Package ‘RVAideMemoire’

January 7, 2020

Encoding  latin1
Type   Package
Title   Testing and Plotting Procedures for Biostatistics
Version 0.9-74
Date 2020-01-04
Author Maxime Hervé
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biocViews

Imports ade4 (>= 1.7-8), boot, car, FactoMineR, graphics, grDevices,
   lme4 (>= 1.0-4), MASS, mixOmics, nnet, pls, pspearman, stats,
   utils, vegan (>= 2.4-3)

Suggests dgof, emmeans, ordinal, survival

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

License GPL-2
LazyLoad yes
NeedsCompilation no
Repository CRAN
Date/Publication 2020-01-07 20:20:28 UTC

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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.

Details

Package: RVAideMemoire
Type: Package
Version: 0.9-74
Date: 2020-01-04
License: GPL-2
LazyLoad: yes

Author(s)

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


**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

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

### Arguments

- **formula**: a typical model formula such as `Y~A+B*C`, but where `Y` is either a dissimilarity object (inheriting from class "dist") or data frame or a matrix; `A`, `B`, and `C` may be factors or continuous variables.
- **data**: the data frame from which `A`, `B` and `C` would be drawn.
- **...**: additional arguments to `adonis`. 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 Hervé <mx.herve@gmail.com>

### Examples

```r
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)
```
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

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

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

Arguments

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

Details

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

Value

See `Anova`.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

`Anova, clm, clmm`
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.

Usage

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

Arguments

- `emm` object returned by `emmeans`.
- `transform` transformation applied to the response variable before building the model on which `emm` is based ("4rt" is fourth-root).
- `base` the base with respect to which the logarithm transformation was computed (if `transform="log"`). Defaults to $e=\exp(1)$.
- `add` value to be added to $x$ before computing the transformation, if needed (e.g. 1 if the initial transformation was $\log(x+1)$).
- `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 Hervé <mx.herve@gmail.com>

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)
```
Description

Simplified version of the `boot` function.

Usage

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

Arguments

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

Details

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

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

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

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

Arguments

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

hist

Examples

data(iris)
byf.hist(Sepal.Length~Species,data=iris)
byf.mqqnorm  QQ-plot for factor levels

Description

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

Usage

byf.mqqnorm(formula, data)

Arguments

formula  a formula of the form a ~ b, where a is a matrix giving the dependent variables (each column giving a variable) and b a factor giving the corresponding groups.

data  an optional data frame containing the variables in the formula formula. By default the variables are taken from environment(formula).

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

mqqnorm, byf.mshapiro, qqPlot

Examples

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

byf.mshapiro  Shapiro-Wilk test for factor levels

Description

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

Usage

byf.mshapiro(formula, data)
byf.qqnorm

Arguments

<table>
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<th>Argument</th>
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<tr>
<td>formula</td>
<td>a formula of the form a ~ b where a is a matrix giving the dependent variables (each column giving a variable) and b a factor giving the corresponding groups.</td>
</tr>
<tr>
<td>data</td>
<td>an optional data frame containing the variables in the formula formula. By default the variables are taken from environment(formula).</td>
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</tbody>
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Value

<table>
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<tr>
<th>Argument</th>
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<td>data.name</td>
<td>a character string giving the names of the data.</td>
</tr>
<tr>
<td>tab</td>
<td>table of results.</td>
</tr>
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</table>

Author(s)

Maxime Hervé <mx.herve@gmail.com>

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>formula</td>
<td>a formula of the form a ~ b where a gives the data values and b a factor giving the corresponding groups.</td>
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</tr>
<tr>
<td>...</td>
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Author(s)

Maxime Hervé <mx.herve@gmail.com>
See Also

link[RVAideMemoire]{byf.shapiro}, qqPlot

Examples

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

byf.shapiro       Shapiro-Wilk test for factor levels

Description

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

Usage

byf.shapiro(formula, data)

Arguments

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

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

byf.qqnorm, shapiro.test

Examples

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

Performs cross validation with correspondence discriminant analyses.

Usage

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

Arguments

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

Details

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

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>
CDA.test

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

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

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

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

Value
An ANOVA or MANOVA table.

Author(s)
Maxime Hervé <mx.herve@gmail.com>

See Also
discrimin.coa, summary.manova
cdf.discrete

Examples

```r
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

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

Arguments

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

Details

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

Examples

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

Expected counts for comparison of response probabilities to given values

Description

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

Usage

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

Arguments

formula a formula of the form a ~ b, where a and b give the data values and corresponding groups, respectively. a can be a numeric vector or a factor, with only two possible values (except NA).

data an optional data frame containing the variables in the formula formula. By default the variables are taken from environment(formula).

p theoretical probabilities.

graph logical. If TRUE a mosaic plot of expected counts is drawn.

Details

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

Value

p.theo theoretical probabilities.

mat contingency table of expected counts.

cochran number of counts which can be < 5.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

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

```r
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)
```

### 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

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

### Arguments

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

### Details

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

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

### Value

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

Author(s)
Maxime Hervé <mx.herve@gmail.com>

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

- \texttt{p.theo} theoretical proportions.
- \texttt{mat} contingency table of expected counts.
- \texttt{cochran} number of counts which can be < 5.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

\texttt{prop.test}, \texttt{chisq.test}, \texttt{mosaicplot}

Examples

```r
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 \hspace{1cm} \textit{Pairwise comparisons after a chi-squared goodness-of-fit test}

Description

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

Usage

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

Arguments

- \texttt{x} numeric vector (counts).
- \texttt{p.method} method for \( p \)-values correction. See help of \texttt{p.adjust}.

Details

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

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 Hervé <mx.herve@gmail.com>

See Also

chisq.test, multinomial.test, multinomial.multcomp

Examples

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

chisq.theo.bintest

Pearson’s Chi-squared test for comparison of response probabilities to given values

Description

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

Usage

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

Arguments

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

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

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

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

Examples

```r
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.multcomp(response~fact,p=p.theo)
```

Description

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

Usage

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

Arguments

- `x` numeric vector (counts).
- `p` theoretical proportions.
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 Hervé <mx.herve@gmail.com>

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

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

Arguments

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

Details

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

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

Examples

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

**Condition number of the Hessian matrix of a multinomial log-linear model**

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

**Usage**
```
cond.multinom(model)
```

**Arguments**
- `model` object of class "multinom".

**Author(s)**
Maxime Hervé <mx.herve@gmail.com>

### coord.proj

**Coordinates of projected points**

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

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

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

**Author(s)**
Maxime Hervé <mx.herve@gmail.com>
**Examples**

```r
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 significative, the function returns the common coefficient, its confidence interval and performs the test for equality to a given value.

