

Package ‘ropls’

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Type Package

Title PCA, PLS(-DA) and OPLS(-DA) for multivariate analysis and feature selection of omics data

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Description Latent variable modeling with Principal Component Analysis (PCA) and Partial Least Squares (PLS) are powerful methods for visualization, regression, classification, and feature selection of omics data where the number of variables exceeds the number of samples and with multicollinearity among variables. Orthogonal Partial Least Squares (OPLS) enables to separately model the variation correlated (predictive) to the factor of interest and the uncorrelated (orthogonal) variation. While performing similarly to PLS, OPLS facilitates interpretation. Successful applications of these chemometrics techniques include spectroscopic data such as Raman spectroscopy, nuclear magnetic resonance (NMR), mass spectrometry (MS) in metabolomics and proteomics, but also transcriptomics data. In addition to scores, loadings and weights plots, the package provides metrics and graphics to determine the optimal number of components (e.g. with the R2 and Q2 coefficients), check the validity of the model by permutation testing, detect outliers, and perform feature selection (e.g. with Variable Importance in Projection or regression coefficients). The package can be accessed via a user interface on the Workflow4Metabolomics.org online resource for computational metabolomics (built upon the Galaxy environment).

Suggests RUnit, BiocGenerics, BiocStyle, faahKO, xcms, CAMERA

Depends methods

License CeCILL

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Description

Latent variable modeling with Principal Component Analysis (PCA) and Partial Least Squares (PLS) are powerful methods for visualization, regression, classification, and feature selection of omics data where the number of variables exceeds the number of samples and with multicollinearity among variables. Orthogonal Partial Least Squares (OPLS) enables to separately model the variation correlated (predictive) to the factor of interest and the uncorrelated (orthogonal) variation. While performing similarly to PLS, OPLS facilitates interpretation. Successful applications of these chemometrics techniques include spectroscopic data such as Raman spectroscopy, nuclear magnetic resonance (NMR), mass spectrometry (MS) in metabolomics and proteomics, but also transcriptomics data. In addition to scores, loadings and weights plots, the package provides metrics and graphics to determine the optimal number of components (e.g. with the R2 and Q2 coefficients), check the validity of the model by permutation testing, detect outliers, and perform feature selection (e.g. with Variable Importance in Projection or regression coefficients). The package can be accessed via a user interface on the Workflow4Metabolomics.org online resource for computational metabolomics (built upon the Galaxy environment).

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Author(s)

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Examples

```
data(sacurine)
attach(sacurine)

#### PCA

sacurine.pca <- opl(s(dataMatrix))
plot(sacurine.pca, parAsColFcVn = sampleMetadata[, "gender"])

#### PLS-DA

sacurine.plsda <- opl(dataMatrix, sampleMetadata[, "gender"])

#### OPLS-DA
```

```
sacurine.oplsda <- opls(dataMatrix, sampleMetadata[, "gender"], predI = 1, orthoI = NA)
detach(sacurine)
```

aminoacids

Amino-Acids Dataset

Description

Quantitative structure property relationship (QSPR)

Usage

```
data(aminoacids)
```

Format

A data frame with the following parameters:

AA amino acid

PIE lipophilicity constant of the AA side chain

PIF lipophilicity constant of the AA side chain

DGR free energy of transfer of an AA side chain from protein interior to water

SAC water-accessible surface area of AA's calculated by MOLSV

MR molecular refractivity

Lam polarity parameter

Vol molecular volume of AA's calculated by MOLSV

DDGTS free energy of unfolding of the tryptophane synthase a unit of bacteriophage T4 lysosome

Value

Data frame (numeric type except the first column, which can be transformed into row names) with 19 rows and the 9 columns containing information about amino acids. For details see the 'Format' section above.

Source

'aminoacids' dataset.

References

Wold et al. (2001). PLS-regression: a basic tool of chemometrics. *Chemometrics and Intelligent Laboratory Systems*. 58:109-130.

cellulose	<i>NIR-Viscosity example data set to illustrate multivariate calibration using PLS, spectral filtering and OPLS</i>
-----------	---

Description

The data were collected at Akzo Nobel, Ornskoldsvik (Sweden). The raw material for their cellulose derivative process is delivered to the factory in form of cellulose sheets. Before entering the process the cellulose sheets are controlled by a viscosity measurement, which functions as a steering parameter for that particular batch. In this data set NIR spectra for 180 cellulose sheets were collected after the sheets had been sent through a grinding process. Hence the NIR spectra were measured on the cellulose raw material in powder form. Data are divided in two parts, one used for modeling and one part for testing.

Usage

```
data(cellulose)
```

Format

A list with the following elements: 1) nirMN: a matrix of 180 samples x 1201 wavelengths in the VIS-NIR region, 2) viscoVn: a vector (length = 180) of viscosity of cellulose powder, and 3) classVn: a vector (length = 180) of class membership (1 or 2)

Value

For details see the Format section above.

References

Multivariate calibration using spectral data. Simca tutorial. Umetrics.

coef.opls	<i>Coefficients method for (O)PLS models</i>
-----------	--

Description

Coefficients of the (O)PLS(-DA) regression model

Usage

```
## S4 method for signature 'opls'  
coef(object, ...)
```

Arguments

object An S4 object of class `opls`, created by `opls` function.
... Currently not used.

