, effective measures, environ network indices, general network indices, pathway analysis, network uncertainty indices

and constraint efficiencies and the trophic level and omnivory indices of food webs. By Karline Soetaert and Julius Kipkeygon Kones.

OPE Fit an outer-product emulator to the multivariate evaluations of a computer model. By Jonathan Rougier.

PBSddesolve Solver for Delay Differential Equations via interfacing numerical routines written by Simon N. Wood, with contributions by Benjamin J. Cairns. Replaces package **ddesolve**. By Alex Couture-Beil, Jon Schnute and Rowan Haigh.

PSM Estimation of linear and non-linear mixed-effects models using stochastic differential equations. Also provides functions for finding smoothed estimates of model states and for simulation. Allows for any multivariate non-linear time-variant model to be specified, and also handles multi-dimensional input, covariates, missing observations and specification of dosage regimen. By Stig Mortensen and Søren Klim.

PolynomF Univariate polynomial operations in R. By Bill Venables.

Pomic Calculations of Pattern Oriented Modeling Information Criterion (POMIC), a non-parsimonious based information criterion, to check the quality of simulations results of ABM/IBM or other non-linear rule-based models. The POMIC is based on the KL divergence and likelihood theory. By Cyril Piou.

PredictiveRegression Prediction intervals for three algorithms described in “On-line predictive linear regression” (Annals of Statistics, 2008). By Vladimir Vovk and Ilia Nourtdinov.

PtProcess Time dependent point process modeling, with an emphasis on earthquake modeling. By David Harte.

R2jags Running JAGS from R. By Yu-Sung Su and Masanao Yajima.

Rltools Tools for randomization inference. By Jake Bowers, Mark Fredrickson and Ben Hansen.

RKEA An R interface to KEA (Version 5.0). By Ingo Feinerer.

RM2 Functions used in revenue management and pricing environments. By Tudor Bodea, Dev Koushik and Mark Ferguson.

RPostgreSQL Database interface and PostgreSQL driver for R. Complies with the database interface definition as implemented in package **DBI**. By Sameer Kumar Prayaga with mentor Dirk Eddelbuettel.

