

# Package: RVAideMemoire (via r-universe)

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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.

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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**

Package: RVAideMemoire  
Type: Package  
Version: 0.9-83-7  
Date: 2023-11-06  
License: GPL-2  
LazyLoad: yes

**Author(s)**

Maxime HERVE

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

**References**

Document : "Aide-memoire de statistique appliquee a la biologie - Construire son etude et analyser les resultat 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 [adonis](#) but performs type II tests (whereas [adonis](#) performs type I).

**Usage**

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

**Arguments**

formula	a typical model formula such as $Y \sim A+B*C$ , 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 <a href="#">adonis</a> . See help of this function.

**Details**

See [adonis](#) for detailed explanation of what is done. The only difference with [adonis](#) 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:
adonis(dune~Management*A1,data=dune.env,permutations=99)
adonis(dune~A1*Management,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 <a href="#">Anova</a> . 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](#), [c1m](#), [c1mm](#)

---

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 <a href="#">emmeans</a> .
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 ( <i>e.g.</i> 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 <a href="#">p.beta</a> .
C	number of categories from which initial continuous proportions were computed. Only used with transform="p.beta", see <a href="#">p.beta</a> .
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 <a href="#">boot</a> . 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 $a \sim b$ 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 <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
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 $a \sim b$ , 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	<i>Shapiro-Wilk test for factor levels</i>
--------------	--

---

**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 $a \sim b$ 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 <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .

**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 $a \sim b$ 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 <code>environment(formula)</code> .
...	other arguments to pass to <a href="#">qqPlot</a> .

**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 $a \sim b$ 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 <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .

**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 <a href="#">predict.coadisc</a> .

**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 <code>nlevels(fact)-1</code> are used. See Details.
...	other arguments to pass to <a href="#">summary.manova</a> . 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**

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

**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 $a \sim b$ , 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 <code>environment(formula)</code> .
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  $\geq 5$ ).

**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 $a \sim b$ , 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 <code>environment(formula)</code> .
correct	a logical indicating whether to apply continuity correction when computing the test statistic for 2 by 2 tables. See help of <a href="#">chisq.test</a> .
alpha	significance level to compute pairwise comparisons.
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .

**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  $\geq 5$ ).

**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 <a href="#">p.adjust</a> .

**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	<i>Pearson's Chi-squared test for comparison of response probabilities to given values</i>
--------------------	--

---

**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 $a \sim b$ , 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 <code>environment(formula)</code> .
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 <a href="#">p.adjust</a> .

**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 $a \sim b \mid c$ , 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 <a href="#">p.adjust</a> .

**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	<i>Condition number of the Hessian matrix of a multinomial log-linear model</i>
---------------	---

---

**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	<i>Coordinates of projected points</i>
------------	--

---

**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 <a href="#">p.adjust</a> .

**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 whether the (square) covariance is higher than expected under random association between the two datasets. The test is relevant parallel to a 2B-PLS.

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

<code>method</code>	a character string indicating the name of the test.
<code>data.name</code>	a character string giving the name(s) of the data, plus additional information.
<code>statistic</code>	the value of the test statistics.
<code>permutations</code>	the number of permutations.
<code>p.value</code>	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	<i>Cramer's association coefficient</i>
-------------	---

---

**Description**

Computes the Cramer's association coefficient between 2 nominal variables, its confidence interval (by bootstrapping) 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 bootstrapping.  
 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	<i>Dendrogram and number of groups to be chosen</i>
-----------	---

---

**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	<i>Deprecated functions in RVAideMemoire package</i>
------------	--

