Package ‘MultBiplotR’

January 20, 2025

Type Package

Title Multivariate Analysis Using Biplots in R

Version 23.11.0

Date 2023-11-16

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Description Several multivariate techniques from a biplot perspective. It is the translation (with many improvements) into R of the previous package developed in 'Matlab'. The package contains some of the main developments of my team during the last 30 years together with some more standard techniques. Package includes: Classical Biplots, HJ-Biplot, Canonical Biplots, MANOVA Biplots, Correspondence Analysis, Canonical Correspondence Analysis, Canonical STATIS-ACT, Logistic Biplots for binary and ordinal data, Multidimensional Unfolding, External Biplots for Principal Coordinates Analysis or Multidimensional Scaling, among many others. References can be found in the help of each procedure.

License GPL (>= 2)

Encoding UTF-8

Repository CRAN

Depends R (>= 4.0.0)

Imports MASS, scales, geometry, deldir, mirt, GPArotation, Hmisc, car, dunn.test, gplots, lattice, polycor, dae, xtable, mvtnorm, psych, ThreeWay, knitr

LazyData yes

Archs i386, x64

NeedsCompilation no

Date/Publication 2023-11-21 15:00:06 UTC

Contents

`MultBiplotR-package` *Multivariate Analysis using Biplots*

Description

Classical PCA biplot with aditional features as non-standard data transformations, scales for the variables, together with many graphical aids as sizes or colors of the points according to their qualities of representation or predictiveness. The package includes also Alternating Least Squares (ALS) or Criss-Cross procedures for the calculation of the reduced rank approximation that can deal with missing data, differencial weights for each element of the data matrix or even ronust versions of the procedure.

This is part of a bigger project called MULTBIPLOT that contains many other biplot techniques and is a translation to R of the package MULBIPLOT programmed in MATLAB. A GUI for the package is also in preparation.

Details

Package:	MultBiplot
Type:	Package
Version:	0.1.00
Date:	2015-01-14
License:	GPL(>=2)

Author(s)

Jose Luis Vicente Villardon Maintainer: Jose Luis Vicente Villardon <villardon@usal.es>

References

Vicente-Villardon, J.L. (2010). MULTBIPLOT: A package for Multivariate Analysis using Biplots. Departamento de Estadistica. Universidad de Salamanca. (http://biplot.usal.es/ClassicalBiplot/index.html).

Vicente-Villardon, J. L. (1992). Una alternativa a las técnicas factoriales clasicas basada en una generalización de los metodos Biplot (Doctoral dissertation, Tesis. Universidad de Salamanca. España. 248 pp.[Links]).

Gabriel KR (1971) The biplot graphic display of matrices with application to principal component analysis. Biometrika 58(3):453-467

Gabriel KR (1998) Generalised bilinear regresion, J. L. (1998). Use of biplots to diagnose independence models in three-way contingency tables. Visualization of Categorical Data. Academic Press. London.

Gabriel, K. R. (2002). Le biplot-outil d'exploration de donnes multidimensionnelles. Journal de la Societe francaise de statistique, 143(3-4).

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Galindo Villardon, M. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Qüestiió. 1986, vol. 10, núm. 1.

Demey J, Vicente-Villardon JL, Galindo MP, Zambrano A (2008) Identifying molecular markers associated with classification of genotypes using external logistic biplots. Bioinformatics 24(24):2832-2838.

Vicente-Villardon JL, Galindo MP, Blazquez-Zaballos A (2006) Logistic biplots. Multiple Correspondence Analysis and related methods pp 491-509.

Santos, C., Munoz, S. S., Gutierrez, Y., Hebrero, E., Vicente, J. L., Galindo, P., Rivas, J. C. (1991). Characterization of young red wines by application of HJ biplot analysis to anthocyanin profiles. Journal of Agricultural and food chemistry, 39(6), 1086-1090.

Rivas-Gonzalo, J. C., Gutierrez, Y., Polanco, A. M., Hebrero, E., Vicente, 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(iris)
bip=PCA.Biplot(iris[,1:4])
plot(bip)
```

AddBinVars2Biplot — *Add suplementary binary variables to a biplot*

Description

Add suplementary binary variables to a biplot of any kind

Usage

```
AddBinVars2Biplot(bip, Y, IncludeConst = TRUE, penalization = 0.2,
freq = NULL, tolerance = 1e-05, maxiter = 100)
```

Arguments

`bip`	A biplot object
`Y`	Matrix of binary variables to add
`IncludeConst`	Should include a constant in the fit
`penalization`	Penalization for the fit
`freq`	frequencies for each row of Y. By default is 1.
`tolerance`	Tolerance for the fit
`maxiter`	Maximum number of iterations

Details

Fits binary variables to an existing biplot using penalized logistic regression.

Value

The biplot object with supplementary binary variables added.

Author(s)

Jose Luis Vicente Villardon

References

Vicente-Villardón, J. L., & Hernández-Sánchez, J. C. (2020). External Logistic Biplots for Mixed Types of Data. In Advanced Studies in Classification and Data Science (pp. 169-183). Springer, Singapore.

Examples

```
## No examples yet
```

`AddCluster2Biplot` *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

```
AddCluster2Biplot(Bip, NGroups=3, ClusterType="hi", Groups=NULL,
                  Original=FALSE, ClusterColors=NULL, ...)
```

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?.
`ClusterColors`	Colors for the clusters.
`...`	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 hirarchical clustering
`ClusterObject`	The object obtained from `hclust`, `kmeans` or `MGC`

Author(s)

Jose Luis Vicente Villardon

References

Demey, J. R., Vicente-Villardon, J. L., Galindo-Villardon, 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-Villardon, 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., & Zabalgogeazcoa, 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`.

Examples

```
data(Protein)
bip=PCA.Biplot(Protein[,3:11])
plot(bip)
# Add user defined clusters containing the region (North, South, Center)
bip=AddCluster2Biplot(bip, ClusterType="us", Groups=Protein$Region)
plot(bip, mode="a", margin=0.1, PlotClus=TRUE)

# Hierarchical clustering on the biplot coordinates using the Ward method
bip=AddCluster2Biplot(bip, ClusterType="hi", method="ward.D")
op <- par(mfrow=c(1,2))
plot(bip, mode="s", margin=0.1, PlotClus=TRUE)
plot(bip$Dendrogram)
par(op)
# K-means cluster on the biplot coordinates using the Ward method
bip=AddCluster2Biplot(bip, ClusterType="hi", method="ward.D")
op <- par(mfrow=c(1,2))
plot(bip, mode="s", margin=0.1, PlotClus=TRUE)
plot(bip$Dendrogram)
par(op)
```

`AddContVars2Biplot` *Adds supplementary continuous variables to a biplot object*

Description

Adds supplementary continuous variables to a biplot object

Usage

```
AddContVars2Biplot(bip, X, dims = NULL, Scaling = 5, Fit = NULL)
```

Arguments

`bip`	A biplot object
`X`	Matrix containing the supplementary continuos variables
`dims`	Dimension of the solution
`Scaling`	Transformation to apply to X
`Fit`	Type of fit. Linear by default.

Details

More types of fit will be added in the future

Value

A biplot object with the coordinates for the supplementary variables added.

Author(s)

Jose Luis Vicente Villardon

See Also

`AddSupVars2Biplot`

Examples

```
# Not yet
```

`AddOrdVars2Biplot` *Adds supplementary ordinal variables to an existing biplot objects.*

Description

Adds supplementary ordinal variables to an existing biplot objects.

Usage

```
AddOrdVars2Biplot(bip, Y, tol = 1e-06, maxiterlogist = 100,
penalization = 0.2, showiter = TRUE, show = FALSE)
```

Arguments

`bip`	A biplot object.
`Y`	A matrix of ordinal variables.
`tol`	Tolerance.
`maxiterlogist`	Maximum number of iterations for the logistic fit.
`penalization`	Penalization for the logistic fit
`showiter`	Should the itrations be shown on screen
`show`	Show details.

Details

Adds supplementary ordinal variables to an existing biplot objects.

Value

An object with the information of the fits

Author(s)

Jose Luis Vicente-Villardon

References

Vicente-Villardon, J. L., & Hernandez-Sanchez, J. C. (2020). External Logistic Biplots for Mixed Types of Data. In Advanced Studies in Classification and Data Science (pp. 169-183). Springer, Singapore.

Examples

```
# not yet
```

`AddSupVars2Biplot` *Adds supplementary variables to a biplot object*

Description

Adds supplementary bariables to a biplot object constructed with any of the biplot methods of the package. The new variables are fitted using the coordinates for the rows. Each variable is fitted using the adequate procedure for its type.

Usage

```
AddSupVars2Biplot(bip, X)
```

Arguments

`bip`	The biplot object
`X`	A data frame with the supplementary variables.

Details

Binary, nominal or ordinal variables are fitted using logistic biplots. Continuous variables are fitted with linear regression.

Value

A biplot object with the coordinates for the supplementary variables added.

Author(s)

Jose Luis Vicente Villardon

See Also

`AddContVars2Biplot`

Examples

```
# Not yet
```

`anova.RidgeBinaryLogistic`

Compares two binary logistic models

Description

Anova for comparing two binary logistic models

Usage

```
## S3 method for class 'RidgeBinaryLogistic'
anova(object, object2, ...)
```

Arguments

`object`	The first model
`object2`	The second model
`...`	Any additional arguments

Details

Anova for comparing two binary logistic models

Value

The comparison of the two models.

Author(s)

Jose Luis Vicente Villardon

Examples

```
# Not yet
```

Bartlett.Tests *Bartlett tests*

Description

Bartlett tests foor the columns of a matrix and a grouping variable

Usage

```
Bartlett.Tests(X, groups = NULL)
```

Arguments

`X`	A data frame or a matrix containing several numerical variables
`groups`	A factor with the groups

Details

Bartlett tests foor the columns of a matrix and a grouping variable

Value

A matrix with the tests for each column

Author(s)

Jose Luis Vicente Villardon

References

Bartlett, M. S. (1937). "Properties of sufficiency and statistical tests". Proceedings of the Royal Statistical Society, Series A 160, 268-282 JSTOR 96803

Examples

```
data(wine)
Bartlett.Tests(wine[,4:8], groups = wine$Origin)
```

BasicDescription *Basic descriptive sataistics*

Description

Basic descriptive sataistics of several variables by the categories of a factor.

Usage

```
BasicDescription(X, groups = NULL, SortByGroups = FALSE, na.rm = FALSE, Intervals = TRUE)
```

Arguments

X	A data frame or a matrix containing several numerical variables
groups	A factor with the groupings
SortByGroups	Sorting by groups
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
Intervals	Should the confidence intervals be calculated?

Details

Basic descriptive sataistics of several variables by the categories of a factor.

Value

A list with the description of each variable.

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(wine)
BasicDescription(wine[,4:8], groups = wine$Origin)
```

BinaryDistances *Binary Distances*

Description

Calculates distances among rows of a binary data matrix or among the rows of two binary matrices. The end user will use BinaryProximities rather than this function. Input must be a matrix with 0 or 1 values.

Usage

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

Arguments

`x`	Main binary data matrix. Distances among rows are calculated if y=NULL.
`y`	Second binary data matrix. If not NULL the distances among the rows of x and y are calculated
`coefficient`	Similarity coefficient. Use the name (see details)
`transformation`	Transformation of the similarities. Use the name (see details)

Details

The following coefficients are calculated

1.- Kulezynski = a/(b + c)

2.- Russell_and_Rao = a/(a + b + c+d)

3.- Jaccard = a/(a + b + c)

4.- Simple_Matching = (a + d)/(a + b + c + d)

5.- Anderberg = a/(a + 2 * (b + c))

6.- Rogers_and_Tanimoto = (a + d)/(a + 2 * (b + c) + d)

7.- Sorensen_Dice_and_Czekanowski = a/(a + 0.5 * (b + c))

8.- Sneath_and_Sokal = (a + d)/(a + 0.5 * (b + c) + d)

9.- Hamman = (a - (b + c) + d)/(a + b + c + d)

10.- Kulezynski = 0.5 * ((a/(a + b)) + (a/(a + c)))

11.- Anderberg2 = 0.25 * (a/(a + b) + a/(a + c) + d/(c + d) + d/(b + d))

12.- Ochiai = a/sqrt((a + b) * (a + c))

13.- S13 = (a * d)/sqrt((a + b) * (a + c) * (d + b) * (d + c))

14.- Pearson_phi = (a * d - b * c)/sqrt((a + b) * (a + c) * (d + b) * (d + c))

15.- Yule = (a * d - b * c)/(a * d + b * c)

The following transformations of the similarity3 are calculated

1.- ‘Identity‘ dis=sim

2.- ‘1-S‘ dis=1-sim

3.- ‘sqrt(1-S)‘ dis = sqrt(1 - sim)

4.- ‘-log(s)‘ dis=-1*log(sim)

5.- ‘1/S-1‘ dis=1/sim -1

6.- ‘sqrt(2(1-S))‘ dis== sqrt(2*(1 - sim))

7.- ‘1-(S+1)/2‘ dis=1-(sim+1)/2

8.- ‘1-abs(S)‘ dis=1-abs(sim)

9.- ‘1/(S+1)‘ dis=1/(sim)+1

Value

An object of class `proximities`.This has components:

`comp1` Description of ’comp1’

Author(s)

Jose Luis Vicente-Villardon

References

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

See Also

PrincipalCoordinates

Examples

```
data(spiders)
```

BinaryLogBiplotEM *Binary logistic biplot with the EM algorithm.*

Description

Binary logistic biplot with the EM algorithm

Usage

```
BinaryLogBiplotEM(x, freq = matrix(1, nrow(x), 1), aini = NULL,
dimens = 2, nnodos = 15, tol = 1e-04, maxiter = 100, penalization = 0.2)
```

Arguments

`x`	A binary data matrix
`freq`	A vector of frequencies.
`aini`	Initial values for the row coordinates.
`dimens`	Dimension of the solution.
`nnodos`	Number of nodes for the gaussian quadrature
`tol`	Tolerance
`maxiter`	Maximum number of iterations.
`penalization`	Penalization for the fit (ridge)

Details

Binary logistic biplot with the EM algorithm based on marginal maximum likelihood.

Value

A logistic biplot object.

Author(s)

Jose Luis Vicente-Villardon

References

Vicente-Villardón, J. L., Galindo-Villardón, M. P., & Blázquez-Zaballos, A. (2006). Logistic biplots. Multiple correspondence analysis and related methods. London: Chapman & Hall, 503-521.

Examples

```
# Not yet
```

`BinaryLogBiplotGD` *Binary Logistic Biplot with Gradient Descent Estimation*

Description

Binary Logistic Biplot with Gradient Descent Estimation. An external optimization function is used to calculate the parameters.

Usage

```
BinaryLogBiplotGD(X, freq = matrix(1, nrow(X), 1), dim = 2, tolerance =
                   1e-07, penalization = 0.01, num_max_iters = 100,
                   RotVarimax = FALSE, seed = 0, OptimMethod = "CG",
                   Initial = "random", Orthogonalize = FALSE, Algorithm =
                   "Joint", ...)
```

Arguments

`X`	A binary data matrix
`freq`	Frequencies of each row. When adequate.
`dim`	Dimension of the final solution.
`tolerance`	Tolerance for convergence of the algorithm.
`penalization`	Ridge penalization constant.
`num_max_iters`	Maximum number of iterations of the algorithm.
`RotVarimax`	Should the final solution be rotated.
`seed`	Seed for the random numbers. Used for reproductibility.
`OptimMethod`	Optimization method used by `optim`.
`Initial`	Initial configuration to start the iterations.
`Orthogonalize`	Should te solution be orthogonalized?.
`Algorithm`	Algorithm for esimation: Joint or alternated.
`...`	Aditional parameters used by the optimization function.

Details

Fits a binary logistic biplot using gradient descent. The general function `optim` is used to optimize the loss function. Conjugate gradien is used as a default although other alternatives can be USED.

Value

An object of class "Binary.Logistic.Biplot".

Author(s)

Jose Luis Vicente-Villardon

References

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez, A. (2006) Logistic Biplots. In Multiple Correspondence Análisis And Related Methods. Grenacre, M & Blasius, J, Eds, Chapman and Hall, Boca Raton.

Demey, J., Vicente-Villardon, J. L., Galindo, M.P. AND Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics, 24(24): 2832-2838.

Examples

```
data(spiders)
X=Dataframe2BinaryMatrix(spiders)

logbip=BinaryLogBiplotGD(X,penalization=0.1)
plot(logbip, Mode="a")
summary(logbip)
```

BinaryLogBiplotGDRecursive
Binary Logistic Biplot with Recursive Gradient Descent Estimation

Description

Binary Logistic Biplot with Recursive Gradient Descent Estimation. An external optimization function is used to calculate the parameters.

Usage

```
BinaryLogBiplotGDRecursive(X, freq = matrix(1, nrow(X), 1), dim = 2, tolerance = 1e-04,
                           penalization = 0.2, num_max_iters = 100,
                           RotVarimax = FALSE, OptimMethod = "CG",
                           Initial = "random", ...)
```

Arguments

X	A binary data matrix
freq	Frequencies of each row. When adequate.
dim	Dimension of the final solution.
tolerance	Tolerance for convergence of the algorithm.
penalization	Ridge penalization constant.
num_max_iters	Maximum number of iterations of the algorithm.
RotVarimax	Should the final solution be rotated.
OptimMethod	Optimization method used by `optim`.
Initial	Initial configuration to start the iterations.
...	Aditional parameters used by the optimization function.

Details

Fits a binary logistic biplot using recursive gradient descent. The general function `optim` is used to optimize the loss function. Conjugate gradien is used as a default although other alternatives can be USED. It can be considered as a generalization of the NIPALS algorithm for a matrix of binary data.

Value

An object of class "Binary.Logistic.Biplot".

Author(s)

José Luis Vicente Villardon

References

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez, A. (2006) Logistic Biplots. In Multiple Correspondence Análisis And Related Methods. Grenacre, M & Blasius, J, Eds, Chapman and Hall, Boca Raton.

Demey, J., Vicente-Villardon, J. L., Galindo, M.P. AND Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics, 24(24): 2832-2838.

Examples

```
data(spiders)
X=Dataframe2BinaryMatrix(spiders)
logbip=BinaryLogBiplotGDRecursive(X,penalization=0.1)
plot(logbip, Mode="a")
summary(logbip)
```

BinaryLogBiplotJoint *Binary logistic biplot with a gradient descent algorithm.*

Description

Binary logistic biplot with a gradient descent algorithm.

Usage

```
BinaryLogBiplotJoint(x, freq = matrix(1, nrow(x), 1), dim = 2,
ainit = NULL, tolerance = 1e-04, maxiter = 30, penalization = 0.2,
maxcond = 7, RotVarimax = FALSE, lambda = 0.1, ...)
```

Arguments

`x`	A binary data matrix
`freq`	A vector of frequencies.
`dim`	Dimension of the solution
`ainit`	Initial values for the row coordinates.
`tolerance`	Tolerance
`maxiter`	Maximum number of iterations.
`penalization`	Penalization for the fit (ridge)
`maxcond`	Naximum condition number
`RotVarimax`	Should a Varimax Rotation be used?
`lambda`	Penalization argument
`...`	Aditional arguments

Details

Binary logistic biplot with a gradient descent algorithm. Estimates row and column parameters at the same time.

Value

A logistic biplot object.

Author(s)

Jose Luis Vicente-Villardon

References

Vicente-Villardón, J. L., Galindo-Villardón, M. P., & Blázquez-Zaballos, A. (2006). Logistic biplots. Multiple correspondence analysis and related methods. London: Chapman & Hall, 503-521.

Vicente-Villardon, J. L., & Vicente-Gonzalez, L. Redundancy Analysis for Binary Data Based on Logistic Responses in Data Analysis and Rationality in a Complex World. Springer.

Examples

```
# not yet
```

`BinaryLogBiplotMirt` *Binary logistic biplot with Item Response Theory.*

Description

Binary logistic biplot with Item Response Theory.

Usage

```
BinaryLogBiplotMirt(x, dimens = 2, tolerance = 1e-04,
maxiter = 30, penalization = 0.2, Rotation = "varimax", ...)
```

Arguments

`x`	The binary Data matrix
`dimens`	Dimension of the solution
`tolerance`	Tolerance of the algorithm
`maxiter`	Maximum number of iterations
`penalization`	Rige Penalization
`Rotation`	Should a rotation be applied?
`...`	Aditional argumaents.

Details

Binary logistic biplot with Item Response Theory.

Value

A logistic biplot object.

Author(s)

Jose Luis Vicente Villardon

References

Vicente-Villardón, J. L., Galindo-Villardón, M. P., & Blázquez-Zaballos, A. (2006). Logistic biplots. Multiple correspondence analysis and related methods. London: Chapman & Hall, 503-521.

Examples

```
# Not yet
```

BinaryLogisticBiplot *Binary Logistic Biplot*

Description

Fits a binary lo gistic biplot to a binary data matrix.

Usage

```
BinaryLogisticBiplot(x, dim = 2, compress = FALSE, init = "mca",
method = "EM", rotation = "none", tol = 1e-04,
maxiter = 100, penalization = 0.2, similarity = "Simple_Matching", ...)
```

Arguments

`x`	The binary data matrix
`dim`	Dimension of the solution
`compress`	Compress the data before the fitting (not yet implemented)
`init`	Type of initial configuration. ("random", "mirt", "PCoA", "mca")
`method`	Method to fit the logistic biplot ("EM", "Joint", "mirt", "JointGD", "AlternatedGD", "External", "Recursive")
`rotation`	Rotation of the solution ("none", "oblimin", "quartimin", "oblimax" ,"entropy", "quartimax", "varimax", "simplimax") see GPARotation
`tol`	Tolerance for the algorithm
`maxiter`	Maximum number of iterations.
`penalization`	Panalization for the different algorithms
`similarity`	Similarity coefficient for the initial configuration or the external model
`...`	Any other argument for each particular method.

Details

Fits a binary lo gistic biplot to a binary data matrix.

Different Initial configurations can be selected:

1.- random : Random coordinates for each point.

2.- mirt: scores of the procedure mirt (Multidimensional Item Response Theory)

3.- PCoA: Principal Coordinates Analysis

4.- mca: Multiple Correspondence Analysis

We can use also different methods for the estimation

1.- Joint: Joint estimation of the row and column parameters. The Initial alorithm.

2.- EM: Marginal Maximum Likelihood

3.- mirt: Similar to the previous but fitted using the package mirt.

4.- JointGD: Joint estimation of the row and column methods using the gradient descent method.

5.- AlternatedGD: Alternated estimation of the row and column methods using the gradient descent method.

6.- External: Logistic fits on the Principal Coordinates Analysis.

7.- Recursive: Recursive (one axis at a time) estimation of the row and column methods using the gradient descent method. This is similar to the NIPALS algorithm for PCA

Value

A Logistic Biplot object.

Author(s)

Jose Luis Vicente Villardon

References

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez, A. (2006) Logistic Biplots. In Multiple Correspondence Análisis And Related Methods. Grenacre, M & Blasius, J, Eds, Chapman and Hall, Boca Raton.

Demey, J., Vicente-Villardon, J. L., Galindo, M.P. AND Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics, 24(24): 2832-2838.

See Also

`BinaryLogBiplotJoint`, `BinaryLogBiplotEM`, `BinaryLogBiplotGD`, `BinaryLogBiplotMirt`,

Examples

```
# data(spiders)
# X=Dataframe2BinaryMatrix(spiders)

# logbip=BinaryLogBiplotGD(X,penalization=0.1)
# plot(logbip, Mode="a")
# summary(logbip)
```

BinaryPLSFit *Binary PLS Regression.*

Description

Fits Binary PLS regression.

Usage

```
BinaryPLSFit(Y, X, S = 2, tolerance = 5e-06, maxiter = 100, show = FALSE,
          penalization = 0.1, OptimMethod = "CG", seed = 0)
```

Arguments

Y	The response
X	The matrix of independent variables
S	The Dimension of the solution
tolerance	Tolerance for convergence of the algorithm
maxiter	Maximum Number of iterations
show	Show the steps of the algorithm
penalization	Penalization for the Ridge Logistic Regression
OptimMethod	Optimization methods from optimr
seed	Seed. By default is 0.

Details

Fits Binary PLS Regression. It is used for a higher level function.

Value

The PLS fit used by the BinaryPLSR function.

Author(s)

Jose Luis Vicente Villardon

References

Ugarte Fajardo, J., Bayona Andrade, O., Criollo Bonilla, R., Cevallos-Cevallos, J., Mariduena-Zavala, M., Ochoa Donoso, D., & Vicente Villardon, J. L. (2020). Early detection of black Sigatoka in banana leaves using hyperspectral images. Applications in plant sciences, 8(8), e11383.

Vicente-Gonzalez, L., & Vicente-Villardon, J. L. (2022). Partial Least Squares Regression for Binary Responses and Its Associated Biplot Representation. Mathematics, 10(15), 2580.

Examples

```
## Not yet
```

`BinaryPLSR` *Partial Least Squares Regression with Binary Data*

Description

Fits Partial Least Squares Regression with Binary Data

Usage

```
BinaryPLSR(Y, X, S = 2, tolerance = 5e-05, maxiter = 100, show = FALSE,
                   penalization = 0.1, OptimMethod = "CG", seed = 0)
```

Arguments

`Y`	The response
`X`	The matrix of independent variables
`S`	The Dimension of the solution
`tolerance`	Tolerance for convergence of the algorithm
`maxiter`	Maximum Number of iterations
`show`	Show the steps of the algorithm
`penalization`	Penalization for the Ridge Logistic Regression
`OptimMethod`	Optimization methods from optim
`seed`	Seed. By default is 0.

Details

The function fits the PLSR method for the case when there are two sets of binary variables, using logistic rather than linear fits to take into account the nature of responses. We term the method BPLSR (Binary Partial Least Squares Regression). This can be considered as a generalization of the NIPALS algorithm when the data are all binary.

Value

`Method`	Description of 'comp1'
`X`	The predictors matrix
`Y`	The responses matrix
`ScaledX`	The scaled X matrix
`tolerance`	Tolerance used in the algorithm
`maxiter`	Maximum number of iterations used
`penalization`	Ridge penalization
`XScores`	Scores of the X matrix, used later for the biplot
`XLoadings`	Loadings of the X matrix
`YScores`	Scores of the Y matrix
`YLoadings`	Loadings of the Y matrix
`XStructure`	Correlations among the X variables and the PLS scores
`InterceptsY`	Intercepts for the Y loadings
`InterceptsX`	Intercepts for the Y loadings
`LinTerm`	Linear terms for each response
`Expected`	Expected probabilities for the responses
`Predictions`	Binary predictions of the responses
`PercentCorrect`	Global percent of correct predictions
`PercentCorrectCols`	Percent of correct predictions for each column

Author(s)

José Luis Vicente Villardon

References

Ugarte Fajardo, J., Bayona Andrade, O., Criollo Bonilla, R., Cevallos-Cevallos, J., Mariduena-Zavala, M., Ochoa Donoso, D., & Vicente Villardon, J. L. (2020). Early detection of black Sigatoka in banana leaves using hyperspectral images. Applications in plant sciences, 8(8), e11383.

Vicente-Gonzalez, L., & Vicente-Villardon, J. L. (2022). Partial Least Squares Regression for Binary Responses and Its Associated Biplot Representation. Mathematics, 10(15), 2580.

Examples

```
X=as.matrix(wine[,4:21])
Y=cbind(Factor2Binary(wine[,1])[,1], Factor2Binary(wine[,2])[,1])
rownames(Y)=wine[,3]
colnames(Y)=c("Year", "Origin")
pls=PLSRBin(Y,X, penalization=0.1, show=TRUE, S=2)
```

BinaryProximities *Proximity Measures for Binary Data*

Description

Calculation of proxymities among rows or columns of a binary data matrix or a data frame that will be converted into a binary data matrix.

Usage

```
BinaryProximities(x, y = NULL, coefficient = "Jaccard", transformation =
                  NULL, transpose = FALSE, ...)
```

Arguments

`x`	A data frame or a binary data matrix. Proximities among the rows of `x` will be calculated
`y`	Supplementary data. The proximities amond the rows of `x` and the rows of `y` will be also calculated
`coefficient`	Similarity coefficient. Use the number or the name (see details)
`transformation`	Transformation of the similarities. Use the number or the name (see details)
`transpose`	Logical. If `TRUE`, proximities among columns are calculated
`...`	Used to provide additional parameters for the conversion of the dataframe into a binary matrix

Details

A binary data matrix is a matrix with values 0 or 1 coding the absence or presence of several binary characters. When a data frame is provided, every variable in the data frame is converted to a binary variable using the function `Dataframe2BinaryMatrix`. Factors with two levels are converted directly to binary variables, factors with more than two levels are converted to a matrix with as meny columns as levels and numerical variables are converted to binary variables using a cut point that can be the median, the mean or a value provided by the user.

The following coefficients are calculated

1.- Kulezynski = a/(b + c)

2.- Russell_and_Rao = a/(a + b + c+d)

3.- Jaccard = a/(a + b + c)

4.- Simple_Matching = (a + d)/(a + b + c + d)

5.- Anderberg = a/(a + 2 * (b + c))

6.- Rogers_and_Tanimoto = (a + d)/(a + 2 * (b + c) + d)

7.- Sorensen_Dice_and_Czekanowski = a/(a + 0.5 * (b + c))

8.- Sneath_and_Sokal = (a + d)/(a + 0.5 * (b + c) + d)

9.- Hamman = (a - (b + c) + d)/(a + b + c + d)

10.- Kulezynski = 0.5 * ((a/(a + b)) + (a/(a + c)))

11.- Anderberg2 = 0.25 * (a/(a + b) + a/(a + c) + d/(c + d) + d/(b + d))

12.- Ochiai = a/sqrt((a + b) * (a + c))

13.- S13 = (a * d)/sqrt((a + b) * (a + c) * (d + b) * (d + c))

14.- Pearson_phi = (a * d - b * c)/sqrt((a + b) * (a + c) * (d + b) * (d + c))

15.- Yule = (a * d - b * c)/(a * d + b * c)

The following transformations of the similarity3 are calculated

1.- 'Identity' dis=sim

2.- '1-S' dis=1-sim

3.- 'sqrt(1-S)' dis = sqrt(1 - sim)

4.- '-log(s)' dis=-1*log(sim)

5.- '1/S-1' dis=1/sim -1

6.- 'sqrt(2(1-S))' dis== sqrt(2*(1 - sim))

7.- '1-(S+1)/2' dis=1-(sim+1)/2

8.- '1-abs(S)' dis=1-abs(sim)

9.- '1/(S+1)' dis=1/(sim)+1

Note that, after transformation the similarities are converted to distances except for "Identity". Not all the transformations are suitable for all the coefficients. Use them at your own risk. The default values are admissible combinations.

Value

An object of class `proximities`.This has components:

`TypeData`	Binary, Continuous or Mixed. Binary in this case.
`Coefficient`	Coefficient used to calculate the proximities
`Transformation`	Transformation used to calculate the proximities
`Data`	Data used to calculate the proximities
`SupData`	Supplementary Data, if any
`Proximities`	Proximities among rows of `x`. May be similarities or dissimilarities depending on the transformation
`SupProximities`	Proximities among rows of `x` and `y`.

Author(s)

Jose Luis Vicente-Villardon

References

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

See Also

BinaryDistances, Dataframe2BinaryMatrix

Examples

```
data(spiders)
D=BinaryProximities(spiders, coefficient="Jaccard", transformation="sqrt(1-S)")
D2=BinaryProximities(spiders, coefficient=3, transformation=3)
```

Biplot.BinaryPLSR *Biplot for a PLSR model with binary data*

Description

Builds a Biplot for a PLSR model with binary data

Usage

```
Biplot.BinaryPLSR(plsr, BinBiplotType=1)
```

Arguments

plsr	A BinaryPLSR object
BinBiplotType	The type of biplot: 1:The biplot resulting from the fit, for the binary data. 2: The biplot for the coefficients

Details

Builds a Biplot for a PLSR model with binary data. The result is a biplot for the matrix with the binary predictors (X) adding the binary responses as suplementary variables. There are two possible types, 1 for the biplot directly obtained in the fit (the default) and 2 for the biplot obtaines after refitting the binary variables using Ridge Logistic Regression.

Value

An object of class Binary.Logistic.Biplot

Author(s)

Jose Luis Vicente Villardon

References

Ugarte Fajardo, J., Bayona Andrade, O., Criollo Bonilla, R., Cevallos-Cevallos, J., Mariduena-Zavala, M., Ochoa Donoso, D., & Vicente Villardon, J. L. (2020). Early detection of black Sigatoka in banana leaves using hyperspectral images. Applications in plant sciences, 8(8), e11383.

Vicente-Gonzalez, L., & Vicente-Villardon, J. L. (2022). Partial Least Squares Regression for Binary Responses and Its Associated Biplot Representation. Mathematics, 10(15), 2580.

Examples

```
X=as.matrix(wine[,4:21])
Y=cbind(Factor2Binary(wine[,1])[,1], Factor2Binary(wine[,2])[,1])
rownames(Y)=wine[,3]
colnames(Y)=c("Year", "Origin")
pls=PLSRBin(Y,X, penalization=0.1, show=TRUE, S=2)
plsbip=Biplot.PLSRBIN(pls, BinBiplotType=1)
plsbip=AddCluster2Biplot(plsbip, ClusterType = "us",
       Groups = wine$Group)
plot(plsbip, margin=0.05, mode="s", PlotClus = TRUE,
    ModeSupBinVars = "s", ShowAxis = FALSE,
    ColorSupBinVars = "blue",     CexInd=0.5,
    ClustCenters = TRUE, LabelInd = FALSE, ShowBox = TRUE)
```

Biplot.PLSR *Partial Least Squares Biplot*

Description

Adds a Biplot to a Partial Lest Squares (plsr) object.

Usage

```
Biplot.PLSR(plsr)
```

Arguments

plsr	A plsr object from the PLSR function

Details

Adds a Biplot to a Partial Lest Squares (plsr) object. The biplot is constructed with the matrix of predictors, the dependent variable is projected onto the biplot as a continuous supplementary variable.

Value

An object of class ContinuousBiplot with the dependent variables as supplemntary.

Author(s)

Jose Luis Vicente Villardon

References

Oyedele, O. F., & Lubbe, S. (2015). The construction of a partial least-squares biplot. Journal of Applied Statistics, 42(11), 2449-2460.

See Also

PLSR

Examples

```
X=as.matrix(wine[,4:21])
y=as.numeric(wine[,2])-1
mifit=PLSR(y,X, Validation="None")
mibip=Biplot.PLSR(mifit)
plot(mibip, PlotVars=TRUE, IndLabels = y, ColorInd=y+1)
```

Biplot.PLSR1BIN *Biplot for a PLSR model with a binary response*

Description

Biplot for a PLSR model with a binary response

Usage

```
Biplot.PLSR1BIN(plsr)
```

Arguments

plsr	An object of class PLSR1BIN.

Details

Biplot for a PLSR model with a binary response

Value

The biplot for the independent variables with the response as supplementary binary variable.

Author(s)

Jose Luis Vicente Villardon

References

Ugarte-Fajardo, J., Bayona-Andrade, O., Criollo-Bonilla, R., Cevallos-Cevallos, J., Mariduena-Zavala, M., Ochoa-Donoso, D., & Vicente-Villardon, J. L. (2020). Early detection of black Sigatoka in banana leaves using hyperspectral images. Applications in plant sciences, 8(8), e11383.

See Also

PLSR1Bin

Examples

```
# Not Yet
```

Biplot.PLSRBIN *Biplot for a PLSR model with binary responses*

Description

Builds a Biplot for a PLSR model with binary responses

Usage

```
Biplot.PLSRBIN(plsr, BinBiplotType = 1)
```

Arguments

plsr	A PLSRBin object
BinBiplotType	The type of biplot: 1:The biplot resulting from the fit, for the binary responses. 2: The biplot for the coefficients

Details

Builds a Biplot for a PLSR model with binary responses. The result is a biplot for the matrix with the predictors (X) adding the binary responses as suplementary variables. There are two possible types, 1 for the biplot directly obtained in the fit (the default) and 2 for the biplot obtaines after refitting the binary variables using Ridge Logistic Regression.