- Ratings** Functions to implement the methods described in “Improving the Presentation and Interpretation of Online Ratings Data with Model-based Figures” by Ho and Quinn (The American Statistician). By Kevin M. Quinn and Daniel E. Ho.
- Read.isi** Automated access to old World Fertility Survey data saved in fixed-width format based on ISI-formatted codebooks. By Rense Nieuwenhuis.
- ResearchMethods** Using GUIs to help teach statistics to non-statistics students. By Sam Stewart and Mohammed Abdolell.
- RobAStBase** Base S4 classes and functions for robust asymptotic statistics. By Matthias Kohl and Peter Ruckdeschel.
- Rsg** Functions for using R with the SGE cluster/grid queuing system. By Dan Bode.
- SASPECT** Significant Analysis of PEptide CounTs. A statistical method for significant analysis of comparative proteomics based on LC-MS/MS Experiments. By Pei Wang and Yan Liu.
- SDDA** Stepwise Diagonal Discriminant Analysis — a fast algorithm for building multivariate classifiers. By CSIRO Bioinformatics, Glenn Stone.
- SGP** Calculate growth percentile and projections for students using large scale, longitudinal assessment data. These norm referenced growth values are presently used in some state testing and accountability systems. The functions use quantile regression techniques package to estimate the conditional density associated with each student’s achievement history. Student Growth Projections (i.e., percentile growth trajectories) help to identify what it will take for students to reach future achievement targets. By Damian W. Betebenner, with contributions from Jonathan Weeks, Jinnie Choi, Xin Wei and Hi Shin Shim.
- SMVar** Structural Model for Variances in order to detect differentially expressed genes from gene expression data. By Guillemette Marot.
- SNPMaP** SNP Microarrays and Pooling in R. Pooling DNA on SNP microarrays is a cost-effective way to carry out genome-wide association studies for heritable disorders or traits. By Oliver SP Davis and Leo C Schalkwyk.
- SNPMaP.cdm** Annotation for SNP Microarrays and Pooling in R: provides cdm objects for the **SNPMaP** package. By Oliver SP Davis and Leo C Schalkwyk.
- SQLiteMap** Manage vector graphical maps using SQLite. By Norbert Solymosi.
- STAR** Spike Train Analysis with R: functions to analyze neuronal spike trains from a single neuron or from several neurons recorded simultaneously. By Christophe Pouzat.
- SiZer** ‘SiZer: Significant Zero Crossings. Calculates and plots the SiZer map for scatterplot data. A SiZer map is a way of examining when the p -th derivative of a scatterplot-smoother is significantly negative, possibly zero or significantly positive across a range of smoothing bandwidths. By Derek Sonderegger.
- SimpleTable** Methods to conduct Bayesian inference and sensitivity analysis for causal effects from 2×2 and $2 \times 2 \times K$ tables when unmeasured confounding is present or suspected. By Kevin M. Quinn.
- SpatialExtremes** Several approaches to spatial extremes modeling. By Mathieu Ribatet.
- StatMatch** Perform statistical matching between two data sources and also for imputing missing values in data sets through hot deck methods. By Marcello D’Orazio.
- StreamMetabolism** Calculate single station metabolism from diurnal Oxygen curves. By Stephen A Sefick Jr.
- TinnR** Tinn-R GUI/editor resources for R. By Jose Claudio Faria, based on code by Philippe Grosjean.
- TraMineR** Sequences and trajectories mining for the field of social sciences, where sequences are sets of states or events describing life histories, for example family formation histories. Provides tools for translating sequences from one format to another, statistical functions for describing sequences and methods for computing distances between sequences using several metrics like optimal matching and some other metrics proposed by C. Elzinga. By Alexis Gabadinho, Matthias Studer, Nicolas S. Müller and Gilbert Ritschard.
- VhayuR** Vhayu R Interface. By The Brookhaven Group.
- apsrtable** Formats \LaTeX tables from one or more model objects side-by-side with standard errors below, not unlike tables found in such journals as the American Political Science Review. By Michael Malecki.
- audio** Interfaces to audio devices (mainly sample-based) from R to allow recording and playback of audio. Built-in devices include Windows MM, Mac OS X AudioUnits and PortAudio (the last one is very experimental). By Simon Urbanek.