---

**Description**

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

## Usage

```
back.lsmmeans(...)  
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.lsmmeans(...)  
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.lsmmeans` and `rating.lsmmeans` 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

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

## Details

The function uses the weighted predicted classification error rate (see [perf](#)).

## Value

<code>repet</code>	number of times the whole procedure was repeated.
<code>k</code>	number of folds.
<code>validation</code>	kind of validation used.
<code>ncomp</code>	number of components used.
<code>method</code>	criterion used to classify individuals of the test sets.
<code>NMC.mean</code>	mean classification error rate (based on <code>repet</code> values).
<code>NMC.se</code>	standard error of the classification error rate (based on <code>repet</code> 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 <a href="#">perf</a> .
validation	a character giving the kind of (internal) validation to use. See <a href="#">perf</a> .
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 <a href="#">perf</a> .

**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	<i>Empirical logistic transformation</i>
--------	--

---

**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	<i>Fisher's exact test for binary variables</i>
----------------	---

---

**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 $a \sim b$ , 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 <code>environment(formula)</code> .
alpha	significance level to compute pairwise comparisons.
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .

**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(0,0,0,0,0,0,1,0,0,0,0,0,1,0,1,1,1,0,0,1,1,1,1,1,0,0,1,1,1)
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	<i>Fligner-Policello test</i>
---------	-------------------------------

---

### 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 $a \sim b$ , 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 <code>environment(formula)</code> .
alpha	significance level to compute pairwise comparisons.
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .

**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**

<code>x</code>	numeric vector (counts).
<code>p.method</code>	method for p-values correction. See help of <a href="#">p.adjust</a> .

**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**

<code>method</code>	name of the test.
<code>data.name</code>	a character string giving the name(s) of the data.
<code>p.adjust.method</code>	method for p-values correction.
<code>p.value</code>	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**

Performs 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 <a href="#">p.adjust</a> .

**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 variables), 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 limited 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  $y \sim x$ , where  $y$  and  $x$  give the  $y$  and  $x$  variable, respectively. The formula can also be  $y \sim x | f$  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 adjustment 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	<a href="#">glm</a> model.
int	number of intervals.
...	other arguments. See help of <a href="#">points</a> and <a href="#">segments</a> .

**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	<i>Creating a nls model for logistic regression from fitted values of a glm model</i>
-------------	---

---

**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	<code>glm</code> 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	<i>Mode</i>
-----	-------------

---

**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 extension, 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 $a \sim b$ , where $a$ and $b$ give the data values and corresponding groups.
data	an optional data frame containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
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 chi-square test).
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic (in case of a chi-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)
```

---

mqnorm

*Multivariate normality QQ-Plot*


---

### Description

Draws a QQ-plot to assess multivariate normality.