Value

An object of class ContinuousBiplot

Author(s)

Jose Luis Vicente Villardon

References

Ugarte Fajardo, J., Bayona Andrade, O., Criollo Bonilla, R., Cevallos-Cevallos, J., Mariduena-Zavala, M., Ochoa Donoso, D., & Vicente Villardon, J. L. (2020). Early detection of black Sigatoka in banana leaves using hyperspectral images. Applications in plant sciences, 8(8), e11383.

Examples

```
X=as.matrix(wine[,4:21])
Y=cbind(Factor2Binary(wine[,1])[,1], Factor2Binary(wine[,2])[,1])
rownames(Y)=wine[,3]
colnames(Y)=c("Year", "Origin")
pls=PLSRBin(Y,X, penalization=0.1, show=TRUE, S=2)
plsbip=Biplot.PLSRBIN(pls, BinBiplotType=1)
plsbip=AddCluster2Biplot(plsbip, ClusterType = "us",
       Groups = wine$Group)
plot(plsbip, margin=0.05, mode="s", PlotClus = TRUE,
    ModeSupBinVars = "s", ShowAxis = FALSE,
    ColorSupBinVars = "blue",     CexInd=0.5,
    ClustCenters = TRUE, LabelInd = FALSE, ShowBox = TRUE)
```

BiplotFPCA *External Biplot for functional data from a functional PCA object.*

Description

The function calculates a biplot from a functional PCA object and the data used tocalculate it.

Usage

```
BiplotFPCA(FPCA, X)
```

Arguments

FPCA	Functional PCA object
X	Data used to calculate the fuctional PCA

Details

The function calculates a biplot from a functional PCA object and the data used tocalculate it. At this moment the function calculates only an external biplot by regressing X o the funcional components. Furure versions will include the internal biplot.

Value

A Continuous biplot object

Author(s)

José Luis Vicente Villardón

Examples

```
# not yet
```

BootstrapDistance *Bootstrap on the distance matrices used for Principal Coordinates Analysis (PCoA)*

Description

Obtains bootstrap replicates of a distance matrix using ramdom samples or permuatations of the residual matrix from a Principal Coordinates (Components) Analysis. The object is to estimate the sampling variability of absorbed variances, coordinates and qualities of representation in a PCoA.

Usage

```
BootstrapDistance(D, W=diag(nrow(D)), nB=200, dimsol=2,
                  ProcrustesRot=TRUE, method=c("Sampling", "Permutation"))
```

Arguments

D	A distance matrix
W	A diagonal matrix containing waiths for the rows of D
nB	Number of Bootstrap replications
dimsol	Dimension of the solution
ProcrustesRot	Should each replication be rotated to match the initial solution?
method	The replications are obtained "Sampling" or "Permutating" the residuals.

Details

The function calculates bootstrap confidence intervals for the inertia, coordinates and qualties of representation of a Principal Coordinates Analysis using a distance matrix as a basis. The funcion uses random sampling or permutations of the residuals to obtain the bootstrap replications. The procedure preserves the length of the points in the multidimensional space perturbating only the angles among the vectors. It is done so to preserve the property of positiveness of the diagonal elements of the scalar product matrices. The procedure may result into a scalar product that does not have an euclidean configuration and then has some negative eigenvalues; to avoid this problem the negative eigenvalues are removed to approximate the perturbated matrix by the closest with the required properties.

It is well known that the eigenvectors of a matrix are unique except for reflections, that is, if we change the sign of each component of the eigenvector we have the same solution. If that happens, an unwanted increase in the variability due to this artifact may invalidate the results. To avoid this we can calculate the scalar product of each eigenvector of the initial matrix with the corresponding eigenvector of the bootstrap replicate and change the signs of the later if the result is negative.

Another artifact of the procedure may arise when the dimension of the solution is higher than 1 because the eigenvectors of a replicate may generate the same subspace although are not in the same directions, i. e., the subspace is referred to a different system. That also may produce an unwanted increase of the variability that invalidates the results. To avoid this, every replicate may be rotated to match as much as possible the subspace generated by the eigenvectors of the initial matrix. This is done by Procrustes Analysis, taking the rotated matrix as solution. The solution to this problem is also a sulution to the reflection, then only this problem is considered.

Value

Returns an object of class "PCoABootstrap" with the information for each bootstrap replication.

`Eigenvalues`	A matrix with dimensions in rows and replicates in columns containing the eigenvalues of each replicate in columns
`Inertias`	A matrix with dimensions in rows and replicates in columns containing the inertias of each replicate in columns
`Coordinates`	A list with a component for each object. A component contains the coordinates of an object for each replicate (in columns)
`Values-Table`	A list with a component for each object. A component contains the qualities of an object for each replicate (in columns)
`NReplicates`	Number of bootstrap replicates

Author(s)

Jose L. Vicente-Villardon

References

Efron, B.; Tibshirani, RJ. (1993). An introduction to the bootstrap. New York: Chapman and Hall. 436p.

Ringrose, T. J. (1992). Bootstrapping and correspondence analysis in archaeology. Journal of Archaeological Science, 19(6), 615-629.

MILAN, L., & WHITTAKER, J. (1995). Application of the parametric bootstrap to models that incorporate a singular value decomposition. Applied statistics, 44(1), 31-49.

See Also

`BootstrapScalar`, ~~~

Examples

```
data(spiders)
D=BinaryProximities(spiders, coefficient="Jaccard", transformation="sqrt(1-S)")
DB=BootstrapDistance(D$Proximities)
```

BootstrapScalar *Bootstrap on the scalar product matrices used for Principal Coordinates Analysis (PCoA)*

Description

Obtains bootstrap replicates of a scalar products matrix using ramdom samples or permuatations of the residual matrix from a Principal Coordinates (Components) Analysis. The object is to estimate the sampling variability of absorbed variances, coordinates and qualities of representation in a PCoA.

Usage

```
BootstrapScalar(B, W=diag(nrow(B)), nB=200, dimsol=2,
                ProcrustesRot=TRUE, method=c("Sampling", "Permutation"))
```

Arguments

`B`	A scalar product matrix
`W`	A diagonal matrix containing waiths for the rows of D
`nB`	Number of Bootstrap replications
`dimsol`	Dimension of the solution
`ProcrustesRot`	Should each replication be rotated to match the initial solution?
`method`	The replications are obtained "Sampling" or "Permutating" the residuals.

Details

The function calculates bootstrap confidence intervals for the inertia, coordinates and qualties of representation of a Principal Coordinates Analysis using a distance matrix as a basis. The funcion uses random sampling or permutations of the residuals to obtain the bootstrap replications. The procedure preserves the length of the points in the multidimensional space perturbating only the angles among the vectors. It is done so to preserve the property of positiveness of the diagonal elements of the scalar product matrices. The procedure may result into a scalar product that does not have an euclidean configuration and then has some negative eigenvalues; to avoid this problem the negative eigenvalues are removed to approximate the perturbated matrix by the closest with the required properties.

It is well known that the eigenvectors of a matrix are unique except for reflections, that is, if we change the sign of each component of the eigenvector we have the same solution. If that happens, an unwanted increase in the variability due to this artifact may invalidate the results. To avoid this we can calculate the scalar product of each eigenvector of the initial matrix with the corresponding eigenvector of the bootstrap replicate and change the signs of the later if the result is negative.

Another artifact of the procedure may arise when the dimension of the solution is higher than 1 because the eigenvectors of a replicate may generate the same subspace although are not in the same directions, i. e., the subspace is referred to a different system. That also may produce an unwanted increase of the variability that invalidates the results. To avoid this, every replicate may be rotated to match as much as possible the subspace generated by the eigenvectors of the initial matrix. This is done by Procrustes Analysis, taking the rotated matrix as solution. The solution to this problem is also a sulution to the reflection, then only this problem is considered.

Value

Returns an object of class "PCoABootstrap" with the information for each bootstrap replication.

`Eigenvalues`	A matrix with dimensions in rows and replicates in columns containing the eigenvalues of each replicate in columns
`Inertias`	A matrix with dimensions in rows and replicates in columns containing the inertias of each replicate in columns
`Coordinates`	A list with a component for each object. A component contains the coordinates of an object for each replicate (in columns)
`Values-Table`	A list with a component for each object. A component contains the qualities of an object for each replicate (in columns)
`NReplicates`	Number of bootstrap replicates

Author(s)

Jose L. Vicente-Villardon

References

Efron, B.; Tibshirani, RJ. (1993). An introduction to the bootstrap. New York: Chapman and Hall. 436p.

Ringrose, T. J. (1992). Bootstrapping and correspondence analysis in archaeology. Journal of Archaeological Science, 19(6), 615-629.

Milan, L., & Whittaker, J. (1995). Application of the parametric bootstrap to models that incorporate a singular value decomposition. Applied statistics, 44(1), 31-49.

See Also

`BootstrapScalar`

Examples

```
## Not yet
```

BootstrapSmacof *Bootstrap on the distance matrices used for MDS with Smacof*

Description

Obtains bootstrap replicates of a distance matrix using ramdom samples or permuatations of a distance matrix. The object is to estimate the sampling variability of the results of the Smacof algorithm.

Usage

```
BootstrapSmacof(D, W=NULL, Model=c("Identity", "Ratio", "Interval", "Ordinal"),
          dimsol=2, maxiter=100, maxerror=0.000001, StandardizeDisparities=TRUE,
               ShowIter=TRUE, nB=200, ProcrustesRot=TRUE,
               method=c("Sampling", "Permutation"))
```

Arguments

D	A distance matrix
W	A diagonal matrix containing waiths for the rows of D
Model	Mesurement level of the distances
dimsol	Dimension of the solution
maxiter	Maximum number of iterations for the smacof algorithm
maxerror	Tolerance for the smacof algorithm
StandardizeDisparities	Should the disparities be standardized in the smacof algorithm?
ShowIter	Should the information on each ieration be printed on the screen?
nB	Number of Bootstrap replications
ProcrustesRot	Should each replication be rotated to match the initial solution?
method	The replications are obtained "Sampling" or "Permutating" the residuals.

Details

The function calculates bootstrap confidence intervals for coordinates and different stress measures using a distance matrix as a basis. The funcion uses random sampling or permutations of the residuals to obtain the bootstrap replications. The procedure preserves the length of the points in the multidimensional space perturbating only the angles among the vectors. It is done so to preserve the property of positiveness of the diagonal elements of the scalar product matrices. The procedure may result into a scalar product that does not have an euclidean configuration and then has some negative eigenvalues; to avoid this problem the negative eigenvalues are removed to approximate the perturbated matrix by the closest with the required properties.

It is well known that the eigenvectors of a matrix are unique except for reflections, that is, if we change the sign of each component of the eigenvector we have the same solution. If that happens, an unwanted increase in the variability due to this artifact may invalidate the results. To avoid this we can calculate the scalar product of each eigenvector of the initial matrix with the corresponding eigenvector of the bootstrap replicate and change the signs of the later if the result is negative.

Another artifact of the procedure may arise when the dimension of the solution is higher than 1 because the eigenvectors of a replicate may generate the same subspace although are not in the same directions, i. e., the subspace is referred to a different system. That also may produce an unwanted increase of the variability that invalidates the results. To avoid this, every replicate may be rotated to match as much as possible the subspace generated by the eigenvectors of the initial matrix. This is done by Procrustes Analysis, taking the rotated matrix as solution. The solution to this problem is also a sulution to the reflection, then only this problem is considered.

Value

Returns an object of class "PCoABootstrap" with the information for each bootstrap replication.

`Info` Information about the procedure

`InitialDistance` Initial distance

`RawStress` A vector containing the raw stress for all the bootstrap replicates

`stress1` A vector containing the value of the stress1 formula for all the bootstrap replicates

`stress2` A vector containing the value of the stress2 formula for all the bootstrap replicates

`sstress1` A vector containing the value of the sstress1 formula for all the bootstrap replicates

`sstress2` A vector containing the value of the sstress2 formula for all the bootstrap replicates

`Coordinates` A list with a component for each object. A component contains the coordinates of an object for all the bootstrap replicates (in columns)

`NReplicates` Number of bootstrap replicates

Author(s)

Jose L. Vicente-Villardon

References

Efron, B.; Tibshirani, RJ. (1993). An introduction to the bootstrap. New York: Chapman and Hall. 436p.

Ringrose, T. J. (1992). Bootstrapping and correspondence analysis in archaeology. Journal of Archaeological Science, 19(6), 615-629.

MILAN, L., & WHITTAKER, J. (1995). Application of the parametric bootstrap to models that incorporate a singular value decomposition. Applied statistics, 44(1), 31-49.

Jacoby, W. G., & Armstrong, D. A. (2014). Bootstrap Confidence Regions for Multidimensional Scaling Solutions. American Journal of Political Science, 58(1), 264-278.

See Also

BootstrapScalar

Examples

```
data(spiders)
D=BinaryProximities(spiders, coefficient="Jaccard", transformation="sqrt(1-S)")
DB=BootstrapDistance(D$Proximities)
```

BoxPlotPanel *Panel of box plots*

Description

Panel of box plots for a set of numerical variables and a grouping factor.

Usage

```
BoxPlotPanel(X, groups = NULL, nrows = NULL, panel = TRUE,
notch = FALSE, GroupsTogether = TRUE, ...)
```

Arguments

X	The matrix of continuous variables
groups	The grouping factor
nrows	Number of rows of the panel.
panel	Should the plots be organized into a panel? (or separated)
notch	Should notches be used in the box plots?
GroupsTogether	Should all the groups be together in the same plot?
...	Other graphical arguments

Details

Panel of box plots for a set of numerical variables and a grouping factor.

Value

The box plot panel

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(wine)
BoxPlotPanel(wine[,4:7], groups = wine$Origin, nrows = 2, ylab="")
```

CA — *Correspondence Analysis*

Description

Correspondence Analysis for a frequency or abundace data matrix.

Usage

```
CA(x, dim = 2, alpha = 1)
```

Arguments

`x`	The frequency or abundance data matrix.
`dim`	Dimension of the final solution
`alpha`	Alpha to determine the kind of biplot to use.

Details

Calculates Correspondence Analysis for a tww-way frequency or abundance table

Value

Correspondence analysis solution

Author(s)

Jose Luis Vicente Villardon

References

Benzécri, J. P. (1992). Correspondence analysis handbook. New York: Marcel Dekker.

Greenacre, M. J. (1984). Theory and applications of correspondence analysis. Academic Press.

Examples

```
data(SpidersSp)
cabip=CA(SpidersSp)
plot(cabip)
```

Canonical.Variate.Analysis
Biplot representation of a Canonical Variate Analysis or a Manova (Canonical-Biplot or MANOVA-Biplot)

Description

Calculates a canonical biplot with confidence regions for the means.

Usage

```
Canonical.Variate.Analysis(X, group, InitialTransform = 5)
```

Arguments

`X`	A data matrix
`group`	A factor containing the groups
`InitialTransform`	Initial transformation of the data matrix

Details

The Biplot method (Gabriel, 1971; Galindo, 1986; Gower and Hand, 1996) is becoming one of the most popular techniques for analysing multivariate data. Biplot methods are techniques for simultaneous representation of the n rows and n columns of a data matrix $\mathbf{X}$, in reduced dimensions, where the rows represent individuals, objects or samples and the columns the variables measured on them. Classical Biplot methods are a graphical representation of a Principal Components Analysis (PCA) that it is used to obtain linear combinations that successively maximize the total variability. PCA is not considered an appropriate approach where there is known a priori group structure in the data. The most general methodology for discrimination among groups, using multiple observed variables, is Canonical Variate Analysis (CVA). CVA allows us to derive linear combinations that successively maximize the ratio of "between-groups"" to "pooled within-group" sample variance. Several authors propose a Biplot representation for CVA called Canonical Biplot (CB) (Vicente-Villardon, 1992 and Gower & Hand, 1996) when it is oriented to the discrimination between groups or MANOVA-Biplot Gabriel (1972, 1995) when the aim is to study the variables responsible for the discrimination. The main advantage of the Biplot version of the technique is that it is possible not only to establish the differences between groups but also to characterise the variables responsible for them. The methodology is not yet widely used mainly because it is still not available in the major statistical packages. Amaro, Vicente-Villardon & Galindo (2004) extend the methodology for two-way designs and propose confidence circles based on univariate and multivariate tests to perform post-hoc analysis of each variable.

Value

An object of class "Canonical.Biplot"

Author(s)

Jose Luis Vicente Villardon

References

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

Vicente-Villardón, J. L. (1992). Una alternativa a las técnicas factoriales clásicas basada en una generalización de los métodos Biplot (Doctoral dissertation, Tesis. Universidad de Salamanca. España. 248 pp.[Links]).

Gabriel KR (1971) The biplot graphic display of matrices with application to principal component analysis. Biometrika 58(3):453-467.

Gabriel, K. R. (1995). MANOVA biplots for two-way contingency tables. WJ Krzanowski (Ed.), Recent advances in descriptive multivariate analysis, Oxford University Press, Toronto. 227-268.

Galindo Villardon, M. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Qüestiió. 1986, vol. 10, núm. 1.

Gower y Hand (1996): Biplots. Chapman & Hall.

Varas, M. J., Vicente-Tavera, S., Molina, E., & Vicente-Villardon, J. L. (2005). Role of canonical biplot method in the study of building stones: an example from Spanish monumental heritage. Environmetrics, 16(4), 405-419.

Santana, M. A., Romay, G., Matehus, J., Villardon, J. L., & Demey, J. R. (2009). simple and low-cost strategy for micropropagation of cassava (Manihot esculenta Crantz). African Journal of Biotechnology, 8(16).

Examples

```
data(wine)
X=wine[,4:21]
canbip=CanonicalBiplot(X, group=wine$Group)
plot(canbip, mode="s")
```

CanonicalBiplot *Biplot representation of a Canonical Variate Analysis or a Manova (Canonical-Biplot or MANOVA-Biplot)*

Description

Calculates a canonical biplot with confidence regions for the means.

Usage

```
CanonicalBiplot(X, group, SUP = NULL, InitialTransform = 5, LDA=FALSE, MANOVA = FALSE)
```

Arguments

`X`	A data matrix
`group`	A factor containing the groups
`SUP`	Supplementary observations to project on the biplot
`InitialTransform`	Initial transformation of the data matrix
`LDA`	A logical to indicate if the discriminant analysis should also be included
`MANOVA`	A logical to indicate if MANOVA should also be included

Details

The Biplot method (Gabriel, 1971; Galindo, 1986; Gower and Hand, 1996) is becoming one of the most popular techniques for analysing multivariate data. Biplot methods are techniques for simultaneous representation of the n rows and n columns of a data matrix $\mathbf{X}$, in reduced dimensions, where the rows represent individuals, objects or samples and the columns the variables measured on them. Classical Biplot methods are a graphical representation of a Principal Components Analysis (PCA) that it is used to obtain linear combinations that successively maximize the total variability. PCA is not considered an appropriate approach where there is known a priori group structure in the data. The most general methodology for discrimination among groups, using multiple observed variables, is Canonical Variate Analysis (CVA). CVA allows us to derive linear combinations that successively maximize the ratio of "between-groups"" to "pooled within-group" sample variance. Several authors propose a Biplot representation for CVA called Canonical Biplot (CB) (Vicente-Villardon, 1992 and Gower & Hand, 1996) when it is oriented to the discrimination between groups or MANOVA-Biplot Gabriel (1972, 1995) when the aim is to study the variables responsible for the discrimination. The main advantage of the Biplot version of the technique is that it is possible not only to establish the differences between groups but also to characterise the variables responsible for them. The methodology is not yet widely used mainly because it is still not available in the major statistical packages. Amaro, Vicente-Villardon & Galindo (2004) extend the methodology for two-way designs and propose confidence circles based on univariate and multivariate tests to perform post-hoc analysis of each variable.

Value

An object of class "Canonical.Biplot"

Author(s)

Jose Luis Vicente Villardon

References

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

Vicente-Villardón, J. L. (1992). Una alternativa a las técnicas factoriales clásicas basada en una generalización de los métodos Biplot (Doctoral dissertation, Tesis. Universidad de Salamanca. España. 248 pp.[Links]).

Gabriel KR (1971) The biplot graphic display of matrices with application to principal component analysis. Biometrika 58(3):453-467.

Gabriel, K. R. (1995). MANOVA biplots for two-way contingency tables. WJ Krzanowski (Ed.), Recent advances in descriptive multivariate analysis, Oxford University Press, Toronto. 227-268.

Galindo Villardon, M. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Qüestiió. 1986, vol. 10, núm. 1.

Gower y Hand (1996): Biplots. Chapman & Hall.

Varas, M. J., Vicente-Tavera, S., Molina, E., & Vicente-Villardon, J. L. (2005). Role of canonical biplot method in the study of building stones: an example from Spanish monumental heritage. Environmetrics, 16(4), 405-419.

Santana, M. A., Romay, G., Matehus, J., Villardon, J. L., & Demey, J. R. (2009). simple and low-cost strategy for micropropagation of cassava (Manihot esculenta Crantz). African Journal of Biotechnology, 8(16).

Examples

```
data(wine)
X=wine[,4:21]
canbip=CanonicalBiplot(X, group=wine$Group)
plot(canbip, mode="s")
```

`CanonicalDistanceAnalysis`
MANOVA and Canonical Analysis of Distances

Description

Performs a MANOVA and a Canonical Analysis based on of Distance Matrices (usally for continuous data)

Usage

```
CanonicalDistanceAnalysis(Prox, group, dimens = 2, Nsamples = 1000,
PCoA = "Standard", ProjectInd = TRUE)
```

Arguments

`Prox`	A object containing proximities
`group`	A factor with the group structure of the rows
`dimens`	The dimension of the solution
`Nsamples`	Number of samples for the permutation test. Number of permutations.
`PCoA`	Type of Principal Coordinates for the Canonical Analysis calculated from the Principal coordinates of the Mean Matrix. "Standard" : Standard Principal Coordinates Analysis, "Weighted": Weighted Principal Coordinates Analysis, "WPCA")
`ProjectInd`	Should the individual points be Projected onto the representation For the moment only available for Continuous Data.

Details

Performs a MANOVA and a Canonical Analysis based on of Distance Matrices (usally for continuous data). The MANOVA statistics is calculated from a decomposition of the distance matrix based on a factor of a external classification. The significance of the test is calculated using a premutation test. The approach depens only on the distances and then is useful with any kind of data.

The Canonical Representation is calculated from a Principal Coordinates Analysis od the distance matrix among the means. Thus, it is only possible for continuous data. The PCoA representation can be "Standard" using the means directly, "Weighted" weighting each group with its sample size or using weighted Princiopal Components Analysis of the matrix of means.

A measure of the quality of representation of the groups is provided. When possible, the measure is also provided for the individual points.

Soon, a biplot representation will also be developed.

Value

An object of class "CanonicalDistanceAnalysis" with:

`Distances`	The Matrix of Distances from which the Analysis has been made
`Groups`	A factor containing the group struture of the individuals
`TSS`	Total sum of squares
`BSS`	Between groups sum of squares
`WSS`	Within groups sum of squares
`Fexp`	Experimental pseudo F-value
`pvalue`	p value based on the permutation test
`Nsamples`	p value based on the permutation test
`ExplainedVariance`	Variances explained by the PCoA
`MeanCoordinates`	Coordinates of the groups for the graphical representation
`Qualities`	Qualities of the representation of the groups
`CummulativeQualities`	Cummulative qualities of the representation of the groups
`RowCoordinates`	Coordinates of the individuals for the graphical representation

Note

The MANOVA and the representation of the means can be applied to any Distance althoug the projection of the individuals can be made only for continuous data.

Author(s)

Jose Luis Vicente Villardon

References

Gower, J. C., & 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.

Krzanowski, W. J. (2004). Biplots for multifactorial analysis of distance. Biometrics, 60(2), 517-524.

Examples

```
data(iris)
group=iris[,5]
X=as.matrix(iris[1:4])
D=ContinuousProximities(X,  coef = 1)
CDA=CanonicalDistanceAnalysis(D, group, dimens=2)
summary(CDA)
plot(CDA)
```

`CanonicalStatisBiplot` *CANONICAL STATIS-ACT for multiple tables with common rows and its associated Biplot*

Description

The procedure performs STATIS-ACT methodology for multiple tables with common rows and its associated biplot

Usage

```
CanonicalStatisBiplot(X, Groups, InitTransform = "Standardize columns", dimens = 2,
                  SameVar = FALSE)
```

Arguments

`X`	A list containing multiple tables with common rows
`Groups`	A factor containing the groups
`InitTransform`	Initial transformation of the data matrices
`dimens`	Dimension of the final solution
`SameVar`	Are the variables the same for all occasions?

Details

The procedure performs Canonical STATIS-ACT methodology for multiple tables with common rows and its associated biplot. When the variables are the same for all occasions trajectories for the variables can also be plotted.

Value

An object of class StatisBiplot

Author(s)

Jose Luis Vicente Villardon

References

Vallejo-Arboleda, A., Vicente-Villardon, J. L., & Galindo-Villardon, M. P. (2007). Canonical STATIS: Biplot analysis of multi-table group structured data based on STATIS-ACT methodology. Computational statistics & data analysis, 51(9), 4193-4205.

Abdi, H., Williams, L.J., Valentin, D., & Bennani-Dosse, M. (2012). STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat, 4, 124-167.

Efron, B.,Tibshirani, RJ. (1993). An introduction to the bootstrap. New York: Chapman and Hall. 436p.

Escoufier, Y. (1976). Operateur associe a un tableau de donnees. Annales de laInsee, 22-23, 165-178.

Escoufier, Y. (1987). The duality diagram: a means for better practical applications. En P. Legendre & L. Legendre (Eds.), Developments in Numerical Ecology, pp. 139-156, NATO Advanced Institute, Serie G. Berlin: Springer.

L'Hermier des Plantes, H. (1976). Structuration des Tableaux a Trois Indices de la Statistique. [These de Troisieme Cycle]. University of Montpellier, France.

Ringrose, T.J. (1992). Bootstrapping and Correspondence Analysis in Archaeology. Journal of Archaeological Science. 19:615-629.

Examples

```
data(Chemical)
x= Chemical[37:144,5:9]
weeks=as.factor(as.numeric(Chemical$WEEKS[37:144]))
levels(weeks)=c("W2" , "W3", "W4")
X=Convert2ThreeWay(x,weeks, columns=FALSE)
Groups=Chemical$Treatment[1:36]
canstbip=CanonicalStatisBiplot(X, Groups, SameVar = TRUE)
plot(canstbip, mode="s", PlotVars=TRUE, ShowBox=TRUE)
```

`CategoricalDistances` *Distances among individuals using nominal variables.*

Description

Distances among individuals using nominal variables.

Usage

```
CategoricalDistances(x, y = NULL, coefficient = "GOW", transformation = "sqrt(1-S)")
```

Arguments

x	Matrix of Categorical Data
y	A second matrix of categorical data with the same variables as x
coefficient	Similarity coefficient to use (see details)
transformation	Transformation of the similarity into a distance

Details

The function calculates similarities and dissimilarities among a set ob ogjects characterized by a set of nominal variables. The function uses similarities and converts into dissimilarities using a variety of transformations controled by the user.

Value

A matrix with distances among the rows of x and y. If y is NULL the interdistances among the rows of x are calculated.

Author(s)

Jose Luis Vicente Villardon

References

dos Santos, T. R., & Zarate, L. E. (2015). Categorical data clustering: What similarity measure to recommend?. Expert Systems with Applications, 42(3), 1247-1260.

Boriah, S., Chandola, V., & Kumar, V. (2008). Similarity measures for categorical data: A comparative evaluation. red, 30(2), 3.

Examples

```
##---- Should be DIRECTLY executable !! ----
```

CategoricalProximities

Proximities among individuals using nominal variables.

Description

Proximities among individuals using nominal variables.

Usage

```
CategoricalProximities(Data, SUP = NULL, coefficient = "GOW", transformation = 3, ...)
```

Arguments

`Data`	A data frame containing categorical (nominal) variables
`SUP`	Supplementary data (Used to project supplementary individuals onto the PCoA configuration, for example)
`coefficient`	Similarity coefficient to use (see details)
`transformation`	Transformation of the similarity into a distance
`...`	Extra parameters

Details

The function calculates similarities and dissimilarities among a set ob ogjects characterized by a set of nominal variables. The function uses similarities and converts into dissimilarities using a variety of transformations controled by the user.

Value

A list of Values

Author(s)

Jose Luis Vicente Villardon

References

dos Santos, T. R., & Zarate, L. E. (2015). Categorical data clustering: What similarity measure to recommend?. Expert Systems with Applications, 42(3), 1247-1260.

Boriah, S., Chandola, V., & Kumar, V. (2008). Similarity measures for categorical data: A comparative evaluation. red, 30(2), 3.

Examples

```
data(Doctors)
Dis=CategoricalProximities(Doctors, SUP=NULL, coefficient="GOW" , transformation=3)
pco=PrincipalCoordinates(Dis)
plot(pco, RowCex=0.7, RowColors=as.integer(Doctors[[1]]), RowLabels=as.character(Doctors[[1]]))
```

CCA *Canonical Correspondence Analysis*

Description

Calculates the solution of a Canonical Correspondence Analysis Biplot

Usage

```
CCA(P, Z, alpha = 1, dimens = 4)
```

Arguments

P	Abundance Matrix of sites by species.
Z	Environmental variables measured at the same sites
alpha	Alpha for the biplot decomposition [0,1]. With alpha=1 the emphasis is on the sites and with alpha=0 the emphasis is on the species
dimens	Dimension of the solution

Details

A pair of ecological tables, made of a species abundance matrix and an environmental variables matrix measured at the same sampling sites, is usually analyzed by Canonical Correspondence Analysis (CCA) (Ter BRAAK, 1986). CCA can be considered as a Correspondence Analysis (CA) in which the ordination axis are constrained to be linear combinations of the environmental variables. Recently the procedure has been extended to other disciplines as Sociology or Psichology and it is potentially useful in many other fields.

Value

A CCA solution object

Author(s)

Jose Luis vicente Villardon

References

Ter Braak, C. J. (1986). Canonical correspondence analysis: a new eigenvector technique for multivariate direct gradient analysis. Ecology, 67(5), 1167-1179.

Johnson, K. W., & Altman, N. S. (1999). Canonical correspondence analysis as an approximation to Gaussian ordination. Environmetrics, 10(1), 39-52.

Graffelman, J. (2001). Quality statistics in canonical correspondence analysis. Environmetrics, 12(5), 485-497.

Graffelman, J., & Tuft, R. (2004). Site scores and conditional biplots in canonical correspondence analysis. Environmetrics, 15(1), 67-80.

Greenacre, M. (2010). Canonical correspondence analysis in social science research (pp. 279-286). Springer Berlin Heidelberg.

Examples

```
data(riano)
Sp=riano[,3:15]
Env=riano[,16:25]
ccabip=CCA(Sp, Env)
plot(ccabip)
```

`CheckBinaryMatrix` *Checks if a data matrix is binary*

Description

Checks if a data matrix is binary

Usage

```
CheckBinaryMatrix(x)
```

Arguments

`x`	Matrix to check.

Details

Checks if all the entries of the matix are either 0 or 1.

Value

`TRUE` if the matrix is binary.

Author(s)

Jose Luis Vicente-Villardon

Examples

```
data(spiders)
sp=Dataframe2BinaryMatrix(spiders)
CheckBinaryMatrix(sp)
```

`CheckBinaryVector` *Checks if a vector is binary*

Description

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

Usage

```
CheckBinaryVector(x)
```

Arguments

`x` he vector to check

Value

The logical result

Author(s)

Jose luis Vicente Villardon

Examples

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

Chemical *Chemical data*

Description

Ecological data

Usage

```
data("Chemical")
```

Format

A data frame with 324 observations on the following 16 variables.

`Treatment` a factor with levels `F0N0` `F0N1` `F0N2` `F0N3` `F1N0` `F1N1` `F1N2` `F1N3` `F2N0` `F2N1` `F2N2` `F2N3`

`FISH` a factor with levels `F0` `F1` `F2`

`NUTRIENTS` a factor with levels `N0` `N1` `N2` `N3`

`WEEKS` a factor with levels `W1` `W2` `W3` `W4` `W5` `W6` `W7` `W8` `W9`

`TEMPERATURE` a numeric vector

`pH` a numeric vector

`ALKALINITYmeql` a numeric vector

`CO2free` a numeric vector

`NNH4mgl` a numeric vector

`NNO3mgl` a numeric vector

`SRPmglP` a numeric vector

`TPmgl` a numeric vector

`TSSmgl` a numeric vector

`CONDUCTIVITYmScm` a numeric vector

`TSPmglP` a numeric vector

`Chlorophyllamgl` a numeric vector

Details

Chemical Data

Source

Department of Ecology. University of Leon. (Spain)

References

To add

Examples

```
data(Chemical)
## maybe str(Chemical) ; plot(Chemical) ...
```

`Circle` *Draws a circle*

Description

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

Usage

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

Arguments

`radius`	radius of the circle
`origin`	Centre of the circle
`col`	Color od the circle
`...`	Aditional 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 Villardon

Examples

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

`Coinertia` *Coinertia Analysis.*

Description

Calculates a Coinertia Analysis for two matrices of continuous data

Usage

```
Coinertia(X, Y, ScalingX = 5, ScalingY = 5, dimsol = 3)
```

Arguments

`X`	The first matrix in the analysis
`Y`	The second matrix in the analysis
`ScalingX`	Transformation of the X matrix
`ScalingY`	Transformation of the Y matrix
`dimsol`	Dimension of the solution

Details

Coinertia analysis for two continuous data matrices.

Value

An object of class Coinertia.SOL

Author(s)

Jose Luis Vicente Villardon

References

Doledec, S., & Chessel, D. (1994). Co-inertia analysis: an alternative method for studying species-environment relationships. Freshwater biology, 31(3), 277-294.

Examples

```
SSI$Year == "a2006"
SSI2D=SSI[SSI$Year == "a2006",3:23]
rownames(SSI2D)=as.character(SSI$Country[SSI$Year == "a2006"])
SSIHuman2D=SSI2D[,1:9]
SSIEnvir2D=SSI2D[,10:16]
SSIEcon2D=SSI2D[,17:21]
Coin=Coinertia(SSIHuman2D, SSIEnvir2D)
```

`ColContributionPlot` *Plots the contributios of a biplot*

Description

Plots the contributios of a biplot

Usage

```
ColContributionPlot(bip, A1 = 1, A2 = 2, Colors = NULL, Labs = NULL,
MinQuality = 0, CorrelationScale = FALSE, ContributionScale = TRUE,
AddSigns2Labs = TRUE, ...)
```

Arguments

`bip`	An object of class ContinuousBiplot
`A1`	First dimension to plot
`A2`	Second dimension to plot
`Colors`	Colors for the variables
`Labs`	Labels for the variables
`MinQuality`	Min quality to plot
`CorrelationScale`	Scales for correlation
`ContributionScale`	Scales for contributions
`AddSigns2Labs`	Add the siggns of the correlations to the labels
`...`	Any other graphical parameter

Details

Plots the contributions on a plot that sows also the sum for both axes-

Value

The contribution plot

Author(s)

Jose Luis Vicente Villardon

Examples

```
## Simple Biplot with arrows
data(Protein)
bip=PCA.Biplot(Protein[,3:11])

# Plot of the Variable Contributions
ColContributionPlot(bip, cex=1)
```

`ConcEllipse` *Concentration ellipse for a se of two-dimensional points*

Description

The function calculates a non-parametric concentration ellipse for a set of two-dimensional points.

Usage

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

Arguments

`data`	The set of two-dimensional points
`confidence`	Percentage of points to be included in the ellipse
`npoints`	Number of points to draw the eelipse contour. The hier the number of points the smouther is the ellipse.

Details

The procedre uses the Mahalanobis distances to determine the points that will be used for the calculations.

Value

A list with the following fields

`data`	Data Used for the calculations
`confidence`	The confidence level used
`ellipse`	The points on the ellipse contour to be plotted
`center`	The center of the points

Author(s)

Jose Luis Vicente Villardon

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

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

ConfidenceInterval *Confidence Interval for the mean*

Description

Calculates Confidence Interval for the mean of a Numerical Variable.

Usage

