- `nls()` now allows more peculiar but reasonable ways of being called, e.g., with `data = list(`*uneven_lengths*`)` or a model without variables.
- `match.arg()` was not behaving as documented when `several.ok = TRUE` (PR#9859), gave spurious warnings when `arg` had the wrong length and was incorrectly documented (exact matches are returned even when there is more than one partial match).
- The `data.frame` method for `split<-()` was broken.
- The test for `-D__NO_MATH_INLINES` was badly broken and returned true on all non-glibc platforms and false on all glibc ones (whether they were broken or not).
- LF was missing after the last prompt when '`--quiet`' was used without '`--slave`'. Use '`--slave`' when no final LF is desired.
- Fixed bug in initialisation code in **grid** package for determining the boundaries of shapes. Problem reported by Hadley Wickham; symptom was error message: '`Polygon edge not found`'.
- `str()` is no longer slow for large `POSIXct` objects. Its output is also slightly more compact for such objects; implementation via new optional argument `give.head`.
- `strsplit(*, fixed = TRUE)`, potentially `iconv()` and internal string formatting is now faster for large strings, thanks to report PR#9902 by John Brzustowski.
- `de.restore()` gave a spurious warning for matrices (Ben Bolker)
- `plot(fn, xlim = c(a, b))` would not set `from` and `to` properly when plotting a function. The argument lists to `curve()` and `plot.function()` have been modified slightly as part of the fix.
- `julian()` was documented to work with `POSIXt` origins, but did not work with `POSIXlt` ones. (PR#9908)
- Dataset `HairEyeColor` has been corrected to agree with Friendly (2000): the change involves the breakdown of the Brown hair / Brown eye cell by Sex, and only totals over Sex are given in the original source.
- Trailing spaces are now consistently stripped from `\alias{}` entries in '.Rd' files, and this is now documented. (PR#9915)
- `.find.packages()`, `packageDescription()` and `sessionInfo()` assumed that attached environments named `"package:foo"` were package environments, although misguided users could use such a name in `attach()`.
- `spline()` and `splinefun()` with `method = "periodic"` could return incorrect results when `length(x)` was 2 or 3.
- `getS3method()` could fail if the method name contained a regexp metacharacter such as `"+"`.
- `help(`*a_character_vector*`)` now uses the name and not the value of the vector unless it has length exactly one, so e.g. `help(letters)` now gives help on `letters`. (Related to PR#9927)
- Ranges in `chartr()` now work better in CJK locales, thanks to Ei-ji Nakama.

Changes on CRAN

by Kurt Hornik

New contributed packages

ADaCGH Analysis and plotting of array CGH data. Allows usage of Circular Binary Segmentation, wavelet-based smoothing, ACE method (CGH Explorer), HMM, BioHMM, GLAD, CGHseg, and Price's modification of Smith & Waterman's algorithm. Most computations are parallelized. Figures are imagemaps with links to IDClight (`http://idclight.bioinfo.cnio.es`). By Ramon Diaz-Uriarte and Oscar M. Rueda. Wavelet-based aCGH smoothing code from Li Hsu and Douglas Grove, imagemap code from Barry Rowlingson.

AIS Tools to look at the data ("Ad Inidicia Spectata"). By Micah Altman.

AcceptanceSampling Creation and evaluation of Acceptance Sampling Plans. Plans can be single, double or multiple sampling plans. By Andreas Kiermeier.

Amelia Amelia II: A Program for Missing Data. Amelia II "multiply imputes" missing data in a single cross-section (such as a survey), from a time series (like variables collected for each year in a country), or from a time-series-cross-sectional data set (such as collected by years for each of several countries). Amelia II implements a bootstrapping-based algorithm that gives essentially the same answers as the standard IP or EMis approaches, is usually considerably faster than existing approaches and can handle many more variables. The program also generalizes existing approaches by allowing for trends in time series across observations within a cross-sectional unit, as well as priors that allow experts to incorporate beliefs they have about the values of missing cells in their data. The program works from the R command line or via a graphical user interface that does not require users to know R. By James Honaker, Gary King, and Matthew Blackwell.

BiodiversityR A GUI (via **Rcmdr**) and some utility functions (often based on the **vegan**) for statistical analysis of biodiversity and ecological communities, including species accumulation curves, diversity indices, Renyi profiles, GLMs for analysis of species abundance and presence-absence, distance matrices, Mantel tests, and cluster, constrained and unconstrained ordination analysis. By Roeland Kindt.

CORREP Multivariate correlation estimator and statistical inference procedures. By Dongxiao Zhu and Youjuan Li.

CPGchron Create radiocarbon-dated depth chronologies, following the work of Parnell and Haslett (2007, submitted to JRSSC). By Andrew Parnell.

Cairo Provides a Cairo graphics device that can be use to create high-quality vector (PDF, PostScript and SVG) and bitmap output (PNG, JPEG, TIFF), and high-quality rendering in displays (X11 and Win32). Since it uses the same back-end for all output, copying across formats is WYSIWYG. Files are created without the dependence on X11 or other external programs. This device supports alpha channel (semi-transparent drawing) and resulting images can contain transparent and semi-transparent regions. It is ideal for use in server environments (file output) and as a replacement for other devices that don't have Cairo's capabilities such as alpha support or anti-aliasing. Backends are modular such that any subset of backends is supported. By Simon Urbanek and Jeffrey Horner.

CarbonEL Carbon Event Loop: hooks a Carbon event loop handler into R. This is useful for enabling UI from a console R (such as using the Quartz device from Terminal or ESS). By Simon Urbanek.