**Usage**

```r
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 Hervé <mx.herve@gmail.com>

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 Hervé <mx.herve@gmail.com>

**See Also**

- cor.test

**Examples**

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

---

**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 difference is significative, the functions performs pairwise comparisons between coefficients.

**Usage**

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

**Arguments**

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

**cor.multcomp**

*Comparison of several Pearson’s linear correlation coefficients*
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 Hervé <mx.herve@gmail.com>

See Also

cor.test

Examples

```r
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)
```

```r
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)
```
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

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

Details

The function deals with the 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 Hervé <mx.herve@gmail.com>
**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**

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

**Arguments**

- `model`: a `coxph` model.

**Author(s)**

Maxime Hervé <mx.herve@gmail.com>, based on an idea of John Fox.

**References**

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

**See Also**

`coxph`

**Examples**

```r
# '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 Cramér’s association coefficient between 2 nominal variables.

**Usage**

```r
cramer(x, y)
```
cramer.test

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 Hervé <mx.herve@gmail.com>

Examples

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

cramer.test Cramer's association coefficient

Description

Computes the Cramér’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 Cramér’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 Hervé <mx.herve@gmail.com>

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

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 Hervé <mx.herve@gmail.com>

Examples
cv(rnorm(30))
Dendrogram and number of groups to be chosen

Description

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

Usage

dendro.gp(dend)

Arguments

dend  a dendrogram obtained from hclust.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

hclust

Examples

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

deprecated

Deprecated functions in RVAideMemoire package

Description

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

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

Arguments

... previous arguments.

Details

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

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

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

CvM.test did actually not perform a Cramer-von Mises test but an alternative Cramer test. Use cramer.test 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

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

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

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

#### Value
- **repet**: number of times the whole procedure was repeated.
- **k**: number of folds.
- **validation**: kind of validation used.
- **ncomp**: number of components used.
- **method**: criterion used to classify individuals of the test sets.
- **NMC.mean**: mean classification error rate (based on `repet` values).
- **NMC.se**: standard error of the classification error rate (based on `repet` values).
**Author(s)**
Maxime Hervé <mx.herve@gmail.com>

**See Also**
`block.plsda`, `block.splsda`, `perf`

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

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

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

**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 Hervé <mx.herve@gmail.com>

**See Also**

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

**Examples**

```r
## 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**

```r
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 Hervé <mx.herve@gmail.com>
Examples
fac <- gl(3,5,labels=LETTERS[1:3])
dummy(fac)

fisher.bintest  
Fisher's exact test for binary variables

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

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

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

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.
**fisher.multcomp**

- **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 Hervé <mx.herve@gmail.com>

**See Also**

chisq.bintest, G.bintest

**Examples**

```r
response <- c(0,0,0,0,0,0,0,1,0,0,0,1,0,1,1,0,1,1,0,1,1,1,0,0,1,1,1)
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**

```r
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).
fp.test

Fligner-Policello test

Description

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

Usage

fp.test(x, ...)

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

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

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

Details

The Fligner-Policello test does not assume that the shape of the distribution is similar in two groups, contrary to the Mann-Whitney-Wilcoxon test. However, it assumes that the 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 Hervé <mx.herve@gmail.com> based on `fp.test`

See Also

`fp.test`, `wilcox.test`

Examples

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

G-test for binary variables

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

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

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

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.
**Description**

Performs pairwise comparisons after a global G-test.

**Usage**

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

**Arguments**

- `x` numeric vector (counts).

**Details**

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

**Value**

- `method` name of the test.
- `data.name` a character string giving the name(s) of the data.
- `p.adjust.method` method for p-values correction.
- `p.value` table of results.
Author(s)
Maxime Hervé <mx.herve@gmail.com>

See Also
G.test, multinomial.test, multinomial.multcomp

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

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 coloums, 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 Hervé <mx.herve@gmail.com>

See Also

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

Examples

```r
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

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

Arguments

- `x` numeric vector (counts).
- `p` theoretical proportions.

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 Hervé <mx.herve@gmail.com>

See Also

- `G.test`
- `multinomial.test`
- `multinomial.theo.multcomp`

Examples

```r
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)
```

Description

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

Usage

```r
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.
- **nb.iteration**: the maximum number of iterations until the algorithm stops.
- **scale**: logical, if TRUE (default) scaling is required.
- **n.perm**: 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 Hervé <mx.herve@gmail.com>

References


See Also

- GPA

Examples

```r
require(FactoMineR)
data(wine)

## Not run: GPA.test(wine[,-(1:2)], group=c(5,3,10,9,2))
```
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 Hervé <mx.herve@gmail.com>

See Also

lm.influence, least.rect

Examples

```r
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)
```
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 \( y \sim x \mid f \) to fit a (separate) regression for each level of the factor \( f \).
- **data**: an optional data frame containing the variables in the formula \( \text{formula} \). By default the variables are taken from \( \text{environment(\text{formula})} \).
- **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 Hervé <mx.herve@gmail.com>
Examples

```r
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**

```r
loc.slp()
```

**Author(s)**

Maxime Hervé <mx.herve@gmail.com>

---

### logis.fit

**Graphical adjsutment 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**

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

**Arguments**

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

Author(s)
Maxime Hervé <mx.herve@gmail.com>

See Also
glm

Examples

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

logis.noise

Creating a nls model for logistic regression from fitted values of a glm model

Description

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

Usage

logis.noise(model, intensity = 25)

Arguments

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

Author(s)
Maxime Hervé <mx.herve@gmail.com>

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(...))
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 Hervé <mx.herve@gmail.com>

See Also

density

Examples

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

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

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

**Mood’s median test**

**Description**

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

**Usage**

mood.medtest(x, ...)

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

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

**Arguments**

- **x**
  - a numeric vector of data values.
- **g**
  - a vector or factor object giving the group for the corresponding elements of x.
- **exact**
  - a logical indicating whether an exact p-value should be computed.
- **formula**
  - a formula of the form a ~ b, where a and b give the data values and corresponding groups.
- **data**
  - an optional data frame containing the variables in the formula formula. By default the variables are taken from environment(formula).
- **subset**
  - an optional vector specifying a subset of observations to be used.
- **...**
  - further arguments to be passed to or from other methods.

**Details**

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

**Value**

- **method**
  - a character string indicating the name of the test.
- **data.name**
  - a character string giving the name(s) of the data.
- **statistic**
  - the value the chi-squared test statistic (in case of a 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 Hervé <mx.herve@gmail.com>

Examples

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

---

mqqnorm

**Multivariate normality QQ-Plot**

---

**Description**

Draws a QQ-plot to assess multivariate normality.

**Usage**

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

**Arguments**

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

**Author(s)**

Maxime Hervé <mx.herve@gmail.com>

**See Also**

`mshapiro.test`, `qqPlot`

**Examples**

```r
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 mvnormtest, for internal convenience.