```
ConfidenceInterval(x, Desv = NULL, df = NULL, Confidence = 0.95)
```

Arguments

x	The numerical variable
Desv	Standard deviation. If NULL, the sd is calculated from the data
df	Degrees of freedom
Confidence	Confidence Level

Details

Calculates Confidence Interval for the mean of a Numerical Variable.

Value

The confidence Interval for the mean

Author(s)

Jose Luis Vicente Villardon

Examples

```
# Not yet
```

`ConstrainedLogisticBiplot` *Constrained Binary Logistic Biplot*

Description

Constrained Binary Logistic Biplot or Redundancy Analysis for Binary Data based on logistic responses

Usage

```
ConstrainedLogisticBiplot(Y, X, dim = 2, Scaling = 5, tolerance = 1e-05,
maxiter = 100, penalization = 0.1)
```

Arguments

`Y`	A binary data matrix
`X`	A matrix of predictors
`dim`	Dimension of the Solution
`Scaling`	Transformation of the columns of the predictor matrix.
`tolerance`	Tolerance for the algorithm
`maxiter`	Maximum number of iterations.
`penalization`	Penalization for the fit (ridge)

Details

Constrained Binary Logistic Biplot or Redundancy Analysis for Binary Data based on logistic responses.

Value

A logistic Biplot with the reponse and the predictive variables projected onto it.

Author(s)

Jose Luis Vicente-Villardon

References

Vicente-Villardon, J. L., & Vicente-Gonzalez, L. Redundancy Analysis for Binary Data Based on Logistic Responses in Data Analysis and Rationality in a Complex World. Springer.

Examples

```
# not yet
```

`ConstrainedOrdinalLogisticBiplot`
Constrained Ordinal Logistic Biplot

Description

Constrained Ordinal Logistic Biplot or Redundancy Analysis for Ordinal Data based on logistic responses

Usage

```
ConstrainedOrdinalLogisticBiplot(Y, X, dim = 2, Scaling = 5,
tolerance = 1e-05, maxiter = 100, penalization = 0.1, show = FALSE)
```

Arguments

`Y`	A binary data matrix
`X`	A matrix of predictors
`dim`	Dimension of the Solution
`Scaling`	Transformation of the columns of the predictor matrix.
`tolerance`	Tolerance for the algorithm
`maxiter`	Maximum number of iterations.
`penalization`	Penalization for the fit (ridge)
`show`	Show each step ot the fit

Details

Constrained Ordinal Logistic Biplot or Redundancy Analysis for Ordinal Data based on logistic responses.

Value

An ordinal logistic Biplot with the reponse and the predictive variables projected onto it.

Author(s)

Jose Luis Vicente-Villardon

References

Vicente-Villardon, J. L., & Vicente-Gonzalez, L. Redundancy Analysis for Binary Data Based on Logistic Responses in Data Analysis and Rationality in a Complex World. Springer.

Examples

```
# not yet
```

ContinuousDistances *Distances for Continuous Data*

Description

Calculates distances among rows of a continuous data matrix or among the rows of two continuous matrices.

Usage

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

Arguments

x	Main data matrix. Distances among rows are calculated if y=NULL.
y	Supplementary data matrix. If not NULL the distances among the rows of x and y are calculated
coef	Distance coefficient. Use the name or the number(see details)
r	Exponent for the Minkowsky

Details

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(abs(y[i,]-x[j,])/r)/p

4.- Minkowski = (sum((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(abs(y[i,]-x[j,])/abs(y[i,]+x[j,]))/p

7.- Camberra = sum(abs(y[i,]-x[j,])/(abs(y[i,])+abs(x[j,])))

8.- Bray_Curtis = sum(abs(y[i,]-x[j,]))/sum(y[i,]+x[j,])

9.- Soergel = sum(abs(y[i,]-x[j,]))/sum(apply(rbind(y[i,],x[j,]),2,max))

10.- Ware_hedges = sum(abs(y[i,]-x[j,]))/sum(apply(rbind(y[i,],x[j,]),2,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)

Jose Luis Vicente-Villardon

References

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

See Also

PrincipalCoordinates

Examples

```
data(wine)
dis=ContinuousDistances(wine[,4:21])
```

ContinuousProximities *Proximities for Continuous Data*

Description

Calculates proximities among rows of a continuous data matrix or among the rows of two continuous matrices.

Usage

```
ContinuousProximities(x, y = NULL, ysup = FALSE,
transpose = FALSE, coef = "Pythagorean", r = 1)
```

Arguments

x	Main data matrix. Distances among rows are calculated if y=NULL.
y	Supplementary data matrix. If not NULL the distances among the rows of x and y are calculated
ysup	Supplementary Y data
transpose	Transpose rows and columns
coef	Distance coefficient. Use the name or the number(see details)
r	Exponent for the Minkowsky

Details

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(abs(y[i,]-x[j,])/r)/p

4.- Minkowski = (sum((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(abs(y[i,]-x[j,])/abs(y[i,]+x[j,]))/p

7.- Camberra = sum(abs(y[i,]-x[j,])/(abs(y[i,])+abs(x[j,])))

8.- Bray_Curtis = sum(abs(y[i,]-x[j,]))/sum(y[i,]+x[j,])

9.- Soergel = sum(abs(y[i,]-x[j,]))/sum(apply(rbind(y[i,],x[j,]),2,max))

10.- Ware_hedges = sum(abs(y[i,]-x[j,]))/sum(apply(rbind(y[i,],x[j,]),2,max))

Value

`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)

Jose Luis Vicente-Villardon

References

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

Examples

```
data(wine)
dis=ContinuousProximities(wine[,4:21])
```

Convert2ThreeWay — *Three way array from a two way matrix*

Description

Converts a two-dimensional matrix into a list where each cell is the two dimensional data matrix for an occasion or group.

Usage

```
Convert2ThreeWay(x, groups, columns = FALSE, RowNames = NULL)
```

Arguments

`x`	The two dimensional matrix
`groups`	A factor defining the groups
`columns`	Are the grouos defined for columns?
`RowNames`	Names for the rows of each table.

Details

Converts a two dimensional matrix into a multitable list according to the groups provided by the user. Each field of the list has the name of the corresponding group.

Value

A Multitable list. Ech filed is the data matrix for a group.

`X`	The multitable list

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(Chemical)
x= Chemical[,5:16]
X=Convert2ThreeWay(x,Chemical$WEEKS, columns=FALSE)
```

Convert3wArray2List *Converts a three way array into a list*

Description

Converts a three way array into a list

Usage

```
Convert3wArray2List(X)
```

Arguments

X	A three way array

Details

Converts a three way array into a list

Value

A list

Author(s)

Jose Luis Vicente-Villardon

Examples

```
#No examples yet
```

ConvertFactors2Integers *Convert a factor to integer numbers*

Description

Convert a factor to integer numbers

Usage

```
ConvertFactors2Integers(x)
```

Arguments

x	A vector with a factor

Details

Convert a factor to integer numbers

Value

a vector with the converted values

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

ConvertList23wArray *Converts a list of matrices into a three way array*

Description

Converts a list of matrices into a three way array. All the matrices in the list must have the same size.

Usage

```
ConvertList23wArray(X)
```

Arguments

X	A list with data matrices.

Details

Converts a list of matrices into a three way array. All the matrices in the list must have the same size.

Value

A three-way array

Author(s)

Jose Luis Vicente-Villardon

Examples

```
# No examples yet
```

`CorrelationCircle` *Circle of correlations*

Description

Circle of correlations among the manifiest variables and the principal comonents (or dimensions of any biplot).

Usage

```
CorrelationCircle(bip, A1 = 1, A2 = 2, Colors = NULL, Labs = NULL, ...)
```

Arguments

`bip`	an biplot object of any kind.
`A1`	First dimension for the representation
`A2`	Second dimension for the representation
`Colors`	Colors of the variables
`Labs`	Labels of the variables
`...`	Any other graphical parameters

Details

Circle of correlations among the manifiest variables and the principal comonents (or dimensions of any biplot).

Value

The plot of the circle of correlations

Author(s)

Jose Luis Vicente Villardon

Examples

```
bip=PCA.Biplot(wine[,4:21])
CorrelationCircle(bip)
```

CrissCross *Alternated Least Squares Biplot*

Description

Alternated Least Squares Biplot with any choice of weigths for each element of the data matrix

Usage

```
CrissCross(x, w = matrix(1, dim(x)[1], dim(x)[2]), dimens = 2, a0 = NULL,
b0 = NULL, maxiter = 100, tol = 1e-04, addsvd = TRUE, lambda = 0)
```

Arguments

`x`	Data Matrix to be analysed
`w`	Weights matrix. Must be of the same size as X.
`dimens`	Dimension of the solution.
`a0`	Starting row coordinates. Random coordinates are calculated if the argument is NULL.
`b0`	Starting column coordinates. Random coordinates are calculated if the argument is NULL.
`maxiter`	Maximum number of iterations
`tol`	Tolerance for the algorithm to converge.
`addsvd`	Calculate an additional SVD at the end of the algorithm. That meakes the final solution more readable
`lambda`	Constant to add to the diagonal of the natrices to be inverted in order to improve stability when the matrices are ill-conditioned.

Details

The function calculates Alternated Least Squares Biplot with any choice of weigths for each element of the data matrix. The function is useful when we want a low rank approximation of a data matrix in which each element of the matrix has a different weight, for example, all the weights are 1 except for the missing elements that are 0, or to model the logarithms of a frequency table using the frequencies as weights.

Value

An object of class .Biplot" with the following components:

`n`	Number of Rows
`p`	Number of Columns
`dim`	Dimension of the Biplot
`EigenValues`	Eigenvalues

`Inertia`	Explained variance (Inertia)
`CumInertia`	Cumulative Explained variance (Inertia)
`RowCoordinates`	Coordinates for the rows
`ColCoordinates`	Coordinates for the columns
`RowContributions`	Contributions for the rows
`ColContributions`	Contributions for the columns
`Scale_Factor`	Scale factor for the traditional plot with points and arrows. The row coordinates are multiplied and the column coordinates divided by that scale factor. The look of the plot is better without changing the inner product. For the HJ-Biplot the scale factor is 1.

Author(s)

Jose Luis Vicente Villardon

References

GABRIEL, K.R. and ZAMIR, S. (1979). Lower rank approximation of matrices by least squares with any choice of weights. Technometrics, 21: 489-498.

See Also

`LogFrequencyBiplot`

Examples

```
data(Protein)
X=as.matrix(Protein[,3:11])
X = InitialTransform(X, transform=5)$X
bip=CrissCross(X)
```

`CumSum` *Cummulative sums*

Description

Cummulative sums

Usage

```
CumSum(X, dimens = 1)
```

Arguments

`X`	Data Matrix
`dimens`	Dimension for summing

Details

Cummulative sums within rows (dimens=1) or columns (dimens=2) of a data matrix

Value

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

Author(s)

Jose Luis Vicente Villardon

Examples

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

Dataframe2BinaryMatrix *Converts a Data Frame into a Binary Data Matrix*

Description

Converts a Data Frame into a Binary Data Matrix

Usage

```
Dataframe2BinaryMatrix(dataf, cuttype = "Median", cut = NULL, BinFact = TRUE)
```

Arguments

dataf	data.frame to be converted
cuttype	Type of cut point for continuous variables. Must be "Median" or "Mean". Does not have any effect for factors
cut	Personalized cut value for continuous variables.
BinFact	Should I treat a factor with two levels as binary. This means that only a single dummy rather than two is used

Details

The function converts a data frame into a Binary Data Matrix (A matrix with entries either 0 or 1).

Factors with two levels are directly transformed into a column of 0/1 entries.

Factors with more than two levels are converted into a binary submatrix with as many rows as x and as many columns as levels or categories. (Indicator matrix)

Integer Variables are treated as factors

Continuous Variables are converted into binary variables using a cut point that can be the median, the mean or a value provided by the user.

Value

A Binary Data Matrix.

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(spiders)
Dataframe2BinaryMatrix(spiders)
```

DataFrame2Matrix4Regression

Prepares a matrix for regression from a data frame

Description

Prepares a matrix for regression from a data frame

Usage

```
DataFrame2Matrix4Regression(X, last = TRUE, Intercept = FALSE)
```

Arguments

X	A data frame
last	Logical to use the last category of nominal variabless as baseline.
Intercept	Logical to tell the function if a constant must be present

Details

Nominal variables are converted to a matrix of dummy variables for regression.

Value

A matrix ready to use as independent variables in a regression

Author(s)

Jose Luis Vicente Vilardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

`DensityBiplot` *Adds Non-parametric densities to a biplot. Separated densities are calculated for different clusters*

Description

Adds Non-parametric densities to a biplot. Separated densities are calculated for different clusters

Usage

```
DensityBiplot(X, y = NULL, grouplabels = NULL, ncontours = 6,
groupcolors = NULL, ncolors=20, ColorType=4)
```

Arguments

`X`	Two dimensional coordinates of the points in a biplot (or any other)
`y`	A factor containing clusters or groups for separate densities.
`grouplabels`	Labels for the groups
`ncontours`	Number of contours to represent on the biplot
`groupcolors`	Colors for the groups
`ncolors`	Number of colors for the density patterns
`ColorType`	One of the following: "1" = rainbow, "2" = heat.colors, "3" = terrain.colors, "4" = topo.colors, "5" = cm.colors

Details

Non parametric densities are used to investigate the concentration of row points on different areas of the biplot representation. The densities can be calculated for different groups or clusters in order to investigate if individuals with differnt characteristics are concentrated on particular areas of the biplot. The procedure is particularly useful with a high number of individuals.

Value

No value returned. It has effect on the graph.

Author(s)

Jose Luis Vicente Villardon

References

Gower, J. C., Lubbe, S. G., & Le Roux, N. J. (2011). Understanding biplots. John Wiley & Sons.

Examples

```
bip=PCA.Biplot(iris[,1:4])
plot(bip, mode="s", CexInd=0.1)
```

Dhats *Calculation of Disparities*

Description

Calculation of Disparities for a MDS model

Usage

```
Dhats(P, D, W, Model = c("Identity", "Ratio", "Interval", "Ordinal"), Standardize = TRUE)
```

Arguments

P	A matrix of proximities (usually dissimilarities)
D	A matrix of distances obtained from an euclidean configuration
W	A matrix of weights
Model	Measurement level of the proximities
Standardize	Should the Disparities be standardized?

Details

Calculation of disparities using standard or monotone regression depending on the MDS model.

Value

Returns the proximities.

Author(s)

Jose L. Vicente Villardon

References

Borg, I., & Groenen, P. J. (2005). Modern multidimensional scaling: Theory and applications. Springer.

Examples

```
## Function is used inside MDS or smacof
```

diagonal — *Diagonal matrix from a vector*

Description

Creates a diagonal matrix from a vector

Usage

```
diagonal(d)
```

Arguments

d	A numerical vector

Value

A diagonal matrix wirh the values of vector in the diagonal a zeros elsewhere

Author(s)

Jose Luis Vicente Villardon

Examples

```
diag(c(1, 2, 3, 4, 5))
```

DimensionLabels — *Labels for the selected dimensions in a biplot*

Description

Creates a character vector with labels for the dimensions of the biplot

Usage

```
DimensionLabels(dimens, Root = "Dim")
```

Arguments

dimens	Number of dimensions
Root	Root of the label

Details

An auxiliary function to cretae labels for the dimensions. Useful to label the matrices of results

Value

Returns a vector of labels

Author(s)

Jose Luis Vicente Villardon

Examples

```
DimensionLabels(dimens=3, Root = "Dim")
```

---

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
```

Doctors *Data set extracted from the Careers of doctorate holders survey carried out by Spanish Statistical Office in 2008.*

Description

The sample data, as part of a large survey, corresponds to 100 people who have the PhD degree and it shows the level of satisfaction of the doctorate holders about some issues.

Usage

```
data(Doctors)
```

Format

This data frame contains 100 observation for the following 5 ordinal variables, with four categories each: (1= "Very Satisfied", 2= "Somewhat Satisfied",3="Somewhat dissatisfied", 4="Very dissatisfied")

Salary

Benefits

Job Security

Job Location

Working conditions

Source

Spanish Statistical Institute. Survey of PDH holders, 2006. URL: http://www.ine.es.

Examples

```
data(Doctors)
## maybe str(Doctors) ; plot(Doctors) ...
```

ErrorBarPlotPanel *Plots a panel of error bars*

Description

Plots a panel of error bars to compare the means of several variables in the levels of a factor using confidence intervals.

Usage

```
ErrorBarPlotPanel(X, groups = NULL, nrows = NULL, panel = TRUE,
GroupsTogether = TRUE, Confidence = 0.95, p.adjust.method = "None",
UseANOVA = FALSE, Colors = "blue", Title = "Error Bar Plot",
sort = TRUE, ...)
```

Arguments

`X`	A matrix containing several variables
`groups`	A factor defining groups of individuals
`nrows`	Number of rows of the panel. The function calculates the number of columns needed.
`panel`	The plots are shown on a panel (TRUE) or in separated graphs (FALSE)
`GroupsTogether`	The groups appear together on the same plot
`Confidence`	Confidence levels for the error bars (confidence intervals)
`p.adjust.method`	Method for adjusting the p-value to cope with multiple comparisons.
`UseANOVA`	If TRUE the function uses the residual variance of the ANOVA to calculate the confidence interval. ("None", "Bonferroni" or "Sidak")
`Colors`	Colors to identyfy the groups
`Title`	Title of the graph
`sort`	Should short the means before plotting
`...`	Other graphical parameters

Details

The funtion plots a panel of error bars plots to compare several groups for several variables.

Value

A panel of error bars plots.

Author(s)

Jose Luis Vicente Villardon

Examples

```
ErrorBarPlotPanel(wine[4:9], wine$Group, UseANOVA=TRUE, Title="", sort=FALSE)
```

`EuclideanDistance` *Classical Euclidean Distance (Pythagorean Distance)*

Description

Calculates the eucliden distances among the rows of an euclidean configurations in any dimensions

Usage

```
EuclideanDistance(x)
```

Arguments

`x`	A matrix containing the euclidean configuration

Details

eucliden distances among the rows of an euclidean configurations in any dimensions

Value

Returns the distance matrix

Author(s)

Jose Luis Vicente Villardon

Examples

```
x=matrix(runif(20),10,2)
D=EuclideanDistance(x)
```

ExpandTable *Expands a compressed table of patterns and frequencies*

Description

Expands a compressed table of patterns and frequencies

Usage

```
ExpandTable(table)
```

Arguments

`table`	A compressed table of patterns and frequencies

Details

To simplify the calculations of some of the algorithms we compress the tables by searching for the distinct patterns and its frequencies. This function recovers the original data. It serves also to assign the corrdinates on the biplot to the original individuals.

Value

A matrix with the original data

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

ExternalBinaryLogisticBiplot *External Logistic Biplot for binary Data*

Description

Fits an External Logistic Biplot to the results of a Principal Coordinates Analysis obtained from binary data.

Usage

```
ExternalBinaryLogisticBiplot(Pco, IncludeConst=TRUE, penalization=0.2, freq=NULL,
tolerance = 1e-05, maxiter = 100)
```

Arguments

`Pco`	An object of class "Principal.Coordinates"
`IncludeConst`	Should the logistic fit include the constant term?
`penalization`	Penalization for the ridge regression
`freq`	frequencies for each observation or pattern (usually 1)
`tolerance`	Tolerance for convergence
`maxiter`	Maximum number of iterations

Details

Let $\mathbf{X}$ be the matrix of binary data scored as present or absent (1 or 0), in which the rows correspond to n individuals or entries (for example, genotypes) and the columns to p binary characters (for example alleles or bands), let $\mathbf{S} = (s_{ij})$ be a matrix containing the similarities among rows, obtained from the binary data matrix , and let $\Delta = (\delta_{ij})$ be the corresponding dissimilarity/distance matrix, taking for example $\delta_{ij} = \sqrt{1 - s_{ij}}$. Despite the fact that, in Cluster Analysis and Principal Coordinates Analysis, interpretation of the variables responsible for grouping or ordination is not straightforward, those methods are normally used to classify individual in which binary variables have been measured. we use a combination of Principal Coordinates Analysis (PCoA), Cluster Analysis (CA) and External Logistic Regression (ELB), as a better way to interpret the binary variables associated to the classification of genotypes. The combination of three standard techniques with some new ideas about the geometry of the procedures, allows to construct a External Logistic Regression (ELB), that helps the interpretation of the variables responsible for the classification or ordination. Suppose we have obtained an euclidean configuration $\mathbf{Y}$ obtained from the Principal Coordinates (PCoA) of the similarity matrix. To search for the variables associated to the ordination obtained in PCoA, we can look for the directions in the ordination diagram that better predict the probability of presence of each allele. More formally, if we defined $\pi_{ij} = E(x_{ij}) = \frac{1}{1+\exp(-(b_{j0}+\sum_{s=1}^{k} b_{js}y_{is}))}$ as the expected probability that the allele j be present at genotype for a genotype with coordinates y_{is} (i=1, ...,n; s=1, ..., k) on the ordination diagram, as where bjs (j=1,..., p) are the logistic regression coefficients that correspond to the jth variable (alleles or bands) in the sth dimension. The model is a generalized linear model having the logit as a link function. where and , y's and b's define a biplot in logit scale. This is called External Logistic Biplot because the coordinates of the genotypes are calculated in an external procedure (PCoA). Given that the y's are known from PCoA, obtaining the b´s is equivalent to performing a logistic regression using the j-th column of X as a response variable and the columns of y as regressors.

Value

An object of class `External.Binary.Logistic.Biplot` with the fields of the `Principal.Coordinates` object with the following fields added.

`ColumnParameters`
: Parameters resulting from fitting a logistic regression to each column of the original binary data matrix

`VarInfo`
: Information of the fit for each variable

`VarInfo$Deviances`
: A vector with the deviances of each variable calculated as the difference with the null model

`VarInfo$Dfs` A vector with degrees of freedom for each variable

`VarInfo$pvalues` A vector with the p values each variable

`VarInfo$Nagelkerke` A vector with the Nagelkerke pseudo R-squared for each variable

`VarInfo$PercentsCorrec` A vector with the percentage of correct classifications for each variable

`DevianceTotal` Total Deviance as the difference with the null model

`p` p value for the complete representation

`TotalPercent` Total percentage of correct classification

Author(s)

Jose Luis Vicente Villardon

References

Demey, J., Vicente-Villardon, J. L., Galindo, M.P. AND Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics, 24(24): 2832-2838.

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez, A. (2006) Logistic Biplots. In Multiple Correspondence Análisis And Related Methods. Grenacre, M & Blasius, J, Eds, Chapman and Hall, Boca Raton.

Examples

```
data(spiders)
x2=Dataframe2BinaryMatrix(spiders)
colnames(x2)=colnames(spiders)
dist=BinaryProximities(x2)
pco=PrincipalCoordinates(dist)
pcobip=ExternalBinaryLogisticBiplot(pco)
```

ExtractTable *Extracts unique patterns and its frequencies for a discrete data matrix (numeric)*

Description

Extracts the patterns and the frequencies of a discrete data matrix reducing the size of the data matrix in order to accelerate calculations in some techniques.

Usage

```
ExtractTable(x)
```

Arguments

x	A matrix of integers containing information of discrete variables. The input matrix must be numerical for the procedure to work properly.

Details

For any numerical matrix, calculates the different patterns and the frequencies associated to each pattern The result contains the pattern matrix, a vector with the frequencies, a list with rows sharing the same pattern. The final pattern matrix has different ordering than the original matrix.

Value

OriginalNames	Names before grouping the equal rows
Patterns	The reduced table with only unique patterns
EqualRows	A list with as many components as unique patterns specifying the original rows with each pattern. That will allow for the reconstruction of the initial matrix

Author(s)

Jose Luis Vicente-Villardon

Examples

```
data(spiders)
spidersbin=Dataframe2BinaryMatrix(spiders)
spiderstable=ExtractTable(spidersbin)
```

FA.Biplot *Biplot for Factor Analysis.*

Description

Biplot used as a graphical representation of Factor Analysis.

Usage

```
FA.Biplot(X, dimension = 3, Extraction="PC", Rotation="varimax",
         InitComunal="A1", normalize=FALSE, Scores= "Regression",
         MethodArgs=NULL, sup.rows = NULL, sup.cols = NULL, ...)
```

Arguments

X	Data Matrix
dimension	Dimension of the solution
Extraction	Method for the extraction of the factors. Can be "PC", "IPF" or "ML" ("Principal Components", "Iterated Principal Factor" or "Maximum Likelihood")
Rotation	Method for the rotation of the factors. Can be "PC", "IPF" or "ML"
InitComunal	Initial communalities for the iterated principal factor method. Can be "A1", "HSC" or "MC" ("All 1", "Highest Simple Correlation" or "Multiple Correlation")
normalize	Should the loadings be normalized
Scores	Method to calculate the Row Scores. Must be "Regression" or "Bartlett".
MethodArgs	Aditional arguments associated to the rotation method.
sup.rows	Supplementary or illustrative rows, if any.
sup.cols	Supplementary or illustrative rows, if any.
...	Additional arguments for the rotation procedure.

Details

Biplots represent the rows and columns of a data matrix in reduced dimensions. Usually rows represent individuals, objects or samples and columns are variables measured on them. The most classical versions can be thought as visualizations associated to Principal Components Analysis (PCA) or Factor Analysis (FA) obtained from a Singular Value Decomposition or a related method. From another point of view, Classical Biplots could be obtained from regressions and calibrations that are essentially an alternated least squares algorithm equivalent to an EM-algorithm when data are normal This routine Calculates a biplot as a graphical representation of a classical Factor Analysis alowing for different extraction methods and different rotations.

Value

An object of class "ContinuousBiplot" with the following components:

Title	A general title
Non_Scaled_Data	Original Data Matrix
Means	Means of the original Variables
Medians	Medians of the original Variables
Deviations	Standard Deviations of the original Variables
Minima	Minima of the original Variables
Maxima	Maxima of the original Variables
P25	25 Percentile of the original Variables
P75	75 Percentile of the original Variables
Gmean	Global mean of the complete matrix

`Sup.Rows`	Supplementary rows (Non Transformed)
`Sup.Cols`	Supplementary columns (Non Transformed)
`Scaled_Data`	Transformed Data
`Scaled_Sup.Rows`	Supplementary rows (Transformed)
`Scaled_Sup.Cols`	Supplementary columns (Transformed)
`n`	Number of Rows
`p`	Number of Columns
`nrowsSup`	Number of Supplementary Rows
`ncolsSup`	Number of Supplementary Columns
`dim`	Dimension of the Biplot
`EigenValues`	Eigenvalues
`Inertia`	Explained variance (Inertia)
`CumInertia`	Cumulative Explained variance (Inertia)
`EV`	EigenVectors
`Structure`	Correlations of the Principal Components and the Variables
`RowCoordinates`	Coordinates for the rows, including the supplementary
`ColCoordinates`	Coordinates for the columns, including the supplementary
`RowContributions`	Contributions for the rows, including the supplementary
`ColContributions`	Contributions for the columns, including the supplementary
`Scale_Factor`	Scale factor for the traditional plot with points and arrows. The row coordinates are multiplied and the column coordinates divided by that scale factor. The look of the plot is better without changing the inner product. For the HJ-Biplot the scale factor is 1.

Author(s)

Jose Luis Vicente Villardon

References

Gabriel, K.R.(1971): The biplot graphic display of matrices with applications to principal component analysis. Biometrika, 58, 453-467.

Gabriel, K. R. AND Zamir, S. (1979). Lower rank approximation of matrices by least squares with any choice of weights. Technometrics, 21(21):489–498, 1979.

Gabriel, K.R.(1998): Generalised Bilinear Regression. Biometrika, 85, 3, 689-700.

Gower y Hand (1996): Biplots. Chapman & Hall.

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez-Zaballos, A. (2006). Logistic Biplots. Multiple Correspondence Analysis and related methods 491-509.

See Also

InitialTransform

Examples

```
data(Protein)
X=Protein[,3:11]
bip=FA.Biplot(X, Extraction="ML", Rotation="oblimin")
plot(bip, mode="s", margin=0.05, AddArrow=TRUE)
```

Fact2Bin *Converts a Factor into its indicator matrix*

Description

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

Usage

```
Factor2Binary(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 Villardon

Examples

```
y=factor(c(1, 1, 2, 2, 2, 2, 3, 3, 3, 3, 2, 2, 2, 1, 1, 1))
Factor2Binary(y)
```

`Fraction` *Selection of a fraction of the data*

Description

Selects a percentage of the data eliminating the observations with higher Mahalanobis distances to the center.

Usage

```
Fraction(data, confidence = 1)
```

Arguments

`data`	Two dimensional data set
`confidence`	Percentage to retain. (0-1)

Details

The function is used to select a fraction of the data to be plotted for example when clusters are used. The function eliminates the extreme values.

Value

An object of class `fraction` with the following fields

`data`	The originaldata
`fraction`	The selected data
`confidence`	The percentage selected

Author(s)

Jose Luis Vicente Villardon

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`, `AddCluster2Biplot`

Examples

```
a=matrix(runif(50), 25,2)
a2=Fraction(a, 0.7)
```

Games_Howell *Games-Howell post-hoc tests for Welch's one-way analysis*

Description

This function produces results from Games-Howell post-hoc tests for Welch's one-way analysis of variance (ANOVA) for a matrix of numeric data and a grouping variable.

Usage

```
Games_Howell(data, group)
```

Arguments

`data`	The matrix of continuous data.
`group`	The grouping variable

Details

This function produces results from Games-Howell post-hoc tests for Welch's one-way analysis of variance (ANOVA) for a matrix of numeric data and a grouping variable.

Value

The tests for each column of the data matrix

Author(s)

Jose Luis Vicente Villardon

References

Ruxton, G. D., & Beauchamp, G. (2008). Time for some a priori thinking about post hoc testing. Behavioral ecology, 19(3), 690-693.

Examples

```
# Not yet
```

GD.Biplot *Biplot for continuous data based on gradient descent methods*

Description

Biplot for continuous data based on gradient descent methods.

Usage

```
GD.Biplot(X, dimension = 2, Scaling = 5,
         lambda = 0.01, OptimMethod = "CG",
         Orthogonalize = FALSE, Algorithm = "Alternated",
         sup.rows = NULL, sup.cols = NULL,
         grouping = NULL, tolerance = 1e-04,
         num_max_iters = 300, Initial = "random")
```

Arguments

`X`	A data matrix with continuous variables.
`dimension`	Dimension of the final solution.
`Scaling`	Transformation of the raw data matrix before the calculation of the biplot.
`lambda`	Constant for the ridge Penalization
`OptimMethod`	Optimization method passed to the `optim` function. By default is CG (Conjugate Gradient).
`Orthogonalize`	Should the solution be ortogonalized.
`Algorithm`	Algorithm to calculate the Biplot. (Alternated, Joint, Recursive)
`sup.rows`	Supplementary Rows. (not working now)
`sup.cols`	Supplementary Columns. (not working now)
`grouping`	Grouping factor for the within groups transformation.
`tolerance`	Tolerance for convergence
`num_max_iters`	Maximum number of iterations.
`Initial`	Initial Configuration

Details

The function calculates a bilot using gradient descent methods. The function `optim` is used to optimize the loss function. By default CG (Conjugate Gradient) method is used althoug other possibilities can be used.

Value

An object of class "ContinuousBiplot" is returned.

Author(s)

Jose Luis Vicente Villardon

Examples

```
data("Protein")
X=Protein[,3:11]
gdbip=GD.Biplot(X, dimension=2, Algorithm="Joint",
Orthogonalize=FALSE, lambda=0.3, Initial="random")
plot(gdbip)
summary(gdbip)
```

GeneralizedProcrustes *Generalized Procrustes Analysis*

Description

Generalized Procrustes Analysis

Usage

```
GeneralizedProcrustes(x, tolerance = 1e-05, maxiter = 100, Plot = FALSE)
```

Arguments

`x`	Three dimensional array with the configurations. The first dimension contains the rows of the configurations, the second contains the columns and the third the number of configurations. So x[,,i] is the *i-th* configuration
`tolerance`	Tolerance for the Procrustes algorithm.
`maxiter`	Maximum number of iterations
`Plot`	Should the results be plotted?

Details

Generalized Procrustes Analysis for several configurations contained in a three-dimensional array.

Value

An object of class `GenProcustes`.This has components:

`History`	History of Iterations
`X`	Initial configurations in a three dimensional array
`RotatedX`	Transformed configurations in a three dimensional array
`Scale`	Scale factors for each configuration
`Rotations`	Rotation Matrices in a three dimensional array
`rss`	Residual Sum of Squares
`Fit`	Goodness of fit as percent of expained variance

Author(s)

Jose Luis Vicente-Villardon

References

Gower, J.C., (1975). Generalised Procrustes analysis. Psychometrika 40, 33-51.

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

See Also

PrincipalCoordinates

Examples

```
data(spiders)
n=dim(spiders)[1]
p=dim(spiders)[2]
prox=array(0,c(n,2,4))

p1=BinaryProximities(spiders,coefficient=5)
prox[,,1]=PrincipalCoordinates(p1)$RowCoordinates
p2=BinaryProximities(spiders,coefficient=2)
prox[,,2]=PrincipalCoordinates(p2)$RowCoordinates
p3=BinaryProximities(spiders,coefficient=3)
prox[,,3]=PrincipalCoordinates(p3)$RowCoordinates
p4=BinaryProximities(spiders,coefficient=4)
prox[,,4]=PrincipalCoordinates(p4)$RowCoordinates
GeneralizedProcrustes(prox)
```

GetBiplotScales *Calculates the scales for the variables on a linear biplot*

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

```
GetBiplotScales(Biplot, nticks = 3, 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 outsite 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 outsite 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 outsite 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 used 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 Villardon

Examples

```
data(iris)
bip=PCA.Biplot(iris[,1:4])
GetBiplotScales(bip)
```

`GetCCAScales` *Calculates scales for plotting the environmental variables in a Canonical Correspondence Analysis*

Description

Calculates scales for plotting the environmental variables in a Canonical Correspondence Analysis

Usage

```
GetCCAScales(CCA, nticks = 7, TypeScale = "Complete", ValuesScale = "Original")
```

Arguments

`CCA`	A CCA solution object
`nticks`	Number of ticks to represent
`TypeScale`	Type of scale to represent
`ValuesScale`	Values to represent (Original or Transformed)

Details

Calculates scales for plotting the environmental variables in a Canonical Correspondence Analysis

Value

Returns the points and the labels for each biplot axis

Author(s)

Jose Luis Vicente Villardon

References

Gower, J. C., & Hand, D. J. (1995). Biplots (Vol. 54). CRC Press.

Gower, J. C., Lubbe, S. G., & Le Roux, N. J. (2011). Understanding biplots. John Wiley & Sons.

Vicente-Villardón, J. L., Galindo Villardón, M. P., & Blázquez Zaballos, A. (2006). Logistic biplots. Multiple correspondence analysis and related methods. London: Chapman & Hall, 503-521.

Examples

```
# No examples yet
```

---

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 Villardon

Examples

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

GowerProximities — *Gower Dissimilarities for mixed types of data*

Description

Gower Dissimilarities for mixed types of data

Usage

```
GowerProximities(x, y = NULL, Binary = NULL, Classes = NULL,
                 transformation = 3, IntegerAsOrdinal = FALSE, BinCoef
                 = "Simple_Matching", ContCoef = "Gower", NomCoef =
                 "GOW", OrdCoef = "GOW")
```

Arguments

`x`	Main data. Distances among rows are calculated if y=NULL. Must be a data frame.
`y`	Suplementary data matrix. If not NULL the distances among the rows of x and y are calculated. Must be a data frame with the same columns as x.
`Binary`	A vector containing the binary variables.
`Classes`	Vector with column types. If NULL the data frame types are used.
`transformation`	Transformation for the similarities.
`IntegerAsOrdinal`	Should integer variables be used as ordinal?
`BinCoef`	Coefficient for the binary data
`ContCoef`	Coefficient for the continuous data
`NomCoef`	Coefficient for the nominal data
`OrdCoef`	Coefficient for the ordinal data

Details

The transformation `sqrt(1-S)` is applied to the similarity.

