Package 'mixOmics'

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Type Package

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Suggests BiocStyle, knitr, rmarkdown, mime, testthat, microbenchmark, magick, vdiffr, kableExtra, devtools

Description Multivariate methods are well suited to large omics data sets where the number of variables (e.g. genes, proteins, metabolites) is much larger than the number of samples (patients, cells, mice). They have the appealing properties of reducing the dimension of the data by using instrumental variables (components), which are defined as combinations of all variables. Those components are then used to produce useful graphical outputs that enable better understanding of the relationships and correlation structures between the different data sets that are integrated. mixOmics offers a wide range of multivariate methods for the exploration and integration of biological datasets with a particular focus on variable selection. The package proposes several sparse multivariate models we have developed to identify the key variables that are highly correlated, and/or explain the biological outcome of interest. The data that can be analysed with mixOmics may come from high throughput sequencing technologies, such as omics data (transcriptomics, metabolomics, proteomics, metagenomics etc) but also beyond the realm of omics (e.g. spectral imaging). The methods implemented in mixOmics can also handle missing values without having to delete entire rows with missing data. A non exhaustive list of methods include variants of generalised Canonical Correlation Analysis, sparse Partial Least Squares and sparse Discriminant Analysis. Recently we implemented integrative methods to combine multiple data sets: N-integration with variants of Generalised Canonical Correlation Analysis and P-integration with variants of multi-group Partial Least Squares.

License GPL (>= 2)

URL http://www.mixOmics.org

BugReports https://github.com/mixOmicsTeam/mixOmics/issues/

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`mixOmics-package` *'Omics Data Integration Project*

Description

Multivariate methods are well suited to large omics data sets where the number of variables (e.g. genes, proteins, metabolites) is much larger than the number of samples (patients, cells, mice). They have the appealing properties of reducing the dimension of the data by using instrumental variables (components), which are defined as combinations of all variables. Those components are then used to produce useful graphical outputs that enable better understanding of the relationships and correlation structures between the different data sets that are integrated.

Details

mixOmics offers a wide range of multivariate methods for the exploration and integration of biological datasets with a particular focus on variable selection. The package proposes several sparse multivariate models we have developed to identify the key variables that are highly correlated, and/or explain the biological outcome of interest. The data that can be analysed with mixOmics may come from high throughput sequencing technologies, such as omics data (transcriptomics, metabolomics, proteomics, metagenomics etc) but also beyond the realm of omics (e.g. spectral imaging).

The methods implemented in mixOmics can also handle missing values without having to delete entire rows with missing data. A non exhaustive list of methods include variants of generalised Canonical Correlation Analysis, sparse Partial Least Squares and sparse Discriminant Analysis. Recently we implemented integrative methods to combine multiple data sets: N-integration with variants of Generalised Canonical Correlation Analysis and P-integration with variants of multigroup Partial Least Squares.

See Also

Useful links:

- http://www.mixOmics.org
- Report bugs at https://github.com/mixOmicsTeam/mixOmics/issues/

---

auroc *Area Under the Curve (AUC) and Receiver Operating Characteristic (ROC) curves for supervised classification*

Description

Calculates the AUC and plots ROC for supervised models from s/plsda, mint.s/plsda and block.plsda, block.splsda or wrapper.sgccda functions.