DAAGbio Data sets and functions useful for the display of microarray and for demonstrations with microarray data. By John Maindonald.

Defaults Set, get, and import global function defaults. By Jeffrey A. Ryan.

Devore7 Data sets and sample analyses from Jay L. Devore (2008), "Probability and Statistics for Engineering and the Sciences (7th ed)", Thomson. Original by Jay L. Devore, modifications by Douglas Bates, modifications for the 7th edition by John Verzani.

G1DBN Perform Dynamic Bayesian Network inference using 1st order conditional dependencies. By Sophie Lebre.

GSA Gene Set Analysis. By Brad Efron and R. Tibshirani.

GSM Gamma Shape Mixture. Implements a Bayesian approach for estimation of a mixture of gamma distributions in which the mixing occurs over the shape parameter. This family provides a flexible and novel approach for modeling heavy-tailed distributions, is computationally efficient, and only requires to specify a prior distribution for a single parameter. By Sergio Venturini.

GeneF Implements several generalized F-statistics, including ones based on the flexible isotonic/monotonic regression or order restricted hypothesis testing. By Yinglei Lai.

HFWutils Functions for Excel connections, garbage collection, string matching, and passing by reference. By Felix Wittmann.

ICEinfer Incremental Cost-Effectiveness (ICE) Statistical Inference. Given two unbiased samples of patient level data on cost and effectiveness for a pair of treatments, make head-to-head treatment comparisons by (i) generating the bivariate bootstrap resampling distribution of ICE uncertainty for a specified value of the shadow price of health, λ, (ii) form the wedge-shaped ICE confidence region with specified confidence fraction within $[0.50, 0.99]$ that is equivariant with respect to changes in λ, (iii) color the bootstrap outcomes within the above confidence wedge with economic preferences from an ICE map with specified values of λ, beta and gamma parameters, (iv) display VAGR and ALICE acceptability curves, and (v) display indifference (iso-preference) curves from an ICE map with specified values of λ, β and γ or η parameters. By Bob Obenchain.

ICS ICS/ICA computation based on two scatter matrices. Implements Oja et al.'s method of two different scatter matrices to obtain an invariant coordinate system or independent components, depending on the underlying assumptions. By Klaus Nordhausen, Hannu Oja, and Dave Tyler.

ICSNP Tools for multivariate nonparametrics, as location tests based on marginal ranks, spatial median and spatial signs computation, Hotelling's T-test, estimates of shape. By Klaus Nordhausen, Seija Sirkia, Hannu Oja, and Dave Tyler.

LLAhclust Hierarchical clustering of variables or objects based on the likelihood linkage analysis method. The likelihood linkage analysis is a general agglomerative hierarchical clustering method developed in France by Lerman in a long series of research articles and books. Initially proposed in the framework of variable clustering, it has been progressively extended to allow the clustering of very general object descriptions. The approach mainly consists in replacing the value of the estimated similarity coefficient by the probability of finding a lower value under the hypothesis of "absence of link". Package **LLAhclust** contains routines for computing various types of probabilistic similarity coefficients between variables or object descriptions. Once the similarity values between variables/objects are computed, a hierarchical clustering can be performed using several probabilistic and non-probabilistic aggregation criteria, and indices measuring the quality of the partitions compatible with the resulting hierarchy can be computed. By Ivan Kojadinovic, Israël-César Lerman, and Philippe Peter.

LLN Learning with Latent Networks. A new framework in which graph-structured data are used to train a classifier in a latent space, and then classify new nodes. During the learning phase, a latent representation of the network is first learned and a supervised classifier is then built in the learned latent space. In order to classify new nodes, the positions of these nodes in the learned latent space are estimated using the existing links between the new nodes and the learning set nodes. It is then possible to apply the supervised classifier to assign each new node to one of the classes. By Charles Bouveyron & Hugh Chipman.

LearnBayes Functions helpful in learning the basic tenets of Bayesian statistical inference. Contains functions for summarizing basic one and two parameter posterior distributions and predictive distributions, MCMC algorithms for summarizing posterior distributions defined by the user, functions for regression models, hierarchical models, Bayesian tests, and illustrations of Gibbs sampling. By Jim Albert.

LogConcDEAD Computes the maximum likelihood estimator from an i.i.d. sample of data from a log-concave density in any number of dimensions. Plots are available for 1- and 2-d data. By Madeleine Cule, Robert Gramacy, and Richard Samworth.

MLDS Maximum Likelihood Difference Scaling. Difference scaling is a method for scaling perceived supra-threshold differences. The package contains functions that allow the user to design and run a difference scaling experiment, to fit the resulting data by maximum likelihood and test the internal validity of the estimated scale. By Kenneth Knoblauch and Laurence T. Maloney, based in part on C code written by Laurence T. Maloney and J. N. Yang.

MLEcens MLE for bivariate (interval) censored data. Contains functions to compute the nonparametric maximum likelihood estimator for the bivariate distribution of (X, Y), when realizations of (X, Y) cannot be observed directly. More precisely, the MLE is computed based on a set of rectangles ("observation rectangles") that are known to contain the unobservable realizations of (X, Y). The methods can also be used for univariate censored data, and for censored data with competing risks. The package contains the functionality of **bicreduc**, which will no longer be maintained. By Marloes Maathuis.

MiscPsycho Miscellaneous Psychometrics: statistical analyses useful for applied psychometricians. By Harold C. Doran.

ORMDR Odds ratio based multifactor-dimensionality reduction method for detecting gene-gene interactions. By Eun-Kyung Lee, Sung Gon Yi, Yoojin Jung, and Taesung Park.