Value

Numeric matrix of coefficients (number of rows equals the number of variables, and the number of columns equals the number of responses)

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)

sacurine.plsda <- opls(dataMatrix,
                      sampleMetadata[, "gender"])

head(coef(sacurine.plsda))

detach(sacurine)
```

cornell

Octane of various blends of gasoline

Description

Twelve mixture component proportions of the blend are analysed

Usage

```
data(cornell)
```

Format

A data frame with the following parameters:

num mixture number
x1 proportion of component 1
x2 proportion of component 2
x3 proportion of component 3
x4 proportion of component 4

x5 proportion of component 5
x6 proportion of component 6
x7 proportion of component 7 Note: the 7 variables are correlated since they sum up to 1
y octane (quantitative variable)

Value

Data frame (numeric type only; the first column can be transformed into row names) with 12 rows and 9 columns corresponding to the 'num'ber of the mixture (column 1), the proportion of each of the 7 'x' components within the mixture (columns 2-8), and the octane indice 'y' (column 9). For details see the 'Format' section above.

Source

Tenenhous (1998), Table 6, page 78.

References

Tenenhous (1998). La regression PLS: theorie et pratique. Paris: Editions Technip.

fitted.opls	<i>Fitted method for 'opls' objects</i>
-------------	---

Description

Returns predictions of the (O)PLS(-DA) model on the training dataset

Usage

```
## S4 method for signature 'opls'  
fitted(object, ...)
```

Arguments

object	An S4 object of class opls, created by the opls function.
...	Currently not used.

Value

Predictions (either a vector, factor, or matrix depending on the y response used for training the model)

Author(s)

Philippe Rinaudo and Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)
sacurine.plsda <- oplS(dataMatrix, sampleMetadata[, "gender"])

fitted(sacurine.plsda)

detach(sacurine)
```

foods

Food consumption patterns across European countries (FOODS)

Description

The relative consumption of 20 food items was compiled for 16 countries. The values range between 0 and 100 percent and a high value corresponds to a high consumption. The dataset contains 3 missing data.

Usage

```
data(foods)
```

Format

A data frame with the following parameters:

Country Name of the country
Gr_Coffe Ground Coffee
Inst_Coffe Instant Coffee
Tea Tea
Sweetner Sweetner
Biscuits Biscuits
Pa_Soup Powder Soup
Ti_Soup Tin Soup
In_Potat Instant Potatoes
Fro_Fish Frozen Fish
Fro_Veg Frozen Vegetables
Apples Apples
Oranges Oranges
Ti_Fruit Tin Fruit
Jam Jam

Garlic Garlic
 Butter Butter
 Margarine Margarine
 Olive_Oil Olive Oil
 Yoghurt Yoghurt
 Crisp_Brea Crisp Bread

Value

Data frame (numeric type except the first column, which can be transformed into row names) with 16 rows and 21 columns, corresponding to the 'Country' (column 1), followed by the consumption of each of the 20 food items (columns 2-21). For details see the 'Format' section above.

References

Eriksson et al. (2006). Multi- and Megarvariate Data Analysis. Umetrics Academy. pp.10, 33, 48.

getLoadingMN	<i>getLoadingMN method for PCA/(O)PLS(-DA) models</i>
--------------	---

Description

(Orthogonal) loadings of the PCA/(O)PLS(-DA) model

Usage

```
## S4 method for signature 'opls'
getLoadingMN(object, orthoL = FALSE)
```

Arguments

object	An S4 object of class <code>opls</code> , created by <code>opls</code> function.
orthoL	Logical: Should the orthogonal loading matrix be returned (default is FALSE and the predictive loading matrix is returned)

Value

Numeric matrix with a number of rows equal to the number of variables and a number of columns equal to the number of components

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)

sacurine.plsda <- opls(dataMatrix,
                      sampleMetadata[, "gender"])

getLoadingMN(sacurine.plsda)

detach(sacurine)
```

getPcaVarVn*getPcaVarVn method for PCA models*

Description

Variance of the components (score vectors)

Usage

```
## S4 method for signature 'opls'
getPcaVarVn(object)
```

Arguments

object An S4 object of class opls, created by opls function.

Value

Numeric vector with the same length as the number of components

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)

sacurine.pca <- opls(dataMatrix)

getPcaVarVn(sacurine.pca)

detach(sacurine)
```

`getScoreMN`*getScoreMN method for PCA/(O)PLS(-DA) models*

Description

(Orthogonal) scores of the (O)PLS(-DA) model

Usage

```
## S4 method for signature 'opls'  
getScoreMN(object, orthoL = FALSE)
```

Arguments

<code>object</code>	An S4 object of class <code>opls</code> , created by <code>opls</code> function.
<code>orthoL</code>	Logical: Should the orthogonal score matrix be returned (default is <code>FALSE</code> and the predictive score matrix is returned)

Value

Numeric matrix with a number of rows equal to the number of samples and a number of columns equal to the number of components

