

# Package ‘packMBPLSDA’

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**Type** Package

**Title** Multi-Block Partial Least Squares Discriminant Analysis

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**Description** Several functions are provided to implement a MBPLSDA : components search, optimal model components number search, optimal model validity test by permutation tests, observed values evaluation of optimal model parameters and predicted categories, bootstrap values evaluation of optimal model parameters and predicted cross-validated categories. The use of this package is described in Brandolini-Bunlon et al (2019. Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134).

**License** GPL (>= 2.0)

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**Imports** MASS, parallel, doParallel, foreach, FactoMineR

**NeedsCompilation** no

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packMBPLSDA-package	<i>Multi-Block Partial Least Squares Discriminant Analysis</i>
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## Description

Several functions are provided to implement a MBPLSDA : components search, optimal model components number search, optimal model validity test by permutation tests, observed values evaluation of optimal model parameters and predicted categories, bootstrap values evaluation of optimal model parameters and predicted cross-validated categories. The use of this package is described in Brandolini-Bunlon et al (2019. Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134).

## Details

Index of help topics:

boot_mbplsda	bootstraped simulations for multi-block partial least squares discriminant analysis
cvpred_mbplsda	Cross-validated predicted categories from a multi-block partial least squares discriminant model
disjunctive	Disjunctive table
ginv	generalized inverse of a matrix X
inertie	inertia of a matrix
mbplsda	Multi-block partial least squares discriminant analysis
medical	medical dataset
nutrition	nutritional dataset
omics	metabolomic dataset
packMBPLSDA-package	Multi-Block Partial Least Squares Discriminant Analysis
permut_mbplsda	Permutation testing of a multi-block partial least squares discriminant model
plot_boot_mbplsda	Plot the results of the fonction boot_mbplsda in a pdf file
plot_cvpred_mbplsda	Plot the results of the fonction cvpred_mbplsda

	in a pdf file
plot_permut_mbplsda	Plot the results of the fonction permut_mbplsda in a pdf file
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pred_mbplsda	Observed parameters and predicted categories from a multi-block partial least squares discriminant model
status	physiopathological status data
testdim_mbplsda	Test of number of components by two-fold cross-validation for a multi-block partial least squares discriminant model

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**References**

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at Chimie 2020, Liege, BEL(01-27-2020 - 01-29-2020).

**See Also**

[mbplsda](#) [testdim\\_mbplsda](#) [plot\\_testdim\\_mbplsda](#) [permut\\_mbplsda](#) [plot\\_permut\\_mbplsda](#) [pred\\_mbplsda](#) [plot\\_pred\\_mbplsda](#) [cvpred\\_mbplsda](#) [plot\\_cvpred\\_mbplsda](#) [boot\\_mbplsda](#) [plot\\_boot\\_mbplsda](#)

**Examples**

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical, nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
```

---

boot_mbplsda	<i>bootstrapped simulations for multi-block partial least squares discriminant analysis</i>
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### Description

Function to perform bootstrapped simulations for multi-block partial least squares discriminant analysis, in order to get confidence intervals for regression coefficients, variable loadings, variable and block importances.

### Usage

```
boot_mbplsda(object, nrepet = 199, optdim, cpus = 1, ...)
```

### Arguments

object	an object created by mbplsda
nrepet	integer indicating the number of repetitions
optdim	integer indicating the optimal number of global components to be introduced in the model
cpus	integer indicating the number of cpus to use when running the code in parallel
...	other arguments to be passed to methods

### Details

no details are needed

### Value

XYcoef	mean, standard deviation, quantiles (0.025;0.975), 95% confidence interval, median for regression coefficients
faX	mean, standard deviation, quantiles (0.025;0.975), 95% confidence interval, median for variable loadings
vipc	mean, standard deviation, quantiles (0.025;0.975), 95% confidence interval, median for cumulated variable importances
bipc	mean, standard deviation, quantiles (0.025;0.975), 95% confidence interval, median for cumulated block importances

### Note

at least 30 bootstrap repetitions may be recommended, more than 100 being preferable

### Author(s)

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

## References

Efron, B., Tibshirani, R.J. (1994). An Introduction to the Bootstrap. Chapman and Hall-CRC Monographs on Statistics and Applied Probability, Norwell, Massachusetts, United States.

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at Chimie 2020, Liege, BEL(01-27-2020 - 01-29-2020).

## See Also

[mbplsda](#) [plot\\_boot\\_mbplsda](#) [packMBPLSDA-package](#)

## Examples

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical, nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
resboot <- boot_mbplsda(modelembplsQ, optdim = ncpopt, nrepet = 30, cpus=1)
```

---

cvpred\_mbplsda

*Cross-validated predicted categories from a multi-block partial least squares discriminant model*

---

## Description

Function to perform 2-fold cross-validation for multi-block partial least squares discriminant analysis, in order to get for each observation the cross-validated predicted categories, and the statistical description of the predictions (mean, sd, 95

## Usage

```
cvpred_mbplsda(object, nrepet = 100, threshold = 0.5, bloY, optdim, cpus = 1,
  algo = c("max", "gravity", "threshold"))
```

**Arguments**

object	an object created by mbplsda
nrepet	integer indicating the number of repetitions
threshold	numeric indicating the threshold, between 0 and 1, to consider the categories are predicted with the threshold prediction method.
bloY	integer vector indicating the number of categories per variable of the Y-block.
optdim	integer indicating the (optimal) number of components of the multi-block partial least squares discriminant model
cpus	integer indicating the number of cpus to use when running the code in parallel
algo	character vector indicating the method(s) of prediction to use (see details)

**Details**

Three different algorithms are available to predict the categories of observations. In the max, and respectively the threshold algorithms, numeric values are calculated from the matrix of explanatory variables and the regression coefficients. Then, the predicted categorie for each variable of the Y-block is the one which corresponds to the higher predicted value, respectively to the values higher than the indicated threshold. In the gravity algorithm, predicted scores of the observations on the components are calculated. Then, each observation is assigned to the observed category of which it is closest to the barycentre in the component space.

