Changes on CRAN

by Kurt Hornik

CRAN package web

The CRAN package web area has substantially been reorganized and enhanced. Most importantly, packages now have persistent package URLs of the form

`http://CRAN.R-project.org/package=`*`foo`*

which is also the recommended package URL for citations. (The `package=`*`foo`* redirections also work for most official CRAN mirrors.) The corresponding package web page now has its package dependency information hyperlinked. It also points to a package check page with check results and timings, and to an archive directory with the sources of older versions of the package (if applicable), which are conveniently gathered into an 'Archive/*foo*' subdirectory of the CRAN 'src/contrib' area.

CRAN package checking

The CRAN Linux continuing ("daily") check processes now fully check packages with dependencies on packages in Bioconductor and Omegahat. All check flavors now give timings for installing and checking installed packages. The check results are available in overall summaries sorted by either package name or maintainer name, and in individual package check summary pages.

New contributed packages

BAYSTAR Bayesian analysis of Threshold autoregressive model (BAYSTAR). By Cathy W. S. Chen, Edward M.H. Lin, F.C. Liu, and Richard Gerlach.

BB Barzilai-Borwein Spectral Methods for solving nonlinear systems of equations, and for optimizing nonlinear objective functions subject to simple constraints. By Ravi Varadhan.

BPHO Bayesian Prediction with High-Order interactions. This software can be used in two situations. The first is to predict the next outcome based on the previous states of a discrete sequence. The second is to classify a discrete response based on a number of discrete covariates. In both situations, we use Bayesian logistic regression models that consider the high-order interactions. The models are trained with slice sampling method, a variant of Markov chain Monte Carlo. The time arising from using high-order interactions is reduced greatly by our compression technique that represents a group of original parameters as a single one in MCMC step. By Longhai Li.

Bchron Create chronologies based on radiocarbon and non-radiocarbon dated depths, following the work of Parnell and Haslett (2007, JRSSC). The package runs MCMC, predictions and plots for radiocarbon (and non radiocarbon) dated sediment cores. By Andrew Parnell.

BootPR Bootstrap Prediction Intervals and Bias-Corrected Forecasting for auto-regressive time series. By Jae H. Kim.

COZIGAM COnstrained Zero-Inflated Generalized Additive Model (COZIGAM) fitting with associated model plotting and prediction. By Hai Liu and Kung-Sik Chan.

CPE Concordance Probability Estimates in survival analysis. By Qianxing Mo, Mithat Gonen and Glenn Heller.

ChainLadder Mack- and Munich-chain-ladder methods for insurance claims reserving. By Markus Gesmann.

CombMSC Combined Model Selection Criteria: functions for computing optimal convex combinations of model selection criteria based on ranks, along with utility functions for constructing model lists, MSCs, and priors on model lists. By Andrew K. Smith.

Containers Object-oriented data structures for R: stack, queue, deque, max-heap, min-heap, binary search tree, and splay tree. By John Hughes.

CoxBoost Cox survival models by likelihood based boosting. By Harald Binder.

DEA Data Envelopment Analysis, performing some basic models in both multiplier and envelopment form. By Zuleyka Diaz-Martinez and Jose Fernandez-Menendez.

DierckxSpline R companion to "Curve and Surface Fitting with Splines", providing a wrapper to the FITPACK routines written by Paul Dierckx. The original Fortran is available from `http://www.netlib.org/dierckx`. By Sundar Dorai-Raj.

EMC Evolutionary Monte Carlo (EMC) algorithm. Random walk Metropolis, Metropolis Hasting, parallel tempering, evolutionary Monte Carlo, temperature ladder construction and placement. By Gopi Goswami.

EMCC Evolutionary Monte Carlo (EMC) methods for clustering, temperature ladder construction and placement. By Gopi Goswami.

EMD Empirical Mode Decomposition and Hilbert spectral analysis. By Donghoh Kim and Hee-Seok Oh.

ETC Tests and simultaneous confidence intervals for equivalence to control. The package allows selecting those treatments of a one-way layout being equivalent to a control. Bonferroni adjusted "two one-sided *t*-tests" (TOST) and related simultaneous confidence intervals are given for both differences or ratios of means of normally distributed data. For the case of equal variances and balanced sample sizes for the treatment groups, the single-step procedure of Bofinger and Bofinger (1995) can be chosen. For non-normal data, the Wilcoxon test is applied. By Mario Hasler.

EffectiveDose Estimates the Effective Dose level for quantal bioassay data by nonparametric techniques and gives a bootstrap confidence interval. By Regine Scheder.

FAiR Factor Analysis in R. This package estimates factor analysis models using a genetic algorithm, which opens up a number of new ways to pursue old ideas, such as those discussed by Allen Yates in his 1987 book "Multivariate Exploratory Data Analysis". The major sources of value added in this package are new ways to transform factors in exploratory factor analysis, and perhaps more importantly, a new estimator for the factor analysis model called semi-exploratory factor analysis. By Ben Goodrich.

