- `demo()` had a 'device' argument that did nothing (although it was documented to): it has been removed.

- Setting new levels on a factor dropped all existing attributes, including class "ordered".

- `format.default(justify="none")` now by default converts NA character strings, as the other values always did.

- `format.info()` often gave a different field width from `format()` for character vectors (e.g. including missing values or non-printable characters).

- `axis()` now ensures that if 'labels' are supplied as character strings or expressions then 'at' is also supplied (since the calculated value for 'at' can change under resizing).

- Defining S4 methods for "[" had resulted in changed behavior of S3 dispatch in a very rare case which no longer happens.

- Fixed segfault when PostScript font loading fails, e.g., when R is unable to find afm files (reported by Ivo Welch).

- R CMD BATCH <file> now also works when <file> does not end in a newline on Unix-alike platforms.

- `terms.formula()` got confused if the 'data' argument was a list with non-syntactic names.

- `prompt()` and hence `package.skeleton()` now produce *.Rd files that give no errors (but warnings) when not edited, much more often.

- `promptClass()` and `promptMethods()` now also escape "%" e.g. in '%*%' and the latter gives a message about the file written.

- `wilcox.test()` now warns when conf.level is set higher than achievable, preventing errors (PR#3666) and incorrect answers with extremely small sample sizes.

- The default (protection pointer) stack size (the default for '–max-ppsize') has been increased from 10000 to 50000 in order to match the increased default `options("expressions")` (in R 2.1.0).

- The R front-end was expecting –gui=tk not Tk as documented, and rejecting –gui=X11.

- Rdconv -t latex protected only the first « and » in a chunk against conversion to guillemets.

- `callNextMethod()` and `callGeneric()` have fixes related to handling arguments.

- `ls.diag()` now works for fits with missing data. (PR#8139)

- `window.default()` had an incorrect tolerance and so sometimes created too short a series if 'start' or 'end' were zero.

- Some (fairly pointless) cases of reshape left a temporary id variable in the result (PR#8152)

- R CMD build used 'tar xhf' which is invalid on FreeBSD systems (and followed tar chf, so there could be no symbolic links in the tarball).

- Subassignment of length zero vectors to NULL gave garbage answers. (PR#8157)

- Automatic coercion of raw vectors to lists was missing, so for a list (or data frame) z, z[["a"]] <- raw_vector did not work and now does. This also affected DF$a <- raw_vector for a data frame DF.

- The internal code for `commandArgs()` was missing PROTECTs.

- The width for `strwrap()` was used as one less than specified.

- R CMD INSTALL was not cleaning up after an unsuccessful install of a non-bundle which was not already installed.

Changes on CRAN

by Kurt Hornik

New contributed packages

ArDec Implements the autoregressive decomposition of a time series based on the constructive approach in West (1997). Particular cases include the extraction of trend and seasonal components from a monthly time series. Uncertainty on the resulting components can be derived from sampling of the autoregressive model which is written as a linear regression model and handled on a Bayesian framework. By S. M. Barbosa.

BACCO Bayesian analysis of computer code software. The bundle contains routines that evaluate the formulae of Kennedy, O'Hagan, and Oakley. By Robin K. S. Hankin.

BMA Bayesian model averaging for linear models, generalizable linear models and survival models (Cox regression). By Adrian Raftery, Jennifer Hoeting, Chris Volinsky, and Ian Painter.

BRugs An R package containing OpenBUGS and its R interface BRugs. The Chief Software Bug is Andrew Thomas, with web assistance from Real Bug Bob O'Hara. Other members of the BUGS team are statisticians David Spiegelhalter, Nicky Best, Dave Lunn, and Ken Rice. Dave Lunn has also made major contributions to the software development. R Code modified, extended and packaged for R by Uwe Ligges and Sibylle Sturtz. Some ideas taken from the R2WinBUGS package based on code by Andrew Gelman.

BSDA Data sets for book "Basic Statistics and Data Analysis" by Larry J. Kitchens. By Alan T. Arnholt.

Biodem Provides a number of functions for Biodemographycal analysis. By Alessio Boattini and Federico C. F. Calboli; Vincente Canto Cassola together with Martin Maechler authored the function `mtx.exp()`.

DDHFm Contains the normalizing and variance stabilizing Data-Driven Haar-Fisz algorithm. Also contains related algorithms for simulating from certain microarray gene intensity models and evaluation of certain transformations. By Efthimios S. Motakis, Guy P. Nason, and Piotr Fryzlewicz.