Value

An object of class `proximities`.This has components:

`comp1`	Description of

Author(s)

Jose Luis Vicente-Villardon

References

J. C. Gower. (1971) A General Coefficient of Similarity and Some of its Properties. Biometrics, Vol. 27, No. 4, pp. 857-871.

Examples

```
data(spiders)
```

`GowerSimilarities` *Gower Dissimilarities for mixed types of data*

Description

Gower Dissimilarities for mixed types of data

Usage

```
GowerSimilarities(x, y = NULL, Classes = NULL, transformation =
                  "sqrt(1-S)", BinCoef = "Simple_Matching", ContCoef =
                  "Gower", NomCoef = "GOW", OrdCoef = "GOW")
```

Arguments

`x`	Main data. Distances among rows are calculated if y=NULL. Must be a data frame.
`y`	Suplementary data matrix. If not NULL the distances among the rows of x and y are calculated. Must be a data frame with the same columns as x.
`Classes`	Vector containing the classes of each variable.
`transformation`	Transformation to apply to the similarities.
`BinCoef`	Coefficient for the binary data
`ContCoef`	Coefficient for the continuous data
`NomCoef`	Coefficient for the nominal data
`OrdCoef`	Coefficient for the ordinal data

Details

Gower Dissimilarities for mixed types of data. The transformation `sqrt(1-S)` is applied to the similarity by default.

Value

An object of class `proximities`.This has components:

`comp1` Description of

Author(s)

Jose Luis Vicente-Villardon

References

J. C. Gower. (1971) A General Coefficient of Similarity and Some of its Properties. Biometrics, Vol. 27, No. 4, pp. 857-871.

Examples

```
data(spiders)
```

`Hermquad` *Gauss-Hermite quadrature*

Description

Find the Gauss-Hermite abscissae and weights.

Usage

```
Hermquad(N)
```

Arguments

`N` Number of nodes of the quadrature

Details

Find the Gauss-Hermite abscissae and weights.

Value

`X` A column vector containing the abscissae.

`W` A vector containing the corresponding weights.

Author(s)

Jose Luis Vicente Villardon (translated from a Matlab function by Greg von Winckel))

References

Press, W. H., Teukolsky, S. A., Vetterling, W. T., & Flannery, B. P. (1992). Numerical Recipes in C: The Art of Scientific Computing (New York. Cambridge University Press, 636-9.

http://www.mathworks.com/matlabcentral/fileexchange/8836-hermite-quadrature/content/hermquad.m

Examples

```
Hermquad(10)
```

`HistogramPanel` *Panel of histograms*

Description

Panel of histograms for a set of numerical variables.

Usage

```
HistogramPanel(X, nrows = NULL, separated = FALSE, ...)
```

Arguments

`X`	The matrix of continuous variables
`nrows`	Number of rows of the panel.
`separated`	Should the plots be organized into a panel? (or separated)
`...`	Aditional graphical arguments

Details

Jose Luis Vicente Villardon

Value

The histogram panel.

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(wine)
HistogramPanel(wine[,4:7], nrows = 2, xlab="")
```

HJ.Biplot *HJ Biplot with added features.*

Description

HJ Biplot with added features.

Usage

```
HJ.Biplot(X, dimension = 3, Scaling = 5, sup.rows = NULL,
         sup.cols = NULL, grouping = NULL)
```

Arguments

`X`	Data Matrix
`dimension`	Dimension of the solution
`Scaling`	Transformation of the original data. See InitialTransform for available transformations.
`sup.rows`	Supplementary or illustrative rows, if any.
`sup.cols`	Supplementary or illustrative rows, if any.
`grouping`	factor to stadadize with the within groups variability

Details

Biplots represent the rows and columns of a data matrix in reduced dimensions. Usually rows represent individuals, objects or samples and columns are variables measured on them. The most classical versions can be thought as visualizations associated to Principal Components Analysis (PCA) or Factor Analysis (FA) obtained from a Singular Value Decomposition or a related method. From another point of view, Classical Biplots could be obtained from regressions and calibrations that are essentially an alternated least squares algorithm equivalent to an EM-algorithm when data are normal.

Value

An object of class ContinuousBiplot with the following components:

`Title`	A general title
`Non_Scaled_Data`	Original Data Matrix
`Means`	Means of the original Variables
`Medians`	Medians of the original Variables
`Deviations`	Standard Deviations of the original Variables
`Minima`	Minima of the original Variables
`Maxima`	Maxima of the original Variables

P25	25 Percentile of the original Variables
P75	75 Percentile of the original Variables
Gmean	Global mean of the complete matrix
Sup.Rows	Supplementary rows (Non Transformed)
Sup.Cols	Supplementary columns (Non Transformed)
Scaled_Data	Transformed Data
Scaled_Sup.Rows	Supplementary rows (Transformed)
Scaled_Sup.Cols	Supplementary columns (Transformed)
n	Number of Rows
p	Number of Columns
nrowsSup	Number of Supplementary Rows
ncolsSup	Number of Supplementary Columns
dim	Dimension of the Biplot
EigenValues	Eigenvalues
Inertia	Explained variance (Inertia)
CumInertia	Cumulative Explained variance (Inertia)
EV	EigenVectors
Structure	Correlations of the Principal Components and the Variables
RowCoordinates	Coordinates for the rows, including the supplementary
ColCoordinates	Coordinates for the columns, including the supplementary
RowContributions	Contributions for the rows, including the supplementary
ColContributions	Contributions for the columns, including the supplementary
Scale_Factor	Scale factor for the traditional plot with points and arrows. The row coordinates are multiplied and the column coordinates divided by that scale factor. The look of the plot is better without changing the inner product. For the HJ-Biplot the scale factor is 1.

Author(s)

Jose Luis Vicente Villardon

References

Galindo Villardon, M. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Questiio. 1986, vol. 10, núm. 1.

See Also

InitialTransform

Examples

```
## Simple Biplot with arrows
data(Protein)
bip=HJ.Biplot(Protein[,3:11])
plot(bip)
```

InBox *Checks if a point is inside a box.*

Description

Checks if a point is inside a box. The point is specified bi its x and y coordinates and the bom 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	x 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)
```

`InitialTransform` *Initial transformation of data*

Description

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

Usage

```
InitialTransform(X, sup.rows = NULL, sup.cols = NULL,
InitTransform = "None", transform = "Standardize columns",
grouping = NULL)
```

Arguments

`X`	Original Raw Data Matrix
`sup.rows`	Supplementary or illustrative rows.
`sup.cols`	Supplementary or illustrative columns.
`InitTransform`	Pevious transformation (to use. See details)none or log.
`transform`	Transformation to use. See details.
`grouping`	factor to stadadize with the within groups variability

Details

Possible Transformations are:

1.- "Raw Data": When no transformation is required.

2.- "Substract the global mean": Eliminate an eefect 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 beetwen 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

A list with the following components

X	Transformed data matrix
sup.rows	Transformed supplementary rows
sup.rows	Transformed supplementary columns

Author(s)

Jose Luis Vicente Villardon

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=InitialTransform(x, transform=4)
x
```

Integer2Binary *Transforms an Integer Variable into a Binary Variable*

Description

Transforms an Integer Variable into a Binary Variable

Usage

```
Integer2Binary(y, name = "My_Factor")
```

Arguments

y	Vector with the factor
name	name of the factor

Details

Transforms an Integer vector into a Binary Indicator Matrix

Value

A Binary Data Matrix

Author(s)

Jose Luis Vicente-Villardon

Examples

```
dat=c(1, 2, 2, 4, 1, 1, 4, 2, 4)
Integer2Binary(dat,"Myfactor")
```

Kruskal.Wallis.Tests *Kruskal Wallis Tests*

Description

Kruskal Wallis Tests for a matrix of continuous variables and a grouping factor.

Usage

```
Kruskal.Wallis.Tests(X, groups, posthoc = "none", alternative = "two.sided", digits = 4)
```

Arguments

X	The matrix of continuous variables
groups	The factor with the groups
posthoc	Method used for multipe comparisons in the Dunn test
alternative	Kind of alternative hypothesis
digits	number of digitd for he output

Details

Kruskal Wallis Tests for a matrix of continuous variables and a grouping factor, including the Dunn test for multiple comparisons.

Value

the organized output.

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(wine)
Kruskal.Wallis.Tests(wine[,4:7], wine$Group, posthoc = "bonferroni")
```

`Levene.Tests` *Levene Tests*

Description

Levene Tests for a matrix of continuous variables and a grouping factor.

Usage

```
Levene.Tests(X, groups = NULL)
```

Arguments

`X`	The matrix of continuous variables
`groups`	The factor with the groups

Details

Levene Tests for a matrix of continuous variables and a grouping factor.

Value

The organized output

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(wine)
Levene.Tests(wine[,4:7], wine$Group)
```

`LogFrequencyBiplot` *Weighted Biplot for a table of frequencies*

Description

Biplot for the logarithms of the frequencies of a contingency table using the frequencies as weights.

Usage

```
LogFrequencyBiplot(x, Scaling = 2, logoffset = 1, freqoffset = logoffset, ...)
```

Arguments

x	The frequency table to be biplotted
Scaling	Transformation of the matrix after the logarithms
logoffset	Constant to add to the frequencies before calculating the logarithms. This is to avoid calculating the logaritm of zero, so, a covenient value for this argument is 1.
freqoffset	Constant to add to the frequencies before calculating the weigths. This is usually the same as the offset used to add to the frequencies but may be different when we do not want the frequencies zero to influence the biplot, i. e., we want zero weigths.
...	Any other parameter for the CrissCross procedure.

Details

Biplot for the logarithms of the frequencies of a contingency table using the frequencies as weigths.

Value

An object of class .Biplot" with the following components:

Title	A general title
Non_Scaled_Data	Original Data Matrix
Means	Means of the original Variables
Medians	Medians of the original Variables
Deviations	Standard Deviations of the original Variables
Minima	Minima of the original Variables
Maxima	Maxima of the original Variables
P25	25 Percentile of the original Variables
P75	75 Percentile of the original Variables
Gmean	Global mean of the complete matrix
Sup.Rows	Supplementary rows (Non Transformed)
Sup.Cols	Supplementary columns (Non Transformed)
Scaled_Data	Transformed Data
Scaled_Sup.Rows	Supplementary rows (Transformed)
Scaled_Sup.Cols	Supplementary columns (Transformed)
n	Number of Rows
p	Number of Columns
nrowsSup	Number of Supplementary Rows
ncolsSup	Number of Supplementary Columns

`dim` Dimension of the Biplot

`EigenValues` Eigenvalues

`Inertia` Explained variance (Inertia)

`CumInertia` Cumulative Explained variance (Inertia)

`EV` EigenVectors

`Structure` Correlations of the Principal Components and the Variables

`RowCoordinates` Coordinates for the rows, including the supplementary

`ColCoordinates` Coordinates for the columns, including the supplementary

`RowContributions`
Contributions for the rows, including the supplementary

`ColContributions`
Contributions for the columns, including the supplementary

`Scale_Factor` Scale factor for the traditional plot with points and arrows. The row coordinates are multiplied and the column coordinates divided by that scale factor. The look of the plot is better without changing the inner product. For the HJ-Biplot the scale factor is 1.

Author(s)

Jose Luis Vicente Villardon

References

Gabriel, K. R., Galindo, M. P. & Vicente-Villardon, J. L. (1995) Use of Biplots to Diagnose Independence Models in Three-Way Contingency Tables. in: M. Greenacre & J. Blasius. eds. Visualization of Categorical Data. Academis Press. London.

GABRIEL, K.R. and ZAMIR, S. (1979). Lower rank approximation of matrices by least squares with any choice of weights. Technometrics, 21: 489-498.

See Also

CrissCross, ~~~

Examples

```
data(smoking)
logbip=LogFrequencyBiplot(smoking, Scaling=1, logoffset=0, freqoffset=0)
```

`logit` *Logit function*

Description

Calculates the logit of a probability

Usage

```
logit(p)
```

Arguments

`p`	A probability

Details

Calculates the logit of a probability

Value

The lo git of the provided probebility

Author(s)

Jose Luis Vicente Villardón

`Matrix2Proximities` *Matrix to Proximities*

Description

Converts a matrix of proximities into a Proximities object as used in Principal Coordinates or MDS

Usage

```
Matrix2Proximities(x, TypeData = "User Provided",
Type = c("dissimilarity", "similarity", "products"),
Coefficient = "None", Transformation = "None", Data = NULL)
```

Arguments

`x`	The matrix of proximities (a symmetrical matrix)
`TypeData`	By default is User provided but could be any type.
`Type`	Type of proximity: dissimilarity, similarity or scalar product. If not provided, the default is dissimilarity
`Coefficient`	Name of the procedure to calculate the proximities (if any).
`Transformation`	Transformation used to calculate dissimilarities from similarities (if any)
`Data`	Raw data used to calculate the proximity (if any).

Details

Converts a matrix of proximities into a Proximities object as used in Principal Coordinates or MDS aading some extra information about the procedure used to obtain the proximities. Is mainly used when the proximities matrix has been provided by the user and not calculated from raw data using BinaryProximities, ContinuousDistances or any other function.

Value

An object of class `Proximities` containing the proximities matrix and some extra information about it.

Author(s)

Jose Luis Vicente Villardon

`matrixsqrt` *Matrix squared root*

Description

Matrix square root of a matrix using the eigendecomposition.

Usage

```
matrixsqrt(S, tol = sqrt(.Machine$double.eps))
```

Arguments

`S`	A squered matrix
`tol`	Tolerance for the igenvalues

Details

Matrix square root of a matrix using the eigendecomposition and removing the eigenvalues smaller than a tolerance

Value

The matrix square root of the argument

Author(s)

Jose Luis Vicente Villardon

Examples

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

---

matrixsqrtinv *Inverse of the Matrix squared root*

Description

Inverse of the Matrix square root of a matrix using the eigendecomposition.

Usage

```
matrixsqrtinv(S, tol = sqrt(.Machine$double.eps))
```

Arguments

S	A squered matrix
tol	Tolerance for the igenvalues

Details

Inverse of the Matrix square root of a matrix using the eigendecomposition and removing the eigenvalues smaller than a tolerance

Value

The inverse matrix square root of the argument

Author(s)

Jose Luis Vicente Villardon

See Also

ginv

Examples

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

MDS *Multidimensional Scaling*

Description

Multidimensional Scaling using SMACOF algorithm and Bootstraping the coordinates.

Usage

```
MDS(Proximities, W = NULL, Model = c("Identity", "Ratio", "Interval", "Ordinal"),
dimsol = 2, maxiter = 100, maxerror = 1e-06, Bootstrap = FALSE, nB = 200,
ProcrustesRot = TRUE, BootstrapMethod = c("Sampling", "Permutation"),
StandardizeDisparities = FALSE, ShowIter = FALSE)
```

Arguments

`Proximities`	An object of class proximities
`W`	A matrix of weigths
`Model`	MDS model. "Identity", "Ratio", "Interval" or "Ordinal".
`dimsol`	Dimension of the solution
`maxiter`	Maximum number of iterations of the algorithm
`maxerror`	Tolerance for convergence of the algorithm
`Bootstrap`	Should Bootstraping be performed?
`nB`	Number of Bootstrap samples.
`ProcrustesRot`	Should the bootstrap replicates be rotated to match the initial configuration using Procrustes?
`BootstrapMethod`	The bootstrap is performed by samplig or permutaing the residuals?
`StandardizeDisparities`	Should the disparities be standardized
`ShowIter`	Show the iteration proccess

Details

Multidimensional Scaling using SMACOF algorithm and Bootstraping the coordinates. MDS performs multidimensional scaling of proximity data to find a least- squares representation of the objects in a low-dimensional space. A majorization algorithm guarantees monotone convergence for optionally transformed, metric and nonmetric data under a variety of models.

Value

An object of class `Principal.Coordinates` and `MDS`. The function adds the information of the MDS to the object of class `proximities`. Together with the information about the proximities the object has:

`Analysis`	The type of analysis performed, "MDS" in this case
`Model`	MDS model used
`RowCoordinates`	Coordinates for the objects in the MDS procedure
`RawStress`	Raw Stress values
`stress1`	stress formula 1
`stress2`	stress formula 2
`sstress1`	sstress formula 1
`sstress2`	sstress formula 2
`rsq`	Squared correlation between disparities and distances
`Spearman`	Spearman correlation between disparities and distances
`Kendall`	Kendall correlation between disparities and distances
`BootstrapInfo`	The result of the bootstrap calculations

Author(s)

Jose Luis Vicente Villardon

References

Commandeur, J. J. F. and Heiser, W. J. (1993). Mathematical derivations in the proximity scaling (PROXSCAL) of symmetric data matrices (Tech. Rep. No. RR- 93-03). Leiden, The Netherlands: Department of Data Theory, Leiden University.

Kruskal, J. B. (1964). Nonmetric multidimensional scaling: A numerical method. Psychometrika, 29, 28-42.

De Leeuw, J. & Mair, P. (2009). Multidimensional scaling using majorization: The R package smacof. Journal of Statistical Software, 31(3), 1-30, http://www.jstatsoft.org/v31/i03/

Borg, I., & Groenen, P. J. F. (2005). Modern Multidimensional Scaling (2nd ed.). Springer.

Borg, I., Groenen, P. J. F., & Mair, P. (2013). Applied Multidimensional Scaling. Springer.

Groenen, P. J. F., Heiser, W. J. and Meulman, J. J. (1999). Global optimization in least squares multidimensional scaling by distance smoothing. Journal of Classification, 16, 225-254.

Groenen, P. J. F., van Os, B. and Meulman, J. J. (2000). Optimal scaling by alternating length-constained nonnegative least squares, with application to distance-based analysis. Psychometrika, 65, 511-524.

See Also

`BootstrapSmacof`

Examples

```
data(spiders)
Dis=BinaryProximities(spiders)
MDSSol=MDS(Dis, Bootstrap=FALSE)
plot(MDSSol)
```

MGC *Mixture Gaussian Clustering*

Description

Model based clustering using mixtures of gaussian distriutions.

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?
...	Maximum number of iterationsAny 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 Villardon

References

Me falta

Examples

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

MonotoneRegression *Weighted Isotonic Regression (Weighted Monotone Regression)*

Description

Performs weighted isotonic (monotone) regression using the non-negative weights in w. The function is a direct translation of the matlab function lsqisotonic.

Usage

```
MonotoneRegression(x, y, w = NULL)
```

Arguments

`x`	The independent variable vector
`y`	The dependent variable vector
`w`	A vector of weigths

Details

YHAT = MonotoneRegression(X,Y) returns a vector of values that minimize the sum of squares (Y - YHAT).^2 under the monotonicity constraint that X(I) > X(J) => YHAT(I) >= YHAT(J), i.e., the values in YHAT are monotonically non-decreasing with respect to X (sometimes referred to as "weak monotonicity"). LSQISOTONIC uses the "pool adjacent violators" algorithm.

If X(I) == X(J), then YHAT(I) may be <, ==, or > YHAT(J) (sometimes referred to as the "primary approach"). If ties do occur in X, a plot of YHAT vs. X may appear to be non-monotonic at those points. In fact, the above monotonicity constraint is not violated, and a reordering within each group of ties, by ascending YHAT, will produce the desired appearance in the plot.

Value

The fitted values after the monotone regression

Note

The function is a direct translation of the matlab function lsqisotonic.

Author(s)

Jose L. Vicente Villardon (from a matlab functiom)

References

Kruskal, J.B. (1964) "Nonmetric multidimensional scaling: a numerical method", Psychometrika 29:115-129.

Cox, R.F. and Cox, M.A.A. (1994) Multidimensional Scaling, Chapman&Hall.

Examples

```
## Used inside MDS
```

---

moth — *Moth data*

Description

Moth data

Usage

```
data("moth")
```

Format

A data frame with 12 observations on the following 14 variables.

- `s1` a numeric vector
- `s2` a numeric vector
- `s3` a numeric vector
- `s4` a numeric vector
- `s5` a numeric vector
- `s6` a numeric vector
- `s7` a numeric vector
- `s8` a numeric vector
- `s9` a numeric vector
- `s10` a numeric vector
- `s11` a numeric vector
- `s12` a numeric vector
- `s13` a numeric vector
- `s14` a numeric vector

Details

Moth data

Source

Withaker

References

Application of the Parametric Bootstrap to Models that Incorporate a Singular Value Decomposition Luis Milan; Joe Whittaker Applied Statistics, Vol. 44, No. 1. (1995), pp. 31-49.

Examples

```
data(moth)
## maybe str(moth) ; plot(moth) ...
```

Multiquad *Multidimensional Gauss-Hermite quadrature*

Description

Multidimensional Gauss-Hermite quadrature

Usage

```
Multiquad(nnodes, dims)
```

Arguments

`nnodes`	Number of nodes of the quadrature
`dims`	Dimension of the solution

Details

Multidimensional Gauss-Hermite quadrature

Value

Multidimensional Gauss-Hermite quadrature

Author(s)

Jose Luis Vicente Villardon

References

Jackel, P. (2005). A note on multivariate Gauss-Hermite quadrature. http://www.awdz65.dsl.pipex.com/ANoteOnMultivariate

Examples

```
Multiquad(5, 3)
```

MultiTableStatistics *Statistics for multiple tables*

Description

Statistics for multiple tables

Usage

```
MultiTableStatistics(X, dual = FALSE)
```

Arguments

X	A multiple table
dual	Is the transformation for the dual versions?

Details

Statistics for multiple tables

Value

A list with vectors of statistics for each table

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

MultiTableTransform — *Initial Transformation of a multi table object*

Description

Initial Transformation of a multi table object

Usage

```
MultiTableTransform(X, InitTransform = "Standardize columns", dual = FALSE,
CommonSD = TRUE)
```

Arguments

`X`	Multi-table object
`InitTransform`	Initial Transformattion
`dual`	Is the transformation for the dual versions?
`CommonSD`	Should a common standard deviation be used for all the groups?

Details

Initial Transformation of a multi table object

Value

he table transformed

Author(s)

Jose Luis Vicente Villardon

NiceNumber — *Nice numbers: simple decimal numbers*

Description

Calculates a close nice number, i. e. a number with simple decimals.

Usage

```
NiceNumber(x = 6, round = TRUE)
```

Arguments

`x`	A number
`round`	Should the number be rounded?

Details

Calculates a close nice number, i. e. a number with simple decimals.

Value

A number with simple decimals

Author(s)

Jose Luis Vicente Villardon

References

Heckbert, P. S. (1990). Nice numbers for graph labels. In Graphics Gems (pp. 61-63). Academic Press Professional, Inc..

See Also

PrettyTicks

Examples

```
NiceNumber(0.892345)
```

NIPALS.Biplot *Biplot using the NIPALS algorithm*

Description

Biplot using the NIPALS algorithm including a truncated and a sparse version.

Usage

```
NIPALS.Biplot(X, alpha = 1, dimension = 3, Scaling = 5,
Type = "Regular", grouping = NULL, ...)
```

Arguments

`X`	The data matrix
`alpha`	A number between 0 and 1. 0 for GH-Biplot, 1 for JK-Biplot and 0.5 for SQRT-Biplot. Use 2 or any other value not in the interval [0,1] for HJ-Biplot.
`dimension`	Dimension of the solution
`Scaling`	Transformation of the original data. See InitialTransform for available transformations.
`Type`	Type of biplot (Regular, Truncated or Sparse)
`grouping`	Grouping fartor when the scaling is made with the within groups variability
`...`	Aditional arguments for the different types of biplots.

Details

Biplot using the NIPALS algorithm including a truncated and a sparse version.

Value

An object of class ContinuousBiplot with the following components:

`Title`	A general title
`Type`	NIPALS
`call`	call
`Non_Scaled_Data`	Original Data Matrix
`Means`	Means of the original Variables
`Medians`	Medians of the original Variables
`Deviations`	Standard Deviations of the original Variables
`Minima`	Minima of the original Variables
`Maxima`	Maxima of the original Variables
`P25`	25 Percentile of the original Variables
`P75`	75 Percentile of the original Variables
`Gmean`	Global mean of the complete matrix
`Sup.Rows`	Supplementary rows (Non Transformed)
`Sup.Cols`	Supplementary columns (Non Transformed)
`Scaled_Data`	Transformed Data
`Scaled_Sup.Rows`	Supplementary rows (Transformed)
`Scaled_Sup.Cols`	Supplementary columns (Transformed)
`n`	Number of Rows
`p`	Number of Columns
`nrowsSup`	Number of Supplementary Rows
`ncolsSup`	Number of Supplementary Columns
`dim`	Dimension of the Biplot
`EigenValues`	Eigenvalues
`Inertia`	Explained variance (Inertia)
`CumInertia`	Cumulative Explained variance (Inertia)
`EV`	EigenVectors
`Structure`	Correlations of the Principal Components and the Variables
`RowCoordinates`	Coordinates for the rows, including the supplementary
`ColCoordinates`	Coordinates for the columns, including the supplementary

RowContributions
: Contributions for the rows, including the supplementary

ColContributions
: Contributions for the columns, including the supplementary

Scale_Factor
: Scale factor for the traditional plot with points and arrows. The row coordinates are multiplied and the column coordinates divided by that scale factor. The look of the plot is better without changing the inner product. For the HJ-Biplot the scale factor is 1.

Author(s)

Jose Luis Vicente Villardon

References

Wold, H. (1966). Estimation of principal components and related models by iterative least squares. Multivariate analysis. ACEDEMIC PRESS. 391-420.

Examples

```
bip1=NIPALS.Biplot(wine[,4:21], Type="Sparse", lambda=0.15)
plot(bip1)
```

NIPALSPCA *NIPALS algorithm for PCA*

Description

Classical NIPALS algorithm for PCA and Biplot.

Usage

```
NIPALSPCA(X, dimens = 2, tol = 1e-06, maxiter = 1000)
```

Arguments

X	The data matrix.
dimens	The dimension of the solution
tol	Tolerance of the algorithm.
maxiter	Maximum number of iteratios.

Details

Classical NIPALS algorithm for the singular value decomposition that allows for the construction of PCA and Biplot.

Value

The singular value decomposition

u	The coordinates of the rows (standardized)
d	The singuklar values
v	The coordinates of the columns (standardized)

Author(s)

Jose Luis Vicente Villardon

References

Wold, H. (1966). Estimation of principal components and related models by iterative least squares. Multivariate analysis. ACEDEMIC PRESS. 391-420.

Examples

```
# Not yet
```

`NominalDistances` *Distances among individuals with nominal variables*

Description

This function computes several measures of distance (or similarity) among individuals from a nominal data matrix.

Usage

```
NominalDistances(X, method = 1, diag = FALSE, upper = FALSE, similarity = TRUE)
```

Arguments

X	Matrix or data.frame with the nominal variables.
method	An integer between 1 and 6. See details
diag	A logical value indicating whether the diagonal of the distance matrix should be printed.
upper	a logical value indicating whether the upper triangle of the distance matrix should be printed.
similarity	A logical value indicating whether the similarity matrix should be computed.

Details

Let be the table of nominal data. All these distances are of type $d = \sqrt{1-s}$ with s a similarity coefficient.

1 = Overlap method The overlap measure simply counts the number of attributes that match in the two data instances.

2 = Eskin Eskin et al. proposed a normalization kernel for record-based network intrusion detection data. The original measure is distance-based and assigns a weight of $\frac{2}{n_k^2}$ for mismatches; when adapted to similarity, this becomes a weight of $\frac{n_k^2}{n_k^2+2}$.This measure gives more weight to mismatches that occur on attributes that take many values.

3=IOF (Inverse Occurrence Frequency .) This measure assigns lower similarity to mismatches on more frequent values. The IOF measure is related to the concept of inverse document frequency which comes from information retrieval, where it is used to signify the relative number of documents that contain a spe- cific word.

4 = OF (Ocurrence Frequency) This measure gives the opposite weighting of the IOF measure for mismatches, i.e., mismatches on less frequent values are assigned lower similarity and mismatches on more frequent values are assigned higher similarity

5 = Goodall3 This measure assigns a high similarity if the matching values are infrequent regardless of the frequencies of the other values.

6 = Lin This measure gives higher weight to matches on frequent values, and lower weight to mismatches on infrequent values.

Value

An object of class distance

Author(s)

Jose L. Vicente-Villardon

References

Boriah, S., Chandola, V. & Kumar,V.(2008). Similarity measures for categorical data: A comparative evaluation. In proceedings of the eight SIAM International Conference on Data Mining, pp 243–254.

See Also

BinaryDistances,ContinuousDistances

Examples

```
## Not run:
data(Env)
Distance<-NominalDistances(Env,upper=TRUE,diag=TRUE,similarity=FALSE,method=1)

## End(Not run)
```

NormalityTests *Normality tests*

Description

Normality tests foor the columns of a matrix and a grouping variable.

Usage

```
NormalityTests(X, groups = NULL, plot = FALSE, SortByGroups = FALSE)
```

Arguments

X	A data frame or a matrix containing several numerical variables
groups	A factor with the groups
plot	If TRUE the qqnorm plots are shown
SortByGroups	Should the results be sorted by groups?

Details

Normality tests foor the columns of a matrix and a grouping variable.

Value

The normality tests and the plots

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(wine)
NormalityTests(wine[,4:6], groups = wine$Origin, plot=TRUE)
```

Numeric2Binary *Converts a numeric variable into a binary one*

Description

Converts a numeric variable into a binary one using a cut point

Usage

```
Numeric2Binary(y, name= "MyVar", cut = NULL)
```

Arguments

`y`	Vector containing the numeric values
`name`	Name of the variable
`cut`	Cut point to cut the values of the variable. If is NULL the median is used.

Details

Converts a numeric variable into a binary one using a cut point. If the cut is NULL the median is used.

Value

A binary Variable

Author(s)

Jose Luis Vicente-Villardon

See Also

Dataframe2BinaryMatrix

Examples

```
y=c(1, 1.2, 3.2, 2.4, 1.7, 2.2, 2.7, 3.1)
Numeric2Binary(y)
```

`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 Villardon

Examples

```
ones(6)
```

`OrdinalLogisticFit` *Fits an ordinal logistic regression with ridge penalization*

Description

This function fits a logistic regression between a dependent ordinal variable y and some independent variables x, and solves the separation problem using ridge penalization.

Usage

```
OrdinalLogisticFit(y, x, penalization = 0.1, tol = 1e-04, maxiter = 200, show = FALSE)
```

Arguments

`y`	Dependent variable.
`x`	A matrix with the independent variables.
`penalization`	Penalization used to avoid singularities.
`tol`	Tolerance for the iterations.
`maxiter`	Maximum number of iterations.
`show`	Should the iteration history be printed?.

Details

The problem of the existence of the estimators in logistic regression can be seen in Albert (1984); a solution for the binary case, based on the Firth's method, Firth (1993) is proposed by Heinze(2002). All the procedures were initially developed to remove the bias but work well to avoid the problem of separation. Here we have chosen a simpler solution based on ridge estimators for logistic regression Cessie(1992).

Rather than maximizing $L_j(\mathbf{G}|\, \mathbf{b}_{j0}, \mathbf{B}_j)$ we maximize

$$L_j(\mathbf{G}|\, \mathbf{b}_{j0}, \mathbf{B}_j) - \lambda\left(\|\mathbf{b}_{j0}\| + \|\mathbf{B}_j\|\right)$$

Changing the values of λ we obtain slightly different solutions not affected by the separation problem.

Value

An object of class `"pordlogist"`. This has components:

`nobs`	Number of observations
`J`	Maximum value of the dependent variable
`nvar`	Number of independent variables
`fitted.values`	Matrix with the fitted probabilities
`pred`	Predicted values for each item
`Covariances`	Covariances matrix
`clasif`	Matrix of classification of the items
`PercentClasif`	Percent of good classifications
`coefficients`	Estimated coefficients for the ordinal logistic regression
`thresholds`	Thresholds of the estimated model
`logLik`	Logarithm of the likelihood
`penalization`	Penalization used to avoid singularities
`Deviance`	Deviance of the model
`DevianceNull`	Deviance of the null model
`Dif`	Diference between the two deviances values calculated
`df`	Degrees of freedom

`pval`	p-value of the contrast
`CoxSnell`	Cox-Snell pseudo R squared
`Nagelkerke`	Nagelkerke pseudo R squared
`MacFaden`	Nagelkerke pseudo R squared
`iter`	Number of iterations made

Author(s)

Jose Luis Vicente-Villardon

References

Albert,A. & Anderson,J.A. (1984),*On the existence of maximum likelihood estimates in logistic regression models*, Biometrika 71(1), 1–10.

Bull, S.B., Mak, C. & Greenwood, C.M. (2002), *A modified score function for multinomial logistic regression*, Computational Statistics and dada Analysis 39, 57–74.

Firth, D.(1993), *Bias reduction of maximum likelihood estimates*, Biometrika 80(1), 27–38

Heinze, G. & Schemper, M. (2002), *A solution to the problem of separation in logistic regression*, Statistics in Medicine 21, 2109–2419

Le Cessie, S. & Van Houwelingen, J. (1992), *Ridge estimators in logistic regression*, Applied Statistics 41(1), 191–201.

Examples

```
# No examples yet
```

`OrdLogBipEM` *Alternated EM algorithm for Ordinal Logistic Biplots*

Description

This function computes, with an alternated algorithm, the row and column parameters of an Ordinal Logistic Biplot for ordered polytomous data. The row coordinates (E-step) are computed using multidimensional Gauss-Hermite quadratures and Expected *a posteriori* (EAP) scores and parameters for each variable or items (M-step) using Ridge Ordinal Logistic Regression to solve the separation problem present when the points for different categories of a variable are completely separated on the representation plane and the usual fitting methods do not converge. The separation problem is present in almost avery data set for which the goodness of fit is high.

Usage

```
OrdLogBipEM(Data, freq=NULL, dim = 2, nnodes = 15,
tol = 0.0001, maxiter = 100, maxiterlogist = 100,
penalization = 0.2, show = FALSE, initial = 1, alfa = 1,
Orthogonalize=TRUE, Varimax=TRUE, ...)
```

Arguments

`Data`	Data frame with the ordinal data. All the variables must be ordered factors.
`freq`	Frequencies for compacted tables
`dim`	Dimension of the solution
`nnodes`	Number of nodes for the multidimensional Gauss-Hermite quadrature
`tol`	Value to stop the process of iterations.
`maxiter`	Maximum number of iterations for the biplot procedure.
`maxiterlogist`	Maximum number of iterations for the logistic regression step or the Mirt initial configuration.
`penalization`	Penalization used in the diagonal matrix to avoid singularities.
`show`	Boolean parameter to specify if the user wants to see every iteration.
`initial`	Method used to choose the initial ability in the algorithm. Default value is 1.
`alfa`	Optional parameter to calculate row and column coordinates in Simple correspondence analysis if the initial parameter is equal to 1.
`Orthogonalize`	Should the final row coordinates be orthogonalized?. The column parameters have to be recalculated.
`Varimax`	Should the final row coordinates be rotated using the varimax procedure?.
`...`	Aditional argunments for mirt.

Value

An object of class `"Ordinal.Logistic.Biplot"`.This has components:

`RowCoordinates`	Coordinates for the rows or the individuals
`ColumnParameters`	List with information about the Ordinal Logistic Models calculated for each variable including: estimated parameters with thresholds,percents of correct classifications,and pseudo-Rsquared
`loadings`	factor loadings
`LogLikelihood`	Logarithm of the likelihood
`r2`	R squared coefficient
`Ncats`	Number of the categories of each variable

Author(s)

Jose Luis Vicente-Villardon

References

Bock,R. & Aitkin,M. (1981),*Marginal maximum likelihood estimation of item parameters: Aplication of an EM algorithm*, Phychometrika 46(4), 443-459.