Usage

mshapiro.test(x)

Arguments

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

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com> 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))
**Description**

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

**Usage**

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

**Arguments**

- `x`: numeric vector (counts). Can also be a factor; in that case `table(x)` is used as counts.

**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 Hervé <mx.herve@gmail.com>

**See Also**

- `multinomial.test`, `binom.test`

**Examples**

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

**Exact multinomial test**

**Description**

Performs an exact multinomial test on a vector of counts.

**Usage**

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

**Arguments**

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

**Details**

The function works as `chisq.test` or `G.test`:
- if theoretical proportions are not given, equality of counts is tested
- if theoretical proportions are given, equality of counts to theoretical counts (given by theoretical proportions) is tested.

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

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

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

**Value**

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

**Author(s)**

Maxime Hervé <mx.herve@gmail.com> based on `multinomial.test`

**See Also**

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

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

**Description**

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

**Usage**

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

**Arguments**

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

**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.
multtest.cor

Author(s)
Maxime Hervé <mx.herve@gmail.com>

See Also
multinomial.test.binom.test

Examples

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

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

Usage

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

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

Arguments

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


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

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

```r
## 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, ...)
```
multtest.gp

Arguments

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

Details

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

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

Examples

```r
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

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

```r
## 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").
- `ordered` logical indicating if variables should be ordered based on p-values.
- `x` object returned from `multtest.gp.bin`.
- `signif` logical indicating if only variables with significant P-value should be plotted.
- `alpha` significance threshold.
- `vars` numeric vector giving variables to plot (rows of `x`). Default to all, which can lead to errors if too many variables.
- `xlab` legend of the x axis.
- `ylab` legend of the y axis
- `titles` titles of the graphs (name of the variables by default).
- `groups` names of the bars (levels of `fac` by default).
- `...` additional arguments to testing functions in `multtest.gp.bin` (especially for `Anova` and `fisher.test`) and to `barplot` in `plot`.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

- `multtest.gp`, `Anova`, `fisher.test`
MVA.anova

Type II permutation test for constrained multivariate analyses

Description

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

Usage

MVA.anova(object, ...)

Arguments

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

Details

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

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

Value

a data frame of class "anova".

Author(s)

Maxime Hervé <mx.herve@gmail.com>

MVA.biplot

Biplot of multivariate analyses

Description

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

Usage

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

- **x**: a multivariate analysis (see Details).
- **xax**: the horizontal axis.
- **yax**: the vertical axis.
- **scaling**: type of scaling (see `MVA.scoreplot`).
- **sco.set**: scores to be displayed, when several sets are available (see `MVA.scoreplot`).
- **cor.set**: correlations to be displayed, when several sets are available (see `MVA.scoreplot`).
- **space**: space to use, when several are available (see `MVA.scoreplot` and `MVA.corplot`).
- **ratio**: constant for 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 `MVA.scoreplot`. All arguments are accepted.
- **cor.args**: list containing optional arguments to pass to `MVA.corplot`. All arguments are accepted except `xlab`, `ylab`, `circle`, `intcircle`, `drawintaxes`, `add` and `add.const`.
- **f.col**: color(s) used for barycenters in case of a constraint analysis (RDA or CCA) containing factor constraint(s). Can be a unique value, a vector giving one color per constraint or a vector giving one color per barycenter (all factors confounded).
- **f.cex**: size(s) used for barycenters in case of a constraint analysis (RDA or CCA) containing factor constraint(s). Can be a unique value, a vector giving one size per constraint or a vector giving one size per barycenter (all factors confounded).

Details

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

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

Examples

```r
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"))
```
Description

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

Usage

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

Arguments

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

a vector of individual weights for the observations, in CPPLS or PPLS-DA (see \texttt{cppls.fit}).

set.prior

only used when a second analysis (LDA or QDA) is performed. If \texttt{TRUE}, the prior probabilities of class membership are defined according to the mean weight of individuals belonging to each class. If \texttt{FALSE}, prior probabilities are obtained from the data sets on which LDA/QDA models are built.

crit.DA

criterion used to predict class membership when a second analysis (LDA or QDA) is used. See \texttt{predict.lda}.

... other arguments to pass to \texttt{plsr} (PLSR, PLS-DA) or \texttt{cppls} (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 \texttt{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 \texttt{scale = TRUE}, the scaling is done as this:

- for each step of the outer loop (i.e. \texttt{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. \texttt{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**

<table>
<thead>
<tr>
<th>Model</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>model</td>
<td>model used.</td>
</tr>
<tr>
<td>type</td>
<td>type of model used.</td>
</tr>
<tr>
<td>repet</td>
<td>number of times the whole 2CV procedure was repeated.</td>
</tr>
<tr>
<td>kout</td>
<td>number of folds in the outer loop.</td>
</tr>
<tr>
<td>kinn</td>
<td>number of folds in the inner loop.</td>
</tr>
<tr>
<td>crit.inn</td>
<td>criterion used to choose the number of components in the inner loop.</td>
</tr>
<tr>
<td>crit.DA</td>
<td>criterion used to classify individuals of the test and validation sets.</td>
</tr>
<tr>
<td>Q2diff</td>
<td>threshold used if the number of components is chosen according to Q2.</td>
</tr>
<tr>
<td>groups</td>
<td>levels of ( Y ) if it is a factor.</td>
</tr>
</tbody>
</table>
models.list  list of of models generated (repet*kout models), for PLSR, CPPLS, PLS-DA and PPLS-DA.
models1.list  list of of (P)PLS-DA models generated (repet*kout models), for PLS-DA/LDA, PLS-DA/QDA, PPLS-DA/LDA and PPLS-DA/QDA.
models2.list  list of of LDA/QDA models generated (repet*kout models), for PLS-DA/LDA, PLS-DA/QDA, PPLS-DA/LDA and PPLS-DA/QDA.
RMSEP        RMSEP computed from the models used in the outer loops (repet values).
Q2           Q2 computed from the models used in the outer loops (repet values).
NMC          Classification error rate computed from the models used in the outer loops (repet values).
confusion    Confusion matrices computed from the models used in the outer loops (repet values).
pred.prob    Probability of each individual of being of each level of Y.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