FinTS R companion to Tsay (2005), "Analysis of Financial Time Series, 2nd ed." (Wiley). Includes data sets, functions and script files required to work some of the examples. Version 0.2-x includes R objects for all data files used in the text and script files to recreate most of the analyses in chapters 1 and 2 plus parts of chapters 3 and 11. By Spencer Graves.

FitAR Subset AR Model fitting. Complete functions are given for model identification, estimation and diagnostic checking for AR and subset AR models. Two types of subset AR models are supported. One family of subset AR models, denoted by ARp, is formed by taking subsets of the original AR coefficients and in the other, denoted by ARz, subsets of the partial autocorrelations are used. The main advantage of the ARz model is its applicability to very large order models. By A.I. McLeod and Ying Zhang.

FrF2 Analyzing Fractional Factorial designs with 2-level factors. The package is meant for completely aliased designs only, i.e., e.g. not for analyzing Plackett-Burman designs with interactions. Enables convenient main effects and interaction plots for all factors simultaneously and offers a cube plot for looking at the simultaneous effects of three factors. An enhanced `DanielPlot` function (modified from **BsMD**) is provided. Furthermore, the alias structure for Fractional Factorial 2-level designs is output in a more readable format than with the built-in function alias. By Ulrike Groemping.

FunNet Functional analysis of gene co-expression networks from microarray expression data. The analytic model implemented in this package involves two abstraction layers: transcriptional and functional (biological roles). A functional profiling technique using Gene Ontology & KEGG annotations is applied to extract a list of relevant biological themes from microarray expression profiling data. Afterwards, multiple-instance representations are built to relate significant themes to their transcriptional instances (i.e., the two layers of the model). An adapted non-linear dynamical system model is used to quantify the proximity of relevant genomic themes based on the similarity of the expression profiles of their gene instances. Eventually an unsupervised multiple-instance clustering procedure, relying on the two abstraction layers, is used to identify the structure of the co-expression network composed from modules of functionally related transcripts. Functional and transcriptional maps of the co-expression network are provided separately together with detailed information on the network centrality of related transcripts and genomic themes. By Corneliu Henegar.

GEOmap Routines for making map projections (forward and inverse), topographic maps, perspective plots, geological maps, geological map symbols, geological databases, interactive plotting and selection of focus regions. By Jonathan M. Lees.

IBrokers R API to Interactive Brokers Trader Workstation. By Jeffrey A. Ryan.

ISA Insieme di funzioni di supporto al volume "INTRODUZIONE ALLA STATISTICA APPLICATA con esempi in R", Federico M. Stefanini, PEARSON Education Milano, 2007. By Fabio Frascati and Federico M. Stefanini.

ISOcodes ISO language, territory, currency, script and character codes. Provides ISO 639 language codes, ISO 3166 territory codes, ISO 4217 currency codes, ISO 15924 script codes, and the ISO 8859 and ISO 10646 character codes as well as the Unicode data table. By Christian Buchta and Kurt Hornik.

Iso Functions to perform isotonic regression. Does linear order and unimodal order isotonic regression. By Rolf Turner.

JM Shared parameter models for the joint modeling of longitudinal and time-to-event data. By Dimitris Rizopoulos.

MCPAN Multiple contrast tests and simultaneous confidence intervals based on normal approximation. With implementations for binomial proportions in a $2 \times k$ setting (risk difference and odds ratio), poly-3-adjusted tumor rates, and multiple comparisons of biodiversity indices. Approximative power calculation for multiple contrast tests of binomial proportions. By Frank Schaarschmidt, Daniel Gerhard, and Martin Sill.

MCPMod Design and analysis of dose-finding studies. Implements a methodology for dose-response analysis that combines aspects of multiple comparison procedures and modeling approaches (Bretz, Pinheiro and Branson, 2005, Biometrics 61, 738–748). The package provides tools for the analysis of dose finding trials as well as a variety of tools necessary to plan a trial to be conducted with the MCPMod methodology. By Bjoern Bornkamp, Jose Pinheiro, and Frank Bretz.

MultEq Tests and confidence intervals for comparing two treatments when there is more than one primary response variable (endpoint) given. The step-up procedure of Quan et al. (2001) is both applied for differences and extended to ratios of means of normally distributed data. A related single-step procedure is also available. By Mario Hasler.

PARccs Estimation of partial attributable risks (PAR) from case-control data, with corresponding percentile or BCa confidence intervals. By Christiane Raemsch.

PASWR Data and functions for the book "Probability and Statistics with R" by M. D. Ugarte, A. F. Militino, and A. T. Arnholt (2008, Chapman & Hall/CRC). By Alan T. Arnholt.