### Usage

```
mqnorm(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 assess multivariate normality. This is a slightly modified copy of the [mshapiro.test](#) function of the package mvnrmtest, 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 <code>table(x)</code> is used as counts.
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .

### 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	<i>Exact multinomial test</i>
------------------	-------------------------------

---

### Description

Performs 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 <code>table(x)</code> 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 <code>table(x)</code> 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 <a href="#">p.adjust</a> .

**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 <a href="#">cor</a> .
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .
ordered	logical indicating if variables should be ordered based on correlation values.
x	object returned from <code>multtest.cor</code> .
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 <a href="#">dotchart</a> ).

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 <code>mult.var</code> .
...	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 <a href="#">p.adjust</a> .
ordered	logical indicating if variables should be ordered based on p-values.
x	object returned from <code>multtest.gp</code> .
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 <code>multtest.gp</code> (especially for <code>var.equal</code> in <a href="#">t.test</a> and <code>nperm</code> in <a href="#">perm.anova</a> and <a href="#">perm.t.test</a> ) and to <a href="#">barplot</a> in <code>plot</code> .

**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 <a href="#">p.adjust</a> .
ordered	logical indicating if variables should be ordered based on p-values.
x	object returned from <code>multtest.gp.bin</code> .
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 <code>multtest.gp.bin</code> (especially for <a href="#">Anova</a> and <a href="#">fisher.test</a> ) and to <a href="#">barplot</a> in <code>plot</code> .

### Author(s)

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

### See Also

[multtest.gp](#), [Anova](#), [fisher.test](#)

---

MVA.anova	<i>Type II permutation test for constrained multivariate analyses</i>
-----------	---

---

**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**

<code>object</code>	a result object from <code>cca</code> , <code>rda</code> , <code>capscale</code> or <code>dbrda</code> .
<code>...</code>	additional arguments to <code>anova.cca</code> (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)**

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

---

MVA.biplot	<i>Biplot of multivariate analyses</i>
------------	--

---

**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 <a href="#">MVA.scoreplot</a> ).
sco.set	scores to be displayed, when several sets are available (see <a href="#">MVA.scoreplot</a> ).
cor.set	correlations to be displayed, when several sets are available (see <a href="#">MVA.scoreplot</a> ).
space	space to use, when several are available (see <a href="#">MVA.scoreplot</a> and <a href="#">MVA.corplot</a> ).
ratio	constant for adjustment 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 <a href="#">MVA.scoreplot</a> . All arguments are accepted.
cor.args	list containing optional arguments to pass to <a href="#">MVA.corplot</a> . 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 <a href="#">cppls.fit</a> ).
upper	a vector of upper limits for power optimisation in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
Y.add	a vector or matrix of additional responses containing relevant information about the observations, in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).

<code>weights</code>	a vector of individual weights for the observations, in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
<code>set.prior</code>	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.
<code>crit.DA</code>	criterion used to predict class membership when a second analysis (LDA or QDA) is used. See <a href="#">predict.lda</a> .
<code>...</code>	other arguments to pass to <a href="#">plsr</a> (PLSR, PLS-DA) or <a href="#">cppls</a> (CPPLS, PPLS-DA).

### Details

Cross model validation is detailed in 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

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

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

**Author(s)**

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

**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 <code>length(xax) &gt; 1</code> ).
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.rgccca`. Space can be 1 to n, the number of blocks (i.e. datasets).
- sGCCA: `wrapper.sgccca`. 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.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 <a href="#">dotchart</a> ).
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 <a href="#">dhist</a> ).
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.rgccca`. 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, "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 <a href="#">cppls.fit</a> ).
upper	a vector of upper limits for power optimisation in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
Y.add	a vector or matrix of additional responses containing relevant information about the observations, in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
weights	a vector of individual weights for the observations, in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
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 <a href="#">predict.lda</a> .
...	other arguments to pass to <a href="#">pls</a> (PLSR, PLS-DA) or <a href="#">cppls</a> (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.rgccca](#). Space can be 1 to n, the number of blocks (i.e. datasets).
- sGCCA: [wrapper.sgccca](#). 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.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 <a href="#">MVA.scoreplot</a> ). 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 <a href="#">MVA.scoreplot</a> .
space	scores to be displayed, when several spaces are available (see Details of <a href="#">MVA.scoreplot</a> ). 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 <code>dhist</code> .

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

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### 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 <code>length(xax) &gt; 1</code> ).
scaling	type of scaling. Only available with some analyses performed with the <code>vegan</code> 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 one 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)

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### 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 explained 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 <a href="#">MVA.cv</a> and <a href="#">MVA.cmv</a> .
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 <a href="#">cppls.fit</a> ).
upper	a vector of upper limits for power optimisation in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
Y.add	a vector or matrix of additional responses containing relevant information about the observations, in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
weights	a vector of individual weights for the observations, in CPPLS or PPLS-DA (see <a href="#">cppls.fit</a> ).
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 <a href="#">predict.lda</a> .
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .
nperm	number of permutations.
progress	logical indicating if the progress bar should be displayed.
...	other arguments to pass to <a href="#">pls</a> (PLSR, PLS-DA) or <a href="#">cppls</a> (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 limited 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)**

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**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 <a href="#">MVA.scoreplot</a> .
set	scores to be displayed, when several sets are available (see Details of <a href="#">MVA.scoreplot</a> ). 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 <a href="#">MVA.scoreplot</a> ). 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	<i>Odds-ratio (multinomial regression)</i>
-------------	--

---

**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**

<code>model</code>	object of class "multinom".
<code>variable</code>	any predictor present in model (unquoted).
<code>conf.level</code>	confidence level.

**Author(s)**

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

---

ord.rw	<i>Re-computation of an ordination using given row weights</i>
--------	--

---

**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**

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

**Author(s)**

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

---

overdisp.glmmer      *Estimation of overdispersion with [glmmer](#) models*

---

### Description

Estimates residual deviance and residual degrees of freedom to check for overdispersion with [glmmer](#) models. This function is directly coming from <http://glmm.wikidot.com/faq>.

### Usage

```
overdisp.glmmer(model)
```

### Arguments

model      a model fitted by [glmmer](#).

### Author(s)

Ben Bolker

### See Also

[glmmer](#)

### Examples

```
require(lme4)

# Example from the 'glmmer' function
gm1 <- glmmer(cbind(incidence,size-incidence)~period+(1|herd),
  family="binomial",data=cbpp)
overdisp.glmmer(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 & Wee-don 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 <a href="#">p.adjust</a> .
...	other arguments to pass to <a href="#">CDA.test</a> .

**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 <a href="#">MVA.scores</a> .
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 <a href="#">p.adjust</a> .
...	optional further arguments to <a href="#">MVA.scores</a> .

**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	<i>Pairwise comparisons for proportions using G-tests</i>
-----------------	---

---

### 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 <a href="#">p.adjust</a> .

### 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 <a href="#">p.adjust</a> .

### 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 <a href="#">p.adjust</a> .
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 <a href="#">MVA.test</a> .

### Details

The function deals with the limited 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 [adonis](#).