Usage

```
auroc(object, ...)

## S3 method for class 'mixo_plsda'
auroc(
  object,
  newdata = object$input.X,
  outcome.test = as.factor(object$Y),
  multilevel = NULL,
  plot = TRUE,
  roc.comp = NULL,
  title = NULL,
  print = TRUE,
  ...
)

## S3 method for class 'mixo_splsda'
auroc(
  object,
  newdata = object$input.X,
  outcome.test = as.factor(object$Y),
  multilevel = NULL,
  plot = TRUE,
  roc.comp = NULL,
  title = NULL,
  print = TRUE,
  ...
)

## S3 method for class 'list'
auroc(object, plot = TRUE, roc.comp = NULL, title = NULL, print = TRUE, ...)

## S3 method for class 'mint.plsda'
auroc(
```

```
  object,
  newdata = object$X,
  outcome.test = as.factor(object$Y),
  study.test = object$study,
  multilevel = NULL,
  plot = TRUE,
  roc.comp = NULL,
  roc.study = "global",
  title = NULL,
  print = TRUE,
  ...
)

## S3 method for class 'mint.splsda'
auroc(
  object,
  newdata = object$X,
  outcome.test = as.factor(object$Y),
  study.test = object$study,
  multilevel = NULL,
  plot = TRUE,
  roc.comp = NULL,
  roc.study = "global",
  title = NULL,
  print = TRUE,
  ...
)

## S3 method for class 'sgccda'
auroc(
  object,
  newdata = object$X,
  outcome.test = as.factor(object$Y),
  multilevel = NULL,
  plot = TRUE,
  roc.block = 1L,
  roc.comp = NULL,
  title = NULL,
  print = TRUE,
  ...
)

## S3 method for class 'mint.block.plsda'
auroc(
  object,
  newdata = object$X,
  study.test = object$study,
  outcome.test = as.factor(object$Y),
  multilevel = NULL,
  plot = TRUE,
  roc.block = 1,
  roc.comp = NULL,
```

```
  title = NULL,
  print = TRUE,
  ...
)

## S3 method for class 'mint.block.splsda'
auroc(
  object,
  newdata = object$X,
  study.test = object$study,
  outcome.test = as.factor(object$Y),
  multilevel = NULL,
  plot = TRUE,
  roc.block = 1,
  roc.comp = NULL,
  title = NULL,
  print = TRUE,
  ...
)
```

Arguments

`object`	Object of class inherited from one of the following supervised analysis function: "plsda", "splsda", "mint.plsda", "mint.splsda", "block.splsda" or "wrapper.sgccda". Alternatively, this can be a named list of plsda and splsda objects if multiple models are to be compared. Note that these multiple models need to have used the same levels in the response variable.
`...`	external optional arguments for plotting - `line.col` for custom colors and `legend.title` for custom legend title
`newdata`	numeric matrix of predictors, by default set to the training data set (see details).
`outcome.test`	Either a factor or a class vector for the discrete outcome, by default set to the outcome vector from the training set (see details).
`multilevel`	Sample information when a newdata matrix is input and when multilevel decomposition for repeated measurements is required. A numeric matrix or data frame indicating the repeated measures on each individual, i.e. the individuals ID. See examples in `splsda`.
`plot`	Whether the ROC curves should be plotted, by default set to TRUE (see details).
`roc.comp`	Specify the component (integer) up to which the ROC will be calculated and plotted from the multivariate model, default to 1.
`title`	Character, specifies the title of the plot.
`print`	Logical, specifies whether the output should be printed.
`study.test`	For MINT objects, grouping factor indicating which samples of `newdata` are from the same study. Overlap with `object$study` are allowed.
`roc.study`	Specify the study for which the ROC will be plotted for a mint.plsda or mint.splsda object, default to "global".
`roc.block`	Specify the block number (integer) or the name of the block (set of characters) for which the ROC will be plotted for a block.plsda or block.splsda object, default to 1.

Details

For more than two classes in the categorical outcome Y, the AUC is calculated as one class vs. the other and the ROC curves one class vs. the others are output.

The ROC and AUC are calculated based on the predicted scores obtained from the `predict` function applied to the multivariate methods (`predict(object)$predict`). Our multivariate supervised methods already use a prediction threshold based on distances (see `predict`) that optimally determine class membership of the samples tested. As such AUC and ROC are not needed to estimate the performance of the model (see `perf`, `tune` that report classification error rates). We provide those outputs as complementary performance measures.

The pvalue is from a Wilcoxon test between the predicted scores between one class vs the others.

External independent data set (`newdata`) and outcome (`outcome.test`) can be input to calculate AUROC. The external data set must have the same variables as the training data set (`object$X`).

If `object` is a named list of multiple `plsda` and `splsda` objects, ensure that these models each have a response variable with the same levels. Additionally, `newdata` and `outcome.test` cannot be passed to this form of `auroc`.

If `newdata` is not provided, AUROC is calculated from the training data set, and may result in overfitting (too optimistic results).

