

Package ‘PERMANOVA’

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Type Package

Title Multivariate Analysis of Variance Based on Distances and Permutations

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Description Calculates multivariate analysis of variance based on permutations and some associated pictorial representations. The pictorial representation is based on the principal coordinates of the group means. There are some original results that will be published soon.

License GPL (>= 2)

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AddClusterToBiplot *Add Clusters to a Biplot Object*

Description

The function add clusters to a biplot object to be represented on the biplot. The clusters can be defined by a nominal variable provided by the user, obtained from the `hclust` function of the base package or from the `kmeans` function.

Usage

```
AddClusterToBiplot(Bip, NGroups = 3, ClusterType = "hi", Groups = NULL,
Original = FALSE, ...)
```

Arguments

Bip	A Biplot object obtained from any biplot procedure. It has to be a list containing a field called Bip\$RowCoordinates in order to calculate the clusters when necessary.
NGroups	Number of groups or clusters. Only necessary when hierarchical or k-means procedures are used.
ClusterType	The type of cluster to add. There are three possibilities "us" (User Defined), "hi" (hierarchical clusters), "km" (kmeans clustering) or "gm" (gaussian mixture).
Groups	A factor defining the groups provided by the user.
Original	Should the clusters be calculated using the original data rather than the reduced dimensions?
...	Any other parameter for the hclust and kmeans procedures.

Details

One of the main shortcomings of cluster analysis is that it is not easy to search for the variables associated to the obtained classification; representing the clusters on the biplot can help to perform that interpretation. If you consider the technique for dimension reduction as a way to separate the signal from the noise, clusters should be constructed using the dimensions retained in the biplot, otherwise the complete original data matrix can be used. The colors used by each cluster should match the color used in the Dendrogram. User defined clusters can also be plotted, for example, to investigate the relation of the biplot solution to an external nominal variable.

Value

The function returns the biplot object with the information about the clusters added in new fields

ClusterType	The method of clustering as defined in the argument ClusterType.
Clusters	A factor containing the solution or the user defined clusters
ClusterNames	The names of the clusters
ClusterColors	The colors of the clusters
Dendrogram	The Dendrogram if we have used hierarchical clustering
ClusterObject	The object obtained from hclust, kmeans or MGC

Author(s)

Jose Luis Vicente-Villardón, Laura Vicente-Gonzalez

References

- Demey, J. R., Vicente-Villardón, J. L., Galindo-Villardón, M. P., & Zambrano, A. Y. (2008). Identifying molecular markers associated with classification of genotypes by External Logistic Biplots. *Bioinformatics*, 24(24), 2832-2838.
- Gallego-Alvarez, I., & Vicente-Villardón, J. L. (2012). Analysis of environmental indicators in international companies by applying the logistic biplot. *Ecological Indicators*, 23, 250-261.

Galindo, P. V., Vaz, T. D. N., & Nijkamp, P. (2011). Institutional capacity to dynamically innovate: an application to the Portuguese case. *Technological Forecasting and Social Change*, 78(1), 3-12.

Vazquez-de-Aldana, B. R., Garcia-Criado, B., Vicente-Tavera, S., & Zabalgoeazcoa, I. (2013). Fungal Endophyte (*Epichloë festucae*) Alters the Nutrient Content of *Festuca rubra* Regardless of Water Availability. *PLoS one*, 8(12), e84539.

See Also

For clusters not provided by the user the function uses the standard procedures in `hclust` and `kmeans`.

BinaryVectorCheck	<i>Checks if a vector is binary</i>
-------------------	-------------------------------------

Description

Checks if all the entries of a vector are 0 or 1.

Usage

```
BinaryVectorCheck(x)
```

Arguments

`x` The vector to check

Value

The logical result.

Author(s)

Jose Luis Vicente-Villardón

Examples

```
x=c(0, 0, 0, 0, 1, 1, 1, 2)
BinaryVectorCheck(x)
```

BiplotVar

Draws a variable on a biplot

Description

Draws a continuous variable on a biplot.

Usage

```
BiplotVar(bi1, bi2, b0 = 0, xmin = -3, xmax = 3, ymin = -3, ymax = 3,
label = "Point", mode = "a", CexPoint = 0.8, PchPoint = 1, Color = "blue",
ticks = c(-3, -2.5, -2, -1.5, -1, -0.5, 0.5, 1, 1.5, 2, 2.5, 3), ticklabels =
round(ticks, digits = 2), tl = 0.03, ts = "Complete", Position = "Angle",
AddArrow = FALSE, ...)
```

Arguments

bi1	First component of the direction vector.
bi2	Second component of the direction vector.
b0	Constant for the regression adjusted biplots.
xmin	Minimum value of the x axis.
xmax	Maximum value of the x axis.
ymin	Minimum value of the y axis.
ymax	Maximum value of the y axis.
label	Label of the variable.
mode	Mode of the biplot: "p", "a", "b", "h", "ah" and "s".
CexPoint	Size for the symbols and labels of the variables.
PchPoint	Symbols for the variable (when represented as a point).
Color	Color for the variable.
ticks	Ticks when the variable is represented as a graded scale.
ticklabels	Labels for the ticks when the variable is represented as a graded scale.
tl	Thick length.
ts	Size of the mark in the graded scale.
Position	If the Position is "Angle" the label of the variable is placed using the angle of the vector.
AddArrow	Add an arrow to the representation of other modes of the biplot.
...	Any other graphical parameters

Details

See plot.PCA.Biplot

Value

No value returned

Author(s)

Jose Luis Vicente-Villardón

BootDisMANOVA

Multivariate Analysis of Variance based on Distances and Bootstrap

Description

Multivariate Analysis of variance based on distances and Bootstrap.

Usage

```
BootDisMANOVA(Distance, groups, C = NULL, Effects = NULL, nB = 1000, seed = NULL,
CoordPrinc = FALSE, dimens = 2, PCoA = "Standard", ProjectInd = TRUE, tol = 1e-04,
DatosIni = TRUE)
```

Arguments

Distance	A matrix of distances.
groups	A factor containing the groups to compare.
C	A matrix of contrasts (if null the identity is used).
Effects	A vector of effects.
nB	Number of Bootstrap replicates.
seed	Seed for the random numbers.
CoordPrinc	Should Principal Coordinates be calculated.
dimens	Dimension of the solution.
PCoA	Type of Principal Coordinates to calculate.
ProjectInd	Should the individuals be projected onto the graph.
tol	Tolerance for convergence of the algorithms.
DatosIni	Should the initial data be included in the results.

Details

Multivariate Analysis of Variance based on distances and Bootstrap.

Value

call	Function
Title	Title of the study
Type	BootMANOVA
Distances	A matrix containing the distances between individuals.
C	Contrasts Matrix.
Initial	Containing two matrices: * Global -> Global contrast. * Contrastes ->Contrasts for groups.
DistMuestral	Sample distribution of F-exp from permutations.
pvalue	Estimate p-value for PERMANOVA.
ExplainedVariance	Explained variance by Principal Coordinates selected.
Inertias	Eigenvalue, Explained variance, Cumulative explained variance.
MeanCoordinates	Mean Coordinates by groups for the dimensions obtained in the Principal Coordinates Analysis.
Qualities	Qualities representation by groups for the dimensions of PCoA.
CummulativeQualities	Cummulative qualities representation.
ClusterType	Cluster type selected.
Clusters	Clusters created.
ClusterNames	Names of clusters
ClusterColors	Colors of clusters, color name and HTML code.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

- Anderson, M. J. (2001). A new method for non-parametric multivariate analysis of variance. *Australian ecology*, 26(1):32–46.
- Anderson, M. J. (2005). *Permanova: a fortran computer program for permutational multivariate analysis of variance*. Department of Statistics, University of Auckland, New Zealand, 24.

Examples

```
data(wine)
X = wine[,4:21]
D = DistContinuous(X)
bootwine=BootDisMANOVA(D, wine$Group)
bootwine
```

 BootDistCanonicalAnalysis

Canonical Analysis based on Distances

Description

Canonical Analysis based on distances. Confidence Regions for the mean vectors are calculated using bootstrap.