- bark** Bayesian Additive Regression Kernels. Implementation of BARK as described in Zhi Ouyang's 2008 Ph.D. thesis. By Zhi Ouyang, Merlise Clyde and Robert Wolpert.
- bayesGARCH** Bayesian estimation of the GARCH(1,1) model with Student's t innovations. By David Ardia.
- bear** An average bioequivalence (ABE) and bioavailability data analysis tool including sample size estimation, noncompartmental analysis (NCA) and ANOVA (lm) for a standard RT/TR 2-treatment, 2-sequence, 2-period, and balanced, cross-over design. By Hsin-ya Lee and Yung-jin Lee.
- betaper** Evaluates and quantifies distance decay of similarity among biological inventories in the face of taxonomic uncertainty. By Luis Cayuela and Marcelino de la Cruz.
- bigmemory** Use C++ to create, store, access, and manipulate massive matrices. Under UNIX, it also supports use of shared memory. By Michael J. Kane and John W. Emerson.
- bise** Some easy-to-use functions for spatial analyses of (plant-) phenological data sets and satellite observations of vegetation. By Daniel Doktor.
- bit** A class for vectors of 1-bit booleans. With bit vectors you can store true binary booleans at the expense of 1 bit only; on a 32 bit architecture this means factor 32 less RAM and factor 32 more speed on boolean operations. By Jens Oehlschlägel.
- bmd** Benchmark dose analysis for continuous and quantal dose-response data. By Christian Ritz.
- bpca** Biplot (2d and 3d) of multivariate data based on principal components analysis and diagnostic tools of the quality of the reduction. By Jose Claudio Faria and Clarice Garcia Borges Demetrio.
- ccgarch** Estimation and simulation of Conditional Correlation GARCH (CC-GARCH) models. By Tomoaki Nakatani.
- cem** Coarsened Exact Matching. Implements the CEM algorithm (and many extensions) described in "Matching for Causal Inference Without Balance Checking" by Stefano M. Iacus, Gary King, and Giuseppe Porro (<http://gking.harvard.edu/files/abs/cem-abs.shtml>). By Stefano Iacus, Gary King and Giuseppe Porro.
- compare** Functions for comparing vectors and data frames. By Paul Murrell.
- compoisson** Routines for density and moments of the Conway-Maxwell-Poisson distribution as well as functions for fitting the COM-Poisson model for over/under-dispersed count data. By Jeffrey Dunn.
- convexHaz** Functions to compute the nonparametric maximum likelihood estimator (MLE) and the nonparametric least squares estimator (LSE) of a convex hazard function, assuming that the data is i.i.d. By Hanna Jankowski, Ivy Wang, Hugh McCague and Jon A. Wellner.
- copas** Statistical methods to model and adjust for bias in meta-analysis. By James Carpenter and Guido Schwarzer.
- coxphw** Weighted estimation for Cox regression. R by Meinhard Ploner, FORTRAN by Georg Heinze.
- curvetest** Test if two curves defined by two data sets are equal, or if one curve is equal to zero. By Zhongfa Zhang and Jiayang Sun.
- dataframes2xls** Write data frames to '.xls' files. Supports multiple sheets and basic formatting. By Guido van Steen.
- ddst** Data driven smooth test. By Przemyslaw Biecek (R code) and Teresa Ledwina (support, descriptions).
- deSolve** General solvers for ordinary differential equations (ODE) and for differential algebraic equations (DAE). The functions provide an interface to the FORTRAN functions lsoda, lsodar, lsode, lsodes, dvide and daspk. The package also contains routines designed for solving uni- and multicomponent 1-D and 2-D reactive transport models. By Karline Soetaert, Thomas Petzoldt and R. Woodrow Setzer.
- denstrip** Graphical methods for compactly illustrating probability distributions, including density strips, density regions, sectioned density plots and varying width strips. By Christopher Jackson.
- dfcrm** Dose-finding by the continual reassessment method. Provides functions to run the CRM and TITE-CRM in phase I trials and calibration tools for trial planning purposes. By Ken Cheung.
- diffractometry** Residual-based baseline identification and peak decomposition for x-ray diffractograms as introduced in the corresponding paper by Davies et al. (2008, *Annals of Applied Statistics*). By P. L. Davies, U. Gather, M. Meise, D. Mergel and T. Mildenerger. Additional Code by T. Bernholt and T. Hofmeister.