Note that for mint.plsda and mint.splsda objects, if `roc.study` is different from "global", then `newdata`), `outcome.test` and `sstudy.test` are not used.

Value

Depending on the type of object used, a list that contains: The AUC and Wilcoxon test pvalue for each 'one vs other' classes comparison performed, either per component (splsda, plsda, mint.plsda, mint.splsda), or per block and per component (wrapper.sgccda, block.plsda, blocksplsda).

Author(s)

Benoit Gautier, Francois Bartolo, Florian Rohart, Al J Abadi

See Also

`tune`, `perf`, and http://www.mixOmics.org for more details.

Examples

```
## example with PLSDA, 2 classes
# ----------------
data(breast.tumors)
X <- breast.tumors$gene.exp
Y <- breast.tumors$sample$treatment

plsda.breast <- plsda(X, Y, ncomp = 2)
auc.plsda.breast = auroc(plsda.breast, roc.comp = 1)
auc.plsda.breast = auroc(plsda.breast, roc.comp = 2)

## Not run:
## example with sPLSDA
# -----------------
splsda.breast <- splsda(X, Y, ncomp = 2, keepX = c(25, 25))
auroc(plsda.breast, plot = FALSE)
```

```
## example with sPLSDA with 4 classes
# -----------------
data(liver.toxicity)
X <- as.matrix(liver.toxicity$gene)
# Y will be transformed as a factor in the function,
# but we set it as a factor to set up the colors.
Y <- as.factor(liver.toxicity$treatment[, 4])

splsda.liver <- splsda(X, Y, ncomp = 2, keepX = c(20, 20))
auc.splsda.liver = auroc(splsda.liver, roc.comp = 2)


## example with mint.plsda
# -----------------
data(stemcells)

res = mint.plsda(X = stemcells$gene, Y = stemcells$celltype, ncomp = 3,
study = stemcells$study)
auc.mint.pslda = auroc(res, plot = FALSE)

## example with mint.splsda
# -----------------
res = mint.splsda(X = stemcells$gene, Y = stemcells$celltype, ncomp = 3, keepX = c(10, 5, 15),
study = stemcells$study)
auc.mint.spslda = auroc(res, plot = TRUE, roc.comp = 3)


## example with block.plsda
# ------------------
data(nutrimouse)
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid)
# with this design, all blocks are connected
design = matrix(c(0,1,1,0), ncol = 2, nrow = 2,
byrow = TRUE, dimnames = list(names(data), names(data)))

block.plsda.nutri = block.plsda(X = data, Y = nutrimouse$diet)
auc.block.plsda.nutri = auroc(block.plsda.nutri, roc.block = 'lipid')

## example with block.splsda
# ---------------
list.keepX = list(gene = rep(10, 2), lipid = rep(5,2))
block.splsda.nutri = block.splsda(X = data, Y = nutrimouse$diet, keepX = list.keepX)
auc.block.splsda.nutri = auroc(block.splsda.nutri, roc.block = 1)

## End(Not run)
```

`background.predict` *Calculate prediction areas*

Description

Calculate prediction areas that can be used in plotIndiv to shade the background.

Usage

```
background.predict(
  object,
  comp.predicted = 1,
  dist = "max.dist",
  xlim = NULL,
  ylim = NULL,
  resolution = 100
)
```

Arguments

object	A list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in matrices, samples x variables, with samples order matching in all data sets.
comp.predicted	Matrix response for a multivariate regression framework. Data should be continuous variables (see block.splsda for supervised classification and factor reponse)
dist	distance to use to predict the class of new data, should be a subset of "centroids.dist", "mahalanobis.dist" or "max.dist" (see predict).
xlim, ylim	numeric list of vectors of length 2, giving the x and y coordinates ranges for the simulated data. By default will be $1.2*$ the range of object$variates$X[,i]
resolution	A total of resolution*resolution data are simulated between xlim[1], xlim[2], ylim[1] and ylim[2].

Details

background.predict simulates resolution*resolution points within the rectangle defined by xlim on the x-axis and ylim on the y-axis, and then predicts the class of each point (defined by two coordinates). The algorithm estimates the predicted area for each class, defined as the 2D surface where all points are predicted to be of the same class. A polygon is returned and should be passed to plotIndiv for plotting the actual background.