DEoptim Provides the DEoptim function which performs Differential Evolution Optimization (evolutionary algorithm). By David Ardia.

DICOM Provides functions to import and manipulate medical imaging data via the Digital Imaging and Communications in Medicine (DICOM) Standard. By Brandon Whitcher.

ElemStatLearn Data sets, functions and examples from the book "The Elements of Statistical Learning, Data Mining, Inference, and Prediction" by Trevor Hastie, Robert Tibshirani and Jerome Friedman.

Epi Useful functions for demographic and epidemiological analysis in the Lexis diagram, i.e., register and cohort follow-up data. Also some useful functions for tabulation and plotting. Contains some epidemiological datasets. By David Clayton, Martyn Plummer, Bendix Carstensen, Mark Myatt et. al.

Fahrmeir Data and functions for the book "Multivariate Statistical Modelling Based on Generalized Linear Models" by Ludwig Fahrmeir and Gerhard Tutz. Compiled by Kjetil Halvorsen.

ICE Kernel Estimators for Interval-Censored Data. By W. John Braun.

JLLprod Implements the Lewbel and Linton (2003), Lewbel and Linton (2005) and Jacho-Chávez, Lewbel and Linton (2005) nonparametric estimators of Homothetic and Generalized Homothetic production functions. By David Tomás Jacho-Chávez.

Kendall Computes the Kendall rank correlation. By A.I. McLeod.

LMGene Analysis of microarray data using a linear model and glog data transformation. By David Rocke and Geun Cheol Lee.

Lmoments Contains functions to estimate L-moments and trimmed L-moments from the data. Also contains functions to estimate the parameters of the normal polynomial quantile mixture and the Cauchy polynomial quantile mixture from L-moments and trimmed L-moments. By Juha Karvanen.

MSBVAR Provides methods for estimating frequentist and Bayesian Vector Autoregression (VAR) models. Also includes methods for the generating posterior inferences for VAR forecasts, impulse responses (using likelihood-based error bands), and forecast error decompositions. Also includes utility functions for plotting forecasts and impulse responses, and generating draws from Wishart and singular multivariate normal densities. Future versions will include Bayesian Structural VAR (B-SVAR) models and possibly some models with Markov switching. By Patrick T. Brandt.

MarkedPointProcess Non-parametric Analysis of the Marks of Marked Point Processes. By Martin Schlather.

POT Some functions useful to perform a Peak Over Threshold analysis. Some piece of code come from the **evd** Package of Alec Stephenson. By Mathieu Ribatet.

R.utils This package provides utility classes and methods useful when programming in R and developing R packages. By Henrik Bengtsson.

RFA Several function to perform a Regional Frequency Analysis. By Mathieu Ribatet.

RGraphics Data and functions from the book "R Graphics". There is a function to produce each figure in the book, plus several functions, classes, and methods defined in Chapter 7. By Paul Murrell.

RLMM A classification algorithm, based on a multi-chip, multi-SNP approach for Affymetrix SNP arrays. Using a large training sample where the genotype labels are known, this algorithm will obtain more accurate classification results on new data. **RLMM** is based on a robust, linear model and uses the Mahalanobis distance for classification. The chip-to-chip non-biological variation is removed through normalization. This model-based algorithm captures the similarities across genotype groups and probes, as well as thousands other SNPs for accurate classification. NOTE: 100K-Xba only at for now. By Nusrat Rabbee and Gary Wong.

RWinEdt A plug in for using WinEdt as an editor for R. By Uwe Ligges.

RXshrink Identify and display TRACEs for a specified shrinkage path and determine the extent of shrinkage most likely, under normal distribution theory, to produce an optimal reduction in MSE Risk in estimates of regression (beta) coefficients. By Bob Obenchain.

RandVar Implementation of random variables by means of S4 classes and methods. By Matthias Kohl.

Rfwdmv Explore Multivariate Data with the Forward Search. By Anthony Atkinson, Andrea Cerioli, and Marco Riani.

Rlsf Functions for using R with the LSF cluster/grid queuing system. By Chris Smith and Gregory Warnes.

Rpad A workbook-style user interface to R through a web browser. Provides convenient plotting, HTML GUI generation, and HTML output routines. Can be used with R in standalone mode or with a web server to serve Rpad pages to other users. By Tom Short and Philippe Grosjean.