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)  
attach(sacurine)  
  
sacurine.plsda <- opls(dataMatrix,  
                      sampleMetadata[, "gender"])  
  
getScoreMN(sacurine.plsda)  
  
detach(sacurine)
```

`getSubsetVi`*getSubsetVi method for (O)PLS(-DA) models*

Description

Extracts the indices of the samples used for building the model (when a subset argument has been specified)

Usage

```
## S4 method for signature 'opls'  
getSubsetVi(object)
```

Arguments

`object` An S4 object of class `opls`, created by `opls` function.

Value

Integer vector with the indices of the samples used for training

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)  
attach(sacurine)  
  
predictorMN <- dataMatrix  
responseFc <- sampleMetadata[, "gender"]  
  
sacurine.plsda <- opsl(predictorMN,  
                      responseFc,  
                      subset = "odd")  
  
trainVi <- getSubsetVi(sacurine.plsda)  
  
table(responseFc[trainVi], fitted(sacurine.plsda))  
  
detach(sacurine)
```

getSummaryDF	<i>getSummaryDF method for PCA/(O)PLS models</i>
--------------	--

Description

Summary of model metrics

Usage

```
## S4 method for signature 'opls'  
getSummaryDF(object)
```

Arguments

object An S4 object of class opls, created by opls function.

Value

Data frame

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)  
attach(sacurine)  
  
sacurine.plsda <- opls(dataMatrix,  
                      sampleMetadata[, "gender"])  
  
getSummaryDF(sacurine.plsda)  
  
detach(sacurine)
```

getVipVn	<i>getVipVn method for (O)PLS(-DA) models</i>
----------	---

Description

(Orthogonal) VIP of the (O)PLS(-DA) model

Usage

```
## S4 method for signature 'opls'  
getVipVn(object, orthoL = FALSE)
```

Arguments

object	An S4 object of class <code>opls</code> , created by <code>opls</code> function.
orthoL	Logical: Should the orthogonal VIP be returned (default is <code>FALSE</code> and the predictive VIP is returned)

Value

Numeric vector with a length equal to the number of variables and a number of columns equal to the number of components

Author(s)

Etienne Thevenot (CEA)

References

Galindo-Prieto B., Eriksson L. and Trygg J. (2014). Variable influence on projection (VIP) for orthogonal projections to latent structures (OPLS). *Journal of Chemometrics* 28, 623-632.

Examples

```
data(sacurine)  
attach(sacurine)  
  
sacurine.plsda <- opls(dataMatrix,  
                      sampleMetadata[, "gender"])  
  
getVipVn(sacurine.plsda)  
  
detach(sacurine)
```

getWeightMN

getWeightMN method for (O)PLS(-DA) models

Description

(Orthogonal) weights of the (O)PLS(-DA) model

Usage

```
## S4 method for signature 'opls'  
getWeightMN(object, orthoL = FALSE)
```

Arguments

object	An S4 object of class <code>opls</code> , created by <code>opls</code> function.
orthol	Logical: Should the orthogonal weight matrix be returned (default is FALSE and the predictive weight matrix is returned)

Value

Numeric matrix with a number of rows equal to the number of variables and a number of columns equal to the number of components

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)

sacurine.plsda <- opls(dataMatrix,
                      sampleMetadata[, "gender"])

getWeightMN(sacurine.plsda)

detach(sacurine)
```

linnerud

Linnerud Dataset

Description

Three physiological and three exercise variables are measured on twenty middle-aged men in a fitness club.

Usage

```
data(linnerud)
```

Format

A data frame with the following parameters:

```
num subject number
weight weight
waist waist
```

pulse pulse
pullUp pull-up
squat situp
jump jump

Value

Data frame (numeric type only; the first column can be transformed into row names) with 20 rows and 7 columns corresponding to the subject's 'num'ber (column 1), the 3 physiological variables (columns 2-4), and the 3 exercise variables (columns 5-7). For details see the 'Format' section above.

Source

'mixOmics' 'linnerud' dataset.

References

Tenenhaus (1998). La regression PLS: theorie et pratique. Paris: Editions Technip.

lowarp

A multi response optimization data set (LOWARP)

Description

This example concerns the development of a polymer similar to that used in the plastic covering of mobile phones. The desired profile of the polymer was low warp and high strength. Four constituents (glas, crtp, mica, and amtp) were varied in the polymer formulation by means of a 17 run mixture design. For each new polymer, i.e., each new experiment in the mixture design, 14 responses relating to both warp and strength were measured on the product. The objective of the data analysis was to uncover which combination of factors (the four ingredients) gave polymers with low warp and high strength. The data set contains 10 missing values (NA).

Usage

```
data(lowarp)
```

Format

A data frame with the following parameters:

num mixture number
glas glas constituent
crtp crtp constituent
mica mica constituent
amtp amtp constituent

wrp1 warp response 1
wrp2 warp response 2
wrp3 warp response 3
wrp4 warp response 4
wrp5 warp response 5
wrp6 warp response 6
wrp7 warp response 7
wrp8 warp response 8
st1 strength response 1
st2 strength response 2
st3 strength response 3
st4 strength response 4
st5 strength response 5
st6 strength response 6

Value

Data frame (numeric type only; the first column can be transformed into row names) with 17 rows and 19 columns corresponding to the subject's 'num'ber (column 1), the 4 constituent variables (columns 2-5), the 8 warp responses (columns 6-13), and the 6 strength responses (columns 14-19). For details see the 'Format' section above.