**Value**

TRUEnrepet	number of repetitions
matPredYc.max	with the max algorithm, boolean matrix indicating the cross-validated predicted categories on the calibration datasets, the prediction accuracy for each categorie, each Y-block variable, and overall
matPredYv.max	with the max algorithm, boolean matrix indicating the cross-validated predicted categories on the validation datasets, the prediction accuracy for each categorie, each Y-block variable, and overall
matPredYc.gravity	with the gravity algorithm, boolean matrix indicating the cross-validated predicted categories on the calibration datasets, the prediction accuracy for each categorie, each Y-block variable, and overall
matPredYv.gravity	with the gravity algorithm, boolean matrix indicating the cross-validated predicted categories on the validation datasets, the prediction accuracy for each categorie, each Y-block variable, and overall
matPredYc.threshold	with the threshold algorithm, boolean matrix indicating the cross-validated predicted categories on the calibration datasets, the prediction accuracy for each categorie, each Y-block variable, and overall
matPredYv.threshold	with the threshold algorithm, boolean matrix indicating the cross-validated predicted categories on the validation datasets, the prediction accuracy for each categorie, each Y-block variable, and overall

- `statPredYc.max` with the max algorithm, matrix indicating the statistical description of prediction categories for each observation on the calibration datasets: number of predictions as an observation of the calibration dataset, modal value, probability to be predicted with its standard deviation, 95% confidence interval, quantiles 0.025 and 0.975, median value
- `statPredYv.max` with the max algorithm, matrix indicating the statistical description of prediction categories for each observation on the validation datasets: number of predictions as an observation of the validation dataset, modal value, probability to be predicted with its standard deviation, 95% confidence interval, quantiles 0.025 and 0.975, median value
- `statPredYc.gravity`  
with the gravity algorithm, matrix indicating the statistical description of prediction categories for each observation on the calibration datasets: number of predictions as an observation of the calibration dataset, modal value, probability to be predicted with its standard deviation, 95% confidence interval, quantiles 0.025 and 0.975, median value
- `statPredYv.gravity`  
with the gravity algorithm, matrix indicating the statistical description of prediction categories for each observation on the validation datasets: number of predictions as an observation of the validation dataset, modal value, probability to be predicted with its standard deviation, 95% confidence interval, quantiles 0.025 and 0.975, median value
- `statPredYc.threshold`  
with the threshold algorithm, matrix indicating the statistical description of prediction categories for each observation on the calibration datasets: number of predictions as an observation of the calibration dataset, modal value, probability to be predicted with its standard deviation, 95% confidence interval, quantiles 0.025 and 0.975, median value
- `statPredYv.threshold`  
with the threshold algorithm, matrix indicating the statistical description of prediction categories for each observation on the validation datasets: number of predictions as an observation of the validation dataset, modal value, probability to be predicted with its standard deviation, 95% confidence interval, quantiles 0.025 and 0.975, median value

**Note**

at least 90 cross-validation repetitions may be recommended

**Author(s)**

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**References**

Stone, M. (1974). Cross-validated choice and assessment of statistical predictions. *Journal of the Royal Statistical Society B*, 36(2), 111-147.

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134

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### See Also

[mbplsda](#) [plot\\_cvpred\\_mbplsda](#) [packMBPLSDA-package](#)

### Examples

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical[,1:10],
nutrition = nutrition[,1:10], omics = omics[,1:20]))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
CVpred <- cvpred_mbplsda(modelembplsQ, nrepet = 30, threshold = 0.5, bloY = bloYobs,
optdim = ncpopt, cpus = 1, algo = c("max"))
```

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical,
nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
CVpred <- cvpred_mbplsda(modelembplsQ, nrepet = 90, threshold = 0.5, bloY = bloYobs,
optdim = ncpopt, cpus = 1, algo = c("max"))
```

---

disjunctive	<i>Disjunctive table</i>
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---

**Description**

Function to transform a boolean matrix in a disjunctive table

**Usage**

```
disjunctive(y)
```

**Arguments**

y                    boolean matrix indicating observations categories

**Details**

no details are needed

**Value**

ydisj                disjunctive table

**Author(s)**

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

**References**

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at Chimie 2020, Liege, BEL(01-27-2020 - 01-29-2020).

**See Also**

[packMBPLSDA-package](#)

**Examples**

```
data(status)
disjonctif <- (disjunctive(status))
```

---

ginv	<i>generalized inverse of a matrix X</i>
------	--

---

**Description**

function to calculate the generalized inverse of a matrix X

**Usage**

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

**Arguments**

X	Matrix for which the generalized inverse is required
tol	A relative tolerance to detect zero singular values

---

inertie	<i>inertia of a matrix</i>
---------	----------------------------

---

**Description**

function to calculate the inertia of a matrix

**Usage**

```
inertie(tab)
```

**Arguments**

tab	a matrix
-----	----------

---

mbplsda	<i>Multi-block partial least squares discriminant analysis</i>
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---

**Description**

Function to perform a multi-block partial least squares discriminant analysis (MBPLSDA) of several explanatory blocks defined as an object of class ktab, to explain a dependent dataset (Y-block) defined as an object of class dudi, in order to get model parameters for the indicated number of components.

