Package ‘RVAideMemoire’

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Description Contains miscellaneous functions useful in biostatistics, mostly univariate and multivariate testing procedures with a special emphasis on permutation tests. Many functions intend to simplify user's life by shortening existing procedures or by implementing plotting functions that can be used with as many methods from different packages as possible.

Enhances glmmADMB

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Contents

`RVAideMemoire-package` *Testing and Plotting Procedures for Biostatistics*

Description

Contains miscellaneous functions useful in biostatistics, mostly univariate and multivariate testing procedures with a special emphasis on permutation tests. Many functions intend to simplify user's life by shortening existing procedures or by implementing plotting functions that can be used with as many methods from different packages as possible.

Details

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Author(s)

Maxime HERVE

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References

Document : "Aide-memoire de statistique appliquee a la biologie - Construire son etude et analyser les resutats a l'aide du logiciel R" (available on CRAN)

`adonis.II` *Type II permutation MANOVA using distance matrices*

Description

This function is a wrapper to `adonis2` but performs type II tests (whereas `adonis2` performs type I).

Usage

```
adonis.II(formula, data, ...)
```

Arguments

`formula`	a typical model formula such as `Y~A+B*C`, but where `Y` is either a dissimilarity object (inheriting from class `"dist"`) or data frame or a matrix; `A`, `B`, and `C` may be factors or continuous variables.
`data`	the data frame from which `A`, `B` and `C` would be drawn.
`...`	additional arguments to `adonis2`. See help of this function.

Details

See `adonis2` for detailed explanation of what is done. The only difference with `adonis2` is that `adonis.II` performs type II tests instead of type I.

Value

a data frame of class `"anova"`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
require(vegan)
data(dune)
data(dune.env)

# Compare:
adonis2(dune~Management*A1,by="terms",data=dune.env,permutations=99)
adonis2(dune~A1*Management,by="terms",data=dune.env,permutations=99)

# With:
adonis.II(dune~Management*A1,data=dune.env,permutations=99)
adonis.II(dune~A1*Management,data=dune.env,permutations=99)
```

`Anova.clm` *Anova Tables for Cumulative Link (Mixed) Models*

Description

These functions are methods for `Anova` to calculate type-II or type-III analysis-of-deviance tables for model objects produced by `clm` and `clmm`. Likelihood-ratio tests are calculated in both cases.

Usage

```
## S3 method for class 'clm'
Anova(mod, type = c("II", "III", 2, 3), ...)

## S3 method for class 'clmm'
Anova(mod, type = c("II", "III", 2, 3), ...)
```

Arguments

`mod`	`clm` or `clmm` object.
`type`	type of test, `"II"`, `"III"`, `2` or `3`.
`...`	additional arguments to `Anova`. Not usable here.

Details

See help of the `Anova` for a detailed explanation of what "type II" and "typ III" mean.

Value

See `Anova`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`Anova`, `clm`, `clmm`

`back.emmeans` *Back-transformation of EMMeans*

Description

Back-transforms EMMeans (produced by `emmeans`) when the model was built on a transformed response variable. This is typically the case when a LM(M) with *log(x+1)* as response variable gives a better fitting than a GLM(M) for count data, or when a beta regression takes as response a variable on the [0;1] interval that has been rescaled to the (0;1) interval using `p.beta`.

Usage

```
back.emmeans(emm, transform = c("log", "logit", "sqrt", "4rt", "inverse", "p.beta"),
  base = exp(1), add = 0, n = NULL, C = 2, ord = FALSE, decreasing = TRUE)
```

Arguments

`emm`	object returned by `emmeans`.
`transform`	transformation applied to the response variable before building the model on which `emm` is based (`"4rt"` is fourth-root). `"p.beta"` assumes that the model (beta regression) was built using a logit link function.
`base`	the base with respect to which the logarithm transformation was computed (if `transform="log"`). Defaults to *e*=`exp(1)`.
`add`	value to be added to *x* before computing the transformation, if needed (*e.g.* `1` if the initial transformation was *log(x+1)*).
`n`	total number of observations in the initial data set. Only used with `transform="p.beta"`, see `p.beta`.
`C`	number of categories from which initial continuous proportions were computed. Only used with `transform="p.beta"`, see `p.beta`.
`ord`	logical indicating if back-transformed EMMeans should be ordered.
`decreasing`	logical indicating in which order back-transformed EMMeans should be ordered, if `order=TRUE`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`emmeans`

Examples

```
require(emmeans)

set.seed(1149)
tab <- data.frame(
  response <- c(rpois(30,0),rpois(30,2),rpois(30,4)),
  fact <- gl(3,30,labels=LETTERS[1:3])
)

model <- lm(log(response+1)~fact,data=tab)
EMM <- emmeans(model,~fact)
back.emmeans(EMM,transform="log",add=1)
```

`bootstrap` *Bootstrap*

Description

Simplified version of the `boot` function.

Usage

```
bootstrap(x, fun, nrep = 1000, conf.level = 0.95, ...)
```

Arguments

`x`	numeric vector.
`fun`	function to be used for computation (`function(x,i) ...(x[i])`).
`nrep`	number of replicates.
`conf.level`	confidence level for confidence interval.
`...`	additional arguments to `boot`. See help of this function.

Details

See help of the `boot` function for more explanations.

Value

`method`	the character string `"Bootstrap"`
`data.name`	a character string giving the name of the data.
`estimate`	the estimated original value
`conf.level`	confidence level for confidence interval.
`rep`	number of replicates.
`conf.int`	limits of the confidence interval.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`boot`

Examples

```
# Confidence interval of a mean
samp <- sample(1:50,10,replace=TRUE)
bootstrap(samp,function(x,i) mean(x[i]))

# Confidence interval of the standard error of the mean
bootstrap(samp,function(x,i) sd(x[i])/sqrt(length(x[i])))
```

`byf.hist` *Histogram for factor levels*

Description

Draws a histogram of a numeric variable per level of a factor.

Usage

```
byf.hist(formula, data, sep = FALSE, density = TRUE, xlab = NULL, ylab = NULL,
  col = NULL)
```

Arguments

`formula`	a formula of the form `a ~ b` where `a` gives the data values and `b` a factor giving the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`sep`	logical. If `TRUE` a histogram is displayed per level of the factor. If `FALSE` all levels are displayed on the same histogram.
`density`	logical. If `TRUE` density polygons are displayed, if `FALSE` classical counts are displayed.
`xlab`	label for x-axis (name of the response variable as default).
`ylab`	label for y-axis ("Density" or "Frequency" as default, depending on the type of histogram).
`col`	color(s) used for density curves or bars.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`hist`

Examples

```
data(iris)
byf.hist(Sepal.Length~Species,data=iris)
```

`byf.mqqnorm` *QQ-plot for factor levels*

Description

Draws a multivariate QQ-plot of numeric variables per level of a factor.

Usage

```
byf.mqqnorm(formula, data)
```

Arguments

`formula`	a formula of the form `a ~ b`, where `a` is a matrix giving the dependent variables (each column giving a variable) and `b` a factor giving the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`mqqnorm`, `byf.mshapiro`, `qqPlot`

Examples

```
data(iris)
byf.mqqnorm(as.matrix(iris[,1:4])~Species,data=iris)
```

`byf.mshapiro` *Shapiro-Wilk test for factor levels*

Description

Performs a multivariate Shapiro-Wilk test on numeric variables per level of a factor.

Usage

```
byf.mshapiro(formula, data)
```

Arguments

`formula`	a formula of the form `a ~ b` where `a` is a matrix giving the dependent variables (each column giving a variable) and `b` a factor giving the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.

Value

`method`	name of the test.
`data.name`	a character string giving the names of the data.
`tab`	table of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`byf.mqqnorm`, `mshapiro.test`, `qqPlot`

Examples

```
data(iris)
byf.mshapiro(as.matrix(iris[,1:4])~Species,data=iris)
```

`byf.qqnorm` *QQ-plot for factor levels*

Description

Draws a QQ-plot of a numeric variable per level of a factor.

Usage

```
byf.qqnorm(formula, data, ...)
```

Arguments

`formula`	a formula of the form `a ~ b` where `a` gives the data values and `b` a factor giving the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`...`	other arguments to pass to `qqPlot`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`link[RVAideMemoire]{byf.shapiro}`, `qqPlot`

Examples

```
data(iris)
byf.qqnorm(Sepal.Length~Species,data=iris)
```

`byf.shapiro` *Shapiro-Wilk test for factor levels*

Description

Performs a Shapiro-Wilk test on a numeric variable per level of a factor.

Usage

```
byf.shapiro(formula, data)
```

Arguments

`formula`	a formula of the form `a ~ b` where `a` gives the data values and `b` a factor giving the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.

Value

`method`	name of the test.
`data.name`	a character string giving the names of the data.
`tab`	table of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`byf.qqnorm`, `shapiro.test`

Examples

```
data(iris)
byf.shapiro(Sepal.Length~Species,data=iris)
```

`CDA.cv` *Cross validation*

Description

Performs cross validation with correspondence discriminant analyses.

Usage

```
CDA.cv(X, Y, repet = 10, k = 7, ncomp = NULL, method = c("mahalanobis",
  "euclidian"))
```

Arguments

`X`	a data frame of dependent variables (typically contingency or presence-absence table).
`Y`	factor giving the groups.
`repet`	an integer giving the number of times the whole procedure has to be repeated.
`k`	an integer giving the number of folds (can be re-set internally if needed).
`ncomp`	an integer giving the number of components to be used for prediction. If `NULL` all components are used.
`method`	criterion used to predict class membership. See `predict.coadisc`.

Details

The training sets are generated in respect to the relative proportions of the levels of `Y` in the original data set (see `splitf`).

Value

`repet`	number of times the whole procedure was repeated.
`k`	number of folds.
`ncomp`	number of components used.
`method`	criterion used to classify individuals of the test sets.
`groups`	levels of `Y`.
`models.list`	list of of models generated (`repet*k` models), for PLSR, CPPLS, PLS-DA, PPLS-DA, LDA and QDA.
`NMC`	Classification error rates (`repet` values).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`discrimin.coa`

Examples

```
require(ade4)
data(perthi02)
## Not run: CDA.cv(perthi02$tab,perthi02$cla)
```

`CDA.test` *Significance test for CDA*

Description

Performs a significance test for correspondence discriminant analysis. See Details.

Usage

```
CDA.test(X, fact, ncomp = NULL, ...)
```

Arguments

`X`	a data frame of dependent variables (typically contingency or presence-absence table).
`fact`	factor giving the groups.
`ncomp`	an integer giving the number of components to be used for the test. If `NULL` `nlevels(fact)-1` are used. See Details.
`...`	other arguments to pass to `summary.manova`. See Details.

Details

CDA consists in two steps: building a correspondence analysis (CA) on `X`, then using row coordinates on all CA components as input variables for a linear discriminant analysis. `CDA.test` builds the intermediate CA, then uses the first `ncomp` components to test for an effect of `fact`. If 1 component is used the test is an ANOVA, if more than 1 component are used the test is a MANOVA.

Value

An ANOVA or MANOVA table.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`discrimin.coa`, `summary.manova`

Examples

```
require(ade4)
data(perthi02)

CDA.test(perthi02$tab,perthi02$cla)
```

`cdf.discrete` *Cumulative Distribution Function of a known discrete distribution*

Description

Returns an object similar to what is produced by `ecdf`, but based on a known discrete distribution.

Usage

```
cdf.discrete(x, dist = c("binom", "geom", "hyper", "nbinom", "pois"), ...)
```

Arguments

`x`	numeric vector of the observations.
`dist`	character string naming a discrete distribution (`"binom"` by default).
`...`	parameters of the distribution specified by `dist`.

Details

The function is intended to be used in goodness-of-fits tests for discrete distributions, such as proposed in the `dgof` package.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
if(require(dgof)) {
  set.seed(1124)
  resp <- rpois(20,2)
  cvm.test(resp,cdf.discrete(resp,"pois",2))
}
```

`chisq.bin.exp` *Expected counts for comparison of response probabilities to given values*

Description

Returns expected counts before comparing response probabilities (i.e. when the response variable is a binary variable) to given values by a chi-squared test. The function is in fact a wrapper to the chi-squared test for comparison of proportions to given values on a contingency table.

Usage

```
chisq.bin.exp(formula, data, p, graph = FALSE)
```

Arguments

`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups, respectively. `a` can be a numeric vector or a factor, with only two possible values (except NA).
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`p`	theoretical probabilities.
`graph`	logical. If `TRUE` a mosaic plot of expected counts is drawn.

Details

The function returns how many counts can be < 5 to respect Cochran's rule (80% of counts must be >= 5).

Value

`p.theo`	theoretical probabilities.
`mat`	contingency table of expected counts.
`cochran`	number of counts which can be < 5.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`prop.test`, `chisq.theo.bintest`, `mosaicplot`

Examples

```
response <- c(rep(0:1,c(40,60)),rep(0:1,c(55,45)),rep(0:1,c(65,35)))
fact <- gl(3,100,labels=LETTERS[1:3])
p.theo <- c(0.5,0.45,0.2)
chisq.bin.exp(response~fact,p=p.theo)
```

`chisq.bintest` *Pearson's Chi-squared test for binary variables*

Description

Performs a Pearson's Chi-squared test for comparing response probabilities (i.e. when the response variable is a binary variable). The function is in fact a wrapper to the chi-squared test for comparison of proportions on a contingency table. If the p-value of the test is significant, the function performs pairwise comparisons by using Pearson's Chi-squared tests.

Usage

```
chisq.bintest(formula, data, correct = TRUE, alpha = 0.05, p.method = "fdr")
```

Arguments

`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups, respectively. `a` can be a numeric vector or a factor, with only two possible values (except NA).
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`correct`	a logical indicating whether to apply continuity correction when computing the test statistic for 2 by 2 tables. See help of `chisq.test`.
`alpha`	significance level to compute pairwise comparisons.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

If the response is a 0/1 variable, the probability of the '1' group is tested. In any other cases, the response is transformed into a factor and the probability of the second level is tested.

Since a chi-squared test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `fisher.bintest` in that case.

Value

`method.test`	a character string giving the name of the global test computed.
`data.name`	a character string giving the name(s) of the data.
`alternative`	a character string describing the alternative hypothesis.
`estimate`	the estimated probabilities.
`null.value`	the value of the difference in probabilities under the null hypothesis, always 0.
`statistic`	test statistics.
`parameter`	test degrees of freedom.
`p.value`	p-value of the global test.
`alpha`	significance level.
`p.adjust.method`	method for p-values correction.
`p.value.multcomp`	data frame of pairwise comparisons result.
`method.multcomp`	a character string giving the name of the test computed for pairwise comparisons.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`G.bintest`, `fisher.bintest`

Examples

```
response <- c(rep(0:1,c(40,60)),rep(0:1,c(55,45)),rep(0:1,c(65,35)))
fact <- gl(3,100,labels=LETTERS[1:3])
chisq.bintest(response~fact)
```

`chisq.exp` *Expected counts for comparison of proportions to given values*

Description

Returns expected counts before comparing proportions to given values by a chi-squared test.

Usage

```
chisq.exp(data, p, graph = FALSE)
```

Arguments

`data`	contingency table.
`p`	theoretical proportions.
`graph`	logical. If `TRUE` a mosaic plot of expected counts is drawn.

Details

The function returns how many counts can be < 5 to respect Cochran's rule (80% of counts must be >= 5).

Value

`p.theo`	theoretical proportions.
`mat`	contingency table of expected counts.
`cochran`	number of counts which can be < 5.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`prop.test`, `chisq.test`, `mosaicplot`

Examples

```
proportions <- sample(c(0,1),200,replace=TRUE)
populations <- sample(LETTERS[1:3],200,replace=TRUE)
tab.cont <- table(populations,proportions)
p.theo <- c(0.4,0.5,0.7)
chisq.exp(tab.cont,p=p.theo)
```

`chisq.multcomp` *Pairwise comparisons after a chi-squared goodness-of-fit test*

Description

Performs pairwise comparisons after a global chi-squared goodness-of-fit test.

Usage

```
chisq.multcomp(x, p.method = "fdr")
```

Arguments

`x`	numeric vector (counts).
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since a chi-squared test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `multinomial.multcomp` in that case.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.adjust.method`	method for p-values correction.
`p.value`	table of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`chisq.test`, `multinomial.test`, `multinomial.multcomp`

Examples

```
counts <- c(49,30,63,59)
chisq.test(counts)
chisq.multcomp(counts)
```

`chisq.theo.bintest` *Pearson's Chi-squared test for comparison of response probabilities to given values*

Description

Performs a Pearson's Chi-squared test for comparing response probabilities (i.e. when the response variable is a binary variable) to given values. The function is in fact a wrapper to the chi-squared test for comparison of proportions to given values on a contingency table.

Usage

```
chisq.theo.bintest(formula, data, p)
```

Arguments

`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups, respectively. `a` can be a numeric vector or a factor, with only two possible values (except NA).
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`p`	theoretical probabilities.

Details

If the response is a 0/1 variable, the probability of the '1' group is tested. In any other cases, the response is transformed into a factor and the probability of the second level is tested.

Value

`method.test`	a character string giving the name of the test.
`data.name`	a character string giving the name(s) of the data.
`alternative`	a character string describing the alternative hypothesis, always two-sided.
`estimate`	the estimated probabilities.
`null.value`	the theoretical probabilities.
`statistic`	test statistics.
`parameter`	test degrees of freedom.
`p.value`	p-value of the test.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`prop.test`, `chisq.bin.exp`, `prop.bin.multcomp`

Examples

```
response <- c(rep(0:1,c(40,60)),rep(0:1,c(55,45)),rep(0:1,c(65,35)))
fact <- gl(3,100,labels=LETTERS[1:3])
p.theo <- c(0.5,0.45,0.2)
chisq.theo.bintest(response~fact,p=p.theo)
```

`chisq.theo.multcomp` *Pairwise comparisons after a chi-squared test for given probabilities*

Description

Performs pairwise comparisons after a global chi-squared test for given probabilities.

Usage

```
chisq.theo.multcomp(x, p = rep(1/length(x), length(x)), p.method = "fdr")
```

Arguments

`x`	numeric vector (counts).
`p`	theoretical proportions.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since a chi-squared test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `multinomial.theo.multcomp` in that case.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`observed`	observed counts.
`expected`	expected counts.
`p.adjust.method`	method for p-values correction.
`statistic`	statistics of each test.
`p.value2`	corrected p-values.
`p.value`	data frame of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`chisq.test`, `multinomial.test`, `multinomial.theo.multcomp`

Examples

```
counts <- c(49,30,63,59)
p.theo <- c(0.2,0.1,0.45,0.25)
chisq.test(counts,p=p.theo)
chisq.theo.multcomp(counts,p=p.theo)
```

`cochran.qtest` *Cochran's Q test*

Description

Performs the Cochran's Q test for unreplicated randomized block design experiments with a binary response variable and paired data. If the p-value of the test is significant, the function performs pairwise comparisons by using the Wilcoxon sign test.

Usage

```
cochran.qtest(formula, data, alpha = 0.05, p.method = "fdr")
```

Arguments

`formula`	a formula of the form `a ~ b | c`, where `a`, `b` and `c` give the data values and corresponding groups and blocks, respectively. `a` can be a numeric vector or a factor, with only two possible values.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`alpha`	significance level to compute pairwise comparisons.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

If the response is a 0/1 variable, the probability of the '1' group is tested. In any other cases, the response is transformed into a factor and the probability of the second level is tested.

Value

`method.test`	a character string giving the name of the global test computed.
`data.name`	a character string giving the name(s) of the data.
`alternative`	a character string describing the alternative hypothesis.
`estimate`	the estimated probabilities.
`null.value`	the value of the difference in probabilities under the null hypothesis, always 0.
`statistic`	test statistics (Pearson's Chi-squared test only).
`parameter`	test degrees of freedom (Pearson's Chi-squared test only).
`p.value`	p-value of the global test.
`alpha`	significance level.
`p.adjust.method`	method for p-values correction.
`p.value.multcomp`	data frame of pairwise comparisons result.
`method.multcomp`	a character string giving the name of the test computed for pairwise comparisons.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
response <- c(0,1,1,0,0,1,0,1,1,1,1,1,0,0,1,1,0,1,0,1,1,0,0,1,0,1,1,0,0,1)
fact <- gl(3,1,30,labels=LETTERS[1:3])
block <- gl(10,3,labels=letters[1:10])
cochran.qtest(response~fact|block)
```

`cond.multinom` *Condition number of the Hessian matrix of a multinomial log-linear model*

Description

Computes the condition number of the Hessian matrix of a model fitted with `multinom`.

Usage

```
cond.multinom(model)
```

Arguments

`model`	object of class `"multinom"`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`coord.proj` *Coordinates of projected points*

Description

Returns the coordinates of a set of points when orthogonally projected on a new axis.

Usage

```
coord.proj(coord,slp)
```

Arguments

`coord`	2-column data frame or matrix giving the original coordinates (left column: x, right column: y).
`slp`	slope of the new axis.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
data(iris)

# Original coordinates
plot(Petal.Length~Sepal.Length,pch=16,col=as.numeric(iris$Species),data=iris)

# New axis
abline(-6,1.6)

# Coordinates on new axis
new.coord <- coord.proj(iris[,c("Sepal.Length","Petal.Length")],1.6)
stripchart(new.coord~Species,data=iris,col=1:3)
```

`cor.2comp` *Comparison of 2 Pearson's linear correlation coefficients*

Description

Performs the test for equality of 2 Pearson's correlation coefficients. If the difference is not significant, the function returns the common coefficient, its confidence interval and performs the test for equality to a given value.