Note that by default xlim and ylim will create a rectangle of simulated data that will cover the plotted area of plotIndiv. However, if you use plotIndiv with ellipse=TRUE or if you set xlim and ylim, then you will need to adapt xlim and ylim in background.predict.

Also note that the white frontier that defines the predicted areas when plotting with plotIndiv can be reduced by increasing resolution.

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017).

Value

background.predict returns a list of coordinates to be used with polygon to draw the predicted area for each class.

Author(s)

Florian Rohart, Al J Abadi

References

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

plotIndiv, predict, polygon.

Examples

```
# Example 1
# ----------------------------------
data(breast.tumors)
X <- breast.tumors$gene.exp
Y <- breast.tumors$sample$treatment

splsda.breast <- splsda(X, Y,keepX=c(10,10),ncomp=2)

# calculating background for the two first components, and the centroids distance

background = background.predict(splsda.breast, comp.predicted = 2, dist = "centroids.dist")

## Not run:
# default option: note that the outcome color is included by default!
plotIndiv(splsda.breast, background = background, legend=TRUE)

# Example 2
# ----------------------------------
data(liver.toxicity)
X = liver.toxicity$gene
Y = as.factor(liver.toxicity$treatment[, 4])

plsda.liver <- plsda(X, Y, ncomp = 2)

# calculating background for the two first components, and the mahalanobis distance
background = background.predict(plsda.liver, comp.predicted = 2, dist = "mahalanobis.dist")

plotIndiv(plsda.liver, background = background, legend = TRUE)



## End(Not run)
```

`biplot` *biplot methods for* pca *family*

Description

biplot methods for pca family

Usage

```
## S3 method for class 'pca'
biplot(
  x,
  comp = c(1, 2),
  block = NULL,
```

```
  ind.names = TRUE,
  group = NULL,
  cutoff = 0,
  col = NULL,
  ind.names.size = 3,
  ind.names.col = color.mixo(4),
  ind.names.repel = TRUE,
  pch = 19,
  pch.size = 2,
  var.names = TRUE,
  var.names.col = "grey40",
  var.names.size = 4,
  var.names.angle = FALSE,
  var.arrow.col = "grey40",
  var.arrow.size = 0.5,
  var.arrow.length = 0.2,
  ind.legend.title = NULL,
  vline = FALSE,
  hline = FALSE,
  legend = if (is.null(group)) FALSE else TRUE,
  legend.title = NULL,
  pch.legend.title = NULL,
  cex = 1.05,
  ...
)

## S3 method for class 'mixo_pls'
biplot(
  x,
  comp = c(1, 2),
  block = NULL,
  ind.names = TRUE,
  group = NULL,
  cutoff = 0,
  col = NULL,
  ind.names.size = 3,
  ind.names.col = color.mixo(4),
  ind.names.repel = TRUE,
  pch = 19,
  pch.size = 2,
  var.names = TRUE,
  var.names.col = "grey40",
  var.names.size = 4,
  var.names.angle = FALSE,
  var.arrow.col = "grey40",
  var.arrow.size = 0.5,
  var.arrow.length = 0.2,
  ind.legend.title = NULL,
  vline = FALSE,
  hline = FALSE,
  legend = if (is.null(group)) FALSE else TRUE,
  legend.title = NULL,
```

```
  pch.legend.title = NULL,
  cex = 1.05,
  ...
)
```