**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 <a href="#">anova.mlm</a> ).
nperm	number of permutations.
progress	logical indicating if the progress bar should be displayed.
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .
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 limited floating point precision, which can bias calculation of p-values based on a discrete test statistic distribution.

If resp is a distance matrix, [adonis](#) 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](#), [adonis](#)

**Examples**

```
require(vegan)
data(iris)

# permutation MANOVA
adonis(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 <a href="#">p.adjust</a> .
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 limited 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 <a href="#">p.adjust</a> .
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 limited 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 <a href="#">p.adjust</a> .
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 <a href="#">cor</a> .
method	same as method of <a href="#">cor</a> .

**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	<i>Tests for (semi-)partial association/correlation between paired samples</i>
-----------	--

---

**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 bootstrapping).
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 bootstrapping, 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 confidence 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	the 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 limited 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 $a \sim b$ where $a$ gives the data values and $b$ the corresponding groups.
data	an optional data frame containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
nperm	number of permutations.
progress	logical indicating if the progress bar should be displayed.

**Details**

The function deals with the limited 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**

<code>x, y</code>	numeric vectors of data values. <code>x</code> and <code>y</code> must have the same length.
<code>alternative</code>	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less".
<code>nperm</code>	number of permutations.
<code>progress</code>	logical indicating if the progress bar should be displayed.

**Details**

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

**Value**

<code>method</code>	name of the test.
<code>data.name</code>	a character string giving the name(s) of the data.
<code>statistic</code>	test statistics of the parametric test.
<code>permutations</code>	number of permutations.
<code>p.value</code>	p-value of the permutation test.
<code>estimate</code>	the estimated correlation coefficient.
<code>alternative</code>	a character string describing the alternative hypothesis.
<code>null.value</code>	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	<i>Permutation Student's t-test</i>
-------------	-------------------------------------

---

### 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 limited 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 $a \sim b$ 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 limited 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 <sup>2</sup> 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](#), [mqnorm](#), [mshapiro.test](#)

---

plotsurvivors	<i>Survivor curve</i>
---------------	-----------------------

---

**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	<i>Variable Importance in the Projection (VIP)</i>
-----------	--

---

**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

<code>object</code>	object of class inheriting from "MVA.cv" or "MVA.cmv".
<code>newdata</code>	vector, matrix or data frame giving new individuals (one row per individual).
<code>conf.level</code>	confidence level for prediction of a quantitative response.
<code>type.DA</code>	for discriminant analyses, should the probability of the most probable class be given ("max", the default) or the probability of each class ("all")?
<code>crit.DA</code>	criterion used to predict class membership when a LDA or QDA is used. See <a href="#">predict.lda</a> .
<code>...</code>	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 $a \sim b$ , 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 <code>environment(formula)</code> .
p	theoretical probabilities.
p.method	method for p-values correction. See help of <a href="#">p.adjust</a> .

### 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 <a href="#">p.adjust</a> .

**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  $\geq 2$ , 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 different 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  $\geq 2$  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 <code>emmeans</code> applied on a <code>clm</code> or <code>clmm</code> 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 <code>type</code> ).

**Details**

A factor named `cut` must have been called in `emmeans`, to compute EMMs 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 EMMs have to be computed.

**Author(s)**

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

**See Also**

[emmeans](#), [clm](#), [clmm](#)

**Examples**

```
require(ordinal)
require(emmeans)

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 ( $F_i$ is frequency of ratings $\leq i$ ) and "class" gives the most frequent rating.

**Author(s)**

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

**Examples**

```
require(ordinal)
data(wine)

# 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 arguments. See help of <a href="#">lines</a> .

**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	<i>Sequence generation</i>
------	----------------------------

---

**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	<i>Confidence interval of a Spearman's rank correlation coefficient</i>
-------------	---

---

**Description**

Computes the confidence interval of a Spearman's rank correlation coefficient by bootstrapping.

**Usage**

```
spearman.ci(var1, var2, nrep = 1000, conf.level = 0.95)
```

**Arguments**

var1	numeric vector (first variable).
var2	numeric vector (second variable).
nrep	number of replicates for bootstrapping.
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 bootstrapping.

**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 bootstrapping.

**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 bootstrapping.

**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 it 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 column 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 <a href="#">p.adjust</a> .

## 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  $H_0$ . 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 response 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 with overdispersion and no blocks.

**Author(s)**

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

**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)**

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

**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)**

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

**Examples**

```
mean(1:10)
wmean(1:10,w=10:1)
```



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