Usage

```
cor.2comp(var1, var2, var3, var4, alpha = 0.05, conf.level = 0.95, theo = 0)
```

Arguments

`var1`	numeric vector (first variable of the first correlation).
`var2`	numeric vector (second variable of the first correlation).
`var3`	numeric vector (first variable of the second correlation).
`var4`	numeric vector (second variable of the second correlation).
`alpha`	significance level.
`conf.level`	confidence level.
`theo`	theoretical coefficient.

Value

`method.test`	a character string giving the name of the global test computed.
`data.name`	a character string giving the name(s) of the data.
`statistic`	test statistics.
`p.value`	p-value for comparison of the 2 coefficients.
`null.value`	the value of the difference in coefficients under the null hypothesis, always 0.
`alternative`	a character string describing the alternative hypothesis.

`estimate`	the estimated correlation coefficients.
`alpha`	significance level.
`conf.level`	confidence level.
`common.name`	a character string explaining the elements of the table below.
`common`	data frame of results if the coefficients are not significantly different (common coefficient).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`cor.test`

Examples

```
cor1.var1 <- 1:30+rnorm(30,0,2)
cor1.var2 <- 1:30+rnorm(30,0,3)
cor2.var1 <- (-1):-30+rnorm(30,0,2)
cor2.var2 <- (-1):-30+rnorm(30,0,3)
cor.2comp(cor1.var1,cor1.var2,cor2.var1,cor2.var2)
```

`cor.conf` *Equality of a Pearson's linear correlation coefficient to a given value*

Description

Performs a test for equality of a Pearson's linear correlation coefficient to a given value.

Usage

```
cor.conf(var1, var2, theo)
```

Arguments

`var1`	numeric vector (first variable).
`var2`	numeric vector (second variable).
`theo`	theoretical value.

Value

`method`	a character string giving the name of the test.
`data.name`	a character string giving the name(s) of the data.
`statistic`	test statistics.
`p.value`	p-value of the test.
`null.value`	the value of the theoretical coefficient.
`alternative`	a character string describing the alternative hypothesis.
`estimate`	the estimated correlation coefficient.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`cor.test`

Examples

```
var1 <- 1:30+rnorm(30,0,4)
var2 <- 1:30+rnorm(30,0,4)
cor.conf(var1,var2,theo=0.5)
```

`cor.multcomp` *Comparison of several Pearson's linear correlation coefficients*

Description

Performs comparisons of several Pearson's linear correlation coefficients. If no difference, the function returns the common correlation coefficient, its confidence interval and test for its equality to a given value. If the difference is significant, the functions performs pairwise comparisons between coefficients.

Usage

```
cor.multcomp(var1, var2, fact, alpha = 0.05, conf.level = 0.95, theo = 0,
  p.method = "fdr")
```

Arguments

`var1`	numeric vector (first variable).
`var2`	numeric vector (second variable).
`fact`	factor (groups).
`alpha`	significance level.
`conf.level`	confidence level.
`theo`	theoretical coefficient.
`p.method`	method for p-values correction. See help of`p.adjust`.

Value

`method.test`	a character string giving the name of the global test computed.
`data.name`	a character string giving the name(s) of the data.
`statistic`	test statistics.
`parameter`	test degrees of freedom.
`p.value`	p-value for comparison of the coefficients.
`null.value`	the value of the difference in coefficients under the null hypothesis, always 0.
`alternative`	a character string describing the alternative hypothesis.
`estimate`	the estimated correlation coefficients.
`alpha`	significance level.
`conf.level`	confidence level.
`p.adjust.method`	method for p-values correction.
`p.value.multcomp`	data frame of pairwise comparisons result.
`common.name`	a character string explaining the elements of the table below.
`common`	data frame of results if the coefficients are not significantly different (common coefficient).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`cor.test`

Examples

```
var1 <- c(1:15+rnorm(15,0,4),1:15+rnorm(15,0,1),1:15+rnorm(15,0,8))
var2 <- c(-1:-15+rnorm(15,0,4),1:15+rnorm(15,0,1),1:15+rnorm(15,0,8))
fact <- gl(3,15,labels=LETTERS[1:3])
cor.multcomp(var1,var2,fact)

var3 <- c(1:15+rnorm(15,0,1),1:15+rnorm(15,0,3),1:15+rnorm(15,0,2))
cor.multcomp(var1,var3,fact)
```

`cov.test` *Significance test for the covariance between two datasets*

Description

Performs a permutation test based on the sum of square covariance between variables of two datasets, to test wether the (square) covariance is higher than expected under random association between the two datasets. The test is relevent parallel to a 2B-PLS.

Usage

```
cov.test(X, Y, scale.X = TRUE, scale.Y = TRUE, nperm = 999, progress = TRUE)
```

Arguments

`X`	a numeric vector, matrix or data frame.
`Y`	a numeric vector, matrix or data frame.
`scale.X`	logical, if `TRUE` (default) scaling of `X` is required.
`scale.Y`	logical, if `TRUE` (default) scaling of `Y` is required.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name(s) of the data, plus additional information.
`statistic`	the value of the test statistics.
`permutations`	the number of permutations.
`p.value`	the p-value of the test.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`cox.resid` *Martingale residuals of a Cox model*

Description

Plots martingale residuals of a Cox model against fitted values, to check for log-linearity of covariates.

Usage

```
cox.resid(model)
```

Arguments

`model`	a `coxph` model.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>, based on an idea of John Fox.

References

Fox, J. 2002 Cox Proportional-Hazards Regression for Survival Data.

See Also

`coxph`

Examples

```
# 'kidney' dataset of package 'survival'
require(survival)
data(kidney)
model <- coxph(Surv(time,status)~age+factor(sex),data=kidney)
cox.resid(model)
```

`cramer` *Cramer's association coefficient*

Description

Computes the Cramer's association coefficient between 2 nominal variables.

Usage

```
cramer(x, y)
```

Arguments

`x`	a contingency table ('matrix' or 'table' object). `x` and `y` can also both be factors.
`y`	ignored if `x` is a contingency table. If not, `y` should be a vector of the same length.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
var1 <- sample(LETTERS[1:3],30,replace=TRUE)
var2 <- sample(letters[1:3],30,replace=TRUE)
cramer(var1,var2)
# or cramer(table(var1,var2))
```

`cramer.test` *Cramer's association coefficient*

Description

Computes the Cramer's association coefficient between 2 nominal variables, its confidence interval (by bootstraping) and tests for its significance.

Usage

```
cramer.test(x, y, nrep = 1000, conf.level = 0.95)
```

Arguments

`x`	a contingency table ('matrix' or 'table' object). `x` and `y` can also both be factors.
`y`	ignored if `x` is a contingency table. If not, `y` should be a vector of the same length.
`nrep`	number of replicates for bootstraping.
`conf.level`	confidence level.

Value

`method`	name of the test.
`statistic`	test statistics.
`parameter`	test degrees of freedom.
`p.value`	test p-value.
`data.name`	a character string giving the names of the data.
`estimate`	Cramer's coefficient.

`conf.level`	confidence level.
`rep`	number of replicates.
`conf.int`	confidence interval.
`alternative`	a character string giving the alternative hypothesis, always `"two.sided"`
`null.value`	the value of the association measure under the null hypothesis, always 0.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`boot`

Examples

```
var1 <- sample(LETTERS[1:3],30,replace=TRUE)
var2 <- sample(letters[1:3],30,replace=TRUE)
cramer.test(var1,var2)
# or cramer.test(table(var1,var2))
```

`cv` *Coefficient of variation*

Description

Computes the coefficient of variation of a vector.

Usage

```
cv(x, abs = TRUE, pc = TRUE)
```

Arguments

`x`	numeric vector.
`abs`	logical. If `TRUE` the coefficient is expressed in absolute value.
`pc`	logical. If `TRUE` the coefficient is expressed in percentage.

Details

The function deals with missing values.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
cv(rnorm(30))
```

`dendro.gp` *Dendrogram and number of groups to be chosen*

Description

Draws a dendrogram and an additional bar plot helping to choose the number of groups to be retained (based on the dendrogram).

Usage

```
dendro.gp(dend)
```

Arguments

`dend`	a dendrogram obtained from `hclust`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`hclust`

Examples

```
data(iris)
distances <- dist(iris[,1:4],method="euclidian")
dendro <- hclust(distances,method="ward.D2")
dendro.gp(dendro)
```

`deprecated` *Deprecated functions in RVAideMemoire package*

Description

Functions that are not usable anymore, and will be entirely removed from the package in future versions.

Usage

```
back.lsmeans(...)
byf.normhist(...)
cor.sparse(...)
CvM.test(...)
DA.confusion(...)
DA.valid(...)
DA.var(...)
dunn.test(...)
fc.multcomp(...)
friedman.rating.test(...)
kruskal.rating.test(...)
pairwise.manova(...)
pairwise.to.groups(...)
pairwise.wilcox.rating.test(...)
plot1comp.ind(...)
plot1comp.var(...)
PLSDA.ncomp(...)
PLSDA.test(...)
rating.lsmeans(...)
s.corcircle2(...)
scat.mix.categorical(...)
scat.mix.numeric(...)
scatter.coa2(...)
wilcox.paired.rating.multcomp(...)
wilcox.rating.signtest(...)
wilcox.rating.test(...)
```

Arguments

`...`	previous arguments.

Details

`back.lsmeans` and `rating.lsmeans` are replaced by `back.emmeans` and `rating.emmeans`. More generally, stop using package `lsmeans` and change to package `emmeans`, its new version.

`byf.normhist` was not very useful and `byf.hist` does nearly the same job.

`cor.sparse` is replaced by the more generic `MVA.plot`.

`CvM.test` did actually not perform a Cramer-von Mises test but an alternative Cramer test. Use `cramer.test` from package `cramer` directly, on which `CvM.test` was based.

`DA.confusion` and `DA.valid` are replaced by the more generic `MVA.cmv` and `MVA.cv`.

`DA.var` is replaced by the more generic `MVA.synt`.

`dunn.test` is not very useful, prefer `dunnTest` from package `FSA`.

`fc.multcomp` is not useful anymore since `emtrends` (package emmeans) does the same job in a much more powerful manner (see argument `var` of `emtrends`).

`friedman.rating.test`, `kruskal.rating.test`, `wilcox.rating.test`, `wilcox.rating.signtest`, `pairwise.wilcox.rating.test` and `wilcox.paired.rating.multcomp` can be problematic with ratings (in which ties and zeroes are very frequent). The use of CLM(M)s (*via* `clm` and `clmm`) is recommended.

`pairwise.manova` is not useful anymore since `emmeans` (package emmeans) does the same job in a much more powerful manner (on `"mlm"` objects, created by `lm` and not `manova`)

`pairwise.to.groups` was not very useful.

`plot1comp.ind`, `plot1comp.var`, `s.corcircle2`, `scat.mix.categorical`, `scat.mix.numeric` and `scatter.coa2` are replaced by the more generic `MVA.plot`.

`PLSDA.ncomp` was not really useful and `mvr` does nearly the same job.

`PLSDA.test` is replaced by the more generic `MVA.test`.

`DIABLO.cv` *Cross validation*

Description

Performs cross validation with DIABLO (`block.plsda` or `block.splsda`).

Usage

```
DIABLO.cv(x, method = c("mahalanobis.dist", "max.dist", "centroids.dist"),
  validation = c("Mfold", "loo"), k = 7, repet = 10, ...)
```

Arguments

`x`	an object of class `"sgccda"`.
`method`	criterion used to predict class membership. See `perf`.
`validation`	a character giving the kind of (internal) validation to use. See `perf`.
`k`	an integer giving the number of folds (can be re-set internally if needed).
`repet`	an integer giving the number of times the whole procedure has to be repeated.
`...`	other arguments to pass to `perf`.

Details

The function uses the weighted predicted classification error rate (see `perf`).

Value

`repet`	number of times the whole procedure was repeated.
`k`	number of folds.
`validation`	kind of validation used.
`ncomp`	number of components used.
`method`	criterion used to classify individuals of the test sets.
`NMC.mean`	mean classification error rate (based on `repet` values).
`NMC.se`	standard error of the classification error rate (based on `repet` values).

Author(s)

Maxime HERVE <mx.herve@gmail.com>

See Also

`block.plsda`, `block.splsda`, `perf`

Examples

```
## Not run:
require(mixOmics)
data(nutrimouse)
data <- list(gene=nutrimouse$gene,lipid=nutrimouse$lipid,Y=nutrimouse$diet)
DIABLO <- block.plsda(X=data,indY=3)
DIABLO.cv(DIABLO)

## End(Not run)
```

`DIABLO.test` *Significance test based on cross-validation*

Description

Performs a permutation significance test based on cross-validation with DIABLO (`block.plsda` or `block.splsda`).

Usage

```
DIABLO.test(x, method = c("mahalanobis.dist", "max.dist", "centroids.dist"),
  validation = c("Mfold", "loo"), k = 7, nperm = 999, progress = TRUE, ...)
```

Arguments

`x`	an object of class `"sgccda"`.
`method`	criterion used to predict class membership. See `perf`.
`validation`	a character giving the kind of (internal) validation to use. See `perf`.
`k`	an integer giving the number of folds (can be re-set internally if needed).
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.
`...`	other arguments to pass to `perf`.

Details

The function uses the weighted predicted classification error rate (see `perf`).

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name of the data, plus additional information.
`statistic`	the value of the test statistics (classification error rate).
`permutations`	the number of permutations.
`p.value`	the p-value of the test.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`block.plsda`, `block.splsda`, `perf`

Examples

```
## Not run:
require(mixOmics)
data(nutrimouse)
data <- list(gene=nutrimouse$gene,lipid=nutrimouse$lipid,Y=nutrimouse$diet)
DIABLO <- block.plsda(X=data,indY=3)
DIABLO.test(DIABLO)

## End(Not run)
```

`dummy` *Dummy responses*

Description

Creates a matrix of dummy responses from a factor. Needed in some multivariate analyses.

Usage

```
dummy(f, simplify = TRUE)
```

Arguments

`f`	vector (internally transformed into factor).
`simplify`	logical indicating if the last column of the response matrix should be removed (to avoid model overfitting).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
fac <- gl(3,5,labels=LETTERS[1:3])
dummy(fac)
```

`elogis` *Empirical logistic transformation*

Description

Empirical logistic transformation for logistic models with data showing (quasi-)complete separation. The function is intended to be used as a link function in GLM(M)s.

Usage

```
elogis()
```

Author(s)

Formula from McCullagh & Nelder in their seminal book 'Generalized Linear Models'. R code from Eric Wajnberg & Jean-Sebastien Pierre.

Examples

```
# An example with 3 groups and complete separation (from E. Wajnberg)
tab <- data.frame(case=letters[1:3],yes=c(25,30,0),no=c(1,0,20))
tab
## Not run:
mod <- glm(cbind(yes,no)~case,family=binomial(link=elogis()),data=tab)
# Warnings are normal
summary(mod)
## End(Not run)
```

`fisher.bintest` *Fisher's exact test for binary variables*

Description

Performs a Fisher's exact test for comparing response probabilities (i.e. when the response variable is a binary variable). The function is in fact a wrapper to the Fisher's exact test for count data. If the p-value of the test is significant, the function performs pairwise comparisons by using Fisher's exact tests.

Usage

```
fisher.bintest(formula, data, alpha = 0.05, p.method = "fdr")
```

Arguments

`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups, respectively. `a` can be a numeric vector or a factor, with only two possible values (except NA).
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`alpha`	significance level to compute pairwise comparisons.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

If the response is a 0/1 variable, the probability of the '1' group is tested. In any other cases, the response is transformed into a factor and the probability of the second level is tested.

Since chi-squared and G tests are approximate tests, exact tests are preferable when the number of individuals is small (200 is a reasonable minimum).

Value

`method.test`	a character string giving the name of the global test computed.
`data.name`	a character string giving the name(s) of the data.
`alternative`	a character string describing the alternative hypothesis.
`estimate`	the estimated probabilities.
`null.value`	the value of the difference in probabilities under the null hypothesis, always 0.
`p.value`	p-value of the global test.
`alpha`	significance level.
`p.adjust.method`	method for p-values correction.
`p.value.multcomp`	data frame of pairwise comparisons result.
`method.multcomp`	a character string giving the name of the test computed for pairwise comparisons.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`chisq.bintest`, `G.bintest`

Examples

```
response <- c(0,0,0,0,0,0,1,0,0,0,0,0,1,0,1,1,1,0,0,1,1,1,1,1,1,0,0,1,1,1)
fact <- gl(3,10,labels=LETTERS[1:3])
fisher.bintest(response~fact)
```

`fisher.multcomp` *Pairwise comparisons using Fisher's exact test*

Description

Performs pairwise comparisons after a comparison of proportions or after a test for independence of 2 categorical variables, by using a Fisher's exact test.

Usage

```
fisher.multcomp(tab.cont, p.method = "fdr")
```

Arguments

`tab.cont`	contingency table.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since chi-squared and G tests are approximate tests, exact tests are preferable when the number of individuals is small (200 is a reasonable minimum).

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.adjust.method`	method for p-values correction.
`p.value`	table of results of pairwise comparisons.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`chisq.test`, `prop.test`, `fisher.test`

Examples

```
# 2-column contingency table: comparison of proportions
tab.cont1 <- matrix(c(17,23,12,24,20,10),ncol=2,dimnames=list(c("Control",
  "Treatment1","Treatment2"),c("Alive","Dead")),byrow=TRUE)
fisher.test(tab.cont1)
fisher.multcomp(tab.cont1)

# 3-column contingency table: independence test
```

```
tab.cont2 <- as.table(matrix(c(25,10,12,6,15,14,9,16,9),ncol=3,dimnames=list(c("fair",
  "dark","russet"),c("blue","brown","green"))))
fisher.test(tab.cont2)
fisher.multcomp(tab.cont2)
```

`fp.test` *Fligner-Policello test*

Description

Performs a Fligner-Policello test of the null that the medians in the two groups (samples) are the same.

Usage

```
fp.test(x, ...)

## Default S3 method:
fp.test(x, y, delta = 0, alternative = "two.sided", ...)

## S3 method for class 'formula'
fp.test(formula, data, subset, ...)
```

Arguments

`x`	a numeric vector of data values.
`y`	a numeric vector of data values.
`delta`	null difference in medians tested.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`.
`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`...`	further arguments to be passed to or from other methods.

Details

The Fligner-Policello test does not assume that the shape of the distribution is similar in two groups, contrary to the Mann-Whitney-Wilcoxon test. However, it assumes that the the distributions are symmetric.

Value

`statistic`	test statistics.
`p.value`	p-value of the test.
`alternative`	a character string describing the alternative hypothesis.
`method`	a character string indicating the name of the test.
`data.name`	a character string giving the names of the data.
`null.value`	the specified hypothesized value of the median difference.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`wilcox.test`

Examples

```
x <- rpois(20,3)
y <- rpois(20,5)
fp.test(x,y)
```

G.bintest *G-test for binary variables*

Description

Performs a G-test for comparing response probabilities (i.e. when the response variable is a binary variable). The function is in fact a wrapper to the G-test for comparison of proportions on a contingency table. If the p-value of the test is significant, the function performs pairwise comparisons by using G-tests.

Usage

```
G.bintest(formula, data, alpha = 0.05, p.method = "fdr")
```

Arguments

`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups, respectively. `a` can be a numeric vector or a factor, with only two possible values (except NA).
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`alpha`	significance level to compute pairwise comparisons.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

If the response is a 0/1 variable, the probability of the '1' group is tested. In any other cases, the response is transformed into a factor and the probability of the second level is tested.

Since a G-test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `fisher.bintest` in that case.

Value

`method.test`	a character string giving the name of the global test computed.
`data.name`	a character string giving the name(s) of the data.
`alternative`	a character string describing the alternative hypothesis.
`estimate`	the estimated probabilities.
`null.value`	the value of the difference in probabilities under the null hypothesis, always 0.
`statistic`	test statistics.
`parameter`	test degrees of freedom.
`p.value`	p-value of the global test.
`alpha`	significance level.
`p.adjust.method`	method for p-values correction.
`p.value.multcomp`	data frame of pairwise comparisons result.
`method.multcomp`	a character string giving the name of the test computed for pairwise comparisons.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`chisq.bintest`, `fisher.bintest`

Examples

```
response <- c(rep(0:1,c(40,60)),rep(0:1,c(55,45)),rep(0:1,c(65,35)))
fact <- gl(3,100,labels=LETTERS[1:3])
G.bintest(response~fact)
```

`G.multcomp` *Pairwise comparisons after a G-test*

Description

Performs pairwise comparisons after a global G-test.

Usage

```
G.multcomp(x, p.method = "fdr")
```

Arguments

`x`	numeric vector (counts).
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since a G-test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `multinomial.multcomp` in that case.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.adjust.method`	method for p-values correction.
`p.value`	table of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`G.test`, `multinomial.test`, `multinomial.multcomp`

Examples

```
counts <- c(49,30,63,59)
G.test(counts)
G.multcomp(counts)
```

`G.test` *G-test*

Description

Perfoms a G-test on a contingency table or a vector of counts.

Usage

```
G.test(x, p = rep(1/length(x), length(x)))
```

Arguments

`x`	a numeric vector or matrix (see Details).
`p`	theoretical proportions (optional).

Details

If `x` is matrix, it must be constructed like this:

- 2 columns giving number of successes (left) and fails (right)

- 1 row per population.

The function works as `chisq.test` :

- if `x` is a vector and theoretical proportions are not given, equality of counts is tested

- if `x` is a vector and theoretical proportions are given, equality of counts to theoretical counts (given by theoretical proportions) is tested

- if `x` is a matrix with two columns, equality of proportion of successes between populations is tested.

- if `x` is a matrix with more than two columns, independence of rows and columns is tested.

Since a G-test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `multinomial.test` in that case with a vector, `fisher.test` with a matrix.

Value

`method`	name of the test.
`statistic`	test statistics.
`parameter`	test degrees of freedom.
`p.value`	p-value.
`data.name`	a character string giving the name(s) of the data.
`observed`	the observed counts.
`expected`	the expected counts under the null hypothesis.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`chisq.test`, `multinomial.test`, `fisher.test` `G.multcomp`, `G.theo.multcomp`, `pairwise.G.test`

Examples