PET Simulation and reconstruction of PET images. Implements different analytic/direct and iterative reconstruction methods of Peter Toft, and offers the possibility to simulate PET data. By Joern Schulz, Peter Toft, Jesper James Jensen, and Peter Philipsen.

PSAgraphics Propensity Score Analysis (PSA) Graphics. Includes functions which test balance within strata of categorical and quantitative covariates, give a representation of the estimated effect size by stratum, provide a graphic and loess based effect size estimate, and various balance functions that provide measures of the balance achieved via a PSA in a categorical covariate. By James E. Helmreich and Robert M. Pruzek.

PerformanceAnalytics Econometric tools for performance and risk analysis. Aims to aid practitioners and researchers in utilizing the latest research in analysis of non-normal return streams. In general, the package is most tested on return (rather than price) data on a monthly scale, but most functions will work with daily or irregular return data as well. By Peter Carl and Brian G. Peterson.

QRMlib Code to examine Quantitative Risk Management concepts, accompanying the book "Quantitative Risk Management: Concepts, Techniques and Tools" by Alexander J. McNeil, Rüdiger Frey and Paul Embrechts. S-Plus original by Alexander McNeil; R port by Scott Ulman.

R.cache Fast and light-weight caching of objects. Methods for memoization, that is, caching arbitrary R objects in persistent memory. Objects can be loaded and saved stratified on a set of hashing objects. By Henrik Bengtsson.

R.huge Methods for accessing huge amounts of data. Provides a class representing a matrix where the actual data is stored in a binary format on the local file system. This way the size limit of the data is set by the file system and not the memory. Currently in an alpha/early-beta version. By Henrik Bengtsson.

RBGL Interface to boost C++ graph library. Demo of interface with full copy of all hpp defining boost. By Vince Carey, Li Long, and R. Gentleman.

RDieHarder An interface to the dieharder test suite of random number generators and tests that was developed by Robert G. Brown, extending earlier work by George Marsaglia and others. By Dirk Eddelbuettel.

RLRsim Exact (Restricted) Likelihood Ratio tests for mixed and additive models. Provides rapid simulation-based tests for the presence of variance components/nonparametric terms with a convenient interface for a variety of models. By Fabian Scheipl.

ROptEst Optimally robust estimation using S4 classes and methods. By Matthias Kohl.

ROptRegTS Optimally robust estimation for regression-type models using S4 classes and methods. By Matthias Kohl.

RSVGTipsDevice An R SVG graphics device with dynamic tips and hyperlinks using the w3.org XML standard for Scalable Vector Graphics. Supports tooltips with 1 to 3 lines and line styles. By Tony Plate, based on **RSvgDevice** by T Jake Luciani.

Rcapture Loglinear Models in Capture-Recapture Experiments. Estimation of abundance and other demographic parameters for closed populations, open populations and the robust design in capture-recapture experiments using loglinear models. By Sophie Baillargeon and Louis-Paul Rivest.

RcmdrPlugin.TeachingDemos Provides an **Rcmdr** "plug-in" based on the **TeachingDemos** package, and is primarily for illustrative purposes. By John Fox.

Reliability Functions for estimating parameters in software reliability models. Only infinite failure models are implemented so far. By Andreas Wittmann.

RiboSort Rapid classification of (TRFLP & ARISA) microbial community profiles, eliminating the laborious task of manually classifying community fingerprints in microbial studies. By automatically assigning detected fragments and their respective relative abundances to appropriate ribotypes, **RiboSort** saves time and greatly simplifies the preparation of DNA fingerprint data sets for statistical analysis. By Úna Scallan & Ann-Kathrin Liliensiek.

Rmetrics Rmetrics — Financial Engineering and Computational Finance. Environment for teaching "Financial Engineering and Computational Finance". By Diethelm Wuertz and many others.

RobLox Optimally robust influence curves in case of normal location with unknown scale. By Matthias Kohl.

RobRex Optimally robust influence curves in case of linear regression with unknown scale and standard normal distributed errors where the regressor is random. By Matthias Kohl.

Rsac Seismic analysis tools in R. Mostly functions to reproduce some of the Seismic Analysis Code (SAC, `http://www.llnl.gov/sac/`) commands in R. This includes reading standard binary '.SAC' files, plotting arrays of seismic recordings, filtering, integration, differentiation, instrument deconvolution, and rotation of horizontal components. By Eric M. Thompson.

Runuran Interface to the UNU.RAN library for Universal Non-Uniform RANdom variate generators. By Josef Leydold and Wolfgang Hörmann.

Ryacas An interface to the yacas computer algebra system. By Rob Goedman, Gabor Grothendieck, Søren Højsgaard, Ayal Pinkus.

SRPM Shared Reproducibility Package Management. A package development and management system for distributed reproducible research. By Roger D. Peng.

SimHap A comprehensive modeling framework for epidemiological outcomes and a multiple-imputation approach to haplotypic analysis of population-based data. Can perform single SNP and multi-locus (haplotype) association analyses for continuous Normal, binary, longitudinal and right-censored outcomes measured in population-based samples. Uses estimation maximization techniques for inferring haplotypic phase in individuals, and incorporates a multiple-imputation approach to deal with the uncertainty of imputed haplotypes in association testing. By Pamela A. McCaskie.

SpatialNP Multivariate nonparametric methods based on spatial signs and ranks. Contains test and estimates of location, tests of independence, tests of sphericity, several estimates of shape and regression all based on spatial signs, symmetrized signs, ranks and signed ranks. By Seija Sirkia, Jaakko Nevalainen, Klaus Nordhausen, and Hannu Oja.