Arguments

x	An object of class 'pca'or mixOmics '(s)pls'.
comp	integer vector of length two (or three to 3d). The components that will be used on the horizontal and the vertical axis respectively to project the individuals.
block	Character, name of the block to show for pls object. Default to 'X'.
ind.names	either a character vector of names for the individuals to be plotted, or FALSE for no names. If TRUE, the row names of the first (or second) data matrix is used as names (see Details). If 'pch' is set this will overwrite the names as shapes. Default is TRUE. Not avaliable for MINT objects.
group	Factor indicating the group membership for each sample.
cutoff	numeric between 0 and 1. Variables with correlations below this cutoff in absolute value are not plotted (see Details).
col	character (or symbol) color to be used. If group provided, should be a vector of the same length as groups, order of colours will be respected to correspond to order of group levels.
ind.names.size	Numeric, sample name size.
ind.names.col	Character, sample name colour.
ind.names.repel	Logical, whether to repel away label names.
pch	A single character or numeric value, or a factor. If a factor, the levels of the factor are used to define the point types. If a character or numeric value, the same point type is used for all points. If NULL, the default point type is used. See examples.
pch.size	Numeric, sample point character size.
var.names	Logical indicating whether to show variable names. Alternatively, a character.
var.names.col	Character, variable name colour.
var.names.size	Numeric, variable name size.
var.names.angle	Logical, whether to align variable names to arrow directions.
var.arrow.col	Character, variable arrow colour. If 'NULL', no arrows are shown.
var.arrow.size	Numeric, variable arrow head size.
var.arrow.length	Numeric, length of the arrow head in 'cm'.
ind.legend.title	Character, title of the legend.
vline	Logical, whether to draw the vertical neutral line.
hline	Logical, whether to draw the horizontal neutral line.
legend	Logical, whether to show the legend if group != NULL.
legend.title	Character, the legend title if group != NULL.

pch.legend.title
: Character, the legend title if pch is a factor.

cex
: Numeric scalar indicating the desired magnification of plot texts. theme function may be used with the output object if further customisation is required.

...
: Not currently used.

pch.legend
: Character, the legend title if pch is a factor.

Details

biplot unifies the reduced representation of both the observations/samples and variables of a matrix of multivariate data on the same plot. Essentially, in the reduced space the samples are shown as points/names and the contributions of features to each dimension are shown as directed arrows or vectors. For pls objects it is possible to use either 'X' or 'Y' latent space using block argument.

Value

A ggplot object.

Author(s)

Al J Abadi

Examples

```
## 'pca' class - examples demonstrate how to control sample colours and customise plots
# ------------------------------------------------------------------------------------
set.seed(42)
data("nutrimouse")
pca.lipid <- pca(nutrimouse$lipid, ncomp = 3, scale = TRUE)

# colors indicate diet
biplot(pca.lipid, group = nutrimouse$diet)

# colors indicate genotype
biplot(pca.lipid, group = nutrimouse$genotype)

# customise colours
biplot(pca.lipid, group = nutrimouse$genotype,
       col = c("red", "blue"))

## correlation cutoff to filter features
biplot(pca.lipid, cutoff = c(0.8))

## tailor threshold for each component
biplot(pca.lipid, cutoff = c(0.8, 0.7))

## customise components
biplot(pca.lipid, cutoff = c(0.8), comp = c(1,3))

## customise ggplot in an arbitrary way
biplot(pca.lipid) + theme_linedraw() +
    # add vline
    geom_vline(xintercept = 0, col = 'green') +
    # add hline
    geom_hline(yintercept = 0, col = 'green') +
```

```
    # customise labs
    labs(x = 'Principal Component 1', y = 'Principal Component 2')

## customise variable labels
biplot(pca.lipid,
       var.names.col = color.mixo(2),
       var.names.size = 4,
       var.names.angle = TRUE
)

## no arrows
biplot(pca.lipid, group = nutrimouse$diet, legend.title = 'Diet',
       var.arrow.col = NULL, var.names.col = 'black')

## add x=0 and y=0 lines in function
biplot(pca.lipid, group = nutrimouse$diet, legend.title = 'Diet',
       var.arrow.col = NULL, var.names.col = 'black',
       vline = TRUE, hline = TRUE)

## 'pls' class - examples demonstrate how to control cutoffs
# ------------------------------------------------------------------------------

data("nutrimouse")
pls.nutrimouse <- pls(X = nutrimouse$gene, Y = nutrimouse$lipid, ncomp = 2)

biplot(pls.nutrimouse, group = nutrimouse$genotype, block = 'X',
       legend.title = 'Genotype', cutoff = 0.878)

biplot(pls.nutrimouse, group = nutrimouse$genotype, block = 'Y',
       legend.title = 'Genotype', cutoff = 0.8)


## 'plsda' class - examples demonstrate how to control point shapes
# ------------------------------------------------------------------------------

data(breast.tumors)
X <- breast.tumors$gene.exp
colnames(X) <- paste0('GENE_', colnames(X))
rownames(X) <- paste0('SAMPLE_', rownames(X))
Y <- breast.tumors$sample$treatment
nrow(X)
grouping <- factor(c(rep("A", 20), rep("B", 20), rep("C", 7)))

plsda.breast <- plsda(X, Y, ncomp = 2)

biplot(plsda.breast, cutoff = 0.72, ind.names = FALSE)

biplot(plsda.breast, cutoff = 0.72, ind.names = FALSE, pch = 2, pch.size = 5)

biplot(plsda.breast, cutoff = 0.72, pch = grouping, pch.size = 5)
```