```
counts <- c(49,30,63,59)
G.test(counts)
```

`G.theo.multcomp` *Pairwise comparisons after a G-test for given probabilities*

Description

Performs pairwise comparisons after a global G-test for given probabilities.

Usage

```
G.theo.multcomp(x, p = rep(1/length(x), length(x)), p.method = "fdr")
```

Arguments

`x`	numeric vector (counts).
`p`	theoretical proportions.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since a G-test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `multinomial.theo.multcomp` in that case.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`observed`	observed counts.
`expected`	expected counts.
`p.adjust.method`	method for p-values correction.
`statistic`	statistics of each test.
`p.value2`	corrected p-values.
`p.value`	data frame of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`G.test`, `multinomial.test`, `multinomial.theo.multcomp`

Examples

```
counts <- c(49,30,63,59)
p.theo <- c(0.2,0.1,0.45,0.25)
G.test(counts,p=p.theo)
G.theo.multcomp(counts,p=p.theo)
```

`GPA.test` *Significance test for GPA*

Description

Performs a permutation significance test based on total variance explained for Generalized Procrustes Analysis. The function uses `GPA`.

Usage

```
GPA.test(df, group, tolerance = 10^-10, nbiteration = 200, scale = TRUE,
  nperm = 999, progress = TRUE)
```

Arguments

`df`	a data frame with n rows (individuals) and p columns (quantitative varaibles), in which all data frames are combined.
`group`	a vector indicating the number of variables in each group (i.e. data frame).
`tolerance`	a threshold with respect to which the algorithm stops, i.e. when the difference between the GPA loss function at step n and n+1 is less than `tolerance`.
`nbiteration`	the maximum number of iterations until the algorithm stops.
`scale`	logical, if `TRUE` (default) scaling is required.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.

Details

Rows of each data frame are randomly and independently permuted.

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name(s) of the data, plus additional information.
`statistic`	the value of the test statistics.
`permutations`	the number of permutations.
`p.value`	the p-value of the test.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

References

Wakeling IN, Raats MM and MacFie HJH (1992) A new significance test for consensus in Generalized Procrustes Analysis. Journal of Sensory Studies 7:91-96.

See Also

`GPA`

Examples

```
require(FactoMineR)
data(wine)

## Not run: GPA.test(wine[,-(1:2)],group=c(5,3,10,9,2))
```

`ind.contrib` *Individual contributions in regression*

Description

Computes difference in regression parameters when each individual is dropped, expressed in proportion of the whole regression coefficients. The function deals with `lm` (including glm) and `least.rect` models.

Usage

```
ind.contrib(model, print.diff = FALSE, graph = TRUE, warning=25)
```

Arguments

`model`	model (of class "`lm`" or "`least.rect`").
`print.diff`	logical. If `TRUE` results are printed.
`graph`	logical. If `TRUE` results are returned in a graphical way.
`warning`	level of graphical warning.

Value

`coefficients`	coefficients of each computed regression.
`coefficients.diff`	difference in coefficients between each computed regression and the whole regression.
`coefficients.prop`	difference in coefficients expressed in proportion of the whole regression coefficients.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`lm.influence`, `least.rect`

Examples

```
x <- 1:30
y <- 1:30+rnorm(30,0,4)
model1 <- lm(y~x)
model2 <- least.rect(y~x)
ind.contrib(model1)
ind.contrib(model2)
```

`least.rect` *Least rectangles linear regression*

Description

Fits a least rectangle linear regression, possibly for each level of a factor.

Usage

```
least.rect(formula, data, conf.level = 0.95, theo = 1, adj = TRUE)
```

Arguments

`formula`	a formula of the form `y ~ x`, where `y` and `x` give the y and x variable, respectively. The formula can also be `y ~ x | f` to fit a (separate) regression for each level of the factor `f`.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`conf.level`	confidence level.
`theo`	theoretical value of the slope. If several regression are fitted, the same value is used for all comparisons of slope vs. theoretical value.

`adj`	logical indicating if, in case of several regressions fitted, confidence intervals and p-values should be Bonferroni-corrected for multiple testing.

Value

`coefficients`	regression parameters.
`residuals`	residuals.
`fitted.values`	fitted values.
`call`	the matched call.
`model`	the model frame used.
`conf.level`	confidence level.
`conf.int`	confidence interval of regression parameters.
`theo`	theoretical value of the slope.
`comp`	data frame of results for equality of the slope(s) to the theoretical value.
`corr`	data frame of results for significativity of the correlation coefficient(s).
`multiple`	logical, `TRUE` if several regressions are fitted.
`adj`	logical, `TRUE` if confidence intervals and p-values are corrected for multiple testing (only if several regressions are fitted).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
x <- 1:30+rnorm(30,0,3)
y <- 1:30+rnorm(30,0,3)
regression1 <- least.rect(y~x)
summary(regression1)

x2 <- c(1:30,1:30)
y2 <- c(1:30+rnorm(30,0,3),seq(10,22,12/29)+rnorm(30,0,3))
fact <- gl(2,30,labels=LETTERS[1:2])
regression2 <- least.rect(y2~x2|fact)
summary(regression2)
```

`loc.slp` *Slope of a hand-defined line*

Description

Returns the slope of a line defined by selecting two points on a graph.

Usage

```
loc.slp()
```

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`logis.fit` *Graphical adujstment of a simple binary logistic regression to data*

Description

Cuts the data into intervals, compute the response probability and its standard error for each interval and add the results to the regression curve. No test is performed but this permits to have a graphical idea of the adjustment of the model to the data.

Usage

```
logis.fit(model, int = 5, ...)
```

Arguments

`model`	`glm` model.
`int`	number of intervals.
`...`	other arguments. See help of `points` and `segments`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`glm`

Examples

```
x <- 1:50
y <- c(rep(0,18),sample(0:1,14,replace=TRUE),rep(1,18))
model <- glm(y~x,family=binomial)
plot(x,y)
lines(x,model$fitted)
logis.fit(model)
```

`logis.noise` *Creating a nls model for logistic regression from fitted values of a glm model*

Description

Adds some noise to the fitted values of a `glm` model to create a `nls` model for logistic regression (creating a `nls` model from exact fitted values can not be done, see help of `nls`).

Usage

```
logis.noise(model, intensity = 25)
```

Arguments

`model`	`glm` model.
`intensity`	intensity of the noise: lower the value, bigger the noise.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`glm`, `nls`

Examples

```
x <- 1:50
y <- c(rep(0,18),sample(0:1,14,replace=TRUE),rep(1,18))
model <- glm(y~x,family=binomial)
y2 <- logis.noise(model)
# Then model2 <- nls(y2~SSlogis(...))
```

`mod` *Mode*

Description

Computes the mode of a vector. The function makes the difference between continuous and discontinuous variables (which are made up of integers only). By extention, it also gives the most frequent value in a character vector or a factor.

Usage

```
mod(x)
```

Arguments

`x`	vector (numeric, character or factor).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`density`

Examples

```
# Continuous variable
x <- rnorm(100)
mod(x)

# Discontinuous variable
y <- rpois(100,2)
mod(y)

# Character vector
z <- sample(LETTERS[1:3],20,replace=TRUE)
mod(z)
```

`mood.medtest` *Mood's median test*

Description

Performs a Mood's median test to compare medians of independent samples.

Usage

```
mood.medtest(x, ...)

## Default S3 method:
mood.medtest(x, g, exact = NULL, ...)

## S3 method for class 'formula'
mood.medtest(formula, data, subset, ...)
```

Arguments

`x`	a numeric vector of data values.
`g`	a vector or factor object giving the group for the corresponding elements of `x`.
`exact`	a logical indicating whether an exact p-value should be computed.

`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`...`	further arguments to be passed to or from other methods.

Details

If `exact=NULL`, a Fisher's exact test is used if the number of data values is < 200; otherwise a chi-square test is used, with Yates continuity correction if necessary.

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name(s) of the data.
`statistic`	the value the chi-squared test statistic (in case of a chis-square test).
`parameter`	the degrees of freedom of the approximate chi-squared distribution of the test statistic (in case of a chis-square test).
`p.value`	the p-value of the test.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
set.seed(1716)
response <- c(rnorm(10,3,1.5),rnorm(10,5.5,2))
fact <- gl(2,10,labels=LETTERS[1:2])
mood.medtest(response~fact)
```

`mqqnorm` *Multivariate normality QQ-Plot*

Description

Draws a QQ-plot to assess multivariate normality.

Usage

```
mqqnorm(x, main = "Multi-normal Q-Q Plot")
```

Arguments

`x`	a data frame or a matrix of numeric variables (each column giving a variable).
`main`	title of the graph.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`mshapiro.test`, `qqPlot`

Examples

```
x <- 1:30+rnorm(30)
y <- 1:30+rnorm(30,1,3)
mqqnorm(cbind(x,y))
```

`mshapiro.test` *Shapiro-Wilk multivariate normality test*

Description

Performs a Shapiro-Wilk test to asses multivariate normality. This is a slightly modified copy of the `mshapiro.test` function of the package mvnormtest, for internal convenience.

Usage

```
mshapiro.test(x)
```

Arguments

`x`	a data frame or a matrix of numeric variables (each column giving a variable).

Value

`method`	name of the test.
`data.name`	a character string giving the names of the data.
`statistic`	test statistics of the test.
`p.value`	p-value of the test.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr> from the work of Slawomir Jarek

See Also

`shapiro.test`, `mshapiro.test`

Examples

```
x <- 1:30+rnorm(30)
y <- 1:30+rnorm(30,1,3)
mshapiro.test(cbind(x,y))
```

`multinomial.multcomp` *Pairwise comparisons after an exact multinomial test*

Description

Performs pairwise comparisons after a global exact multinomial test. These comparisons are performed using exact binomial tests.

Usage

```
multinomial.multcomp(x, p.method = "fdr")
```

Arguments

`x`	numeric vector (counts). Can also be a factor; in that case `table(x)` is used as counts.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since chi-squared and G tests are approximate tests, exact tests are preferable when the number of individuals is small (200 is a reasonable minimum).

An exact multinomial test with two groups is strictly the same than an exact binomial test.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.adjust.method`	method for p-values correction.
`p.value`	table of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`multinomial.test`, `binom.test`

Examples

```
counts <- c(5,15,23)
multinomial.test(counts)
multinomial.multcomp(counts)
```

`multinomial.test` *Exact multinomial test*

Description

Perfoms an exact multinomial test on a vector of counts.

Usage

```
multinomial.test(x, p = rep(1/length(x), length(x)))
```

Arguments

`x`	numeric vector (counts). Can also be a factor; in that case `table(x)` is used as counts.
`p`	theoretical proportions (optional).

Details

The function works as `chisq.test` or `G.test` :

- if theoretical proportions are not given, equality of counts is tested

- if theoretical proportions are given, equality of counts to theoretical counts (given by theoretical proportions) is tested.

Since chi-squared and G tests are approximate tests, exact tests are preferable when the number of individuals is small (200 is a reasonable minimum).

Be aware that the calculation time increases with the number of individuals (i.e. the sum of `x`) and the number of groups (i.e. the length of `x`).

An exact multinomial test with two groups is strictly the same as an exact binomial test.

Value

`method`	name of the test.
`p.value`	p-value.
`data.name`	a character string giving the name(s) of the data.
`observed`	the observed counts.
`expected`	the expected counts under the null hypothesis.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr> based on `multinomial.test`

See Also

`chisq.test`, `G.test`, `binom.test`, `multinomial.multcomp`, `multinomial.theo.multcomp`

Examples

```
counts <- c(5,15,23)
multinomial.test(counts)
```

---

multinomial.theo.multcomp

Pairwise comparisons after an exact multinomial test for given probabilities

---

Description

Performs pairwise comparisons after a global exact multinomial test for given probabilities. These comparisons are performed using exact binomial tests.

Usage

```
multinomial.theo.multcomp(x, p = rep(1/length(x), length(x)), prop = FALSE,
  p.method = "fdr")
```

Arguments

`x`	numeric vector (counts). Can also be a factor; in that case `table(x)` is used as counts.
`p`	theoretical proportions.
`prop`	logical indicating if results should be printed as counts (`FALSE`) or proportions (`TRUE`).
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since chi-squared and G tests are approximate tests, exact tests are preferable when the number of individuals is small (200 is a reasonable minimum).

An exact multinomial test with two groups is strictly the same than an exact binomial test.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`observed`	observed counts.
`expected`	expected counts.
`p.adjust.method`	method for p-values correction.
`p.value2`	corrected p-values.
`p.value`	data frame of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`multinomial.test`, `binom.test`

Examples

```
counts <- c(5,15,23)
p.theo <- c(0.2,0.5,0.3)
multinomial.test(counts,p=p.theo)
multinomial.theo.multcomp(counts,p=p.theo)
```

`multtest.cor` *Univariate correlation test for multiple variables*

Description

Performs correlation tests between one variable and a series of other variables, and corrects p-values.

Usage

```
multtest.cor(mult.var, uni.var, method = "pearson", p.method = "fdr",
  ordered = TRUE)

## S3 method for class 'multtest.cor'
plot(x, arrows = TRUE, main = NULL, pch = 16,
  cex = 1, col = c("red", "orange", "black"), labels = NULL, ...)
```

Arguments

`mult.var`	data frame containing a series of numeric variables.
`uni.var`	numeric variable (vector).
`method`	a character string indicating which correlation coefficient is to be computed. See help of `cor`.
`p.method`	method for p-values correction. See help of `p.adjust`.
`ordered`	logical indicating if variables should be ordered based on correlation values.
`x`	object returned from `multtest.cor`.
`arrows`	logical indicating if arrows should be plotted. If `FALSE`, points are displayed at the extremity of the arrows.
`main`	optional title of the graph.
`pch`	symbol(s) used for points, when points are displayed (see `arrows`).
`cex`	size of points and labels (see help of `dotchart`).

`col`	vector of three colors: first for variables with P < 0.05, second for variables with 0.05 < P < 0.1, third for variables with P > 0.1. Recycled if only one value.
`labels`	names of the variables. If `NULL` (default), labels correspond to names found in `mult.var`.
`...`	not used.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`cor.test`

Examples

```
data(iris)

# Original coordinates
plot(Petal.Length~Sepal.Length,pch=16,col=as.numeric(iris$Species),data=iris)

# New axis
abline(-6,1.6)

# Coordinates on new axis
new.coord <- coord.proj(iris[,c(”Sepal.Length”,”Petal.Length”)],1.6)

# Correlation between the whole dataset and new coordinates
mult.cor <- multtest.cor(iris[,1:4],new.coord)
plot(mult.cor)
```

`multtest.gp` *Univariate comparison of groups for multiple variables*

Description

Performs group comparisons for multiple variables using parametric, permutational or rank tests, and corrects p-values. Gives also group means and standards errors for each variable.

Usage

```
multtest.gp(tab, fac, test = c(”param”, ”perm”, ”rank”),
  transform = c(”none”, ”sqrt”, ”4rt”, ”log”), add = 0, p.method = ”fdr”,
  ordered = TRUE, ...)

## S3 method for class 'multtest.gp'
plot(x, signif = FALSE, alpha = 0.05,
  vars = NULL, xlab = ”Group”, ylab = ”Mean (+/- SE) value”,
  titles = NULL, groups = NULL, ...)
```

Arguments

`tab`	data frame containing response variables.
`fac`	factor defining groups to compare.
`test`	type of test to use: parametric (default), permutational (non parametric) or rank-based (non parametric). See Details.
`transform`	transformation to apply to response variables before testing (none by default; `"4rt"` is fourth-root). Only used for parametric and permutational tests.
`add`	value to add to response variables before a log-transformation.
`p.method`	method for p-values correction. See help of `p.adjust`.
`ordered`	logical indicating if variables should be ordered based on p-values.
`x`	object returned from `multtest.gp`.
`signif`	logical indicating if only variables with significant P-value should be plotted.
`alpha`	significance threshold.
`vars`	numeric vector giving variables to plot (rows of `x`). Default to all, which can lead to errors if too many variables.
`xlab`	legend of the x axis.
`ylab`	legend of the y axis
`titles`	titles of the graphs (name of the variables by default).
`groups`	names of the bars (levels of `fac` by default).
`...`	additional arguments to testing functions in `multtest.gp` (especially for `var.equal` in `t.test` and `nperm` in `perm.anova` and `perm.t.test`) and to `barplot` in `plot`.

Details

In case of parametric tests, t-tests or ANOVAs are used depending on the number of groups (2 or more, respectively). In case of permutational tests: permutational t-tests or permutational ANOVAs. In case of rank-based tests: Mann-Whitney-Wilcoxon or Kruskal-Wallis tests.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`perm.anova`, `perm.t.test`

Examples

```
data(iris)
mult <- multtest.gp(iris[,1:4],iris$Species)
plot(mult)
```

`multtest.gp.bin` *Univariate comparison of groups for multiple binary variables*

Description

Performs group comparisons for multiple binary variables using a parametric or an exact test, and corrects p-values. Gives also group proportions and standards errors for each variable.

Usage

```
multtest.gp.bin(tab, fac, test = c("LRT", "Fisher"),
  p.method = "fdr", ordered = TRUE, ...)

## S3 method for class 'multtest.gp.bin'
plot(x, signif = FALSE, alpha = 0.05,
  vars = NULL, xlab = "Group", ylab = "Mean (+/- SE) proportion",
  titles = NULL, groups = NULL, ...)
```

Arguments

`tab`	data frame containing response variables.
`fac`	factor defining groups to compare.
`test`	type of test to use: likelihood ratio test based on binomial GLM (`"LRT"`, default) or Fisher's exact test (`"Fisher"`).
`p.method`	method for p-values correction. See help of `p.adjust`.
`ordered`	logical indicating if variables should be ordered based on p-values.
`x`	object returned from `multtest.gp.bin`.
`signif`	logical indicating if only variables with significant P-value should be plotted.
`alpha`	significance threshold.
`vars`	numeric vector giving variables to plot (rows of `x`). Default to all, which can lead to errors if too many variables.
`xlab`	legend of the x axis.
`ylab`	legend of the y axis
`titles`	titles of the graphs (name of the variables by default).
`groups`	names of the bars (levels of `fac` by default).
`...`	additional arguments to testing functions in `multtest.gp.bin` (especially for `Anova` and `fisher.test`) and to `barplot` in `plot`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`multtest.gp`, `Anova`, `fisher.test`

`MVA.anova` *Type II permutation test for constrained multivariate analyses*

Description

This function is a wrapper to `anova.cca(...,by="terms")` but performs type II tests (whereas `anova.cca` performs type I).

Usage

```
MVA.anova(object, ...)
```

Arguments

`object`	a result object from `cca`, `rda`, `capscale` or `dbrda`.
`...`	additional arguments to `anova.cca` (can be `permutations`, `model`, `parallel` and/or `strata`). See help of this function.

Details

See `anova.cca` for detailed explanation of what is done. The only difference with `anova.cca` is that `MVA.anova` performs type II tests instead of type I.

See example of `adonis.II` for the difference between type I (sequential) and type II tests.

Value

a data frame of class `"anova"`.

Author(s)

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`MVA.biplot` *Biplot of multivariate analyses*

Description

Displays a biplot of a multivariate analysis. This just consists in superimposing a score plot and a correlation circle (plus centroids of factor levels in constrained analyses, RDA or CCA). The correlation circle is adjusted to fit the size of the score plot.

Usage

```
MVA.biplot(x, xax = 1, yax = 2, scaling = 2, sco.set = c(12, 1, 2),
  cor.set = c(12, 1, 2), space = 1, ratio = 0.9, weights = 1,
  constraints = c("nf", "n", "f", NULL), sco.args = list(),
  cor.args = list(), f.col = 1, f.cex = 1)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	the horizontal axis.
`yax`	the vertical axis.
`scaling`	type of scaling (see `MVA.scoreplot`).
`sco.set`	scores to be displayed, when several sets are available (see `MVA.scoreplot`).
`cor.set`	correlations to be displayed, when several sets are available (see `MVA.scoreplot`).
`space`	space to use, when several are available (see `MVA.scoreplot` and `MVA.corplot`).
`ratio`	constant for adjustement of correlations to the size of the score plot (`0.9` means the longest arrows is 90% of the corresponding axis).
`weights`	only used with constrained analyses (RDA or CCA) where some constraints are factors. Individual weights, used to calculate barycenter positions.
`constraints`	only used with constrained analyses (RDA or CCA). Type of constraints to display: quantitative (`"n"`), factors (`"f"`), both (`"nf", default`) or none (`"NULL"`).
`sco.args`	list containing optional arguments to pass to `MVA.scoreplot`. All arguments are accepted.
`cor.args`	list containing optional arguments to pass to `MVA.corplot`. All arguments are accepted except `xlab`, `ylab`, `circle`, `intcircle`, `drawintaxes`, `add` and `add.const`.
`f.col`	color(s) used for barycenters in case of a constraint analysis (RDA or CCA) containing factor constraint(s). Can be a unique value, a vector giving one color per constraint or a vector giving one color per barycenter (all factors confounded).
`f.cex`	size(s) used for barycenters in case of a constraint analysis (RDA or CCA) containing factor constraint(s). Can be a unique value, a vector giving one size per constraint or a vector giving one size per barycenter (all factors confounded).

Details

This function should not be use directly. Prefer the general `MVA.plot`, to which all arguments can be passed.