SAGx Retrieval, preparation and analysis of data from the Affymetrix GeneChip. In particular the issue of identifying differentially expressed genes is addressed. By Per Broberg.

SensoMineR For analysing sensory data. By François Husson and Sébastien Lê.

SharedHT2 Derives per gene means and fits the Wishart/inverse Wishart conjugate family to the per gene empirical covariance matrices. Derives a Hotelling T^2 statistic having an F-distribution using an empirical Bayes variance. By Grant Izmirlian.

SwissAir Ozone, NO_x (= Sum of Nitrogenmonoxide and Nitrogendioxide), Nitrogenmonoxide, ambient temperature, dew point, wind speed and wind direction at 3 sites around lake of Lucerne in Central Switzerland in 30 min time resolution for year 2004. By Rene Locher.

TeachingDemos A set of demonstration functions that can be used in a classroom to demonstrate statistical concepts, or on your own to better understand the concepts or the programming. By Greg Snow.

USPS Identify and display the distribution of Local Treatment Differences (LTDs) and Local Average Treatment Effects (LATEs) in Outcome within Clusters of patients chosen to be relatively well matched on baseline X-covariates. By Bob Obenchain.

WhatIf Inferences about counterfactuals are essential for prediction, answering what if questions, and estimating causal effects. However, when the counterfactuals posed are too far from the data at hand, conclusions drawn from well-specified statistical analyses become based largely on speculation hidden in convenient modeling assumptions that few would be willing to defend. Unfortunately, standard statistical approaches assume the veracity of the model rather than revealing the degree of model-dependence, which makes this problem hard to detect. **WhatIf** offers easy-to-apply methods to evaluate counterfactuals that do not require sensitivity testing over specified classes of models. If an analysis fails the tests offered here, then we know that substantive inferences will be sensitive to at least some modeling choices that are not based on empirical evidence, no matter what method of inference one chooses to use. **WhatIf** implements the methods for evaluating counterfactuals discussed in Gary King and Langche Zeng (2006), The Dangers of Extreme Counterfactuals, *Political Analysis* **14**(2), and Gary King and Langche Zeng (2006), When Can History Be Our Guide? The Pitfalls of Counterfactual Inference, *International Studies Quarterly*. By Heather Stoll, Gary King, and Langche Zeng.

aaMI Contains five functions. `read.FASTA()` reads in a FASTA format alignment file and parses it into a data frame. `read.CX()` reads in a ClustalX '.aln' format file and parses it into a data frame. `read.Gdoc()` reads in a GeneDoc '.msf' format file and parses it into a data frame. The alignment data frame returned by each of these functions has the sequence IDs as the row names and each site in the alignment is a column in the data frame. `aaMI()` calculates the mutual information between each pair of sites (columns) in the protein sequence alignment data frame. `aaMIn()` calculates the normalized mutual information between pairs of sites

in the protein sequence alignment data frame. The normalized mutual information of sites i and j is the mutual information of these sites divided by their joint entropy. By Kurt Wollenberg.

aod Provides a set of functions to analyze overdispersed counts or proportions. Most of the methods are already available elsewhere but are scattered in different packages. The proposed functions should be considered as complements to more sophisticated methods such as generalized estimating equations (GEE) or generalized linear mixed effect models (GLMM). By Matthieu Lesnoff and Renaud Lancelot.

apTreeshape Mainly dedicated to simulation and analysis of phylogenetic tree topologies using statistical indices. It is a companion library of the **ape** package. It provides additional functions for reading, plotting, manipulating phylogenetic trees. It also offers convenient web-access to public databases, and enables testing null models of macroevolution using corrected test statistics. Trees of class `"phylo"` (from package **ape**) can be converted easily. By Nicolas Bortolussi, Eric Durand, Michael Blum, and Olivier François.

aster Functions and datasets for Aster modeling (forest graph exponential family conditional or unconditional canonical statistic models for life history analysis). By Charles J. Geyer.

baymvb Fits multivariate binary data using Bayesian approach. By S. M. Mwalili.

bicreduc Reduction algorithm for the NPMLE for the distribution function of bivariate interval-censored data. The main function is `HMA()`, the HeightMapAlgorithm. This algorithm is based on the idea of an "height map", and is described in the following paper: "Reduction algorithm for the NPMLE for the distribution function of bivariate interval-censored data", by Marloes Maathuis, *Journal of Computational and Graphical Statistics*, **14** (2) (to appear). By Marloes Maathuis.