References


See Also

predict.MVA.cmv, mvr, lda, qda

Examples

```
require(pls)
require(MASS)

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

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

*Correlations of multivariate analyses*

Description

Returns correlations of a multivariate analysis.

Usage

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

Arguments

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

Details

Many multivariate analyses are supported, from various packages:

- PCA: `dudi.pca`, `rda`.
- sPCA: `spca`.
- IPCA: `ipca`.
- sIPCA: `sipca`.
- LDA: `lda`, `discrimin`.
- PLS-DA (PLS2 on a dummy-coded factor): `plsdas` 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, pcaiivortho, rda. With rda, space 1 is constrained space, space 2 is unconstrained space. Only constrained space is available with pcaiv, the opposite for pcaiivortho. Set 1 is constraints (only quantitative constraints are extracted), set 2 is dependent variables (only set 2 is available for pcaiivortho). 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**: cointertia. 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, lwd can be defined differently for each set.

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

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

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

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

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

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

**Author(s)**

Maxime Hervé <mx.herve@gmail.com>
MVA.corplot

Correlation circle of multivariate analyses

Description
Displays a correlation circle of a multivariate analysis.

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

Arguments

x
  a multivariate analysis (see Details).

xax
  the horizontal axis.

yax
  the vertical axis. This can be set to NULL for a one-dimensional graph, which is a dotchart.

thresh
  threshold (in absolute value of the correlation coefficient) of variables to be plotted.

fac
  an optional factor defining groups of variables.

set
  variables to be displayed, when several sets are available (see Details). 12 (default) for both sets, 1 for X or constraints, 2 for Y or constrained variables.

space
  variables to be displayed, when several spaces are available (see Details). space is the number of the space to be plotted.

xlab
  legend of the horizontal axis. If NULL (default), automatic labels are used depending on the multivariate analysis.

ylab
  only used for two-dimensional graphs. Legend of the vertical axis. If NULL (default), automatic labels are used depending on the multivariate analysis.

main
  optional title of the graph.

circle
  only used for two-dimensional graphs. Logical indicating if the circle of radius 1 should be plotted.

intcircle
  only used for two-dimensional graphs. Vector of one or several values indicating radii of circles to be plotted inside the main circle. Can be set to NULL.

points
  only used for two-dimensional graphs. If FALSE, arrows or points (see arrows) are replaced with their corresponding label (defined by labels).

ident
  only used for two-dimensional graphs when points=TRUE. A logical indicating if variable names should be displayed.
arrows only used if points=TRUE. Logical indicating if arrows should be plotted. If FALSE, points are displayed at the extremity of the arrows.

labels names of the variables. If NULL (default), labels correspond to variable names found in the data used in the multivariate analysis. For two-dimensional graphs, only used if ident=TRUE.

main.pos position of the title, if main is not NULL. Default to "bottomleft".

main.cex size of the title, if main is not NULL.

legend only used for two-dimensional graphs. Logical indicating if a legend should be added to the graph.

legend.pos position of the legend, if legend is TRUE. Default to "topleft".

legend.title optional title of the legend, if legend is TRUE.

legend.lab legend labels, if legend is TRUE. If NULL, levels of the factor defined by fac are used.

pch symbol(s) used for points, when points are displayed (see arrows). If fac is not NULL, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.

cex size of the points and/or of the variable names. For two-dimensional graphs: if fac is not NULL, can be a vector of length one or a vector giving one value per group; otherwise a vector of any length can be defined, which is recycled if necessary. For dotcharts, gives the size used for points and all labels (see dotchart).

col color(s) used for points and/or variable names. If fac is not NULL, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.

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

- rGCCA: wrapper.rgcca. Space can be 1 to n, the number of blocks (i.e. datasets).
- sGCCA: wrapper.sgcca. Space can be 1 to n, the number of blocks (i.e. datasets).
- DIABLO: block.plsda, block.splsda. Space can be 1 to n, the number of blocks (i.e. datasets).

Author(s)
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Examples

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

Description

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

Usage

```r
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>a data frame of independent variables.</td>
</tr>
<tr>
<td>Y</td>
<td>the dependent variable(s): numeric vector, data frame of quantitative variables or factor.</td>
</tr>
<tr>
<td>repet</td>
<td>an integer giving the number of times the whole procedure has to be repeated.</td>
</tr>
<tr>
<td>k</td>
<td>an integer giving the number of folds (can be re-set internally if needed).</td>
</tr>
<tr>
<td>ncomp</td>
<td>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).</td>
</tr>
<tr>
<td>scale</td>
<td>logical indicating if data should be scaled (see Details).</td>
</tr>
<tr>
<td>model</td>
<td>the model to be fitted (see Details).</td>
</tr>
</tbody>
</table>
lower  a vector of lower limits for power optimisation in CPPLS or PPLS-DA (see cppls.fit).
upper  a vector of upper limits for power optimisation in CPPLS or PPLS-DA (see cppls.fit).
Y.add  a vector or matrix of additional responses containing relevant information about the observations, in CPPLS or PPLS-DA (see cppls.fit).
weights a vector of individual weights for the observations, in CPPLS or PPLS-DA (see cppls.fit).
set.prior only used when a LDA or QDA is performed (coupled or not with a PLS model). If TRUE, the prior probabilities of class membership are defined according to the mean weight of individuals belonging to each class. If FALSE, prior probabilities are obtained from the data sets on which LDA/QDA models are built.
crit.DA  criterion used to predict class membership when a LDA or QDA is used. See predict.lda.
... other arguments to pass to plsr (PLSR, PLS-DA) or cppls (CPPLS, PPLS-DA).

Details

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

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

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

Value

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

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, pcaR.
- 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 Hervé <mx.herve@gmail.com>
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.