All multivariate analyses covered by `MVA.corplot` can be used for biplots.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
require(vegan)
data(iris)
RDA <- rda(iris[,1:4]~Species,data=iris)
MVA.plot(RDA,"biplot",cor.args=list(col="purple"),ratio=0.8,f.col=c("red","green","blue"))
```

`MVA.cmv` *Cross model validation*

Description

Performs cross model validation (2CV) with different PLS analyses.

Usage

```
MVA.cmv(X, Y, repet = 10, kout = 7, kinn = 6, ncomp = 8, scale = TRUE,
  model = c("PLSR", "CPPLS", "PLS-DA", "PPLS-DA", "PLS-DA/LDA", "PLS-DA/QDA",
  "PPLS-DA/LDA", "PPLS-DA/QDA"), crit.inn = c("RMSEP", "Q2", "NMC"),
 Q2diff = 0.05, lower = 0.5, upper = 0.5, Y.add = NULL, weights = rep(1, nrow(X)),
  set.prior = FALSE, crit.DA = c("plug-in", "predictive", "debiased"), ...)
```

Arguments

`X`	a data frame of independent variables.
`Y`	the dependent variable(s): numeric vector, data frame of quantitative variables or factor.
`repet`	an integer giving the number of times the whole 2CV procedure has to be repeated.
`kout`	an integer giving the number of folds in the outer loop (can be re-set internally if needed).
`kinn`	an integer giving the number of folds in the inner loop (can be re-set internally if needed). Cannot be > `kout`.
`ncomp`	an integer giving the maximal number of components to be tested in the inner loop (can be re-set depending on the size of the train sets).
`scale`	logical indicating if data should be scaled (see Details).
`model`	the model to be fitted (see Details).
`crit.inn`	the criterion to be used to choose the number of components in the inner loop. Root Mean Square Error of Prediction (`"RMSEP"`, default) and Q2 (`"Q2"`) are only used for PLSR and CPPLS, whereas the Number of MisClassifications (`"NMC"`) is only used for discriminant analyses.
`Q2diff`	the threshold to be used if the number of components is chosen according to Q2. The next component is added only if it makes the Q2 increase more than `Q2diff` (5% by default).
`lower`	a vector of lower limits for power optimisation in CPPLS or PPLS-DA (see `cppls.fit`).
`upper`	a vector of upper limits for power optimisation in CPPLS or PPLS-DA (see `cppls.fit`).
`Y.add`	a vector or matrix of additional responses containing relevant information about the observations, in CPPLS or PPLS-DA (see `cppls.fit`).

`weights`	a vector of individual weights for the observations, in CPPLS or PPLS-DA (see `cppls.fit`).
`set.prior`	only used when a second analysis (LDA or QDA) is performed. If `TRUE`, the prior probabilities of class membership are defined according to the mean weight of individuals belonging to each class. If `FALSE`, prior probabilities are obtained from the data sets on which LDA/QDA models are built.
`crit.DA`	criterion used to predict class membership when a second analysis (LDA or QDA) is used. See `predict.lda`.
`...`	other arguments to pass to `plsr` (PLSR, PLS-DA) or `cppls` (CPPLS, PPLS-DA).

Details

Cross model validation is detailed is Szymanska et al (2012). Some more details about how this function works:

- when a discriminant analysis is used (`"PLS-DA"`, `"PPLS-DA"`, `"PLS-DA/LDA"`, `"PLS-DA/QDA"`, `"PPLS-DA/LDA"` or `"PPLS-DA/QDA"`), the training sets (test set itself in the inner loop, test+validation sets in the outer loop) are generated in respect to the relative proportions of the levels of `Y` in the original data set (see `splitf`).

- `"PLS-DA"` is considered as PLS2 on a dummy-coded response. For a PLS-DA based on the CPPLS algorithm, use `"PPLS-DA"` with `lower` and `upper` limits of the power parameters set to `0.5`.

- if a second analysis is used (`"PLS-DA/LDA"`, `"PLS-DA/QDA"`, `"PPLS-DA/LDA"` or `"PPLS-DA/QDA"`), a LDA or QDA is built on scores of the first analysis (PLS-DA or PPLS-DA) also in the inner loop. The classification error rate, based on this second analysis, is used to choose the number of components.

If `scale = TRUE`, the scaling is done as this:

- for each step of the outer loop (i.e. `kout` steps), the rest set is pre-processed by centering and unit-variance scaling. Means and standard deviations of variables in the rest set are then used to scale the test set.

- for each step of the inner loop (i.e. `kinn` steps), the training set is pre-processed by centering and unit-variance scaling. Means and standard deviations of variables in the training set are then used to scale the validation set.

Value

`model`	model used.
`type`	type of model used.
`repet`	number of times the whole 2CV procedure was repeated.
`kout`	number of folds in the outer loop.
`kinn`	number of folds in the inner loop.
`crit.inn`	criterion used to choose the number of components in the inner loop.
`crit.DA`	criterion used to classify individuals of the test and validation sets.
`Q2diff`	threshold used if the number of components is chosen according to Q2.
`groups`	levels of `Y` if it is a factor.

`models.list`	list of of models generated (`repet*kout` models), for PLSR, CPPLS, PLS-DA and PPLS-DA.
`models1.list`	list of of (P)PLS-DA models generated (`repet*kout` models), for PLS-DA/LDA, PLS-DA/QDA, PPLS-DA/LDA and PPLS-DA/QDA.
`models2.list`	list of of LDA/QDA models generated (`repet*kout` models), for PLS-DA/LDA, PLS-DA/QDA, PPLS-DA/LDA and PPLS-DA/QDA.
`RMSEP`	RMSEP computed from the models used in the outer loops (`repet` values).
`Q2`	Q2 computed from the models used in the outer loops (`repet` values).
`NMC`	Classification error rate computed from the models used in the outer loops (`repet` values).
`confusion`	Confusion matrices computed from the models used in the outer loops (`repet` values).
`pred.prob`	Probability of each individual of being of each level of `Y`.

Author(s)

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References

Szymanska E, Saccenti E, Smilde AK and Westerhuis J (2012) Double-check: validation of diagnostic statistics for PLS-DA models in metabolomics studies. Metabolomics (2012) 8:S3-S16.

See Also

`predict.MVA.cmv`, `mvr`, `lda`, `qda`

Examples

```
require(pls)
require(MASS)

# PLSR
data(yarn)
## Not run: MVA.cmv(yarn$NIR,yarn$density,model="PLSR")

# PPLS-DA coupled to LDA
data(mayonnaise)
## Not run: MVA.cmv(mayonnaise$NIR,factor(mayonnaise$oil.type),model="PPLS-DA/LDA",crit.inn="NMC")
```

`MVA.cor` *Correlations of multivariate analyses*

Description

Returns correlations of a multivariate analysis.

Usage

```
MVA.cor(x, xax = 1, yax = 2, set = c(12, 1, 2), space = 1, ...)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	axis or axes for which to extract correlations.
`yax`	axis for which to extract correlations (ignored if `length(xax)` > 1).
`set`	variables to be displayed, when several sets are available (see Details). `12` (default) for both sets, `1` for X or constraints, `2` for Y or constrained variables.
`space`	variables to be displayed, when several spaces are available (see Details). `space` is the number of the space to be plotted.
`...`	not used.

Details

Many multivariate analyses are supported, from various packages:

- PCA: `dudi.pca`, `rda`.

- sPCA: `spca`.

- IPCA: `ipca`.

- sIPCA: `sipca`.

- LDA: `lda`, `discrimin`.

- PLS-DA (PLS2 on a dummy-coded factor): `plsda`. X space only.

- sPLS-DA (sPLS2 on a dummy-coded factor): `splsda`. X space only.

- CPPLS: `mvr`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch,cex`, `col`, `lwd` can be defined differently for each set. X space only.

- PLSR: `mvr`, `pls`, `plsR` (plsRglm package). Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch,cex`, `col`, `lwd` can be defined differently for each set. X space only.

- sPLSR: `pls`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch,cex`, `col`, `lwd` can be defined differently for each set. X space only.

- PLS-GLR: `plsRglm` (plsRglm package). Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch,cex`, `col`, `lwd` can be defined differently for each set. Correlations are computed with Y on the link scale.

- PCR: `mvr`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- CDA: `discrimin`, `discrimin.coa`.

- NSCOA: `dudi.nsc`. For NSCOA there is no real correlation, but the classical representation of columns is arrows. This is why MVA.corplot was made able to deal with this analysis.

- CCA: `cca`, `pcaiv`. Constraints (only quantitative constraints are extracted) in constrained space only.

- Mix analysis: `dudi.mix`, `dudi.hillsmith`. Only quantitative variables are displayed.

- RDA (or PCAIV): `pcaiv`, `pcaivortho`, `rda`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`, the opposite for `pcaivortho`. Set 1 is constraints (only quantitative constraints are extracted), set 2 is dependent variables (only set 2 is available for `pcaivortho`). If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- CCorA: `CCorA`, `rcc`. Space 1 is X, space 2 is Y. With `rcc` a third space is available, in which coordinates are means of X and Y coordinates. In this third space, set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- rCCorA: `rcc`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates. In space 3, set 1 is X and set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- CIA: `coinertia`. Space 1 is X, space 2 is Y, space 3 is a "common" space where X and Y scores are normed. In space 3, set 1 is X and set 2 is Y. If `set=12` in space 3 (default), `fac` is not available and `pch`,`cex`, `col`, `lws` can be defined differently for each set.

- GPA: `GPA`. Only the consensus ordination can be displayed.

- 2B-PLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates. In space 3, set 1 is X and set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- 2B-sPLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates. In space 3, set 1 is X and set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- rGCCA: `wrapper.rgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- sGCCA: `wrapper.sgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- DIABLO: `block.plsda`, `block.splsda`. Space can be 1 to n, the number of blocks (i.e. datasets).

Author(s)

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`MVA.corplot` *Correlation circle of multivariate analyses*

Description

Displays a correlation circle of a multivariate analysis.

Usage

```
MVA.corplot(x, xax = 1, yax = 2, thresh = 0, fac = NULL, set = c(12, 1, 2), space = 1,
  xlab = NULL, ylab = NULL, main = NULL, circle = TRUE, intcircle = 0.5, points = TRUE,
  ident = TRUE, arrows = TRUE, labels = NULL, main.pos = c("bottomleft", "topleft",
  "bottomright", "topright"), main.cex = 1.3, legend = FALSE, legend.pos = c("topleft",
  "topright", "bottomleft", "bottomright"), legend.title = NULL, legend.lab = NULL,
  pch = 16, cex = 1, col = 1, lwd = 1, drawintaxes = TRUE, add = FALSE, add.const = 1,
   keepmar = FALSE)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	the horizontal axis.
`yax`	the vertical axis. This can be set to `NULL` for a one-dimensional graph, which is a dotchart.
`thresh`	threshold (in absolute value of the correlation coefficient) of variables to be plotted.
`fac`	an optional factor defining groups of variables.
`set`	variables to be displayed, when several sets are available (see Details). `12` (default) for both sets, `1` for X or constraints, `2` for Y or constrained variables.
`space`	variables to be displayed, when several spaces are available (see Details). `space` is the number of the space to be plotted.
`xlab`	legend of the horizontal axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`ylab`	only used for two-dimensional graphs. Legend of the vertical axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`main`	optional title of the graph.
`circle`	only used for two-dimensional graphs. Logical indicating if the circle of radius 1 should be plotted.
`intcircle`	only used for two-dimensional graphs. Vector of one or several values indicating radii of circles to be plotted inside the main circle. Can be set to `NULL`.
`points`	only used for two-dimensional graphs. If `FALSE`, arrows or points (see `arrows`) are replaced with their corresponding label (defined by `labels`).
`ident`	only used for two-dimensional graphs when `points=TRUE`. A logical indicating if variable names should be displayed.

`arrows`	only used if `points=TRUE`. Logical indicating if arrows should be plotted. If `FALSE`, points are displayed at the extremity of the arrows.
`labels`	names of the variables. If `NULL` (default), labels correspond to variable names found in the data used in the multivariate analysis. For two-dimensional graphs, only used if `ident=TRUE`.
`main.pos`	position of the title, if `main` is not `NULL`. Default to `"bottomleft"`.
`main.cex`	size of the title, if `main` is not `NULL`.
`legend`	only used for two-dimensional graphs. Logical indicating if a legend should be added to the graph.
`legend.pos`	position of the legend, if `legend` is `TRUE`. Default to `"topleft"`.
`legend.title`	optional title of the legend, if `legend` is `TRUE`.
`legend.lab`	legend labels, if `legend` is `TRUE`. If `NULL`, levels of the factor defined by `fac` are used.
`pch`	symbol(s) used for points, when points are displayed (see `arrows`). If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.
`cex`	size of the points and/or of the variable names. For two-dimensional graphs: if `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group; otherwise a vector of any length can be defined, which is recycled if necessary. For dotcharts, gives the size used for points and all labels (see `dotchart`).
`col`	color(s) used for points and/or variable names. If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary (not available for density histograms, see `dhist`).
`lwd`	only used if arrows are displayed. Width of arrows. If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.
`drawintaxes`	logical indicating if internal axes should be drawn.
`add`	only used for two-dimensional graphs. Logical indicating if the correlation circle should be added to an existing graph.
`add.const`	only used for two-dimensional graphs and if `add` is `TRUE`. Constant by which correlations are multiplied to fit onto the original graph.
`keepmar`	only used for two-dimensional graphs. Logical indicating if margins defined by MVA.corplot should be kept after plotting (necessary in some cases when `add=TRUE`).

Details

This function should not be use directly. Prefer the general `MVA.plot`, to which all arguments can be passed.

Many multivariate analyses are supported, from various packages:

- PCA: `dudi.pca`, `rda`.

- sPCA: `spca`.

- IPCA: `ipca`.

- sIPCA: `sipca`.

- LDA: `lda`, `discrimin`.

- PLS-DA (PLS2 on a dummy-coded factor): `plsda`. X space only.

- sPLS-DA (sPLS2 on a dummy-coded factor): `splsda`. X space only.

- CPPLS: `mvr`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set. X space only.

- PLSR: `mvr`, `pls`, `plsR` (plsRglm package). Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set. X space only.

- sPLSR: `pls`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set. X space only.

- PLS-GLR: `plsRglm` (plsRglm package). Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set. Correlations are computed with Y on the link scale.

- PCR: `mvr`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- CDA: `discrimin`, `discrimin.coa`.

- NSCOA: `dudi.nsc`. For NSCOA there is no real correlation, but the classical representation of columns is arrows. This is why MVA.corplot was made able to deal with this analysis.

- CCA: `cca`, `pcaiv`. Constraints (only quantitative constraints are extracted) in constrained space only.

- Mix analysis: `dudi.mix`, `dudi.hillsmith`. Only quantitative variables are displayed.

- RDA (or PCAIV): `pcaiv`, `pcaivortho`, `rda`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`, the opposite for `pcaivortho`. Set 1 is constraints (only quantitative constraints are extracted), set 2 is dependent variables (only set 2 is available for `pcaivortho`). If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- db-RDA: `capscale`, `dbrda`. Constraints (only quantitative constraints are extracted) in constrained space only.

- CCorA: `CCorA`, `rcc`. Space 1 is X, space 2 is Y. With `rcc` a third space is available, in which coordinates are means of X and Y coordinates. In this third space, set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- rCCorA: `rcc`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates. In space 3, set 1 is X and set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- CIA: `coinertia`. Space 1 is X, space 2 is Y, space 3 is a "common" space where X and Y scores are normed. In space 3, set 1 is X and set 2 is Y. If `set=12` in space 3 (default), `fac` is not available and `pch`,`cex`, `col`, `lws` can be defined differently for each set.

- PCIA: `procuste`. Set 1 is X, set 2 is Y.

- 2B-PLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates. In space 3, set 1 is X and set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- 2B-sPLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates. In space 3, set 1 is X and set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col`, `lwd` can be defined differently for each set.

- rGCCA: `wrapper.rgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- sGCCA: `wrapper.sgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- DIABLO: `block.plsda`, `block.splsda`. Space can be 1 to n, the number of blocks (i.e. datasets).

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Examples

```
require(ade4)
data(olympic)
PCA <- dudi.pca(olympic$tab,scannf=FALSE)
MVA.plot(PCA,"corr")
```

`MVA.cv` *Cross validation*

Description

Performs cross validation with different PLS and/or discriminant analyses.

Usage

```
MVA.cv(X, Y, repet = 10, k = 7, ncomp = 8, scale = TRUE, model = c("PLSR",
  "CPPLS", "PLS-DA", "PPLS-DA", "LDA", "QDA", "PLS-DA/LDA", "PLS-DA/QDA",
  "PPLS-DA/LDA", "PPLS-DA/QDA"), lower = 0.5, upper = 0.5, Y.add = NULL,
  weights = rep(1, nrow(X)), set.prior = FALSE, crit.DA = c("plug-in",
  "predictive", "debiased"), ...)
```

Arguments

`X`	a data frame of independent variables.
`Y`	the dependent variable(s): numeric vector, data frame of quantitative variables or factor.
`repet`	an integer giving the number of times the whole procedure has to be repeated.
`k`	an integer giving the number of folds (can be re-set internally if needed).
`ncomp`	an integer giving the number of components to be used for all models except LDA and QDA (can be re-set depending on the size of the train sets).
`scale`	logical indicating if data should be scaled (see Details).
`model`	the model to be fitted (see Details).

`lower`	a vector of lower limits for power optimisation in CPPLS or PPLS-DA (see `cppls.fit`).
`upper`	a vector of upper limits for power optimisation in CPPLS or PPLS-DA (see `cppls.fit`).
`Y.add`	a vector or matrix of additional responses containing relevant information about the observations, in CPPLS or PPLS-DA (see `cppls.fit`).
`weights`	a vector of individual weights for the observations, in CPPLS or PPLS-DA (see `cppls.fit`).
`set.prior`	only used when a LDA or QDA is performed (coupled or not with a PLS model). If `TRUE`, the prior probabilities of class membership are defined according to the mean weight of individuals belonging to each class. If `FALSE`, prior probabilities are obtained from the data sets on which LDA/QDA models are built.
`crit.DA`	criterion used to predict class membership when a LDA or QDA is used. See `predict.lda`.
`...`	other arguments to pass to `plsr` (PLSR, PLS-DA) or `cppls` (CPPLS, PPLS-DA).

Details

When a discriminant analysis is used (`"PLS-DA"`, `"PPLS-DA"`, `"LDA"`, `"QDA"`, `"PLS-DA/LDA"`, `"PLS-DA/QDA"`, `"PPLS-DA/LDA"` or `"PPLS-DA/QDA"`), the training sets are generated in respect to the relative proportions of the levels of `Y` in the original data set (see `splitf`).

`"PLS-DA"` is considered as PLS2 on a dummy-coded response. For a PLS-DA based on the CPPLS algorithm, use `"PPLS-DA"` with `lower` and `upper` limits of the power parameters set to `0.5`.

If `scale = TRUE`, the scaling is done as this: for each step of the validation loop (i.e. `k` steps), the training set is pre-processed by centering and unit-variance scaling. Means and standard deviations of variables in the training set are then used to scale the test set.

Value

`model`	model used.
`type`	type of model used.
`repet`	number of times the whole procedure was repeated.
`k`	number of folds.
`ncomp`	number of components used.
`crit.DA`	criterion used to classify individuals of the test sets.
`groups`	levels of `Y` if it is a factor.
`models.list`	list of of models generated (`repet*k` models), for PLSR, CPPLS, PLS-DA, PPLS-DA, LDA and QDA.
`models1.list`	list of of (P)PLS-DA models generated (`repet*k` models), for PLS-DA/LDA, PLS-DA/QDA, PPLS-DA/LDA and PPLS-DA/QDA.
`models2.list`	list of of LDA/QDA models generated (`repet*k` models), for PLS-DA/LDA, PLS-DA/QDA, PPLS-DA/LDA and PPLS-DA/QDA.

`RMSEP`	RMSEP vales (`repet` values).
`Q2`	Q2 values (`repet` values).
`NMC`	Classification error rates (`repet` values).
`confusion`	Confusion matrices (`repet` values).
`pred.prob`	Probability of each individual of being of each level of `Y`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`predict.MVA.cmv`, `mvr`, `lda`, `qda`

Examples

```
require(pls)
require(MASS)

# PLSR
data(yarn)
## Not run: MVA.cv(yarn$NIR,yarn$density,model="PLSR")

# PPLS-DA coupled to LDA
data(mayonnaise)
## Not run: MVA.cv(mayonnaise$NIR,factor(mayonnaise$oil.type),model="PPLS-DA/LDA")
```

`MVA.load` *Loadings of multivariate analyses*

Description

Returns loadings of a multivariate analysis.

Usage

```
MVA.load(x, xax = 1, yax = 2, set = c(12, 1, 2), space = 1, ...)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	axis or axes for which to extract loadings.
`yax`	axis for which to extract loadings (ignored if `length(xax)` > 1).
`set`	variables to be displayed, when several sets are available (see Details). `12` (default) for both sets, `1` for X, `2` for Y.
`space`	variables to be displayed, when several spaces are available (see Details). `space` is the number of the space to be plotted.
`...`	not used.

Details

Many multivariate analyses are supported, from various packages:

- PCA: `prcomp`, `princomp`, `dudi.pca`, `rda`, `pca`, `pca`.

- sPCA: `spca`.

- IPCA: `ipca`.

- sIPCA: `sipca`.

- LDA: `lda`, `discrimin`.

- PLS-DA (PLS2 on a dummy-coded factor): `plsda`. X space only.

- sPLS-DA (sPLS2 on a dummy-coded factor): `splsda`. X space only.

- CPPLS: `mvr`. X space only.

- PLSR: `mvr`, `pls`, `plsR` (plsRglm package). X space only.

- sPLSR: `pls`. X space only.

- PLS-GLR: `plsRglm` (plsRglm package).

- PCR: `mvr`.

- CDA: `discrimin`, `discrimin.coa`.

- NSCOA: `dudi.nsc`.

- MCA: `dudi.acm`.