biopara A parallel system designed to be used with R. By Peter Lazar and David Schoenfeld.

bivpois Fitting Bivariate Poisson Models using the EM algorithm. Details can be found in Karlis and Ntzoufras (2003, JRSS D; 2004, AUEB Technical Report). By Dimitris Karlis and Ioannis Ntzoufras.

butler Testing, profiling and benchmarking of code. By Hadley Wickham.

caMassClass Processing and classification of protein mass spectra (SELDI) data. Also includes reading and writing of mzXML files. By Jarek Tuszynski.

caTools Several basic utility functions including: moving (rolling, running) window statistic functions, read/write for GIF and ENVI binary files, fast calculation of AUC, LogitBoost classifier, base64 encoder/decoder, round-off error free sum and cumsum, etc. By Jarek Tuszynski.

cba Clustering techniques such as Proximus and Rock, utility functions for efficient computation of cross distances and data manipulation. By Christian Buchta.

compositions Provides functions for the consistent analysis of compositional data (e.g., portions of substances) and positive numbers (e.g., concentrations) in the way proposed by Aitchison. By K. Gerald van den Boogaart and Raimon Tolosana, with contributions of Matevz Bren.

copula Classes (S4) of commonly used copulas including elliptical and Archimedean copulas. Implemented copulas include normal, t, Clayton, Frank, and Gumbel. Methods for `density()`, distribution, random number generators, `persp()`, and `contour()`. By Jun Yan.

corpcor Implements a shrinkage estimator to allow the efficient inference of large-scale covariance matrices from small sample data. The resulting estimates are always positive definite, more accurate than the empirical estimate, well conditioned, computationally inexpensive, and require only little a priori modeling. The package also contains similar functions for inferring correlations and partial correlations. In addition, it provides functions for fast SVD computation, for computing the pseudoinverse, and for checking the rank and positive definiteness of a matrix. By Juliane Schaefer and Korbinian Strimmer.

corpora Utility functions for the statistical analysis of corpus frequency data. By Stefan Evert.

cslogistic Functions for likelihood and posterior analysis of conditionally specified logistic regression models. All calculus and simulation is done in compiled FORTRAN. By Alejandro Jara Vallejos and Maria Jose Garcia-Zattera.

depmix Fit (multigroup) mixtures of latent Markov models on mixed categorical and continuous (time series) data. By Ingmar Visser.

dglm Fitting double generalized linear models. By Peter K Dunn and Gordon K Smyth.

distrEx Extensions of package **distr** and some additional functionality. By Matthias Kohl.

distrSim Simulation (S4-)classes based on package **distr**. By Florian Camphausen, Matthias Kohl, Peter Ruckdeschel, and Thomas Stabla.

distrTEst Evaluation (S4-)classes based on package **distr** for evaluating procedures (estimators/tests) at data/simulation in a unified way. By Florian Camphausen, Matthias Kohl, Peter Ruckdeschel, and Thomas Stabla.

dprep Functions for normalization, treatment of missing values, discretization, outlier detection, feature selection, and visualization. By Edgar Acuna and Caroline Rodriguez.

dyn Time series regression. The dyn class interfaces `ts`, `irts`, `its`, `zoo` and `zooreg` time series classes to `lm()`, `glm()`, `loess()`, `quantreg::rq()`, `MASS::rlm()`, `randomForest::randomForest()` and other regression functions allowing those functions to be used with time series including specifications that may contain lags, diffs and missing values. By Gabor Grothendieck.

dynlm Dynamic linear models and time series regression. By Achim Zeileis.

elliptic A suite of elliptic and related functions including Weierstrass and Jacobi forms. Also includes various tools for manipulating and visualizing complex functions. By Robin K. S. Hankin.

equivalence Provides some statistical tests and graphics for assessing tests of equivalence. Such tests have similarity as the alternative hypothesis instead of the null. Sample datasets are included. By Andrew Robinson.

fCalendar The Rmetrics module for "Date, Time and Calendars".

fMultivar The Rmetrics module for "Multivariate Data Analysis".

fPortfolio The Rmetrics module for "Pricing and Hedging of Options".

fgac Generalized Archimedean Copula. Bi-variate data fitting is done by two ingredients: the margins and the dependency structure. The dependency structure is modeled through a copula. An algorithm was implemented considering seven families of copulas (Generalized Archimedean Copulas), the best fitting can be obtained looking all copula's options. By Veronica Andrea Gonzalez-Lopez.