`block.pls` *N-integration with Projection to Latent Structures models (PLS)*

Description

Integration of multiple data sets measured on the same samples or observations, ie. N-integration. The method is partly based on Generalised Canonical Correlation Analysis.

Usage

```
block.pls(
  X,
  Y,
  indY,
  ncomp = 2,
  design,
  mode,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in matrices, samples x variables, with samples order matching in all data sets.
Y	Matrix response for a multivariate regression framework. Data should be continuous variables (see ?block.plsda for supervised classification and factor response).
indY	To supply if Y is missing, indicates the position of the matrix response in the list X.
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.

near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

block.spls function fits a horizontal integration PLS model with a specified number of components per block). An outcome needs to be provided, either by Y or by its position indY in the list of blocks X. Multi (continuous)response are supported. X and Y can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm block.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the impute.nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and ?pls for more details). Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Note that our method is partly based on Generalised Canonical Correlation Analysis and differs from the MB-PLS approaches proposed by Kowalski et al., 1989, J Chemom 3(1) and Westerhuis et al., 1998, J Chemom, 12(5).

Value

block.pls returns an object of class 'block.pls', a list that contains the following components:

X	the centered and standardized original predictor matrix.
indY	the position of the outcome Y in the output list X.
ncomp	the number of components included in the model for each block.
mode	the algorithm used to fit the model.
variates	list containing the variates of each block of X.
loadings	list containing the estimated loadings for the variates.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
iter	Number of iterations of the algorithm for each component
prop_expl_var	Percentage of explained variance for each component and each block
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

Wold H. (1966). Estimation of principal components and related models by iterative least squares. In: Krishnaiah, P. R. (editors), *Multivariate Analysis*. Academic Press, N.Y., 391-420.

Tenenhaus A. and Tenenhaus M., (2011), Regularized Generalized Canonical Correlation Analysis, Psychometrika, Vol. 76, Nr 2, pp 257-284.

See Also

plotIndiv, plotArrow, plotLoadings, plotVar, predict, perf, selectVar, block.spls, block.plsda and http://www.mixOmics.org for more details.

Examples

```
# Example with TCGA multi omics study
# ----------------------------------
data("breast.TCGA")
# this is the X data as a list of mRNA and miRNA; the Y data set is a single data set of proteins
data = list(mrna = breast.TCGA$data.train$mrna, mirna = breast.TCGA$data.train$mirna)
# set up a full design where every block is connected
design = matrix(1, ncol = length(data), nrow = length(data),
dimnames = list(names(data), names(data)))
diag(design) =  0
design
# set number of component per data set
ncomp = c(2)

TCGA.block.pls = block.pls(X = data, Y = breast.TCGA$data.train$protein,
                           ncomp = ncomp, design = design)
TCGA.block.pls
## use design = 'full'
TCGA.block.pls = block.pls(X = data, Y = breast.TCGA$data.train$protein,
                           ncomp = ncomp, design = 'full')
# in plotindiv we color the samples per breast subtype group but the method is unsupervised!
# here Y is the protein data set
plotIndiv(TCGA.block.pls, group =  breast.TCGA$data.train$subtype, ind.names = FALSE)
```

---

block.plsda *N-integration with Projection to Latent Structures models (PLS) with Discriminant Analysis*

Description

Integration of multiple data sets measured on the same samples or observations to classify a discrete outcome, ie. N-integration with Discriminant Analysis. The method is partly based on Generalised Canonical Correlation Analysis.

Usage

```
block.plsda(
  X,
  Y,
```

```
  indY,
  ncomp = 2,
  design,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in matrices, samples x variables, with samples order matching in all data sets.
Y	a factor or a class vector for the discrete outcome.
indY	To supply if Y is missing, indicates the position of the matrix response in the list X.
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

block.plsda function fits a horizontal integration PLS-DA model with a specified number of components per block). A factor indicating the discrete outcome needs to be provided, either by Y or by its position indY in the list of blocks X.