**Usage**

```
mbplsda(dudiY, ktabX, scale = TRUE, option = c("uniform", "none"),
scannf = TRUE, nf = 2)
```

**Arguments**

dudiY	an object of class dudi containing the dependent variables
ktabX	an object of class ktab containing the blocks of explanatory variables
scale	logical value indicating whether the explanatory variables should be standardized
option	option for the block weighting. If uniform, the weight of each explanatory block is equal to 1/number of explanatory blocks, and the weight of the Y-block is equal to 1. If none, the block weight is equal to the block inertia.
scannf	logical value indicating whether the eigenvalues bar plot should be displayed
nf	integer indicating the number of components to be calculated

**Details**

no details are needed

**Value**

call	the matching call
tabX	data frame of explanatory variables centered, eventually scaled (if scale=TRUE)and weighted (if option="uniform")
tabY	data frame of dependent variables centered, eventually scaled (if scale=TRUE)and weighted (if option="uniform")
nf	integer indicating the number of kept dimensions
lw	numeric vector of row weights
X.cw	numeric vector of column weights for the explanalatory dataset
blo	vector of the numbers of variables in each explanatory dataset
rank	rank of the analysis
eig	numeric vector containing the eigenvalues
TL	dataframe useful to manage graphical outputs
TC	dataframe useful to manage graphical outputs
faX	matrix containing the global variable loadings associated with the global explanatory dataset
Tc1	matrix containing the partial variable loadings associated with each explanatory dataset(unit norm)
Yc1	matrix of the variable loadings associated with the dependent dataset
lX	matrix of the global components associated with the whole explanatory dataset(scores of the individuals)
TlX	matrix containing the partial components associated with each explanatory dataset
lY	matrix of the components associated with the dependent dataset
cov2	squared covariance between lY and TlX
XYcoef	list of matrices of the regression coefficients of the whole explanatory dataset onto the dependent dataset

intercept	intercept of the regression of the whole explanatory dataset onto the dependent dataset
XYcoef.raw	list of matrices of the regression coefficients of the whole raw explanatory dataset onto the raw dependent dataset
intercept.raw	intercept of the regression of the whole raw explanatory dataset onto the raw dependent dataset
bip	block importances for a given dimension
bipc	cumulated block importances for a given number of dimensions
vip	variable importances for a given dimension
vipc	cumulated variable importances for a given number of dimensions

**Note**

This function is coming from the mbpls function of the R package ade4 (application in order to explain a disjunctive table, limitation of the number of calculated components)

**Author(s)**

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**References**

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

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Bougeard, S. and Dray, S. (2018) Supervised Multiblock Analysis in R with the ade4 Package. *Journal of Statistical Software*, 86(1), 1-17.

**See Also**

[packMBPLSDA-package](#)

**Examples**

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical, nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
```

---

medical	<i>medical dataset</i>
---------	------------------------

---

**Description**

extract of modified medical data obtained from physical examination and questionnaires in a human cohort study

**Usage**

```
data("medical")
```

**Format**

A data frame with 40 observations on the following 18 variables.

medic1 a numeric vector  
medic2 a numeric vector  
medic3 a numeric vector  
medic4 a numeric vector  
medic5 a numeric vector  
medic6 a numeric vector  
medic7 a numeric vector  
medic8 a numeric vector  
medic9 a numeric vector  
medic10 a numeric vector  
medic11 a numeric vector  
medic12 a numeric vector  
medic13 a numeric vector  
medic14 a numeric vector  
medic15 a numeric vector  
medic16 a numeric vector  
medic17 a numeric vector  
medic18 a numeric vector

**Details**

no details are needed

**Source**

non-real data

**Examples**

```
data(medical)
```

---

nutrition	<i>nutritional dataset</i>
-----------	----------------------------

---

**Description**

extract of modified nutritional data obtained by analysis of food questionnaires in a human cohort study

**Usage**

```
data("nutrition")
```

**Format**

A data frame with 40 observations on the following 33 variables.

nutri1 a numeric vector  
nutri2 a numeric vector  
nutri3 a numeric vector  
nutri4 a numeric vector  
nutri5 a numeric vector  
nutri6 a numeric vector  
nutri7 a numeric vector  
nutri8 a numeric vector  
nutri9 a numeric vector  
nutri10 a numeric vector  
nutri11 a numeric vector  
nutri12 a numeric vector  
nutri13 a numeric vector  
nutri14 a numeric vector  
nutri15 a numeric vector  
nutri16 a numeric vector  
nutri17 a numeric vector  
nutri18 a numeric vector  
nutri19 a numeric vector  
nutri20 a numeric vector  
nutri21 a numeric vector  
nutri22 a numeric vector  
nutri23 a numeric vector  
nutri24 a numeric vector

nutri25 a numeric vector  
nutri26 a numeric vector  
nutri27 a numeric vector  
nutri28 a numeric vector  
nutri29 a numeric vector  
nutri30 a numeric vector  
nutri31 a numeric vector  
nutri32 a numeric vector  
nutri33 a numeric vector

**Details**

no details are needed

**Source**

non-real data

**Examples**

```
data(nutrition)
```

---

omics

*metabolomic dataset*

---

**Description**

extract of modified metabolomic data obtained by LC-MS analysis of human plasma samples in a cohort study

**Usage**