Examples

```
## Not run:
    data(Doctors)
    olb = OrdLogBipEM(Doctors,dim = 2, nnodes = 10, initial=4,
    tol = 0.001, maxiter = 100, penalization = 0.1, show=TRUE)
    olb
    summary(olb)
    PlotOrdinalResponses(olb)

## End(Not run)
```

OrdVarBiplot *Plots an ordinal variable on the biplot*

Description

Plots an ordinal variable on the biplot from its fitted parameters

Usage

```
OrdVarBiplot(bi1, bi2, threshold, xmin = -3, xmax = 3, ymin = -3,
ymax = 3, label = "Point", mode = "a", CexPoint = 0.8,
PchPoint = 1, Color = "green", tl = 0.03, textpos = 1, CexScale= 0.5, ...)
```

Arguments

bi1	Slope for the first dimension to plot
bi2	Slope for the second dimension to plot
threshold	Thresholds for each category of the variable
xmin	Minimum value of the X on the plot
xmax	Maximum value of the X on the plot
ymin	Minimum value of the Y on the plot
ymax	Maximum value of the X on the plot
label	Label of the variable
mode	Mode of the plot (as in a regular biplot)
CexPoint	Size of the point
PchPoint	Mark for the point
Color	Color
tl	Tick Length
textpos	Position of the label
CexScale	Sizes of the scales
...	Any aditional graphical parameter

Details

Plots an ordinal variable on the biplot from its fitted parameters. The plot uses the same parameters as any other biplot.

Value

Returns a graphical representation of the ordinal variable on the current plot

Author(s)

Jose Luis Vicente Villardon

References

Vicente-Villardon, J. L., & Sanchez, J. C. H. (2014). Logistic Biplots for Ordinal Data with an Application to Job Satisfaction of Doctorate Degree Holders in Spain. arXiv preprint arXiv:1405.0294.

Examples

```
##---- Should be DIRECTLY executable !! ----
```

OrdVarCoordinates *Coordinates of an ordinal variable on the biplot.*

Description

Coordinates of an ordinal variable on the biplot.

Usage

```
OrdVarCoordinates(tr, b = c(1, 1), inf = -12, sup = 12, step = 0.01,
                  plotresponse = FALSE, label = "Item", labx = "z", laby
                  = "Probability", catnames = NULL, Legend = TRUE,
                  LegendPos = 1)
```

Arguments

`tr`	A vector containing the thresholds of the model, that is, the constatn for each category of the ordinal variable
`b`	Vector containing the common slopes for all categories of the ordinal variable
`inf`	The inferior limit of the values to be sampled on the biplot axis (it depends on the scale of the biplot).
`sup`	The superior limit of the values to be sampled on the biplot axis (it depends on the scale of the biplot).
`step`	Increment (step) of the squence
`plotresponse`	Should the item be plotted

label	Label of the item.
labx	Label for the X axis in the summary of the item.
laby	Label for the Y axis in the summary of the item.
catnames	Names of the categories.
Legend	Should a legend be plotted
LegendPos	Position of the legend.

Details

The function calculates the coordinates of the points that define the separation among the categories of an ordinal variable projected onto an ordinal logistic biplot.

Value

An object of class OrdVarCoord

z	Values of the cut points on the scale of the biplot axis (not used)
points	The points for the marks to be represented on the biplot.
labels	The labels for the points
hidden	Are there any hidden categories? (Categories whose probability is never hier than the probabilities of the rest)
cathidden	Number of the hidden cateories

Author(s)

Jose Luis Vicente Villardon

References

Vicente-Villardon, J. L., & Sanchez, J. C. H. (2014). Logistic Biplots for Ordinal Data with an Application to Job Satisfaction of Doctorate Degree Holders in Spain. arXiv preprint arXiv:1405.0294.

Examples

```
# No examples
```

`OrthogonalizeScores` *Orthogonalize a set of Scores calculated by other procedure*

Description

Orthogonalize a set of Scores calculated by other procedure

Usage

```
OrthogonalizeScores(scores)
```

Arguments

`scores`	A matrix containing the scores

Details

Orthogonalize a set of Scores calculated by other procedure proyecting onto the dimensions defined by the eigenvectors of the covariance matrix

Value

The orthogonalised scores.

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

`PCA.Analysis` *Classical PCA Biplot with added features.*

Description

Classical PCA Biplot with added features.

Usage

```
PCA.Analysis(X, dimension = 3, Scaling = 5, ...)
```

Arguments

X	Data Matrix
dimension	Dimension of the solution
Scaling	Transformation of the original data. See InitialTransform for available transformations.
...	Any other useful argument

Details

Biplots represent the rows and columns of a data matrix in reduced dimensions. Usually rows represent individuals, objects or samples and columns are variables measured on them. The most classical versions can be thought as visualizations associated to Principal Components Analysis (PCA) or Factor Analysis (FA) obtained from a Singular Value Decomposition or a related method. From another point of view, Classical Biplots could be obtained from regressions and calibrations that are essentially an alternated least squares algorithm equivalent to an EM-algorithm when data are normal.

Value

An object of class ContinuousBiplot with the following components:

Title	A general title
Non_Scaled_Data	Original Data Matrix
Means	Means of the original Variables
Medians	Medians of the original Variables
Deviations	Standard Deviations of the original Variables
Minima	Minima of the original Variables
Maxima	Maxima of the original Variables
P25	25 Percentile of the original Variables
P75	75 Percentile of the original Variables
Gmean	Global mean of the complete matrix
Sup.Rows	Supplementary rows (Non Transformed)
Sup.Cols	Supplementary columns (Non Transformed)
Scaled_Data	Transformed Data
Scaled_Sup.Rows	Supplementary rows (Transformed)
Scaled_Sup.Cols	Supplementary columns (Transformed)
n	Number of Rows
p	Number of Columns
nrowsSup	Number of Supplementary Rows

ncolsSup Number of Supplementary Columns

dim Dimension of the Biplot

EigenValues Eigenvalues

Inertia Explained variance (Inertia)

CumInertia Cumulative Explained variance (Inertia)

EV EigenVectors

Structure Correlations of the Principal Components and the Variables

RowCoordinates Coordinates for the rows, including the supplementary

ColCoordinates Coordinates for the columns, including the supplementary

RowContributions
Contributions for the rows, including the supplementary

ColContributions
Contributions for the columns, including the supplementary

Scale_Factor Scale factor for the traditional plot with points and arrows. The row coordinates are multiplied and the column coordinates divided by that scale factor. The look of the plot is better without changing the inner product. For the HJ-Biplot the scale factor is 1.

Author(s)

Jose Luis Vicente Villardon

References

Gabriel, K.R.(1971): The biplot graphic display of matrices with applications to principal component analysis. Biometrika, 58, 453-467.

Galindo Villardon, M. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Questiio. 1986, vol. 10, núm. 1.

Gabriel, K. R. AND Zamir, S. (1979). Lower rank approximation of matrices by least squares with any choice of weights. Technometrics, 21(21):489–498, 1979.

Gabriel, K.R.(1998): Generalised Bilinear Regression. Biometrika, 85, 3, 689-700.

Gower y Hand (1996): Biplots. Chapman & Hall.

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez-Zaballos, A. (2006). Logistic Biplots. Multiple Correspondence Analysis and related methods 491-509.

Demey, J., Vicente-Villardon, J. L., Galindo, M. P. and Zambrano, A. (2008). Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics 24 2832-2838.

See Also

InitialTransform

Examples

```
## Simple Biplot with arrows
data(Protein)
bip=PCA.Biplot(Protein[,3:11])
plot(bip)

## Biplot with scales on the variables
plot(bip, mode="s", margin=0.2)

# Structure plot (Correlations)
CorrelationCircle(bip)

# Plot of the Variable Contributions
ColContributionPlot(bip, cex=1)
```

PCA.Biplot *Classical PCA Biplot with added features.*

Description

Classical PCA Biplot with added features.

Usage

```
PCA.Biplot(X, alpha = 1, dimension = 2, Scaling = 5, sup.rows = NULL,
           sup.cols = NULL, grouping = NULL)
```

Arguments

X	Data Matrix
alpha	A number between 0 and 1. 0 for GH-Biplot, 1 for JK-Biplot and 0.5 for SQRT-Biplot. Use 2 or any other value not in the interval [0,1] for HJ-Biplot.
dimension	Dimension of the solution
Scaling	Transformation of the original data. See InitialTransform for available transformations.
sup.rows	Supplementary or illustrative rows, if any.
sup.cols	Supplementary or illustrative rows, if any.
grouping	A factor to standardize with the variability within groups

Details

Biplots represent the rows and columns of a data matrix in reduced dimensions. Usually rows represent individuals, objects or samples and columns are variables measured on them. The most classical versions can be thought as visualizations associated to Principal Components Analysis (PCA) or Factor Analysis (FA) obtained from a Singular Value Decomposition or a related method. From another point of view, Classical Biplots could be obtained from regressions and calibrations that are essentially an alternated least squares algorithm equivalent to an EM-algorithm when data are normal.

Value

An object of class ContinuousBiplot with the following components:

`Title`	A general title
`Non_Scaled_Data`	Original Data Matrix
`Means`	Means of the original Variables
`Medians`	Medians of the original Variables
`Deviations`	Standard Deviations of the original Variables
`Minima`	Minima of the original Variables
`Maxima`	Maxima of the original Variables
`P25`	25 Percentile of the original Variables
`P75`	75 Percentile of the original Variables
`Gmean`	Global mean of the complete matrix
`Sup.Rows`	Supplementary rows (Non Transformed)
`Sup.Cols`	Supplementary columns (Non Transformed)
`Scaled_Data`	Transformed Data
`Scaled_Sup.Rows`	Supplementary rows (Transformed)
`Scaled_Sup.Cols`	Supplementary columns (Transformed)
`n`	Number of Rows
`p`	Number of Columns
`nrowsSup`	Number of Supplementary Rows
`ncolsSup`	Number of Supplementary Columns
`dim`	Dimension of the Biplot
`EigenValues`	Eigenvalues
`Inertia`	Explained variance (Inertia)
`CumInertia`	Cumulative Explained variance (Inertia)
`EV`	EigenVectors
`Structure`	Correlations of the Principal Components and the Variables

`RowCoordinates` Coordinates for the rows, including the supplementary

`ColCoordinates` Coordinates for the columns, including the supplementary

`RowContributions`
Contributions for the rows, including the supplementary

`ColContributions`
Contributions for the columns, including the supplementary

`Scale_Factor` Scale factor for the traditional plot with points and arrows. The row coordinates are multiplied and the column coordinates divided by that scale factor. The look of the plot is better without changing the inner product. For the HJ-Biplot the scale factor is 1.

Author(s)

Jose Luis Vicente Villardon

References

Gabriel, K.R.(1971): The biplot graphic display of matrices with applications to principal component analysis. Biometrika, 58, 453-467.

Galindo Villardon, M. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Questiio. 1986, vol. 10, núm. 1.

Gabriel, K. R. AND Zamir, S. (1979). Lower rank approximation of matrices by least squares with any choice of weights. Technometrics, 21(21):489–498, 1979.

Gabriel, K.R.(1998): Generalised Bilinear Regression. Biometrika, 85, 3, 689-700.

Gower y Hand (1996): Biplots. Chapman & Hall.

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez-Zaballos, A. (2006). Logistic Biplots. Multiple Correspondence Analysis and related methods 491-509.

Demey, J., Vicente-Villardon, J. L., Galindo, M. P. and Zambrano, A. (2008). Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics 24 2832-2838.

See Also

InitialTransform

Examples

```
## Simple Biplot with arrows
data(Protein)
bip=PCA.Biplot(Protein[,3:11])
plot(bip)

## Biplot with scales on the variables
plot(bip, mode="s", margin=0.2)

# Structure plot (Correlations)
CorrelationCircle(bip)
```

```
# Plot of the Variable Contributions
ColContributionPlot(bip, cex=1)
```

PCA.Bootstrap *Principal Components Analysis with bootstrap confidence intervals.*

Description

Calculates a Principal Components Analysis with bootstrap confidence intervals for its parameters

Usage

```
PCA.Bootstrap(X, dimens = 2, Scaling = "Standardize columns", B = 1000, type = "np")
```

Arguments

X	The original raw data matrix
dimens	Desired dimension of the solution.
Scaling	Transformation that should be applied to the raw data.
B	Number of Bootstrap samples to draw.
type	Type of Bootstrap ("np", "pa", "spper", "spres")

Details

The types of bootstrap used are:

"np : " Non Parametric

"pa : " parametric (data is obtained from a Multivariate Normal Distribution)

"spper : " Semi-parametric Residuals are permutated

"spres : " Semi-parametric Residuals are resampled

For the moment, only the non-parametric bootstrap is implemented.

The Principal Components (eigenvectors) are obtained using bootstrap samples.

The Row scotes are obtained projecting the completen data matrix into the bootstrap Principal Components. In this way all the individulas have the same number of replications.

Value

Type	The type of Bootstrap used
InitTransform	Transformation of the raw data
InitData	Initial data provided to the function'
TransformedData	Transformed Data
InitialSVD	Singular value decomposition of the transformed data
InitScores	Row Scores for the initial Data
InitCorr	Correlation among variables and Principal Components for the Initial Data
Samples	Matrix containing the members of the Bootstrap Samples
EigVal	Matrix containing the eigenvalues (columns) for each bootstrap sample (columns)
Inertia	Matrix containing the proportions of accounted variance (columns) for each bootstrap sample (columns)
Us	Three-dimensional array containing the left singular vectors for each bootstrap sample
Vs	Three-dimensional array containing the right singular vectors for each bootstrap sample
As	Projection of the bootstrap sampled matrix onto the bottstrap principal components
Bs	Projection of the bootstrap sampled matrix onto the bottstrap principal coordinates
Scores	Projection of the original matrix onto the bootstrap principal components
Struct	Correlation of the Initial Variabblñes and the PCs for each bootstrap sample

Author(s)

Jose Luis Vicente Villardon

References

Daudin, J. J., Duby, C., & Trecourt, P. (1988). Stability of principal component analysis studied by the bootstrap method. Statistics: A journal of theoretical and applied statistics, 19(2), 241-258.

Chateau, F., & Lebart, L. (1996). Assessing sample variability in the visualization techniques related to principal component analysis: bootstrap and alternative simulation methods. COMPSTAT, Physica-Verlag, 205-210.

Babamoradi, H., van den Berg, F., & Rinnan, Å. (2013). Bootstrap based confidence limits in principal component analysis—A case study. Chemometrics and Intelligent Laboratory Systems, 120, 97-105.

Fisher, A., Caffo, B., Schwartz, B., & Zipunnikov, V. (2016). Fast, exact bootstrap principal component analysis for p> 1 million. Journal of the American Statistical Association, 111(514), 846-860.

See Also

PCA.Biplot

Examples

```
## Not run: X=wine[,4:21]
grupo=wine$Group
rownames(X)=paste(1:45, grupo, sep="-")
pcaboot=PCA.Bootstrap(X, dimens=2, Scaling = "Standardize columns", B=1000)
plot(pcaboot, ColorInd=as.numeric(grupo))
summary(pcaboot)

## End(Not run)
```

---

plot.Binary.Logistic.Biplot
Plots the results of a Binary Logistic Biplot

Description

Plots the results of a Binary Logistic Biplot

Usage

```
## S3 method for class 'Binary.Logistic.Biplot'
plot(x, F1 = 1, F2 = 2, ShowAxis = FALSE, margin = 0,
PlotVars = TRUE, PlotInd = TRUE, WhatRows = NULL, WhatCols = NULL,
LabelRows = TRUE, LabelCols = TRUE, ShowBox = FALSE, RowLabels = NULL,
ColLabels = NULL, RowColors = NULL, ColColors = NULL, Mode = "s",
TickLength = 0.01, RowCex = 0.8, ColCex = 0.8, SmartLabels = FALSE,
MinQualityRows = 0, MinQualityCols = 0, dp = 0, PredPoints = 0,
SizeQualRows = FALSE, SizeQualCols = FALSE, ColorQualRows = FALSE,
ColorQualCols = FALSE, PchRows = NULL, PchCols = NULL, PlotClus = FALSE,
TypeClus = "ch", ClustConf = 1, Significant = TRUE, alpha = 0.05,
Bonferroni = TRUE, PlotSupVars = TRUE, AbbreviateLabels = FALSE, MainTitle = TRUE, Title =
                    NULL, RemoveXYlabs = FALSE, CenterCex = 1.5,  ...)
```

Arguments

`x`	An object of class Binary.Logistic.Biplot
`F1`	Dimension for the first axis of the representation. Default = 1
`F2`	Dimension for the second axis of the representation. Default = 2
`ShowAxis`	Should the axis of the representation be shown?
`margin`	Margin of the plot as a percentage. It gets some space for the labels.
`PlotVars`	Should the variables be plotted?
`PlotInd`	Should the individuals be plotted?
`WhatRows`	What Rows should be plotted. A binary vector containing which rows (individuals) should be plotted (1) and which should not (0).

WhatCols	What Columns should be plotted. A binary vector containing which columns (variables) should be plotted (1) and which should not (0).
LabelRows	Should the individuals be labeled?
LabelCols	Should the individuals be labeled?
ShowBox	Should a box around the points be plotted?
RowLabels	A vector of row labels. If NULL the labels contained in the object will be used.
ColLabels	A vector of column labels. If NULL the labels contained in the object will be used.
RowColors	A vector of alternative row colors.
ColColors	A vector of alternative column colors.
Mode	Mode of the biplot: "p", "a", "b", "h", "ah" and "s".
TickLength	Length of the scale ticks for the biplot variables.
RowCex	Cex (Size) of the rows (marks and labels). Can be a single common size for all the points or a vector with individual sizes.
ColCex	Cex (Size) of the columns (marks and labels). Can be a single common size for all the points or a vector with individual sizes.
SmartLabels	Should the labels be placed in a smart way?
MinQualityRows	Minimum quality of the rows to be plotted. (Between 0 and 1)
MinQualityCols	Minimum quality of the columns to be plotted. (Between 0 and 1)
dp	A vector of variable indices to project all the individuals onto each variable of the vector.
PredPoints	A vector of row indices to project onto each variable.
SizeQualRows	Should the size of the Row points be related to its quality?
SizeQualCols	Should the size of the Column points be related to its quality?
ColorQualRows	Should the color of the Row points be related to its quality?
ColorQualCols	Should the color of the Column points be related to its quality?
PchRows	Marks for the rows (numbers). Can be a single common mark for all the points or a vector with individual marks.
PchCols	Marks for the columns (numbers). Can be a single common mark for all the points or a vector with individual marks.
PlotClus	Should the clusters be plotted?
TypeClus	Type of plot for the clusters. ("ch"- Convex Hull, "el"- Ellipse or "st"- Star)
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
Significant	Should only the significant variables be plotted?
alpha	Signification level.
Bonferroni	Should the Bonferroni correction be used?
PlotSupVars	Should the Supplementary variables be plotted?
AbbreviateLabels	Should labels be abbreviated?

`MainTitle`	Should the mail Title be displayed?
`Title`	Title to display.
`RemoveXYlabs`	Should the axis labs be removed?
`CenterCex`	Size of the point for 0.5 probability.
`...`	Any other graphical parameter.

Details

Plots a biplot for binary data. The Biplot for binary data is taken as the basis of the plot. If there are a mixture of different types of variables (binary, nominal, abundance, ...) are added to the biplot as supplementary parts.

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.

Value

The plot of the biplot.

Author(s)

Jose Luis Vicente Villardon

References

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez, A. (2006) Logistic Biplots. In Multiple Correspondence Análisis And Related Methods. Grenacre, M & Blasius, J, Eds, Chapman and Hall, Boca Raton.

Demey, J., Vicente-Villardon, J. L., Galindo, M.P. AND Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics, 24(24): 2832-2838.

Examples

```
data(spiders)
X=Dataframe2BinaryMatrix(spiders)

logbip=BinaryLogBiplotGD(X,penalization=0.1)
plot(logbip, Mode="a")
summary(logbip)
```

plot.CA.sol *Plot the solution of a Coorespondence Analysis*

Description

Plots the solution of a Correspondence Analysis

Usage

```
## S3 method for class 'CA.sol'
plot(x, ...)
```

Arguments

x	A CA.sol object
...	Any other biplot and graphical parameters

Details

Plots the solution of a Correspondence Analysis

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

References

Add some references here

See Also

plot.ContinuousBiplot

Examples

```
data(riano)
Sp=riano[,3:15]
cabip=CA(Sp)
plot(cabip)
```

plot.Canonical.Biplot *Plots a Canonical Biplot*

Description

Plots a Canonical Biplot

Usage

```
## S3 method for class 'Canonical.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 "Canonical.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	Shoud the group centers be plotted?
PlotVars	Should the variables be plotted?
PlotInd	Should the individuals be plotted?
WhatInds	Logical vector to control what individuals (Rows) are plotted. (Can be also a binary vector)
WhatVars	Logical vector to control what variables (Columns) are plotted. (Can be also a binary vector)
WhatGroups	Logical vector to control what groups are plotted. (Can be also a binary vector)

`IndLabels`	A set of labels for the individuals. If NULL the default object labels are used
`VarLabels`	A set of labels for the variables. If NULL the default object labels are used
`GroupLabels`	A set of labels for the groups. If NULL the default object labels are used
`AbbreviateLabels`	Should labels be abbreviated?
`LabelInd`	Should the individuals be labeled?
`LabelVars`	Should the variables be labeled?
`CexGroup`	Sizes of the points for the groups
`PchGroup`	Markers for the group
`margin`	margin for the graph
`AddLegend`	Should a legend with the groups be added?
`ShowAxes`	Should outside axes be shown?
`LabelAxes`	Should outside axes be labelled?
`LabelGroups`	Should the groups be labeled?
`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 regións for each group be plotted?
`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"
`MinQualityVars`	Minimum quality of representation for a variable to be plotted
`dpg`	A set of indices with the variables that will show the projections of the gorups
`dpi`	A set of indices with the individuasl that will show the projections on the variables
`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`	Marhers 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 poitns be plotted?
ShowTitle	Should the title be shown?
PlotClus	Should the clusters be plotted?
TypeClus	Type of plot for the clusters. ("ch"- Convex Hull, "el"- Ellipse or "st"- Star)
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
ClustCenters	Should the cluster centers be plotted?
UseClusterColors	Should the cluster colors be used in the plot
CexClustCenters	Size of the cluster centres
...	Any other graphical parameters

Details

The function plots the results of a Canononical 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

No value returned

Author(s)

Jose Luis Vicente Villardon

References

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

Varas, M. J., Vicente-Tavera, S., Molina, E., & Vicente-Villardon, J. L. (2005). Role of canonical biplot method in the study of building stones: an example from Spanish monumental heritage. Environmetrics, 16(4), 405-419.

Santana, M. A., Romay, G., Matehus, J., Villardon, J. L., & Demey, J. R. (2009). simple and low-cost strategy for micropropagation of cassava (Manihot esculenta Crantz). African Journal of Biotechnology, 8(16).

Examples

```
data(wine)
X=wine[,4:21]
canbip=CanonicalBiplot(X, group=wine$Group)
plot(canbip, TypeCircle="U")
```

`plot.CanonicalDistanceAnalysis`
Plots a Canonical Distance Analysis

Description

Plots a Canonical Distance Analysis

Usage

```
## S3 method for class 'CanonicalDistanceAnalysis'
plot(x, A1 = 1, A2 = 2, ScaleGraph = TRUE,
ShowAxis = FALSE, ShowAxes = FALSE, LabelAxes = TRUE, margin = 0.1,
PlotAxis = FALSE, ShowBox = TRUE, PlotGroups = TRUE, LabelGroups = TRUE,
CexGroup = 1.5, PchGroup = 16, ColorGroup = NULL, voronoi = TRUE,
VoronoiColor = "black", PlotInd = TRUE, 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 "CanonicalDistanceAnalysis"
`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.
`ShowAxis`	Should the axis be shown?
`ShowAxes`	Not used
`LabelAxes`	Shoud the axis be labelled?
`margin`	Margin of the plot
`PlotAxis`	Should the axis be plotted?
`ShowBox`	Show a box around the plot
`PlotGroups`	Should the groups be plotted?
`LabelGroups`	Should the groups be labelled?
`CexGroup`	Sizes for the groups
`PchGroup`	Marks for the groups
`ColorGroup`	Colors for the groups
`voronoi`	Should a voronoi diagram separating the groups be plotted?
`VoronoiColor`	Color for the voronoi diagram
`PlotInd`	Should the individuals be plotted?
`LabelInd`	Should the individuals be labelled?
`CexInd`	Sizes for the individuals
`PchInd`	Marks for the individuals
`ColorInd`	Colors for the individuals
`WhatInds`	What indivduals are plotted
`IndLabels`	Labels for the individuals
`PlotVars`	Should the variables be plotted?
`LabelVar`	Should the variables be labelled?
`CexVar`	Sizes for the variables
`PchVar`	Marks for the variables
`ColorVar`	User colors for the variables. Default colors will be used if NULL.
`WhatVars`	What Variables are plotted
`VarLabels`	User 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`	Plot the labels 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)
`MinQualityVars`	Minimum quality of representation for a variable to be plotted
`dpg`	A set of indices with the variables that will show the projections of the gorups
`dpi`	A set of indices with the individuasl that will show the projections on the variables
`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)
`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
`CexClustCenters`	SIze of the cluster centers.
`ClustCenters`	Should the cluster centers be plotted?
`UseClusterColors`	Should the cluster colors be used in the plot
`...`	Any other graphical parameters

Details

Plots a Canonical Distance Analysis

Value

The plot of a Canonical Distance Analysis

Author(s)

Jose Luis Vicente Villardon

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.

See Also

`plot.Canonical.Biplot`

Examples

```
# Not yet
```

---

plot.CCA.sol *Plots the solution of a Canonical Correspondence Analysisis*

Description

Plots the solution of a Canonical Correspondence Analysisis using similar parameters to the continuous biplot

Usage

```
## S3 method for class 'CCA.sol'
plot(x, A1 = 1, A2 = 2, ShowAxis = FALSE, margin = 0,
                 PlotSites = TRUE, PlotSpecies = TRUE, PlotEnv = TRUE,
                 LabelSites = TRUE, LabelSpecies = TRUE, LabelEnv =
                 TRUE, TypeSites = "wa", SpeciesQuality = FALSE,
                 MinQualityVars = 0.3, dp = 0, pr = 0, PlotAxis =
                 FALSE, TypeScale = "Complete", ValuesScale =
                 "Original", mode = "a", CexSites = NULL, CexSpecies =
                 NULL, CexVar = NULL, ColorSites = NULL, ColorSpecies =
                 NULL, ColorVar = NULL, PchSites = NULL, PchSpecies =
                 NULL, PchVar = NULL, SizeQualSites = FALSE,
                 SizeQualSpecies = FALSE, SizeQualVars = FALSE,
                 ColorQualSites = FALSE, ColorQualSpecies = FALSE,
                 ColorQualVars = FALSE, SmartLabels = FALSE, ...)
```

Arguments

`x`	The results of a CCA model
`A1`	Dimension for the first axis
`A2`	Dimension for the second axis
`ShowAxis`	Logical variable to control if the coordinate axes should appear in the plot. The default value is FALSE because for most of the biplots its presence is irrelevant.
`margin`	Margin for the labels in some of the biplot modes (percentage of the plot width). Default is 0. Increase the value if the labels are not completely plotted.
`PlotSites`	Should the sites be plotted?
`PlotSpecies`	Should the species be plotted?
`PlotEnv`	Should the environmental variables be plotted?
`LabelSites`	Labels for the sites
`LabelSpecies`	Labels for the species
`LabelEnv`	Labels for the environmental variables.

`TypeSites`	Type for the sites plot
`SpeciesQuality`	Quality for the species
`MinQualityVars`	Minimum quality to plot a variable
`dp`	A set of indices with the variables that will show the projections of the individuals.
`pr`	A set of indices with the individuals to show the projections on the variables.
`PlotAxis`	Should the axis be plotted?
`TypeScale`	Type of scale to use : "Complete", "StdDev" or "BoxPlot"
`ValuesScale`	Values to show on the scale: "Original" or "Transformed"
`mode`	Mode of the biplot: "p", "a", "b", "h", "ah" and "s".
`CexSites`	Size for the symbols and labels of the sites. Can be a single common size for all the points or a vector with individual sizes.
`CexSpecies`	Size for the symbols and labels of the species. Can be a single common size for all the points or a vector with individual sizes.
`CexVar`	Size for the symbols and labels of the variables. Can be a single common size for all the points or a vector with individual sizes.
`ColorSites`	Color for the symbols and labels of the sites. Can be a single common color for all the points or a vector with individual colors.
`ColorSpecies`	Color for the symbols and labels of the species. Can be a single common color for all the points or a vector with individual colors.
`ColorVar`	Color for the symbols and labels of the variables. Can be a single common color for all the points or a vector with individual colors.
`PchSites`	Symbol for the sites points. See `help(points)` for details.
`PchSpecies`	Symbol for the species points. See `help(points)` for details.
`PchVar`	Symbol for the variables points. See `help(points)` for details.
`SizeQualSites`	Should the size of the site points be related to their qualities of representation (predictiveness)?
`SizeQualSpecies`	Should the size of the species points be related to their qualities of representation (predictiveness)?
`SizeQualVars`	Should the size of the variables points be related to their qualities of representation (predictiveness)?
`ColorQualSites`	Should the color of the sites points be related to their qualities of representation (predictiveness)?
`ColorQualSpecies`	Should the color of the species points be related to their qualities of representation (predictiveness)?
`ColorQualVars`	Should the color of the variables points be related to their qualities of representation (predictiveness)?
`SmartLabels`	Plot the labels in a smart way
`...`	Aditional graphical parameters.

Details

The plotting procedure is similar to the one used for continuous biplots including the calibration of the environmental variables.

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

References

CCA

See Also

plot.ContinuousBiplot

Examples

```
##---- Should be DIRECTLY executable !! ----
```

---

plot.ContinuousBiplot *Plots a biplot for continuous data.*

Description

Plots a biplot for continuous data.

Usage

```
## S3 method for class 'ContinuousBiplot'
plot(x, A1 = 1, A2 = 2, ShowAxis = FALSE, margin = 0,
                    PlotVars = TRUE, PlotInd = TRUE, WhatInds = NULL,
                    WhatVars = NULL, LabelVars = TRUE, LabelInd = TRUE,
                    IndLabels = NULL, VarLabels = NULL, mode = "a", CexInd
                    = NULL, CexVar = NULL, ColorInd = NULL, ColorVar =
                    NULL, LabelPos = 1, SmartLabels = FALSE,
                    AbbreviateLabels = FALSE, MinQualityInds = 0,
                    MinQualityVars = 0, dp = 0, PredPoints = 0, PlotAxis =
                    FALSE, TypeScale = "Complete", ValuesScale =
                    "Original", SizeQualInd = FALSE, SizeQualVars = FALSE,
                    ColorQualInd = FALSE, ColorQualVars = FALSE, PchInd =
                    NULL, PchVar = NULL, PlotClus = FALSE, TypeClus =
                    "ch", ClustConf = 1, ClustLegend = FALSE,
                    ClustLegendPos = "topright", ClustCenters = FALSE,
```

```
UseClusterColors = TRUE, CexClustCenters = 1,
PlotSupVars = TRUE, SupMode = "a", ShowBox = FALSE,
nticks = 5, NonSelectedGray = FALSE, PlotUnitCircle =
TRUE, PlotContribFA = TRUE, AddArrow = FALSE,
ColorSupContVars = "red", ColorSupBinVars = "red",
ColorSupOrdVars = "red", ModeSupContVars="a",
ModeSupBinVars="a", ModeSupOrdVars="a",
WhatSupBinVars = NULL, Title = NULL, Xlab = NULL,
Ylab = NULL, add = FALSE, PlotTrajVars = FALSE,
PlotTrajInds = FALSE, LabelTraj = "end", Limits = NULL,
PlotSupInds = FALSE, WhatSupInds = NULL,
ColorSupInd = "black", CexSupInd = 0.8, PchSupInd =
16, LabelSupInd = TRUE, PredSupPoints = 0,  CexScale =
0.5, ...)
```

Arguments

x	An object of class "Biplot"
A1	Dimension for the first axis. 1 is the default.
A2	Dimension for the second axis. 2 is the default.
ShowAxis	Logical variable to control if the coordinate axes should appear in the plot. The default value is FALSE because for most of the biplots its presence is irrelevant.
margin	Margin for the labels in some of the biplot modes (percentage of the plot width). Default is 0. Increase the value if the labels are not completely plotted.
PlotVars	Logical to control if the Variables (Columns) are plotted.
PlotInd	Logical to control if the Individuals (Rows) are plotted.
WhatInds	Logical vector to control what individuals (Rows) are plotted. (Can be also a binary vector)
WhatVars	Logical vector to control what variables (Columns) are plotted. (Can be also a binary vector)
LabelVars	Logical to control if the labels for the Variables are shown
LabelInd	Logical to control if the labels for the individuals are shown
IndLabels	A set of labels for the individuals. If NULL the default object labels are used
VarLabels	A set of labels for the variables. If NULL the default object labels are used
mode	Mode of the biplot: "p", "a", "b", "h", "ah" and "s".
CexInd	Size for the symbols and labels of the individuals. Can be a single common size for all the points or a vector with individual sizes.
CexVar	Size for the symbols and labels of the variables. Can be a single common size for all the points or a vector with individual sizes.
ColorInd	Color for the symbols and labels of the individuals. Can be a single common color for all the points or a vector with individual colors.
ColorVar	Color for the symbols and labels of the variables. Can be a single common color for all the points or a vector with individual colors.

- `LabelPos` Position of the labels in relation to the point. (Se the graphical parameter `pos`)
- `SmartLabels` Plot the labels in a smart way
- `AbbreviateLabels` Should labels be abbreviated?
- `MinQualityInds` Minimum quality of representation for an individual to be plotted.
- `MinQualityVars` Minimum quality of representation for a variable to be plotted.
- `dp` A set of indices with the variables that will show the projections of the individuals.
- `PredPoints` A vector with integers. The row points listed in the vector are projected onto all the variables.
- `PlotAxis` Not Used
- `TypeScale` Type of scale to use : "Complete", "StdDev" or "BoxPlot"
- `ValuesScale` Values to show on the scale: "Original" or "Transformed"
- `SizeQualInd` Should the size of the row points be related to their qualities of representation (predictiveness)?
- `SizeQualVars` Should the size of the column points be related to their qualities of representation (predictiveness)?
- `ColorQualInd` Should the color of the row points be related to their qualities of representation (predictiveness)?
- `ColorQualVars` Should the color of the column points be related to their qualities of representation (predictiveness)?
- `PchInd` Symbol for the row points. See `help(points)` for details.
- `PchVar` Symbol for the column points. See `help(points)` for details.
- `PlotClus` Should the clusters be plotted?
- `TypeClus` Type of plot for the clusters. ("ch"- Convex Hull, "el"- Ellipse or "st"- Star)
- `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
- `ClustLegend` Should a legend for the clusters be plotted? Default FALSE
- `ClustLegendPos` Position of the legend for the clusters. Default "topright"
- `ClustCenters` Should the cluster centers be plotted
- `UseClusterColors` Should the cluster colors be used in the plot
- `CexClustCenters` Size of the cluster centres
- `PlotSupVars` Should the supplementary variables be plotted?
- `SupMode` Mode of the supplementary variables.
- `ShowBox` Should a box around the poitns be plotted?
- `nticks` Number of ticks for the representation of the variables
- `NonSelectedGray` The nonselected individuals and variables aplotted in light gray colors

`PlotUnitCircle`	Plot the unit circle in the biplot for a Factor Analysis in which the lenght of the column arrows is smaller than 1 and is the quality of representation.
`PlotContribFA`	Plot circles in the biplot for a Factor Analysis with different values of the quality of representation.
`AddArrow`	Add an arrow to the representation of other modes of the biplot.
`ColorSupContVars`	Colors for the continuous supplementary variables.
`ColorSupBinVars`	Colors for the binary supplementary variables.
`ColorSupOrdVars`	Colors for the ordinal supplementary variables.
`ModeSupContVars`	Mode for the continuous supplementary variables.
`ModeSupBinVars`	Mode for the binary supplementary variables.
`ModeSupOrdVars`	Mode for the ordinal supplementary variables.
`WhatSupBinVars`	What supplementary binary variables should be plotted?
`Title`	Title of the plot.
`Xlab`	Label for the X axis
`Ylab`	Label for the Y axis
`add`	Should the plot be added to an existing plot?
`PlotTrajVars`	Plot trajectories for the variables (when appropriate)?
`PlotTrajInds`	Plot trajectories for the individuals (when appropriate)?
`LabelTraj`	Label trajectories for the variables (when appropriate)?
`Limits`	Limits of the axis for the plot
`PlotSupInds`	Should the supplementary individuals be plotted?
`WhatSupInds`	What supplementary individuals are going to be plotted
`ColorSupInd`	Colors for the supplementary individuals
`CexSupInd`	Sizes for the supplementary individuals
`PchSupInd`	Symbols for the supplementary individuals
`LabelSupInd`	Labels for the supplementary individuals
`PredSupPoints`	Predictions for the supplementary individuals
`CexScale`	Sizes of the scales
`...`	Any other graphical parameters.