Peaks Spectrum manipulation: background estimation, Markov smoothing, deconvolution and peaks search functions. Ported from ROOT/TSpectrum class. By Miroslav Morhac.

PwrGSD Tools to compute power in a group sequential design. SimPwrGSD C-kernel is a simulation routine that is similar in spirit to '`dssp2.f`' by Gu and Lai, but with major improvements. AsyPwrGSD has exactly the same range of application as SimPwrGSD but uses asymptotic methods and runs *much* faster. By Grant Izmirlian.

QuantPsyc Quantitative psychology tools. Contains functions useful for data screening, testing moderation, mediation and estimating power. By Thomas D. Fletcher.

R.methodsS3 Methods that simplify the setup of S3 generic functions and S3 methods. Major effort has been made in making definition of methods as simple as possible with a minimum of maintenance for package developers. For example, generic functions are created automatically, if missing, and name conflict are automatically solved, if possible. The method `setMethodS3()` is a good start for those who in the future want to migrate to S4. This is a cross-platform package implemented in pure R and is generating standard S3 methods. By Henrik Bengtsson.

RExcelInstaller Integration of R and Excel (use R in Excel, read/write XLS files). RExcel, an add-in for MS Excel on MS Windows, allows to transfer data between R and Excel, writing VBA macros using R as a library for Excel, and calling R functions as worksheet function in Excel. RExcel integrates nicely with R Commander (**Rcmdr**). This R package installs the Excel add-in for Excel versions from 2000 to 2007. It only works on MS Windows. By Erich Neuwirth, with contributions by Richard Heiberger and Jurgen Volkering.

RFreak An R interface to a modified version of the Free Evolutionary Algorithm Kit FrEAK (`http://sourceforge.net/projects/freak427/`), a toolkit written in Java to design and analyze evolutionary algorithms. Both the R interface an extended version of FrEAK are contained in the RFreak package. By Robin Nunkesser.

RSEIS Tools for seismic time series analysis via spectrum analysis, wavelet transforms, particle motion, and hodograms. By Jonathan M. Lees.

RSeqMeth Package for analysis of Sequenom EpiTYPER Data. By Aaron Statham.

RTOMO Visualization for seismic tomography. Plots tomographic images, and allows one to interact and query three-dimensional tomographic models. Vertical cross-sectional cuts can be extracted by mouse click. Geographic information can be added easily. By Jonathan M. Lees.

RankAggreg Performs aggregation of ordered lists based on the ranks using three different algorithms: Cross-Entropy Monte Carlo algorithm, Genetic algorithm, and a brute force algorithm (for small problems). By Vasyl Pihur, Somnath Datta, and Susmita Datta.

RcmdrPlugin.Export Graphically export objects to LaTeX or HTML. This package provides facilities to graphically export **Rcmdr** output to LaTeX or HTML code. Essentially, at the moment, the plug-in is a graphical front-end to `xtable()`. It is intended to (1) facilitate exporting **Rcmdr** output to formats other than ASCII text and (2) provide R novices with an easy to use, easy to access reference on exporting R objects to formats suited for printed output. By Liviu Andronic.

RcmdrPlugin.IPSUR Accompanies "Introduction to Probability and Statistics Using R" by G. Andy Chang and G. Jay Kerns (in progress). Contributes functions unique to the book as well as specific configuration and selected functionality to the R Commander by John Fox. By G. Jay Kerns, with contributions by Theophilius Boye and Tyler Drombosky, adapted from the work of John Fox et al.

RcmdrPlugin.epack Rcmdr plugin for time series. By Erin Hodgess.

Rcplex R interface to CPLEX solvers for linear, quadratic, and (linear and quadratic) mixed integer programs. A working installation of CPLEX is required. Support for Windows platforms is currently not available. By Hector Corrada Bravo.

Rglpk R interface to the GNU Linear Programing Kit (GLPK). GLPK is open source software for solving large-scale linear programming (LP), mixed integer linear programming (MILP) and other related problems. By Kurt Hornik and Stefan Theussl.

Rsymphony An R interface to the SYMPHONY MILP solver (version 5.1.7). By Reinhard Harter, Kurt Hornik and Stefan Theussl.

SMC Sequential Monte Carlo (SMC) Algorithm, and functions for particle filtering and auxiliary particle filtering. By Gopi Goswami.

SyNet Inference and analysis of sympatry networks. Infers sympatry matrices from distributional data and analyzes them in order to identify groups of species cohesively sympatric. By Daniel A. Dos Santos.

TSA Functions and data sets detailed in the book "Time Series Analysis with Applications in R (second edition)" by Jonathan Cryer and Kung-Sik Chan. By Kung-Sik Chan.

TSHRC Two-stage procedure for comparing hazard rate functions which may or may not cross each other. By Jun Sheng, Peihua Qiu, and Charles J. Geyer.