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 used 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`.
- sIPCA: `ipca`.
- sIPCA: `sipca`.
- LDA: `lda`, `discrimin`.
- PLS-DA (PLS2 on a dummy-coded factor): `plsd`. 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`.
- PCA: `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 Hervé <mx.herve@gmail.com>

**Examples**
```r
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**

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

**Arguments**

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

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 Hervé <mx.herve@gmail.com>

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)

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MV A.
scoreplot

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 dotchart). Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

col color(s) used for points or labels (see points). If fac is not NULL, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary (not available for density
histograms, see dhist). Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

points only used for two-dimensional graphs. If FALSE, points are replaced with their corresponding label (defined by labels). Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

labels used in two-dimensional graphs when points=FALSE and in dotcharts (see dhist). Names of the individuals. If NULL (default), labels correspond to row names of the data used in the multivariate analysis. Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

main.pos position of the title, if main is not NULL. Default to "bottomleft". Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

main.cex size of the title, if main is not NULL. Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

fac.lab only used if fac is not NULL. Labels used to display barycenters in two-dimensional graphs or on the vertical axis of a dotchart in the one-dimensional case (see dhist). If NULL, levels of the factor defined by fac are used. In case of a MCA or a mix analysis with byfac=TRUE (see byfac), labels cannot be changed and correspond to the levels of the factor displayed on each graph.

fac.cex only used if fac is not NULL and in two-dimensional graphs. Labels used to display barycenters. Can be a vector of length one or a vector giving one value per group. Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

legend logical indicating if a legend should be added to the graph. Available for two-dimensional graphs and for density histograms in the one-dimensional case (see dhist).

legend.pos position of the legend, if legend is TRUE. Default to "topleft".

legend.title optional title of the legend, if legend is TRUE. Not available for MCA and mix analyses when byfac=TRUE (see byfac).

legend.lab legend labels, if legend is TRUE. If NULL, labels defined by fac.labels are used (see fac.labels).

legend.cex size of legend labels, if legend is TRUE.

drawextaxes logical indicating if external axes should be drawn. Available for two-dimensional graphs and for density histograms in the one-dimensional case (see dhist).

drawintaxes logical indicating if internal axes should be drawn.

xlim limits of the horizontal axis. If NULL, limits are computed automatically. Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

ylim only used in two-dimensional graphs. Limits of the vertical axis. If NULL, limits are computed automatically. Re-used for all graphs for MCA and mix analyses when byfac=TRUE (see byfac).

keepmar only used in two-dimensional graphs. Logical indicating if margins defined by MVA.scoreplot should be kept after plotting (necessary for biplots).
Details

This function should not be used 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 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: `plsr`. X space only.
- PLS-GLR: `plsr` (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.
- PCA: `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: `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 Hervé <mx.herve@gmail.com>

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

### MVA.scores

**Scores of multivariate analyses**

**Description**
Returns scores of a multivariate analysis.

**Usage**

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

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

Details

Many multivariate analyses are supported, from various packages:
- PCA: prcomp, princomp (if scores=TRUE), dudi.pca, rda, pca, pca. scaling can be defined for rda (see scores.rda).
- sPCA: spca.
- IPCA: ipca.
- sIPCA: sipca.
- PCoA: cmdscale (with at least one non-default argument), dudi.pco, wcmdscale (with at least one non-default argument), capscale, pco, pcoa.
- nMDS: monoMDS, metaMDS, nmmds, 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: **procruste**. 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: **sgcca**, **wrapper.sgcca**. Space can be 1 to n, the number of blocks (i.e. datasets).

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

**Author(s)**

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---

**MVA.synt**

*Synthesis quality of multivariate analyses*

**Description**

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

MVA.synt(x, rows = 5)

Arguments

x
a multivariate analysis (see Details).

rows
maximum number of axes to print in the output.

Details

Many multivariate analyses are supported, from various packages.
- PCA: prcomp, princomp, dudi.pca, rda, pca, pca: % of total variance explained by each axis.
- sPCA: spca: % of total variance explained by each axis.
- IPCA: ipca: kurtosis of each axis.
- sIPCA: sipca: kurtosis of each axis.
- PCoA: cmdscale (with eig=TRUE), dudi.pco, wcmdscale (with eig=TRUE), capscale, pco, pcoa: % of total variance explained by each axis.
- 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.
- PL SR: 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).
- C Cor A: 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: \texttt{rgcca, wrapper.rgcca}: \% of total intra-block variance explained by each axis, correlation between each pair of axes (canonical correlations).
- DIABLO: \texttt{block.plsda, block.splsda}: \% of total intra-block variance explained by each axis, correlation between each pair of axes (canonical correlations).
- CIA: \texttt{coinertia}: RV coefficient, \% of co-inertia explained by each pair of axes, correlation between each pair of axes (canonical correlations).
- PCIA: \texttt{procuste: m2}.

\textbf{Author(s)}

Maxime Hervé <mx.herve@gmail.com>

\textbf{Examples}

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

---

\textbf{MVA.test}

\textit{Significance test based on cross (model) validation}

\textbf{Description}

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

\textbf{Usage}

\texttt{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, ...)}

\textbf{Arguments}

- \texttt{X}: a data frame of independent variables.
- \texttt{Y}: the dependent variable(s): numeric vector, data frame of quantitative variables or factor.
- \texttt{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).
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)

Maxime Hervé <mx.herve@gmail.com>

References


See Also

- `MVA.cv`, `MVA.cmv`

Examples

```r
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.
MVA.trajplot

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 trajec labels.

scaling type of scaling. Only available with some analyses performed with the vegan package. See Details of MVA.scoreplot.

set scores to be displayed, when several sets are available (see Details of MVA.scoreplot). 12 (default) for both sets, 1 for rows or X, 2 for columns or Y.

space scores to be displayed, when several spaces are available (see Details of MVA.scoreplot). space is the number of the space to be plotted.

xlab legend of the horizontal axis. If NULL (default), automatic labels are used depending on the multivariate analysis.

ylab legend of the vertical axis. If NULL (default), automatic labels are used depending on the multivariate analysis.

main optional title of the graph.

pch symbols used for points. Can be a vector giving one value per trajectory (and a last one for non-linked points if allpoints=TRUE).

cex size of the labels. Can be a vector giving one value per trajectory (and a last one for non-linked points if allpoints=TRUE).

trajlab.cex size of trajectory labels. Can be a vector giving one value per trajectory.

col color(s) used for arrows and labels. If fac is not NULL, can be a vector of length one or a vector giving one value per group. Otherwise a vector of any length can be defined, which is recycled if necessary.

lwd width of trajectory segments. Can be a vector giving one value per trajectory.

lty type of trajectory segments. Can be a vector giving one value per trajectory.