- dirichlet** Dirichlet model of consumer buying behavior for marketing research. The Dirichlet (aka NBD-Dirichlet) model describes the purchase incidence and brand choice of consumer products. Provides model estimation and summaries of various theoretical quantities of interest to marketing researchers. Also provides functions for making tables that compare observed and theoretical statistics. By Feiming Chen.
- distrMod** Object orientated implementation of probability models based on packages **distr** and **distrEx**. By Matthias Kohl and Peter Ruckdeschel.
- distrTeach** Extensions of package **distr** for teaching stochastics/statistics in secondary school. By Peter Ruckdeschel, Matthias Kohl, Anja Hueller and Eleonara Feist.
- divagis** Tools for quality checks of georeferenced plant species accessions. By Reinhard Simon.
- dti** DTI Analysis. Diffusion Weighted Imaging is a Magnetic Resonance Imaging modality that measures diffusion of water in tissues like the human brain. The package contains unctions to process diffusion-weighted data in the context of the diffusion tensor model (DTI), including the calculation of anisotropy measures and, the implementation of the structural adaptive smoothing algorithm described in "Diffusion Tensor Imaging: Structural Adaptive Smoothing" by K. Tabelow, J. Polzehl, V. Spokoiny, and H.U. Voss (2008, Neuroimage 39(4), 1763-1773). By Karsten Tabelow and Joerg Polzehl.
- dynamo** Routines for estimation, simulation, regularization and prediction of univariate dynamic models including: ARMA, ARMA-GARCH, ACD, MEM. By Christian T. Brownlees.
- ecolMod** Figures, data sets and examples from the book "A practical guide to ecological modelling — using R as a simulation platform" by Karline Soetaert and Peter MJ Herman (2008, Springer). By Karline Soetaert and Peter MJ Herman.
- empiricalBayes** A bundle providing a simple solution to the extreme multiple testing problem by estimating local false discovery rates. Contains two packages, **localFDR** and **HighProbability**. Given a vector of p -values, the former estimates local false discovery rates and the latter determines which p -values are low enough that their alternative hypotheses can be considered highly probable. By Zahra Montazeri and David R. Bickel.
- entropy** Implements various estimators of entropy, such as the shrinkage estimator by Hausser and Strimmer, the maximum likelihood and the Millow-Madow estimator, various Bayesian estimators, and the Chao-Shen estimator. It also offers an R interface to the NSB estimator. Furthermore, it provides functions for estimating mutual information. By Jean Hauser and Korbinian Strimmer.
- eqtl** Analysis of experimental crosses to identify genes (called quantitative trait loci, QTLs) contributing to variation in quantitative traits, a complementary to Karl Broman's **qtl** package for genome-wide analysis. By Ahmid A. Khalili and Olivier Loudet.
- etm** Empirical Transition Matrix: matrix of transition probabilities for any time-inhomogeneous multistate model with finite state space. By Arthur Allignol.
- expert** Modeling without data using expert opinion. Expert opinion (or judgment) is a body of techniques to estimate the distribution of a random variable when data is scarce or unavailable. Opinions on the quantiles of the distribution are sought from experts in the field and aggregated into a final estimate. Supports aggregation by means of the Cooke, Mendel-Sheridan and predefined weights models. By Mathieu Pigeon, Michel Jacques and Vincent Goulet.
- fbati** Family-based gene by environment interaction tests, and joint gene, gene-environment interaction test. By Thomas Hoffmann.
- fgui** Function GUI: rapidly create a GUI for a function by automatically creating widgets for arguments of the function. By Thomas Hoffmann.
- fossil** Palaeoecological and palaeogeographical analysis tools. Includes functions for estimating species richness (Chao 1 and 2, ACE, ICE, Jackknife), shared species/beta diversity, species area curves and geographic distances and areas. By Matthew Vavrek.
- frontier** Maximum Likelihood Estimation of stochastic frontier production and cost functions. Two specifications are available: the error components specification with time-varying efficiencies (Battese and Coelli, 1992) and a model specification in which the firm effects are directly influenced by a number of variables (Battese and Coelli, 1995). By Tim Coelli and Arne Henningsen.
- fts** R interface to tslib (a time series library in C++). By Whit Armstrong.