Usage

```
BootDistCanonicalAnalysis(Distance, groups, dimens = NULL, nB = 100, seed = NULL,
  PCoA = "Standard", ProcrustesRot = TRUE, DatosIni = TRUE, tol = 1e-04)
```

Arguments

Distance	A list of three elements containing the data, the distances between individuals and type of distance used.
groups	A factor containing the groups to compare.
dimens	Number of dimensions to choose . By default is 2.
nB	Number of Bootstrap samples.
seed	Seed for the generation of the random samples (Added for reproducibility)
PCoA	The type of Principal Coordinates Analysis. There are two possibilities: * Standard * Weighted By default is Standard.
ProcrustesRot	Should Procrustes rotation be applied to the configurations?
DatosIni	The input object contains the initial data?. By default is TRUE.
tol	Tolerance

Details

Calculates a Canonical Analysis based on distance matrices with confidence regions based on bootstrap resampling.

Value

D	The distance matrix used for calculations
Coefficient	Dissimilarity coefficient used to calculate the proximities
nB	Number of bootstrap samples
Groups	Factor containing the groups to compare
GroupNames	Names of the groups

Inertia	Variance accounted for each canonical coordinate
Inertias	able with the eigenvalue, variance accounted and cumulated variance
MeanCoordinates	Coordinates of the groups in the representation
Qualities	Qualities of the representation of the group means
CumulativeQualities	Cumulative Qualities of the representation
CoordBoot	Coordinates of the bootstrap replicates
RowCoordinates	Coordinates of the individuals

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

Gower, J. C. and Krzanowski, W. J. (1999). Analysis of distance for structured multivariate data and extensions to multivariate analysis of variance. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 48(4):505–519.

Examples

```
data(wine)
X=wine[,4:21]
Dist=DistContinuous(X)
canon=BootDistCanonicalAnalysis(Dist, groups=wine$Group, nB=10)
```

Circle2

Draws a circle.

Description

Draws a circle for a given radius at the specified center with the given color.

Usage

```
Circle2(radius = 1, origin = c(0, 0), col = 1, ...)
```

Arguments

radius	Radius of the circle.
origin	Centre of the circle.
col	Color of the circle.
...	Additional graphical parameters.

Details

Draws a circle for a given radius at the specified center with the given color.

Value

No value is returned.

Author(s)

Jose Luis Vicente-Villardón

Examples

```
plot(0,0)
Circle2(1,c(0,0))
```

ConcEllipse

Non-parametric concentration ellipses

Description

Calculates non-parametric concentration ellipses for a two-dimensional set of points

Usage

```
ConcEllipse(data, center = NULL, confidence = 1, npoints = 100)
```

Arguments

data	A two dimensional set of points.
center	Center of the data.
confidence	Confidence for the concentration ellipse.
npoints	Number of points to plot.

Details

Calculates non-parametric concentration ellipses for a two-dimensional set of points using distances to the center.

Value

data	Original data
confidence	Percent of points selected for the ellipse
ellipse	points to plot the ellipse
center	center of the ellipse

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

Meulman, J. J., & Heiser, W. J. (1983). The display of bootstrap solutions in multidimensional scaling. Murray Hill, NJ: Bell Laboratories.

Linting, M., Meulman, J. J., Groenen, P. J., & Van der Kooij, A. J. (2007). Stability of nonlinear principal components analysis: An empirical study using the balanced bootstrap. *Psychological Methods*, 12(3), 359.

Examples

```
x=runif(30)
y=x+rnorm(30)*0.3
plot(x, y)
el=ConcEllipse(cbind(x,y), confidence=0.95)
plot(el)
```

ConstructContrasts *Construction of contrasts for several factors*

Description

Constructs the contrasts for main effects and interaction for a dataframe of factors.

Usage

```
ConstructContrasts(Factors, MaxOrderIter = 2)
```

Arguments

Factors	A data frame of factors (For general data frames the functions extracts all the columns that are factors).
MaxOrderIter	Maximum order of the interaction to construct.

Details

Constructs the contrasts for main effects and interaction for a dataframe of factors. For a general data frame the functions extracts all the factors first. The function constructs the contrasts for all the main effects and the interactions up to order MaxOrderIter.

Value

Groups	The groups resulting of combining the levels of all the factors.
Contrasts	A matrix of contrasts containing the contrasts that are associated to the main affects and interaction. The rows contain contrasts and the columns the groups to combine.
Effects	A factor describing which contrasts correspond to each effect.

Author(s)

Jose Luis Vicente-Villardón, Laura Vicente-Gonzalez

References

Bapat, R. B. (2012). Linear algebra and linear models. Springer Science & Business Media.

Examples

```
ConstructContrasts(wine[,1:2])
```

Cumsum

Cumulative sums

Description

Cumulative sums.

Usage

```
Cumsum(X, dims = 1)
```

Arguments

X	Data Matrix.
dims	Dimension for summing.

Details

Cumulative sums within rows (dims=1) or columns (dims=2) of a data matrix.

Value

A matrix of the same size as X with cumulative sums within each row or each column.

Author(s)

Jose Luis Vicente-Villardón

Examples

```
data(wine)
X=wine[,4:21]
Cumsum(X,1)
Cumsum(X,2)
```

DistBinary	<i>Distances for binary data</i>
------------	----------------------------------

Description

Calculates distances among individuals for binary data. It is possible to introduce two matrices (x, y) and calculate the distances between them or introduce only one matrix (x) and calculate the distances among individuals in the single matrix.

Usage

```
DistBinary(x, y = NULL, coefficient = "Simple_Matching", transformation = "sqrt(1-S)")
```

Arguments

x	A matrix containing binary data.
y	A matrix containing binary data different than x. By default it is null because if we want to calculate the distances between individuals it's not necessary.
coefficient	Similarity coefficients for binary data. By default it is Simple_Matching. See details.
transformation	Transformations of similarities into distances. By default it is sqrt(1-S). See details.

Details

The function calculates coefficients of similarity (among individuals) for binary data and converts them into measures of distance.

We have 17 different coefficients (numbers instead of names can be used as arguments of the function) :

- * 1.- Kulezynski
- * 2.- Russell_and_Rao
- * 3.- Jaccard
- * 4.- Simple_Matching
- * 5.- Anderberg
- * 6.- Rogers_and_Tanimoto
- * 7.- Sorensen_Dice_and_Czekanowski
- * 8.- Sneath_and_Sokal
- * 9.- Hamman
- * 10.- Kulezynski2
- * 11.- Anderberg2
- * 12.- Ochiai
- * 13.- S13

- * 14.- Pearson_phi
- * 15.- Yule
- * 16.- Sorensen
- * 17.- Dice

There are nine possible transformations of the initial similarities:

- * 1.- Identity
- * 2.- 1-S
- * 3.- $\sqrt{1-S}$
- * 4.- $(-\log(S))$
- * 5.- $(1/S-1)$
- * 6.- $(\sqrt{2(1-S)})$
- * 7.- $(1-(S+1)/2)$
- * 8.- $1-\text{abs}(S)$
- * 9.- $1/(S+1)$

Value

The DistBinary function creates a list that return:

Data	A matrix with initial data.
D	A matrix containing binary distancies.
Coefficient	Character containing the name of the coefficient used.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

Gower, J. C. (2006) Similarity dissimilarity and Distance, measures of. Encyclopedia of Statistical Sciences. 2nd. ed. Volume 12. Wiley

Examples

```
data(spidersb)
DD=DistBinary(spidersb)
```

DistContinuous

*Distances among individuals with continuous data***Description**

Calculate distances among individuals for continuous data. It is possible to introduce two matrices (x, y) and calculate the distances between the two sets of rows or introduce only one matrix (x) and calculate the distances between its rows.

Usage

```
DistContinuous(x, y = NULL, coef = "Pythagorean", r = 1)
```

Arguments

x	A matrix containing continuous data.
y	A matrix containing continuous data different from x. By default it is null.
coef	Coefficient to calculate continuous distances. By default we use Pythagorean distances.
r	For Minkowski distances. By default it is 1.

Details

The function calculates distances among individuals for matrices of continuous data using different distance measures. If two matrices are provided, distances among individuals, one from the first matrix and another from the second, are calculated. If only one matrix is provided, interdistances among its rows are calculated.