VIM Visualization and Imputation of Missing values. Can be used for exploring the data and the structure of the missing values. Depending on this structure, the tool can be helpful for identifying the mechanism generating the missings. A graphical user interface allows an easy handling of the implemented plot methods. By Matthias Templ.

WINRPACK Reads in WIN pickfile and waveform file, prepares data for **RSEIS**. By Jonathan M. Lees.

XReg Implements extreme regression estimation as described in LeBlanc, Moon and Kooperberg (2006, Biostatistics 7, 71–84). By Michael LeBlanc.

adk Anderson-Darling *K*-sample test and combinations of such tests. By Fritz Scholz.

anacor Simple and canonical correspondence analysis. Performs simple correspondence analysis (CA) on a two-way frequency table (with missings) by means of SVD. Different scaling methods (standard, centroid, Benzecri, Goodman) as well as various plots including confidence ellipsoids are provided. By Jan de Leeuw and Patrick Mair.

anapuce Functions for normalization, differential analysis of microarray data and others functions implementing recent methods developed by the Statistic and Genome Team from UMR 518 AgroParisTech/INRA Appl. Math. Comput. Sc. By J. Aubert.

backfitRichards Computation and plotting of backfitted independent values of Richards curves. By Jens Henrik Badsberg.

bentcableAR Bent-Cable regression for independent data or auto-regressive time series. The bent cable (linear-quadratic-linear) generalizes the broken stick (linear-linear), which is also handled by this package. By Grace Chiu.

biclust BiCluster Algorithms. The main function `biclust()` provides several algorithms to find biclusters in two-dimensional data: Cheng and Church, Spectral, Plaid Model, Xmotifs and Bimax. In addition, the package provides methods for data preprocessing (normalization and discretization), visualization, and validation of bicluster solutions. By Sebastian Kaiser, Rodrigo Santamaria, Roberto Theron, Luis Quintales and Friedrich Leisch.

bifactorial Global and multiple inferences for given bi- and trifactorial clinical trial designs using bootstrap methods and a classical approach. By Peter Frommolt.

bipartite Visualizes bipartite networks and calculates some ecological indices. By Carsten F. Dormann and Bernd Gruber, with additional code from Jochen Fruend, based on the C-code developed by Nils Bluethgen.

birch Dealing with very large data sets using BIRCH. Provides an implementation of the algorithms described in Zhang et al. (1997), and provides functions for creating CF-trees, along with algorithms for dealing with some combinatorial problems, such as `covMcd` and `ltsReg`. It is very well suited for dealing with very large data sets, and does not require that the data can fit in physical memory. By Justin Harrington and Matias Salibian-Barrera.

brglm Bias-reduction in binomial-response GLMs. Fit binomial-response GLMs using either a modified-score approach to bias-reduction or maximum penalized likelihood where penalization is by Jeffreys invariant prior. Fitting takes place by iteratively fitting a local GLM on a pseudo-data representation. The interface is essentially the same as `glm`. More flexibility is provided by the fact that custom pseudo-data representations can be specified and used for model fitting. Functions are provided for the construction of confidence intervals for the bias-reduced estimates. By Ioannis Kosmidis.

bspec Bayesian inference on the (discrete) power spectrum of time series. By Christian Roever.

bvls An R interface to the Stark-Parker algorithm for bounded-variable least squares. By Katharine M. Mullen.

candisc Functions for computing and graphing canonical discriminant analyses. By Michael Friendly and John Fox.

cheb Discrete linear Chebyshev approximation. By Jan de Leeuw.

chemometrics An R companion to the book "Introduction to Multivariate Statistical Analysis in Chemometrics" by K. Varmuza and P. Filzmoser (CRC Press). By P. Filzmoser and K. Varmuza.

cir Nonparametric estimation of monotone functions via isotonic regression and centered isotonic regression. Provides the well-known isotonic regression (IR) algorithm and an improvement called Centered Isotonic Regression (CIR) for the case the true function is known to be smooth and strictly monotone. Also features percentile estimation for dose-response experiments (e.g., ED50 estimation of a medication) using CIR. By Assaf P. Oron.

compHclust Performs the complementary hierarchical clustering procedure and returns X' (the expected residual matrix), and a vector of the relative gene importance. By Gen Nowak and Robert Tibshirani.

contfrac Various utilities for evaluating continued fractions. By Robin K. S. Hankin.

corrperm Three permutation tests of correlation useful when there are repeated measurements. By Douglas M. Potter.

crank Functions for completing and recalculating rankings. By Jim Lemon.

degreenet Likelihood-based inference for skewed count distributions used in network modeling. Part of the "statnet" suite of packages for network analysis. By Mark S. Handcock.