- fuzzyOP** Fuzzy numbers and the main mathematical operations for these. By Aklan Semagul, Altindas Emine, Macit Rabiye, Umar Senay and Unal Hatice.
- gWidgetsWWW** Toolkit implementation of **gWidgets** for www. By John Verzani.
- gbs** Utilities for analyzing censored and uncensored data from generalized Birnbaum-Saunders distributions. By Michelli Barros, Victor Leiva and Gilberto A. Paula.
- gene2pathway** Prediction of KEGG pathway membership for individual genes based on InterPro domain signatures. By Holger Froehlich, with contributions by Tim Beissbarth.
- geonames** Interface to `www.geonames.org` web service. By Barry Rowlingson.
- glmmBUGS** Generalized Linear Mixed Models with WinBUGS. By Patrick Brown.
- glmnet** Extremely efficient procedures for fitting the entire lasso or elastic-net regularization path for linear regression, logistic and multinomial regression models, using cyclical coordinate descent in a pathwise fashion. By Jerome Friedman, Trevor Hastie and Rob Tibshirani.
- gmm** Estimation of parameters using the generalized method of moments (GMM) of Hansen (1982). By Pierre Chausse.
- grade** Binary Grading functions for R. By Leif Johnson.
- gtm** Generative topographic mapping. By Ondrej Such.
- hlr** Hidden Logistic Regression. Implements the methods described in Rousseeuw and Christman (2003) to cope with separation issues and outliers in logistic regression. Original S-PLUS code by Peter J. Rousseeuw and Andreas Christmann, R port by Tobias Verbeke.
- hwriter** HTML Writer: easy-to-use and versatile functions to output R objects in HTML format. By Gregoire Pau.
- ic.infer** Inequality constrained inference in linear normal situations. Implements parameter estimation in normal (linear) models under linear equality and inequality constraints as well as likelihood ratio tests involving inequality-constrained hypotheses. By Ulrike Groemping.
- ic50** Standardized high-throughput evaluation of compound screens. Calculation of IC50 values, automatic drawing of dose-response curves and validation of compound screens on 96- and 384-well plates. By Peter Frommolt.
- icomp** Calculates the ICOMP criterion and its variations. By Jake Ferguson.
- imputeMDR** Multifactor Dimensionality Reduction (MDR) analysis for incomplete data. By Junghyun Namkung, Taeyoung Hwang, Min-Seok Kwon, Sunggon Yi and Wonil Chung.
- intervals** Tools for working with and comparing sets of points and intervals. By Richard Bourgon.
- kml** K-Means for Longitudinal data (kml), a non parametric algorithm for clustering longitudinal data. By Christophe M. Genolini.
- laercio** Functions to compare group means (Duncan test, Tukey test and Scott-Knott test). By Laercio Junio da Silva.
- lda.cv** Cross-validation for linear discriminant analysis. By Wenxuan Zhong.
- lmom** L-moments: computation of L-moments of distributions and data samples, parameter estimation, L-moment ratio diagram, and plot against quantiles of an extreme-value distribution. By J. R. M. Hosking.
- loglognorm** Double log normal distribution functions. By Heike Trautmann, Detlef Steuer and Olaf Mersmann.
- lpSolveAPI** An R interface to the `lp_solve` library API. `lp_solve` is a Mixed Integer Linear Programming (MILP) solver with support for pure linear, (mixed) integer/binary, semi-continuous and special ordered sets (SOS) models. By Kjell Konis.
- lpc** Implements the Lassoed Principal Components (LPC) method of Witten & Tibshirani (2008) for identification of significant genes in a microarray experiment. By Daniela M Witten and Robert Tibshirani.
- marelac** Datasets, chemical and physical constants and functions, routines for unit conversions, etc, for the marine and lacustrine sciences. By Karline Soetaert and Filip Meysman.
- marginalmodelplots** Marginal model plots for linear and generalized linear models, including tools for bandwidth exploration. By Andrew Redd.
- mco** Functions for multi criteria optimization using genetic algorithms and related test problems. By Heike Trautmann, Detlef Steuer and Olaf Mersmann.
- mi** Missing-data imputation and model checking. By Andrew Gelman, Jennifer Hill, Masanao Yajima, Yu-Sung Su and Maria Grazia Pittau.

