Reference card to "shipunov" package

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1 `asmisc.r`

1.1 System

`Alldups(vec1)` Finds duplicates from both ends, optionally returns indexes of duplicates' groups

`Aggregate1(df1, by, fun)` Aggregates by one vector and uses it for row names

`Toclip(df1)` Insert content to Linux X11 clipboard (uses xclip)

`Xpager(pager)` Separate terminal pager for Linux X11 (uses some terminal and less)

`Table2df(table1)` Convert table to data frame saving structure

`Cdate()` System date in yyyymmdd format

`Str(df1)` Enhanced str() (with variable numbers, row names and missing data indication)

`Files()` Textual filesystem browser

`Ls()` Advanced object listing (with type, memory size etc.)

`Read.tri.nts(file1)` Read NTSYSpc files

`Tobin(df1)` Binarize (make dummy variables)

`Peaks(vec1)` Find local maxima

1.2 Statistics

`Normality(vec1)` Check normality

`CVs(vec1)` Coefficients of variation

`K(vec1)` Lyubishchev's coefficient of divergence ($SSMD^2$)

`Mag(num)` Interpreter for R^2-related effect sizes

`pairwise.Eff(vec1, factor1, effect)` Pairwise table of effects with magnitudes

`Rro.test(vec1, vec2)` Robust rank order test

`pairwise.Rro.test(vec1, factor1)` ... and its pairwise *post hoc* derivative

`pairwise.Table2.test(table1)` Pairwise Chi-squared or Fisher test for 2-dimensional tables

`VTcoeffs(table1)` Effect sizes of association between categorical variables

`Fibonacci(num)` Calculates the n's Fibonacci's number

`Phyllotaxis(num)` Outputs the phyllotaxis formula or angle of divergence

`PlotBest.dist(data)` Plots dotchart with best base distance method

`PlotBest.mdist(data)` Plots dotchart with best distance method, use multiple non-base distances

`PlotBest.hclust(dist)` Plots dotchart with best clustering method

`Misclass(vec1, vec2)` Misclassification (confusion) table

`BootRF(data, group)` How to bootstrap with randomForest()

`BootKNN(data, group)` How to bootstrap with KNN

`Dev(df)` Allows to know which object is predicted with less accuracy

`Co.test(hclust, dist)` Correlation test between cophenetic and original distances

`Jclust(df1)` Simple bootstrap and jackknife clustering

`BootA(df)` How to bootstrap clustering with ape

`Hclust.match(hc1, hc2)` Counts matches between two hierarchical clusterings

`MDSv(scores)` MDS: explained variance (surrogate)

`Missing.map(df1)` Textual plot of missing data

1.3 Plots

`Points(vec1, vec2)` Number of cases in each location reflected in the point size

`PPoints(factor1, vec1, vec2)` Same as above, for multiple subgroups

`Histp(vec1)` Histogram with percents on the top of bars

`Histr(vec1)` Histogram with overlaid normal curve or density, optionally with rug

`Cladd(lm)` Adds confidence bands to the simple linear model plots

`Boxplots(df1, factor1)` Boxplots for every scaled variable grouped by "group" factor

`Dotchart1(vec1)` and `Dotchart(vec1)` Like a dotchart(vec1) but with better left margin

`Dotchart3(values, left, right)` Dotchart which shows values together with ranges

`Linechart(df1, factor1)` Dotchart-like plot sfor every scaled variable grouped by "group" factor

`Ellipses(points, groups)` Groups' confidence ellipses

`Hulls(points, groups)` Groups' hulls with centroids calculation

`Overlap(hulls)` Polygons' overlap

`Squares(hulls)` Polygons' squares

`Ploth(hclust)` Changes the appearance of cluster dendrogram

1.4 Correlation

`Topm(df1)` Stacks (correlation) matrix and selects values which are above the "level"

`Cor(df1)` Correlation matrix with p-values

`Cor2(df1)` Another (faster) variant of correlation matrix with p-values based on F-statistic

`Coeff.det(df1)` Average coefficients of determination for each variable

`Cor.vec(df1)` Calculates correlation and converts results into the named long vector

`Rostova.tbl(df1, factor1)` Calculates multiple correlation matrices (via factor1) and stacks them together

`Pleiad(table1)` Correlation circles (correlation pleiads)

2 `recode.r`: multiple recode

`Recode(var, from, to)` Basic multiple recoding (similar to SQL left join)

`Recode4(var, from, to, missed)` Multiple recoding which cares of non-recoded values (partly similar to SQL inner join)

`RecodeR(var, from, to)` Running multiple recoding

`Recode4R(var, from, to, missed)` Running multiple recoding, considers non-recoded

3 `infill.r`: strictly biological

`Read.fasta(file1)` Simple reading of FASTA files

`Write.fasta(df1, file1)` Simple writing of FASTA files

`Gap.code(seqs)` Gap coding of nucleotide alignments

`MrBayes(...)` A slight improvement of ips::mrbayes()

`Infill(data, perm)` Rarefaction curves

`Coml(df1, df2)` Compare species checklists

`Is.tax.inform.char(vec)` Is the character potentially taxonomically informative?

`Make.treesc(list)` Phylogenetic trees unification, requires specific label format

`Plot.phylocl(tree, df)` Plot phylogenetic tree with clades collapsed into triangles or rectangles

4 gmoon.r

4.1 Graphical examples

`Ex.lty()` or `Ex.lines()` Line type examples

`Ex.pch()` or `Ex.points()` Point (pch) examples

`Ex.col(all=FALSE)` or `Ex.cols(all=FALSE)` Examples of standard colors (also shows all colors)

`Ex.font()` or `Ex.fonts()` Examples of standard fonts

`Ex.plots()` or `Ex.types()` Examples of plot types

`Ex.margins()` Example of plot margins

`Ex.boxplot()` Boxplot explanation

4.2 Grapical fun

`A.locator()` Add arrow to the plot interactively

`Saynodynamite()` Say "no" to dynamite plots!

`Gridmoon(config)` Painting with R

`Ell(config)` Plot ellipse

`R(x1, y1)` Imitation (!) of the modern R logo

`Miney(cells)` Miney game, modified from `miney` package of Roland Rau

`Life(config)` Conway's Game of Life

4.3 Special multivariate

`Gradd(model)` Adds to the 2D ordination plot small semi-transparent points which make color classification grid

`plot.nnet(nnet)` Plots `nnet` object