TIMP Problem solving environment for fitting superposition models. Measurements often represent a superposition of the contributions of distinct sub-systems resolved with respect to many experimental variables (time, temperature, wavelength, pH, polarization, etc). **TIMP** allows parametric models for such superpositions to be fit and validated. The package has been extensively applied to modeling data arising in spectroscopy experiments. By Katharine M. Mullen and Ivo H. M. van Stokkum.

TwslmSpikeWeight Normalization of cDNA microarray data with the two-way semilinear model(TW-SLM). It incorporates information from control spots and data quality in the TW-SLM to improve normalization of cDNA microarray data. Huber's and Tukey's bisquare weight functions are available for robust estimation of the TW-SLM. By Deli Wang and Jian Huang.

Umacs Universal Markov chain sampler. By Jouni Kerman.

WilcoxCV Functions to perform fast variable selection based on the Wilcoxon rank sum test in the cross-validation or Monte-Carlo cross-validation settings, for use in microarray-based binary classification. By Anne-Laure Boulesteix.

YaleToolkit Tools for the graphical exploration of complex multivariate data developed at Yale University. By John W. Emerson and Walton Green.

adegenet Genetic data handling for multivariate analysis using **ade4**. By Thibaut Jombart.

ads Spatial point patterns analysis. Perform first- and second-order multi-scale analyses derived from Ripley's K-function, for univariate, multivariate and marked mapped data in rectangular, circular or irregular shaped sampling windows, with test of statistical significance based on Monte Carlo simulations. By R. Pelissier and F. Goreaud.

argosfilter Functions to filter animal satellite tracking data obtained from Argos. Especially indicated for telemetry studies of marine animals, where Argos locations are predominantly of low quality. By Carla Freitas.

arrayImpute Missing imputation for microarray data. By Eun-kyung Lee, Dankyu Yoon, and Taesung Park.

ars Adaptive Rejection Sampling. By Paulino Perez Rodriguez; original C++ code from Arnost Komarek.

arulesSequences Add-on for **arules** to handle and mine frequent sequences. Provides interfaces to the C++ implementation of cSPADE by Mohammed J. Zaki. By Christian Buchta and Michael Hahsler.

asuR Functions and data sets for a lecture in Advanced Statistics using R. Especially the functions `mancontr()` and `inspect()` may be of general interest. With the former, it is possible to specify your own contrasts and give them useful names. Function `inspect()` shows a wide range of inspection plots to validate model assumptions. By Thomas Fabbro.

bayescount Bayesian analysis of count distributions with JAGS. A set of functions to apply a zero-inflated gamma Poisson (equivalent to a zero-inflated negative binomial), zero-inflated Poisson, gamma Poisson (negative binomial) or Poisson model to a set of count data using JAGS (Just Another Gibbs Sampler). Returns information on the possible values for mean count, overdispersion and zero inflation present in count data such as faecal egg count data. By Matthew Denwood.

benchden Full implementation of the 28 distributions introduced as benchmarks for nonparametric density estimation by Berlinet and Devroye (1994). Includes densities, cdfs, quantile functions and generators for samples. By Thoralf Mildenberger, Henrike Weinert, and Sebastian Tiemeyer.

biOps Basic image operations and image processing. Includes arithmetic, logic, look up table and geometric operations. Some image processing functions, for edge detection (several algorithms including Roberts, Sobel, Kirsch, Marr-Hildreth, Canny) and operations by convolution masks (with predefined as well as user defined masks) are provided. Supported file formats are jpeg and tiff. By Matias Bordese and Walter Alini.

binMto Asymptotic simultaneous confidence intervals for comparison of many treatments with one control, for the difference of binomial proportions, allows for Dunnett-like-adjustment, Bonferroni or unadjusted intervals. Simulation of power of the above interval methods, approximate calculation of any-pair-power, and sample size iteration based on approximate any-pair power. Exact conditional maximum test for many-to-one comparisons to a control. By Frank Schaarschmidt.

bio.infer Compute biological inferences. Imports benthic count data, reformats this data, and computes environmental inferences from this data. By Lester L. Yuan.

blockTools Block, randomly assign, and diagnose potential problems between units in randomized experiments. Blocks units into experimental blocks, with one unit per treatment condition, by creating a measure of multivariate distance between all possible pairs of units. Maximum, minimum, or an allowable range of differences between units on one variable can be set. Randomly assign units to treatment conditions. Diagnose potential interference problems between units assigned to different treatment conditions. Write outputs to '`.tex`' and '`.csv`' files. By Ryan T. Moore.

bootStepAIC Model selection by bootstrapping the `stepAIC()` procedure. By Dimitris Rizopoulos.

brew A templating framework for mixing text and R code for report generation. Template syntax is similar to PHP, Ruby's erb module, Java Server Pages, and Python's psp module. By Jeffrey Horner.

ca Computation and visualization of simple, multiple and joint correspondence analysis. By Michael Greenacre and Oleg Nenadic.

catmap Case-control And Tdt Meta-Analysis Package. Conducts fixed-effects (inverse variance) and random-effects (DerSimonian and Laird, 1986) meta-analyses of case-control or family-based (TDT) genetic data; in addition, performs meta-analyses combining these two types of study designs. The fixed-effects model was first described by Kazeem and Farrell (2005); the random-effects model is described in Nicodemus (submitted for publication). By Kristin K. Nicodemus.