- mirf** Multiple Imputation and Random Forests for unobservable phase, high-dimensional data. Applies a combination of missing haplotype imputation via the EM algorithm of Excoffier and Slatkin (1995) and modeling trait-haplotype associations via the Random Forest algorithm, as described in "Multiple imputation and random forests (MIRF) for unobservable high-dimensional data" by B.A.S. Nonyane and A.S. Foulkes (2007, *The International Journal of Biostatistics* 3(1): Article 12). By Yimin Wu, B. Aletta S. Nonyane and Andrea S. Foulkes.
- mixer** Estimation of Erdős-Rényi mixture for graphs. By Christophe Ambroise, Gilles Grasseau, Mark Hoebeke and Pierre Latouche.
- mixlow** Assessing drug synergism/antagonism. By John Boik.
- mlogit** Estimation of the multinomial logit model with alternative and/or individual specific variables. By Yves Croissant.
- mpm** Multivariate Projection Methods: exploratory graphical analysis of multivariate data, specifically gene expression data with different projection methods: principal component analysis, correspondence analysis, spectral map analysis. By Luc Wouters.
- mrdr** Model-Robust Concentration-Response Analysis semi-parametric modeling of continuous and quantal concentration/dose-response data. By Christian Ritz and Mads Jeppe Tarp-Johansen.
- msBreast** A dataset of 96 protein mass spectra generated from a pooled sample of nipple aspirate fluid (NAF) from healthy breasts and breasts with cancer. By Lixin Gong, William Constantine and Yu Alex Chen.
- msDilution** A dataset of 280 MALDI-TOF mass spectra generated from a dilution experiment aimed at elucidating which features in MALDI-TOF mass spectrometry data are informative for quantifying peptide content. By Lixin Gong, William Constantine and Yu Alex Chen.
- msProstate** A dataset of protein mass spectra generated from patients with prostate cancer, benign prostatic hypertrophy, and normal controls. By Lixin Gong, William Constantine and Alex Chen.
- nparcomp** Computation of nonparametric simultaneous confidence intervals and simultaneous p -values for relative contrast effects in the unbalanced one way layout. The simultaneous confidence intervals can be computed using multivariate normal distribution, multivariate t -distribution with a Satterthwaite Approximation of the degree of freedom, or using multivariate range preserving transformations with logit or probit as transformation function. By Frank Konietzschke.
- onemap** Software for constructing genetic maps in outcrossing species. Analysis of molecular marker data from non-model systems to simultaneously estimate linkage and linkage phases. By Gabriel Rodrigues Alves Margarido, with contributions from Antonio Augusto Franco Garcia.
- opentick** Provide an interface to opentick real time and historical market data. By Josh Ulrich.
- orloca** The Operations Research LOCational Analysis models. Deals with the min-sum or center location problems. By Fernando Fernandez-Palacin and Manuel Munoz-Marquez.
- orloca.es** Spanish version of package **orloca**. By Fernando Fernandez-Palacin and Manuel Munoz-Marquez.
- orth** Performs multivariate logistic regressions by way of orthogonalized residuals. As a special case, the methodology recasts alternating logistic regressions in a way that is consistent with standard estimating equation theory. Cluster diagnostics and observation level diagnostics such as leverage and Cook's distance are computed based on an approximation. By Kunthel By, Bahjat F. Qaqish and John S. Preisser.
- pack** Functions to easily convert data to binary formats other programs/machines can understand. By Josh Ulrich.
- packClassic** Illustration of the tutorial "S4: From Idea To Package". By Christophe Genolini and some reader that sent useful comments.
- paltran** Functions for paleolimnology: wa-regression (see also package **analogue**), wa-pls and MW regression. By Sven Adler.
- pec** Prediction Error Curves for survival models: validation of predicted survival probabilities using inverse weighting and resampling. By Thomas A. Gerds.
- peperr** Parallelized Estimation of Prediction Error. Prediction error estimation through resampling techniques, possibly accelerated by parallel execution on a computer cluster. By Christine Porzelius and Harald Binder.
- picante** Phylocom integration, community analyses, null-models, traits and evolution in R. By Steve Kembel, David Ackerly, Simon Blomberg, Peter Cowan, Matthew Helmus and Cam Webb.