filehash Simple file-based hash table. By Roger D. Peng.

gamlss The GAMLSS library and datasets. By Mikis Stasinopoulos and Bob Rigby, with contributions from Calliope Akantziliotou.

geometry Makes the qhull library (`www.qhull.org`) available in R, in a similar manner as in Octave and MATLAB. Qhull computes convex hulls, Delaunay triangulations, halfspace intersections about a point, Voronoi diagrams, furthest-site Delaunay triangulations, and furthest-site Voronoi diagrams. It runs in 2-d, 3-d, 4-d, and higher dimensions. It implements the Quickhull algorithm for computing the convex hull. Qhull does not support constrained Delaunay triangulations, or mesh generation of non-convex objects, but the package does include some R functions that allow for this. Currently the package only gives access to Delaunay triangulation and convex hull computation. By Raoul Grasman.

giRaph Supply data structures and algorithms for computations on graphs. By Jens Henrik Badsberg, Claus Dethlefsen, and Luca La Rocca.

glpk The GNU Linear Programming Kit (GLPK) version 4.8. This interface mirrors the GLPK C API. Almost all GLPK lpx routines are supported. This release is beta status due to the fact that not all routines have been tested. Suggestions and improvements are solicited. By Lopaka Lee.

gmt Interface between GMT 4.0 map-making software and R, enabling the user to manipulate geographic data within R and call GMT programs to draw and annotate maps in postscript format. By Arni Magnusson.

gnm Functions to specify and fit generalized nonlinear models, including models with multiplicative interaction terms such as the UNIDIFF model from sociology and the AMMI model from crop science. This is a major re-working of an earlier Xlisp-Stat package, "Llama". Overparameterized representations of models are used throughout; functions are provided for inference on estimable parameter combinations, as well as standard methods for diagnostics etc. By Heather Turner and David Firth.

grouped Regression models for grouped and coarse data, under the Coarsened At Random assumption. By Dimitris Rizopoulos and Spyridoula Tsonaka.

hapsim Package for haplotype data simulation. Haplotypes are generated such that their allele frequencies and linkage disequilibrium coefficients match those estimated from an input data set. By Giovanni Montana.

hoa A bundle with various functions for higher order likelihood-based inference. Contains **cond** for approximate conditional inference for logistic and log-linear models, **csampling** for conditional simulation in regression-scale models, **marg** for approximate marginal inference for regression-scale models, and **nlreg** for higher order inference for nonlinear heteroscedastic models. By Alessandra R. Brazzale.

howmany When testing multiple hypotheses simultaneously, this package provides functionality to calculate a lower bound for the number of correct rejections (as a function of the number of rejected hypotheses), which holds simultaneously—with high probability—for all possible number of rejections. As a special case, a lower bound for the total number of false null hypotheses can be inferred. Dependent test statistics can be handled for multiple tests of associations. For independent test statistics, it is sufficient to provide a list of p-values. By Nicolai Meinshausen.

iid.test Testing whether data is independent and identically distributed. By Rasmus E. Benestad.

kappalab Kappalab, which stands for "laboratory for capacities", is an S4 tool box for capacity (or non-additive measure, fuzzy measure) and integral manipulation on a finite setting. It contains routines for handling various types of set functions such as games or capacities. It can be used to compute several non-additive integrals: the Choquet integral, the Sugeno integral, and the symmetric and asymmetric Choquet integrals. An analysis of capacities in terms of decision behavior can be performed through the computation of various indices such as the Shapley value, the interaction index, the orness degree, etc. The well-known Möbius transform, as well as other equivalent representations of set functions can also be computed. **Kappalab** further contains four capacity identification routines: two least squares based approaches, a maximum entropy like method based on variance minimization and an unsupervised approach grounded on parametric entropies. The functions contained in **Kappalab** can for instance be used for multicriteria decision making or in the framework of cooperative game theory. By Michel Grabisch, Ivan Kojadinovic, and Patrick Meyer.

latentnet Latent position and cluster models for statistical networks. These models are fit within the "ergm" framework of the **statnet** package. By Mark S. Handcock, based on original code from Jeremy Tantrum, Susan Shortreed, and Peter Hoff.

lodplot Assorted plots of location score versus genetic map position. By David L Duffy.

longmemo Data sets and functionality from the textbook "Statistics for Long-Memory Processes" by Jan Beran. Original S code by Jan Beran, data sets via Brandon Whitcher, top-level R functions and much more by Martin Maechler.