References

Eriksson et al. (2006). Multi- and Megarvariate Data Analysis. Umetrics Academy. pp.16, 77, 209.

mark	<i>'mark' Dataset</i>
------	-----------------------

Description

Examination marks obtained by French students in Mathematics, Physics, French and English

Usage

data(mark)

Format

A data frame with the following parameters:

nom names of the students
math marks in mathematics
phys marks in physics
fran marks in french
angl marks in english

Value

Data frame (numeric type except the first column, which can be transformed into row names) with 9 rows and 5 columns, corresponding to the name of the students (column 1), followed by the marks obtained in Maths, Physics, French and English (columns 2-5). For details see the 'Format' section above.

Source

'mark' dataset.

References

Baccini (2010). Statistique Descriptive Multidimensionnelle (pour les nuls).

opls

PCA, PLS(-DA), and OPLS(-DA)

Description

PCA, PLS, and OPLS regression, classification, and cross-validation with the NIPALS algorithm

Usage

```
## S4 method for signature 'data.frame'
opls(x, ...)
## S4 method for signature 'matrix'
opls(x,
y = NULL,
predI = NA,
orthoI = 0,
algoC = c("default", "nipals", "svd")[1],
crossvalI = 7,
log10L = FALSE,
permI = 20,
scaleC = c("none", "center", "pareto", "standard")[4],
subset = NULL,
printL = TRUE,
plotL = TRUE,

.sinkC = NULL,
...)
```

Arguments

x	Numerical data frame or matrix (observations x variables); NAs are allowed
y	Response to be modelled: Either 1) 'NULL' for PCA (default) or 2) a numerical vector (same length as 'x' row number) for single response (O)PLS, or 3) a numerical matrix (same row number as 'x') for multiple response PLS or 4) a factor (same length as 'x' row number) for (O)PLS-DA. Note that, for convenience, character vectors are also accepted for (O)PLS-DA as well as single column numerical (resp. character) matrices for (O)PLS (respectively (O)PLS-DA). NAs are allowed in numeric responses.
predI	Integer: number of components (predictive components in case of PLS and OPLS) to extract; for OPLS, predI is (automatically) set to 1; if set to NA [default], autofit is performed: a maximum of 10 components are extracted until (i) PCA case: the variance is less than the mean variance of all components (note that this rule requires all components to be computed and can be quite time-consuming for large datasets) or (ii) PLS case: either R2Y of the component is < 0.01 (N4 rule) or Q2Y is < 0 (for more than 100 observations) or 0.05 otherwise (R1 rule)
orthoI	Integer: number of orthogonal components (for OPLS only); when set to 0 [default], PLS will be performed; otherwise OPLS will be performed; when set to NA, OPLS is performed and the number of orthogonal components is automatically computed by using the cross-validation (with a maximum of 9 orthogonal components).
algoC	Default algorithm is 'svd' for PCA (in case of no missing values in 'x'; 'nipals' otherwise) and 'nipals' for PLS and OPLS; when asking to use 'svd' for PCA on an 'x' matrix containing missing values, NAs are set to half the minimum of non-missing values and a warning is generated
crossvalI	Integer: number of cross-validation segments (default is 7); The number of samples (rows of 'x') must be at least >= crossvalI
log10L	Should the 'x' matrix be log10 transformed? Zeros are set to 1 prior to transformation
permI	Integer: number of random permutations of response labels to estimate R2Y and Q2Y significance by permutation testing [default is 20 for single response models (without train/test partition), and 0 otherwise]
scaleC	Character: either no centering nor scaling ('none'), mean-centering only ('center'), mean-centering and pareto scaling ('pareto'), or mean-centering and unit variance scaling ('standard') [default]
subset	Integer vector: indices of the observations to be used for training (in a classification scheme); use NULL [default] for no partition of the dataset; use 'odd' for a partition of the dataset in two equal sizes (with respect to the classes proportions)
printL	Logical: Should informations regarding the data set and the model be printed? [default = TRUE]
plotL	Logical: Should the 'summary' plot be displayed? [default = TRUE]
.sinkC	Character: Name of the file for R output diversion [default = NULL: no diversion]; Diversion of messages is required for the integration into Galaxy

... Currently not used.

Value

An S4 object of class 'opls' containing the following slots:

typeC	Character: model type (PCA, PLS, PLS-DA, OPLS, or OPLS-DA)
descriptionMC	Character matrix: Description of the data set (number of samples, variables, etc.)
modelDF	Data frame with the model overview (number of components, R2X, R2X(cum), R2Y, R2Y(cum), Q2, Q2(cum), significance, iterations)
summaryDF	Data frame with the model summary (cumulated R2X, R2Y and Q2); RMSEE is the square root of the mean error between the actual and the predicted responses
subsetVi	Integer vector: Indices of observations in the training data set
pcaVarVn	PCA: Numerical vector of variances of length: predI
vipVn	PLS(-DA): Numerical vector of Variable Importance in Projection; OPLS(-DA): Numerical vector of Variable Importance for Prediction (VIP4,p from Galindo-Prieto et al, 2014)
orthoVipVn	OPLS(-DA): Numerical vector of Variable Importance for Orthogonal Modeling (VIP4,o from Galindo-Prieto et al, 2014)
xMeanVn	Numerical vector: variable means of the 'x' matrix
xSdVn	Numerical vector: variable standard deviations of the 'x' matrix
yMeanVn	(O)PLS: Numerical vector: variable means of the 'y' response (transformed into a dummy matrix in case it is of 'character' mode initially)
ySdVn	(O)PLS: Numerical vector: variable standard deviations of the 'y' response (transformed into a dummy matrix in case it is of 'character' mode initially)
xZeroVarVi	Numerical vector: indices of variables with variance < 2.22e-16 which were excluded from 'x' before building the model
scoreMN	Numerical matrix of x scores (T; dimensions: nrow(x) x predI) $X = TP' + E$; $Y = TC' + F$
loadingMN	Numerical matrix of x loadings (P; dimensions: ncol(x) x predI) $X = TP' + E$
weightMN	(O)PLS: Numerical matrix of x weights (W; same dimensions as loadingMN)
orthoScoreMN	OPLS: Numerical matrix of orthogonal scores (Tortho; dimensions: nrow(x) x number of orthogonal components)
orthoLoadingMN	OPLS: Numerical matrix of orthogonal loadings (Portho; dimensions: ncol(x) x number of orthogonal components)
orthoWeightMN	OPLS: Numerical matrix of orthogonal weights (same dimensions as orthoLoadingMN)
cMN	(O)PLS: Numerical matrix of Y weights (C; dimensions: number of responses or number of classes in case of qualitative response) x number of predictive components; $Y = TC' + F$
coMN:	(O)PLS: Numerical matrix of Y orthogonal weights; dimensions: number of responses or number of classes in case of qualitative response with more than 2 classes x number of orthogonal components

uMN	(O)PLS: Numerical matrix of Y scores (U; same dimensions as scoreMN); $Y = UC' + G$
weightStarMN	Numerical matrix of projections (W^* ; same dimensions as loadingMN); whereas columns of weightMN are derived from successively deflated matrices, columns of weightStarMN relate to the original 'x' matrix: $T = XW^*$; $W^* = W(P'W)^{-1}$
suppLs	List of additional objects to be used internally by the 'print', 'plot', and 'predict' methods

Author(s)

Etienne Thevenot (CEA)

References

Eriksson et al. (2006). Multi- and Megarvariate Data Analysis. Umetrics Academy. Rosipal and Kramer (2006). Overview and recent advances in partial least squares Tenenhaus (1990). La regression PLS : theorie et pratique. Technip. Wehrens (2011). Chemometrics with R. Springer. Wold et al. (2001). PLS-regression: a basic tool of chemometrics

Examples

```
#### PCA

data(foods) ## see Eriksson et al. (2001); presence of 3 missing values (NA)
head(foods)
foodMN <- as.matrix(foods[, colnames(foods) != "Country"])
rownames(foodMN) <- foods[, "Country"]
head(foodMN)
foo.pca <- opls(foodMN)

#### PLS with a single response

data(cornell) ## see Tenenhaus, 1998
head(cornell)
cornell.pls <- opls(as.matrix(cornell[, grep("x", colnames(cornell))]),
                  cornell[, "y"])

## Complementary graphics

plot(cornell.pls, typeVc = c("outlier", "predict-train", "xy-score", "xy-weight"))

#### PLS with multiple (quantitative) responses

data(lowarp) ## see Eriksson et al. (2001); presence of NAs
head(lowarp)
lowarp.pls <- opls(as.matrix(lowarp[, c("glas", "crtp", "mica", "amtp")]),
                  as.matrix(lowarp[, grepl("^wrp", colnames(lowarp)) |
                                grepl("^st", colnames(lowarp))]))

#### PLS-DA
```

```

data(sacurine)
attach(sacurine)
sacurine.plsda <- opls(dataMatrix, sampleMetadata[, "gender"])

#### OPLS-DA

sacurine.oplsda <- opls(dataMatrix, sampleMetadata[, "gender"], predI = 1, orthoI = NA)

detach(sacurine)

```

opls-class

Class "opls"

Description

The opls object class

Objects from the Class

Objects can be created by calls of the form `new("opls", ...)` or by calling the `opls` function

Slots

`typeC`: character: model type (PCA, PLS, PLS-DA, OPLS, or OPLS-DA)

`descriptionMC`: character matrix: Description of the data set (number of samples, variables, etc.)