The following coefficients are calculated

- 1.- Pythagorean = $\sqrt{\sum((y[i,] - x[j,])^2)/p}$
- 2.- Taxonomic = $\sqrt{\sum(((y[i,]-x[j,])^2)/r^2)/p}$
- 3.- City = $\sum(\text{abs}(y[i,]-x[j,])/r)/p$
- 4.- Minkowski = $(\sum((\text{abs}(y[i,]-x[j,])/r)^t)/p)^{1/t}$
- 5.- Divergence = $\sqrt{\sum((y[i,]-x[j,])^2/(y[i,]+x[j,])^2)/p}$
- 6.- dif_sum = $\sum(\text{abs}(y[i,]-x[j,])/(\text{abs}(y[i,]+x[j,]))) / p$
- 7.- Camberra = $\sum(\text{abs}(y[i,]-x[j,]) / (\text{abs}(y[i,]) + \text{abs}(x[j,])))$
- 8.- Bray_Curtis = $\sum(\text{abs}(y[i,]-x[j,])) / \sum(y[i,]+x[j,])$
- 9.- Soergel = $\sum(\text{abs}(y[i,]-x[j,])) / \sum(\text{apply}(\text{rbind}(y[i,],x[j,]),2,\text{max}))$
- 10.- Ware_hedges = $\sum(\text{abs}(y[i,]-x[j,])) / \sum(\text{apply}(\text{rbind}(y[i,],x[j,]),2,\text{max}))$

Value

A list with:

Data	A matrix with the initial data (x matrix).
SupData	A matrix with the supplementary data (y matrix).
D	The matrix of distances.
Coefficient	The coefficient used.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

Gower, J. C. (2006) Similarity dissimilarity and Distance, measures of. Encyclopedia of Statistical Sciences. 2nd. ed. Volume 12. Wiley

Examples

```
data(wine)
X = wine[,4:21]
D=DistContinuous(X)
```

Dlines

Connects two sets of points by lines

Description

Connects two sets of points by lines in a rowwise manner. Adapted from Graffelman(2013).

Usage

```
Dlines(SetA, SetB, lin = "dotted", color = "black", ...)
```

Arguments

SetA	First set of points.
SetB	Second set of points.
lin	Line style.
color	Line color.
...	Any other graphical parameters.

Details

Connects two sets of points by lines.

Value

NULL

Author(s)

Based on Graffelman (2013)

References

Jan Graffelman (2013). calibrate: Calibration of Scatterplot and Biplot Axes. R package version 1.7.2. <http://CRAN.R-project.org/package=calibrate>

Examples

```
## No examples
```

FactorToBinary	<i>Converts a Factor into its indicator matrix</i>
----------------	--

Description

Converts a factor into a binary matrix with as many columns as categories of the factor.

Usage

```
FactorToBinary(y, Name = NULL)
```

Arguments

y	A factor.
Name	Name to use in the final matrix.

Value

An indicator binary matrix.

Author(s)

Jose Luis Vicente-Villardón

Examples

```
y=factor(c(1, 1, 2, 2, 2, 2, 3, 3, 3, 3, 2, 2, 2, 1, 1, 1))
FactorToBinary(y)
```

GetScalesBiplot	<i>Calculates the scales for the variables on a linear biplot</i>
-----------------	---

Description

Calculates the scales for the variables on a linear prediction biplot. There are several types of scales and values that can be shown on the graphical representation. See details.

Usage

```
GetScalesBiplot(Biplot, nticks = 4, TypeScale = "Complete", ValuesScale = "Original")
```

Arguments

Biplot	Object of class PCA.Biplot.
nticks	Number of ticks for the biplot axes.
TypeScale	Type of scale to use : "Complete", "StdDev" or "BoxPlot".
ValuesScale	Values to show on the scale: "Original" or "Transformed".

Details

The function calculates the points on the biplot axes where the scales should be placed.

There are three types of scales when the transformations of the raw data are made by columns:

"Complete": Covers the whole range of the variable using the number of ticks specified in "nticks". A smaller number of points could be shown if some fall outside the range of the scatter.

"StdDev": The mean +/- 1, 2 and 3 times the standard deviation. A smaller number of points could be shown if some fall outside the range of the scatter.

"BoxPlot": Median, 25, 75 percentiles maximum and minimum values are shown. The extremes of the interquartile range are connected with a thicker line. A smaller number of points could be shown if some fall outside the range of the scatter.

There are two kinds of values that can be shown on the biplot axis:

"Original": The values before transformation. Only makes sense when the transformations are for each column.

"Transformed": The values after transformation, for example, after standardization.

Although the function is public, the end user will not normally use it.

Value

A list with the following components:

Ticks	A list containing the ticks for each variable.
Labels	A list containing the labels for each variable.

Author(s)

Jose Luis Vicente-Villardón

Ginv

G inverse

Description

Calculates the g-inverse of a squared matrix using the eigen decomposition and removing the eigenvalues smaller than a tolerance.

Usage

```
Ginv(X, tol = sqrt(.Machine$double.eps))
```

Arguments

X	Matrix to calculate the g-inverse.
tol	Tolerance.

Details

The function is useful to avoid singularities.

Value

Returns the g-inverse.

Author(s)

Jose Luis Vicente-Villardón

Examples

```
data(iris)
x=as.matrix(iris[,1:4])
S= t(x)
Ginv(S)
```

inbox

Checks if a point is inside a box

Description

Checks if a point is inside a box. The point is specified by its x and y coordinates and the box with the minimum and maximum values on both coordinate axis: xmin, xmax, ymin, ymax. The vertices of the box are then (xmin, ymin), (xmax, ymin), (xmax, ymax) and (xmin, ymax).

Usage

```
inbox(x, y, xmin, xmax, ymin, ymax)
```

Arguments

x	x coordinate of the point.
y	y coordinate of the point.
xmin	Minimum value of X.
xmax	Maximum value of X.
ymin	Minimum value of Y.
ymax	Maximum value of Y.

Value

Returns a logical value: TRUE if the point is inside the box and FALSE otherwise.

Author(s)

Jose Luis Vicente Villardon

Examples

```
inbox(0, 0, -1, 1, -1, 1)
```

IniTransform

Initial transformation of a data matrix

Description

Initial transformation of data before the construction of a biplot (or any other technique).

Usage

```
IniTransform(X, InitTransform = "None", transform = "Standardize columns")
```

Arguments

X	Original Raw Data Matrix.
InitTransform	Previous transformation (Logarithm or logit).
transform	Transformation to use. See details.

Details

Possible Transformations are:

- 1.- "Raw Data": When no transformation is required.
- 2.- "Subtract the global mean": Eliminate an effect common to all the observations
- 3.- "Double centering" : Interaction residuals. When all the elements of the table are comparable. Useful for AMMI models.
- 4.- "Column centering": Remove the column means.
- 5.- "Standardize columns": Remove the column means and divide by its standard deviation.
- 6.- "Row centering": Remove the row means.
- 7.- "Standardize rows": Divide each row by its standard deviation.
- 8.- "Divide by the column means and center": The resulting dispersion is the coefficient of variation.
- 9.- "Normalized residuals from independence" for a contingency table.

The transformation can be provided to the function by using the string between the quotes or just the associated number.

The supplementary rows and columns are not used to calculate the parameters (means, standard deviations, etc). Some of the transformations are not compatible with supplementary data.

Value

X Transformed data matrix.

Author(s)

Jose Luis Vicente-Villardón

References

M. J. Baxter (1995) Standardization and Transformation in Principal Component Analysis, with Applications to Archaeometry. *Journal of the Royal Statistical Society. Series C (Applied Statistics)*. Vol. 44, No. 4 (1995) , pp. 513-527

Kroonenberg, P. M. (1983). *Three-mode principal component analysis: Theory and applications* (Vol. 2). DSWO press. (Chapter 6)

Examples

```
data(iris)
x=as.matrix(iris[,1:4])
x=IniTransform(x, transform=4)
x
```

MANOVA

Multivariate Analysis of Variance (MANOVA)

Description

Performs a Multivariate Analysis of Variance (MANOVA) based on matrix calculations. Is an extension of the function in the base package of R.

The function can take care of matrices of contrasts and matrices of linear combinations of variables in order to cope with complex designs.