celsius Retrieve Affymetrix microarray measurements and metadata from Celsius web services, see `http://genome.ucla.edu/projects/celsius`. By Allen Day, Marc Carlson.

cghFLasso Spatial smoothing and hot spot detection using the fused lasso regression. By Robert Tibshirani and Pei Wang.

choplump Choplump tests: permutation tests for comparing two groups with some positive but many zero responses. By M. P. Fay.

clValid Statistical and biological validation of clustering results. By Guy Brock, Vasyl Pihur, Susmita Datta, and Somnath Datta.

classGraph Construct directed graphs of S4 class hierarchies and visualize them. Typically, these graphs are DAGs (directed acyclic graphs) in general, though often trees. By Martin Maechler partly based on code from Robert Gentleman.

clinfun Clinical Trial Design and Data Analysis Functions. Utilities to make your clinical collaborations easier if not fun. By E. S. Venkatraman.

clusterfly Explore clustering interactively using R and GGobi. Contains both general code for visualizing clustering results and specific visualizations for model-based, hierarchical and SOM clustering. By Hadley Wickham.

clv Cluster Validation Techniques. Contains most of the popular internal and external cluster validation methods ready to use for the most of the outputs produced by functions coming from package **cluster**. By Lukasz Nieweglowski.

codetools Code analysis tools for R. By Luke Tierney.

colorRamps Builds single and double gradient color maps. By Tim Keitt.

contrast Contrast methods, in the style of the **Design** package, for fit objects produced by the `lm`, `glm`, `gls`, and `geese` functions. By Steve Weston, Jed Wing and Max Kuhn.

coxphf Cox regression with Firth's penalized likelihood. R by Meinhard Ploner, Fortran by Georg Heinze.

crosshybDetector Identification of probes potentially affected by cross-hybridizations in microarray experiments. Includes functions for diagnostic plots. By Paolo Uva.

ddesolve Solver for Delay Differential Equations by interfacing numerical routines written by Simon N. Wood, with contributions by Benjamin J. Cairns. These numerical routines first appeared in Simon Wood's solv95 program. By Alex Couture-Beil, Jon T. Schnute, and Rowan Haigh.

desirability Desirability Function Optimization and Ranking. S3 classes for multivariate optimization using the desirability function by Derringer and Suich (1980). By Max Kuhn.

dplR Dendrochronology Program Library in R. Contains functions for performing some standard tree-ring analyses. By Andy Bunn.

dtt Discrete Trigonometric Transforms. Functions for 1D and 2D Discrete Cosine Transform (DCT), Discrete Sine Transform (DST) and Discrete Hartley Transform (DHT). By Lukasz Komsta.

earth Multivariate Adaptive Regression Spline Models. Build regression models using the techniques in Friedman's papers "Fast MARS" and "Multivariate Adaptive Regression Splines". (The term "MARS" is copyrighted and thus not used as the name of the package.). By Stephen Milborrow, derived from code in package **mda** by Trevor Hastie and Rob Tibshirani.

eigenmodel Semiparametric factor and regression models for symmetric relational data. Estimates the parameters of a model for symmetric relational data (e.g., the above-diagonal part of a square matrix) using a model-based eigenvalue decomposition and regression. Missing data is accommodated, and a posterior mean for missing data is calculated under the assumption that the data are missing at random. The marginal distribution of the relational data can be arbitrary, and is fit with an ordered probit specification. By Peter Hoff.

epibasix Elementary tools for the analysis of common epidemiological problems, ranging from sample size estimation, through 2×2 contingency table analysis and basic measures of agreement (kappa, sensitivity/specificity). Appropriate print and summary statements are also written to facilitate interpretation wherever possible. The target audience includes biostatisticians and epidemiologists who would like to apply standard epidemiological methods in a simple manner. By Michael A Rotondi.

experiment Various statistical methods for designing and analyzing randomized experiments. One main functionality is the implementation of randomized-block and matched-pair designs based on possibly multivariate pretreatment covariates. Also provides the tools to analyze various randomized experiments including cluster randomized experiments, randomized experiments with noncompliance, and randomized experiments with missing data. By Kosuke Imai.

fCopulae Rmetrics — Dependence Structures with Copulas. Environment for teaching "Financial Engineering and Computational Finance". By Diethelm Wuertz and many others.

forensic Statistical Methods in Forensic Genetics. Statistical evaluation of DNA mixtures, DNA profile match probability. By Miriam Marusiakova.

fractal Insightful Fractal Time Series Modeling and Analysis. Software to book in development entitled "Fractal Time Series Analysis in S-PLUS and R" by William Constantine and Donald B. Percival, Springer. By William Constantine and Donald Percival.

fso Fuzzy Set Ordination: a multivariate analysis used in ecology to relate the composition of samples to possible explanatory variables. While differing in theory and method, in practice, the use is similar to "constrained ordination". Contains plotting and summary functions as well as the analyses. By David W. Roberts.

gWidgetstcltk Toolkit implementation of the **gWidgets** API for the **tcltk** package. By John Verzani.

gamlss.mx A GAMLSS add on package for fitting mixture distributions. By Mikis Stasinopoulos and Bob Rigby.

gcl Computes a fuzzy rules classifier (Vinterbo, Kim & Ohno-Machado, 2005). By Staal A. Vinterbo.

geiger Analysis of evolutionary diversification. Features running macroevolutionary simulation and estimating parameters related to diversification from comparative phylogenetic data. By Luke Harmon, Jason Weir, Chad Brock, Rich Glor, and Wendell Challenger.