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

Details

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

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

Examples

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

Odds-ratio (multinomial regression)

Description
Computes the odds ratios and their confidence interval for a predictor of a model fitted with \texttt{multinom}.

Usage
\texttt{OR.multinom(model, variable, conf.level = 0.95)}

Arguments
\texttt{model} \hspace{1cm} \texttt{variable} \hspace{1cm} \texttt{conf.level}
\begin{itemize}
  \item object of class "multinom".
  \item any predictor present in \texttt{model} (unquoted).
  \item confidence level.
\end{itemize}

Author(s)
Maxime Hervé <mx.herve@gmail.com>

ord.rw

Re-computation of an ordination using given row weights

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

Usage
\texttt{ord.rw(ord, CA = NULL, rw = NULL)}

Arguments
\texttt{ord} \hspace{1cm} \texttt{CA} \hspace{1cm} \texttt{rw}
\begin{itemize}
  \item an ordination to re-compute. Must come from the ade4 package or be supported by \texttt{to.dudi}. In any case the resulting ordination will be in the ade4 format.
  \item an optional correspondence analysis from which row weights should be extracted. Must come from \texttt{dudi.coa} or \texttt{cca}.
  \item an optional vector of row weights. Used only if \texttt{CA} is \texttt{NULL}.
\end{itemize}

Author(s)
Maxime Hervé <mx.herve@gmail.com>
**overdisp.glmer**  
*Estimation of overdispersion with glmer models*

**Description**

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

**Usage**

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

**Arguments**

- `model`  
a model fitted by glmer.

**Author(s)**

Ben Bolker

**See Also**

glmer

**Examples**

```r
require(lme4)

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

---

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

**Description**

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

**Usage**

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

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.
...    other arguments to pass to CDA.test.

Details

See CDA.test.

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

CDA.test

Examples

require(ade4)
data(perthi02)
CDA.test(perthi02$tab,perthi02$cla)
pairwise.CDA.test(perthi02$tab,perthi02$cla)
pairwise.factorfit  
Pairwise comparisons of groups displayed on a factorial map

Description

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

Usage

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

Arguments

- ord: any multivariate analysis handled by MVA.scores.
- fact: grouping factor.
- xax: first axis of the factorial map.
- yax: second axis of the factorial map.
- nperm: number of permutations.
- ... optional further arguments to MVA.scores.

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

factorfit
Examples

```r
require(vegan)
data(iris)

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

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

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

---

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

Description

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

Usage

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

Arguments

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

Details

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

Value

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

See Also

- `G.test`, `fisher.multcomp`
Examples

```r
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

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

Arguments

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

Details

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

Value

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

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

`mood.medtest`
Examples

```r
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)
```

Description

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

Usage

```r
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.
- `cmv`: a logical indicating if the test statistic (NMC) should be generated through cross-validation (classical K-fold process) or cross model validation (inner + outer loops).
- `ncomp`: an integer giving the number of components to be used to generate all submodels (cross-validation) or the maximal number of components to be tested in the inner loop (cross model validation). Can be re-set internally if needed. Does not concern LDA and QDA.
- `kout`: an integer giving the number of folds (cross-validation) or the number of folds in the outer loop (cross model validation). Can be re-set internally if needed.
- `kinn`: an integer giving the number of folds in the inner loop (cross model validation only). Can be re-set internally if needed. Cannot be > `kout`.
- `model`: the model to be fitted.
- `nperm`: number of permutations.
- `progress`: logical indicating if the progress bar should be displayed.
- `...`: other arguments to pass to `MVA.test`. 
pairwise.perm.manova

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 Hervé <mx.herve@gmail.com>

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
Arguments

resp response. Either a matrix (one column per variable; objects of class "data.frame" are accepted and internally converted into matrices) or a distance matrix.

fact grouping factor.

test choice of test statistic when resp is a matrix (see anova.mlm).
nperm number of permutations.

progress logical indicating if the progress bar should be displayed.

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 Hervé <mx.herve@gmail.com>

See Also

anova.mlm, adonis

Examples

require(vegan)
data(iris)

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

# Pairwise comparisons
pairwise.perm.t.test

Pairwise permutation t tests

Description
Perform 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.
- 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.
pairwise.perm.var.test

Description
Perform 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.
- 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.
pairwise.var.test

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 Hervé <mx.herve@gmail.com>

See Also
- pairwise.var.test

Examples
```r
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)
```

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

Usage
```r
pairwise.var.test(resp, fact, p.method = "fdr", alternative = c("two.sided","less","greater"))
```
Arguments

resp  response vector.

fact  grouping factor.


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 Hervé <mx.herve@gmail.com>

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", "kendall", "spearman"))
Arguments

x  a numeric vector.
y  a numeric vector.
z  a numeric vector, matrix, data frame or list giving the controlling variables. For matrices, variables must be placed in columns.

semi  logical. If TRUE the semi-partial correlation coefficient is computed. In that case only y is controlled for z.

use  same as use of cor.

method  same as method of cor.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

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.test

Tests for (semi-)partial association/correlation between paired samples

Description

Tests for (semi-)partial association between paired samples while controlling for other variables, using one of Pearson’s product moment correlation coefficient or Spearman’s rho.

Usage

pcor.test(x, y, z, semi = FALSE, conf.level = 0.95, nrep = 1000, method = c("pearson", "spearman"))
Arguments

- **x**: a numeric vector.
- **y**: a numeric vector.
- **z**: a numeric vector, matrix, data frame or list giving the controlling variables. For matrices, variables must be placed in columns.
- **semi**: logical. If `TRUE` the semi-partial correlation coefficient is computed and tested. In that case only **y** is controlled for **z**.
- **conf.level**: confidence level for confidence interval.
- **nrep**: number of replicates for computation of the confidence interval of a Spearman’s rank correlation coefficient (by 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 Hervé <mx.herve@gmail.com>

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 (factor-
    2).
    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 Hervé <mx.herve@gmail.com>

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)
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 formula. By default the variables are taken from `environment(formula)`.
- **nperm**: number of permutations.
- **progress**: logical indicating if the progress bar should be displayed.

Details

The function deals with the 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 Hervé <mx.herve@gmail.com>

See Also

- **bartlett.test**

Examples

```r
response <- c(rnorm(12),rpois(12,1),rnorm(12,2,1))
fact <- gl(3,12,labels=LETTERS[1:3])
perm.bartlett.test(response~fact)
```

Description

Performs a permutation Pearson’s product-moment correlation test.