Details

Plots a biplot for continuous data. The Biplot for continuous data is taken as the basis of the plot. If there are a mixture of different types of variables (binary, nominal, abundance, ...) are added to the biplot as supplementary parts.

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.

It is possible to associate the color and the size of the points with the quality of representation. Bigger points correspond to better representation quality.

Value

No value Returned

Author(s)

Jose Luis Vicente Villardon

References

Gabriel, K. R. (1971). The biplot graphic display of matrices with application to principal component analysis. Biometrika, 58(3), 453-467.

Galindo Villardon, M. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Questiio. 1986, vol. 10, num. 1.

Vicente-Villardon, J. L., Galindo Villardon, M. P., & Blazquez Zaballos, A. (2006). Logistic biplots. Multiple correspondence analysis and related methods. London: Chapman & Hall, 503-521.

Gower, J. C., & Hand, D. J. (1995). Biplots (Vol. 54). CRC Press.

Gower, J. C., Lubbe, S. G., & Le Roux, N. J. (2011). Understanding biplots. John Wiley & Sons.

Blasius, J., Eilers, P. H., & Gower, J. (2009). Better biplots. Computational Statistics & Data Analysis, 53(8), 3145-3158.

Examples

```
data(Protein)
bip=PCA.Biplot(Protein[,3:11])
plot(bip, mode="s", margin=0.2, ShowAxis=FALSE)
```

---

plot.CVA *Plot of a Canonical Variate Analysis*

Description

Plot of a Canonical Variate Analysis

Usage

```
## S3 method for class 'CVA'
plot(x, A1 = 1, A2 = 2, ...)
```

Arguments

x	Object of class CVA
A1	Dimension for the first axis of the representation
A2	Dimension for the second axis of the representation
...	Additional arguments

Details

Plot of a Canonical Variate Analysis

Value

Te Vanonical variate plot

Author(s)

Jose Luis Vicente Villardon

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 Villardon

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, 0.95)
plot(E, labeled=TRUE, center=TRUE)
```

---

plot.External.Binary.Logistic.Biplot
Plots an External Logistic Biplot for binary data

Description

Plot of an External Binary Logistic Biplot with many arguments controling different aspects of the representation

Usage

```
## S3 method for class 'External.Binary.Logistic.Biplot'
plot(x, F1 = 1, F2 = 2,
                    ShowAxis = FALSE, margin = 0.1,
                    PlotVars = TRUE, PlotInd = TRUE, WhatRows = NULL,
                    WhatCols = NULL, LabelRows = TRUE, LabelCols = TRUE,
                    RowLabels = NULL, ColLabels = NULL, RowColors = NULL,
                    ColColors = NULL, Mode = "s", TickLength = 0.01,
                    RowCex = 0.8, ColCex = 0.8, SmartLabels = FALSE,
                    MinQualityRows = 0, MinQualityCols = 0, dp = 0,
                    PredPoints = 0, SizeQualRows = FALSE, ShowBox = FALSE,
                    SizeQualCols = FALSE, ColorQualRows = FALSE,
                    ColorQualCols = FALSE, PchRows = NULL, PchCols = NULL,
                    PlotClus = FALSE, TypeClus = "ch", ClustConf = 1,
                    Significant = FALSE, alpha = 0.05, Bonferroni = FALSE,
                    PlotSupVars = TRUE, ...)
```

Arguments

x	An object of type External.Binary.Logistic.Biplot
F1	Latent factor to represent at the X axis
F2	Latent factor to represent at the Y axis
ShowAxis	Should the axis be plotted?
margin	Margin for the labels in some of the biplot modes (percentage of the plot width). Default is 0. Increase the value if the labels are not completely plotted.
PlotVars	Should Variables be plotted
PlotInd	Should Individuals be plotted

WhatRows	A binary vector (0 and 1) that indicates if each individual row should be plotted or not
WhatCols	A binary vector (0 and 1) that indicates if each individual column should be plotted or not
LabelRows	Should Variables be labelled
LabelCols	Should Individuals be labelled
RowLabels	A vector of Labels for the rows if you do not want to use the data labels
ColLabels	A vector of Labels for the columns if you do not want to use the data labels
RowColors	A vector of colors for the rows
ColColors	A vector of colors for the rows
Mode	Mode of the biplot: "p", "a", "b", "ah" and "s". See details.
TickLength	Lenght of the tick marks. Depends on the scale of the graph.
RowCex	A scalar or a vector containing the sizes of the poitns ans labels for the rows. Default value is 0.8 if the sizes are not provided.
ColCex	A scalar or a vector containing the sizes of the poitns ans labels for the columns. Default value is 0.8 if the sizes are not provided.
SmartLabels	Plot the labels in a smart way
MinQualityRows	Minimum quality of representation for a row or individual to be plotted
MinQualityCols	Minimum quality of representation for a column or variable to be plotted
dp	"Drop Points" on the variables, a vector with integers. The row points are projected on the directions of the variables listed in the vector.
PredPoints	A vector with integers. The row points listed in the vector are projected onto all the variables.
SizeQualRows	Should the size of the row points be related to their qualities of representation (predictiveness)?
ShowBox	Should abox around the point be displayed?
SizeQualCols	Should the size of the column points be related to their qualities of representation (predictiveness)?
ColorQualRows	Should the color of the row points be related to their qualities of representation (predictiveness)?
ColorQualCols	Should the color of the column points be related to their qualities of representation (predictiveness)?
PchRows	Symbol for the row points. See `help(points)` for details.
PchCols	Symbol for the column points. See `help(points)` for details.
PlotClus	Should the clusters be plotted?
TypeClus	Type of plot for the clusters. ("ch"- Convex Hull, "el"- Ellipse or "st"- Star)
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
Significant	If TRUE, only the significant variables are plotted
alpha	Significance Level
Bonferroni	Should the Bonferroni correction be used
PlotSupVars	Should supplementary variables be plotted
...	Any other graphical parameter you want to use

Details

The logistic regression equation predicts the probability that a caracter will be present in an individual. Geometrically the y´s can be represented as point in the reduced dimension space and the b's are the vectors showing the directions that best predict the probability of presence of each allele . For a com-plete explanation of the geometrical properties of the ELB see Vicente-Villardón et al (2006). The prediction of the probabilities is made in the same way as in a linear Biplot, i. e., the projection of a genotype point on the direction of an variable vector predicts the probability of presence of that variable in the individual. To facilitate the interpretation of the graph, fixed prediction probabilities points are situated on each allele vector. To simplify the graph, in our ap-plication, a vector joining the points for 0.5 and 0.75 are placed; this shows the cut point for prediction of presence and the direction of increasing probabilities. The length of the vector can be interpreted as an inverse measure of the discriminatory power of the alleles or bands, in the sense that shorter vectors correspond to alleles that better differentiate individuals. Two alleles pointing in the same direction are highly correlated, two alleles pointing in opposite directions are negatively correlated, and two alleles forming an angle close to 90º are not correlated. A more complete scale with probabilities from 0.1 to 0.9 can also be plotted with this function. For each variable, the ordination diagram can be divided into two separate regions predicting presence or absence, the two regions are separated by the line that is perpendicular to the variable vector in the Biplot and cuts the vector in the point predicting 0.5. The variables associated to the configuration are those that predict the presences adequately. In a practical situation not all the variables are associated to the ordination. Due to the high number usually studied, it is convenient to situate on the graph only those that are related to the configuration, i. e., those that have an adequate goodness of fit after adjusting the logistic regression.

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

References

Demey, J., Vicente-Villardon, J. L., Galindo, M.P. AND Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. Bioinformatics, 24(24): 2832-2838.

Vicente-Villardon, J. L., Galindo, M. P. and Blazquez, A. (2006) Logistic Biplots. In Multiple Correspondence Analysis And Related Methods. Grenacre, M & Blasius, J, Eds, Chapman and Hall, Boca Raton.

See Also

ExternalBinaryLogisticBiplot

Examples

```
data(spiders)
dist=BinaryProximities(spiders)
```

```
pco=PrincipalCoordinates(dist)
pcobip=ExternalBinaryLogisticBiplot(pco)
plot(pcobip, Mode="s")
pcobip=AddCluster2Biplot(pcobip, NGroups=3, ClusterType="hi")
op <- par(mfrow=c(1,2))
plot(pcobip, Mode="s", PlotClus = TRUE)
plot(pcobip$Dendrogram)
par(op)
```

`plot.fraction` *Plots a fraction of the data as a cluster*

Description

Plots a convex hull or a star containing a specified percentage of the data. Used to plot clusters.

Usage

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

Arguments

`x`	An object with class `fraction` obtained from `Fraction`.
`add`	Should the fraction be added to the current plot?
`center`	Should the center be plotted?
`centerlabel`	Label for the center.
`initial`	Should the initial data be plotted?
`type`	Type of plot. Can be: "ch"- Convex Hull or "st" - Star (Joining each point with the center)
`...`	Any other graphical parameter that can affects the plot (as color, etc ...)

Details

Plots a convex hull or a star containing a specified percentage of the data.

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

See Also

Fraction

Examples

```
a=matrix(runif(50), 25,2)
a2=Fraction(a, 0.7)
plot(a2, add=FALSE, type="ch", initial=TRUE, center=TRUE, col="blue")
plot(a2, add=TRUE, type="st", col="red")
```

---

plot.MGC *Plot the results of Model-Based Gaussian Clustering algorithms*

Description

PLots an object of type MGC (Model-based Gaussian Clustering)

Usage

```
## S3 method for class 'MGC'
plot(x, vars = NULL, groups = x$Classification, CexPoints = 0.2, Confidence = 0.95, ...)
```

Arguments

x	An object of type MGC
vars	A subset of indices of the variables to be plotted
groups	A factor containing groups to represent. Usually the clusters obtained from the algorithm.
CexPoints	Size of the points.
Confidence	Confidence of the ellipses
...	Anay additional graphical parameters

Details

PLots an object of type MGC (Model-based Gaussian Clustering) using a splom plot.

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(iris)
```

plot.Ordinal.Logistic.Biplot

Plots an ordinal Logistic Biplot

Description

Plots an ordinal Logistic Biplot

Usage

```
## S3 method for class 'Ordinal.Logistic.Biplot'
plot(x, A1 = 1, A2 = 2,
ShowAxis = FALSE, margin = 0, PlotVars = TRUE, PlotInd = TRUE,
LabelVars = TRUE, LabelInd = TRUE, mode = "a", CexInd = NULL,
CexVar = NULL, ColorInd = NULL, ColorVar = NULL, SmartLabels = TRUE,
MinQualityVars = 0, dp = 0, PredPoints = 0, PlotAxis = FALSE,
TypeScale = "Complete", ValuesScale = "Original",
SizeQualInd = FALSE, SizeQualVars = FALSE, ColorQualInd = FALSE,
ColorQualVars = FALSE, PchInd = NULL, PchVar = NULL,
PlotClus = FALSE, TypeClus = "ch", ClustConf = 1,
ClustCenters = FALSE, UseClusterColors = TRUE, ClustLegend = TRUE,
ClustLegendPos = "topright", TextVarPos = 1, PlotSupVars = FALSE,...)
```

Arguments

x	Plots and object of type "Ordinal.Logistic.Biplot"
A1	First dimension to plot
A2	Second dimension to plot
ShowAxis	Should the axis be shown
margin	Margin for the graph (in order to have space for the variable levels)
PlotVars	Should the variables be plotted?
PlotInd	Should the individuals be plotted?
LabelVars	Should the variables be labelled?
LabelInd	Should the variables be labelled?
mode	Mode of the biplot (see the classical biplot)
CexInd	Type of marker used for the individuals
CexVar	Type of marker used for the variables
ColorInd	Colors used for the individuals
ColorVar	Colors used for the cariables
SmartLabels	Should smart placement for the labels be used?
MinQualityVars	Minimum quality of representation for a variable to be displayed
dp	Set of variables in which the individuals are projected

`PredPoints`	Set of points thet will be projected on all the variables
`PlotAxis`	Should the axis be plotted?
`TypeScale`	See continuous biplots
`ValuesScale`	See continuous biplots
`SizeQualInd`	Should the size of the labels and points be related to the quality of representation for individuals?
`SizeQualVars`	Should the size of the labels and points be related to the quality of representation for variables?
`ColorQualInd`	Should the intensity of the color of the labels and points be related to the quality of representation for individuals?
`ColorQualVars`	Should the intensity of the color of the labels and points be related to the quality of representation for variables?
`PchInd`	Markers for the individuals
`PchVar`	Markers for the individuals
`PlotClus`	Should the added clusters for the individuals be plotted?
`TypeClus`	Type of plot for the clusters. The types are "ch", "el" and "st" for "Convex Hull", "Ellipse" and "Star" repectively.
`ClustConf`	Confidence level for the cluster
`ClustCenters`	Should the centers of the clsters be plotted
`UseClusterColors`	Should the colors of the clusters be used to plot the individuals.
`ClustLegend`	Should a legend for the clusters be added?
`ClustLegendPos`	Position of the legend
`TextVarPos`	Position of the labels for the variables
`PlotSupVars`	Should the supplementary variables be plotted
`...`	Any other aditional parameters

Details

Plots an ordinal Logistic Biplot

Value

The plot ....

Author(s)

Jose Luis Vicente Villardon

References

Vicente-Villardón, J. L., & Sánchez, J. C. H. (2014). Logistic Biplots for Ordinal Data with an Application to Job Satisfaction of Doctorate Degree Holders in Spain. arXiv preprint arXiv:1405.0294.

See Also

plot.ContinuousBiplot

Examples

```
data(Doctors)
olb = OrdLogBipEM(Doctors,dim = 2, nnodes = 10, initial=4,  tol = 0.001,
maxiter = 100, penalization = 0.1, show=TRUE)
plot(olb, mode="s", ColorInd="gray", ColorVar=1:5)
```

---

plot.PCA.Analysis *Plots a Principal Component Analysis*

Description

Plots the results of a Principal Component Analysis.

Usage

```
## S3 method for class 'PCA.Analysis'
plot(x, A1 = 1, A2 = 2, CorrelationCircle = FALSE, ...)
```

Arguments

x	The object with the results of a PCA
A1	Dimension for the first axis of the representation
A2	Dimension for the second axis of the representation
CorrelationCircle	Should the correlation circle be plotted? If false the scores plot is done.
...	Any other arguments of the function plot.ContinuousBiplot

Details

Plots theresults of a Principal Component Analysis. The plot can be the correlation circle containing the correlations of the variables with the components or a plot of the scores of the individuals.

Value

The PCA plot.

Author(s)

Jose Luis Vicente Villardon

See Also

plot.ContinuousBiplot

Examples

```
# Not yet
```

`plot.PCA.Bootstrap` *Plots the Bootstrap information for Principal Components Analysis (PCA)*

Description

Plots an object of class "PCA.Bootstrap"

Usage

```
## S3 method for class 'PCA.Bootstrap'
plot(x, Eigenvalues = TRUE,
Inertia = FALSE, EigenVectors = TRUE, Structure = TRUE,
Squared = TRUE, Scores = TRUE, ColorInd = "black", TypeScores = "ch", ...)
```

Arguments

`x`	An object of class "PCA.Bootstrap"
`Eigenvalues`	Should the information for the eigenvalues be plotted?
`Inertia`	Should the information for the inertia be plotted?
`EigenVectors`	Should the information for the eigenvectors be plotted?
`Structure`	Should the information for the correlations (variables-dimensions) be plotted?
`Squared`	Should the information for the correlations (variables-dimensions) be plotted?
`Scores`	Should the row (individual) scores be plotted?
`ColorInd`	Colors for the rows
`TypeScores`	Type of plot for the scores
`...`	Any other graphical argument

Details

For each parameter, box-plots and confidence intervals are plotted. The initial estimator and the bootstrap mean are plotted.

For the eigenvectors, loadings and contributions, the graph is divided into as many rows as dimensions, each row contains a plot of the hole set of variables.

The scores are plotted on a two dimensional

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

References

Daudin, J. J., Duby, C., & Trecourt, P. (1988). Stability of principal component analysis studied by the bootstrap method. Statistics: A journal of theoretical and applied statistics, 19(2), 241-258.

Chateau, F., & Lebart, L. (1996). Assessing sample variability in the visualization techniques related to principal component analysis: bootstrap and alternative simulation methods. COMPSTAT, Physica-Verlag, 205-210.

Babamoradi, H., van den Berg, F., & Rinnan, Å. (2013). Bootstrap based confidence limits in principal component analysis: A case study. Chemometrics and Intelligent Laboratory Systems, 120, 97-105.

Fisher, A., Caffo, B., Schwartz, B., & Zipunnikov, V. (2016). Fast, exact bootstrap principal component analysis for p> 1 million. Journal of the American Statistical Association, 111(514), 846-860.

See Also

PCA.Bootstrap

Examples

```
X=wine[,4:21]
grupo=wine$Group
rownames(X)=paste(1:45, grupo, sep="-")
pcaboot=PCA.Bootstrap(X, dimens=2, Scaling = "Standardize columns", B=1000)
plot(pcaboot, ColorInd=as.numeric(grupo))
summary(pcaboot)
```

---

plot.PCoABootstrap *Plots an object of class PCoABootstrap*

Description

Plots an object of class PCoABootstrap

Usage

```
## S3 method for class 'PCoABootstrap'
plot(x, F1=1, F2=2, Move2Center=TRUE,
BootstrapPlot="Ellipse", confidence=0.95, Colors=NULL, ...)
```

Arguments

`x`	An object of class "PCoABootstrap"
`F1`	First dimension to plot
`F2`	Second dimension to plot
`Move2Center`	Translate the ellipse center to the coordinates
`BootstrapPlot`	Type of Bootstrap plot to draw: "Ellipse", "ConvexHull", "Star"
`confidence`	Confidence level for the bootstrap plot
`Colors`	Colors of the objects
`...`	Additional parameters for graphical representations

Details

Draws the bootstrap confidence regions for the coordinates of the points obtained from a Principal Coodinates Analysis

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

References

J.R. Demey, J.L. Vicente-Villardon, M.P. Galindo, A.Y. Zambrano, Identifying molecular markers associated with classifications of genotypes by external logistic biplot, Bioinformatics 24 (2008) 2832.

Examples

```
data(spiders)
Dis=BinaryProximities(spiders)
pco=PrincipalCoordinates(Dis, Bootstrap=TRUE, BootstrapType="Products")
plot(pco, Bootstrap=TRUE)
```

plot.Principal.Coordinates
Plots an object of class Principal.Coordinates

Description

Plots an object of class Principal.Coordinates

Usage

```
## S3 method for class 'Principal.Coordinates'
plot(x, A1 = 1, A2 = 2, LabelRows = TRUE,
WhatRows = NULL, RowCex = 1, RowPch = 16, Title = "", RowLabels = NULL,
RowColors = NULL, ColColors = NULL, ColLabels = NULL, SizeQualInd = FALSE,
SmartLabels = TRUE, ColorQualInd = FALSE, ColorQual = "black", PlotSup = TRUE,
Bootstrap = FALSE, BootstrapPlot = c("Ellipse", "CovexHull", "Star"),
margin = 0, PlotClus = FALSE, TypeClus = "ch", ClustConf = 1,
CexClustCenters = 1, LegendClust = TRUE, ClustCenters = FALSE,
UseClusterColors = TRUE, ShowAxis = FALSE, PlotBinaryMeans = FALSE,
MinIncidence = 0, ShowBox = FALSE, ColorSupContVars = NULL,
ColorSupBinVars = NULL, ColorSupOrdVars = NULL, TypeScale = "Complete",
SupMode = "s", PlotSupVars = FALSE, ...)
```

Arguments

x	Object of class "Principal.Coordinates"
A1	First dimenssion of the plot
A2	Second dimenssion of the plot
LabelRows	Controls if the points are labelled. Usually TRUE.
WhatRows	What Rows to plot. A vector of 0/1 elements. If NULL all rows are plotted
RowCex	Size of the points. Can be a single number or a vector.
RowPch	Symbols for the points.
Title	Title for the graph
RowLabels	Labels for the rows. If NULL row names of the data matrix are used.
RowColors	Colors for the rows. If NULL row deafault colors are assigned. Can be a single value or avector of colors.
ColColors	Colors for the columns (Variables)
ColLabels	Labels for the columns (Variables)
SizeQualInd	Controls if the size of points depends on the quality of representation.
SmartLabels	Controls the way labels are plotted on the graph. If TRUE labels for points with positive x values are placed to the right of the point and labels for points with negative values to the left

ColorQualInd	Controls if the color of the points depends on the quality of representation.
ColorQual	Darker color for the quality scale.
PlotSup	Controls if the supplementary points are plotted.
Bootstrap	Controls if the bootstrap points are plotted.
BootstrapPlot	Type of plot of the Bootstrap Information. The types are "Ellipse", "CovexHull" or "Star".
margin	Margin for the graph.
PlotClus	Should the clusters be plotted?
TypeClus	Type of plot for the clusters. ("ch"- Convex Hull, "el"- Ellipse or "st"- Star)
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
CexClustCenters	Size of the cluster centers
LegendClust	Legends for the clusters
ClustCenters	Should the cluster centers be plotted
UseClusterColors	Should the cluster colors be used in the plot
ShowAxis	Logical variable to control if the coordinate axes should appear in the plot. The default value is FALSE because for most of the biplots its presence is irrelevant.
PlotBinaryMeans	Plot the mean of the presence points for each variable
MinIncidence	Minimum incidence to keep a variable
ShowBox	Should a box around the poitns be plotted?
ColorSupContVars	Colors for the supplementary continuous variables
ColorSupBinVars	Colors for the supplementary binary variables
ColorSupOrdVars	Colors for the supplementary ordinal variables
TypeScale	Type of scales for the plot
SupMode	Mode of the supplementary variables
PlotSupVars	Should the supplementary variables be plotted
...	Additional parameters for graphical representations

Details

Graphical representation of an Principal coordinates Analysis controlling visual aspects of the plot as colors, symbols or sizes of the points.

Value

No value is returned

Author(s)

Jose Luis Vicente-Villardon

References

J.R. Demey, J.L. Vicente-Villardon, M.P. Galindo, A.Y. Zambrano, Identifying molecular markers associated with classifications of genotypes by external logistic biplot, Bioinformatics 24 (2008) 2832.

See Also

BinaryProximities

Examples

```
data(spiders)
dist=BinaryProximities(spiders)
pco=PrincipalCoordinates(dist)
plot(pco)
```

`plot.Procrustes` *Plots an object of class "Procrustes"*

Description

Plots Simple Procrustes Analysis

Usage

```
## S3 method for class 'Procrustes'
plot(x, F1=1, F2=2, ...)
```

Arguments

`x`	Object of class "Procrustes"
`F1`	First dimenssion of the plot
`F2`	Second dimenssion of the plot
`...`	Additional parameters for graphical representations

Details

Graphical representation of an Orthogonal Procrustes Analysis.

Value

No value is returned

Author(s)

Jose Luis Vicente-Villardon

See Also

BinaryProximities

Examples

```
data(spiders)
dist=BinaryProximities(spiders)
pco=PrincipalCoordinates(dist)
plot(pco)
```

---

plot.StatisBiplot *Plots a Statis Biplot Object*

Description

Plots a Statis Biplot Object

Usage

```
## S3 method for class 'StatisBiplot'
plot(x, A1 = 1, A2 = 2, PlotType = "Biplot",
PlotRowTraj = FALSE, PlotVarTraj = FALSE, LabelTraj = "Begining",
VarColorType = "ByVar", VarColors = NULL, VarLabels = NULL,
RowColors = NULL, TableColors = NULL, RowRandomColors = FALSE,
TypeTraj = "line", ...)
```

Arguments

x	A Statis object
A1	First dimension of the plot
A2	Second dimension of the plot
PlotType	Type of plot: Interstructure, Correlations, Contributions or Biplot
PlotRowTraj	Should the row trajectories be plotted?
PlotVarTraj	Should the variables trajectories be plotted?
LabelTraj	Where the trajecories should be labelled: Begining or End.
VarColorType	The colors for the variables should be set by table (ByTable) or by variable (ByVar)
VarColors	Colors for the variables.
VarLabels	Labels for the variables
RowColors	Colors for the rows

TableColors	Colors for each table
RowRandomColors	Use random colors for the variables.
TypeTraj	Type of trajectory to plot: Lines or stars
...	Aditional parameters

Details

Plots a Statis Biplot Object. The arguments of the general biplot are as in a Continuous Biplot.

Value

A biplot

Author(s)

Jose Luis Vicente Villardon

References

Vallejo-Arboleda, A., Vicente-Villardon, J. L., & Galindo-Villardon, M. P. (2007). Canonical STATIS: Biplot analysis of multi-table group structured data based on STATIS-ACT methodology. Computational statistics & data analysis, 51(9), 4193-4205.

See Also

plot.ContinuousBiplot

Examples

```
data(Chemical)
x= Chemical[,5:16]
X=Convert2ThreeWay(x,Chemical$WEEKS, columns=FALSE)
stbip=StatisBiplot(X)
```

---

plot.TetraDualStatis *Plots an object of class "tetraDualStatis".*

Description

Plots an object the results of TetraDualStatis.

Usage

```
## S3 method for class 'TetraDualStatis'
plot(x, A1 = 1, A2 = 2, PlotType = "InterStructure",
                PlotRowTraj = FALSE, PlotVarTraj = FALSE, LabelTraj = "Begining",
                    VarColorType = "Biplot", VarColors = NULL, VarLabels = NULL,
                  RowColors = NULL, TableColors = NULL, RowRandomColors = FALSE,
                    TypeTraj = "line", ...)
```

Arguments

`x`	An object of class TetraDualStatis
`A1`	Dimension for the X-axis
`A2`	Dimension for the Y-axis
`PlotType`	Type of plot: "Biplot", "Compromise", "Correlations", "Contributions", "Inter-Structure".
`PlotRowTraj`	Should the row trajectories be plotted?
`PlotVarTraj`	Should the variables trajectories be plotted?
`LabelTraj`	Should the trajectories be labelled.
`VarColorType`	One of the following: "Biplot", "ByTable", "ByVar".
`VarColors`	User colors for the variables.
`VarLabels`	User labels for the variables.
`RowColors`	User colors for the rows.
`TableColors`	User colors for the different tables.
`RowRandomColors`	Should use random colors for the rows?
`TypeTraj`	Type of trajectory. Normally a line.
`...`	Additional graphical arguments.

Details

Plots an object the results of TetraDualStatis.

Value

The plot of the results

Author(s)

Laura Vicente-Gonzalez, Jose Luis Vicente-Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

plot.Unfolding *Plots an Unfolding Representation*

Description

Plots an Unfolding Representation

Usage

```
## S3 method for class 'Unfolding'
plot(x, A1 = 1, A2 = 2, ShowAxis = FALSE,
margin = 0.1, PlotSites = TRUE, PlotSpecies = TRUE, PlotEnv = TRUE,
LabelSites = TRUE, LabelSpecies = TRUE, LabelEnv = TRUE,
SpeciesQuality = FALSE, MinQualityVars = 0, dp = 0,
PlotAxis = FALSE, TypeScale = "Complete", ValuesScale = "Original",
mode = "h", CexSites = NULL, CexSpecies = NULL, CexVar = NULL,
ColorSites = NULL, ColorSpecies = NULL, ColorVar = NULL,
PchSites = NULL, PchSpecies = NULL, PchVar = NULL,
SizeQualSites = FALSE, SizeQualSpecies = FALSE,
SizeQualVars = FALSE, ColorQualSites = FALSE,
ColorQualSpecies = FALSE, ColorQualVars = FALSE, SmartLabels = FALSE,
PlotTol = FALSE, ...)
```

Arguments

x	An object of class Unfolding
A1	Axis 1 of the representation.
A2	Axis 1 of the representation.
ShowAxis	Should the axis be shown?
margin	Margin for the plot (precentage)
PlotSites	Should the sites be plotted?
PlotSpecies	Should the species be plotted?
PlotEnv	Should the environmental variables be plotted?
LabelSites	Should the sites be labelled?
LabelSpecies	Should the species be labelled?
LabelEnv	Should the environmental variables be labelled?
SpeciesQuality	Min species quality to plot
MinQualityVars	Minimum quality of a var to be plotted.
dp	A set of indices with the variables that will show the projections of the individuals.
PlotAxis	Should the axis be plotted?
TypeScale	Type of scale to use : "Complete", "StdDev" or "BoxPlot"

ValuesScale	Values to show on the scale: "Original" or "Transformed"
mode	Mode of the biplot: "p", "a", "b", "h", "ah" and "s".
CexSites	Size for the symbols and labels of the sites. Can be a single common size for all the points or a vector with individual sizes.
CexSpecies	Size for the symbols and labels of the species. Can be a single common size for all the points or a vector with individual sizes.
CexVar	Size for the symbols and labels of the variables. Can be a single common size for all the points or a vector with individual sizes.
ColorSites	Color for the symbols and labels of the sites. Can be a single common color for all the points or a vector with individual colors.
ColorSpecies	Color for the symbols and labels of the species. Can be a single common color for all the points or a vector with individual colors.
ColorVar	Color for the symbols and labels of the variables. Can be a single common color for all the points or a vector with individual colors.
PchSites	Symbol for the sites points. See `help(points)` for details.
PchSpecies	Symbol for the species points. See `help(points)` for details.
PchVar	Symbol for the variables points. See `help(points)` for details.
SizeQualSites	Should the size of the site points be related to their qualities of representation (predictiveness)?
SizeQualSpecies	Should the size of the species points be related to their qualities of representation (predictiveness)?
SizeQualVars	Should the size of the variables points be related to their qualities of representation (predictiveness)?
ColorQualSites	Should the color of the sites points be related to their qualities of representation (predictiveness)?
ColorQualSpecies	Should the color of the species points be related to their qualities of representation (predictiveness)?
ColorQualVars	Should the color of the variables points be related to their qualities of representation (predictiveness)?
SmartLabels	Plot the labels in a smart way
PlotTol	Should the tolerances be plotted
...	Aditional graphical parameters.

Details

Plots an Unfolding Representation

Value

A plot of the unfolding representation.

Author(s)

Jose Luis Vicente-Villardon

References

de Leeuw, J. (2005). Multidimensional unfolding. Encyclopedia of statistics in behavioral science.

Examples

```
# Not yet
```

PlotBiplotClusters *Plot clusters on a biplot.*

Description

Highlights several groups or clusters on a biplot representation.