ggplot An implementation of the grammar of graphics in R. Combines the advantages of both **base** and **lattice** graphics: conditioning and shared axes are handled automatically, and one can still build up a plot step by step from multiple data sources. Also implements a more sophisticated multidimensional conditioning system and a consistent interface to map data to aesthetic attributes. By Hadley Wickham.

ghyp Provides all about univariate and multivariate generalized hyperbolic distributions and its special cases (Hyperbolic, Normal Inverse Gaussian, Variance Gamma and skewed Student t distribution). Especially fitting procedures, computation of the density, quantile, probability, random variates, expected shortfall and some portfolio optimization and plotting routines. Also contains the generalized inverse Gaussian distribution. By Wolfgang Breymann and David Luethi.

glmmAK Generalized Linear Mixed Models. By Arnost Komarek.

granova Graphical Analysis of Variance. Provides distinctive graphics for display of ANOVA results. Functions were written to display data for any number of groups, regardless of their sizes (however, very large data sets or numbers of groups are likely to be problematic) using a specialized approach to construct data-based contrast vectors with respect to which ANOVA data are displayed. By Robert M. Pruzek and James E. Helmreich.

graph Implements some simple graph handling capabilities. By R. Gentleman, Elizabeth Whalen, W. Huber, and S. Falcon.

grasp Generalized Regression Analysis and Spatial Prediction for R. GRASP is a general method for making spatial predictions of response variables (RV) using point surveys of the RV and spatial coverages of predictor variables (PV). Originally, GRASP was developed to analyse, model and predict vegetation distribution over New Zealand. It has been used in all sorts of applications since then. By Anthony Lehmann, Fabien Fivaz, John Leathwick and Jake Overton, with contributions from many specialists from around the world.

hdeco Hierarchical DECOmposition of Entropy for Categorical Map Comparisons. A flexible and hierarchical framework for comparing categorical map composition and configuration (spatial pattern) along spatial, thematic, or external grouping variables. Comparisons are based on measures of mutual information between thematic classes (colors) and location (spatial partitioning). Results are returned in textual, tabular, and graphical forms. By Tarmo K. Remmel, Sandor Kabos, and Ferenc (Ferko) Csillag.

heatmap.plus Heatmaps with more sensible behavior. Allows the heatmap matrix to have non-identical x and y dimensions, and multiple tracks of annotation for `RowSideColors` and `ColSideColors`. By Allen Day.

hydrosanity Graphical user interface for exploring hydrological time series. Designed to work with catchment surface hydrology data (rainfall and streamflow); but could also be used with other time series data. Hydrological time series typically have many missing values, and varying accuracy of measurement (indicated by data quality codes). Furthermore, the spatial coverage of data varies over time. Much of the functionality of this package attempts to understand these complex data sets, detect errors and characterize sources of uncertainty. Emphasis is on graphical methods. The GUI is based on **rattle**. By Felix Andrews.

identity Calculate identity coefficients, based on Mark Abney's C code. By Na Li.

ifultools Insightful Research Tools. By William Constantine.

inetwork Network Analysis and Plotting. Implements a network partitioning algorithm to identify communities (or modules) in a network. A network plotting function then utilizes the identified community structure to position the vertices for plotting. Also contains functions to calculate the assortativity and transitivity of a vertex. By Sun-Chong Wang.

inline Functionality to dynamically define R functions and S4 methods with in-lined C, C++ or Fortran code supporting `.C` and `.Call` calling conventions. By Oleg Sklyar, Duncan Murdoch, and Mike Smith.

irtoys A simple common interface to the estimation of item parameters in IRT models for binary responses with three different programs (ICL, BILOG-MG, and `ltm`), and a variety of functions useful with IRT models. By Ivailo Partchev.

kin.cohort Analysis of kin-cohort studies. Provides estimates of age-specific cumulative risk of a disease for carriers and noncarriers of a mutation. The cohorts are retrospectively built from relatives of probands for whom the genotype is known. Currently the method of moments and marginal maximum likelihood are implemented. Confidence intervals are calculated from bootstrap samples. Most of the code is a translation from previous MATLAB code by Chatterjee. By Victor Moreno, Nilanjan Chatterjee, and Bhramar Mukherjee.

kzs Kolmogorov-Zurbenko Spline. A collection of functions utilizing splines to smooth a noisy data set in order to estimate its underlying signal. By Derek Cyr and Igor Zurbenko.

lancet.iraqmortality Surveys of Iraq mortality published in The Lancet. The Lancet has published two surveys on Iraq mortality before and after the US-led invasion. The package facilitates access to the data and a guided tour of some of their more interesting aspects. By David Kane, with contributions from Arjun Navi Narayan and Jeff Enos.

ljr Fits and tests logistic joinpoint models. By Michal Czajkowski, Ryan Gill, and Greg Rempala.

luca Likelihood Under Covariate Assumptions (LUCA). Likelihood inference in case-control studies of a rare disease under independence or simple dependence of genetic and non-genetic covariates. By Ji-Hyung Shin, Brad McNeney, and Jinko Graham.

meifly Interactive model exploration using GGobi. By Hadley Wickham.

mixPHM Mixtures of proportional hazard models. Fits multiple variable mixtures of various parametric proportional hazard models using the EM algorithm. Proportionality restrictions can be imposed on the latent groups and/or on the variables. Several survival distributions can be specified. Missing values are allowed. Independence is assumed over the single variables. By Patrick Mair and Marcus Hudec.

mlmmm Computational strategies for multivariate linear mixed-effects models with missing values (Schafer and Yucel, 2002). By Recai Yucel.