- Mix analysis: `dudi.mix`, `dudi.hillsmith`.

- PCIA: `procuste`. Set 1 is X, set 2 is Y.

- RDA (or PCAIV): `pcaiv`, `pcaivortho`, `rda`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`, the opposite for `pcaivortho`.

- CCorA: `rcc`. Space 1 is X, space 2 is Y.

- rCCorA: `rcc`. Space 1 is X, space 2 is Y.

- CIA: `coinertia`. Space 1 is X, space 2 is Y.

- 2B-PLS: `pls`. Space 1 is X, space 2 is Y.

- 2B-sPLS: `pls`. Space 1 is X, space 2 is Y.

- rGCCA: `wrapper.rgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- sGCCA: `wrapper.sgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- DIABLO: `block.plsda`, `block.splsda`. Space can be 1 to n, the number of blocks (i.e. datasets).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`MVA.loadplot` *Loading plot of multivariate analyses*

Description

Displays a loading plot of a multivariate analysis.

Usage

```
MVA.loadplot(x, xax = 1, yax = 2, fac = NULL, set = c(12, 1, 2), space = 1, map = TRUE,
  xlab = NULL, ylab = NULL, main = NULL, points = TRUE, ident = TRUE, links = TRUE,
  line = TRUE, labels = NULL, main.pos = c("bottomleft", "topleft","bottomright",
  "topright"), main.cex = 1.3, legend = FALSE, legend.pos = c("topleft", "topright",
  "bottomleft", "bottomright"), legend.title = NULL, legend.lab = NULL, pch = 16,
  cex = 1, col = 1, lwd = 1, lty = 1, drawextaxes = TRUE, drawintaxes = TRUE, xlim = NULL,
  ylim = NULL)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	the horizontal axis.
`yax`	the vertical axis. This can be set to `NULL` for a one-dimensional graph.
`fac`	only used for one-dimensional graphs. An optional factor defining groups of variables.
`set`	variables to be displayed, when several sets are available (see Details). `12` (default) for both sets, `1` for X, `2` for Y.
`space`	variables to be displayed, when several spaces are available (see Details). `space` is the number of the space to be plotted.
`map`	logical indicating if a two-dimensional (`TRUE`, default) or a one-dimensional graph should be drawn. A one-dimensional graph can show loadings for one or two dimensions, both horizontally.
`xlab`	only used for two-dimensional graphs. Legend of the horizontal axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`ylab`	legend of the vertical axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`main`	optional title of the graph.
`points`	only used for two-dimensional graphs. If `FALSE`, lines or points (see `links`) are replaced with their corresponding label (defined by `labels`).
`ident`	logical indicating if variable names should be displayed. Only used when `points=TRUE` for two-dimensional graphs.
`links`	only used for two-dimensional graphs when `points=TRUE`. Logical indicating if variables should be linked to the origin of the graph. If `FALSE`, points are displayed at the extremity of the segments.

`line`	only used for one-dimensional graphs when `yax=NULL`. Logical indicating if loadings should be linked (default) as displayed as sticks.
`labels`	only used if `ident=TRUE`. Names of the variables. If `NULL` (default), labels correspond to variable names found in the data used in the multivariate analysis.
`main.pos`	only used for one-dimensional graphs. Position of the title, if `main` is not `NULL`. Default to `"bottomleft"`.
`main.cex`	size of the title, if `main` is not `NULL`.
`legend`	logical indicating if a legend should be added to the graph.
`legend.pos`	position of the legend, if `legend` is `TRUE`. Default to `"topleft"`.
`legend.title`	optional title of the legend, if `legend` is `TRUE`.
`legend.lab`	legend labels, if `legend` is `TRUE`. If `NULL` for a one-dimensional graph, dimension names are used. If `NULL` for a two-dimensional graph, levels of the factor defined by `fac` are used.
`pch`	only used for two-dimensional graphs. Symbol(s) used for points, when points are displayed (see `links`). If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.
`cex`	size of the points and/or of the variable names. For two-dimensional graphs: if `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group; otherwise a vector of any length can be defined, which is recycled if necessary.
`col`	color(s) used for points, variable names and/or lines/sticks. For one-dimensional graphs, can be a vector of length one or a vector giving one value per line. For two-dimensional graphs: if `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary (not available for density histograms, see `dhist`).
`lwd`	width of lines. For one-dimensional graphs, can be a vector of length one or a vector giving one value per line. For two-dimensional graphs: if `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.
`lty`	only used for one-dimensional graphs. Can be a vector of length one or a vector giving one value per line.
`drawextaxes`	logical indicating if external axes should be drawn.
`drawintaxes`	only used for two-dimensional graphs. Logical indicating if internal axes should be drawn.
`xlim`	only used in two-dimensional graphs. Limits of the horizontal axis. If `NULL`, limits are computed automatically.
`ylim`	limits of the vertical axis. If `NULL`, limits are computed automatically.

Details

This function should not be use directly. Prefer the general `MVA.plot`, to which all arguments can be passed.

Many multivariate analyses are supported, from various packages:

- PCA: `prcomp`, `princomp`, `dudi.pca`, `rda`, `pca`, `pca`.

- sPCA: `spca`.

- IPCA: `ipca`.

- sIPCA: `sipca`.

- LDA: `lda`, `discrimin`.

- PLS-DA (PLS2 on a dummy-coded factor): `plsda`. X space only.

- sPLS-DA (sPLS2 on a dummy-coded factor): `splsda`. X space only.

- CPPLS: `mvr`. X space only.

- PLSR: `mvr`, `pls`, `plsR` (plsRglm package). X space only.

- sPLSR: `pls`. X space only.

- PLS-GLR: `plsRglm` (plsRglm package).

- PCR: `mvr`.

- CDA: `discrimin`, `discrimin.coa`.

- NSCOA: `dudi.nsc`.

- MCA: `dudi.acm`.

- Mix analysis: `dudi.mix`, `dudi.hillsmith`.

- PCIA: `procuste`. Set 1 is X, set 2 is Y.

- RDA (or PCAIV): `pcaiv`, `pcaivortho`, `rda`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`, the opposite for `pcaivortho`.

- CCorA: `rcc`. Space 1 is X, space 2 is Y.

- rCCorA: `rcc`. Space 1 is X, space 2 is Y.

- CIA: `coinertia`. Space 1 is X, space 2 is Y.

- 2B-PLS: `pls`. Space 1 is X, space 2 is Y.

- 2B-sPLS: `pls`. Space 1 is X, space 2 is Y.

- rGCCA: `wrapper.rgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- sGCCA: `wrapper.sgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- DIABLO: `block.plsda`, `block.splsda`. Space can be 1 to n, the number of blocks (i.e. datasets).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
require(ade4)
data(olympic)
PCA <- dudi.pca(olympic$tab,scannf=FALSE)
MVA.plot(PCA,"load")
```

`MVA.pairplot` *Paired plot of multivariate analyses*

Description

Displays a paired plot (*i.e.* a score plot of paired points) of a multivariate analysis.

Usage

```
MVA.pairplot(x, xax = 1, yax = 2, pairs = NULL, scaling = 2, space = 1, fac = NULL,
  xlab = NULL, ylab = NULL, main = NULL, ident = TRUE, labels = NULL, cex = 0.7, col = 1,
   lwd = 1, main.pos = c("bottomleft", "topleft", "bottomright", "topright"),
  main.cex = 1.3, legend = FALSE, legend.pos = c("topleft", "topright", "bottomleft",
   "bottomright"), legend.title = NULL, legend.lab = NULL, drawextaxes = TRUE,
   drawintaxes = TRUE, xlim = NULL, ylim = NULL)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	the horizontal axis.
`yax`	the vertical axis. Cannot be `NULL`, only two-dimensional graphs can be drawn.
`pairs`	two-level factor identifying paired individuals (in the same order in both sets of points). Can be omitted with multivariate analyses where two sets of points are available in the same space (see `MVA.scoreplot`). In this case these sets are automatically detected.
`scaling`	type of scaling. Only available with some analyses performed with the `vegan` package. See Details of `MVA.scoreplot`.
`space`	scores to be displayed, when several spaces are available (see Details of `MVA.scoreplot`). `space` is the number of the space to be plotted.
`fac`	an optional factor defining groups pairs.
`xlab`	legend of the horizontal axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`ylab`	legend of the vertical axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`main`	optional title of the graph.
`ident`	logical indicating if variable names should be displayed.
`labels`	names of the individuals. If `NULL` (default), labels correspond to row names of the data used in the multivariate analysis.
`cex`	size of the labels. If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.
`col`	color(s) used for arrows and labels. If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.

`lwd`	width of arrows. If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.
`main.pos`	position of the title, if `main` is not `NULL`. Default to `"bottomleft"`.
`main.cex`	size of the title, if `main` is not `NULL`.
`legend`	logical indicating if a legend should be added to the graph.
`legend.pos`	position of the legend, if `legend` is `TRUE`. Default to `"topleft"`.
`legend.title`	optional title of the legend, if `legend` is `TRUE`.
`legend.lab`	legend labels, if `legend` is `TRUE`. If `NULL` and `fac` is defined, levels of `fac` are used.
`drawextaxes`	logical indicating if external axes should be drawn..
`drawintaxes`	logical indicating if internal axes should be drawn.
`xlim`	limits of the horizontal axis. If `NULL`, limits are computed automatically.
`ylim`	limits of the vertical axis. If `NULL`, limits are computed automatically.

Details

This function should not be use directly. Prefer the general `MVA.plot`, to which all arguments can be passed.

All multivariate analyses supported by `MVA.scoreplot` can be used for a paired plot.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
require(ade4)
data(macaca)
PCIA <- procuste(macaca$xy1,macaca$xy2)
MVA.plot(PCIA,"pairs")
```

`MVA.plot` *Plotting of multivariate analyses*

Description

Displays several kinds of plots for multivariate analyses.

Usage

```
MVA.plot(x, type = c("scores", "loadings", "correlations", "biplot", "pairs",
  "trajectories"), ...)
```

Arguments

`x`	a multivariate analysis (see Details).
`type`	the type of plot to be displayed: score plot (default), loading plot, correlation circle, biplot, score plot showing paired samples or score plot showing trajectories, respectively.
`...`	arguments to be passed to subfunctions. See Details.

Details

Different subfunctions are used depending on the type of plot to be displayed: `MVA.scoreplot`, `MVA.loadplot`, `MVA.corplot`, `MVA.biplot`, `MVA.pairplot` or `MVA.trajplot`. These functions should not be used directly (everything can be done with the general `MVA.plot`) but for convenience, arguments and analyses supported are detailed in separate help pages.

Warning: the use of `attach` before running a multivariate analysis can prevent `MVA.plot` to get the values it needs, and make it fail.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`MVA.scoreplot` *Score plot of multivariate analyses*

Description

Displays a score plot of a multivariate analysis.

Usage

```
MVA.scoreplot(x, xax = 1, yax = 2, scaling = 2, set = c(12, 1, 2), space = 1,
  byfac = TRUE, fac = NULL, barycenters = TRUE, stars = TRUE, contours = FALSE,
  dhist = TRUE, weights = 1, xlab = NULL, ylab = NULL, main = NULL, pch = 16,
  cex = 1, col = 1, points = TRUE, labels = NULL, main.pos = c("bottomleft",
  "topleft", "bottomright", "topright"), main.cex = 1.3, fac.lab = NULL,
 fac.cex = 1, legend = FALSE, legend.pos = c("topleft", "topright", "bottomleft",
  "bottomright"), legend.title = NULL, legend.lab = NULL, legend.cex = 1,
  drawextaxes = TRUE, drawintaxes = TRUE, xlim = NULL, ylim = NULL,
  keepmar = FALSE)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	the horizontal axis.
`yax`	the vertical axis. This can be set to `NULL` for a one-dimensional graph. The type of graph to be drawn in this case depends on the value of `dhist`.

`scaling`	type of scaling. Only available with some analyses performed with the `vegan` package. See Details.
`set`	scores to be displayed, when several sets are available (see Details). `12` (default) for both sets, `1` for rows or X, `2` for columns or Y.
`space`	scores to be displayed, when several spaces are available (see Details). `space` is the number of the space to be plotted.
`byfac`	only used with MCA and mix analyses (see Details). If `TRUE`, a separate score plot is displayed for each factor included in the analysis. In this case `fac` cannot be used and if `main=NULL`, the factor names are displayed as titles on the graphs.
`fac`	an optional factor defining groups of individuals.
`barycenters`	only used if `fac` is not `NULL`. If `TRUE` (default), the name of each group (defined by `fac.lab`) is diplayed at the position of the barycenter of this group. Available for two-dimensional graphs and for dotcharts in the one-dimensional case (see `dhist`).
`stars`	only used if `fac` is not `NULL`. If `TRUE` (default), the individual of each group are linked to their corresponding barycenter.
`contours`	only used if `fac` is not `NULL`. If `TRUE`, a polygon of contour is displayed for each group.
`dhist`	only used in the one-dimensional case. If `TRUE` (default), a density histogram is displayed. If `FALSE`, a dotchart is displayed.
`weights`	individual weights, used to calculate barycenter positions (see `barycenters`).
`xlab`	legend of the horizontal axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`ylab`	legend of the vertical axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis. Available for two-dimensional graphs and for density histograms in the one-dimensional case (see `dhist`).
`main`	optional title of the graph. Can be a vector of several values for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`pch`	symbol(s) used for points, when points are displayed (see `points`). If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary. Available for two-dimensional graphs and for dotcharts in the one-dimensional case (see `dhist`). Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`cex`	size of the points or of the labels (see `points`). Available for two-dimensional graphs and for dotcharts in the one-dimensional case (see `dhist`). For two-dimensional graphs: if `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group; otherwise a vector of any length can be defined, which is recycled if necessary. For dotcharts, gives the size used for points and all labels (see `dotchart`). Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`col`	color(s) used for points or labels (see `points`). If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary (not available for density

	histograms, see `dhist`). Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`points`	only used for two-dimensional graphs. If `FALSE`, points are replaced with their corresponding label (defined by `labels`). Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`labels`	used in two-dimensional graphs when `points=FALSE` and in dotcharts (see `dhist`). Names of the individuals. If `NULL` (default), labels correspond to row names of the data used in the multivariate analysis. Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`main.pos`	position of the title, if `main` is not `NULL`. Default to `"bottomleft"`. Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`main.cex`	size of the title, if `main` is not `NULL`. Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`fac.lab`	only used if `fac` is not `NULL`. Labels used to display barycenters in two-dimensional graphs or on the vertical axis of a dotchart in the one-dimensional case (see `dhist`). If `NULL`, levels of the factor defined by `fac` are used. In case of a MCA or a mix analysis with `byfac=TRUE` (see `byfac`), labels cannot be changed and correspond to the levels of the factor displayed on each graph.
`fac.cex`	only used if `fac` is not `NULL` and in two-dimensional graphs. Labels used to display barycenters. Can be a vector of length one or a vector giving one value per group. Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`legend`	logical indicating if a legend should be added to the graph. Available for two-dimensional graphs and for density histograms in the one-dimensional case (see `dhist`).
`legend.pos`	position of the legend, if `legend` is `TRUE`. Default to `"topleft"`.
`legend.title`	optional title of the legend, if `legend` is `TRUE`. Not available for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`legend.lab`	legend labels, if `legend` is `TRUE`. If `NULL`, labels defined by `fac.labels` are used (see `fac.labels`).
`legend.cex`	size of legend labels, if `legend` is `TRUE`.
`drawextaxes`	logical indicating if external axes should be drawn. Available for two-dimensional graphs and for density histograms in the one-dimensional case (see `dhist`).
`drawintaxes`	logical indicating if internal axes should be drawn.
`xlim`	limits of the horizontal axis. If `NULL`, limits are computed automatically. Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`ylim`	only used in two-dimensional graphs. Limits of the vertical axis. If `NULL`, limits are computed automatically. Re-used for all graphs for MCA and mix analyses when `byfac=TRUE` (see `byfac`).
`keepmar`	only used in two-dimensional graphs. Logical indicating if margins defined by MVA.scoreplot should be kept after plotting (necessary for biplots).

Details

This function should not be use directly. Prefer the general `MVA.plot`, to which all arguments can be passed.

Many multivariate analyses are supported, from various packages:

- PCA: `prcomp`, `princomp` (if `scores=TRUE`), `dudi.pca`, `rda`, `pca`, `pca`. `scaling` can be defined for `rda` (see `scores.rda`).

- sPCA: `spca`.

- IPCA: `ipca`.

- sIPCA: `sipca`.

- PCoA: `cmdscale` (with at least on non-default argument), `dudi.pco`, `wcmdscale` (with at least one non-default argument), `capscale`, `pco`, `pcoa`.

- nMDS: `monoMDS`, `metaMDS`, `nmds`, `isoMDS`.

- LDA: `lda`, `discrimin`.

- PLS-DA (PLS2 on a dummy-coded factor): `plsda`. X space only.

- sPLS-DA (sPLS2 on a dummy-coded factor): `splsda`. X space only.

- CPPLS: `mvr`. X space only.

- PLSR: `mvr`, `pls`, `plsR` (plsRglm package). X space only.

- sPLSR: `pls`. X space only.

- PLS-GLR: `plsRglm` (plsRglm package).

- PCR: `mvr`.

- CDA: `discrimin`, `discrimin.coa`.

- NSCOA: `dudi.nsc`.

- MCA: `dudi.acm`.

- Mix analysis: `dudi.mix`, `dudi.hillsmith`.

- COA: `dudi.coa`, `cca`. Set 1 is rows, set 2 is columns. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set. `scaling` can be defined for `cca` (see `scores.cca`).

- DCOA: `dudi.dec`. Set 1 is rows, set 2 is columns. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- PCIA: `procuste`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- Procrustean superimposition: `procrustes`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- GPA: `GPA`. Only the consensus ordination can be displayed.

- DPCoA: `dpcoa`. Set 1 is categories, set 2 is collections. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- RDA (or PCAIV): `pcaiv`, `pcaivortho`, `rda`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`, the opposite for `pcaivortho`. `scaling` can be defined for `rda` (see `scores.rda`).

- db-RDA (or CAP): `capscale`, `dbrda`. Space 1 is constrained space, space 2 is unconstrained space.

- CCA: `pcaiv`, `cca`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`. Set 1 is rows, set 2 is columns. `scaling` can be defined for `cca` (see `scores.cca`).

- CCorA: `CCorA`, `rcc`. Space 1 is X, space 2 is Y. With `rcc` a third space is available, in which coordinates are means of X and Y coordinates.

- rCCorA: `rcc`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates.

- CIA: `coinertia`. Space 1 is X, space 2 is Y, space 3 is a "common" space where X and Y scores are normed. In space 3, set 1 is X and set 2 is Y. If `set=12` in space 3 (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- 2B-PLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates.

- 2B-sPLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates.

- rGCCA: `rgcca`, `wrapper.rgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- sGCCA: `rgcca`, `wrapper.sgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- DIABLO: `block.plsda`, `block.splsda`. Space can be 1 to n, the number of blocks (i.e. datasets).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
data(iris)
PCA <- prcomp(iris[,1:4])
MVA.plot(PCA,"scores")
MVA.plot(PCA,"scores",fac=iris$Species,col=1:3,pch=15:17)
```

`MVA.scores` *Scores of multivariate analyses*

Description

Returns scores of a multivariate analysis.