- plyr** Tools for splitting, applying and combining data. By Hadley Wickham.
- qdg** QTL Directed Graphs: infer QTL-directed dependency graphs for phenotype networks. By Elias Chaibub Neto and Brian S. Yandell.
- qlspack** Quasi Least Squares (QLS) package. QLS is a two-stage computational approach for estimation of the correlation parameters within the framework of GEE. It helps solving parameters in mean, scale, and correlation structures for longitudinal data. By Jichun Xie and Justine Shults.
- rPorta** An R interface to a modified version of PORTA (see <http://www.zib.de/Optimization/Software/Porta/>). By Robin Nunkesser, Silke Straatmann and Simone Wenzel.
- randtoolbox** Toolbox for pseudo and quasi random number generation and RNG tests. Provides general linear congruential generators (Park Miller) and multiple recursive generators (Knuth TAOCP), generalized feedback shift register (SF-Mersenne Twister algorithm and WELL generator), the Torus algorithm, and some additional tests (gap test, serial test, poker test, ...). By Christophe Dutang, with the SFMT algorithm from M. Matsumoto and M. Saito, the WELL generator from P. L'Ecuyer, and the Knuth-TAOCP RNG from D. Knuth).
- rbounds** Perform Rosenbaum bounds sensitivity tests for matched data. Calculates bounds for binary data, Hodges-Lehmann point estimates, Wilcoxon signed-rank test, and for data with multiple matched controls. Is designed to work with package **Matching**. By Luke J. Keele.
- rdetools** Functions for Relevant Dimension Estimation (RDE) of a data set in feature spaces, applications to model selection, graphical illustrations and prediction. By Jan Saputra Mueller.
- repolr** Repeated measures proportional odds logistic regression via generalized estimating equations. By Nick Parsons.
- rjags** Bayesian graphical models via an interface to the JAGS MCMC library. By Martyn Plummer.
- rootSolve** Nonlinear root finding, equilibrium and steady-state analysis of ordinary differential equations. Includes routines that: (1) generate gradient and Jacobian matrices (full and banded), (2) find roots of non-linear equations by the Newton-Raphson method, (3) estimate steady-state conditions of a system of (differential) equations in full, banded or sparse form, using the Newton-Raphson method, or by dynamically running, (4) solve the steady-state conditions for uni-and multicomponent 1-D and 2-D reactive transport models (boundary value problems of ODE) using the method of lines approach. By Karline Soetaert.
- roxygen** Literate Programming in R: a Doxygen-like in-source documentation system for Rd, collation, namespace and callgraphs. By Peter Dabenberg and Manuel Eugster.
- rscproxy** Provides a portable C-style interface to R (StatConnector) used by third party applications, most notable, but not limited to, rcom/R Scilab (D)COM Server, ROOo and other systems. By Thomas Baier.
- runjags** Run Bayesian MCMC models in the BUGS syntax from within R. Includes functions to read external WinBUGS type text files, and allows several ways of automatically specifying model data from existing R objects or R functions. Also includes functions to automatically calculate model run length, autocorrelation and Gelman Rubin statistic diagnostics for all models to simplify the process of achieving chain convergence. Requires Just Another Gibbs Sampler (JAGS, <http://www-fis.iarc.fr/~martyn/software/jags/>) for most functions. By Matthew Denwood (funded as part of the DEFRA VTRI project 0101).
- rwm** APL-like functions for managing R workspaces. By A.I. McLeod.
- sdalt** Signal detection theory measures and alternatives, as detailed in the book "Functions for traditional and multilevel approaches to signal detection theory" by D.B. Wright, R. Horry and E.M. Skagerberg, E.M. (in press, Behavior Research Methods). By Daniel B. Wright.
- sensR** Thurstonian models for sensory discrimination. By Rune Haubo B Christensen and Per Bruun Brockhoff.
- singlecase** Various functions for the single-case research in neuropsychology, mainly dealing with the comparison of a patient's test score (or score difference) to a control or normative sample. These methods also provide a point estimate of the percentage of the population that would obtain a more extreme score (or score difference) and, for some problems, an accompanying interval estimate (i.e., confidence limits) on this percentage. By Matthieu Dubois.
- smacof** provides the following approaches to multidimensional scaling (MDS) based on stress minimization by means of majorization (smacof): Simple smacof on symmetric dissimilarity matrices, smacof for rectangular matrices (unfolding models), smacof with constraints

on the configuration, three-way smacof for individual differences (including constraints for idioscal, indscal, and identity), and spherical smacof (primal and dual algorithm). Each of these approaches is implemented in a metric and nonmetric manner including primary, secondary, and tertiary approaches for tie handling. By Jan de Leeuw and Patrick Mair.