```
data("omics")
```

**Format**

A data frame with 40 observations on the following 46 variables.

omic1 a numeric vector of relative intensities  
omic2 a numeric vector of relative intensities  
omic3 a numeric vector of relative intensities  
omic4 a numeric vector of relative intensities  
omic5 a numeric vector of relative intensities  
omic6 a numeric vector of relative intensities

omic7 a numeric vector of relative intensities  
omic8 a numeric vector of relative intensities  
omic9 a numeric vector of relative intensities  
omic10 a numeric vector of relative intensities  
omic11 a numeric vector of relative intensities  
omic12 a numeric vector of relative intensities  
omic13 a numeric vector of relative intensities  
omic14 a numeric vector of relative intensities  
omic15 a numeric vector of relative intensities  
omic16 a numeric vector of relative intensities  
omic17 a numeric vector of relative intensities  
omic18 a numeric vector of relative intensities  
omic19 a numeric vector of relative intensities  
omic20 a numeric vector of relative intensities  
omic21 a numeric vector of relative intensities  
omic22 a numeric vector of relative intensities  
omic23 a numeric vector of relative intensities  
omic24 a numeric vector of relative intensities  
omic25 a numeric vector of relative intensities  
omic26 a numeric vector of relative intensities  
omic27 a numeric vector of relative intensities  
omic28 a numeric vector of relative intensities  
omic29 a numeric vector of relative intensities  
omic30 a numeric vector of relative intensities  
omic31 a numeric vector of relative intensities  
omic32 a numeric vector of relative intensities  
omic33 a numeric vector of relative intensities  
omic34 a numeric vector of relative intensities  
omic35 a numeric vector of relative intensities  
omic36 a numeric vector of relative intensities  
omic37 a numeric vector of relative intensities  
omic38 a numeric vector of relative intensities  
omic39 a numeric vector of relative intensities  
omic40 a numeric vector of relative intensities  
omic41 a numeric vector of relative intensities  
omic42 a numeric vector of relative intensities  
omic43 a numeric vector of relative intensities  
omic44 a numeric vector of relative intensities  
omic45 a numeric vector of relative intensities  
omic46 a numeric vector of relative intensities

**Details**

no details are needed

**Source**

non-real data

**Examples**

```
data(omics)
```

---

permut_mbplsda	<i>Permutation testing of a multi-block partial least squares discriminant model</i>
----------------	--

---

**Description**

Function to perform permutation testing with 2-fold cross-validation for multi-block partial least squares discriminant analysis, in order to evaluate model validity and predictivity

**Usage**