depmixS4 Fit latent (hidden) Markov models on mixed categorical and continuous (time series) data, otherwise known as dependent mixture models. By Ingmar Visser and Maarten Speekenbrink.

diagram Visualization of simple graphs (networks) based on a transition matrix, utilities to plot flow diagrams and visualize webs, and more. Support for the book "A guide to ecological modelling" by Karline Soetaert and Peter Herman (in preparation). By Karline Soetaert.

dynamicTreeCut Methods for detection of clusters in hierarchical clustering dendrograms. By Peter Langfelder and Bin Zhang, with contributions from Steve Horvath.

emu Provides an interface to the Emu speech database system and many special purpose functions for display and analysis of speech data. By Jonathan Harrington and others.

epiR Functions for analyzing epidemiological data. Contains functions for directly and indirectly adjusting measures of disease frequency, quantifying measures of association on the basis of single or multiple strata of count data presented in a contingency table, and computing confidence intervals around incidence risk and incidence rate estimates. Miscellaneous functions for use in meta-analysis, diagnostic test interpretation, and sample size calculations. By Mark Stevenson with contributions from Telmo Nunes, Javier Sanchez, and Ron Thornton.

ergm An integrated set of tools to analyze and simulate networks based on exponential-family random graph models (ERGM). Part of the "statnet" suite of packages for network analysis. By Mark S. Handcock, David R. Hunter, Carter T. Butts, Steven M. Goodreau, and Martina Morris.

fpca A geometric approach to MLE for functional principal components. By Jie Peng and Debashis Paul.

gRain Probability propagation in graphical independence networks, also known as probabilistic expert systems (which includes Bayesian networks as a special case). By Søren Højsgaard.

geozoo Zoo of geometric objects, allowing for display in GGobi through the use of **rggobi**. By Barret Scloerke, with contributions from Dianne Cook and Hadley Wickham.

getopt C-like getopt behavior. Use this with Rscript to write "`#!`" shebang scripts that accept short and long flags/options. By Allen Day.

gibbs.met Naive Gibbs sampling with Metropolis steps. Provides two generic functions for performing Markov chain sampling in a naive way for a user-defined target distribution which involves only continuous variables. `gibbs_met()` performs Gibbs sampling with each 1-dimensional distribution sampled with Metropolis update using Gaussian proposal distribution centered at the previous state. `met_gaussian` updates the whole state with Metropolis method using independent Gaussian proposal distribution centered at the previous state. The sampling is carried out without considering any special tricks for improving efficiency. This package is aimed at only routine applications of MCMC in moderate-dimensional problems. By Longhai Li.

gmaps Extends the functionality of the **maps** package for the **grid** graphics system. This enables more advanced plots and more functionality. It also makes use of the grid structure to fix problems encountered with the traditional graphics system, such as resizing of graphs. By Andrew Redd.

goalprog Functions to solve weighted and lexicographical goal programming problems as specified by Lee (1972) and Ignizio (1976). By Frederick Novomestky.

gsarima Functions for Generalized SARIMA time series simulation. Write SARIMA models in (finite) AR representation and simulate generalized multiplicative seasonal autoregressive moving average (time) series with Normal/Gaussian, Poisson or negative binomial distribution. By Olivier Briet.

helloJavaWorld Hello Java World. A dummy package to demonstrate how to interface to a jar file that resides inside an R package. By Tobias Verbeke.

hsmm Computation of Hidden Semi Markov Models. By Jan Bulla, Ingo Bulla, Oleg Nenadic.

hydrogeo Groundwater data presentation and interpretation. Contains one function for drawing Piper (also called Piper-Henn) digrammes from water analysis for major ions. By Myles English.

hypergeo The hypergeometric function for complex numbers. By Robin K. S. Hankin.

ivivc A menu-driven package for in vitro-in vivo correlation (IVIVC) model building and model validation. By Hsin Ya Lee and Yung-Jin Lee.

jit Enable just-in-time (JIT) compilation. The functions in this package are useful only under Ra and have no effect under R. See `http://www.milbo.users.sonic.net/ra/index.html`. By Stephen Milborrow.

kerfdr Semi-parametric kernel-based approaches to local fdr estimations useful for the testing of multiple hypothesis (in large-scale genetic, genomic and post-genomic studies for instance). By M Guedj and G Nuel, with contributions from S. Robin and A. Celisse.

knorm Knorm correlations between genes (or probes) from microarray data obtained across multiple biologically interrelated experiments. The Knorm correlation adjusts for experiment dependencies (correlations) and reduces to the Pearson coefficient when experiment dependencies are absent. The Knorm estimation approach can be generally applicable to obtain between-row correlations from data matrices with two-way dependencies. By Siew-Leng Teng.