Usage

```
MANOVA(Y, Group, C = NULL, M = NULL, Effects = NULL, InitialTransform = 5,  
AddOnes = FALSE, Contrasts = TRUE)
```

Arguments

Y	A matrix containing the response variables.
Group	A factor containing the groups to compare (or the treatments).
C	A matrix of contrasts on the groups.
M	A matrix with the linear combinations of the variables to test.
Effects	A factor with the effects in the rows of C.
InitialTransform	Initial transformation of the response variables.
AddOnes	Add a column of ones to the design matrix. By default is false.
Contrasts	Should each contrast be tested separately?. By default is TRUE.

Details

Performs a general MANOVA to compare several groups or treatments. Additional contrasts can be tested using the contrasts matrix **C**. This can also be separated into several effects.

Here we use an approach with matrices rather than the usual multivariate general linear model. Several designs can be obtained using the appropriate matrix of contrasts.

Value

An object of class "MANOVA" and "Canonical.Biplot".

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

- Amaro, I. R., Vicente-Villardón, J. L., & Galindo-Villardón, M. P. (2004). Manova Biplot para arreglos de tratamientos con dos factores basado en modelos lineales generales multivariantes. *Interciencia*, 29(1), 26-32.
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Examples

```
data(wine)
Y=as.matrix(wine[,4:21])
group=wine$Group
manvin=MANOVA(Y, Group=group)
summary(manvin)
```

MANOVA.Estimation	<i>Estimation of the MANOVA parameters.</i>
-------------------	---

Description

The function estimates the parameters of the MANOVA for a set of contrasts and a set of linear combinations of the dependent variables.

Usage

```
MANOVA.Estimation(Y, X, C, M)
```

Arguments

- | | |
|---|---|
| Y | The matrix of dependent variables. |
| X | The matrix of independent variables. |
| C | A matrix containing a set of contrasts on the columns of X. |
| M | A matrix containing a set of linear combinations of the columns of Y. |

Details

The function estimates the parameters of the MANOVA for a set of contrasts contained in a matrix C and a set of linear combinations of the dependent variables in a matrix M. The function is actually used in a more general procedure called MANOVA.

Value

Returns the main results of the MANOVA.

Author(s)

Jose Luis Vicente-Villardón, Laura Vicente-Gonzalez

References

Seber, G. A. (2009). *Multivariate observations* (Vol. 252). John Wiley & Sons.

mgc

Mixture Gaussian Clustering

Description

Model based clustering using mixtures of gaussian distributions.

Usage

```
mgc(x, NG = 2, init = "km", RemoveOutliers = FALSE, ConfidOutliers = 0.995,
tolerance = 1e-07, maxiter = 100, show = TRUE, ...)
```

Arguments

x	The data matrix.
NG	Number of groups or clusters to obtain.
init	Initial centers can be obtained from k-means ("km") or at random ("rd").
RemoveOutliers	Should the extreme values be removed to calculate the clusters?
ConfidOutliers	Percentage of the points to keep for the calculations when RemoveOutliers is true.
tolerance	Tolerance for convergence.
maxiter	Maximum number of iterations.
show	Should the likelihood at each iteration be shown?
...	Any other parameter that can affect k-means if that is the initial configuration.

Details

A basic algorithm for clustering with mixtures of gaussians with no restrictions on the covariance matrices.

Value

Clusters.

Author(s)

Jose Luis Vicente-Villardón

Examples

```
X=as.matrix(iris[,1:4])
mod1=mgc(X,NG=3)
plot(iris[,1:4], col=mod1$Classification)
table(iris[,5],mod1$Classification)
```

Ones

Matrix of ones

Description

Square matrix of ones

Usage

Ones(n)

Arguments

n Order of the matrix.

Details

Square matrix of ones.

Value

A matrix of ones of order n.

Author(s)

Jose Luis Vicente-Villardón

Examples

```
Ones(6)
```

PERMANOVA

*PERMANOVA: MANOVA based on distances***Description**

The correct application of MANOVA needs normal and homocedastic data and the number of variables be much smaller than the number of individuals, but for many applications the conditions do not hold. To extend the application to this data Anderson develops PERMANOVA. This non-parametric test based on distances uses permutation to approximate the sampling distribution of the test statistic.

Contrasts and Effects can be added to the calculations.

Usage

```
PERMANOVA(Distance, group, C = NULL, Effects = NULL, nperm = 1000, seed = NULL,
CoordPrinc = FALSE, dimens = 2, PCoA = "Standard", ProjectInd = TRUE, tol = 1e-04,
DatosIni = TRUE, PostHoc="bonferroni")
```

Arguments

Distance	A list of three elements containing the data, the distances between individuals and type of distance used.
group	A factor containing the groups to compare.
C	Contrast matrix. By default it is null and the identity is used.
Effects	A factor with the effects in the rows of C. By default it is null and each row is considered as an effect.
nperm	Number of permutations to perform. By default is 1000.
seed	Seed to start permutations. By default is null.
CoordPrinc	Should the principal coordinates be calculated?. By default is FALSE.
dimens	Number of dimensions to choose in the PCoA. By default is 2.
PCoA	The type of Principal Coordinates Analysis. There are two possibilities: * Standard * Weighted By default is Standard.
ProjectInd	Show the row coordinates. By default is TRUE.
tol	Tolerance.
DatosIni	It contains the initial data. By default is TRUE.
PostHoc	Correction method. There are eight possibilities: *holm: Holm *hochberg: Hochberg *hommel: Hommel

*bonferroni: Bonferroni. By default is this method.
 *BH: Benjamini & Hochberg
 *BY: Benjamini & Yekutieli
 *fdr: Benjamini & Hochberg
 *none

Details

The function performs a PERMANOVA Analysis.

Value

The PERMANOVA function create a list that return:

call	Function.
Title	Permutation based MANOVA.
Type	PERMANOVA.
Distances	A matrix containing the distances between individuals.
C	Contrasts Matrix.
Initial	Containing two matrices: * Global -> Global contrast. * Contrastes -> Contrasts for groups.
DistMuestral	Sample distribution of F-exp from permutations.
pvalue	Estimate p-value for PERMANOVA.
ExplainedVariance	Explained variance by Principal Coordinates selected.
Inertias	Eigenvalue, Explained variance, Cumulative explained variance.
MeanCoordinates	Mean Coordinates by groups for the dimensions obtained in the Principal Coordinates Analysis.
Qualities	Qualities representation by groups for the dimensions of PCoA.
CummulativeQualities	Cumulative qualities representation.
ClusterType	Cluster type selected.
Clusters	Clusters created.
ClusterNames	Names of clusters.
ClusterColors	Colors of clusters, color name and HTML code.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

Anderson, M. J. (2008). A new method for non-parametric multivariate analysis of variance. *Austral ecology*, 26(1):32–46.

Anderson, M. J. (2005). *Permanova: a fortran computer program for permutational multivariate analysis of variance*. Department of Statistics, University of Auckland, New Zealand, 24.

Examples

```
data(wine)
X = wine[,4:21]
X=IniTransform(X)
D = DistContinuous (X)
perwine=PERMANOVA(D, wine$Group)
perwine
```

```
C = matrix(c(1, 1, -1, 1, 1, -1, 1, 1, 1, -1, -1, 1), nrow=3, byrow=TRUE)
rownames(C)=c("C1", "C2", "C3")
colnames(C)=levels(wine$Group)
```

```
effects=factor(c(1,2,3))
levels(effects)=c("Origin", "Year", "Interaction")
perwine2=PERMANOVA(D, wine$Group, C=C, Effects=effects, CoordPrinc = TRUE)
summary(perwine2)
```

PERMANOVA.Estimation *Estimation of the PERMANOVA parameters*

Description

Estimation of the PERMANOVA parameters.

Usage

```
PERMANOVA.Estimation(D, X, C, Effects = NULL)
```

Arguments

D	A matrix of distances.
X	A matrix of independent variables.
C	Contrast matrix. By default it is null and the identity is used.
Effects	A factor with the effects in the rows of C. By default it is null and each row is considered as an effect.

Details

Estimation of the PERMANOVA parameters.

Value

Global	Significance for the global effect
Contrastes	Significance for each contrast

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

Anderson, M. J. (2008). A new method for non-parametric multivariate analysis of variance. *Austral ecology*, 26(1):32–46.

Anderson, M. J. (2005). *Permanova: a fortran computer program for permutational multivariate analysis of variance*. Department of Statistics, University of Auckland, New Zealand, 24.