```
permut_mbplsda(object, optdim, bloY, algo = c("max", "gravity", "threshold"),
  threshold = 0.5, nrepet = 100, npermut = 100, nbObsPermut = NULL,
  outputs = c("ER", "ConfMat", "AUC"), cpus = 1)
```

**Arguments**

object	an object created by mbplsda_nfX
optdim	integer indicating the (optimal) number of components of the multi-block partial least squares discriminant model
bloY	integer vector indicating the number of categories per variable of the Y-block.
algo	character vector indicating the method(s) of prediction to use (see details)
threshold	numeric indicating the threshold, between 0 and 1, to consider the categories are predicted with the threshold prediction method.
nrepet	integer indicating the number of repetitions
npermut	integer indicating the number of Y-block with switching observations
nbObsPermut	integer indicating the number of switching observations in all the modified Y-blocks
outputs	character vector indicating the wanted outputs (see details)
cpus	integer indicating the number of cpus to use when running the code in parallel

## Details

Three different algorithms are available to predict the categories of observations. In the max, and respectively the threshold algorithms, numeric values are calculated from the matrix of explanatory variables and the regression coefficients. Then, the predicted categorie for each variable of the Y-block is the one which corresponds to the higher predicted value, respectively to the values higher than the indicated threshold. In the gravity algorithm, predicted scores of the observations on the components are calculated. Then, each observation is assigned to the observed category of which it is closest to the barycentre in the component space.

If nbObsPermut is not NULL, t-test are performed to compare mean cross-validated overall prediction error rates (or aera under ROC curve) evaluated on permuted Y-blocks, with the cross-validated overall prediction error rate (or aera under ROC curve) evaluated on the original Y-block.

Available outputs are Error Rates (ER), Confusion Matrix (ConfMat), Aera Under Curve (AUC).

## Value

RV.YYpermut.values  
RV coefficient between Y-block and each Y-block with permuted values

cor.YYpermut.values  
correlation coefficient between categories in the Y-block and each Y-block with permuted values

prctGlob.Ychange.values  
overall percentage of modified values in each Y-block with permuted values

prct.Ychange.values  
percentage per category of modified values in each Y-block with permuted values

descrYperm  
statistical description of RV.YYpermut, cor.YYpermut, prctGlob.Ychange, prct.Ychange

TruePosC.max, TruePosC.gravity, TruePosC.threshold  
statistical description of cross-validated percentages of true positive observations per category, evaluated on calibration datasets, with the different algorithms (TruePosC.max for "max", TruePosC.gravity for "gravity", TruePosC.threshold for "threshold"), for each Y-block with permuted values

TruePosV.max, TruePosV.gravity, TruePosV.threshold  
statistical description of cross-validated percentages of true positive observations per category, evaluated on validation datasets, with the different algorithms (TruePosV.max for "max", TruePosV.gravity for "gravity", TruePosV.threshold for "threshold"), for each Y-block with permuted values

TrueNegC.max, TrueNegC.gravity, TrueNegC.threshold  
statistical description of cross-validated percentages of true negative observations per category, evaluated on calibration datasets, with the different algorithms (TrueNegC.max for "max", TrueNegC.gravity for "gravity", TrueNegC.threshold for "threshold"), for each Y-block with permuted values

TrueNegV.max, TrueNegV.gravity, TrueNegV.threshold  
statistical description of cross-validated percentages of true negative observations per category, evaluated on validation datasets, with the different algorithms (TrueNegV.max for "max", TrueNegV.gravity for "gravity", TrueNegV.threshold for "threshold"), for each Y-block with permuted values

FalsePosC.max, FalsePosC.gravity, FalsePosC.threshold	statistical description of cross-validated percentages of false positive observations per category, evaluated on calibration datasets, with the different algorithms (FalsePosC.max for "max", FalsePosC.gravity for "gravity", FalsePosC.threshold for "threshold"), for each Y-block with permuted values
FalsePosV.max, FalsePosV.gravity, FalsePosV.threshold	statistical description of cross-validated percentages of false positive observations per category, evaluated on validation datasets, with the different algorithms (FalsePosV.max for "max", FalsePosV.gravity for "gravity", FalsePosV.threshold for "threshold"), for each Y-block with permuted values
FalseNegC.max, FalseNegC.gravity, FalseNegC.threshold	statistical description of cross-validated percentages of false negative observations per category, evaluated on calibration datasets, with the different algorithms (FalseNegC.max for "max", FalseNegC.gravity for "gravity", FalseNegC.threshold for "threshold"), for each Y-block with permuted values
FalseNegV.max, FalseNegV.gravity, FalseNegV.threshold	statistical description of cross-validated percentages of false negative observations per category, evaluated on validation datasets, with the different algorithms (FalseNegV.max for "max", FalseNegV.gravity for "gravity", FalseNegV.threshold for "threshold"), for each Y-block with permuted values
ErrorRateC.max, ErrorRateC.gravity, ErrorRateC.threshold	statistical description of cross-validated prediction error rates per category, evaluated on calibration datasets, with the different algorithms (ErrorRateC.max for "max", ErrorRateC.gravity for "gravity", ErrorRateC.threshold for "threshold"), for each Y-block with permuted values
ErrorRateV.max, ErrorRateV.gravity, ErrorRateV.threshold	statistical description of cross-validated prediction error rates per category, evaluated on validation datasets, with the different algorithms (ErrorRateV.max for "max", ErrorRateV.gravity for "gravity", ErrorRateV.threshold for "threshold"), for each Y-block with permuted values
ErrorRateCglobal.max, ErrorRateCglobal.gravity, ErrorRateCglobal.threshold	statistical description of cross-validated overall prediction error rates, evaluated on calibration datasets, with the different algorithms (ErrorRateCglobal.max for "max", ErrorRateCglobal.gravity for "gravity", ErrorRateCglobal.threshold for "threshold"), for each Y-block with permuted values
ErrorRateVglobal.max, ErrorRateVglobal.gravity, ErrorRateVglobal.threshold	statistical description of cross-validated overall prediction error rates, evaluated on validation datasets, with the different algorithms (ErrorRateVglobal.max for "max", ErrorRateVglobal.gravity for "gravity", ErrorRateVglobal.threshold for "threshold"), for each Y-block with permuted values
AUCc	if all Y-block variables are binary, statistical description of cross-validated area under ROC curve values per category, evaluated on the validation datasets, for each Y-block with permuted values
AUCv	if all Y-block variables are binary, statistical description of cross-validated area under ROC curve values per category, evaluated on the validation datasets, for each Y-block with permuted values

AUCc.global	if all Y-block variables are binary, statistical description of cross-validated overall aera under ROC curve values, evaluated on the validation datasets, for each Y-block with permuted values
AUCv.global	if all Y-block variables are binary, statistical description of cross-validated overall aera under ROC curve values, evaluated on the validation datasets, for each Y-block with permuted values
reg.GlobalRes_prctYchange	results of linear regression of overall prediction error rates, and overall aera under ROC curve, onto percentages of modified values in Y-block
ttestMeanERv	if nbObsPermut is not NULL, results of the t-test comparing mean cross-validated overall prediction error rates (and eventually aera under ROC curve) evaluated on permuted Y-blocks, with the cross-validated overall prediction error rate (and eventually aera under ROC curve) evaluated on the original Y-block

**Note**

at least 30 cross-validation repetitions and 100 Y-block with switching observations may be recommended

**Author(s)**

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

**References**

Westerhuis, J.A., Hoefsloot, H.C.J., Smit, S., Vis, D.J., Smilde, A.K., van Velzen, E.J.J., van Duinhoven, J.P.M., van Dorsten, F.A. (2008). Assessment of PLS-DA cross validation. *Metabolomics*, 4, 81-89.

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journées Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at Chimie 2020, Liege, BEL(01-27-2020 - 01-29-2020).

**See Also**

[mbplsda](#) [plot\\_permut\\_mbplsda](#) [packMBPLSDA-package](#)

**Examples**

```
data(status)
data(medical)
data(omics)
```

```
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical[1:20,], omics = omics[1:20,]))
disjonctif <- (disjunctive(data.frame(status=status[1:20,],
row.names = rownames(status)[1:20])))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform",
scannf = FALSE, nf = 1)
rtsPermut <- permut_mbplsda(modelembplsQ, nrepet = 30, npermut = 100, optdim = ncpopt,
outputs = c("ER"), bloY = bloYobs, nbObsPermut = 10, cpus=1, algo = c("max"))
```

---

plot\_boot\_mbplsda      *Plot the results of the fonction boot\_mbplsda in a pdf file*

---

## Description

Fonction to draw the results of the fonction boot\_mbplsda (2-fold cross-validated parameter values) in a pdf file

## Usage