lago An efficient kernel algorithm for rare target detection and unbalanced classification. LAGO is a kernel method much like the SVM, except that it is constructed without the use of any iterative optimization procedure and hence very efficient (Technometrics 48, 193–205; The American Statistician 62, 97–109, Section 4.2). By Alexandra Laflamme-Sanders, Wanhua Su, and Mu Zhu.

latentnetHRT Latent position and cluster models for statistical networks. This package implements the original specification in Handcock, Raftery and Tantrum (2007) and corresponds to version 0.7 of the original **latentnet**. The current package **latentnet** implements the new specification in Krivitsky and Handcock (2008), and represents a substantial rewrite of the original package. Part of the "statnet" suite of packages for network analysis. By Mark S. Handcock, Jeremy Tantrum, Susan Shortreed, and Peter Hoff.

limSolve Solving linear inverse models. Functions that (1) Find the minimum/maximum of a linear or quadratic function: min or $\max(f(x))$, where f(x) = $||Ax - b||^2$ or $f(x) = \sum a_i x_i$ subject to equality constraints $Ex = f$ and/or inequality constraints $Gx >= h$. (2) Sample an under-determined or over-determined system $Ex = f$ subject to $Gx >= h$, and if applicable $Ax = b$. (3) Solve a linear system $Ax = B$ for the unknown x. Includes banded and tridiagonal linear systems. The package calls Fortran functions from LINPACK. By Karline Soetaert, Karel Van den Meersche, and Dick van Oevelen.

lnMLE Maximum likelihood estimation of the Logistic-Normal model for clustered binary data. S original by Patrick Heagerty, R port by Bryan Comstock.

locpol Local polynomial regression. By Jorge Luis Ojeda Cabrera.

logregperm A permutation test for inference in logistic regression. The procedure is useful when parameter estimates in ordinary logistic regression fail to converge or are unreliable due to small sample size, or when the conditioning in exact conditional logistic regression restricts the sample space too severely. By Douglas M. Potter.

marginTree Margin trees for high-dimensional classification, useful for more than 2 classes. By R. Tibshirani.

maxLik Tools for Maximum Likelihood Estimation. By Ott Toomet and Arne Henningsen.

minet Mutual Information NEtwork Inference. Implements various algorithms for inferring mutual information networks from data. All the algorithms compute the mutual information matrix in order to infer a network. Several mutual information estimators are implemented. By P. E. Meyer, F. Lafitte, and G. Bontempi.

mixdist Contains functions for fitting finite mixture distribution models to grouped data and conditional data by the method of maximum likelihood using a combination of a Newton-type algorithm and the EM algorithm. By Peter Macdonald, with contributions from Juan Du.

moduleColor Basic module functions. Methods for color labeling, calculation of eigengenes, merging of closely related modules. By Peter Langfelder and Steve Horvath.

mombf This package computes moment and inverse moment Bayes factors for linear models, and approximate Bayes factors for GLM and situations having a statistic which is asymptotically normally distributed and sufficient. Routines to evaluate prior densities, distribution functions, quantiles and modes are included. By David Rossell.

moonsun A collection of basic astronomical routines for R based on "Practical astronomy with your calculator" by Peter Duffet-Smith. By Lukasz Komsta.

msProcess Tools for protein mass spectra processing including data preparation, denoising, noise estimation, baseline correction, intensity normalization, peak detection, peak alignment, peak quantification, and various functionalities for data ingestion/conversion, mass calibration, data quality assessment, and protein mass spectra simulation. Also provides auxiliary tools for data representation, data visualization, and pipeline processing history recording and retrieval. By Lixin Gong, William Constantine, and Alex Chen.

multipol Various utilities to manipulate multivariate polynomials. By Robin K. S. Hankin.

mvna Computes the Nelson-Aalen estimator of the cumulative transition hazard for multistate models. By Arthur Allignol.

ncf Functions for analyzing spatial (cross-) covariance: the nonparametric (cross-) covariance, the spline correlogram, the nonparametric phase coherence function, and related. By Ottar N. Bjornstad.

netmodels Provides a set of functions designed to help in the study of scale free and small world networks. These functions are high level abstractions of the functions provided by the **igraph** package. By Domingo Vargas.

networksis Simulate bipartite graphs with fixed marginals through sequential importance sampling, with the degrees of the nodes fixed and specified. Part of the "statnet" suite of packages for network analysis. By Ryan Admiraal and Mark S. Handcock.

neuralnet Training of neural networks using the Resilient Backpropagation with (Riedmiller, 1994) or without Weightbacktracking (Riedmiller, 1993) or the modified globally convergent version by Anastasiadis et. al. (2005). The package allows flexible settings through custom choice of error and activation functions. Furthermore the calculation of generalized weights (Intrator & Intrator, 1993) is implemented. By Stefan Fritsch and Frauke Guenther, following earlier work by Marc Suling.