PerMANOVA.Simple	<i>PERMANOVA from a matrix of distances</i>
------------------	---

Description

This function makes a PERMANOVA from distances matrix and factor for groups.

Usage

```
PerMANOVA.Simple(D, grupo, nperm = 999, seed = NULL, C = NULL)
```

Arguments

D	A matrix containing the distances between individuals.
grupo	A factor containing the groups to compare.
nperm	Number of permutation that want to perform. By default it is 999.
seed	Seed to start permutations. By default it is null.
C	Contrast matrix. By default it is null.

Value

The PERMANOVA.Simple function create a list that return:

call	Function
nperm	Number of permutation.

Inicial	Containing: * TSS -> Total sum of squares. * BSS -> Between groups sum of squares. * WSS -> Within groups sum of squares. * glt -> Total degrees of freedom. * glb -> Between groups degrees of freedom. * glw -> Within groups degrees of freedom. * Fexp -> Experimental F.
Fvals	F values of the permutation.
pval	Estimate p-value for PERMANOVA.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

References

Anderson, M. J. (2001). A new method for non-parametric multivariate analysis of variance. *Austral ecology*, 26(1):32–46.

Anderson, M. J. (2005). *Permanova: a fortran computer program for permutational multivariate analysis of variance*. Department of Statistics, University of Auckland, New Zealand, 24.

Examples

```
data(wine)
X = wine[,4:21]
Dist = DistContinuous(X)
PerMANOVA.Simple(Dist$D, wine$Group)
```

plot.BootCanonAnalysis

Plots the principal coordinates of the group centers and the bootstrap confidence regions

Description

Plots the principal coordinates of the group centers and the bootstrap confidence regions.

Usage

```
## S3 method for class 'BootCanonAnalysis'
plot(x, A1 = 1, A2 = 2, centred = FALSE, confidence = 0.9,
     PlotReplicates = TRUE, MeanCex = 1.5, MeanPch = 16,
     Title = "Bootstrap Canonical Analysis based on Distances",
     LabelMeans = TRUE, MeanLabels = NULL, MeanColors = NULL, SmartLabels = TRUE,
     BootstrapPlot = "e1", PlotIndiv = FALSE, LabelInd = FALSE, IndLabels = NULL,
     IndColors = NULL, CexInd = 0.5, PchInd = 1, ConvexHullsInd = FALSE, ...)
```

Arguments

x	The object to plot.
A1	Dimension to plot on the X axis.
A2	Dimension to plot on the Y axis.
centred	Plot centers of the bootstrap regions.
confidence	Confidence for the bootstrap regions.
PlotReplicates	Should all the bootstrap replicates be plotted.
MeanCex	Size of the points and text representing the centroids of the groups.
MeanPch	Marks of the points and text representing the centroids of the groups.
Title	Main title of the graph.
LabelMeans	Should the groups be labelled?
MeanLabels	Labels for the group means.
MeanColors	Colors for the group means.
SmartLabels	Should the labels be placed in a smart way?
BootstrapPlot	Should the bootstrap regions be plotted?
PlotIndiv	Should the individuals be plotted?
LabelInd	Should individuals be labelled?
IndLabels	Labels for the individuals.
IndColors	Colors for the rows (individuals).
CexInd	Sizes for the rows (individuals).
PchInd	Marks for the rows (individuals).
ConvexHullsInd	Convex hulls containing the individuals of each group.
...	Any other graphical parameters.

Details

Plots the principal coordinates of the means of the groups with the confidence bootstrap region.

Value

The plot.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

plot.ellipse *Plot a concentration ellipse*

Description

Plot a concentration ellipse obtained from ConcEllipse.

Usage

```
## S3 method for class 'ellipse'  
plot(x, add = TRUE, labeled = FALSE, center = FALSE, centerlabel = "Center",  
initial = FALSE, ...)
```

Arguments

x	An object with class ellipse obtained from ConcEllipse.
add	Should the ellipse be added to the current plot?
labeled	Should the ellipse be labelled with the confidence level?
center	Should the center be plotted?
centerlabel	Label for the center.
initial	Should the initial data be plotted?
...	Any other graphical parameter that can affects the plot (as color, etc ...).

Details

Plots an ellipse containing a specified percentage of the data.

Value

No value returned.

Author(s)

Jose Luis Vicente-Villardón

References

Meulman, J. J., & Heiser, W. J. (1983). The display of bootstrap solutions in multidimensional scaling. Murray Hill, NJ: Bell Laboratories.

Linting, M., Meulman, J. J., Groenen, P. J., & Van der Kooij, A. J. (2007). Stability of nonlinear principal components analysis: An empirical study using the balanced bootstrap. *Psychological Methods*, 12(3), 359.

See Also

[ConcEllipse](#)

Examples

```

data(iris)
dat=as.matrix(iris[1:50,1:2])
plot(iris[,1], iris[,2],col=iris[,5], asp=1)
E=ConcEllipse(dat, confidence=0.95)
plot(E, add=TRUE, center=TRUE)

```

plot.MANOVA

*Plots the results of a MANOVA Biplot***Description**

Plots the results of a MANOVA Biplot.

Usage

```

## S3 method for class 'MANOVA'
plot(x, A1 = 1, A2 = 2, ScaleGraph = TRUE, PlotGroups = TRUE,
     PlotVars = TRUE, PlotInd = TRUE, WhatInds=NULL,WhatVars=NULL, WhatGroups=NULL,
     IndLabels=NULL, VarLabels=NULL, GroupLabels=NULL, AbbreviateLabels=FALSE,
     LabelInd=TRUE, LabelVars = TRUE, CexGroup=1, PchGroup=16, margin=0.1,
     AddLegend=FALSE, ShowAxes=FALSE, LabelAxes=FALSE, LabelGroups=TRUE,
     PlotCircle = TRUE, ConvexHulls = FALSE, TypeCircle = "M", ColorGroups = NULL,
     ColorVars = NULL, LegendPos="topright", ColorInd = NULL, voronoi = TRUE,
     mode="a", TypeScale = "Complete", ValuesScale = "Original", MinQualityVars = 0,
     dpq = 0, dpi=0, dp=0, PredPoints=0, PlotAxis = FALSE, CexInd = NULL,
     CexVar = NULL, PchInd = NULL, PchVar = NULL, ColorVar=NULL, ShowAxis=FALSE,
     VoronoiColor="black", ShowBox=FALSE, ShowTitle=TRUE,PlotClus = FALSE,
     TypeClus = "ch", ClustConf = 1, ClustCenters = FALSE, UseClusterColors = TRUE,
     CexClustCenters=1, ...)

```

Arguments

x	An object of class "MANOVA.Biplot".
A1	Dimension for the first axis. 1 is the default.
A2	Dimension for the second axis. 2 is the default.
ScaleGraph	Rescale the coordinates to optimal matching.
PlotGroups	Should the group centers be plotted?
PlotVars	Should the variables be plotted?
PlotInd	Should the individuals be plotted?
WhatInds	What individuals should be plotted? A vector.
WhatVars	What variables should be plotted? A vector.
WhatGroups	What groups should be plotted? A vector.
IndLabels	Labels for the individuals.

VarLabels	Labels for the variables.
GroupLabels	Labels for the groups.
AbbreviateLabels	Should the labels be Abbreviated for simplicity of the graph?
LabelInd	Should the individuals be labelled?
LabelVars	Should the variables be labelled?
CexGroup	Size of the points for groups.
PchGroup	Mark of the points for groups.
margin	Margin for labels (in percentage).
AddLegend	Should a legend be added?
ShowAxes	Should the axes be shown?
LabelAxes	Should the axes be labelled?
LabelGroups	Should the groups be labelled?
PlotCircle	Should the confidence regions for the groups be plotted?
ConvexHulls	Should the convex hulls containing the individuals for each group be plotted?
TypeCircle	Type of confidence region: Univariate (U), Bonferroni(B), Multivariate (M) or Classical (C). By default is "M".
ColorGroups	User colors for the groups. Default colors will be used if NULL.
ColorVars	User colors for the variables. Default colors will be used if NULL.
LegendPos	Position of the legend.
ColorInd	User colors for the individuals. Default colors will be used if NULL.
voronoi	Should the Voronoi diagram with the prediction regions for each group be plotted?
mode	Mode of the biplot: "p", "a", "b", "h", "ah" and "s". See details.
TypeScale	Type of scale to use : "Complete", "StdDev" or "BoxPlot". See details.
ValuesScale	Values to show on the scale: "Original" or "Transformed".
MinQualityVars	Minimum quality of representation for a variable to be plotted.
dpg	A set of indices with the variables that will show projections onto the variables.
dpi	A set of indices with the individuals that will show the projections.
dp	A set of indices with the variables that will show the projections of the individuals.
PredPoints	A vector with integers. The group centers listed in the vector are projected onto all the variables.
PlotAxis	Not Used
CexInd	Size of the points for individuals.
CexVar	Size of the points for variables.
PchInd	Markers of the points for individuals.
PchVar	Markers of the points for variables.