snowfall Top-level wrapper around **snow** for easier development of parallel R programs. All functions work in sequential mode, too, if no cluster is present or wished. By Jochen Knaus.

spssDDI Read SPSS System files and produce valid DDI version 3.0 documents. By Guido Gay.

ssize.fdr Sample size calculations for microarray experiments, featuring appropriate sample sizes for one-sample *t*-tests, two-sample *t*-tests, and *F*-tests for microarray experiments based on desired power while controlling for false discovery rates. For all tests, the standard deviations (variances) among genes can be assumed fixed or random. This is also true for effect sizes among genes in one-sample experiments and differences in mean treatment expressions for two-sample experiments. Functions also output a chart of power versus sample size, a table of power at different sample sizes, and a table of critical test values at different sample sizes. By Megan Orr and Peng Liu.

tframePlus Time Frame coding kernel extensions. By Paul Gilbert.

tileHMM Hidden Markov Models for ChIP-on-Chip Analysis. Provided parameter estimation methods include the Baum-Welch algorithm and Viterbi training as well as a combination of both. By Peter Humbug.

timereg Programs for the book “Dynamic Regression Models for Survival Data” by T. Martinussen and T. Scheike (2006, Springer Verlag), plus more recent developments. By Thomas Scheike, with contributions from Torben Martinussen and Jeremy Silver.

tis Functions and S3 classes for time indexes and time indexed series, which are compatible with FAME frequencies. By Jeff Hallman.

topmodel An R implementation of TOPMODEL, based on the 1995 FORTRAN version by Keith Beven. Adapted from the C translation by Huidae Cho. By Wouter Buytaert.

tossm Testing Of Spatial Structure Methods. Provides a framework under which methods for using genetic data to detect population structure and define management units can be tested. By Karen Martien, Dave Gregovich and Mark Bravington.

treelet Treelet: a novel construction of multi-scale bases that extends wavelets to non-smooth signals. Returns a hierarchical tree and a multi-scale orthonormal basis which both reflect the internal structure of the data. By Di Liu.

tsModel Time Series Modeling for Air Pollution and Health. By Roger D. Peng, with contributions from Aidan McDermott.

uncompress Functionality for decompressing ‘.Z’ files. By Nicholas Vinen.

waveclock Time-frequency analysis of cycling cell luminescence data. Provides function `waveclock` designed to assess the period and amplitude of cycling cell luminescence data. The function reconstructs the modal frequencies from a continuous wavelet decomposition of the luminescence data using the “crazy climbers” algorithm described in the book “Practical Time-Frequency Analysis: Gabor and Wavelet Transforms with an Implementation in S” by René Carmona, Wen L. Hwang and Bruno Torresani (1998, Academic Press). By Tom Price.

wgaim Whole Genome Average Interval Mapping for QTL detection using mixed models. Integrates sophisticated mixed modeling methods with a whole genome approach to detecting significant QTLs in linkage maps. By Julian Taylor, Simon Diffey, Ari Verbyla and Brian Cullis.

Other changes

- Package **PARccs** was renamed to **pARccs**.
- Package **BRugs** was moved to the Archive (available via CRANextras now).
- Package **HighProbability** was moved to the Archive (now contained in bundle **empirical-Bayes**).
- Package **brlr** was moved to the Archive.
- Package **paleoTSalt** was moved to the Archive (integrated in package **paleoTS**).
- Package **torus** was moved to the Archive (replaced by package **randtoolbox**).
- Packages **data.table** and **elasticnet** were resurrected from the Archive.

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