nlrwr Data sets and functions for non-linear regression, supporting software for the book "Nonlinear regression with R". By Christian Ritz.

nls2 Non-linear regression with brute force. By G. Grothendieck.

nlt A nondecimated lifting transform for signal denoising. By Marina Knight.

nlts functions for (non)linear time series analysis. A core topic is order estimation through cross-validation. By Ottar N. Bjornstad.

noia Implementation of the Natural and Orthogonal InterAction (NOIA) model. The NOIA model, as described extensively in Alvarez-Castro & Carlborg (2007, Genetics 176(2):1151-1167), is a framework facilitating the estimation of genetic effects and genotype-to-phenotype maps. This package provides the basic tools to perform linear and multilinear regressions from real populations (provided the phenotype and the genotype of every individuals), estimating the genetic effects from different reference points, the genotypic values, and the decomposition of genetic variances in a multi-locus, 2 alleles system. By Arnaud Le Rouzic.

normwn.test Normality and white noise testing, including omnibus univariate and multivariate normality tests. One variation allows for the possibility of weak dependence rather than independence in the variable(s). Also included is an univariate white noise test where the null hypothesis is for "white noise" rather than "strict white noise". The package deals with similar approaches to testing as the **nortest**, **moments**, and **mvnormtest** packages in R. By Peter Wickham.

npde Routines to compute normalized prediction distribution errors, a metric designed to evaluate non-linear mixed effect models such as those used in pharmacokinetics and pharmacodynamics. By Emmanuelle Comets, Karl Brendel and France Mentré.

nplplot Plotting non-parametric LOD scores from multiple input files. By Nandita Mukhopadhyay and Daniel E. Weeks.

obsSens Sensitivity analysis for observational studies. Observational studies are limited in that there could be an unmeasured variable related to both the response variable and the primary predictor. If this unmeasured variable were included in the analysis it would change the relationship (possibly changing the conclusions). Sensitivity analysis is a way to see how much of a relationship needs to exist with the unmeasured variable before the conclusions change. This package provides tools for doing a sensitivity analysis for regression (linear, logistic, and Cox) style models. By Greg Snow.

ofw Implements the stochastic meta algorithm called Optimal Feature Weighting for two multiclass classifiers, CART and SVM. By Kim-Anh Le Cao and Patrick Chabrier.

openNLP An interface to openNLP (`http://opennlp.sourceforge.net/`), a collection of natural language processing tools including a sentence detector, tokenizer, pos-tagger, shallow and full syntactic parser, and named-entity detector, using the Maxent Java package for training and using maximum entropy models. By Ingo Feinerer.

openNLPmodels English and Spanish models for **openNLP**. By Ingo Feinerer.

pga An ensemble method for variable selection by carrying out Darwinian evolution in parallel universes. PGA is an ensemble algorithm similar in spirit to AdaBoost and random forest. It can "boost up" the performance of "bad" selection criteria such as AIC and GCV. (Technometrics 48, 491–502; The American Statistician 62, 97–109, Section 4.3). By Dandi Qiao and Mu Zhu.

phangorn Phylogenetic analysis in R (estimation of phylogenetic trees and networks using maximum likelihood, maximum parsimony, distance methods & Hadamard conjugation). By Klaus Schliep.

plotSEMM Graphing nonlinear latent variable interactions in SEMM. Contains functions which generate the diagnostic plots proposed by Bauer (2005) to investigate nonlinear latent variable interactions in SEMM using LISREL output. By Bethany E. Kok, Jolynn Pek, Sonya Sterba and Dan Bauer.

poilog Functions for obtaining the density, random deviates and maximum likelihood estimates of the Poisson log-normal distribution and the bivariate Poisson log-normal distribution. By Vidar Grøtan and Steinar Engen.

prob Provides a framework for performing elementary probability calculations on finite sample spaces, which may be represented by data frames or lists. Functionality includes setting up sample spaces, counting tools, defining probability spaces, performing set algebra, calculating probability and conditional probability, tools for simulation and checking the law of large numbers, adding random variables, and finding marginal distributions. By G. Jay Kerns.

profileModel Tools that can be used to calculate, evaluate, plot and use for inference the profiles of *arbitrary* inference functions for *arbitrary* `glm`-like fitted models with linear predictors. By Ioannis Kosmidis.

profr An alternative data structure and visual rendering for the profiling information generated by `Rprof`. By Hadley Wickham.

qAnalyst Control charts for variables and attributes according to the book "Introduction to Statistical Quality Control" by Douglas C. Montgomery. Moreover, capability analysis for normal and non-normal distributions is implemented. By Andrea Spanó and Giorgio Spedicato.

qpcR Model fitting, optimal model selection and calculation of various features that are essential in the analysis of quantitative real-time polymerase chain reaction (qPCR). By Andrej-Nikolai Spiess and Christian Ritz.