ColorVar	Colors of the points for variables.
ShowAxis	Should axis scales be shown?
VoronoiColor	Color for the Voronoi diagram.
ShowBox	Should a box around the points be plotted?
ShowTitle	Should Title be shown?
PlotClus	Should the clusters be plotted?
TypeClus	Type of plot for the clusters. ("ch"- Convex Hull, "el"- Ellipse or "st"- Star)
ClusConf	Percent of points included in the cluster. Only the ClusConf percent of the points nearest to the center will be used to calculate the cluster.
ClusCenters	Should the cluster centers be plotted?
UseClusterColors	Should the cluster colors be used in the plot?
CexClusCenters	Size of the cluster centres.
...	Any other graphical parameter.

Details

The function plots the results of a MANOVA Biplot. The coordinates for Groups, Individuals and Variables can be shown or not on the plot, each of the three can also be labeled separately. The are parameters to control the way each different set of coordinates is plotted and labeled.

There are several modes for plotting the biplot.

"p".- Points (Rows and Columns are represented by points)

"a".- Arrows (The traditional representation with points for rows and arrows for columns)

"b".- The arrows for the columns are extended to both extremes of the plot and labeled outside the plot area.

"h".- The arrows for the columns are extended to the positive extreme of the plot and labeled outside the plot area.

"ah".- Same as arrows but labeled outside the plot area.

"s".- The directions (or biplot axes) have a graded scale for prediction of the original values.

The *TypeScale* argument applies only to the "s" mode. There are three types:

"Complete".- An equally spaced scale covering the whole range of the data is calculates.

"StdDev".- Mean with one, two and three standard deviations

"BoxPlot".- Box-Plot like Scale (Median, 25 and 75 percentiles, maximum and minimum values.)

The *ValuesScale* argument applies only to the "s" mode and controls if the labels show the *Original* ot *Transformed* values.

Some of the initial transformations are not compatible with some of the types of biplots and scales. For example, It is not possible to recover by projection the original values when you double centre de data. In that case you have the residuals for interaction and only the transformed values make sense.

Value

A plot is returned.

Author(s)

Jose Luis Vicente-Villardón, Laura Vicente-Gonzalez

References

Gabriel, K. R. (1972). Analysis of meteorological data by means of canonical decomposition and biplots. *Journal of Applied Meteorology*, 11(7), 1071-1077.

Amaro, I. R., Vicente-Villardón, J. L., & Galindo Villardón, M. P. (2004). Manova Biplot para arreglos de tratamientos con dos factores basado en modelos lineales generales multivariantes. *Interciencia*, 29(1), 26-32.

Sierra, C., Ruiz-Barzola, O., Menendez, M., Demey, J. R., & Vicente-Villardón, J. L. (2017). Geochemical interactions study in surface river sediments at an artisanal mining area by means of Canonical (MANOVA)-Biplot. *Journal of Geochemical Exploration*, 175, 72-81.

Examples

```
data(wine)
X=wine[,4:21]
manbip=MANOVA(X, Group=wine$Group)
plot(manbip, TypeCircle="B", Voronoi=FALSE)
```

plot.MANOVA.Biplot *Plots the results of a MANOVA Biplot*

Description

Plots the results of a MANOVA Biplot

Usage

```
## S3 method for class 'MANOVA.Biplot'
plot(x, A1 = 1, A2 = 2, ScaleGraph = TRUE, PlotGroups = TRUE,
PlotVars = TRUE, PlotInd = TRUE, WhatInds = NULL, WhatVars = NULL, WhatGroups = NULL,
IndLabels = NULL, VarLabels = NULL, GroupLabels = NULL, AbbreviateLabels = FALSE,
LabelInd = TRUE, LabelVars = TRUE, CexGroup = 1, PchGroup = 16, margin = 0.1,
AddLegend = FALSE, ShowAxes = FALSE, LabelAxes = FALSE, LabelGroups = TRUE,
PlotCircle = TRUE, ConvexHulls = FALSE, TypeCircle = "M", ColorGroups = NULL,
ColorVars = NULL, LegendPos = "topright", ColorInd = NULL, voronoi = TRUE,
mode = "a", TypeScale = "Complete", ValuesScale = "Original", MinQualityVars = 0,
dpg = 0, dpi = 0, dp = 0, PredPoints = 0, PlotAxis = FALSE, CexInd = NULL,
CexVar = NULL, PchInd = NULL, PchVar = NULL, ColorVar = NULL, ShowAxis = FALSE,
VoronoiColor = "black", ShowBox = FALSE, ShowTitle = TRUE, PlotClus = FALSE,
```

```
TypeClus = "ch", ClustConf = 1, ClustCenters = FALSE, UseClusterColors = TRUE,
CexClustCenters = 1, ...)
```

Arguments

x	An object of class "MANOVA.Biplot"
A1	Dimension for the first axis. 1 is the default.
A2	Dimension for the second axis. 2 is the default.
ScaleGraph	Reescale the coordinates to optimal matching.
PlotGroups	Should the group centers be plotted?
PlotVars	Should the variables be plotted?
PlotInd	Should the individuals be plotted?
WhatInds	What individuals should be plotted? A vector.
WhatVars	What variables should be plotted? A vector.
WhatGroups	What groups should be plotted? A vector.
IndLabels	Labels for the individuals
VarLabels	Labels for the variables
GroupLabels	Labels for the groups
AbbreviateLabels	Should the labels be Abbreviated for simplicity of the graph?
LabelInd	Should the individuals be labelled?
LabelVars	Should the variables be labelled?
CexGroup	Size of the points for groups
PchGroup	Mark of the points for groups
margin	Margin for labels (in percentage)
AddLegend	Should a legend be added?
ShowAxes	Should the axes be shown?
LabelAxes	Should the axes be labelled?
LabelGroups	Should the groups be labelled?
PlotCircle	Should the confidence regions for the groups be plotted?
ConvexHulls	Should the convex hulls containing the individuals for each group be plotted?
TypeCircle	Type of confidence region: Univariate (U), Bonferroni(B), Multivariate (M) or Classical (C)
ColorGroups	User colors for the groups. Default colors will be used if NULL.
ColorVars	User colors for the variables. Default colors will be used if NULL.
LegendPos	Position of the legend.
ColorInd	User colors for the individuals. Default colors will be used if NULL.
voronoi	Should the voronoi diagram with the prediction regions for each group be plotted?

<code>mode</code>	Mode of the biplot: "p", "a", "b", "h", "ah" and "s".
<code>TypeScale</code>	Type of scale to use : "Complete", "StdDev" or "BoxPlot"
<code>ValuesScale</code>	Values to show on the scale: "Original" or "Transformed"
<code>MinQualityVars</code>	Minimum quality of representation for a variable to be plotted
<code>dpg</code>	A set of indices with the variables that will show projections onto the variables
<code>dpi</code>	A set of indices with the individuals that will show the projections
<code>dp</code>	A set of indices with the variables that will show the projections of the individuals
<code>PredPoints</code>	A vector with integers. The group centers listed in the vector are projected onto all the variables.
<code>PlotAxis</code>	Not Used
<code>CexInd</code>	Size of the points for individuals.
<code>CexVar</code>	Size of the points for variables.
<code>PchInd</code>	Markers of the points for individuals.
<code>PchVar</code>	Markers of the points for variables.
<code>ColorVar</code>	Colors of the points for variables.
<code>ShowAxis</code>	Should axis scales be shown?
<code>VoronoiColor</code>	Color for the Voronoi diagram
<code>ShowBox</code>	Should a box around the points be plotted?
<code>ShowTitle</code>	Should Title be shown?
<code>PlotClus</code>	Should the clusters be plotted?
<code>TypeClus</code>	Type of cluster to plot (convex hull, ellipse or star)
<code>ClustConf</code>	Confidence level for the clusters (percentage plotted)
<code>ClustCenters</code>	Should the cluster centres be plotted?
<code>UseClusterColors</code>	Use cluster colors for individuals
<code>CexClustCenters</code>	Size of the cluster centers
<code>...</code>	Any other graphical parameter

Details

The function plots the results of a MANOVA Biplot. The coordinates for Groups, Individuals and Variables can be shown or not on the plot, each of the three can also be labeled separately. The are parameters to control the way each different set of coordinates is plotted and labeled.