Usage

```
MVA.scores(x, xax = 1, yax = 2, scaling = 2, set = c(12, 1, 2), space = 1, ...)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	axis or axes for which to extract scores.
`yax`	axis for which to extract scores (ignored if `length(xax) > 1`).
`scaling`	type of scaling. Only available with some analyses performed with the `vegan` package. See Details.
`set`	scores to be displayed, when several sets are available (see Details). `12` (default) for both sets, `1` for rows or X, `2` for columns or Y.
`space`	scores to be displayed, when several spaces are available (see Details). `space` is the number of the space to be plotted.
`...`	not used.

Details

Many multivariate analyses are supported, from various packages:

- PCA: `prcomp`, `princomp` (if `scores=TRUE`), `dudi.pca`, `rda`, `pca`, `pca`. `scaling` can be defined for `rda` (see `scores.rda`).

- sPCA: `spca`.

- IPCA: `ipca`.

- sIPCA: `sipca`.

- PCoA: `cmdscale` (with at least on non-default argument), `dudi.pco`, `wcmdscale` (with at least one non-default argument), `capscale`, `pco`, `pcoa`.

- nMDS: `monoMDS`, `metaMDS`, `nmds`, `isoMDS`.

- LDA: `lda`, `discrimin`.

- PLS-DA (PLS2 on a dummy-coded factor): `plsda`. X space only.

- sPLS-DA (sPLS2 on a dummy-coded factor): `splsda`. X space only.

- CPPLS: `mvr`. X space only.

- PLSR: `mvr`, `pls`, `plsR` (plsRglm package). X space only.

- sPLSR: `pls`. X space only.

- PLS-GLR: `plsRglm` (plsRglm package).

- PCR: `mvr`.

- CDA: `discrimin`, `discrimin.coa`.

- NSCOA: `dudi.nsc`.

- MCA: `dudi.acm`.

- Mix analysis: `dudi.mix`, `dudi.hillsmith`.

- COA: `dudi.coa`, `cca`. Set 1 is rows, set 2 is columns. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set. `scaling` can be defined for `cca` (see `scores.cca`).

- DCOA: `dudi.dec`. Set 1 is rows, set 2 is columns. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- PCIA: `procuste`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- Procrustean superimposition: `procrustes`. Set 1 is X, set 2 is Y. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- GPA: `GPA`. Only the consensus ordination can be displayed.

- DPCoA: `dpcoa`. Set 1 is categories, set 2 is collections. If `set=12` (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- RDA (or PCAIV): `pcaiv`, `pcaivortho`, `rda`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`, the opposite for `pcaivortho`. `scaling` can be defined for `rda` (see `scores.rda`).

- db-RDA (or CAP): `capscale`, `dbrda`. Space 1 is constrained space, space 2 is unconstrained space.

- CCA: `pcaiv`, `cca`. With `rda`, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with `pcaiv`. Set 1 is rows, set 2 is columns. `scaling` can be defined for `cca` (see `scores.cca`).

- CCorA: `CCorA`, `rcc`. Space 1 is X, space 2 is Y. With `rcc` a third space is available, in which coordinates are means of X and Y coordinates.

- rCCorA: `rcc`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates.

- CIA: `coinertia`. Space 1 is X, space 2 is Y, space 3 is a "common" space where X and Y scores are normed. In space 3, set 1 is X and set 2 is Y. If `set=12` in space 3 (default), `fac` is not available and `pch`,`cex`, `col` can be defined differently for each set.

- 2B-PLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates.

- 2B-sPLS: `pls`. Space 1 is X, space 2 is Y, space 3 is a "common" space in which coordinates are means of X and Y coordinates.

- rGCCA: `rgcca`, `wrapper.rgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- sGCCA: `rgcca`, `wrapper.sgcca`. Space can be 1 to n, the number of blocks (i.e. datasets).

- DIABLO: `block.plsda`, `block.splsda`. Space can be 1 to n, the number of blocks (i.e. datasets).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`MVA.synt` *Synthesis quality of multivariate analyses*

Description

Gives a simple estimator of the quality of the (descriptive) synthesis performed by a wide range of multivariate analyses.

Usage

```
MVA.synt(x, rows = 5)
```

Arguments

`x`	a multivariate analysis (see Details).
`rows`	maximum number of axes to print in the output.

Details

Many multivariate analyses are supported, from various packages.

- PCA: `prcomp`, `princomp`, `dudi.pca`, `rda`, `pca`, `pca`: % of total variance explained by each axis.

- sPCA: `spca`: % of total variance explained by each axis.

- IPCA: `ipca`: kurtosis of each axis.

- sIPCA: `sipca`: kurtosis of each axis.

- PCoA: `cmdscale` (with `eig=TRUE`), `dudi.pco`, `wcmdscale` (with `eig=TRUE`), `capscale`, `pco`, `pcoa`: % of total variance explained by each axis.

- nMDS: `monoMDS`, `metaMDS`, `nmds`, `isoMDS`: stress.

- RDA: `pcaiv`, `pcaivortho`, `rda`: % of constrained and unconstrained total variance, % of constrained variance explained by constrained axes (`pcaiv` and `rda`), % of unconstrained variance explained by unconstrained axes (`pcaivortho` and `rda`).

- db-RDA (or CAP): `capscale`, `dbrda`: % of constrained and unconstrained total variance, % of constrained variance explained by constrained axes, % of unconstrained variance explained by unconstrained axes.

- COA: `dudi.coa`, `cca`: % of total inertia explained by each axis.

- CCA: `pcaiv`, `cca`: % of constrained and unconstrained total inertia, % of constrained inertia explained by constrained axes, % of unconstrained inertia explained by unconstrained axes (`cca` only).

- CPPLS: `mvr`: % of X and Y variances explained by each axis.

- PLSR: `mvr`, `plsR` (plsRglm package): % of X and Y variances explained by each axis (only Y for the moment with `plsR`).

- 2B-PLS: `pls`: % of X/Y square covariance explained by each pair of axes, correlation between each pair of axes (canonical correlations).

- CCorA: `CCorA`, `rcc`: correlation between each pair of axes (canonical correlations).

- rCCorA: `rcc`: correlation between each pair of axes (canonical correlations).

- PCR: `mvr`: % of X and Y variances explained by each axis.

- MCA: `dudi.acm`: % of total inertia explained by each axis.

- Mix analysis: `dudi.mix`, `dudi.hillsmith`: % of total inertia explained by each axis.

- GPA: `GPA`: % of consensus and residual variance, % of total variance exlained by each axis, % of consensus variance explained by each axis, % of residual variance coming from each group of variables.

- RGCCA: `rgcca`, `wrapper.rgcca`: % of total intra-block variance explained by each axis, correlation between each pair of axes (canonical correlations).

- DIABLO: `block.plsda`, `block.splsda`: % of total intra-block variance explained by each axis, correlation between each pair of axes (canonical correlations).

- CIA: `coinertia`: RV coefficient, % of co-inertia explained by each pair of axes, correlation between each pair of axes (canonical correlations).

- PCIA: `procuste`: m2.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
data(iris)
PCA <- prcomp(iris[,1:4])
MVA.synt(PCA)
```

`MVA.test` *Significance test based on cross (model) validation*

Description

Performs a permutation significance test based on cross (model) validation with different PLS and/or discriminant analyses. See `MVA.cv` and `MVA.cmv` for more details about how cross (model) validation is performed.

Usage

```
MVA.test(X, Y, cmv = FALSE, ncomp = 8, kout = 7, kinn = 6, scale = TRUE,
  model = c("PLSR", "CPPLS", "PLS-DA", "PPLS-DA", "LDA", "QDA", "PLS-DA/LDA",
  "PLS-DA/QDA", "PPLS-DA/LDA","PPLS-DA/QDA"), Q2diff = 0.05, lower = 0.5,
  upper = 0.5, Y.add = NULL, weights = rep(1, nrow(X)), set.prior = FALSE,
  crit.DA = c("plug-in", "predictive", "debiased"), p.method = "fdr",
  nperm = 999, progress = TRUE, ...)
```

Arguments

`X`	a data frame of independent variables.
`Y`	the dependent variable(s): numeric vector, data frame of quantitative variables or factor.
`cmv`	a logical indicating if the values (Q2 or NMC) should be generated through cross-validation (classical K-fold process) or cross model validation (inner + outer loops).

`ncomp`	an integer giving the number of components to be used to generate all submodels (cross-validation) or the maximal number of components to be tested in the inner loop (cross model validation). Can be re-set internally if needed. Does not concern LDA and QDA.
`kout`	an integer giving the number of folds (cross-validation) or the number of folds in the outer loop (cross-model validation). Can be re-set internally if needed.
`kinn`	an integer giving the number of folds in the inner loop (cross model validation only). Can be re-set internally if needed. Cannot be > `kout`.
`scale`	logical indicating if data should be scaled. See help of `MVA.cv` and `MVA.cmv`.
`model`	the model to be fitted.
`Q2diff`	the threshold to be used if the number of components is chosen according to Q2 (cross model validation only).
`lower`	a vector of lower limits for power optimisation in CPPLS or PPLS-DA (see `cppls.fit`).
`upper`	a vector of upper limits for power optimisation in CPPLS or PPLS-DA (see `cppls.fit`).
`Y.add`	a vector or matrix of additional responses containing relevant information about the observations, in CPPLS or PPLS-DA (see `cppls.fit`).
`weights`	a vector of individual weights for the observations, in CPPLS or PPLS-DA (see `cppls.fit`).
`set.prior`	only used when a LDA or QDA is performed (coupled or not with a PLS model). If `TRUE`, the prior probabilities of class membership are defined according to the mean weight of individuals belonging to each class. If `FALSE`, prior probabilities are obtained from the data sets on which LDA/QDA models are built.
`crit.DA`	criterion used to predict class membership when a LDA or QDA is used. See `predict.lda`.
`p.method`	method for p-values correction. See help of `p.adjust`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.
`...`	other arguments to pass to `plsr` (PLSR, PLS-DA) or `cppls` (CPPLS, PPLS-DA).

Details

When `Y` consists in quantitative response(s), the null hypothesis is that each response is not predicted better than what would happen by chance. In this case, Q2 is used as the test statistic. When `Y` contains several responses, a p-value is computed for each response and p-values are corrected for multiple testing.

When `Y` is a factor, the null hypothesis is that the factor has no discriminant ability. In this case, the classification error rate (NMC) is used as the test statistic.

Whatever the response, the reference value of the test statistics is obtained by averaging 20 values coming from independently performed cross (model) validation on the original data.

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name(s) of the data, plus additional information.
`statistic`	the value of the test statistics.
`permutations`	the number of permutations.
`p.value`	the p-value of the test.
`p.adjust.method`	a character string giving the method for p-values correction.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

References

Westerhuis J, Hoefsloot HCJ, Smit S, Vis DJ, Smilde AK, van Velzen EJJ, van Duijnhoven JPM and van Dorsten FA (2008) Assessment of PLSDA cross validation. Metabolomics 4:81-89.

See Also

`MVA.cv`, `MVA.cmv`

Examples

```
require(pls)
require(MASS)

# PLSR
data(yarn)
## Not run: MVA.test(yarn$NIR,yarn$density,cmv=TRUE,model="PLSR")

# PPLS-DA coupled to LDA
data(mayonnaise)
## Not run: MVA.test(mayonnaise$NIR,factor(mayonnaise$oil.type),model="PPLS-DA/LDA")
```

`MVA.trajplot` *Trajectory plot of multivariate analyses*

Description

Displays a trajectory plot (*i.e.* a score plot with trajectories linking defined points) of a multivariate analysis.

Usage

```
MVA.trajplot(x, xax = 1, yax = 2, trajects, trajlab = NULL, scaling = 2,
  set = c(12, 1, 2), space = 1, xlab = NULL, ylab = NULL, main = NULL,
  pch = 16, cex = 1, trajlab.cex = 1, col = 1, lwd = 1, lty = 1,
  points = TRUE, allpoints = TRUE, arrows = TRUE, labels = NULL,
  main.pos = c("bottomleft", "topleft", "bottomright", "topright"),
  main.cex = 1.3, legend = FALSE, legend.pos = c("topleft", "topright",
  "bottomleft", "bottomright"), legend.title = NULL, legend.lab = NULL,
  legend.cex = 1, drawextaxes = TRUE, drawintaxes = TRUE, xlim = NULL,
  ylim = NULL)
```

Arguments

`x`	a multivariate analysis (see Details).
`xax`	the horizontal axis.
`yax`	the vertical axis. Cannot be `NULL`, only two-dimensional graphs can be drawn.
`trajects`	vector or list of vectors identifying trajectories. Each vector should give the number of the individuals to be linked, ordered from the first to the last one.
`trajlab`	optional traject labels.
`scaling`	type of scaling. Only available with some analyses performed with the `vegan` package. See Details of `MVA.scoreplot`.
`set`	scores to be displayed, when several sets are available (see Details of `MVA.scoreplot`). `12` (default) for both sets, `1` for rows or X, `2` for columns or Y.
`space`	scores to be displayed, when several spaces are available (see Details of `MVA.scoreplot`). `space` is the number of the space to be plotted.
`xlab`	legend of the horizontal axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`ylab`	legend of the vertical axis. If `NULL` (default), automatic labels are used depending on the multivariate analysis.
`main`	optional title of the graph.
`pch`	symbols used for points. Can be a vector giving one value per trajectory (and a last one for non-linked points if `allpoints=TRUE`).
`cex`	size of the labels. Can be a vector giving one value per trajectory (and a last one for non-linked points if `allpoints=TRUE`).
`trajlab.cex`	size of trajectory labels. Can be a vector giving one value per trajectory.
`col`	color(s) used for arrows and labels. If `fac` is not `NULL`, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.
`lwd`	width of trajectory segments. Can be a vector giving one value per trajectory.
`lty`	type of trajectory segments. Can be a vector giving one value per trajectory.
`points`	logical indicating if points should be displayed. If `FALSE`, points are replaced with their corresponding label (defined by `labels`).

`allpoints`	logical indicating if points which do not belong to any trajectory should be drawn.
`arrows`	logical indicating if trajectories should be oriented with arrows.
`labels`	names of the individuals. If `NULL` (default), labels correspond to row names of the data used in the multivariate analysis.
`main.pos`	position of the title, if `main` is not `NULL`. Default to `"bottomleft"`.
`main.cex`	size of the title, if `main` is not `NULL`.
`legend`	logical indicating if a legend should be added to the graph.
`legend.pos`	position of the legend, if `legend` is `TRUE`. Default to `"topleft"`.
`legend.title`	optional title of the legend, if `legend` is `TRUE`.
`legend.lab`	legend labels, if `legend` is `TRUE`. If `NULL` and `trajlab` is defined, values of `trajlab` are used.
`legend.cex`	size of legend labels, if `legend` is `TRUE`.
`drawextaxes`	logical indicating if external axes should be drawn..
`drawintaxes`	logical indicating if internal axes should be drawn.
`xlim`	limits of the horizontal axis. If `NULL`, limits are computed automatically.
`ylim`	limits of the vertical axis. If `NULL`, limits are computed automatically.

Details

This function should not be use directly. Prefer the general `MVA.plot`, to which all arguments can be passed.

All multivariate analyses supported by `MVA.scoreplot` can be used for a paired plot.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
require(ade4)
data(olympic)
PCA <- dudi.pca(olympic$tab,scannf=FALSE)
MVA.plot(PCA,"traject",trajects=list(1:10,25:30),col=c(2,3,1),trajlab=c("T1","T2"))
```

`OR.multinom` *Odds-ratio (multinomial regression)*

Description

Computes the odds ratios and their confidence interval for a predictor of a model fitted with `multinom`.

Usage

```
OR.multinom(model, variable, conf.level = 0.95)
```

Arguments

`model`	object of class `"multinom"`.
`variable`	any predictor present in `model` (unquoted).
`conf.level`	confidence level.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`ord.rw` *Re-computation of an ordination using given row weights*

Description

Re-computes an ordination using given row weights (possibly extracted from a correspondence analysis). The function is intended to be used prior to `coinertia` when row weights have to be equalized.

Usage

```
ord.rw(ord, CA = NULL, rw = NULL)
```

Arguments

`ord`	an ordination to re-compute. Must come from the `ade4` package or be supported by `to.dudi`. In any case the resulting ordination will be in the `ade4` format.
`CA`	an optional correspondence analysis from which row weights should be extracted. Must come from `dudi.coa` or `cca`.
`rw`	an optional vector of row weights. Used only is `CA` is `NULL`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`overdisp.glmer` *Estimation of overdispersion with `glmer` models*

Description

Estimates residual deviance and residual degrees of freedom to check for overdispersion with `glmer` models. This function is directly comming from `http://glmm.wikidot.com/faq`.

Usage

```
overdisp.glmer(model)
```

Arguments

`model`	a model fitted by `glmer`.

Author(s)

Ben Bolker

See Also

`glmer`

Examples

```
require(lme4)

# Example from the 'glmer' function
gm1 <- glmer(cbind(incidence,size-incidence)~period+(1|herd),
 family="binomial",data=cbpp)
overdisp.glmer(gm1)
```

`p.beta` *Rescaling of a [0,1] variable into the (0,1) interval (and vice-versa)*

Description

The function uses the formula presented in Douma & Weedon (2019). It is primarily intended to be used in beta regression (regression for continuous proportions) when data contain zeroes and/or ones, but can be applied to any variable initially bounded in the [0,1] interval when rescaling is necessary. The function can also perform back-transformation.

Usage

```
p.beta(p, n = length(p), C = 2, back = FALSE)
```

Arguments

`p`	numeric vector of values in the [0,1] interval.
`n`	total number of observations in the initial data set. Not very useful when the transformation is applied to the initial data set, but needed when back-transformation is applied from predicted values.
`C`	number of categories from which `p` was computed.
`back`	logical. If `TRUE`, back-transformation is performed rather than transformation.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr> from the following paper: Douma JC & Weedon JT (2019) Analysing continuous proportions in ecology and evolution: A practical introduction to beta and Dirichlet regression. Methods in Ecology and Evolution, 10: 1412-1430

Examples

```
# A fictive example with four animals performing a behavioral choice-test where time
#   can be spent in three branches (total time 20 min)
(tab <- data.frame(Individual=c("Ind1","Ind2","Ind3","Ind4"),Branch1=c(0,12,20,4),
  Branch2=c(8,4,0,6),Branch3=c(12,4,0,10)))
# Raw proportions of time spent in branch 1:
(p1 <- tab$Branch1/rowSums(tab[,-1]))
# Scaled proportions:
p.beta(p1,C=3)
```

`pairwise.CDA.test` *Pairwise comparisons for CDA*

Description

Performs pairwise comparisons between group levels with corrections for multiple testing, using `CDA.test`.

Usage

```
pairwise.CDA.test(X, fact, ncomp = NULL, p.method = "fdr", ...)
```

Arguments

`X`	a data frame of dependent variables (typically contingency or presence-absence table).
`fact`	factor giving the groups.
`ncomp`	an integer giving the number of components to be used for the test. If `NULL` `nlevels(fact)-1` are used.
`p.method`	method for p-values correction. See help of `p.adjust`.
`...`	other arguments to pass to `CDA.test`.

Details

See `CDA.test`.

Value

`method`	a character string indicating what type of tests were performed.
`data.name`	a character string giving the name(s) of the data.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`CDA.test`

Examples

```
require(ade4)
data(perthi02)

CDA.test(perthi02$tab,perthi02$cla)
pairwise.CDA.test(perthi02$tab,perthi02$cla)
```

`pairwise.factorfit` *Pairwise comparisons of groups displayed on a factorial map*

Description

Performs pairwise comparisons between group levels with corrections for multiple testing. Tests are computed using `factorfit`.

Usage

```
pairwise.factorfit(ord, fact, xax = 1, yax = 2, nperm = 999,
  p.method = "fdr", ...)
```

Arguments

`ord`	any multivariate analysis handled by `MVA.scores`.
`fact`	grouping factor.
`xax`	first axis of the factorial map.
`yax`	second axis of the factorial map.
`nperm`	number of permutations.
`p.method`	method for p-values correction. See help of `p.adjust`.
`...`	optional further agruments to `MVA.scores`.

Value

`method`	a character string giving the name of the test.
`data.name`	a character string giving the name(s) of the data and the number of permutations.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`factorfit`

Examples

```
require(vegan)
data(iris)

PCA <- rda(iris[,1:4])
MVA.plot(PCA,fac=iris$Species,col=1:3)

# Global test
envfit(PCA~Species,data=iris)

# Pairwise comparisons
# (not enough permutations here but faster to run)
pairwise.factorfit(PCA,iris$Species,nperm=49)
```

`pairwise.G.test` *Pairwise comparisons for proportions using G-tests*

Description

Performs pairwise comparisons between pairs of proportions with correction for multiple testing.

Usage

```
pairwise.G.test(x, p.method = "fdr")
```

Arguments

`x`	matrix with 2 columns giving the counts of successes and failures, respectively.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

Since a G-test is an approximate test, an exact test is preferable when the number of individuals is small (200 is a reasonable minimum). See `fisher.multcomp` in that case.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.adjust.method`	method for p-values correction.
`p.value`	table of results.

See Also

`G.test`, `fisher.multcomp`

Examples

```
x <- matrix(c(44,56,36,64,64,40),ncol=2,dimnames=list(c("Control","Treatment1","Treatment2"),
  c("Alive","Dead")),byrow=TRUE)
G.test(x)
pairwise.G.test(x)
```

`pairwise.mood.medtest` *Pairwise Mood's median tests*

Description

Performs pairwise comparisons between group levels with corrections for multiple testing.

Usage

```
pairwise.mood.medtest(resp, fact, exact = NULL, p.method = "fdr")
```

Arguments

`resp`	response vector.
`fact`	grouping factor.
`exact`	a logical indicating whether exact p-values should be computed.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

If `exact=NULL`, Fisher's exact tests are used if the number of data values is < 200; otherwise chi-square tests are used (with Yates continuity correction).

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`mood.medtest`

Examples

```
set.seed(0904)
response <- c(rnorm(10),rnorm(10,0.8),rnorm(10,2))
fact <- gl(3,10,labels=LETTERS[1:3])
mood.medtest(response~fact)
pairwise.mood.medtest(response,fact)
```

`pairwise.MVA.test` *Pairwise permutation tests based on cross (model) validation*

Description

Performs pairwise comparisons between group levels with corrections for multiple testing, using `MVA.test`.

Usage

```
pairwise.MVA.test(X, fact, p.method = "fdr", cmv = FALSE, ncomp = 8,
  kout = 7, kinn = 6, model = c("PLS-DA", "PPLS-DA", "LDA", "QDA",
  "PLS-DA/LDA", "PLS-DA/QDA", "PPLS-DA/LDA","PPLS-DA/QDA"),
  nperm = 999, progress = TRUE, ...)
```

Arguments

`X`	a data frame of independent variables.
`fact`	grouping factor.
`p.method`	method for p-values correction. See help of `p.adjust`.
`cmv`	a logical indicating if the test statistic (NMC) should be generated through cross-validation (classical K-fold process) or cross model validation (inner + outer loops).
`ncomp`	an integer giving the number of components to be used to generate all submodels (cross-validation) or the maximal number of components to be tested in the inner loop (cross model validation). Can be re-set internally if needed. Does not concern LDA and QDA.
`kout`	an integer giving the number of folds (cross-validation) or the number of folds in the outer loop (cross-model validation). Can be re-set internally if needed.
`kinn`	an integer giving the number of folds in the inner loop (cross model validation only). Can be re-set internally if needed. Cannot be > `kout`.
`model`	the model to be fitted.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.
`...`	other arguments to pass to `MVA.test`.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	a character string indicating what type of tests were performed.
`data.name`	a character string giving the name(s) of the data.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.
`permutations`	number of permutations.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`MVA.test`

Examples

```
require(pls)
data(mayonnaise)

# PPLS-DA
## Not run: pairwise.MVA.test(mayonnaise$NIR,factor(mayonnaise$oil.type),model="PPLS-DA")

# The function needs a long calculation time!
```

`pairwise.perm.manova` *Pairwise permutation MANOVAs*

Description

Performs pairwise comparisons between group levels with corrections for multiple testing. These pairwise comparisons are relevant after a permutation MANOVA, such as performed by `adonis2`.

Usage