modeest Provides estimators of the mode of univariate unimodal data or univariate unimodal distributions. Also allows to compute the Chernoff distribution. By Paul Poncet.

modehunt Multiscale Analysis for Density Functions. Given independent and identically distributed observations $X(1), \ldots, X(n)$ from a density f, this package provides five methods to perform a multiscale analysis about f as well as the necessary critical values. The first method, introduced in Duembgen and Walther (2006), provides simultaneous confidence statements for the existence and location of local increases (or decreases) of f, based on all intervals I(all) spanned by any two observations $X(j), X(k)$. The second method approximates the latter approach by using only a subset of I(all) and is therefore computationally much more efficient, but asymptotically equivalent. Omitting the additive correction term Gamma in either method offers another two approaches which are more powerful on small scales and less powerful on large scales, however, not asymptotically minimax optimal anymore. Finally, the block procedure is a compromise between adding Gamma or not, having intermediate power properties. The latter is again asymptotically equivalent to the first and was introduced in Rufibach and Walther (2007). By Kaspar Rufibach and Guenther Walther.

monomvn Estimation of multivariate normal data of arbitrary dimension where the pattern of missing data is monotone. Through the use of parsimonious/shrinkage regressions (plsr, pcr, lasso, ridge, etc.), where standard regressions fail, the package can handle an (almost) arbitrary amount of missing data. The current version supports maximum likelihood inference. Future versions will provide a means of sampling from a Bayesian posterior. By Robert B. Gramacy.

mota Mean Optimal Transformation Approach for detecting nonlinear functional relations. Originally designed for the identifiability analysis of nonlinear dynamical models. However, the underlying concept is very general and allows to detect groups of functionally related variables whenever there are multiple estimates for each variable. By Stefan Hengl.

nlstools Tools for assessing the quality of fit of a Gaussian nonlinear model. By Florent Baty and Marie-Laure Delignette-Muller, with contributions from Sandrine Charles, Jean-Pierre Flandrois.

oc OC Roll Call Analysis Software. Estimates Optimal Classification scores from roll call votes supplied though a `rollcall` object from package **pscl**. By Keith Poole, Jeffrey Lewis, James Lo and Royce Carroll.

oce Analysis of Oceanographic data. Supports CTD measurements, sea-level time series, coastline files, etc. Also includes functions for calculating seawater properties such as density, and derived properties such as buoyancy frequency. By Dan Kelley.

pairwiseCI Calculation of parametric and nonparametric confidence intervals for the difference or ratio of location parameters and for the difference, ratio and odds-ratio of binomial proportion for comparison of independent samples. CIs are *not* adjusted for multiplicity. A `by` statement allows calculation of CI separately for the levels of one further factor. By Frank Schaarschmidt.

paran An implementation of Horn's technique for evaluating the components retained in a principle components analysis (PCA). Horn's method contrasts eigenvalues produced through a PCA on a number of random data sets of uncorrelated variables with the same number of variables and observations as the experimental or observational data set to produce eigenvalues for components that are adjusted for the sample error-induced inflation. Components with adjusted eigenvalues greater than one are retained. The package may also be used to conduct parallel analysis following Glorfeld's (1995) suggestions to reduce the likelihood of over-retention. By Alexis Dinno.

pcse Estimation of panel-corrected standard errors. Data may contain balanced or unbalanced panels. By Delia Bailey and Jonathan N. Katz.

penalized L1 (lasso) and L2 (ridge) penalized estimation in Generalized Linear Models and in the Cox Proportional Hazards model. By Jelle Goeman.

plRasch Fit log linear by linear association models. By Zhushan Li & Feng Hong.

plink Separate Calibration Linking Methods. Uses unidimensional item response theory methods to compute linking constants and conduct chain linking of tests for multiple groups under a nonequivalent groups common item design. Allows for mean/mean, mean/sigma, Haebara, and Stocking-Lord calibrations of single-format or mixed-format dichotomous (1PL, 2PL, and 3PL) and polytomous (graded response partial credit/generalized partial credit, nominal, and multiple-choice model) common items. By Jonathan Weeks.

plotAndPlayGTK A GUI for interactive plots using GTK+. When wrapped around plot calls, a window with the plot and a tool bar to interact with it pop up. By Felix Andrews, with contributions from Graham Williams.

pomp Inference methods for partially-observed Markov processes. By Aaron A. King, Ed Ionides, and Carles Breto.

poplab Population Lab: a tool for constructing a virtual electronic population of related individuals evolving over calendar time, by using vital statistics, such as mortality and fertility, and disease incidence rates. By Monica Leu, Kamila Czene, and Marie Reilly.

proftools Profile output processing tools. By Luke Tierney.

proj4 A simple interface to lat/long projection and datum transformation of the PROJ.4 cartographic projections library. Allows transformation of geographic coordinates from one projection and/or datum to another. By Simon Urbanek.

proxy Distance and similarity measures. An extensible framework for the efficient calculation of auto- and cross-proximities, along with implementations of the most popular ones. By David Meyer and Christian Buchta.

psych Routines for personality, psychometrics and experimental psychology. Functions are primarily for scale construction and reliability analysis, although others are basic descriptive stats. By William Revelle.

psyphy Functions that could be useful in analyzing data from pyschophysical experiments, including functions for calculating d' from several different experimental designs, links for mafc to be used with the binomial family in glm (and possibly other contexts) and self-Start functions for estimating gamma values for CRT screen calibrations. By Kenneth Knoblauch.

qualV Qualitative methods for the validation of models. By K.G. van den Boogaart, Stefanie Jachner and Thomas Petzoldt.