```
plot_boot_mbplsda(obj, filename = "PlotBootstrapMbplsda", propbestvar = 0.5)
```

## Arguments

obj	object type list containing the results of the fonction boot_mbplsda
filename	a string of characters indicating the given pdf filename
propbestvar	numeric value between 0 and 1, indicating the pourcentage of variables with the best VIPc values to plot

## Details

no details are needed

## Value

no numeric result

## Author(s)

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

## References

Efron, B., Tibshirani, R.J. (1994). An Introduction to the Bootstrap. Chapman and Hall-CRC Monographs on Statistics and Applied Probability, Norwell, Massachusetts, United States.

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at Chimie 2020, Liege, BEL(01-27-2020 - 01-29-2020).

## See Also

[mbplsda](#) [boot\\_mbplsda](#) [packMBPLSDA-package](#)

## Examples

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical, nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
resboot <- boot_mbplsda(modelembplsQ, optdim = ncpopt, nrepet = 30, cpus=1)
plot_boot_mbplsda(resboot,"plotBoot_nf1_30rep", propbestvar=0.20)
```

---

plot\_cvpred\_mbplsda *Plot the results of the fonction cvpred\_mbplsda in a pdf file*

---

## Description

Fonction to draw the results of the fonction cvpred\_mbplsda (2-fold cross-validated predictions) in a pdf file

## Usage

```
plot_cvpred_mbplsda(obj, filename = "PlotCVpredMbplsda")
```

**Arguments**

obj                    object type list containing the results of the fonction cvpred\_mbplsda  
filename               a string of characters indicating the given pdf filename

**Details**

no details are needed

**Value**

no numeric result

**Author(s)**

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

**References**

Stone, M. (1974). Cross-validated choice and assessment of statistical predictions. *Journal of the Royal Statistical Society B*, 36(2), 111-147.

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at *Chimiometrie 2020*, Liege, BEL(01-27-2020 - 01-29-2020).

**See Also**

[mbplsda](#) [cvpred\\_mbplsda](#) [packMBPLSDA-package](#)

**Examples**

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical[,1:10],
nutrition = nutrition[,1:10], omics = omics[,1:20]))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform",
scannf = FALSE, nf = 2)
```

```
CVpred <- cvpred_mbplsda(modelembplsQ, nrepet = 30, threshold = 0.5, bloY=bloYobs,
optdim=ncpopt, cpus = 1, algo = c("max"))
plot_cvpred_mbplsda(CVpred,"plotCVPred_nf1_30rep")
```

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical,
nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform",
scannf = FALSE, nf = 2)
CVpred <- cvpred_mbplsda(modelembplsQ, nrepet = 90, threshold = 0.5, bloY=bloYobs,
optdim=ncpopt, cpus = 1, algo = c("max"))
plot_cvpred_mbplsda(CVpred,"plotCVPred_nf1_90rep")
```

---

plot\_permut\_mbplsda *Plot the results of the fonction permut\_mbplsda in a pdf file*

---

### Description

Fonction to draw the results of the fonction permut\_mbplsda (plot and regression line of cross validated prediction error rates, evaluated on the validation datasets, in function of the percent of modified Y-block values) in a pdf file

### Usage

```
plot_permut_mbplsda(obj, filename = "PlotPermutationTest",
MainPlot = "Permutation test results \n (subset of validation)")
```

### Arguments

obj	object type list containing the results of the fonction permut_mbplsda
filename	a string of characters indicating the given pdf filename
MainPlot	a string of characters indicating the given main title

### Details

no details are needed

### Value

no numeric result

**Author(s)**

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

**References**

Westerhuis, J.A., Hoefsloot, H.C.J., Smit, S., Vis, D.J., Smilde, A.K., van Velzen, E.J.J., van Duinhoven, J.P.M., van Dorsten, F.A. (2008). Assessment of PLS-DA cross validation. *Metabolomics*, 4, 81-89.

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journées Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

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**See Also**

[mbplsda](#) [permut\\_mbplsda](#) [packMBPLSDA-package](#)

**Examples**

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical[1:20,], omics = omics[1:20,]))
disjonctif <- (disjunctive(data.frame(status=status[1:20,],
row.names = rownames(status)[1:20])))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 1)
ncpopt <- 1
rtsPermut <- permut_mbplsda(modelembplsQ, nrepet = 30, npermut = 100, optdim = ncpopt,
outputs = c("ER"), bloY=bloYobs, nbObsPermut = 10, cpus = 1, algo = c("max"))
plot_permut_mbplsda(rtsPermut,"plotPermut_nf1_30rep_100perm")
```

---

plot\_pred\_mbplsda

*Plot the results of the fonction pred\_mbplsda in a pdf file*

---

**Description**

Fonction to draw the results of the fonction `pred_mbplsda` (observed parameter values and predictions) in a pdf file

**Usage**

```
plot_pred_mbplsda(obj, filename = "PlotPredMbplsda", propbestvar = 0.5)
```

**Arguments**

obj	object type list containing the results of the fonction pred_mbplsda
filename	a string of characters indicating the given pdf filename
propbestvar	numeric value between 0 and 1, indicating the pourcentage of variables with the best VIPc values to plot

**Details**

no details are needed

**Value**

no numeric result

**Author(s)**

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

**References**

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

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**See Also**

[mbplsda](#) [pred\\_mbplsda](#) [packMBPLSDA-package](#)

**Examples**

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical, nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
```

```
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
predictions <- pred_mbplsda(modelembplsQ, optdim = ncpopt, threshold = 0.5,
bloY=bloYobs, algo = c("max", "gravity", "threshold"))
plot_pred_mbplsda(predictions,"plotPred_nf1", propbestvar=0.20)
```

---

plot\_testdim\_mbplsda *Plot the results of the fonction testdim\_mbplsda in a pdf file*

---

### Description

Fonction to draw the results of the fonction testdim\_mbplsda (cross validated prediction error rates, or aera under ROC curve, in function of the number of components in the model) in a pdf file

### Usage

```
plot_testdim_mbplsda(obj, filename = "PlotTestdimMbplsda")
```

### Arguments

obj	object type list containing the results of the fonction testdim_mbplsda
filename	a string of characters indicating the given pdf filename

### Details

no details are needed

### Value

no numeric result

### Author(s)

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

### References

Stone, M. (1974). Cross-validatory choice and assessment of statistical predictions. Journal of the Royal Statistical Society B, 36(2), 111-147.