`modelDF`: Data frame with the model overview (number of components, R2X, R2X(cum), R2Y, R2Y(cum), Q2, Q2(cum), significance, iterations)

`summaryDF`: Data frame with the model summary (cumulated R2X, R2Y and Q2); RMSEE is the square root of the mean error between the actual and the predicted responses

`subsetVi`: Integer vector: Indices of observations in the training data set

`pcaVarVn`: PCA: Numerical vector of variances of length: `predI`

`vipVn`: PLS(-DA): Numerical vector of Variable Importance in Projection; OPLS(-DA): Numerical vector of Variable Importance for Prediction (VIP4,p from Galindo-Prieto et al, 2014)

`orthoVipVn`: OPLS(-DA): Numerical vector of Variable Importance for Orthogonal Modeling (VIP4,o from Galindo-Prieto et al, 2014)

`coefficientMN`: (O)PLS(-DA): Numerical matrix of regression coefficients (B; dimensions: `ncol(x)` x number of responses; $B = W * C'$ and $Y = XB + F$)

`xMeanVn`: Numerical vector: variable means of the 'x' matrix

`xSdVn`: Numerical vector: variable standard deviations of the 'x' matrix

`yMeanVn`: (O)PLS: Numerical vector: variable means of the 'y' response (transformed into a dummy matrix in case it is of 'character' mode initially)

`ySdVn`: (O)PLS: Numerical vector: variable standard deviations of the 'y' response (transformed into a dummy matrix in case it is of 'character' mode initially)

xZeroVarVi: Numerical vector: indices of variables with variance $< 2.22e-16$ which were excluded from 'x' before building the model

scoreMN: Numerical matrix of x scores (T; dimensions: $nrow(x) \times predI$) $X = TP' + E$; $Y = TC' + F$

loadingMN: Numerical matrix of x loadings (P; dimensions: $ncol(x) \times predI$) $X = TP' + E$

weightMN: (O)PLS: Numerical matrix of x weights (W; same dimensions as loadingMN)

orthoScoreMN: OPLS: Numerical matrix of orthogonal scores (Tortho; dimensions: $nrow(x) \times$ number of orthogonal components)

orthoLoadingMN: OPLS: Numerical matrix of orthogonal loadings (Portho; dimensions: $ncol(x) \times$ number of orthogonal components)

orthoWeightMN: OPLS: Numerical matrix of orthogonal weights (same dimensions as orthoLoadingMN)

cMN: (O)PLS: Numerical matrix of Y weights (C); dimensions: number of responses or number of classes in case of qualitative response with more than 2 classes \times number of predictive components; $Y = TC' + F$

coMN: (O)PLS: Numerical matrix of Y orthogonal weights; dimensions: number of responses or number of classes in case of qualitative response with more than 2 classes \times number of orthogonal components

uMN: (O)PLS: Numerical matrix of Y scores (U; same dimensions as scoreMN); $Y = UC' + G$

weightStarMN: Numerical matrix of projections (W*; same dimensions as loadingMN); whereas columns of weightMN are derived from successively deflated matrices, columns of weightStarMN relate to the original 'x' matrix: $T = XW^*$; $W^* = W(P'W)^{inv}$

suppLs: List of additional objects to be used internally by the 'print', 'plot', and 'predict' methods

Methods

print signature(object = "opls"): print method for (O)PLS(-DA) models

show signature(object = "opls"): show method for (O)PLS(-DA) models

plot signature(object = "opls"): plot method for (O)PLS(-DA) models

predict signature(object = "opls"): plot method for (O)PLS(-DA) models

coef signature(object = "opls"):

fitted signature(object = "opls"): returns predictions of the (O)PLS(-DA) model

residuals signature(object = "opls"): returns the residuals of the (O)PLS(-DA) regression model

tested signature(object = "opls"): returns the predictions of the (O)PLS(-DA) trained on the 'subset' observations only

getSummaryDF signature(object = "opls"): returns summary information about the model

getPcaVarVn signature(object = "opls"): returns the variance of the components (score vectors)

getScoreMN signature(object = "opls"): returns the (orthogonal) score matrix of the PCA/(O)PLS(-DA) model

getLoadingMN signature(object = "opls"): returns the (orthogonal) loading matrix of the PCA/(O)PLS(-DA) model

getWeightMN signature(object = "opls"): returns the (orthogonal) weight matrix of the (O)PLS(-DA) model

getVipVn signature(object = "opls"): returns the (orthogonal) VIP values of the (O)PLS(-DA) model

getSubsetVi signature(object = "opls"): extracts the indices of the samples used for building the model (when a subset argument has been specified)

Author(s)

Etienne Thevenot (CEA)

See Also

[opls](#),

Examples

```
#### PCA

data(foods) ## see Eriksson et al. (2001); presence of 3 missing values (NA)
head(foods)
foodMN <- as.matrix(foods[, colnames(foods) != "Country"])
rownames(foodMN) <- foods[, "Country"]
head(foodMN)
foo.pca <- opls(foodMN)

#### PLS with a single response

data(cornell) ## see Tenenhaus, 1998
head(cornell)
cornell.pls <- opls(as.matrix(cornell[, grep("x", colnames(cornell))]),
                  cornell[, "y"])

## Complementary graphics

plot(cornell.pls, typeVc = c("outlier", "predict-train", "xy-score", "xy-weight"))

#### PLS with multiple (quantitative) responses

data(lowarp) ## see Eriksson et al. (2001); presence of NAs
head(lowarp)
lowarp.pls <- opls(as.matrix(lowarp[, c("glas", "crtp", "mica", "amtp")]),
                  as.matrix(lowarp[, grepl("^wrp", colnames(lowarp)) |
                                grepl("^st", colnames(lowarp))]))

#### PLS-DA

data(sacurine)
```



```
attach(sacurine)
sacurine.plsda <- opls(dataMatrix, sampleMetadata[, "gender"])

#### OPLS-DA

sacurine.oplsda <- opls(dataMatrix, sampleMetadata[, "gender"], predI = 1, orthoI = NA)

detach(sacurine)
```

plot.opls

Plot Method for (O)PLS(-DA)

Description

This function plots values based upon a model trained by opls.