```
pairwise.perm.manova(resp, fact, test = c("Pillai", "Wilks",
  "Hotelling-Lawley", "Roy", "Spherical"), nperm = 999,
  progress = TRUE, p.method = "fdr", F = FALSE, R2 = FALSE)
```

Arguments

`resp`	response. Either a matrix (one column per variable; objects of class `"data.frame"` are accepted and internally converted into matrices) or a distance matrix.
`fact`	grouping factor.
`test`	choice of test statistic when `resp` is a matrix (see `anova.mlm`).
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.
`p.method`	method for p-values correction. See help of `p.adjust`.
`F`	should the table of F values be returned?
`R2`	should the table of R2 values be returned? For tests based on distance matrices only.

Details

If `resp` is a matrix, a classical MANOVA is performed and the distribution of the (pseudo-)F is computed through permutations. The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

If `resp` is a distance matrix, `adonis2` is used to perform each comparison.

Value

`method`	a character string giving the name of the test.
`data.name`	a character string giving the name(s) of the data and the number of permutations.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.
`F.value`	table of F values (if required).
`R2.value`	table of R2 values (if required).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`anova.mlm`, `adonis2`

Examples

```
require(vegan)
data(iris)

# permutation MANOVA
adonis2(iris[,1:4]~Species,data=iris,method="euclidean")

# Pairwise comparisons
```

```
# (not enough permutations here but faster to run)
pairwise.perm.manova(iris[,1:4],iris$Species,nperm=49)

# or
pairwise.perm.manova(dist(iris[,1:4],"euclidean"),iris$Species,nperm=49)
```

`pairwise.perm.t.test` *Pairwise permutation t tests*

Description

Performs pairwise comparisons between group levels with corrections for multiple testing.

Usage

```
pairwise.perm.t.test(resp, fact, p.method = "fdr", paired = FALSE,
  alternative = c("two.sided","less", "greater"), nperm = 999,
  progress = TRUE)
```

Arguments

`resp`	response vector.
`fact`	grouping factor.
`p.method`	method for p-values correction. See help of `p.adjust`.
`paired`	a logical indicating whether you want paired (permutation) t-tests.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	a character string indicating what type of t-tests were performed.
`data.name`	a character string giving the name(s) of the data.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.
`permutations`	number of permutations.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`pairwise.t.test`

Examples

```
set.seed(1203)
response <- c(rnorm(5),rpois(5,0.5),rnorm(5,2,1))
fact <- gl(3,5,labels=LETTERS[1:3])

# Not enough permutations here but it runs faster

# permutation ANOVA
perm.anova(response~fact,nperm=49)

# Pairwise comparisons
pairwise.perm.t.test(response,fact,nperm=49)
```

---

pairwise.perm.var.test

Pairwise permutation F tests

Description

Performs pairwise comparisons between group levels with corrections for multiple testing.

Usage

```
pairwise.perm.var.test(resp, fact, p.method = "fdr",
  alternative = c("two.sided","less", "greater"), nperm = 999,
  progress = TRUE)
```

Arguments

`resp`	response vector.
`fact`	grouping factor.
`p.method`	method for p-values correction. See help of `p.adjust`.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	a character string giving the name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.
`permutations`	number of permutations.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`pairwise.var.test`

Examples

```
set.seed(0921)
response <- c(rnorm(10),rpois(10,0.2),rnorm(10,,2))
fact <- gl(3,10,labels=LETTERS[1:3])

# Not enough permutations here but it runs faster

# permutation Bartlett test
perm.bartlett.test(response~fact,nperm=49)

# Pairwise comparisons
pairwise.perm.var.test(response,fact,nperm=49)
```

`pairwise.var.test` *Pairwise F tests*

Description

Performs pairwise comparisons between group levels with corrections for multiple testing.

Usage

```
pairwise.var.test(resp, fact, p.method = "fdr",
  alternative = c("two.sided","less", "greater"))
```

Arguments

`resp`	response vector.
`fact`	grouping factor.
`p.method`	method for p-values correction. See help of `p.adjust`.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`.

Value

`method`	a character string giving the name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.value`	table of results.
`p.adjust.method`	method for p-values correction.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`pairwise.perm.var.test`

Examples

```
require(graphics)

# Bartlett test
bartlett.test(count~spray,data=InsectSprays)

# Pairwise comparisons
pairwise.var.test(InsectSprays$count,InsectSprays$spray)
```

`pcor` *(Semi-)Partial correlation*

Description

Computes the (semi-)partial correlation of `x` and `y`, controlling for `z`.

Usage

```
pcor(x, y, z, semi = FALSE, use = "complete.obs", method = c("pearson",
  "spearman"))
```

Arguments

`x`	a numeric vector.
`y`	a numeric vector.
`z`	a numeric vector, matrix, data frame or list giving the controlling variables. For matrices, variables must be placed in columns.
`semi`	logical. If `TRUE` the semi-partial correlation coefficient is computed. In that case only `y` is controlled for `z`.
`use`	same as `use` of `cor`.
`method`	same as `method` of `cor`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`pcor.test` for confidence intervals (and tests).

Examples

```
set.seed(1444)
x <- 1:30
y <- 1:30+rnorm(30,0,2)
z1 <- runif(30,0,4)
z2 <- 30:1+rnorm(30,0,3)
pcor(x,y,z1)
pcor(x,y,list(z1,z2))
```

`pcor.test` *Tests for (semi-)partial association/correlation between paired samples*

Description

Tests for (semi-)partial association between paired samples while controlling for other variables, using one of Pearson's product moment correlation coefficient or Spearman's *rho*.

Usage

```
pcor.test(x, y, z, semi = FALSE, conf.level = 0.95, nrep = 1000,
  method = c("pearson", "spearman"))
```

Arguments

`x`	a numeric vector.
`y`	a numeric vector.
`z`	a numeric vector, matrix, data frame or list giving the controlling variables. For matrices, variables must be placed in columns.
`semi`	logical. If `TRUE` the semi-partial correlation coefficient is computed and tested. In that case only `y` is controlled for `z`.
`conf.level`	confidence level for confidence interval..
`nrep`	number of replicates for computation of the confidence interval of a Spearman's rank correlation coefficient (by bootstraping).
`method`	a character string indicating which correlation coefficient is to be used for the test. One of "pearson" or "spearman".

Details

If `method` is `"pearson"` and if there are at least 4+*k* complete series of observation (where *k* is the number of controlling variables), an asymptotic confidence interval of the correlation coefficient is given based on Fisher's Z transform.

If `method` is `"spearman"`, the p-value is computed through the AS89 algorithm if the number of complete series of observation is less than 10, otherwise via the asymptotic *t* approximation (in both cases the `pspearman` function is used). A confidence interval of the correlation coefficient, computed by bootstraping, is given.

Value

`data.name`	a character string giving the name(s) of the data.
`alternative`	a character string describing the alternative hypothesis, always two-sided.
`method`	a character string indicating how the association was measured.
`conf.int`	a condidence interval for the measure of association.
`statistic`	the value of the test statistic.
`parameter`	the degrees of freedom of the test (only for a Pearson's correlation coefficient).
`p.value`	the p-value of the test.
`estimate`	the estimated measure of association, with name `"cor"` or `"rho"` corresponding to the method employed.
`null.value`	he value of the association measure under the null hypothesis, always 0.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`pcor`

Examples

```
set.seed(1444)
x <- 1:30
y <- 1:30+rnorm(30,0,2)
z1 <- runif(30,0,4)
z2 <- 30:1+rnorm(30,0,3)
pcor.test(x,y,z1)
pcor.test(x,y,list(z1,z2))
```

`perm.anova` *Permutation Analysis of Variance*

Description

Performs a permutation analysis of variance for 1 to 3 factors. For 2 and 3 factors, experiment design must be balanced. For 2 factors, the factors can be crossed with or without interaction, or nested. The second factor can be a blocking (random) factor. For 3 factors, design is restricted to 2 fixed factors crossed (with or without interaction) inside blocks (third factor).

Usage

```
perm.anova(formula, nest.f2 = c("fixed", "random"), data, nperm = 999,
  progress = TRUE)
```

Arguments

`formula`	a formula of the form `response ~ factor(s)` (see Details).
`nest.f2`	in case of 2 nested factors, precision is needed if the nested factor (factor2) is `"fixed"` (default) or `"random"`.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.

Details

For 2 factors, the formula can be:

`response ~ factor1 + factor2` for 2 fixed factors without interaction

`response ~ factor1 * factor2` for 2 fixed factors with interaction

`response ~ factor1 / factor2` for 2 fixed factors with factor2 nested into factor1 (if factor2 is a random factor, argument `nest.f2` must be changed from `"fixed"` (default) to `"random"`)

`response ~ factor1 | factor2` for 1 fixed factor (factor1) and 1 blocking (random) factor (factor2).

For 3 factors, the formula can only be:

`response ~ factor1 + factor2 | factor3` or

`response ~ factor1 * factor2 | factor3`. The 2 factors are here fixed and crossed inside each level of the third, blocking (random), factor.

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

a data frame of class `"anova"`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
set.seed(1203)
response <- c(rnorm(12),rpois(12,0.5),rnorm(12,2,1))
fact1 <- gl(3,12,labels=LETTERS[1:3])
fact2 <- gl(3,1,36,labels=letters[1:3])
fact3 <- gl(6,6,labels=letters[1:6])
block <- gl(2,6,36,labels=letters[1:2])

# Not enough permutations here but faster to run

# 2 crossed fixed factors with interaction
perm.anova(response~fact1*fact2,nperm=49)

# 2 nested fixed factors
perm.anova(response~fact1/fact2,nperm=49)

# 2 nested factors, fact2 being random
perm.anova(response~fact1/fact3,nest.f2="random",nperm=49)

# 1 fixed factor and 1 blocking (random) factor
perm.anova(response~fact1|block,nperm=49)
```

`perm.bartlett.test` *Permutation Bartlett's test of homogeneity of variances*

Description

Performs a permutation Bartlett's test of homogeneity of k variances.

Usage

```
perm.bartlett.test(formula, data, nperm = 999, progress = TRUE)
```

Arguments

`formula`	a formula of the form `a ~ b` where `a` gives the data values and `b` the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`statistic`	test statistics of the parametric test.
`permutations`	number of permutations.
`p.value`	p-value of the permutation test.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`bartlett.test`

Examples

```
response <- c(rnorm(12),rpois(12,1),rnorm(12,2,1))
fact <- gl(3,12,labels=LETTERS[1:3])
perm.bartlett.test(response~fact)
```

`perm.cor.test` *Permutation Pearson's correlation test*

Description

Performs a permutation Pearson's product-moment correlation test.

Usage

```
perm.cor.test(x, y, alternative = c("two.sided", "less", "greater"),
  nperm = 999, progress = TRUE)
```

Arguments

`x, y`	numeric vectors of data values. `x` and `y` must have the same length.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`statistic`	test statistics of the parametric test.
`permutations`	number of permutations.
`p.value`	p-value of the permutation test.
`estimate`	the estimated correlation coefficient.
`alternative`	a character string describing the alternative hypothesis.
`null.value`	the value of the association measure under the null hypothesis, always 0.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`cor.test`

Examples

```
x <- rnorm(50)
y <- runif(50)
perm.cor.test(x,y)
```

`perm.t.test` *Permutation Student's t-test*

Description

Performs a permutation Student's t-test.

Usage

```
perm.t.test(x, ...)

## Default S3 method:
perm.t.test(x, y, paired = FALSE, ...)

## S3 method for class 'formula'
perm.t.test(formula, data, alternative = c("two.sided", "less", "greater"),
  paired = FALSE, nperm = 999, progress = TRUE, ...)
```

Arguments

`x`	a numeric vector of data values.
`y`	a numeric vector of data values.
`paired`	a logical indicating whether you want a paired t-test.
`formula`	a formula of the form `a ~ b` where `a` gives the data values and `b` a factor with 2 levels giving the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.
`...`	further arguments to be passed to or from other methods.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`statistic`	test statistics of the parametric test.
`permutations`	number of permutations.
`p.value`	p-value of the permutation test.

`estimate`	the estimated mean or difference in means depending on whether it was a paired or not paired test.
`alternative`	a character string describing the alternative hypothesis.
`method`	a character string indicating what type of t-test was performed.
`data.name`	a character string giving the name(s) of the data.
`null.value`	the specified hypothesized value of the mean difference, always 0.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`t.test`

Examples

```
response <- c(rnorm(5),rnorm(5,2,1))
fact <- gl(2,5,labels=LETTERS[1:2])

# Not enough permutations here but faster to run

# Unpaired test
perm.t.test(response~fact,nperm=49)

# Paired test
perm.t.test(response~fact,paired=TRUE,nperm=49)
```

`perm.var.test` *Permutation F test to compare two variances*

Description

Performs a permutation F test to compare two variances.

Usage

```
perm.var.test(x, ...)

## Default S3 method:
perm.var.test(x, y, ...)

## S3 method for class 'formula'
perm.var.test(formula, data, alternative = c("two.sided", "less",
  "greater"), nperm = 999, progress = TRUE, ...)
```

Arguments

`x`	a numeric vector of data values.
`y`	a numeric vector of data values.
`formula`	a formula of the form `a ~ b` where `a` gives the data values and `b` a factor with 2 levels giving the corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`alternative`	a character string specifying the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"less"`.
`nperm`	number of permutations.
`progress`	logical indicating if the progress bar should be displayed.
`...`	further arguments to be passed to or from other methods.

Details

The function deals with the limitted floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

Value

`method`	name of the test.
`statistic`	test statistics of the parametric test.
`permutations`	number of permutations.
`p.value`	p-value of the permutation test.
`estimate`	the ratio of the two variances.
`alternative`	a character string describing the alternative hypothesis.
`data.name`	a character string giving the name(s) of the data.
`null.value`	the ratio of population variances under the null hypothesis, always 1.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`var.test`

Examples

```
response <- c(rpois(8,1),rpois(8,3))
fact <- gl(2,8,labels=LETTERS[1:2])
perm.var.test(response~fact)
```

`plotresid` *Simple analysis of model residuals*

Description

Plots residuals of a model against fitted values and for some models a QQ-plot of these residuals. Optionally, a Shapiro-Wilk test can be performed on residuals. The function deals with `lm` (including `glm`, `lmList`, `lmList`, `glm.nb`, `mlm` and `manova`), `lmer`, `glmer`, `glmmPQL`, `glmmadmb`, `lme`, `gls`, `nls`, `nlsList`, `survreg`, `least.rect`, `betareg` or `glmmTMB` models.

Usage

```
plotresid(model, shapiro = FALSE)
```

Arguments

`model`	an object of class `"lm"`, `"lmList"`, `"lmList4"`, `"merMod"`, `"glmmadmb"`, `"lme"`, `"glmmPQL"`, `"gls"`, `"nls"`, `"nlsList"`, `"survreg"`, `"least.rect"`, `"betareg"` or `"glmmTMB"`.
`shapiro`	logical. If `TRUE` and if `model` is based on a Gaussian distribution, a Shapiro-Wilk test is performed on residuals.

Details

Response residuals are used for linear models, non linear models and generalized linear models based on an identity link (except with `"quasi"` distributions where response residuals are used only if `variance="constant"`). Pearson or studentized residuals are used whenever there is a link function which is not identity (and with `"quasi"` distributions when `variance` is not `"constant"`), except for `betareg` models where standardized weighted residuals 2 are used (see `residuals.betareg`).

QQ-plots and Shapiro-Wilk tests are available whenever the model is based on a Gaussian distribution (and with `"quasi"` distributions when `variance="constant"`).

With a `mlm` or `manova` model, only a multivariate QQ-plot is drawn. The test performed when `shapiro=TRUE` is a Shapiro-Wilk test for multivariate normality.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`lm`, `lmList`, `lmList`, `glm`, `glm.nb`, `manova`, `lmer`, `glmer`, `lmer`, `glmer.nb`, `lme`, `glmmPQL`, `glmmadmb`, `glmmTMB`, `gls`, `nls`, `nlsList`, `survreg`, `least.rect`, `betareg`, `qresiduals`, `qqPlot`, `shapiro.test`, `mqqnorm`, `mshapiro.test`

`plotsurvivors` *Survivor curve*

Description

Plots the survivor curve (log(survivors) against time) of a dataset to check for constancy of hazard.

Usage

```
plotsurvivors(x, status = rep(1, length(x)))
```

Arguments

`x`	time to event.
`status`	status (1: event observed, 0: event not observed).

Value

`n`	initial number of individuals.
`time`	time of events.
`alive`	number of survivors at each time.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
# 'kidney' dataset of package 'survival'
require(survival)
data(kidney)
plotsurvivors(kidney$time,kidney$status)
```

`PLSDA.VIP` *Variable Importance in the Projection (VIP)*

Description

Returns VIP score of each X-variable in a PLS-DA (obtained from `plsda`).

Usage

```
PLSDA.VIP(model, graph = FALSE)
```

Arguments

`model`	object of class `"plsda"` (from `plsda`).
`graph`	logical: should VIP scores be displayed?

Value

`tab`	table of results.
`sup1`	name of X-variables having a VIP score > 1.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`plsda`

Examples

```
if (require(mixOmics)) {
  data(yeast)
  model.PLSDA <- plsda(t(yeast$data),yeast$strain.cond)
  PLSDA.VIP(model.PLSDA)
}
```

`predict.CDA.cv` *Predict method for cross-validated CDA submodels*

Description

Predicts response based on CDA (correspondence discriminant analysis) submodels generated by cross validation. The predicted class is given with its probability (computed from the values predicted by all submodels).

Usage

```
## S3 method for class 'CDA.cv'
predict(object, newdata, type = c("max", "all"), method = c("mahalanobis",
  "euclidian"), ...)
```

Arguments

`object`	object of class inheriting from `"CDA.cv"`.
`newdata`	vector, matrix or data frame giving new individuals (one row per individual).
`type`	should the probability of the most probable class be given (`"max"`, the default) or the probability of each class (`"all"`)?
`method`	criterion used to predict class membership. See `predict.coadisc`.
`...`	further arguments to be passed to or from other methods.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`CDA.cv`, `predict.coadisc`

`predict.coadisc` *Predict method for CDA*

Description

Predicts class of the grouping factor based on a Correspondence Discriminant Analysis (performed using `discrimin.coa`).

Usage

```
## S3 method for class 'coadisc'
predict(object, newdata, method = c("mahalanobis", "euclidian"), ...)
```

Arguments

`object`	object of class inheriting from `"coadisc"`.
`newdata`	contingency table (either a `"matrix"`, `"table"` or `"data.frame"` object) giving new individuals (one row per individual).
`method`	distance metric to be used for prediction. In all cases the predicted class corresponds to the minimum distance between the new individual and the centroid of each class. Default is Mahalanobis distance.
`...`	further arguments to be passed to or from other methods.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`discrimin.coa`

Examples

```
require(ade4)
data(perthi02)

CDA <- discrimin.coa(perthi02$tab,perthi02$cla,scan=FALSE)
new <- matrix(c(17,45,32,17,17,52,28,29,6,10,7,7,7,5,10,4,37,34,23,9),ncol=20)
predict(CDA,new)
```

`predict.MVA.cv` *Predict method for cross-validated submodels*

Description

Predicts response based on submodels generated by cross (model) validation. For regression models (PLSR and CPPLS), the predicted value is given with its confidence interval. For discriminant analyses, the predicted class is given with its probability (computed from the values predicted by all submodels).

Usage

```
## S3 method for class 'MVA.cv'
predict(object, newdata, conf.level = 0.95, type.DA = c("max", "all"),
   crit.DA = c("plug-in", "predictive", "debiased"), ...)
## S3 method for class 'MVA.cmv'
predict(object, newdata, conf.level = 0.95, type.DA = c("max", "all"),
  crit.DA = c("plug-in", "predictive", "debiased"), ...)
```

Arguments

`object`	object of class inheriting from `"MVA.cv"` or `"MVA.cmv"`.
`newdata`	vector, matrix or data frame giving new individuals (one row per individual).
`conf.level`	confidence level for prediction of a quantitative response.
`type.DA`	for discriminant analyses, should the probability of the most probable class be given (`"max"`, the default) or the probability of each class (`"all"`)?
`crit.DA`	criterion used to predict class membership when a LDA or QDA is used. See `predict.lda`.
`...`	further arguments to be passed to or from other methods.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`MVA.cv`, `MVA.cmv`

`prop.bin.multcomp` *Pairwise comparisons after a test for given probabilities*

Description

Performs pairwise comparisons after a global test for given response probabilities (i.e. when the response variable is a binary variable), by using exact binomial tests. The function is in fact a wrapper to pairwise comparisons of proportions to given values on a contingency table.

Usage

```
prop.bin.multcomp(formula, data, p, p.method = "fdr")
```

Arguments

`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups, respectively. `a` can be a numeric vector or a factor, with only two possible values (except NA).
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`p`	theoretical probabilities.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

If the response is a 0/1 variable, the probability of the '1' group is tested. In any other cases, the response is transformed into a factor and the probability of the second level is tested.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`observed`	observed probabilities.
`expected`	expected probabilities.
`p.adjust.method`	method for p-values correction.
`p.value2`	corrected p-values.
`p.value`	table or results of pairwise comparisons.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`prop.multcomp`, `chisq.theo.bintest`

Examples

```
response <- c(rep(0:1,c(40,60)),rep(0:1,c(55,45)),rep(0:1,c(65,35)))
fact <- gl(3,100,labels=LETTERS[1:3])
p.theo <- c(0.5,0.45,0.2)
chisq.theo.bintest(response~fact,p=p.theo)
prop.bin.multcomp(response~fact,p=p.theo)
```

`prop.multcomp` *Pairwise comparisons after a test for given proportions*

Description

Performs pairwise comparisons after a global test for given proportions, by using exact binomial tests.

Usage