There are several modes for plotting the biplot.

"p".- Points (Rows and Columns are represented by points)

"a" .- Arrows (The traditional representation with points for rows and arrows for columns)

"b" .- The arrows for the columns are extended to both extremes of the plot and labeled outside the plot area.

"h" .- The arrows for the columns are extended to the positive extreme of the plot and labeled outside the plot area.

"ah" .- Same as arrows but labeled outside the plot area.

"s" .- The directions (or biplot axes) have a graded scale for prediction of the original values.

The *TypeScale* argument applies only to the "s" mode. There are three types:

"Complete" .- An equally spaced scale covering the whole range of the data is calculates.

"StdDev" .- Mean with one, two and three stadard deviations

"BoxPlot" .- Box-Plot like Scale (Median, 25 and 75 percentiles, maximum and minimum values.)

The *ValuesScale* argument applies only to the "s" mode and controls if the labels show the *Original* ot *Transformed* values.

Some of the initial transformations are not compatible with some of the types of biplots and scales. For example, It is not possible to recover by projection the original values when you double centre de data. In that case you have the residuals for interaction and only the transformed values make sense.

Value

A plot is returned

Author(s)

Jose Luis Vicente Villardon, Laura Vicente Gonzalez

References

Gabriel, K. R. (1972). Analysis of meteorological data by means of canonical decomposition and biplots. *Journal of Applied Meteorology*, 11(7), 1071-1077.

Amaro, I. R., Vicente-Villardón, J. L., & Galindo Villardón, M. P. (2004). Manova Biplot para arreglos de tratamientos con dos factores basado en modelos lineales generales multivariantes. *In-terciencia*, 29(1), 26-32.

Sierra, C., Ruíz-Barzola, O., Menéndez, M., Demey, J. R., & Vicente-Villardón, J. L. (2017). Geochemical interactions study in surface river sediments at an artisanal mining area by means of Canonical (MANOVA)-Biplot. *Journal of Geochemical Exploration*, 175, 72-81.

Examples

```
data(wine)
X=wine[,4:21]
manbip=MANOVA(X, Group=wine$Group)
plot(manbip, TypeCircle="U", Voronoi=FALSE)
```

plot.Permanova

Plots the results of the PERMANOVA function

Description

Plots the principal coordinates of the group centers and the bootstrap confidence regions.

Usage

```
## S3 method for class 'PERMANOVA'
plot(x, A1 = 1, A2 = 2, ScaleGraph = TRUE, ShowAxis = FALSE,
     ShowAxes = FALSE, LabelAxes = TRUE, margin = 0.1, ShowBox = TRUE, PlotGroups = TRUE,
     LabelGroups = TRUE, CexGroup = 1.5, PchGroup = 16, ColorGroup = NULL, voronoi = TRUE,
     VoronoiColor = "black", PlotInd = FALSE, LabelInd = TRUE, CexInd = 0.8, PchInd = 3,
     ColorInd = NULL, WhatInds = NULL, IndLabels = NULL, PlotVars = TRUE, LabelVar = TRUE,
     CexVar = NULL, PchVar = NULL, ColorVar = NULL, WhatVars = NULL, VarLabels = NULL,
     mode = "a", TypeScale = "Complete", ValuesScale = "Original", SmartLabels = TRUE,
     AddLegend = TRUE, LegendPos = "topright", PlotCircle = TRUE, ConvexHulls = FALSE,
     TypeCircle = "M", MinQualityVars = 0, dpg = 0, dpi = 0, PredPoints = 0,
     PlotClus = TRUE, TypeClus = "ch", ClustConf = 1, CexClustCenters=1, ClustCenters = FALSE,
     UseClusterColors = TRUE, ...)
```

Arguments

x	An object of class "PERMANOVA"
A1	Dimension for the first axis. 1 is the default.
A2	Dimension for the second axis. 2 is the default.
ScaleGraph	Rescale the coordinates to optimal matching.
ShowAxis	Should the axis passing through the origin be plotted?
ShowAxes	Should the axes be shown?
LabelAxes	Should the axes be labelled?
margin	Margin for labels (in percentage).
ShowBox	Should a box around the points be plotted?
PlotGroups	Should the group centers be plotted?
LabelGroups	Should the groups be labelled?
CexGroup	Size of the points for groups.
PchGroup	Mark of the points for groups.
ColorGroup	User colors for the groups. Default colors will be used if NULL.
voronoi	Should the Voronoi diagram with the prediction regions for each group be plotted?
VoronoiColor	Color for the Voronoi diagram.
PlotInd	Should the individuals be plotted?

LabelInd	Should the individuals be labelled?
CexInd	Size of the points for individuals.
PchInd	Markers of the points for individuals.
ColorInd	User colors for the individuals. Default colors will be used if NULL.
WhatInds	What individuals should be plotted? A vector.
IndLabels	Labels for the individuals.
PlotVars	Should the variables be plotted?
LabelVar	Should the variables be labelled?
CexVar	Size of the points for variables.
PchVar	Markers of the points for variables.
ColorVar	Colors of the points for variables.
WhatVars	What variables should be plotted? A vector.
VarLabels	Labels for the variables.
mode	Mode of the biplot: "p", "a", "b", "h", "ah" and "s".
TypeScale	Type of scale to use : "Complete", "StdDev" or "BoxPlot".
ValuesScale	Values to show on the scale: "Original" or "Transformed".
SmartLabels	Should the labels be plotted in a smart way?
AddLegend	Should a legend be added?
LegendPos	Position of the legend.
PlotCircle	Should the confidence regions for the groups be plotted?
ConvexHulls	Should the convex hulls containing the individuals for each group be plotted?
TypeCircle	Type of confidence region: Univariate (U), Bonferroni(B), Multivariate (M) or Classical (C). By default is "M".
MinQualityVars	Minimum quality of representation for a variable to be plotted.
dpg	A set of indices with the variables that will show projections onto the variables.
dpi	A set of indices with the individuals that will show the projections.
PredPoints	A vector with integers. The group centers listed in the vector are projected onto all the variables.
PlotClus	Should the clusters be plotted?
TypeClus	Type of plot for the clusters. ("ch"- Convex Hull, "el"- Ellipse or "st"- Star)
ClusConf	Percent of points included in the cluster. only the ClusConf percent of the points nearest to the center will be used to calculate the cluster.
CexClusCenters	Size of the cluster centers.
ClusCenters	Should the cluster centers be plotted.
UseClusterColors	Should the cluster colors be used in the plot.
...	Any other graphical parameter.

Details

Plots the principal coordinates of the group centers and the bootstrap confidence regions.

Value

The plot.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

Examples

```
data(wine)
X = wine[,4:21]
X=IniTransform(X)
D = DistContinuous (X)
perwine=PERMANOVA(D, wine$Group, CoordPrinc=TRUE)
plot(perwine)
```

PlotClustersBiplot *Plot clusters on a biplot.*

Description

Highlights several groups or clusters on a biplot representation.

Usage

```
PlotClustersBiplot(A, Groups = Ones(c(nrow(A), 1)), TypeClus = "st", ClusterColors =
NULL, ClusterNames = NULL, centers = TRUE, ClustConf = 1, Legend = FALSE, LegendPos =
"topright", CexClustCenters = 1, ...)
```

Arguments

A	Coordinates of the points in the scattergram.
Groups	Factor defining the groups to be highlighted.
TypeClus	Type of representation of the clusters. For the moment just a convex hull but in the future ellipses and stars will be added.
ClusterColors	A vector of colors with as many elements as clusters. If NULL the function selects the rainbow colors.
ClusterNames	A vector of names with as many elements as clusters.
centers	Logical variable to control if centres of the clusters are plotted.