Usage

```
## S4 method for signature 'opls'
plot(x,
y,
typeVc = c("correlation",
"outlier",
"overview",
"permutation",
"predict-train",
"predict-test",
"summary",
"x-loading",
"x-score",
"x-variance",
"xy-score",
"xy-weight")[7],
parAsColFcVn = NA,
parCexN = 0.8,
parCompVi = c(1, 2),
parDevNewL = TRUE,
parEllipsesL = NA,
parLabVc = NA,
parTitleL = TRUE,
file.pdfC = NULL,
.sinkC = NULL,
...)
```

Arguments

x	An S4 object of class <code>opls</code> , created by the <code>opls</code> function.
y	Currently not used.
typeVc	Character vector: the following plots are available: <code>'correlation'</code> : Variable correlations with the components, <code>'outlier'</code> : Observation diagnostics (score and orthogonal distances), <code>'overview'</code> : Model overview showing <code>R2Ycum</code> and <code>Q2cum</code> (or <code>'Variance explained'</code> for PCA), <code>'permutation'</code> : Scatterplot of <code>R2Y</code> and <code>Q2Y</code> actual and simulated models after random permutation of response values; <code>'predict-train'</code> and <code>'predict-test'</code> : Predicted vs Actual Y for reference and test sets (only if Y has a single column), <code>'summary'</code> [default]: 4-plot summary showing permutation, overview, outlier, and x-score together, <code>'x-variance'</code> : Spread of raw variables corresp. with min, median, and max variances, <code>'x-loading'</code> : X-loadings (the 6 of variables most contributing to loadings are colored in red to facilitate interpretation), <code>'x-score'</code> : X-Scores, <code>'xy-score'</code> : XY-Scores, <code>'xy-weight'</code> : XY-Weights
parAsColFcVn	Optional factor character or numeric vector to be converted into colors for the score plot; default is NA [ie colors will be converted from 'y' in case of (O)PLS(-DA) or will be 'black' for PCA]
parCexN	Numeric: amount by which plotting text should be magnified relative to the default
parCompVi	Integer vector of length 2: indices of the two components to be displayed on the score plot (first two components by default)
parDevNewL	Should the graphics be displayed in a new window [default]; If FALSE, <code>parLayL</code> must be set to FALSE also
parEllipsesL	Should the Mahalanobis ellipses be drawn? If 'NA' [default], ellipses are drawn when either a character <code>parAsColVcn</code> is provided (PCA case), or when 'y' is a character factor ((O)PLS-DA cases).
parLabVc	Optional character vector for the labels of observations on the plot; default is NA [ie row names of 'x', if available, or indices of 'x', otherwise, will be used]
parTitleL	Should the titles of the plots be printed on the graphics (default = TRUE); It may be convenient to set this argument to FALSE when the user wishes to add specific titles a posteriori
file.pdfC	Figure filename (e.g. in case of batch mode) ending with '.pdf'; for multiple graphics, set <code>parLayL</code> to TRUE; default is NULL (no saving; displaying instead)
.sinkC	Character: Name of the file for R output diversion [default = NULL: no diversion]; Diversion of messages is required for the integration into Galaxy
...	Currently not used.

Author(s)

Etienne Thevenot (CEA)

Examples

```

data(sacurine)
attach(sacurine)

for(typeC in c("correlation", "outlier", "overview",
              "permutation", "predict-train", "predict-test",
              "summary", "x-loading", "x-score", "x-variance",
              "xy-score", "xy-weight")) {

  print(typeC)

  if(grepl("predict", typeC))
    subset <- "odd"
  else
    subset <- NULL

  opLs <- opls(dataMatrix, sampleMetadata[, "gender"],
              predI = ifelse(typeC != "xy-weight", 1, 2),
              orthoI = ifelse(typeC != "xy-weight", 1, 0),
              permI = ifelse(typeC == "permutation", 10, 0),
              subset = subset,
              printL = FALSE, plotL = FALSE)

  plot(opLs, typeVc = typeC)

}

detach(sacurine)

```

predict.opls

Predict method for (O)PLS models

Description

Returns predictions of the (O)PLS(-DA) model on a new dataset

Usage

```

## S4 method for signature 'opls'
predict(object, newdata, ...)

```

Arguments

object	An S4 object of class opls, created by opls function.
newdata	Either a data frame or a matrix, containing numeric columns only, with the same number of columns (variables) as the 'x' used for model training with 'opls'.
...	Currently not used.