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. Metabolomics, 15(10):134

Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at Chimie 2020, Liege, BEL(01-27-2020 - 01-29-2020).

### See Also

[mbplsda](#) [testdim\\_mbplsda](#) [packMBPLSDA](#)-package

### Examples

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical[,1:10],
nutrition = nutrition[,1:10], omics = omics[,1:20]))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 3)
resdim <- testdim_mbplsda(object=modelembplsQ, nrepet = 30, threshold = 0.5,
bloY=bloYobs, cpus=1, algo = c("max"), outputs = c("ER"))
plot_testdim_mbplsda(resdim, "plotTDim")
```

---

pred_mbplsda	<i>Observed parameters and predicted categories from a multi-block partial least squares discriminant model</i>
--------------	---

---

### Description

Fonction to perform categories predictions from a multi-block partial least squares discriminant model.

### Usage

```
pred_mbplsda(object, optdim , threshold = 0.5, bloY,
algo = c("max", "gravity", "threshold"))
```

### Arguments

object	an object created by mbplsda
optdim	integer indicating the (optimal) number of components of the multi-block partial least squares discriminant model
threshold	numeric indicating the threshold, between 0 and 1, to consider the categories are predicted with the threshold prediction method.
bloY	integer vector indicating the number of categories per variable of the Y-block.
algo	character vector indicating the method(s) of prediction to use (see details)

## Details

Three different algorithms are available to predict the categories of observations. In the max, and respectively the threshold algorithms, numeric values are calculated from the matrix of explanatory variables and the regression coefficients. Then, the predicted categorie for each variable of the Y-block is the one which corresponds to the higher predicted value, respectively to the values higher than the indicated threshold. In the gravity algorithm, predicted scores of the observations on the components are calculated. Then, each observation is assigned to the observed category of which it is closest to the barycentre in the component space.

## Value

XYcoef	list of matrices of the regression coefficients of the whole explanatory dataset onto the dependent dataset
VIPc	cumulated variable importances for a given number of dimensions
BIPc	cumulated block importances for a given number of dimensions
faX	matrix containing the global variable loadings associated with the global explanatory dataset
lX	matrix of the global components associated with the whole explanatory dataset(scores of the individuals)
ConfMat.ErrorRate	confidence matrix and prediction error rate per category
ErrorRate.global	confidence matrix and prediction error rate, per Y-block variable and overall
PredY.max	predictions and accuracy of predictions with the "max" algorithm
PredY.gravity	predictions and accuracy of predictions with the "gravity" algorithm
PredY.threshold	predictions and accuracy of predictions with the "threshold" algorithm
AUC	aera under ROC cuve value and 95% confidence interval, per category, per Y-block variable and overall

## Author(s)

Marion Brandolini-Bunlon (<marion.brandolini-bunlon@inra.fr>) and Stephanie Bougeard (<stephanie.bougeard@anses.fr>)

## References

- Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at 12emes Journees Scientifiques RFMF, Clermont-Ferrand, FRA(05-21-2019 - 05-23-2019).
- Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2019). Multi-block PLS discriminant analysis for the joint analysis of metabolomic and epidemiological data. *Metabolomics*, 15(10):134
- Brandolini-Bunlon, M., Petera, M., Gaudreau, P., Comte, B., Bougeard, S., Pujos-Guillot, E.(2020). A new tool for multi-block PLS discriminant analysis of metabolomic data: application to systems epidemiology. Presented at Chimietrie 2020, Liege, BEL(01-27-2020 - 01-29-2020).

**See Also**

[mbplsda plot\\_pred\\_mbplsda packMBPLSDA-package](#)

**Examples**

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical, nutrition = nutrition, omics = omics))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
ncpopt <- 1
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 2)
predictions <- pred_mbplsda(modelembplsQ, optdim = ncpopt, threshold = 0.5, bloY=bloYobs,
algo = c("max", "gravity", "threshold"))
```

---

status

*physiopathological status data*

---

**Description**

physiopathological status of men in a human cohort study

**Usage**

```
data("status")
```

**Format**

A data frame with 40 observations on the following variable.

status a factor with levels cas temoin

**Details**

no details are needed

**Source**

extract of data not yet published

**Examples**

```
data(status)
```

---

testdim_mbplsda	<i>Test of number of components by two-fold cross-validation for a multi-block partial least squares discriminant model</i>
-----------------	---

---

### Description

Function to perform a two-fold cross-validation in order to select the optimal number of dimensions of a multi-block partial least squares discriminant model, according to the classification error rate or to the area under ROC curve

### Usage

```
testdim_mbplsda(object, nrepet = 100, algo = c("max", "gravity", "threshold"),
  threshold = 0.5, bloY, outputs = c("ER", "ConfMat", "AUC"), cpus = 1)
```

### Arguments

object	an object created by mbplsda_nfX
nrepet	integer indicating the number of repetitions
algo	character vector indicating the method(s) of prediction to use (see details)
threshold	numeric indicating the threshold, between 0 and 1, to consider the categories are predicted with the threshold prediction method.
bloY	integer vector indicating the number of categories per variable of the Y-block.
outputs	character vector indicating the wanted outputs (see details)
cpus	integer indicating the number of cpus to use when running the code in parallel

### Details

Three different algorithms are available to predict the categories of observations. In the max, and respectively the threshold algorithms, numeric values are calculated from the matrix of explanatory variables and the regression coefficients. Then, the predicted categorie for each variable of the Y-block is the one which corresponds to the higher predicted value, respectively to the values higher than the indicated threshold. In the gravity algorithm, predicted scores of the observations on the components are calculated. Then, each observation is assigned to the observed category of which it is closest to the barycentre in the component space.