Usage

```r
perm.cor.test(x, y, alternative = c("two.sided", "less", "greater"),
              nperm = 999, progress = TRUE)
```
perm.cor.test

Arguments

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

Details

The function deals with the 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.
  estimate     the estimated correlation coefficient.
  alternative  a character string describing the alternative hypothesis.
  null.value   the value of the association measure under the null hypothesis, always 0.

Author(s)

  Maxime Hervé <mx.herve@gmail.com>

See Also

  cor.test

Examples

  x <- rnorm(50)
  y <- runif(50)
  perm.cor.test(x,y)
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.
perm.var.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 Hervé <mx.herve@gmail.com>

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 Hervé <mx.herve@gmail.com>

See Also

- var.test

Examples

```r
response <- c(rpois(8,1),rpois(8,3))
fact <- gl(2,8,labels=LETTERS[1:2])
perm.var.test(response=fact)
```
plotresid

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 \texttt{lm} (including \texttt{glm}, \texttt{lmList}, \texttt{lmList4}, \texttt{glm.nb}, \texttt{mlm} and \texttt{manova}), \texttt{lmer}, \texttt{glmer}, \texttt{glmmPQL}, \texttt{glmmadmb}, \texttt{lme}, \texttt{gls}, \texttt{nls}, \texttt{nlsList}, \texttt{survreg} and \texttt{least.rect} models.

Usage

\begin{verbatim}
plotresid(model, shapiro = FALSE)
\end{verbatim}

Arguments

- \texttt{model} an object of class \texttt{"lm"}, \texttt{"lmList"}, \texttt{"lmList4"}, \texttt{"merMod"}, \texttt{"glmmadmb"}, \texttt{"lme"}, \texttt{"glmmPQL"}, \texttt{"gls"}, \texttt{"nls"}, \texttt{"nlsList"}, \texttt{"survreg"} or \texttt{"least.rect"}.
- \texttt{shapiro} logical. If \texttt{TRUE} and if \texttt{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 \texttt{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").

QQ-plots and Shapiro-Wilk tests are available whenever the model is based on a Gaussian distribution (and with "quasi" distributions when \texttt{variance}="constant").

With a \texttt{mlm} or \texttt{manova} model, only a multivariate QQ-plot is drawn. The test performed when \texttt{shapiro=TRUE} is a Shapiro-Wilk test for multivariate normality.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

\texttt{lm, lmList, lmList4, glm, glm.nb, manova, lmer, glmer, lmer.nb, lme, glmmPQL, gls, nls, nlsList, survreg, least.rect, qresiduals, qqPlot, shapiro.test, mqqnorm, mshapiro.test}
plotsurvivors  

**Description**

Plots the survivor curve (log(survivors) against time) of a dataset to check for constancy of hazard.

**Usage**

```r
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 Hervé <mx.herve@gmail.com>

**Examples**

```r
# 'kidney' dataset of package 'survival'
require(survival)
data(kidney)
plotsurvivors(kidney$time, kidney$status)
```

---

**PLSDA.VIP**  

**Variable Importance in the Projection (VIP)**

**Description**

Returns VIP score of each X-variable in a PLS-DA (obtained from `plsd`).

**Usage**

```r
PLSDA.VIP(model, graph = FALSE)
```
**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

```r
## S3 method for class 'CDA.cv'
predict(object, newdata, type = c("max", "all"), method = c("mahalanobis", "euclidian"), ...)
```

### 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 Hervé <mx.herve@gmail.com>

### See Also

`plsda`

### Examples

```r
if (require(mixOmics)) {
  data(yeast)
  model.PLSDA <- plsda(t(yeast$data), yeast$strain.cond)
  PLSDA.VIP(model.PLSDA)
}
```
predict.coadisc

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 Hervé <mx.herve@gmail.com>

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

```r
## 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 Hervé <mx.herve@gmail.com>
**predict.MVA.cv**

**See Also**

discrim.coa

**Examples**

```r
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, 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**

```r
## S3 method for class 'MVA.cv'
predict(object, newdata, conf.level = 0.95, type.DA = c("max", "all"),
         crit.DA = c("plug-in", "predictive", "debiased"), ...)

## S3 method for class 'MVA.cmv'
predict(object, newdata, conf.level = 0.95, type.DA = c("max", "all"),
         crit.DA = c("plug-in", "predictive", "debiased"), ...)
```

**Arguments**

- `object`: object of class inheriting from "MVA.cv" or "MVA.cmv".
- `newdata`: vector, matrix or data frame giving new individuals (one row per individual).
- `conf.level`: confidence level for prediction of a quantitative response.
- `type.DA`: for discriminant analyses, should the probability of the most probable class be given ("max", the default) or the probability of each class ("all")?
- `crit.DA`: criterion used to predict class membership when a LDA or QDA is used. See `predict.lda`.
- `...`: further arguments to be passed to or from other methods.

**Author(s)**

Maxime Hervé <mx.herve@gmail.com>
prop.bin.multcomp

Pairwise comparisons after a test for given probabilities

Description

Performs pairwise comparisons after a global test for given response probabilities (i.e. when the response variable is a binary variable), by using exact binomial tests. The function is in fact a wrapper to pairwise comparisons of proportions to given values on a contingency table.

Usage

prop.bin.multcomp(formula, data, p, p.method = "fdr")

Arguments

formula: a formula of the form a ~ b, where a and b give the data values and corresponding groups, respectively. a can be a numeric vector or a factor, with only two possible values (except NA).

data: an optional data frame containing the variables in the formula formula. By default the variables are taken from environment(formula).

p: theoretical probabilities.


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 Hervé <mx.herve@gmail.com>
prop.multcomp

See Also

prop.multcomp, chisq.theo.bintest

Examples

```r
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**

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

**Arguments**

- **x**: contingency table.
- **p**: theoretical proportions.
- **p.method**: method for p-values correction. See help of `p.adjust`.

**Value**

- **method**: name of the test.
- **data.name**: a character string giving the name(s) of the data.
- **observed**: observed proportions.
- **expected**: expected proportions.
- **p.adjust.method**: method for p-values correction.
- **p.value2**: corrected p-values.
- **p.value**: table or results of pairwise comparisons.

**Author(s)**

Maxime Hervé <mx.herve@gmail.com>
prop.multinom

See Also

prop.test

Examples

```r
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)
```

Description

Computes proportions (and their standard errors) when the number of classes is >= 2, based on predicted values of a model. The function is intended to be used parallel to a multinomial log-linear model.