mblm Linear models based on Theil-Sen single median and Siegel repeated medians. They are very robust (29 or 50 percent breakdown point, respectively), and if no outliers are present, the estimators are very similar to OLS. By Lukasz Komsta.

micEcdat Individual data sets for microeconometrics, which come mainly from the Journal of Applied Econometrics' and the Journal of Business and Economic Statistics' data archives. By Yves Croissant.

mice Multivariate Imputation by Chained Equations. By S. Van Buuren and C.G.M. Oudshoorn.

misc3d A collection of miscellaneous 3d plots, including rgl-based isosurfaces. By Dai Feng and Luke Tierney.

modeltools A collection of tools to deal with statistical models. The functionality is experimental and the user interface is likely to change in the future. The documentation is rather terse, but packages **coin** and **party** have some working examples. By Torsten Hothorn and Friedrich Leisch.

moments Functions to calculate: moments, Pearson's kurtosis, Geary's kurtosis and skewness; tests related to them (Anscombe-Glynn, D'Agostino, Bonett-Seier). By Lukasz Komsta.

monoProc Monotonizes a given fit in one or two variables. By Regine Scheder.

multtest Non-parametric bootstrap and permutation resampling-based multiple testing procedures for controlling the family-wise error rate (FWER), generalized family-wise error rate (gFWER), tail probability of the proportion of false positives (TPPFP), and false discovery rate (FDR). Single-step and step-wise methods are implemented. Tests based on a variety of t- and F-statistics (including t-statistics based on regression parameters from linear and survival models) are included. Results are reported in terms of adjusted p-values, confidence regions and test statistic cutoffs. By Katherine S. Pollard, Yongchao Ge, and Sandrine Dudoit.

nFDR Implements the non-parametric estimate of FDR based on Bernstein polynomials. It calculates the proportion of true null hypotheses, FDR, FNR, and q-values. By Zhong Guan, Baolin Wu and Hongyu Zhao.

network Tools to create and modify network objects. The network class can represent a range of relational data types, and supports arbitrary vertex/edge/graph attributes. By Carter T. Butts, with help from David Hunter and Mark S. Handcock.

neural RBF and MLP neural networks with graphical user interface. By Ádám Nagy.

onion A collection of routines to manipulate and visualize quaternions and octonions. By Robin K. S. Hankin.

optmatch Functions to perform optimal matching, particularly full matching. By Ben B. Hansen, with embedded Fortran code due to Dimitri P. Bertsekas and Paul Tseng.

papply Similar to `apply()` and `lapply()`, applies a function to all items of a list, and returns a list with the results. Uses **Rmpi** to distribute the processing evenly across a cluster. If **Rmpi** is not available, implements this as a non-parallel algorithm. Includes some debugging support. By Duane Currie.

partsm Basic functions to fit and predict periodic autoregressive time series models. These models are discussed in the book "Periodicity and Stochastic Trends in Economic Time Series" by P.H. Franses. Data sets analyzed in that book are also provided. By Javier López-de-Lacalle.

party Unbiased recursive partitioning in a conditional inference framework. This package implements a unified framework for recursive partitioning which embeds tree-structured regression models into a well defined theory of conditional inference procedures. Stopping criteria based on multiple test procedures are implemented. The methodology is applicable to all kinds of regression problems, including nominal, ordinal, numeric, censored as well as multivariate response variables and arbitrary measurement scales of the covariates. Extensible functionality for visualizing tree-structured regression models is available. By Torsten Hothorn, Kurt Hornik, and Achim Zeileis.

permtest Uses permutations in order to compare the variability within and distance between two groups within a set of microarray data. By Douglas Hayden.

pgirmess Miscellaneous functions for analysis and display of ecological and spatial data. By Patrick Giraudoux.

popgen Implements a variety of statistical and population genetic methodology. By J L Marchini.

powerpkg Power analyses for the affected sib pair and the TDT design. By Daniel E. Weeks.

pscl Classes and/or methods for discrete data models; e.g., models for counts, ordinal data, item-response theory (IRT) models for binary data, computing highest density regions. By Simon Jackman.