quantmod Specify, build, trade, and analyze quantitative financial trading strategies. By Jeffrey A. Ryan.

rateratio.test Exact rate ratio test. By Michael Fay.

regtest Functions for unary and binary regression tests. By Jens Oehlschlägel.

relations Data structures for k-ary relations with arbitrary domains, predicate functions, and fitters for consensus relations. By Kurt Hornik and David Meyer.

rgcvpack Interface to the GCVPACK Fortran package for thin plate spline fitting and prediction. By Xianhong Xie.

rgr Geological Survey of Canada (GSC) functions for exploratory data analysis with applied geochemical data, with special application to the estimation of background ranges to support both environmental studies and mineral exploration. By Robert G. Garrett.

rindex Indexing for R. Index structures allow quickly accessing elements from large collections. With btree optimized for disk databases and ttree for RAM databases, uses hybrid static indexing which is quite optimal for R. By Jens Oehlschlägel.

rjson JSON for R. Converts R object into JSON objects and vice-versa. By Alex Couture-Beil.

rsbml R support for SBML. Links R to libsbml for SBML parsing and output, provides an S4 SBML DOM, converts SBML to R graph objects, and more. By Michael Lawrence.

sapa Insightful Spectral Analysis for Physical Applications. Software for the book "Spectral Analysis for Physical Applications" by Donald B. Percival and Andrew T. Walden, Cambridge University Press, 1993. By William Constantine and Donald Percival.

scagnostics Calculates Tukey's scagnostics which describe various measures of interest for pairs of variables, based on their appearance on a scatterplot. They are useful tool for weeding out interesting or unusual scatterplots from a scatterplot matrix, without having to look at ever individual plot. By Heike Hofmann,, Lee Wilkinson, Hadley Wickham, Duncan Temple Lang, and Anushka Anand.

schoolmath Functions and data sets for math used in school. A main focus is set to prime-calculation. By Joerg Schlarmann and Josef Wienand.

sdcMicro Statistical Disclosure Control methods for the generation of public- and scientific-use files. Data from statistical agencies and other institutions are mostly confidential. The package can be used for the generation of safe (micro)data, i.e., for the generation of public- and scientific-use files. By Matthias Templ.

seriation Infrastructure for seriation with an implementation of several seriation/sequencing techniques to reorder matrices, dissimilarity matrices, and dendrograms. Also contains some visualizations techniques based on seriation. By Michael Hahsler, Christian Buchta and Kurt Hornik.

signalextraction Real-Time Signal Extraction (Direct Filter Approach). The Direct Filter Approach (DFA) provides efficient estimates of signals at the current boundary of time series in real-time. For that purpose, one-sided ARMA-filters are computed by minimizing customized error criteria. The DFA can be used for estimating either the level or turning-points of a series, knowing that both criteria are incongruent. In the context of real-time turning-point detection, various risk-profiles can be operationalized, which account for the speed and/or the reliability of the one-sided filter. By Marc Wildi & Marcel Dettling.

simba Functions for similarity calculation of binary data (for instance presence/absence species data). Also contains wrapper functions for reshaping species lists into matrices and vice versa and some other functions for further processing of similarity data (Mantel-like permutation procedures) as well as some other useful stuff. By Gerald Jurasinski.

simco A package to import Structure files and deduce similarity coefficients from them. By Owen Jones.

snpXpert Tools to analysis SNP data. By Eun-kyung Lee, Dankyu Yoon, and Taesung Park.

spam SPArse Matrix: functions for sparse matrix algebra (used by **fields**). Differences with **SparseM** and **Matrix** are: (1) support for only one sparse matrix format, (2) based on transparent and simple structure(s) and (3) S3 and S4 compatible. By Reinhard Furrer.

spatgraphs Graphs, graph visualization and graph based summaries to be used with spatial point pattern analysis. By Tuomas Rajala.

splus2R Insightful package providing missing S-PLUS functionality in R. Currently there are many functions in S-PLUS that are missing in R. To facilitate the conversion of S-PLUS modules and libraries to R packages, this package helps to provide missing S-PLUS functionality in R. By William Constantine.

sqldf Manipulate R data frames using SQL. By G. Grothendieck.

sspline Smoothing splines on the sphere. By Xianhong Xie.

stochasticGEM Fitting Stochastic General Epidemic Models: Bayesian inference for partially observed stochastic epidemics. The general epidemic model is used for estimating the parameters governing the infectious and incubation period length, and the parameters governing susceptibility. In real-life epidemics the infection process is unobserved, and the data consists of the times individuals are detected, usually via appearance of symptoms. The package fits several variants of the general epidemic model, namely the stochastic SIR with Markovian and non-Markovian infectious periods. The estimation is based on Markov chain Monte Carlo algorithm. By Eugene Zwane.

surveyNG An experimental revision of the **survey** package for complex survey samples (featuring a database interface and sparse matrices). By Thomas Lumley.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Other changes

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

Kurt Hornik
Wirtschaftsuniversität Wien, Austria
`Kurt.Hornik@R-project.org`

R Foundation News

by Kurt Hornik

Donations and new members

Donations

AT&T Research (USA)
Jaimison Fargo (USA)
Stavros Panidis (Greece)
Saxo Bank (Denmark)
Julian Stander (United Kingdom)

New benefactors

Shell Statistics and Chemometrics, Chester, UK

New supporting institutions

AT&T Labs, New Jersey, USA

BC Cancer Agency, Vancouver, Canada

Black Mesa Capital, Santa Fe, USA

Department of Statistics, Unviersity of Warwick, Coventry, UK