Usage

```r
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 Hervé <mx.herve@gmail.com>
prop.multinom.test

See Also

multinom, glm

Examples

```r
response <- data.frame(A=c(2,2,4,0,2,14,6,16,0,0),
                       B=c(2,0,0,6,2,10,6,0,0),
                       C=c(12,6,0,6,2,0,0,0,0,0),
                       D=c(0,0,0,14,0,0,0,2,0),
                       E=c(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**

```r
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.
rating.emmeans

EMMeans for Cumulative Link (Mixed) Models

Description

Extracts EMMMeans (produced by \texttt{emmeans}) from Cumulative Link (Mixed) Models (produced by \texttt{clm} or \texttt{clmm}), with different possible formats.

Usage

\begin{verbatim}
rating.emmeans(emm, type = c("prob", "cumprob", "class1", "class2"), level = 0.9)
\end{verbatim}

Arguments

- \texttt{emm} object returned by \texttt{emmeans} applied on a \texttt{clm} or \texttt{clmm} object.
- \texttt{type} type of output to be returned: "prob" (default) gives probability of each rating, "cumprob" gives cumulative probabilities (\(P_i\) is probability to be \(\leq\) to rating \(i\)), "class1" gives the most probable rating and "class2" gives the first rating for which the cumulative probability is \(\geq\) to \texttt{level}.
- \texttt{level} used only for type "class2" (see \texttt{type}).

Details

A factor named \texttt{cut} must have been called in \texttt{emmeans}, to compute EMMMeans per cut point (i.e. rating). Additionally, the argument \texttt{mode} of \texttt{emmeans} must have been set to "linear.predictor". Finally, the call to \texttt{emmeans} is typically like \texttt{emmeans(model,~factor|cut,mode="linear.predictor")} where \texttt{factor} is the factor (or interaction) giving levels for which EMMMeans have to be computed.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

\texttt{emmeans,clm,clmm}
rating.prob

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="class!")

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 \(<= i\)) and
"class" gives the most frequent rating.

Author(s)
Maxime Hervé <mx.herve@gmail.com>

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**

```r
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 `lines`.

**Author(s)**
Maxime Hervé <mx.herve@gmail.com>

**See Also**
`lm`

**Examples**

```r
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")
```
"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 Hervé <mx.herve@gmail.com>, based on an idea of Stéphane 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)

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**

```r
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 Hervé <mx.herve@gmail.com>

**Examples**

```r
# Standard error of a mean
se(rnorm(30))

# Standard error of a proportion
se(9, 25)
```

---

**seq2**

*Sequence generation*

**Description**

Generates a regular sequence from the minimum to the maximum of a vector.

**Usage**

```r
seq2(x, int = 999)
```
spearman.ci

Arguments

  x  numeric vector.
  int  number of values to be generated (int breaks).

Author(s)

Maxime Hervé <mx.herve@gmail.com>

See Also

  seq

Examples

  seq2(rnorm(30))

---

**spearman.ci**  
*Confidence interval of a Spearman’s rank correlation coefficient*

Description

Computes the confidence interval of a Spearman’s rank correlation coefficient by bootstraping.

Usage

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

Arguments

  var1  numeric vector (first variable).
  var2  numeric vector (second variable).
  nrep  number of replicates for bootstraping.
  conf.level  confidence level of the interval.

Value

  method  name of the test.
  data.name  a character string giving the name(s) of the data.
  conf.level  confidence level.
  rep  number of replicates.
  estimate  Spearman’s rank correlation coefficient.
  conf.int  confidence interval.

Author(s)

Maxime Hervé <mx.herve@gmail.com>
spearman.cor.multcomp

See Also
cor.test, boot

Examples

    var1 <- sample(1:50,15,replace=TRUE)
    var2 <- sample(1:50,15,replace=TRUE)
    spearman.ci(var1,var2)

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 bootstraping.

Details

Confidence intervals which do not overlap indicate correlation coefficients significantly different at alpha.

Value

    method    name of the test.
    data.name a character string giving the name(s) of the data.
    tab       data frame of correlation coefficients with confidence intervals
    alpha     significance level.
    nrep      number of replicates for bootstraping.

Author(s)

    Maxime Hervé <mx.herve@gmail.com>
**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**

```r
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 Hervé <mx.herve@gmail.com>

**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.
test.multinom

Author(s)
Maxime Hervé <mx.herve@gmail.com>

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")

desc 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 Hervé <mx.herve@gmail.com>
to.dudi  Synthesis quality of multivariate analyses

Description

Converts some ordinations performed with the vegan package to objects compatible with coinertia.

Usage

to.dudi(ord)

Arguments

ord an ordination (see Details).

Details

The function supports:
- PCA computed from rda. If data were scaled (prior to the analysis or using scale of rda) it is assumed that is was with the standard deviation using n-1; As in dudi.pca, to.dudi rescales the data with the standard deviation using n.
- PCoA computed from wcmdscale, capscale or dbrrda.
- CA computed from cca.

Author(s)

Maxime Hervé <mx.herve@gmail.com>

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 Hervé <mx.herve@gmail.com>

**See Also**

`emmeans`

**Examples**

```r
require(car)
require(emmeans)

# Create data
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(levels(fact),1:3))
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.

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 Hervé <mx.herve@gmail.com>

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**
onoptional blocking (random) factor.
- **p**
hypothesized probability of success.

**Details**
The function builds a logistic (mixed) regression and applies a Wald test to compare the estimated value of the intercept to its theoretical value under H0. Eventual overdispersion is taken into account, by using a quasi-binomial law in case of no blocks or by introducing an individual-level random factor if blocks are present.

If the response is a 0/1 vector, the probability of the '1' group is tested. With other vectors, the response is transformed into a factor and the probability of the second level is tested.

If the response is a two-column matrix, the probability of the left column is tested.

If the 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 Hervé <mx.herve@gmail.com>

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).
**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 Hervé <mx.herve@gmail.com>

**See Also**

pairwise.wilcox.test, wilcox.test

**Examples**

```r
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**

```r
wilcox.signtest(x, ...)
```

## Default S3 method:

```r
wilcox.signtest(x, y = NULL, mu = 0, conf.level = 0.95, ...)
```

## S3 method for class 'formula'

```r
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 Hervé <mx.herve@gmail.com>

See Also

- `wilcox.test`

Examples

```r
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 Hervé <mx.herve@gmail.com>

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