Value

Predictions (either a vector, factor, or matrix depending on the y response used for training the model)

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)

predictorMN <- dataMatrix
responseFc <- sampleMetadata[, "gender"]

sacurine.plsda <- opls(predictorMN,
                      responseFc,
                      subset = "odd")

trainVi <- getSubsetVi(sacurine.plsda)

table(responseFc[trainVi], fitted(sacurine.plsda))

table(responseFc[-trainVi],
       predict(sacurine.plsda, predictorMN[-trainVi, ]))

detach(sacurine)
```

print.opls

Print method for 'opls' objects

Description

Displays information about the dataset and the model.

Usage

```
## S4 method for signature 'opls'
print(x, ...)
```

Arguments

x An S4 object of class opls, created by the opls function.
... Currently not used.

Value

Invisible.

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)
sacurine.plsda <- oplS(dataMatrix, sampleMetadata[, "gender"])

print(sacurine.plsda)

detach(sacurine)
```

residuals.opls	<i>Residuals method for (O)PLS models</i>
----------------	---

Description

Returns the residuals from the (O)PLS(-DA) regression models

Usage

```
## S4 method for signature 'opls'
residuals(object, ...)
```

Arguments

object	An S4 object of class oplS, created by oplS function.
...	Currently not used.

Value

Numeric matrix or vector (same dimensions as the modeled y response); if y is a character vector or a factor (in case of classification), the residuals equal 0 (predicted class identical to the true class) or 1 (prediction error)

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)

sacurine.pls <- opls(dataMatrix,
                    sampleMetadata[, "age"])

head(residuals(sacurine.pls))

detach(sacurine)
```

sacurine	<i>Analysis of the human adult urinary metabolome variations with age, body mass index and gender</i>
----------	---

Description

Urine samples from 183 human adults were analyzed by liquid chromatography coupled to high-resolution mass spectrometry (LTQ Orbitrap) in the negative ionization mode. A total of 109 metabolites were identified or annotated at the MSI level 1 or 2. After retention time alignment with XCMS, peaks were integrated with Quan Browser. After signal drift and batch effect correction of intensities, each urine profile was normalized to the osmolality of the sample. Finally, the data were log10 transformed.

Usage

```
data(sacurine)
```

Format

A list with the following elements: 1) `dataMatrix`: a 183 samples x 109 variables matrix of numeric type corresponding to the intensity profiles (values have been log10-transformed); 2) `sampleMetadata`: a 183 x 3 data frame, with the volunteers' age (`'age'`, numeric), body mass index (`'bmi'`, numeric), and gender (`'gender'`, factor), and 3) `variableMetadata`: a 109 x 3 data frame, with the metabolites' MSI identification level (`'msiLevel'`: either 1 or 2), HMDB ID when available (`'hmdb'`, character), chemical class according to the 'super class' taxonomy of HMDB (`'chemicalClass'`, character)

Value

List containing the `'dataMatrix'` matrix (numeric) of data (samples as rows, variables as columns), the `'sampleMetadata'` data frame of sample metadata, and the `variableMetadata` data frame of variable metadata. Row names of `'dataMatrix'` and `'sampleMetadata'` are identical. Column names of `'dataMatrix'` are identical to row names of `'variableMetadata'`. For details see the `'Format'` section above.

References

Thevenot E.A., Roux A., Xu Y., Ezan E. and Junot C. (2015). Analysis of the human adult urinary metabolome variations with age, body mass index and gender by implementing a comprehensive workflow for univariate and OPLS statistical analyses. *Journal of Proteome Research*, DOI: 10.1021/acs.jproteome.5b00354

show.opls

Show method for 'opls' objects

Description

Displays information about the dataset and the model.

Usage

```
## S4 method for signature 'opls'  
show(object)
```

Arguments

object An S4 object of class op`ls`, created by the `opls` function.

Value

Invisible.

Author(s)

Philippe Rinaudo and Etienne Thevenot (CEA)

Examples

```
data(sacurine)  
attach(sacurine)  
sacurine.plsda <- opls(dataMatrix, sampleMetadata[, "gender"])  
  
show(sacurine.plsda)  
  
detach(sacurine)
```

strF *Printed summary of an R object*

Description

Displays the class, mode, size and first...last values of the object

Usage

```
strF(inpMF, borderN = 2, bigMarkC = ",")
```

Arguments

inpMF	Input matrix, dataframe or vector
borderN	Number of border (first and last) rows and columns to display
bigMarkC	Big mark separator for summary results

Value

This function has no output.

Author(s)

Etienne Thevenot (CEA)

See Also

[str](#)

Examples

```
data(sacurine)
strF(sacurine[['dataMatrix']])
strF(sacurine[['sampleMetadata']])
```

tested *Tested method for (O)PLS models*

Description

Returns predictions of the (O)PLS(-DA) model on the out of the box samples (when a 'subset' of samples has been selected when training the model)

Usage

```
## S4 method for signature 'opls'
tested(object)
```


Arguments

object An S4 object of class `opls`, created by `opls` function.

Value

Predictions (either a vector, factor, or matrix depending on the `y` response used for training the model)

Author(s)

Etienne Thevenot (CEA)

Examples

```
data(sacurine)
attach(sacurine)

testedorMN <- dataMatrix
responseFc <- sampleMetadata[, "gender"]

sacurine.plsda <- opls(testedorMN,
                      responseFc,
                      subset = "odd")

trainVi <- getSubsetVi(sacurine.plsda)

table(responseFc[trainVi], fitted(sacurine.plsda))

detach(sacurine)
```

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