X can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm block.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the impute.nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and ?pls for more details).

Note that our method is partly based on Generalised Canonical Correlation Analysis and differs from the MB-PLS approaches proposed by Kowalski et al., 1989, J Chemom 3(1) and Westerhuis et al., 1998, J Chemom, 12(5).

Value

block.plsda returns an object of class "block.plsda","block.pls", a list that contains the following components:

X	the centered and standardized original predictor matrix.
indY	the position of the outcome Y in the output list X.
ncomp	the number of components included in the model for each block.
mode	the algorithm used to fit the model.
variates	list containing the variates of each block of X.
loadings	list containing the estimated loadings for the variates.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
iter	Number of iterations of the algorithm for each component
prop_expl_var	Percentage of explained variance for each component and each block
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

On PLSDA:

Barker M and Rayens W (2003). Partial least squares for discrimination. *Journal of Chemometrics* **17**(3), 166-173. Perez-Enciso, M. and Tenenhaus, M. (2003). Prediction of clinical outcome with microarray data: a partial least squares discriminant analysis (PLS-DA) approach. *Human Genetics* **112**, 581-592. Nguyen, D. V. and Rocke, D. M. (2002). Tumor classification by partial least squares using microarray gene expression data. *Bioinformatics* **18**, 39-50.

On multiple integration with PLS-DA: Gunther O., Shin H., Ng R. T. , McMaster W. R., McManus B. M. , Keown P. A. , Tebbutt S.J. , Lê Cao K-A. , (2014) Novel multivariate methods for integration of genomics and proteomics data: Applications in a kidney transplant rejection study, OMICS: A journal of integrative biology, 18(11), 682-95.

On multiple integration with sPLS-DA and 4 data blocks:

Singh A., Gautier B., Shannon C., Vacher M., Rohart F., Tebbutt S. and Lê Cao K.A. (2016). DIABLO: multi omics integration for biomarker discovery. BioRxiv available here: http://biorxiv.org/content/early/2016/08/03/067611

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

plotIndiv, plotArrow, plotLoadings, plotVar, predict, perf, selectVar, block.pls, block.splsda and http://www.mixOmics.org for more details.

Examples

```
data(nutrimouse)
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = nutrimouse$diet)
# with this design, all blocks are connected
design = matrix(c(0,1,1,1,0,1,1,1,0), ncol = 3, nrow = 3,
byrow = TRUE, dimnames = list(names(data), names(data)))

res = block.plsda(X = data, indY = 3) # indY indicates where the outcome Y is in the list X
plotIndiv(res, ind.names = FALSE, legend = TRUE)
plotVar(res)

## Not run:
# when Y is provided
res2 = block.plsda(list(gene = nutrimouse$gene, lipid = nutrimouse$lipid),
Y = nutrimouse$diet, ncomp = 2)
plotIndiv(res2)
plotVar(res2)

## End(Not run)
```

---

block.spls *N-integration and feature selection with sparse Projection to Latent Structures models (sPLS)*

Description

Integration of multiple data sets measured on the same samples or observations, with variable selection in each data set, ie. N-integration. The method is partly based on Generalised Canonical Correlation Analysis.