quantchem Statistical evaluation of calibration curves by different regression techniques: ordinary, weighted, robust (up to 4th order polynomial). Log-log and Box-Cox transform, estimation of optimal power and weighting scheme. Tests for heteroscedascity and normality of residuals. Different kinds of plots commonly used in illustrating calibrations. Easy "inverse prediction" of concentration by given responses and statistical evaluation of results (comparison of precision and accuracy by common tests). By Lukasz Komsta.

randaes The deterministic part of the Fortuna cryptographic pseudorandom number generator, described in "Practical Cryptography" by Scheier and Ferguson. By Thomas Lumley.

rcdd R interface to (some of) cddlib. By Charles J. Geyer and Glen D. Meeden.

relax Functions for report writing, presentation, and programming. By Hans Peter Wolf.

reshape Flexibly reshape data. By Hadley Wickham.

sac Semi-parametric empirical likelihood ratio based test of change-point with one-change or epidemic alternatives with data-based model diagnostic. By Zhong Guan.

sampling A set of tools to select and to calibrate samples. By Yves Tillé and Alina Matei.

samr Significance Analysis of Microarrays. By R. Tibshirani, G. Chu, T. Hastie, and Balasubramanian Narasimhan.

scape Import and plot results from statistical catch-at-age models, used in fisheries stock assessments. By Arni Magnusson.

scapeMCMC Markov-chain Monte Carlo diagnostic plots, accompanying the **scape** package. The purpose of the package is to combine existing tools from the **coda** and **lattice** packages, and make it easy to adjust graphical details. It can

be useful for anyone using MCMC analysis, regardless of the application. By Arni Magnusson and Ian Stewart.

simex Implementation of the SIMEX-Algorithm by Cook & Stefanski and MCSIMEX by Küchenhoff, Mwalili & Lesaffre. By Wolfgang Lederer.

sp Classes and methods for spatial data. The classes document where the spatial location information resides, for 2D or 3D data. Utility functions are provided, e.g. for plotting data as maps, spatial selection, as well as methods for retrieving coordinates, for subsetting, print, summary, etc. By Edzer J. Pebesma, Roger Bivand and others.

spectralGP Routines for creating, manipulating, and performing Bayesian inference about Gaussian processes in one and two dimensions using the Fourier basis approximation: simulation and plotting of processes, calculation of coefficient variances, calculation of process density, coefficient proposals (for use in MCMC). It uses R environments to store GP objects as references/pointers. By Chris Paciorek.

sspir A glm-like formula language to define dynamic generalized linear models (state space models). Includes functions for Kalman filtering and smoothing. By Claus Dethlefsen and Søren Lundbye-Christensen.

tdthap TDT tests for extended haplotypes. By David Clayton.

time A function for drawing a progress bar using standard text output, and additional time-tracking routines that allow developers to track how long their processor-intensive calculations take. By Toby Dylan Hocking.

tlnise Functions for two level normal models as described in Everson and Morris (2000), JRSS B. S-PLUS original by Phil Everson; R port by Roger D. Peng.

trust Local optimization using two derivatives and trust regions. By Charles J. Geyer.

tseriesChaos Routines for the analysis of nonlinear time series. This work is largely inspired by the TISEAN project, by Rainer Hegger, Holger Kantz and Thomas Schreiber (`http://www.mpipks-dresden.mpg.de/~tisean/`). By Antonio Fabio Di Narzo.

ump Uniformly most powerful tests. By Charles J. Geyer and Glen D. Meeden.

varSelRF Variable selection from random forests using both backwards variable elimination (for the selection of small sets of non-redundant variables) and selection based on the importance spectrum (somewhat similar to scree plots; for the selection of large, potentially highly-correlated variables). Main applications in high-dimensional data (e.g., microarray data, and other genomics and proteomics applications). By Ramon Diaz-Uriarte.

varmixt Performs mixture models on the variance for the analysis of gene expression data. By Paul Delmar and Julie Aubert.

wavelets Functions for computing and plotting discrete wavelet transforms (DWT) and maximal overlap discrete wavelet transforms (MODWT), as well as their inverses. Additionally, it contains functionality for computing and plotting wavelet transform filters that are used in the above decompositions as well as multi-resolution analyses. By Eric Aldrich.

Other changes

- Packages **anm**, **fdim**, **haplo.score**, **meanscore**, **mscalib**, **phyloarray**, **seao**, **seao.gui**, **sound**, and **twostage** were moved from the main CRAN section to the Archive.

- Package **gpls** was resurrected from the Archive.

- Packages **rcom** and **GPArotation** were moved from the Devel section of CRAN into the main section.

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