Usage

```
PlotBiplotClusters(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 highlited
`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 slects the raibow 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 cluster centres.
`...`	Any other graphical parameters

Details

The clusters to plot should be added to the biplot object using the function `AddCluster2Biplot`.

Value

It takes effects on a plot

Author(s)

Jose Luis Vicente Villardon

See Also

`AddCluster2Biplot`

Examples

```
data(iris)
bip=PCA.Biplot(iris[,1:4])
bip=AddCluster2Biplot(bip, NGroups=3, ClusterType="us", Groups=iris[,5], Original=FALSE)
plot(bip, PlotClus = TRUE)
```

PlotOrdinalResponses *Plot the response functions along the directions of best fit.*

Description

Plot the response functions along the directions of best fit for the selected dimensions

Usage

```
PlotOrdinalResponses(olb, A1 = 1, A2 = 2, inf = -12, sup = 12,
Legend = TRUE, WhatVars=NULL)
```

Arguments

`olb`	An object of class "Ordinal.Logistic.Biplot"
`A1`	First dimension of the plot.
`A2`	Second dimension of the plot
`inf`	Lower limit of the representation
`sup`	Upper limit of the representation
`Legend`	Should a legend be plotted
`WhatVars`	A vector with the numbers of the variables to be plotted. If NULL all the variables are plotted.

Details

Plot the response functions along the directions of best fit for the selected dimensions

Value

A plot describing the behaviour of the variable

Author(s)

Jose Luis Vicente Villardon

Examples

```
data(Doctors)
    olb = OrdLogBipEM(Doctors,dim = 2, nnodes = 10, initial=4,  tol = 0.001,
    maxiter = 100, penalization = 0.1, show=TRUE)
    PlotOrdinalResponses(olb, WhatVars=c(1,2,3,4))
```

PLSR *Partial Least Squares Regression*

Description

Partial Least Squares Regression for numerical variables.

Usage

```
PLSR(Y, X, S = 2, InitTransform = 5, grouping = NULL,
centerY = TRUE, scaleY = TRUE, tolerance = 5e-06,
maxiter = 100, show = FALSE, Validation = NULL, nB = 500)
```

Arguments

`Y`	Matrix of Dependent Variables
`X`	Matrix of Independent Variables
`S`	Dimension of the solution
`InitTransform`	Initial transformation of the independent variables.
`grouping`	Fator when the init transformation is the standardization with the within groups deviation.
`centerY`	Should the dependent variables be centered?
`scaleY`	Should the dependent variables be standadized?
`tolerance`	Tolerance for the algorithm
`maxiter`	Maximum number of iterations
`show`	Show the progress of the algorithm?
`Validation`	Validation (None, Cross, Bootstrap)
`nB`	number of samples for the bottstrap validation

Details

Partial Least Squares Regression for numerical variables.

Value

An object of class plsr with fiends

`Method`	PLSR
`X`	The X matrix
`Y`	The Y matrix
`centerY`	Is the Y matrix centered
`scaleY`	Is the Y matrix scaled
`Initial_Transformation`	Initial transformation of the Y matrix
`ScaledX`	Transformed X matrix
`ScaledY`	Transformed Y matrix
`Intercept`	Intercept of the model
`XScores`	Scores for the individals from the X matrix
`XWeights`	Weigths for the X set
`XLoadings`	Loadings for the X set
`YScores`	Scores for the individals from the Y matrix
`YWeights`	Weigths for the Y set
`YLoadings`	Loadings for the Y set
`RegParameters`	Final Regression Parameters
`ExpectedY`	Expected values of Y
`R2`	R-squared
`XStructure`	Relation of the X variables with its structure
`YStructure`	Relation of the Y variables with its structure
`YXStructure`	Relation of the Y variables with the X components

Author(s)

Jose Luis Vicente Villardon

References

H. Abdi, Partial least squares regression and projection on latent structure regression (PLS regression), WIREs Comput. Stat. 2 (2010), pp. 97-106.

See Also

`Biplot.PLSR`

Examples

```
X=as.matrix(wine[,4:21])
y=as.numeric(wine[,2])-1
mifit=PLSR(y,X, Validation="None")
```

PLSR1Bin *Partial Least Squares Regression with Binary Response*

Description

Fits Partial Least Squares Regression with Binary Response

Usage

```
PLSR1Bin(Y, X, S = 2, InitTransform = 5, grouping = NULL,
tolerance = 5e-06, maxiter = 100, show = FALSE, penalization = 0,
cte = TRUE, Algorithm = 1, OptimMethod = "CG")
```

Arguments

Y	The response
X	The matrix of independent variables
S	The Dimension of the solution
InitTransform	Initial transform for the X matrix
grouping	Factor for grouping the observations
tolerance	Tolerance for convergence of the algorithm
maxiter	Maximum Number of iterations
show	Show the steps of the algorithm
penalization	Penalization for the Ridge Logistic Regression
cte	Should a constant be included in the model?
Algorithm	Algorithm used in the calculations
OptimMethod	Optimization methods from optim

Details

The procedure uses the algorithm proposed by Bastien et al () to fit a Partial Lest Squares Regression when the response is Binary. The procedure will be later converted into a Biplot to visulize the results.

Value

Still to be finished

Author(s)

Jose Luis Vicente Villardon

Examples

```
# No examples yet
```

PLSRBin *Partial Least Squares Regression with several Binary Responses*

Description

Fits Partial Least Squares Regression with several Binary Responses

Usage

```
PLSRBin(Y, X, S = 2, InitTransform = 5, grouping = NULL,
tolerance = 5e-05, maxiter = 100, show = FALSE, penalization = 0.1,
cte = TRUE, OptimMethod = "CG", Multiple = FALSE)
```

Arguments

Y	The response
X	The matrix of independent variables
S	The Dimension of the solution
InitTransform	Initial transform for the X matrix
grouping	Grouping variable when the inial transformation is standardization within groups.
tolerance	Tolerance for convergence of the algorithm
maxiter	Maximum Number of iterations
show	Show the steps of the algorithm
penalization	Penalization for the Ridge Logistic Regression
cte	Should a constant be included in the model?
OptimMethod	Optimization methods from optim
Multiple	The responses are the indicators of a multinomial variable?

Details

The function fits the PLSR method for the case when there is a set binary dependent variables, using logistic rather than linear fits to take into account the nature of responses. We term the method PLS-BLR (Partial Least Squares Binary Logistic Regression). This can be considered as a generalization of the NIPALS algorithm when the responses are all binary.

Value

`Method`	Description of 'comp1'
`X`	The predictors matrix
`Y`	The responses matrix
`Initial_Transformation`	Initial Transformation of the X matrix
`ScaledX`	The scaled X matrix
`tolerance`	Tolerance used in the algorithm
`maxiter`	Maximum number of iterations used
`penalization`	Ridge penalization
`IncludeConst`	Is the constant included in the model?
`XScores`	Scores of the X matrix, used later for the biplot
`XLoadings`	Loadings of the X matrix
`YScores`	Scores of the Y matrix
`YLoadings`	Loadings of the Y matrix
`Coefficients`	Regression coefficients
`XStructure`	Correlations among the X variables and the PLS scores
`Intercepts`	Intercepts for the Y loadings
`LinTerm`	Linear terms for each response
`Expected`	Expected probabilities for the responses
`Predictions`	Binary predictions of the responses
`PercentCorrect`	Global percent of correct predictions
`PercentCorrectCols`	Percent of correct predictions for each column
`Maxima`	Column with the maximum probability. Useful when the responses are the indicators of a multinomial variable

Author(s)

José Luis Vicente Villardon

References

Ugarte Fajardo, J., Bayona Andrade, O., Criollo Bonilla, R., Cevallos-Cevallos, J., Mariduena-Zavala, M., Ochoa Donoso, D., & Vicente Villardon, J. L. (2020). Early detection of black Sigatoka in banana leaves using hyperspectral images. Applications in plant sciences, 8(8), e11383.

Examples

```
X=as.matrix(wine[,4:21])
Y=cbind(Factor2Binary(wine[,1])[,1], Factor2Binary(wine[,2])[,1])
rownames(Y)=wine[,3]
colnames(Y)=c("Year", "Origin")
pls=PLSRBin(Y,X, penalization=0.1, show=TRUE, S=2)
```

`PLSRBinFit` *PLS binary regression.*

Description

Fits PLS binary regression.

Usage

```
PLSRBinFit(Y, X, S = 2, tolerance = 5e-06, maxiter = 100,
show = FALSE, penalization = 0.1, cte = TRUE, OptimMethod = "CG")
```

Arguments

`Y`	The response
`X`	The matrix of independent variables
`S`	The Dimension of the solution
`tolerance`	Tolerance for convergence of the algorithm
`maxiter`	Maximum Number of iterations
`show`	Show the steps of the algorithm
`penalization`	Penalization for the Ridge Logistic Regression
`cte`	Should a constant be included in the model?
`OptimMethod`	Optimization methods from optim

Details

Fits PLS binary regression. It is used for a higher level function.

Value

The PLS fit used by the PLSRBin function.

Author(s)

Jose Luis Vicente Villardon

References

Ugarte Fajardo, J., Bayona Andrade, O., Criollo Bonilla, R., Cevallos-Cevallos, J., Mariduena-Zavala, M., Ochoa Donoso, D., & Vicente Villardon, J. L. (2020). Early detection of black Sigatoka in banana leaves using hyperspectral images. Applications in plant sciences, 8(8), e11383.

Examples

```
## Not yet
```

PLSRfit *Partial Least Squares Regression (PLSR)*

Description

Fits a Partial Least Squares Regression (PLSR) to two continuous data matrices

Usage

```
PLSRfit(Y, X, S = 2, tolerance = 5e-06,
maxiter = 100, show = FALSE)
```

Arguments

Y	The matrix of dependent variables
X	The Matrix of Independent Variables
S	Dimension of the solution. The default is 2
tolerance	Tolerance for the algorithm.
maxiter	Maximum number of iterations for the algorithm.
show	Logical. Should the calculation process be shown on the screen

Details

Fits a Partial Least Squares Regression (PLSR) to a set of two continuous data matrices

Value

An object of class "PLSR"

Method	PLSR1
X	Independent Variables
Y	Dependent Variables
center	Are data centered?
scale	Are data scaled?
ScaledX	Scaled Independent Variables
ScaledY	Scaled Dependent Variables
XScores	Scores for the Independent Variables
XWeights	Weights for the Independent Variables - coefficients of the linear combination
XLoadings	Factor loadings for the Independent Variables
YScores	Scores for the Dependent Variables
YWeights	Weights for the Dependent Variables - coefficients of the linear combination
YLoadings	Factor loadings for the Dependent Variables
XStructure	Structure Correlations for the Independent Variables
YStructure	Structure Correlations for the Dependent Variables
YXStructure	Structure Correlations two groups

Author(s)

Jose Luis Vicente Villardon

References

Wold, S., Sjöström, M., & Eriksson, L. (2001). PLS-regression: a basic tool of chemometrics. Chemometrics and intelligent laboratory systems, 58(2), 109-130.

PoliticalFigures *Political Figures in the USA*

Description

Does the American public actively differentiate political stimuli along ideological lines?. Dissimilarities among 13 political figurein the USA.

Usage

```
data("PoliticalFigures")
```

Format

A data frame with the dissimilarities among 13 political figures in the USA.

`G._W._Bush` a numeric vector with the dissimilarities with the other figures

`John_Kerry` a numeric vector with the dissimilarities with the other figures

`Ralph_Nader` a numeric vector with the dissimilarities with the other figures

`Dick_Cheney` a numeric vector with the dissimilarities with the other figures

`John_Edwards` a numeric vector with the dissimilarities with the other figures

`Laura_Bush` a numeric vector with the dissimilarities with the other figures

`Hillary_Clinton` a numeric vector with the dissimilarities with the other figures

`Bill_Clinton` a numeric vector with the dissimilarities with the other figures

`Colin_Powell` a numeric vector with the dissimilarities with the other figures

`John_Ashcroft` a numeric vector with the dissimilarities with the other figures

`John_McCain` a numeric vector with the dissimilarities with the other figures

`Democ._Party` a numeric vector with the dissimilarities with the other figures

`Repub._Party` a numeric vector with the dissimilarities with the other figures

Details

We have taken information from the 2004 CPS American National Election Study. Specifically 711 NES respondents' feeling thermometer ratings of thirteen prominent political figures from the period of the 2004 election: George W. Bush; John Kerry; Ralph Nader; Richard Cheney; John Edwards; Laura Bush; Hillary Clinton; Bill Clinton; Colin Powell; John Ashcroft; John McCain; the Democratic party; and the Republican party. With the respondent scores, a dissimilarity among each pair of figures

Source

Jacoby, W. G., & Armstrong, D. A. (2014). Bootstrap Confidence Regions for Multidimensional Scaling Solutions. American Journal of Political Science, 58(1), 264-278.

References

Jacoby, W. G., & Armstrong, D. A. (2014). Bootstrap Confidence Regions for Multidimensional Scaling Solutions. American Journal of Political Science, 58(1), 264-278.

Examples

```
# Not yet
```

`PolyOrdinalLogBiplot` *Factor Analysis Biplot based on polychoric correlations*

Description

Calculates a biplot for ordinal data based on polychoric correlations

Usage

```
PolyOrdinalLogBiplot(X, dimension = 3, method = "principal",
rotate = "varimax", RescaleCoordinates = TRUE, ...)
```

Arguments

`X`	A matrix of ordinal data
`dimension`	Number of dimensiona to retain
`method`	Principal components (principal) or factor analysis (fa)
`rotate`	Rotation for the analysis
`RescaleCoordinates`	Rescale coordinates as in a continuous data biplot
`...`	Any aditional arguments for the principal and fa functions

Details

The procedure calculates

Value

A biplot (Continuous or ordinal)

Author(s)

Jose Luis Vicente Villardon

See Also

fa, principal

Examples

```
## Not Yet
```

PrettyTicks *Calculates loose axis ticks and labels using nice numbers*

Description

Calculates axis ticks and labels using nice numbers

Usage

```
PrettyTicks(min = -3, max = 3, ntick = 5)
```

Arguments

min	Minimum value on the axis
max	maximum value on the axis.
ntick	Approximated number of desired ticks

Details

Calculates axis ticks and labels using nice numbers. The resulting labels are known as loose labels.

Value

A list with the following fields

ticks	Ticks for the axis
labels	The corresponding labels

Author(s)

Jose Luis Vicente Villardon

References

Heckbert, P. S. (1990). Nice numbers for graph labels. In Graphics Gems (pp. 61-63). Academic Press Professional, Inc..

See Also

NiceNumber

Examples

```
PrettyTicks(-4, 4, 5)
```

`PrincipalCoordinates` *Principal Coordinates Analysis*

Description

Principal coordinates Analysis for a matrix of proximities obtained from binary, categorical, continuous or mixed data

Usage

```
PrincipalCoordinates(Proximities, w = NULL, dimension = 2,
method = "eigen", tolerance = 1e-04, Bootstrap = FALSE,
BootstrapType = c("Distances", "Products"), nB = 200,
ProcrustesRot = TRUE, BootstrapMethod = c("Sampling", "Permutation"))
```

Arguments

`Proximities`	An object of class `proximities`.
`w`	An set of weights.
`dimension`	Dimension of the solution
`method`	Method to calculate the eigenvalues and eigenvectors. The default is the usual eigen function although the Power Method to calculate only tre first eigenvectors can be used.
`tolerance`	Tolerance for the eigenvalues
`Bootstrap`	Should Bootstrap be calculated?
`BootstrapType`	Bootstrap on the residuals of the "distance" or "scalar products" matrix.
`nB`	Number of Bootstrap replications
`ProcrustesRot`	Should each replication be rotated to match the initial solution?
`BootstrapMethod`	The replications are obtained "Sampling" or "Permutating" the residuals.

Details

Principal Coordinates Analysis for a proximity matrix previously calculated from a matrix of raw data or directly obsrved proximities.

Value

An object of class `Principal.Coordinates`. The function adds the information of the Principal Coordinates to the object of class `proximities`. Together with the information about the proximities the object has:

`Analysis`	The type of analysis performed, "Principal Coordinates" in this case
`Eigenvalues`	The eigenvalues of the PCoA
`Inertia`	The Inertia of the PCoA
`RowCoordinates`	Coordinates for the objects in the PCoA
`RowQualities`	Qualities of representation for the objects in the PCoA
`RawStress`	Raw Stress values
`stress1`	stress formula 1
`stress2`	stress formula 2
`sstress1`	sstress formula 1
`sstress2`	sstress formula 2
`rsq`	Squared correlation between disparities and distances
`Spearman`	Spearman correlation between disparities and distances
`Kendall`	Kendall correlation between disparities and distances
`BootstrapInfo`	The result of the bootstrap calculations

Author(s)

Jose Luis Vicente-Villardon

References

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

Gower, J.C. (1966). Some distance properties of latent root and vector methods used in multivariate analysis. Biometrika 53: 325-338.

J.R. Demey, J.L. Vicente-Villardon, M.P. Galindo, A.Y. Zambrano, Identifying molecular markers associated with classifications of genotypes by external logistic biplot, Bioinformatics 24 (2008) 2832.

See Also

`BinaryProximities`, `BootstrapDistance`, `BootstrapDistance`, `BinaryProximities`

Examples

```
data(spiders)
Dis=BinaryProximities(spiders)
pco=PrincipalCoordinates(Dis)
Dis=BinaryProximities(spiders)
pco=PrincipalCoordinates(Dis, Bootstrap=TRUE)
```

`print.MGC` *Prints the results of Model-Based Gaussian Clustering algorithms*

Description

Prints the results of Model-Based Gaussian Clustering algorithms

Usage

```
## S3 method for class 'MGC'
print(x, ...)
```

Arguments

`x`	An object of class "MGC"
`...`	Any aditional parameters

Details

Prints the results of Model-Based Gaussian Clustering algorithms

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.
```

`print.RidgeBinaryLogistic`
prints an object of class RidgeBinaryLogistic

Description

prints an object of class RidgeBinaryLogistic

Usage

```
## S3 method for class 'RidgeBinaryLogistic'
print(x, ...)
```

Arguments

`x`	An object of class
`...`	Aditional Arguments

Details

Prints an object of class RidgeBinaryLogistic

Value

The main resuls of a binary logistic regression

Author(s)

Jose Luis Vicente Villardon

Examples

```
# Not yet
```

`Protein` *Protein consumption data.*

Description

Protein consumption in twenty-five European countries for nine food groups.

Usage

```
data(Protein)
```

Format

A data frame with 25 observations on the following 11 variables.

`Comunist` a factor with levels `No` `Yes`

`Region` a factor with levels `North` `Center` `South`

`Red_Meat` a numeric vector

`White_Meat` a numeric vector

`Eggs` a numeric vector

`Milk` a numeric vector

`Fish` a numeric vector

`Cereal` a numeric vector

`Starch` a numeric vector

`Nuts` a numeric vector

`Fruits_Vegetables` a numeric vector

Details

These data measure protein consumption in twenty-five European countries for nine food groups. It is possible to use multivariate methods to determine whether there are groupings of countries and whether meat consumption is related to that of other foods.

Source

http://lib.stat.cmu.edu/DASL/Datafiles/Protein.html

References

Weber, A. (1973) Agrarpolitik im Spannungsfeld der internationalen Ernaehrungspolitik, Institut fuer Agrarpolitik und marktlehre, Kiel.

Gabriel, K.R. (1981) Biplot display of multivariate matrices for inspection of data and diagnosis. In Interpreting Multivariate Data (Ed. V. Barnett), New York: John Wiley & Sons, 147-173.

Hand, D.J., et al. (1994) A Handbook of Small Data Sets, London: Chapman & Hall, 297-298.

Examples

```
data(Protein)
## maybe str(Protein) ; plot(Protein) ...
```

RAPD *Sugar Cane Data*

Description

Molecular characteristics of 50 varieties of sugar cane.

Usage

```
data(RAPD)
```

Format

A data frame with 50 observations on 168 variables. 1-120: Random aplified polymorphic DNA and 121-168: Microsatellites

Details

Dta are codified as presence or absence of the dominant marker.

Examples

```
data(RAPD)
## maybe str(RAPD) ; plot(RAPD) ...
```

RemoveRowsWithNaNs *Remove rows that contains NaNs (missing data)*

Description

Remove rows that contains NaNs to obtain a matrix wothout missind data

Usage

```
RemoveRowsWithNaNs(x, cols = NULL)
```

Arguments

x	The matrix to be arranged
cols	A set of columns to check as a vector of integers

Details

Remove rows that contains NaNs to obtain a matrix wothout missind data

Value

x	Matrix without missing data

Author(s)

Jose Luis Vicente-Villardon

`riano` *Ecological data from Riano (Spain)*

Description

Ecological data from Riano (Spain)

Usage

```
data("riano")
```

Format

A data frame with 70 observations on the following 25 variables.

`Week` a factor with levels `A` `B` `C` `D` `E` `F` `G` `H` `I` `J`

`Depth` a factor with levels `0` `2` `5` `10` `15` `20` `Bottom`

`Cianof` a numeric vector

`Crisof` a numeric vector

`Haptof` a numeric vector

`Crasp` a numeric vector

`Cripto` a numeric vector

`Dinof` a numeric vector

`Diatom` a numeric vector

`Euglen` a numeric vector

`Prasin` a numeric vector

`Clorof` a numeric vector

`Zigofi` a numeric vector

`Xantof` a numeric vector

`malgas` a numeric vector

`Ta` a numeric vector

`X02` a numeric vector

`pH` a numeric vector

`COND` a numeric vector

`SiO2` a numeric vector

`P.PO4` a numeric vector

`Chla` a numeric vector

`Chlb` a numeric vector

`Chlc` a numeric vector

`IM` a numeric vector

Details

Ecological data from Riano (Spain). Abundance of several algae taxonomic groups and several environmental variables

Source

Department of Ecology. University of Leon. Spain

Examples

```
data(riano)
## maybe str(riano) ; plot(riano) ...
```

`RidgeBinaryLogistic` *Ridge Binary Logistic Regression for Binary data*

Description

This function performs a logistic regression between a dependent binary variable `y` and some independent variables `x`, solving the separation problem in this type of regression using ridge penalization.

Usage

```
RidgeBinaryLogistic(y, X = NULL, data = NULL, freq = NULL,
tolerance = 1e-05, maxiter = 100, penalization = 0.2,
cte = FALSE, ref = "first", bootstrap = FALSE, nmB = 100,
RidgePlot = FALSE, MinLambda = 0, MaxLambda = 2, StepLambda = 0.1)
```

Arguments

`y`	A binary dependent variable or a formula
`X`	A set of independent variables when y is not a formula.
`data`	data frame for the formula
`freq`	frequencies for each observation (usually 1)
`tolerance`	Tolerance for convergence
`maxiter`	Maximum number of iterations
`penalization`	Ridige penalization: a non negative constant. Penalization used in the diagonal matrix to avoid singularities.
`cte`	Should the model have a constant?
`ref`	Category of reference
`bootstrap`	Should bootstrap confidence intervals be calculated?
`nmB`	Number of bootstrap samples.
`RidgePlot`	Should the ridge plot be plotted?

MinLambda	Minimum value of lambda for the rigge plot
MaxLambda	Maximum value of lambda for the rigge plot
StepLambda	Step for increasing the values of lambda

Details

Logistic Regression is a widely used technique in applied work when a binary, nominal or ordinal response variable is available, due to the fact that classical regression methods are not applicable to this kind of variables. The method is available in most of the statistical packages, commercial or free. Maximum Likelihood together with a numerical method as Newton-Raphson, is used to estimate the parameters of the model. In logistic regression, when in the space generated by the independent variables there are hyperplanes that separate among the individuals belonging to the different groups defined by the response, maximum likelihood does not converge and the estimations tend to the infinity. That is known in the literature as the separation problem in logistic regression. Even when the separation is not complete, the numerical solution of the maximum likelihood has stability problems. From a practical point of view, that means the estimated model is not accurate precisely when there should be a perfect, or almost perfect, fit to the data.

The problem of the existence of the estimators in logistic regression can be seen in Albert (1984), a solution for the binary case, based on the Firth method, Firth (1993) is proposed by Heinze(2002). The extension to nominal logistic model was made by Bull (2002). All the procedures were initially developed to remove the bias but work well to avoid the problem of separation. Here we have chosen a simpler solution based on ridge estimators for logistic regression Cessie(1992).

Rather than maximizing $L_j(\mathbf{G}|\,\mathbf{b}_{j0},\mathbf{B}_j)$ we maximize

$$L_j(\mathbf{G}|\,\mathbf{b}_{j0},\mathbf{B}_j) - \lambda\left(\|\mathbf{b}_{j0}\| + \|\mathbf{B}_j\|\right)$$

Changing the values of λ we obtain slightly different solutions not affected by the separation problem.

Value

An object of class RidgeBinaryLogistic with the following components

beta	Estimates of the coefficients
fitted	Fitted probabilities
residuals	Residuals of the model
Prediction	Predictions of presences and absences
Covariances	Covariances among the estimates
Deviance	Deviance of the current model
NullDeviance	Deviance of the null model
Dif	Difference between the deviances of the cirrent and null models
df	Degrees of freedom of the difference
p	p-value
CoxSnell	Cox-Snell pseudo R-squared

`Nagelkerke`	Nagelkerke pseudo R-squared
`MacFaden`	MacFaden pseudo R-squared
`R2`	Pseudo R-squared using the residuals
`Classification`	Classification table
`PercentCorrect`	Percentage of correct classification

Author(s)

Jose Luis Vicente Villardon

References

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Albert, A. and Anderson, J. A. (1984) On the existence of maximum likelihood estimates in logistic regression models. Biometrika, 71(1): 1-10.

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Malo, N., Libiger, O. and Schork, N. J. (2008) Accommodating Linkage Disequilibrium in Genetic-Association Analyses via Ridge Regression. Am J Hum Genet. 82(2): 375-385.

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Zhu, J. and Hastie, T. (2004) Classification of gene microarrays by penalized logistic regression. Biostatistics. 5(3):427-43.

Examples

```
# not yet
```

`RidgeBinaryLogisticFit` *Fits a binary logistic regression with ridge penalization*

Description

This function fits a logistic regression between a dependent variable y and some independent variables x, and solves the separation problem in this type of regression using ridge regression and penalization.

Usage

```
RidgeBinaryLogisticFit(y, xd, freq, tolerance = 1e-05, maxiter = 100, penalization = 0.2)
```

Arguments

`y`	A vector with the values of the dependent variable
`xd`	A matrix with the independent variables
`freq`	Frequencies of each pattern
`tolerance`	Tolerance for the iterations.
`maxiter`	Maximum number of iterations for convergenc~
`penalization`	Penalization used in the diagonal matrix to avoid singularities.

Details

Fits a binary logistic regression with ridge penalization

Value

The parameters of the fit

Author(s)

Jose Luis Vicente Villardon

See Also

RidgeBinaryLogistic

Examples

```
##---- Should be DIRECTLY executable !! ----
```

RidgeMultinomialLogisticFit

Multinomial logistic regression with ridge penalization

Description

This function does a logistic regression between a dependent variable y and some independent variables x, and solves the separation problem in this type of regression using ridge regression and penalization.

Usage

```
RidgeMultinomialLogisticFit(y, x, penalization = 0.2,
tol = 1e-04, maxiter = 200, show = FALSE)
```

Arguments

y	Dependent variable.
x	A matrix with the independent variables.
penalization	Penalization used in the diagonal matrix to avoid singularities.
tol	Tolerance for the iterations.
maxiter	Maximum number of iterations.
show	Should the iteration history be printed?.

Details

The problem of the existence of the estimators in logistic regression can be seen in Albert (1984), a solution for the binary case, based on the Firth's method, Firth (1993) is proposed by Heinze(2002). The extension to nominal logistic model was made by Bull (2002). All the procedures were initially developed to remove the bias but work well to avoid the problem of separation. Here we have chosen a simpler solution based on ridge estimators for logistic regression Cessie(1992).

Rather than maximizing $L_j(\mathbf{G}|\,\mathbf{b}_{j0},\mathbf{B}_j)$ we maximize

$$L_j(\mathbf{G}|\,\mathbf{b}_{j0},\mathbf{B}_j) - \lambda\,(\|\mathbf{b}_{j0}\| + \|\mathbf{B}_j\|)$$

Changing the values of λ we obtain slightly different solutions not affected by the separation problem.

Value

An object of class "rmlr" with components

fitted	Matrix with the fitted probabilities
cov	Covariance matrix among the estimates
Y	Indicator matrix for the dependent variable
beta	Estimated coefficients for the multinomial logistic regression
stderr	Standard error of the estimates
logLik	Logarithm of the likelihood
Deviance	Deviance of the model
AIC	Akaike information criterion indicator
BIC	Bayesian information criterion indicator

Author(s)

Jose Luis Vicente-Villardon

References

Albert,A. & Anderson,J.A. (1984),*On the existence of maximum likelihood estimates in logistic regression models*, Biometrika 71(1), 1–10.

Bull, S.B., Mak, C. & Greenwood, C.M. (2002), *A modified score function for multinomial logistic regression*, Computational Statistics and dada Analysis 39, 57–74.

Firth, D.(1993), *Bias reduction of maximum likelihood estimates*, Biometrika 80(1), 27–38

Heinze, G. & Schemper, M. (2002), *A solution to the problem of separation in logistic regression*, Statistics in Medicine 21, 2109–2419

Le Cessie, S. & Van Houwelingen, J. (1992), *Ridge estimators in logistic regression*, Applied Statistics 41(1), 191–201.

Examples

```
# No examples yet
```

RidgeMultinomialLogisticRegression
Ridge Multinomial Logistic Regression

Description

Function that calculates an object with the fitted multinomial logistic regression for a nominal variable. It compares with the null model, so that we will be able to compare which model fits better the variable.

Usage

```
RidgeMultinomialLogisticRegression(formula, data, penalization = 0.2,
cte = TRUE, tol = 1e-04, maxiter = 200, showIter = FALSE)
```

Arguments

formula	The usual formula notation (or the dependent variable)
data	The dataframe used by the formula. (or a matrix with the independent variables).
penalization	Penalization used in the diagonal matrix to avoid singularities.
cte	Should the model have a constant?
tol	Value to stop the process of iterations.
maxiter	Maximum number of iterations.
showIter	Should the iteration history be printed?.

Value

An object that has the following components:

fitted	Matrix with the fitted probabilities
cov	Covariance matrix among the estimates
Y	Indicator matrix for the dependent variable
beta	Estimated coefficients for the multinomial logistic regression
stderr	Standard error of the estimates
logLik	Logarithm of the likelihood
Deviance	Deviance of the model
AIC	Akaike information criterion indicator
BIC	Bayesian information criterion indicator
NullDeviance	Deviance of the null model
Difference	Difference between the two deviance values
df	Degrees of freedom
p	p-value asociated to the chi-squared estimate

CoxSnell	Cox and Snell pseudo R squared
Nagelkerke	Nagelkerke pseudo R squared
MacFaden	MacFaden pseudo R squared
Table	Cross classification of observed and predicted responses
PercentCorrect	Percentage of correct classifications

Author(s)

Jose Luis Vicente-Villardon

References

Albert,A. & Anderson,J.A. (1984),*On the existence of maximum likelihood estimates in logistic regression models*, Biometrika 71(1), 1–10.

Bull, S.B., Mak, C. & Greenwood, C.M. (2002), *A modified score function for multinomial logistic regression*, Computational Statistics and dada Analysis 39, 57–74.

Firth, D.(1993), *Bias reduction of maximum likelihood estimates*, Biometrika 80(1), 27–38

Heinze, G. & Schemper, M. (2002), *A solution to the problem of separation in logistic regression*, Statistics in Medicine 21, 2109–2419

Le Cessie, S. & Van Houwelingen, J. (1992), *Ridge estimators in logistic regression*, Applied Statistics 41(1), 191–201.

See Also

RidgeMultinomialLogisticFit

Examples

```
data(Protein)
y=Protein[[2]]
X=Protein[,c(3,11)]
rmlr = RidgeMultinomialLogisticRegression(y,X,penalization=0.0)
summary(rmlr)
```

RidgeOrdinalLogistic *Ordinal logistic regression with ridge penalization*

Description

This function performs a logistic regression between a dependent ordinal variable y and some independent variables x, and solves the separation problem using ridge penalization.

Usage

```
RidgeOrdinalLogistic(y, x, penalization = 0.1, tol = 1e-04, maxiter = 200, show = FALSE)
```

Arguments

`y`	Dependent variable.
`x`	A matrix with the independent variables.
`penalization`	Penalization used to avoid singularities.
`tol`	Tolerance for the iterations.
`maxiter`	Maximum number of iterations.
`show`	Should the iteration history be printed?.

Details

The problem of the existence of the estimators in logistic regression can be seen in Albert (1984); a solution for the binary case, based on the Firth's method, Firth (1993) is proposed by Heinze(2002). All the procedures were initially developed to remove the bias but work well to avoid the problem of separation. Here we have chosen a simpler solution based on ridge estimators for logistic regression Cessie(1992).

Rather than maximizing $L_j(\mathbf{G}|\,\mathbf{b}_{j0}, \mathbf{B}_j)$ we maximize

$$L_j(\mathbf{G}|\,\mathbf{b}_{j0}, \mathbf{B}_j) - \lambda\,(\|\mathbf{b}_{j0}\| + \|\mathbf{B}_j\|)$$

Changing the values of λ we obtain slightly different solutions not affected by the separation problem.

Value

An object of class `"pordlogist"`. This has components:

`nobs`	Number of observations
`J`	Maximum value of the dependent variable
`nvar`	Number of independent variables
`fitted.values`	Matrix with the fitted probabilities
`pred`	Predicted values for each item
`Covariances`	Covariances matrix
`clasif`	Matrix of classification of the items
`PercentClasif`	Percent of good classifications
`coefficients`	Estimated coefficients for the ordinal logistic regression
`thresholds`	Thresholds of the estimated model
`logLik`	Logarithm of the likelihood
`penalization`	Penalization used to avoid singularities
`Deviance`	Deviance of the model
`DevianceNull`	Deviance of the null model
`Dif`	Diference between the two deviances values calculated
`df`	Degrees of freedom

pval	p-value of the contrast
CoxSnell	Cox-Snell pseudo R squared
Nagelkerke	Nagelkerke pseudo R squared
MacFaden	Nagelkerke pseudo R squared
iter	Number of iterations made

Author(s)

Jose Luis Vicente-Villardon

References

Albert,A. & Anderson,J.A. (1984),*On the existence of maximum likelihood estimates in logistic regression models*, Biometrika 71(1), 1–10.

Bull, S.B., Mak, C. & Greenwood, C.M. (2002), *A modified score function for multinomial logistic regression*, Computational Statistics and dada Analysis 39, 57–74.

Firth, D.(1993), *Bias reduction of maximum likelihood estimates*, Biometrika 80(1), 27–38

Heinze, G. & Schemper, M. (2002), *A solution to the problem of separation in logistic regression*, Statistics in Medicine 21, 2109–2419

Le Cessie, S. & Van Houwelingen, J. (1992), *Ridge estimators in logistic regression*, Applied Statistics 41(1), 191–201.

Examples

```
data(Doctors)
olb = OrdLogBipEM(Doctors,dim = 2, nnodos = 10,
            tol = 0.001, maxiter = 100, penalization = 0.2)
model = RidgeOrdinalLogistic(Doctors[, 1], olb$RowCoordinates, tol = 0.001,
        maxiter = 100, penalization = 0.2)
model
```

---

scores.CCA.sol *Extract the scores of a CCA solution object*

Description

Extract the scores of a CCA solution object

Usage

```
scores.CCA.sol(CCA.sol)
```

Arguments

CCA.sol	The results of a CCA model

Details

Extract the scores of a CCA solution object

Value

The species, sites and environmental variables scores of a CCA solution

Author(s)

Jose Luis Vicente Villardon

See Also

CCA

Examples

```
##---- Should be DIRECTLY executable !! ----
```

`SeparateVarTypes` *Separation of different types of variables into a list*

Description

The procedure creates a list in which each field contains the variables of the same type.

Usage

```
SeparateVarTypes(X, TypeVar = NULL, TypeFit = NULL)
```

Arguments

`X`	A data frame
`TypeVar`	A vector of characters defining the type of each variable. If not provided the procedure tries to gess the type of each variable. See details for types
`TypeFit`	A vector of characters defining the type of fit for each variable. If not provided the procedure tries to gess the type of fit for each variable. See details for types

Details

The procedure creates a list in which each field contains the variables of the same type. The type of Variable can be specified in a vector TypeVar and the type of fit in a vector TypeFit. The TypeVar is a vector of characters with as many components as variables with types coded as:

"c" - Continuous (1)

"b" - Binary (2)

"n" - Nominal (3)

"o" - Ordinal (4)

"f" - Frequency (5)

"a" - Abundance (5)

Numbers rhather than characters can also be used. Unless specified in TypeVar, numerical variables are "Continuous", factors are "Nominal", ordered factors are "Ordinal". Factors with just two values are considered as "Binary". "Frequencies" and "abundances" should be specified by the user. If Typevar has length 1, all the variables are supposed to have the same type.

The typeFit is a vector of characters containing the type of fit used for each variable, coded as:

"a" - Average (1)

"wa" - Weighted Average (2)

"r" - Regression (Linear or logistic depending on the type of variable) (3)

"g" - Gaussian (Equal tolerances) (4)

"g1" - Gaussian (Different tolerances) (5)

Numbers rhather than characters can also be used. Unless specified numerical variables are fitted with linear regression, factors with logistic biplots, frequencies with weighted averages and abundances with gaussian regression.

Value

A list containing the following fields

`Continuous`	A list containing a data frame with the numeric variables and a character vector with the type of fit for each variable
`Binary`	A list containing a data frame with the binary variables and a character vector with the type of fit for each variable
`Nominal`	A list containing a data frame with the nominal variables and a character vector with the type of fit for each variable
`Ordinal`	A list containing a data frame with the ordinal variables and a character vector with the type of fit for each variable
`Frequency`	A list containing a data frame with the frequency variables and a character vector with the type of fit for each variable
`Abundance`	A list containing a data frame with the abundance variables and a character vector with the type of fit for each variable

Author(s)

Jose Luis Vicente Villardon

Examples

```
# Not yet
```

`SimpleProcrustes` *Simple Procrustes Analysis*

Description

Simple Procrustes Analysis for two matrices

Usage

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

Arguments

`X`	Matrix of the first configuration.
`Y`	Matrix of the second configuration.
`centre`	Should the matrices be centred 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 expained variance
`correlations`	Correlations among the columns of X and Z

Author(s)

Jose Luis Vicente-Villardon

References

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

See Also

PrincipalCoordinates

Examples

```
data(spiders)
```

SMACOF *SMACOF*

Description

SMACOF algorithm for symmetric proximity matrices

Usage

```
SMACOF(P, X = NULL, W = NULL,
Model = c("Identity", "Ratio", "Interval", "Ordinal"),
dimsol = 2, maxiter = 100, maxerror = 1e-06,
StandardizeDisparities = TRUE, ShowIter = FALSE)
```

Arguments

P	A matrix of proximities
X	Inial configuration
W	A matrix of weights~
Model	MDS model.
dimsol	Dimension of the solution
maxiter	Maximum number of iterations of the algorithm
maxerror	Tolerance for convergence of the algorithm
StandardizeDisparities	Should the disparities be standardized
ShowIter	Show the iteration proccess

Details

SMACOF performs multidimensional scaling of proximity data to find a least- squares representation of the objects in a low-dimensional space. A majorization algorithm guarantees monotone convergence for optionally transformed, metric and nonmetric data under a variety of models.

Value

An object of class Principal.Coordinates and MDS. The function adds the information of the MDS to the object of class proximities. Together with the information about the proximities the object has:

Analysis	The type of analysis performed, "MDS" in this case
X	Coordinates for the objects
D	Distances
Dh	Disparities
stress	Raw Stress
stress1	stress formula 1
stress2	stress formula 2
sstress1	sstress formula 1
sstress2	sstress formula 2
rsq	Squared correlation between disparities and distances
rho	Spearman correlation between disparities and distances
tau	Kendall correlation between disparities and distances

Author(s)

Jose Luis Vicente-Villardon

References

Commandeur, J. J. F. and Heiser, W. J. (1993). Mathematical derivations in the proximity scaling (PROXSCAL) of symmetric data matrices (Tech. Rep. No. RR- 93-03). Leiden, The Netherlands: Department of Data Theory, Leiden University.

Kruskal, J. B. (1964). Nonmetric multidimensional scaling: A numerical method. Psychometrika, 29, 28-42.

De Leeuw, J. & Mair, P. (2009). Multidimensional scaling using majorization: The R package smacof. Journal of Statistical Software, 31(3), 1-30, http://www.jstatsoft.org/v31/i03/

Borg, I., & Groenen, P. J. F. (2005). Modern Multidimensional Scaling (2nd ed.). Springer.

Borg, I., Groenen, P. J. F., & Mair, P. (2013). Applied Multidimensional Scaling. Springer.

Groenen, P. J. F., Heiser, W. J. and Meulman, J. J. (1999). Global optimization in least squares multidimensional scaling by distance smoothing. Journal of Classification, 16, 225-254.

Groenen, P. J. F., van Os, B. and Meulman, J. J. (2000). Optimal scaling by alternating length-constained nonnegative least squares, with application to distance-based analysis. Psychometrika, 65, 511-524.

See Also

MDS, PrincipalCoordinates

Examples

```
data(spiders)
Dis=BinaryProximities(spiders)
MDSSol=SMACOF(Dis$Proximities)
```

---

smoking *Smoking habits*

Description

Frequency table representing smoking habits of different employees in a company

Usage

```
data(smoking)
```

Format

A data frame with 5 observations on the following 4 variables.