```
prop.multcomp(x, p, p.method = "fdr")
```

Arguments

`x`	contingency table.
`p`	theoretical proportions.
`p.method`	method for p-values correction. See help of `p.adjust`.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`observed`	observed proportions.
`expected`	expected proportions.
`p.adjust.method`	method for p-values correction.
`p.value2`	corrected p-values.
`p.value`	table or results of pairwise comparisons.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`prop.test`

Examples

```
proportions <- sample(c(0,1),200,replace=TRUE)
populations <- sample(LETTERS[1:3],200,replace=TRUE)
tab.cont <- table(populations,proportions)
p.theo <- c(0.4,0.5,0.7)
prop.test(tab.cont,p=p.theo)
prop.multcomp(tab.cont,p=p.theo)
```

`prop.multinom` *Proportions and standard errors*

Description

Computes proportions (and their standard errors) when the number of classes is >= 2, based on predicted values of a model. The function is intended to be used parallel to a multinomial log-linear model.

Usage

```
prop.multinom(x)
```

Arguments

`x`	either a factor or a matrix with K columns giving the counts for each of the K classes.

Details

The proportions can be computed through the `predict` function applied on a multinomial log-linear model (see `multinom`). However, standard errors (or confidence intervals) cannot be obtained this way. The present function uses differents GLMs (in each case considering one category vs. the sum of all others) to obtain proportions and standard errors. Overdispersion is taken into account by default, using a quasibinomial law in all GLMs built.

Value

`probs`	the calculated proportions.
`se`	the calculated standard errors.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`multinom`, `glm`

Examples

```
response <- data.frame(A=c(2,2,4,0,2,14,6,16,0,0),
     B=c(2,0,0,0,6,2,10,6,0,0),
     C=c(12,6,0,6,2,0,0,0,0,0),
     D=c(0,0,0,14,0,0,0,0,2,0),
     E=c(0,0,0,0,0,0,0,0,16,15))
prop.multinom(response)
```

`prop.multinom.test` *Wald tests for comparison of proportions*

Description

Performs pairwise comparisons of proportions when the number of classes is >= 2 with corrections for multiple testing.

Usage

```
prop.multinom.test(x, p.method = "fdr")
```

Arguments

`x`	either a factor or a matrix with K columns giving the counts for each of the K classes.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

The function builds multinomial log-linear models (using `multinom`) and applies Wald tests to compare the intercepts to 0. All necessary models (each time using a different reference level/class) are built to get p-values of all possible comparisons among levels/classes.

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name(s) of the data.
`p.adjust.method`	method for p-values correction.
`p.value`	table of results.
`z.tab`	table of z values.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`multinom`, `binom.test`

Examples

```
response <- factor(rep(LETTERS[1:4],c(20,40,42,13)))
table(response)/length(response)
prop.multinom.test(response)
```

`quasibinomial.QAIC` *QAIC(c) calculation with GLMs of the quasi- family*

Description

Allows for the calculation of QAIC(c) with `glm` models built with a `quasibinomial` or `quasipoisson` distribution. The function is directly coming from QAIC.

Usage

```
quasibinomial.QAIC(link = "logit")
quasipoisson.QAIC(link = "log")
```

Arguments

`link`	see family and QAIC.

Author(s)

This function is only intended to make the suggestion of Kamil Barton in QAIC available.

Examples

```
# See ?QAIC from the MuMIn package
```

`rating.emmeans` *EMMeans for Cumulative Link (Mixed) Models*

Description

Extracts EMMeans (produced by `emmeans`) from Cumulative Link (Mixed) Models (produced by `clm` or `clmm`), with different possible formats.

Usage

```
rating.emmeans(emm, type = c("prob", "cumprob", "class1", "class2"), level = 0.9)
```

Arguments

`emm`	object returned by `emmeans` applied on a `clm` or `clmm` object.
`type`	type of output to be returned: `"prob"` (default) gives probability of each rating, `"cumprob"` gives cumulative probabilities (Pi is probability to be <= to rating i), `"class1"` gives the most probable rating and `"class2"` gives the first rating for which the cumulative probability is >= to `level`.
`level`	used only for type `"class2"` (see `type`).

Details

A factor named `cut` must have been called in `emmeans`, to compute EMMeans per cut point (i.e. rating). Additionally, the argument `mode` of `emmeans` must have been set to "linear.predictor". Finally, the call to `emmeans` is typically like `emmeans(model,~factor|cut,mode="linear.predictor")` where `factor` is the factor (or interaction) giving levels for which EMMeans have to be computed.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`emmeans`, `clm`, `clmm`

Examples

```
if (require("ordinal",quietly=TRUE) & require("emmeans",quietly=TRUE)) {
  model <- clm(rating~contact*temp,data=wine)
  EMM <- emmeans(model,~contact:temp|cut,mode="linear.predictor")

  # Probabilities
  rating.emmeans(EMM)

  # Cumulative probabilities
  rating.emmeans(EMM,type="cumprob")

  # Most probable rating
  rating.emmeans(EMM,type="class1")
}
```

`rating.prob` *Observed rating frequencies*

Description

Computes observed rating frequencies per level of a factor, in various formats.

Usage

```
rating.prob(x, g, type = c("prob", "cumprob", "class"))
```

Arguments

`x`	ordered factor (ratings).
`g`	factor giving groups to be compared.
`type`	type of output to be returned: `"prob"` (default) gives frequency of each rating, `"cumprob"` gives cumulative frequencies (Fi is frequence of ratings <= i) and `"class"` gives the most frequent rating.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
if (require("ordinal",quietly=TRUE)) {
  data(wine,package="ordinal")

  # Frequencies
  rating.prob(wine$rating,wine$contact:wine$temp)

  # Cumulative frequencies
  rating.prob(wine$rating,wine$contact:wine$temp,type="cumprob")

  # Most frequent rating
  rating.prob(wine$rating,wine$contact:wine$temp,type="class")
}
```

`reg.ci` *Confidence intervals of a simple linear regression*

Description

Computes and add to a graph the confidence interval of a simple regression line or of individual values.

Usage

```
reg.ci(model, conf.level = 0.95, type = c("mean", "ind"), ...)
```

Arguments

`model`	`lm` model.
`conf.level`	confidence level.
`type`	interval type : `"mean"` for the interval of the regression line (default), `"ind"` for the interval of individual values (also called "prediction interval").
`...`	other agruments. See help of `lines`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`lm`

Examples

```
x <- 1:50
y <- 1:50+rnorm(50,0,4)
regression <- lm(y~x)
plot(x,y)
abline(regression)
reg.ci(regression,type="mean",col="red")
reg.ci(regression,type="ind",col="blue")
```

`scat.cr` *"Correlation" of variables to axes in MCA or mix analyses*

Description

Represents the "correlation" of variables to axes in a MCA (from `dudi.acm`) or a mix analysis (from `dudi.hillsmith` or `dudi.mix`).

Usage

```
scat.cr(dudi.obj, axis = 1)
```

Arguments

`dudi.obj`	object obtained from `dudi.acm`, `dudi.hillsmith` or `dudi.mix`.
`axis`	axis to be represented (the first by default).

Details

For quantitative variables, the squared correlation coefficient is displayed. For ordered factors, the squared multiple correlation coefficient is displayed. For unordered factors, the correlation ratio is displayed.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>, based on an idea of Stephane Champely.

See Also

`dudi.acm`, `dudi.hillsmith`, `dudi.mix`

Examples

```
require(ade4)

# Fictive dataset
age <- sample(15:60,50,replace=TRUE)
sex <- sample(c("M","F"),50,replace=TRUE)
size <- sample(155:190,50,replace=TRUE)
hair <- sample(c("Fair","Dark","Russet"),50,replace=TRUE)
eyes <- sample(c("Blue","Green","Brown"),50,replace=TRUE)
weight <- sample(50:85,50,replace=TRUE)
hand <- sample(c("Left.handed","Right.handed"),50,replace=TRUE)
tab <- data.frame(age,sex,size,weight,hand,eyes,hair,stringsAsFactors=TRUE)

amix <- dudi.hillsmith(tab,scannf=FALSE,nf=2)
scat.cr(amix)
```

`se` *Standard error*

Description

Computes the standard error of a mean or of a proportion.

Usage

```
se(x, y = NULL)
```

Arguments

`x`	numeric vector or number of successes.
`y`	number of trials. If `NULL`, the standard error of the mean of `x` is computed. If not, the standard error of the proportion `x/y` is computed.

Details

The function deals with missing values.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

Examples

```
# Standard error of a mean
se(rnorm(30))

# Standard error of a proportion
se(9,25)
```

`seq2` *Sequence generation*

Description

Generates a regular sequence from the minimum to the maximum of a vector.

Usage

```
seq2(x, int = 999)
```

Arguments

`x`	numeric vector.
`int`	number of values to be generated (`int` breaks).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`seq`

Examples

```
seq2(rnorm(30))
```

`spearman.ci` *Confidence interval of a Spearman's rank correlation coefficient*

Description

Computes the confidence interval of a Spearman's rank correlation coefficient by bootstraping.

Usage

```
spearman.ci(var1, var2, nrep = 1000, conf.level = 0.95)
```

Arguments

`var1`	numeric vector (first variable).
`var2`	nuermic verctor (second variable).
`nrep`	number of replicates for bootstraping.
`conf.level`	confidence level of the interval.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`conf.level`	confidence level.
`rep`	number of replicates.
`estimate`	Spearman's rank correlation coefficient.
`conf.int`	confidence interval.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`cor.test`, `boot`

Examples

```
var1 <- sample(1:50,15,replace=TRUE)
var2 <- sample(1:50,15,replace=TRUE)
spearman.ci(var1,var2)
```

`spearman.cor.multcomp` *Comparison of several Spearman's rank correlation coefficients*

Description

Computes Bonferroni-adjusted confidence intervals of a series of Spearman's rank correlation coefficients, for multiple comparisons. Confidence intervals are computed by bootstraping.

Usage

```
spearman.cor.multcomp(var1, var2, fact, alpha = 0.05, nrep = 1000)
```

Arguments

`var1`	numeric vector (first variable).
`var2`	numeric vector (second variable).
`fact`	factor (groups).
`alpha`	significance level.
`nrep`	number of replicates for bootstraping.

Details

Confidence intervals which do not overlap indicate correlation coefficients significantly different at `alpha`.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`tab`	data frame of correlation coefficients with confidence intervals
`alpha`	significance level.
`nrep`	number of replicates for bootstraping.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`spearman.ci`

Examples

```
set.seed(1510)
var1 <- c(1:15+rnorm(15,0,2),1:15+rnorm(15,0,2),1:15+rnorm(15,0,2))
var2 <- c(-1:-15+rnorm(15,0,2),1:15+rnorm(15,0,2),1:15+rnorm(15,0,2))
fact <- gl(3,15,labels=LETTERS[1:3])
spearman.cor.multcomp(var1,var2,fact)
# B and C similar but different from A
```

`splitf` *Divide into groups respecting relative proportions*

Description

Divides a data frame randomly, but respecting the relative proportions of levels of a factor in the original data frame. Each subset has roughly the same number of individuals, and the same relative proportions in respect to levels of the given factor.

Usage

```
splitf(set, fac, k)
```

Arguments

`set`	a data frame containing values to be divided into groups.
`fac`	a reference factor giving the relative proportions to be respected in each subset of `set`.
`k`	an integer giving the number of subsets to be generated.

Value

A list of subsets of `set`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`split`

Examples

```
data(iris)
iris2 <- iris[c(1:50,51:80,101:120),]

# Proportions to be respected
table(iris2$Species)/nrow(iris2)

# Splitting
result <- splitf(iris2,iris2$Species,3)

# All subsets have the same size
lapply(result,nrow)

# And respect the initial proportions
lapply(result,function(x) table(x$Species)/nrow(x))
```

`stand` *Standardization of a data frame based on another data frame*

Description

Centers and scales a data frame. See Details.

Usage

```
stand(tab, ref.tab=NULL, center=NULL, scale=NULL)
```

Arguments

`tab`	data frame to scale.
`ref.tab`	optional reference data frame, from which centering and scaling parameters are obtained (see Details).
`center`	optional vector of centering parameters (one per column of `tab`). See Details.
`scale`	optional vector of scaling parameters (one per column of `tab`). See Details.

Details

If `ref.tab` is not `NULL`, centering and scaling parameters are looked for into this data frame. If it has a `"scaled:center"` attribute, this one is used to center `tab`. Otherwise means of `ref.tab`'s columns are used. The same happens for scaling parameters (with the `"scaled:scale"` attribute and standard deviations).

If `ref.tab` is `NULL`, values of `center` and `scale` are used to standardize `tab`.

If `ref.tab` and `center` are `NULL`, means of `tab`'s columns are used for centering. If `ref.tab` and `scale` are `NULL`, standard deviations of `tab`'s columns are used for scaling.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`scale`

Examples

```
data(iris)
set.seed(1131)
iris.samp <- iris[sample(1:150,10),1:4]

# Centering parameters of the complete dataset
attr(scale(iris[,1:4]),"scaled:center")
# Centering parameters of the reduced dataset
attr(scale(iris.samp),"scaled:center")

# Standardization based on the reduced dataset only
attr(stand(iris.samp),"scaled:center")
# Standardization based on the complete dataset
attr(stand(iris.samp,iris[,1:4]),"scaled:center")
```

`test.multinom` *Significance tests of coefficients (multinomial regression)*

Description

Tests for significance of coefficients associated with a given predictor of a model fitted with `multinom`. Wald tests are used. All coefficients are generated and tested through the building of models using different reference classes (for the response but also for qualitative predictors with more than 2 levels).

Usage

```
test.multinom(model, variable)
```

Arguments

`model`	object of class `"multinom"`.
`variable`	any predictor present in `model` (unquoted).

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`to.dudi` *Synthesis quality of multivariate analyses*

Description

Converts some ordinations performed with the `vegan` package to objects compatible with `coinertia`.

Usage

```
to.dudi(ord)
```

Arguments

`ord`	an ordination (see Details).

Details

The function supports:

- PCA computed from `rda`. If data were scaled (prior to the analysis or using `scale` of `rda`) it is assumed that is was with the standard deviation using `n-1`; As in `dudi.pca`, `to.dudi` rescales the data with the standard deviation using `n`.

- PCoA computed from `wcmdscale`, `capscale` or `dbrda`.

- CA computed from `cca`.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

`user.cont` *User defined contrasts for EMMeans*

Description

Returns a function usable by `emmeans` for user defined contrasts.

Usage

```
user.cont(cont)
```

Arguments

`cont`	any matrix of contrasts (see 'Details').

Details

In these matrices, each line is a comparison (= contrast) and each colum is a level of the factor. Rules for writing contrasts are:

- levels not involved in the comparison must have a null value

- levels to be compared must have opposite signs

- levels can be grouped (for example 2 -1 -1 give a comparison of the first level against the group composed by the two others)

- the sum of all values of a contrast must be null.

Value

`user.cont.emmc`	the function to be called by `emmeans`

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`emmeans`

Examples

```
require(car)
require(emmeans)

tab <- data.frame(
  response <- c(rpois(30,1),rpois(30,3),rpois(30,10)) ,
  fact <- gl(3,30,labels=LETTERS[1:3])
)
model <- glm(response~fact,family="poisson",data=tab)
```

```
Anova(model)
mat <- matrix(c(1,-1,0,0,1,-1,2,-1,-1),nrow=3,byrow=TRUE,dimnames=list(1:3,levels(fact)))
mat
cont.emmc <- user.cont(mat)
EMM <- emmeans(model,~fact)
contrast(EMM,"cont")
```

`wald.ptheo.multinom.test` *Wald tests for comparison of proportions to theoretical values*

Description

Performs pairwise comparisons of proportions to theoretical values.

Usage

```
wald.ptheo.multinom.test(x, p, p.method = "fdr")
```

Arguments

`x`	either a factor or a matrix with K columns giving the counts for each of the K classes.
`p`	theoretical proportions.
`p.method`	method for p-values correction. See help of `p.adjust`.

Details

The function builds K logistic regressions (in each case considering one class vs. the sum of all others) and uses `wald.ptheo.test` to test the hypothesis that the proportion of this class is equal to `p[K]`.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`observed`	observed proportions.
`expected`	theoretical proportions.
`p.adjust.method`	method for p-values correction.
`statistic`	statistics of each test.
`p.value2`	corrected p-values.
`p.value`	data frame of results.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`wald.ptheo.test`, `prop.multinom`

Examples

```
response <- factor(rep(LETTERS[1:4],c(20,40,42,13)))
wald.ptheo.multinom.test(response,p=c(0.15,0.25,0.3,0.3))
```

`wald.ptheo.test` *Wald test for comparison of a proportion to a theoretical value*

Description

Performs a Wald test for comparison of a proportion to a theoretical value.

Usage

```
wald.ptheo.test(y, blocks = NULL, p = 0.5)
```

Arguments

`y`	either a binary response (numeric vector or factor, with only two possible values except NA) or a two-column matrix with the columns giving the numbers of successes (left) and failures (right).
`blocks`	optional blocking (random) factor.
`p`	hypothesized probability of success.

Details

The function builds a logistic (mixed) regression and applies a Wald test to compare the estimated value of the intercept to its theoretical value under H0. Eventual overdispersion is taken into account, by using a quasi-binomial law in case of no blocks or by introducing an individual-level random factor if blocks are present.

If the response is a 0/1 vector, the probability of the '1' group is tested. With other vectors, the response is transformed into a factor and the probability of the second level is tested.

If the response is a two-column matrix, the probability of the left column is tested.

If the reponse is a vector and no blocking factor is present, the exact binomial test performed by `binom.test` should be preferred since it is an exact test, whereas the Wald test is an approximate test.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`statistic`	test statistics of the test.
`p.value`	p-value of the test.
`estimate`	the estimated proportion (calculated without taking into account the blocking factor, if present).
`alternative`	a character string describing the alternative hypothesis, always `"two.sided"`.
`null.value`	the value of the proportion under the null hypothesis.
`parameter`	the degrees of freedom for the t-statistic, only whith overdispersion and no blocks.

Author(s)

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See Also

`binom.test`, `glm`, `glmer`

Examples

```
set.seed(2006)
response <- sample(0:1,60,replace=TRUE)

# Comparison to p=0.5
wald.ptheo.test(response)

# Comparison to p=0.8
wald.ptheo.test(response,p=0.8)

# With a blocking factor

require(lme4)
blocks <- gl(3,20)
wald.ptheo.test(response,blocks)
```

`wilcox.paired.multcomp`
Non parametric pairwise comparisons for paired data

Description

Performs non parametric pairwise comparisons of paired samples by Wilcoxon signed rank tests for paired data.

Usage

```
wilcox.paired.multcomp(formula, data, p.method = "fdr")
```

Arguments

`formula`	a formula of the form `a ~ b	c`, where `a`, `b` and `c` give the data values and corresponding groups and blocks, respectively.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`p.method`	method for p-values correction. See help of `p.adjust`.

Value

`method`	name of the test.
`data.name`	a character string giving the name(s) of the data.
`method`	a character string indicating the name of the test.
`p.adjust.method`	method for p-values correction.
`p.value`	table of results of pairwise comparisons.

Author(s)

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See Also

`pairwise.wilcox.test`, `wilcox.test`

Examples

```
response <- c(rnorm(10,0,3),rnorm(10,5,3),rnorm(10,8,2))
fact <- gl(3,10,labels=LETTERS[1:3])
block <- gl(10,1,30,labels=letters[1:10])
friedman.test(response~fact|block)
wilcox.paired.multcomp(response~fact|block)
```

`wilcox.signtest` *Wilcoxon sign test*

Description

Performs a Wilcoxon sign test to compare medians of two paired samples or one median to a given value.

Usage

```
wilcox.signtest(x, ...)

## Default S3 method:
wilcox.signtest(x, y = NULL, mu = 0, conf.level = 0.95, ...)

## S3 method for class 'formula'
wilcox.signtest(formula, data, subset, ...)
```

Arguments

`x`	a numeric vector of data values.
`y`	an optional numeric vector of data values (for paired two-sample test).
`mu`	theoretical median (one-sample test) or theoretical median of `x-y` differences.
`conf.level`	confidence level of the interval.
`formula`	a formula of the form `a ~ b`, where `a` and `b` give the data values and corresponding groups.
`data`	an optional data frame containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`subset`	an optional vector specifying a subset of observations to be used.
`...`	further arguments to be passed to or from other methods.

Details

If zeroes (i.e. null differences with `mu`) are present, the median of the data different from `mu` is tested in the one-sample situation; the median of the `x-y` differences different from `mu` in the two-sample situation.

Value

`method`	a character string indicating the name of the test.
`data.name`	a character string giving the name(s) of the data.
`null.value`	the specified hypothesized value of the median or median difference depending on the test performed.
`p.value`	the p-value of the test.
`alternative`	a character string giving the alternative hypothesis, always `"two.sided"`
`estimate`	the estimated median or median of `x-y` differences, depending on the test performed.
`conf.int`	a confidence interval for the median tested.

Author(s)

Maxime HERVE <maxime.herve@univ-rennes1.fr>

See Also

`wilcox.test`

Examples

```
set.seed(1706)
response <- c(rnorm(7,3,1.5),rnorm(7,5.5,2))

# Comparison of 2 samples
fact <- gl(2,7,labels=LETTERS[1:2])
wilcox.signtest(response~fact)

# Comparison to a given value
theo <- 4
wilcox.signtest(response,mu=theo)
```

`wmean` *Weighted arithmetic mean*

Description

Computes the weighted arithmetic mean of a vector.

Usage

```
wmean(x, w = rep(1, length(x)), na.rm = TRUE)
```

Arguments

`x`	numeric vector.
`w`	numeric vector of weights.
`na.rm`	a logical value indicating whether `NA` values should be stripped before the computation proceeds.

Author(s)

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Examples

```
mean(1:10)
wmean(1:10,w=10:1)
```

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