ClustConf	Percent of points included in the cluster. Only the ClusConf percent of the points nearest to the center will be used to calculate the cluster.
Legend	Should a legend be plotted?
LegendPos	Position of the legend.
CexClustCenters	Size of the centers.
...	Any other graphical parameters.

Details

The clusters to plot should be added to the biplot object using the function `AddClusterToBiplot`.

Value

It takes effects on a plot.

Author(s)

Jose Luis Vicente-Villardón

See Also

[AddClusterToBiplot](#)

PostHocComp	<i>Post Hoc pairwise comparisons</i>
-------------	--------------------------------------

Description

Creates a contrast C matrix of post hoc comparisons among groups.

Usage

```
PostHocComp(grupo)
```

Arguments

grupo A factor containing the groups or treatments.

Details

Creates a contrast C matrix of post hoc comparisons among groups. The rows of the contrast matrix are not orthogonal.

Value

The `PostHocComp` function return a matrix to compare the levels of groups introduced.

Author(s)

Laura Vicente-Gonzalez and Jose Luis Vicente-Villardón

Examples

```
data(wine)
PostHocComp(wine$Group)
```

ProcrustesSimple *Simple Procrustes Analysis*

Description

Simple Procrustes Analysis for two matrices

Usage

```
ProcrustesSimple(X, Y, centre = FALSE)
```

Arguments

X	Matrix of the first configuration.
Y	Matrix of the second configuration.
centre	Should the matrices be centered before the calculations?

Details

Orthogonal Procrustes Analysis for two configurations X and Y. The first configuration X is used as a reference and the second, Y, is transformed to match the reference as much as possible. $X = s Y T + 1t + E = Z + E$

Value

An object of class Procrustes. This has components:

X	First Configuration.
Y	Second Configuration.
Yrot	Second Configuration after the transformation.
T	Rotation Matrix.
t	Translation Vector.
s	Scale Factor.
rsss	Residual Sum of Squares.
fit	Goodness of fit as percent of explained variance.
correlations	Correlations among the columns of X and Z.

Author(s)

Jose Luis Vicente-Villardón

References

Ingwer Borg, I. & Groenen, P. J.F. (2005). Modern Multidimensional Scaling. Theory and Applications. Second Edition. Springer

spiders

Hunting Spiders Data

Description

Hunting spiders data transformed into Presence/Absence.

Usage

```
data("spiders")
```

Format

A data frame with 28 observations of presence/absence on the following 12 hunting spider species.

Alopacce a factor with levels Absent Present of the species Alopecosa accentuata.

Alopcune a factor with levels Absent Present of the species Alopecosa cuneata.

Alopfabr a factor with levels Absent Present of the species Alopecosa fabrilis.

Arctlute a factor with levels Absent Present of the species Arctosa lutetiana.

Arctperi a factor with levels Absent Present of the species Arctosa perita.

Auloalbi a factor with levels Absent Present of the species Aulonia albimana.

Pardlugu a factor with levels Absent Present of the species Pardosa lugubris.

Pardmont a factor with levels Absent Present of the species Pardosa monticola.

Pardnigr a factor with levels Absent Present of the species Pardosa nigriceps.

Pardpull a factor with levels Absent Present of the species Pardosa pullata.

Trocterr a factor with levels Absent Present of the species Trochosa terricola.

Zoraspin a factor with levels Absent Present of the species Zora spinimana.

Source

van der Aart, P. J. M., and Smeenk-Enserink, N. (1975) Correlations between distributions of hunting spiders (Lycosidae, Ctenidae) and environmental characteristics in a dune area. Netherlands Journal of Zoology 25, 1-45.

Examples

```
data(spiders)
```

spidersb

Hunting Spiders Data

Description

Hunting spiders data transformed into 1/0.

Usage

```
data("spidersb")
```

Format

A data frame with 28 observations of presence/absence of 12 hunting spider species

Alopacce Presence/Absence of the species *Alopecosa accentuata*

Alopcune Presence/Absence of the species *Alopecosa cuneata*

Alopfabr Presence/Absence of the species *Alopecosa fabrilis*

Arctlute Presence/Absence of the species *Arctosa lutetiana*

Arctperi Presence/Absence of the species *Arctosa perita*

Auloalbi Presence/Absence of the species *Aulonia albimana*

Pardlugu Presence/Absence of the species *Pardosa lugubris*

Pardmont Presence/Absence of the species *Pardosa monticola*

Pardnigr Presence/Absence of the species *Pardosa nigriceps*

Pardpull Presence/Absence of the species *Pardosa pullata*

Trocterr Presence/Absence of the species *Trochosa terricola*

Zoraspin Presence/Absence of the species *Zora spinimana*

Source

van der Aart, P. J. M., and Smeenk-Enserink, N. (1975) Correlations between distributions of hunting spiders (Lycosidae, Ctenidae) and environmental characteristics in a dune area. *Netherlands Journal of Zoology* 25, 1-45.

Examples

```
data(spidersb)
```

summary.BootDisMANOVA *Summarizes the results of a Bootstrap Manova based on distances*

Description

Summarizes the results of a Bootstrap Manova based on distances.

Usage

```
## S3 method for class 'BootDisMANOVA'  
summary(object, Latex = FALSE, ...)
```

Arguments

object	An object of class "BootDisMANOVA".
Latex	Should Latex tables be provided?
...	Any other parameter.

Details

Summarizes the results of a Bootstrap Manova based on distances including Latex tables.

Value

Prints the results.

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardón

Examples

```
data(wine)  
X = wine[,4:21]  
D = DistContinuous(X)  
bootwine=BootDisMANOVA(D, wine$Group)  
summary(bootwine)
```

 TextSmart

Labels of a Scatter

Description

Plots labels of points in a scattergram. labels for points with positive x are placed on the right of the points, and labels for points with negative values on the left.

Usage

```
TextSmart(A, Labels, CexPoints = 1, ColorPoints = "black", ...)
```

Arguments

A	Coordinates of the points for the scattergram.
Labels	Labels for the points.
CexPoints	Size of the labels.
ColorPoints	Colors of the labels.
...	Additional graphical arguments.

Details

The function is used to improve the readability of the labels in a scattergram.

Value

No value returned.

Author(s)

Jose Luis Vicente-Villardón

 wine

Wine data

Description

Comparison of young wines of Ribera de Duero and Toro.

Usage

```
data("wine")
```


Format

A data frame with 45 observations on the following 21 variables.

Year A factor with levels 1986 1987

Origin A factor with levels Ribera Toro

Group A factor with levels R86 R87 T86 T87

A Alcoholic content (percentage)

VA volatil acidity - g acetic acid/l

TA Total tritable acidity - g tartaric acid/l

FA Fixed acidity - g tartaric acid/l

pH pH

TPR Total phenolics - g gallic acid /l - Folin

TPS Total phenolics - Somers

V Substances reactive to vanilin - mg catechin/l

PC Procyanidins - mg cyanidin/l

ACR Total Anthocyanins - mg/l - method 1

ACS Total Anthocyanins - mg/l - methods 2

ACC Malvidin - malvidin-3-glucoside mg/l

CI Color density -

CI2 Color density 2

H Wine Hue Color

I Degree of Ionization - Percent

CA Chemical Age

VPC ratio V/PC

Details

Comparison of young wines of Ribera de Duero and Toro.

Source

Rivas-Gonzalo, J. C., Gutierrez, Y., Polanco, A. M., Hebrero, E., Vicente-Villardón, J. L., Galindo, P., & Santos-Buelga, C. (1993). Biplot analysis applied to enological parameters in the geographical classification of young red wines. *American journal of enology and viticulture*, 44(3), 302-308.

References

Rivas-Gonzalo, J. C., Gutierrez, Y., Polanco, A. M., Hebrero, E., Vicente-Villardón, J. L., Galindo, P., & Santos-Buelga, C. (1993). Biplot analysis applied to enological parameters in the geographical classification of young red wines. *American journal of enology and viticulture*, 44(3), 302-308.

Examples

```
data(wine)
```

Zeros

Matrix of zeros

Description

Matrix of zeros as in Matlab.

Usage

Zeros(n)

Arguments

n Dimension of the matrix.

Value

A matrix of zeros.

Author(s)

Jose Luis Vicente-Villardón

Examples

Zeros(6)

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