`None` a numeric vector

`Light` a numeric vector

`Medium` a numeric vector

`Heavy` a numeric vector

Details

Frequency table representing smoking habits of different employees in a company

Source

http://orange.biolab.si/docs/latest/reference/rst/Orange.projection.correspondence/

References

Greenacre, Michael (1983). Theory and Applications of Correspondence Analysis. London: Academic Press.

Examples

```
data(smoking)
## maybe str(smoking) ; plot(smoking) ...
```

`Sparse.NIPALSPCA` *Sparse version of the NIPALS algorithm for PCA.*

Description

Sparse version of the NIPALS algorithm for PCA.

Usage

```
Sparse.NIPALSPCA(X, dimens = 2, tol = 1e-06, maxiter = 1000, lambda = 0.02)
```

Arguments

`X`	The data matrix.
`dimens`	The dimension of the solution
`tol`	Tolerance of the algorithm.
`maxiter`	Maximum number of iteratios.
`lambda`	Value used for sparsity

Details

Sparse version of the NIPALS algorithm for the singular value decomposition that allows for the construction of PCA and Biplot.

Value

The singular value decomposition

`u`	The coordinates of the rows (standardized)
`d`	The singuklar values
`v`	The coordinates of the columns (standardized)

Author(s)

Jose Luis Vicente Villardon

References

Have to be written

Examples

```
# Not yet
```

`spiders` *Hunting Spiders Data*

Description

Hunting spiders data transformed into Presence/Abscense.

Usage

```
data(spiders)
```

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 (Lycos- idae, Ctenidae) and environmental characteristics in a dune area. Netherlands Journal of Zoology 25, 1-45.

Examples

```
data(spiders)
```

SpidersEnv — *Hunting spiders environmental data.*

Description

Hunting spiders environmental data.

Usage

```
data("SpidersEnv")
```

Format

A data frame with 28 observations on the following 6 variables.

`Watcont` Water content

`Barsand` Bare sand

`Covmoss` Cover moss

`Ligrefl` Light reflection

`Falltwi` Fallen Twings

`Coverher` Cover Herbs

Details

Hunting spiders environmental data.

Source

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

References

Ter Braak, C. J. (1986). Canonical correspondence analysis: a new eigenvector technique for multivariate direct gradient analysis. Ecology, 67(5), 1167-1179.

Examples

```
data(SpidersEnv)
## maybe str(SpidersEnv) ; plot(SpidersEnv) ...
```

SpidersSp *Hunting Spiders Data*

Description

Hunting spiders abundances data.

Usage

```
data("SpidersSp")
```

Format

A data frame with 28 observations of abundance of 12 hunting spider species

Alopacce Abundance of the species Alopecosa accentuata

Alopcune Abundance of the species Alopecosa cuneata

Alopfabr Abundance of the species Alopecosa fabrilis

Arctlute Abundance of the species Arctosa lutetiana

Arctperi Abundance of the species Arctosa perita

Auloalbi Abundance of the species Aulonia albimana

Pardlugu Abundance of the species Pardosa lugubris

Pardmont Abundance of the species Pardosa monticola

Pardnigr Abundance of the species Pardosa nigriceps

Pardpull Abundance of the species Pardosa pullata

Trocterr Abundance of the species Trochosa terricola

Zoraspin Abundance of the species Zora spinimana

Source

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

References

Ter Braak, C. J. (1986). Canonical correspondence analysis: a new eigenvector technique for multivariate direct gradient analysis. Ecology, 67(5), 1167-1179.

Examples

```
data(SpidersSp)
## maybe str(SpidersSp) ; plot(SpidersSp) ...
```

SSI *Sustainability Society Index*

Description

Sustainability Society Index

Usage

```
data("SSI")
```

Format

A data frame with 924 observations on the following 23 variables.

Year a factor with levels a2006 a2008 a2010 a2012 a2014 a2016

Country a factor with levels Albania Algeria Angola Argentina Armenia Australia Austria Azerbaijan Bangladesh Belarus Belgium Benin Bhutan Bolivia Bosnia-Herzegovina Botswana Brazil Bulgaria Burkina_Faso Burundi Cambodia Cameroon Canada Central_African_Republic Chad Chile China Colombia Congo Congo_Democratic_Rep. Costa_Rica Cote_dIvoire Croatia Cuba Cyprus Czech_Republic Denmark Dominican_Republic Ecuador Egypt El_Salvador Estonia Ethiopia Finland France Gabon Gambia Georgia Germany Ghana Greece Guatemala Guinea Guinea-Bissau Guyana Haiti Honduras Hungary Iceland India Indonesia Iran Iraq Ireland Israel Italy Jamaica Japan Jordan Kazakhstan Kenya Korea._North Korea._South Kuwait Kyrgyz_Republic Laos Latvia Lebanon Lesotho Liberia Libya Lithuania Luxembourg Macedonia Madagascar Malawi Malaysia Mali Malta Mauritania Mauritius Mexico Moldova Mongolia Montenegro Morocco Mozambique Myanmar Namibia Nepal Netherlands New_Zealand Nicaragua Niger Nigeria Norway Oman Pakistan Panama Papua_New_Guinea Paraguay Peru Philippines Poland Portugal Qatar Romania Russia Rwanda Saudi_Arabia Senegal Serbia Sierra_Leone Singapore Slovak_Republic Slovenia South_Africa Spain Sri_Lanka Sudan Sweden Switzerland Syria Taiwan Tajikistan Tanzania Thailand Togo Trinidad_and_Tobago Tunisia Turkey Turkmenistan Uganda Ukraine United_Arab_Emirates United_Kingdom United_States Uruguay Uzbekistan Venezuela Vietnam Yemen Zambia Zimbabwe

Sufficient_Food a numeric vector

Sufficient_to_Drink a numeric vector

Safe_Sanitation a numeric vector

Education_ a numeric vector

Healthy_Life a numeric vector

Gender_Equality a numeric vector

Income_Distribution a numeric vector

Population_Growth a numeric vector

Good_Governance a numeric vector

Biodiversity_ a numeric vector

`Renewable_Water_Resources` a numeric vector

`Consumption` a numeric vector

`Energy_Use` a numeric vector

`Energy_Savings` a numeric vector

`Greenhouse_Gases` a numeric vector

`Renewable_Energy` a numeric vector

`Organic_Farming` a numeric vector

`Genuine_Savings` a numeric vector

`GDP` a numeric vector

`Employment` a numeric vector

`Public_Debt` a numeric vector

Details

Sustainability Society Index

Source

https://ssi.wi.th-koeln.de

References

Gallego-Alvarez, I., Galindo-Villardon, M. P., & Rodriguez-Rosa, M. (2015). Analysis of the Sustainable Society Index Worldwide: A Study from the Biplot Perspective. Social Indicators Research, 120(1), 29-65. https://doi.org/10.1007/s11205-014-0579-9

Examples

```
data(SSI)
## maybe str(SSI) ; plot(SSI) ...
```

`SSI3w` *Sustainability Society Index (3w)*

Description

Sustainability Society Index, Three way table

Usage

```
data("SSI3w")
```

Format

The format is: List of 6 $ a2006: num [1:154, 1:21] 10 9.3 6.6 10 8.9 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:21] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2008: num [1:154, 1:21] 10 9.4 7.1 10 9.3 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:21] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2010: num [1:154, 1:21] 10 9.4 7.7 10 9.4 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:21] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2012: num [1:154, 1:21] 10 10 8.1 10 9.3 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:21] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2014: num [1:154, 1:21] 10 10 8.4 10 9.3 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:21] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2016: num [1:154, 1:21] 10 10 8.6 10 9.4 10 10 10 8.4 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:21] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ...

Details

Sustainability Society Index

Source

https://ssi.wi.th-koeln.de

References

Gallego-Alvarez, I., Galindo-Villardon, M. P., & Rodriguez-Rosa, M. (2015). Analysis of the Sustainable Society Index Worldwide: A Study from the Biplot Perspective. Social Indicators Research, 120(1), 29-65. https://doi.org/10.1007/s11205-014-0579-9

Examples

```
data(SSI3w)
## maybe str(SSI3w) ; plot(SSI3w) ...
```

SSIEcon3w *Sustainability Society Index*

Description

Sustainability Society Index

Usage

```
data("SSIEcon3w")
```

Format

The format is: List of 6 $ a2006: num [1:154, 1:5] 1.2 1 1 4.6 1 5.4 9.9 1.9 1 1 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:5] "Organic_Farming" "Genuine_Savings" "GDP" "Employment" ... $ a2008: num [1:154, 1:5] 1 1 1 4.2 1 5.6 9.9 1.9 1 1 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:5] "Organic_Farming" "Genuine_Savings" "GDP" "Employment" ... $ a2010: num [1:154, 1:5] 1.1 1 1 5.8 1.1 5.6 9.9 2 1 1 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:5] "Organic_Farming" "Genuine_Savings" "GDP" "Employment" ... $ a2012: num [1:154, 1:5] 1.1 1 1 5.7 1.1 5.7 9.9 2 1 1 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:5] "Organic_Farming" "Genuine_Savings" "GDP" "Employment" ... $ a2014: num [1:154, 1:5] 1.1 1 1 5.3 1.1 5.7 9.9 2.1 1.2 1 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:5] "Organic_Farming" "Genuine_Savings" "GDP" "Employment" ... $ a2016: num [1:154, 1:5] 1.1 1 1 4.8 1.1 6.8 9.9 2 1.2 1 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:5] "Organic_Farming" "Genuine_Savings" "GDP" "Employment" ...

Details

Sustainability Society Index

Source

https://ssi.wi.th-koeln.de

References

Gallego-Alvarez, I., Galindo-Villardon, M. P., & Rodriguez-Rosa, M. (2015). Analysis of the Sustainable Society Index Worldwide: A Study from the Biplot Perspective. Social Indicators Research, 120(1), 29-65. https://doi.org/10.1007/s11205-014-0579-9

Examples

```
data(SSIEcon3w)
## maybe str(SSIEcon3w) ; plot(SSIEcon3w) ...
```

`SSIEnvir3w` *Sustainability Society Index*

Description

Sustainability Society Index

Usage

```
data("SSIEnvir3w")
```

Format

The format is: List of 6 $ a2006: num [1:154, 1:7] 4.2 6.5 4 4.9 7.7 5.7 8.1 4.9 2.8 6.3 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:7] "Biodiversity_" "Renewable_Water_Resources" "Consumption" "Energy_Use" ... $ a2008: num [1:154, 1:7] 4.8 6.5 4 5.1 7.7 5.7 8 5.7 2.8 6 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:7] "Biodiversity_" "Renewable_Water_Resources" "Consumption" "Energy_Use" ... $ a2010: num [1:154, 1:7] 5.4 6.6 4 5.2 7.7 5.7 8 6.4 2.8 5.8 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:7] "Biodiversity_" "Renewable_Water_Resources" "Consumption" "Energy_Use" ... $ a2012: num [1:154, 1:7] 5.3 6.6 4 5.3 7.7 6.1 8 6.8 2.8 5.8 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:7] "Biodiversity_" "Renewable_Water_Resources" "Consumption" "Energy_Use" ... $ a2014: num [1:154, 1:7] 5.6 6.6 4 5.3 7.7 7 7.9 7.3 2.8 6 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:7] "Biodiversity_" "Renewable_Water_Resources" "Consumption" "Energy_Use" ... $ a2016: num [1:154, 1:7] 5.5 6.6 4.1 5.4 7.8 7.3 7.9 7.3 2.9 5.9 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:7] "Biodiversity_" "Renewable_Water_Resources" "Consumption" "Energy_Use" ...

Details

Sustainability Society Index

Source

https://ssi.wi.th-koeln.de

References

Gallego-Alvarez, I., Galindo-Villardon, M. P., & Rodriguez-Rosa, M. (2015). Analysis of the Sustainable Society Index Worldwide: A Study from the Biplot Perspective. Social Indicators Research, 120(1), 29-65. https://doi.org/10.1007/s11205-014-0579-9

Examples

```
data(SSIEnvir3w)
## maybe str(SSIEnvir3w) ; plot(SSIEnvir3w) ...
```

`SSIHuman3w` *Sustainability Society Index*

Description

Sustainability Society Index

Usage

```
data("SSIHuman3w")
```

Format

The format is: List of 6 $ a2006: num [1:154, 1:9] 10 9.3 6.6 10 8.9 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:9] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2008: num [1:154, 1:9] 10 9.4 7.1 10 9.3 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:9] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2010: num [1:154, 1:9] 10 9.4 7.7 10 9.4 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:9] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2012: num [1:154, 1:9] 10 10 8.1 10 9.3 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:9] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2014: num [1:154, 1:9] 10 10 8.4 10 9.3 10 10 10 8.3 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:9] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ... $ a2016: num [1:154, 1:9] 10 10 8.6 10 9.4 10 10 10 8.4 10 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:154] "Albania" "Algeria" "Angola" "Argentina" ... .$: chr [1:9] "Sufficient_Food" "Sufficient_to_Drink" "Safe_Sanitation" "Education_" ...

Details

Sustainability Society Index

Source

https://ssi.wi.th-koeln.de

References

Gallego-Alvarez, I., Galindo-Villardon, M. P., & Rodriguez-Rosa, M. (2015). Analysis of the Sustainable Society Index Worldwide: A Study from the Biplot Perspective. Social Indicators Research, 120(1), 29-65. https://doi.org/10.1007/s11205-014-0579-9

Examples

```
data(SSIHuman3w)
## maybe str(SSIHuman3w) ; plot(SSIHuman3w) ...
```

`StatisBiplot` *STATIS-ACT for multiple tables with common rows and its associated Biplot*

Description

The procedure performs STATIS-ACT methodology for multiple tables with common rows and its associated biplot

Usage

```
StatisBiplot(X, InitTransform = "Standardize columns", dimens = 2,
                SameVar = FALSE)
```

Arguments

`X`	A list containing multiple tables with common rows.
`InitTransform`	Initial transformation of the data matrices
`dimens`	Dimension of the final solution
`SameVar`	Are the variables the same for all occasions? If so, Biplot trajectories for each variable will be calculated.

Details

The procedure performs STATIS-ACT methodology for multiple tables with common rows and its associated biplot. When the variables are the same for all occasions trajectories for the variables can also be plotted. Basic plotting includes the consensus individuals and all the variables. Traditional trajectories for individuals and biplot trajectories for variables (when adequate) are optional. The original matrix will be provided as a list each cell of the list is the data matrix for one ocassion the number of rows for each occasion must be the same

Value

An object of class StatisBiplot

Author(s)

Jose Luis Vicente Villardon

References

Abdi, H., Williams, L.J., Valentin, D., & Bennani-Dosse, M. (2012). STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat, 4, 124-167.

Efron, B.,Tibshirani, RJ. (1993). An introduction to the bootstrap. New York: Chapman and Hall. 436p.

Escoufier, Y. (1976). Operateur associe a un tableau de donnees. Annales de laInsee, 22-23, 165-178.

Escoufier, Y. (1987). The duality diagram: a means for better practical applications. En P. Legendre & L. Legendre (Eds.), Developments in Numerical Ecology, pp. 139-156, NATO Advanced Institute, Serie G. Berlin: Springer.

L'Hermier des Plantes, H. (1976). Structuration des Tableaux a Trois Indices de la Statistique. [These de Troisieme Cycle]. University of Montpellier, France.

Ringrose, T.J. (1992). Bootstrapping and Correspondence Analysis in Archaeology. Journal of Archaeological. Science.19:615-629.

Examples

```
data(Chemical)
# Extract continous data from the original data frame.
x= Chemical[,5:16]
# Obtaining the three way table as a list
X=Convert2ThreeWay(x,Chemical$WEEKS, columns=FALSE)
# Calculating the Biplot associated to STATIS-ACT
stbip=StatisBiplot(X, SameVar=TRUE)
# Basic plot of the results
plot(stbip)
# Colors By Table
plot(stbip, VarColorType="ByTable")
# Colors By Variable
plot(stbip, VarColorType="ByVar", mode="s",  MinQualityVars = 0.5)

plot(stbip, PlotRowTraj = TRUE, PlotVars=FALSE, RowColors=1:36)
```

`summary.Canonical.Biplot` *Summary of the solution of a Canonical Biplot Analysis*

Description

Summary of the solution of a Canonical Biplot Analysis

Usage

```
## S3 method for class 'Canonical.Biplot'
summary(object, ...)
```

Arguments

`object`	The result of a Canonical Biplot
`...`	Aditional arguments

Details

Summary of the results of a Canonical Biplot

Value

The summary

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

`summary.CCA.sol` *Summary of the solution of a CCA*

Description

Summary of the solution of a CCA

Usage

```
## S3 method for class 'CCA.sol'
summary(object, ...)
```

Arguments

`object`	An object of class CCA.sol
`...`	Aditional arguments

Details

Summary of the solution of a CCA

Value

The main results of a CCA

Author(s)

Jose Luis Vicente Villardon

See Also

CCA

Examples

```
##---- Should be DIRECTLY executable !! ----
```

`summary.ContinuousBiplot` *Summary of the solution of a Biplot for Continuous Data*

Description

Summary of the solution of a Biplot for Continuous Data

Usage

```
## S3 method for class 'ContinuousBiplot'
summary(object, latex = FALSE, ...)
```

Arguments

`object`	An object of class "ContinuousBiplot"
`latex`	Should the results be in latex tables
`...`	Any aditional parameters

Details

Summary of the solution of a Biplot for Continuous Data

Value

The summary

Author(s)

Jose Luis Vicente Villardon

Examples

```
## Simple Biplot with arrows
data(Protein)
bip=PCA.Biplot(Protein[,3:11])
summary(bip)
```

summary.CVA *Summary of a Canonical Variate Analysis*

Description

Summary of a Canonical Variate Analysis

Usage

```
## S3 method for class 'CVA'
summary(object, ...)
```

Arguments

object	An object of class CVA
...	Any aditional arguments

Details

Summary of a Canonical Variate Analysis

Value

The summary

Author(s)

Jose Luis Vicente Villardon

Examples

```
# Not yet
```

summary.MGC *Summary of Model-Based Gaussian Clustering results*

Description

Summarizes the results of Model-Based Gaussian Clustering algorithms

Usage

```
## S3 method for class 'MGC'
summary(object, Centers = TRUE, Covariances = TRUE, ...)
```

Arguments

`object`	An object of class "MGC"
`Centers`	Should the Centers be shown
`Covariances`	Should the Covariances be shown
`...`	Any aditional Parameters

Details

Summarizes the results of Model-Based Gaussian Clustering algorithms

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
```

---

summary.PCA.Analysis   *Summary of the results of a PCA.*

Description

Sumarizes the results of a PCA Analysis.

Usage

```
## S3 method for class 'PCA.Analysis'
summary(object, latex = FALSE, ...)
```

Arguments

`object`	The object with the results of s PCA Analysis.
`latex`	Should return latex tables?
`...`	Aditional arguments.

Details

Sumarizes the results of a PCA Analysis, including latex tables for presentation.

Value

A summary of the main results

Author(s)

Jose Luis Vicente Villardon

Examples

```
# Not yet
```

---

summary.PCA.Bootstrap *Summary of a PCA.Bootstrap object*

Description

Summary of a PCA.Bootstrap object

Usage

```
## S3 method for class 'PCA.Bootstrap'
summary(object, ...)
```

Arguments

object	An object of class PCA.Bootstrap
...	Additional arguments

Details

Summary of a PCA.Bootstrap object

Value

The summary

Author(s)

Jose Luis Vicente Villardon

`summary.PLSR` *Summary of a PLSR object*

Description

Summary of a PLSR object

Usage

```
## S3 method for class 'PLSR'
summary(object, ...)
```

Arguments

`object`	An object of class PLSR
`...`	Additional arguments

Details

Summary of a PLSR object

Value

The summary of the object

Author(s)

Jose Luis Vicente Villardon

`summary.PLSR1Bin` *Summary of PLSR with a Binary Response*

Description

Summary of PLSR with a single binary Response

Usage

```
## S3 method for class 'PLSR1Bin'
summary(object, ...)
```

Arguments

`object`	An object of class PLSR1Bin
`...`	Aditional arguments

Details

Summary of PLSR with a single binary Response

Value

The summary

Author(s)

Jose Luis Viecente Villardon

Examples

```
#Not yet
```

`summary.Principal.Coordinates`
Summary of the results of a Principal Coordinates Analysis

Description

Summary of the results of a Principal Coordinates Analysis

Usage

```
## S3 method for class 'Principal.Coordinates'
summary(object, printdata=FALSE, printproximities=FALSE,
printcoordinates=FALSE, printqualities=FALSE,...)
```

Arguments

`object`	An object of Type `Principal.Coordinates`
`printdata`	Should original data be printed. Default is FALSE
`printproximities`	Should proximities be printed. Default is FALSE
`printcoordinates`	Should proximities be printed. Default is FALSE
`printqualities`	Should qualoties of representation be printed. Default is FALSE
`...`	Additional parameters to summary.

Details

This function is a method for the generic function summary() for class "Principal.Coordinates". It can be invoked by calling summary(x) for an object x of the appropriate class.

Value

The summary

Author(s)

Jose Luis Vicente-Villardon

Examples

```
data(spiders)
dist=BinaryProximities(spiders)
pco=PrincipalCoordinates(dist)
summary(pco)
```

`summary.RidgeBinaryLogistic`
Summary of a Binary Logistic Regression with Ridge Penalization

---

Description

Summarizes the results of a Binary Logistic Regression with Ridge Penalization

Usage

```
## S3 method for class 'RidgeBinaryLogistic'
summary(object, ...)
```

Arguments

`object`	The object with te results of the logistic regression.
`...`	Any other arguments

Details

Summarizes the results of a Binary Logistic Regression with Ridge Penalization.

Value

The summary

Author(s)

Jose Luis Vicente Villardon

Examples

```
# Not Yet
```

`summary.TetraDualStatis` *Summary of the results of TetraDualStatis*

Description

Summary of the results of TetraDualStatis

Usage

```
## S3 method for class 'TetraDualStatis'
summary(object, ...)
```

Arguments

`object`	The result of a Tetra Dual Statis Analysis
`...`	aditional arguments

Details

Summarizes the results of TetradUalStatis

Value

No value returned

Author(s)

Laura Vicente-Gonzalez, José Luis Vicente-Villardon

Examples

```
# No examples yet
```

`t3pcovr` *Tucker 3 Principal Covariates Regression*

Description

Tucker 3 Principal Covariates Regression

Usage

```
t3pcovr(X, Y, I, J, K, L, r1 = 2, r2 = 2, r3 = 2,
       conv = 1e-06, OriginalAlfa = 0.5, AlternativeLossF = 1,
       nRuns = 100, StartSeed = 0)
```

Arguments

`X`	A two way data matrix with the predictors.
`Y`	A three way data matrix with the responses.
`I`	Number of elements of first mode of 3D/2D (the common mode: rows)
`J`	number of elements of second mode of 3D (columns 3D)
`K`	number of elements of third mode of 3D (slabs)
`L`	number of elements of second mode of 2D (columns 2D)
`r1`	Number of extracted components for the A-mode
`r2`	Number of extracted components for the B-mode
`r3`	Number of extracted components for the C-mode
`conv`	value for convergence (tolerance value)
`OriginalAlfa`	(0-1): importance that degree reduction and prediction have in the analysis
`AlternativeLossF`	Using the alternative loss function? 0 = no (use original loss function: weighted SSQ; weighted met alfa) 1 = yes (use weighted loss function with scaled SSQ: scaled by the SSQ in X and y)
`nRuns`	Number of runs
`StartSeed`	Seed for the analysis

Details

In behavioral research it is very common to have to deal with several data sets which include information relative to the same set of individuals, in such a way that one data set tries to explain the others. The class of models known as PCovR focuses on the analysis of a three-way data array explained by a two-way data matrix. In this paper the Tucker3-PCovR model is proposed that is a particular case of PCovR class. Tucker3-PCovR model reduces the predictors to a few components and predict the criterion by using these components and, at the same time, the three way data is fitted through the Tucker3 model. Both, the reduction of the predictors and the prediction of the criterion are done simultaneously. An alternating least squares algorithm to estimate the Tucker3-PCovR model is proposed. A biplot representation to facilitate the interpretation of the results is presented. A couple of applications are made to coupled empirical data sets related to the field of psychology.

Value

`A`	Component matrix for the A-mode)
`B1`	Component matrix for the B-mode
`C`	Component matrix for the C-mode
`H`	Matrized core array (frontal slices)
`B2`	Loading matrix of components (components x predictors)
`...`	Further arguments

Author(s)

Elisa Frutos Bernal (<efb@usal.es>)

References

De Jong, S., & Kiers, H. A. (1992). Principal covariates regression: Part I. Theory. Chemometrics and Intelligent Laboratory Systems , 155-164.

Marlies Vervloet, Henk A. Kiers, Wim Van den Noortgate, Eva Ceulemans (2015). PCovR: An R Package for Principal Covariates Regression. Journal of Statistical Software, 65(8), 1-14. URL http://www.jstatsoft.org/v65/i08/.

Smilde, A. K., Bro, R., & Geladi, P. (2004). Multi-way analysis with applications in the chemical sciences. Chichester, UK: Wiley.

Examples

```
#Not yet
```

`TetraDualStatis` *Dual STATIS-ACT for binary data based on Tetrachoric Correlations*

Description

Dual STATIS-ACT for binary data based on Tetrachoric Correlations

Usage

```
TetraDualStatis(X, dimens = 2, SameInd = FALSE, RotVarimax = FALSE,
                OptimMethod = "L-BFGS-B", penalization = 0.01)
```

Arguments

`X`	A three way binary data matrix
`dimens`	Dimension of the solution
`SameInd`	Are the individuals the same in all occassions?
`RotVarimax`	Should the solution be rotated?
`OptimMethod`	Optimization method for the gradients
`penalization`	Penalization for the ridge solution

Details

The general aim of STATIS-ACT methods is to extract information common to a set of datasets with the same individuals. They will also be represented as a Euclidean configuration or map of points (or vectors), in the same way as in Principal Component Analysis (PCA) or Principal Coordinate Analysis (PCoA). If the object is to analyze the variables and the correlation structures between them we will use a Factor Analysis (FA). When we have tables in which we measure a set of common variables and we want to obtain a consensus structure of all of them, we will use the named STATIS-Dual.

The method was initially designed to work with individuals common to all the tables, but in this work, we will focus on the dual version, which works with variables common to all of them.

When we have several tables of binary dataset, the classical methods for continuous data are not suitable. If the individuals are the same in all tables, we can use a STATIS based on distances, also known as DISTATIS. El procedimiento consiste en calcular una matriz de distancias a partir de para un coeficiente de similaridad para datos binarios. Las distancias se convierten en productos escalares, como en ACoP, y se trabaja a partir de ellos como en el STATIS tradicional.

When we have common variables, and we are interested in the association between them, we could use a coefficient that, instead of similarity, shows the association between the variables. In this work we propose the use of the tetrachoric correlation matrix for each table and develop the necessary adaptations to the method.

Value

An object with the results

Author(s)

Laura Vicente-Gonzalez, José Luis Vicente-Villardon

Examples

```
# Not yet
```

`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, ColorPoints, ...)
```

Arguments

`A`	Coordinates of the points for the scaterrgram
`Labels`	Labels for the points
`CexPoints`	Size of the labels
`ColorPoints`	Colors of the labels
`...`	Aditional graphical arguments

Details

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

Value

No value returned

Author(s)

Jose Luis Vicente-Villardon

See Also

`plot.Principal.Coordinates`

Examples

```
data(spiders)
dist=BinaryProximities(spiders)
pco=PrincipalCoordinates(dist)
plot(pco, SmartLabels =TRUE)
```

`Three2TwoWay` *Converts a multitable list to a two way matrix*

Description

Takes a multitable list of matrices X and converts it to a two way matrix with the structure required by the Statis programs using a _ to separate variable and occassion or study.

Usage

```
Three2TwoWay(X, whatlines = 2)
```

Arguments

`X`	The multitable list.
`whatlines`	Concatenate the rows (1) or the columns (2)

Details

Takes a multitable list of matrices X and converts it to a two way matrix with the structure required by the Statis programs using a _ to separate variable and occassion or study. When whatlines is 1 the final matrix adds the rows of the three dimensional array, then the columns must be the same for all studies. When whatlines is 2 the columns are concatenated and then the number of rows must be the same for all studies.

Value

A two way matrix

`x`	A two way matrix

Author(s)

Jose Luis Vicente Villardon

Examples

```
# No examples yet
```

`ThreeWay2FrontalSlices` *Three to two way data*

Description

Three to two way data.

Usage

```
ThreeWay2FrontalSlices(X, Slice = 1)
```

Arguments

`X`	A three way array.
`Slice`	The mode for the rows

Details

Three to two way data. The provided mode is placen on the rows. The columns are the result of intercatively coding the other two modes.

Value

A two way matrix.

Author(s)

José Luis Vicente- Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

TransformIni *Initial transformation of a data matrix*

Description

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

Usage

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

Arguments

`X`	Original Raw Data Matrix
`InitTransform`	Initial transform of the data (usually logarithm)
`transform`	Transformation to use. See details.

Details

Possible Transformations are:

1.- "Raw Data": When no transformation is required.

2.- "Substract the global mean": Eliminate an eefect 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 beetwen 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 Villardon

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=TransformIni(x, transform=4)
x
```

`Truncated.NIPALSPCA` *Truncated version of the NIPALS algorithm for PCA.*

Description

Truncated version of the NIPALS algorithm for PCA.

Usage

```
Truncated.NIPALSPCA(X, dimens = 2, tol = 1e-06, maxiter = 1000, lambda = 0.02)
```

Arguments

`X`	The data matrix.
`dimens`	The dimension of the solution
`tol`	Tolerance of the algorithm.
`maxiter`	Maximum number of iteratios.
`lambda`	Value used for truncation

Details

Classical NIPALS algorithm for the singular value decomposition that allows for the construction of PCA and Biplot.

Value

The singular value decomposition

u	The coordinates of the rows (standardized)
d	The singuklar values
v	The coordinates of the columns (standardized)

Author(s)

Jose Luis Vicente Villardon

References

Have to be written

See Also

NIPALS.Biplot

Examples

```
# Not yet
```

Unfolding *Multidimensional Unfolding*

Description

Multidimensional Unfolding with some adaptations for vegetation analysis

Usage

```
Unfolding(A, ENV = NULL, TransAbund = "Gaussian Columns", offset = 0.5,
weight = "All_1", Constrained = FALSE,
TransEnv = "Standardize columns",
InitConfig = "SVD", model = "Ratio",
condition = "Columns", Algorithm = "SMACOF",
OptimMethod = "CG", r = 2, maxiter = 100,
tolerance = 1e-05, lambda = 1, omega = 0, plot = FALSE)
```

Arguments

`A`	The original proximities matrix
`ENV`	The matrix of environmental variables
`TransAbund`	Initial transformation of the abundances : "None", "Gaussian", "Column Percent", "Gaussian Columns", "Inverse Square Root", "Divide by Column Maximum")
`offset`	offset is the quantity added to the zeros of the table
`weight`	A matrix of weights for each cell of the table
`Constrained`	Should fit a constrained analysis
`TransEnv`	Transformation of the environmental variables
`InitConfig`	Init configuration for the algorithm
`model`	Type of model to be fitted: "Identity", "Ratio", "Interval" or "Ordinal".
`condition`	"Matrix", "Columns" to condition to the whole matrix or to each column
`Algorithm`	Algorithm to fit the model: "SMACOF", "GD", "Genefold"
`OptimMethod`	Optimization method for gradient descent
`r`	Dimension of the solution
`maxiter`	Maximum number of iterations in the algorithm
`tolerance`	Tolerace for the algorithm
`lambda`	First penalization parameter
`omega`	Second penalization parameter
`plot`	Should the results be plotted?

Details

ological data

Value

An object of class "Unfolding"

Author(s)

Jose Luis Vicente Villardon

References

Ver Articulos

Examples

```
unf=Unfolding(SpidersSp, ENV=SpidersEnv, model="Ratio", Constrained = FALSE, condition="Matrix")
plot(unf, PlotTol=TRUE, PlotEnv = FALSE)
plot(unf, PlotTol=TRUE, PlotEnv = TRUE)
cbind(unf$QualityVars, unf$Var_Fit)
unf2=Unfolding(SpidersSp, ENV=SpidersEnv, model="Ratio", Constrained = TRUE, condition="Matrix")
plot(unf2, PlotTol=FALSE, PlotEnv = TRUE, mode="s")
cbind(unf2$QualityVars, unf2$Var_Fit)
```

VarBiplot *Draws a variable on a biplot*

Description

Draws a continuous variable on a biplot

Usage

```
VarBiplot(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 = 0.04, ts = "Complete",
                 Position = "Angle", AddArrow=FALSE, CexScale=0.8, ...)
```

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 gradedv 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.
`CexScale`	Sizes of the scales
`...`	Any other graphical parameters

Details

See plot.PCA.Biplot

Value

No value returned

Author(s)

Jose Luis Vicente Villardon

See Also

`plot.ContinuousBiplot`

Examples

```
data(Protein)
bip=PCA.Biplot(Protein[,3:11])
plot(bip)
```

`wa` *Extracts the weighted averages of a CCA solution*

Description

Extracts the weighted averages of a CCA solution

Usage

```
wa(CCA.sol, transformed = FALSE)
```

Arguments

`CCA.sol`	The solution of a CCA
`transformed`	Average of the transformed or the original data?

Details

Extracts the weighted averages of a CCA solution

Value

A matrix with the averages

Author(s)

icente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

`wcor` *Weighted correlations*

Description

Weighted correlations

Usage

```
wcor(d1, d2, w = rep(1, nrow(d1))/nrow(d1))
```

Arguments

`d1`	First Vector
`d2`	Second vector to correlate
`w`	weights for ecah element of the vectors

Details

Weighted correlations

Value

Weighted correlation

Author(s)

Jose Luis Vicente Villardon

weighted.quantile *Weighted quantiles*

Description

Weighted quantiles

Usage

```
weighted.quantile(x, w, q = 0.5)
```

Arguments

x	The numerical variable.
w	Weights
q	Quantile

Value

The quantile

Author(s)

Jose Luis Vicente Villardon

Examples

```
##---- Should be DIRECTLY executable !! ----
```

WeightedPCoA *Weighted Principal Coordinates Analysis*

Description

Weighted Principal Coordinates Analysis

Usage

```
WeightedPCoA(Proximities,
weigths = matrix(1,dim(Proximities$Proximities)[1],1),
dimension = 2, tolerance=0.0001)
```

Arguments

`Proximities`	A matrix containing the proximities among a set of objetcs
`weigths`	Weigths
`dimension`	Dimension of the solution
`tolerance`	Tolerance for the eigenvalues

Details

Weighted Principal Coordinates Analysis

Value

data(spiders) dist=BinaryProximities(spiders) pco=WeightedPCoA(dist) An object of class `Principal.Coordinates`

Author(s)

Jose Luis Vicente-Villardon

References

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

Gower, J.C. (1966). Some distance properties of latent root and vector methods used in multivariate analysis. Biometrika 53: 325-338.

J.R. Demey, J.L. Vicente-Villardon, M.P. Galindo, A.Y. Zambrano, Identifying molecular markers associated with classifications of genotypes by external logistic biplot, Bioinformatics 24 (2008) 2832.

Cuadras, C. M., Fortiana, J. Metric scaling graphical representation of Categorical Data. Proceedings of Statistics Day, The Center for Multivariate Analysis, Pennsylvania State University, Part 2, pp.1-27, 1995.

See Also

`BinaryProximities`

Examples

```
data(spiders)
dist=BinaryProximities(spiders)
pco=WeightedPCoA(dist)
```

`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-Villardon, 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-Villardon, 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)
## maybe str(wine) ; plot(wine) ...
```

---

zeros — *Matrix of zeros as in Matlab*

Description

Matrix of zeros

Usage

```
zeros(n)
```

Arguments

n	Dimension of the matrix

Value

A matrix of zeros

Author(s)

Jose Luis Vicente Villardon

Examples

```
zeros(6)
```

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