Available outputs are Error Rates (ER), Confusion Matrix (ConfMat), Area Under Curve (AUC).

### Value

TRUEnrepet	number of repetitions
TruePosC.max, .gravity, .threshold	statistical description of percentages of true positive observations per category, evaluated on the calibration dataset, with the different algorithms (TPcM for "max", TPcG for "gravity", TPcT for "threshold"), for a number of components ranging from 1 to its maximum value

TruePosV.max, .gravity, .threshold  
statistical description of percentages of true positive observations per category, evaluated on the validation dataset, with the different algorithms (TPvM for "max", TPvG for "gravity", TPvT for "threshold"), for a number of components ranging from 1 to its maximum value

TrueNegC.max, .gravity, .threshold  
statistical description of percentages of true negative observations per category, evaluated on the calibration dataset, with the different algorithms (TNcM for "max", TNcG for "gravity", TNcT for "threshold"), for a number of components ranging from 1 to its maximum value

TrueNegV.max, .gravity, .threshold  
statistical description of percentages of true negative observations per category, evaluated on the validation dataset, with the different algorithms (TNvM for "max", TNvG for "gravity", TNvT for "threshold"), for a number of components ranging from 1 to its maximum value

FalsePosC.max, .gravity, .threshold  
statistical description of percentages of false positive observations per category, evaluated on the calibration dataset, with the different algorithms (FPcM for "max", FPcG for "gravity", FPcT for "threshold"), for a number of components ranging from 1 to its maximum value

FalsePosV.max, .gravity, .threshold  
statistical description of percentages of false positive observations per category, evaluated on the validation dataset, with the different algorithms (FPvM for "max", FPvG for "gravity", FPvT for "threshold"), for a number of components ranging from 1 to its maximum value

FalseNegC.max, .gravity, .threshold  
statistical description of percentages of false negative observations per category, evaluated on the calibration dataset, with the different algorithms (FNcM for "max", FNcG for "gravity", FNcT for "threshold"), for a number of components ranging from 1 to its maximum value

FalseNegV.max, .gravity, .threshold  
statistical description of percentages of false negative observations per category, evaluated on the validation dataset, with the different algorithms (FNvM for "max", FNvG for "gravity", FNvT for "threshold"), for a number of components ranging from 1 to its maximum value

ErrorRateC.max, .gravity, .threshold  
statistical description of prediction error rates per category, evaluated on the calibration dataset, with the different algorithms (ERcM for "max", ERcG for "gravity", ERcT for "threshold"), for a number of components ranging from 1 to its maximum value

ErrorRateV.max, .gravity, .threshold  
statistical description of prediction error rates per category, evaluated on the validation dataset, with the different algorithms (ERvM for "max", ERvG for "gravity", ERvT for "threshold"), for a number of components ranging from 1 to its maximum value

ErrorRateCglobal.max, .gravity, .threshold  
statistical description of global prediction error rates, evaluated on the calibration dataset, with the different algorithms (ERcM.global for "max", ERcG.global

	for "gravity", ERcT.global for "threshold"), for a number of components ranging from 1 to its maximum value
ErrorRateVglobal.max, .gravity, .threshold	statistical description of global prediction error rates, evaluated on the validation dataset, with the different algorithms (ERvM.global for "max", ERvG.global for "gravity", ERvT.global for "threshold"), for a number of components ranging from 1 to its maximum value
AUCc	statistical description of aera under ROC curve values per category, evaluated on the calibration dataset, if all Y-block variables are binary, for a number of components ranging from 1 to its maximum value
AUCv	statistical description of aera under ROC curve values per category, evaluated on the validation dataset, if all Y-block variables are binary, for a number of components ranging from 1 to its maximum value
AUCc.global	statistical description of global aera under ROC curve values, evaluated on the calibration dataset, if all Y-block variables are binary, for a number of components ranging from 1 to its maximum value
AUCv.global	statistical description of global aera under ROC curve values, evaluated on the validation dataset, if all Y-block variables are binary, for a number of components ranging from 1 to its maximum value

**Note**

at least 30 cross-validation repetitions may be recommended

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**References**

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**See Also**

[mbplsda plot\\_testdim\\_mbplsda packMBPLSDA-package](#)

**Examples**

```
data(status)
data(medical)
data(omics)
data(nutrition)
ktabX <- ktab.list.df(list(medical = medical[,1:10],
nutrition = nutrition[,1:10], omics = omics[,1:20]))
disjonctif <- (disjunctive(status))
dudiY <- dudi.pca(disjonctif , center = FALSE, scale = FALSE, scannf = FALSE)
bloYobs <- 2
modelembplsQ <- mbplsda(dudiY, ktabX, scale = TRUE, option = "uniform", scannf = FALSE, nf = 3)
resdim <- testdim_mbplsda(object = modelembplsQ, nrepet = 30, threshold = 0.5,
bloY = bloYobs, cpus = 1, algo = c("max"), outputs = c("ER"))
```

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