r2lUniv R to LaTeX Univariate. Performs some basic analysis and generate the corresponding LaTeX code. The basic analysis depends of the variable type (nominal, ordinal, discrete, continuous). By Christophe Genolini.

randomLCA Fits random effects latent class models, as well as standard latent class models. By Ken Beath.

richards Fit Richards curves. By Jens Henrik Badsberg.

risksetROC Compute time-dependent incident/dynamic accuracy measures (ROC curve, AUC, integrated AUC) from censored survival data under proportional or non-proportional hazard assumption of Heagerty & Zheng (2005, Biometrics 61:1, 92–105). By Patrick J. Heagerty, packaging by Paramita Saha.

robfilter A set of functions to filter time series based on concepts from robust statistics. By Roland Fried and Karen Schettlinger.

s20x Stats 20x functions. By Andrew Balemi, James Curran, Brant Deppa, Mike Forster, Michael Maia, and Chris Wild.

sampleSelection Estimation of sample selection models. By Arne Henningsen and Ott Toomet.

scrime Tools for the analysis of high-dimensional data developed/implemented at the group "Statistical Complexity Reduction In Molecular Epidemiology" (SCRIME). Main focus is on SNP data, but most of the functions can also be applied to other types of categorical data. By Holger Schwender and Arno Fritsch.

segclust Segmentation and segmentation/clustering. Corresponds to the implementation of the statistical model described in Picard et. al., "A segmentation/clustering model for the analysis of array CGH data" (2007, Biometrics, 63(3)). Segmentation functions are also available (from Picard et al., "A statistical approach for array CGH data analysis" (2005, BMC Bioinformatics 11;6:27)). By Franck Picard.

shape Plotting functions for creating graphical shapes such as ellipses, circles, cylinders, arrows, and more. Support for the book "A guide to ecological modelling" by Karline Soetaert and Peter Herman (in preparation). By Karline Soetaert.

siar Stable Isotope Analysis in R. This package takes data on organism isotopes and fits a Bayesian model to their dietary habits based upon a Gaussian likelihood with a mixture Dirichlet-distributed prior on the mean. By Andrew Parnell.

similarityRichards Computing and plotting of values for similarity of backfitted independent values of Richards curves. By Jens Henrik Badsberg.

space Partial correlation estimation with joint sparse regression model. By Jie Peng, Pei Wang, Nengfeng Zhou, and Ji Zhu.

stab A menu-driven package for data analysis of drug stability based on ICH guideline (such as estimation of shelf-life from a 3-batch profile.). By Hsin-ya Lee and Yung-jin Lee.

statnet An integrated set of tools for the representation, visualization, analysis and simulation of network data. By Mark S. Handcock, David R. Hunter, Carter T. Butts, Steven M. Goodreau, Martina Morris.

subplex The subplex algorithm for unconstrained optimization, developed by Tom Rowan. By Aaron A. King, Rick Reeves.

survivalROC Compute time-dependent ROC curve from censored survival data using Kaplan-Meier (KM) or Nearest Neighbor Estimation (NNE) method of Heagerty, Lumley & Pepe (2000, Biometrics 56:2, 337–344). By Patrick J. Heagerty, packaging by Paramita Saha.

torus Torus algorithm for quasi random number generation (for Van Der Corput low-discrepancy sequences, use **fOptions** from Rmetrics). Also implements a general linear congruential pseudo random generator (such as Park Miller) to make comparison with Mersenne Twister (default in R) and the Torus algorithm. By Christophe Dutang and Thibault Marchal.

tpr Regression models for temporal process responses with time-varying coefficient. By Jun Yan.

xts Extensible Time Series. Provide for uniform handling of R's different time-based data classes by extending **zoo**, maximizing native format information preservation and allowing for user level customization and extension, while simplifying cross-class interoperability. By Jeffrey A. Ryan and Josh M. Ulrich.

yaml Methods to convert R to YAML and back, implementing the Syck YAML parser (`http://www.whytheluckystiff.net/syck`) for R. By Jeremy Stephens.

Other changes

- New task views `Optimization` (packages which offer facilities for solving optimization problems, by Stefan Theussl) and `ExperimentalDesign` (packages for experimental design and analysis of data from experiments, by Ulrike Groemping).
- Packages **JLLprod**, **butler**, **elasticnet**, **epsi**, **gtkDevice**, **km.ci**, **ncvar**, **riv**, **rpart.permutation**, **rsbml**, **taskPR**, **treeglia**, **vardiag** and **zicounts** were moved to the Archive.
- Package **CPGchron** was moved to the Archive (replaced by **Bchron**).
- Package **IPSUR** was moved to the Archive (replaced by **RcmdrPlugin.IPSUR**).
- Package **gRcox** was renamed to **gRc**.
- Package **pwt** was re-added to CRAN.

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