Usage

```
block.spls(
  X,
  Y,
  indY,
  ncomp = 2,
  keepX,
  keepY,
```

```
  design,
  mode,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in matrices, samples x variables, with samples order matching in all data sets.
Y	Matrix response for a multivariate regression framework. Data should be continuous variables (see ?block.splsda for supervised classification and factor response).
indY	To supply if Y is missing, indicates the position of the matrix response in the list X.
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
keepX	A named list of same length as X. Each entry is the number of variables to select in each of the blocks of X for each component. By default all variables are kept in the model.
keepY	Only if Y is provided (and not indY). Each entry is the number of variables to select in each of the blocks of Y for each component.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

block.spls function fits a horizontal sPLS model with a specified number of components per block). An outcome needs to be provided, either by Y or by its position indY in the list of blocks X. Multi (continuous)response are supported. X and Y can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm block.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and ?pls for more details).

Note that our method is partly based on sparse Generalised Canonical Correlation Analysis and differs from the MB-PLS approaches proposed by Kowalski et al., 1989, J Chemom 3(1), Westerhuis et al., 1998, J Chemom, 12(5) and sparse variants Li et al., 2012, Bioinformatics 28(19); Karaman et al (2014), Metabolomics, 11(2); Kawaguchi et al., 2017, Biostatistics.

Variable selection is performed on each component for each block of X, and for Y if specified, via input parameter keepX and keepY.

Note that if Y is missing and indY is provided, then variable selection on Y is performed by specifying the input parameter directly in keepX (no keepY is needed).

Value

block.spls returns an object of class "block.spls", a list that contains the following components:

X	the centered and standardized original predictor matrix.
indY	the position of the outcome Y in the output list X.
ncomp	the number of components included in the model for each block.
mode	the algorithm used to fit the model.
keepX	Number of variables used to build each component of each block
keepY	Number of variables used to build each component of Y
variates	list containing the variates of each block of X.
loadings	list containing the estimated loadings for the variates.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
iter	Number of iterations of the algorithm for each component
prop_expl_var	Percentage of explained variance for each component and each block after setting possible missing values in the centered data to zero
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

Wold H. (1966). Estimation of principal components and related models by iterative least squares. In: Krishnaiah, P. R. (editors), *Multivariate Analysis*. Academic Press, N.Y., 391-420.

Tenenhaus A. and Tenenhaus M., (2011), Regularized Generalized Canonical Correlation Analysis, Psychometrika, Vol. 76, Nr 2, pp 257-284.

Tenenhaus A., Philippe C., Guillemot V, Lê Cao K.A., Grill J, Frouin V. Variable selection for generalized canonical correlation analysis. *Biostatistics*. kxu001

See Also

plotIndiv, plotArrow, plotLoadings, plotVar, predict, perf, selectVar, block.pls, block.splsda and http://www.mixOmics.org for more details.

Examples

```
# Example with multi omics TCGA study
# ----------------------------
data("breast.TCGA")
# this is the X data as a list of mRNA and miRNA; the Y data set is a single data set of proteins
data = list(mrna = breast.TCGA$data.train$mrna, mirna = breast.TCGA$data.train$mirna)
# set up a full design where every block is connected
design = matrix(1, ncol = length(data), nrow = length(data),
dimnames = list(names(data), names(data)))
diag(design) =  0
design
# set number of component per data set
ncomp = c(2)
# set number of variables to select, per component and per data set (this is set arbitrarily)
list.keepX = list(mrna = rep(10, 2), mirna = rep(10,2))
list.keepY = c(rep(10, 2))

TCGA.block.spls = block.spls(X = data, Y = breast.TCGA$data.train$protein,
ncomp = ncomp, keepX = list.keepX, keepY = list.keepY, design = design)
TCGA.block.spls
# in plotindiv we color the samples per breast subtype group but the method is unsupervised!
plotIndiv(TCGA.block.spls, group = breast.TCGA$data.train$subtype, ind.names = FALSE, legend=TRUE)
# illustrates coefficient weights in each block
plotLoadings(TCGA.block.spls, ncomp = 1)
plotVar(TCGA.block.spls, style = 'graphics', legend = TRUE)

## plot markers (selected markers) for mrna and mirna
group <- breast.TCGA$data.train$subtype
# mrna: show each selected feature separately and group by subtype
plotMarkers(object = TCGA.block.spls, comp = 1, block = 'mrna', group = group)
# mrna: aggregate all selected features, separate by loadings signs and group by subtype
plotMarkers(object = TCGA.block.spls, comp = 1, block = 'mrna', group = group, global = TRUE)
# proteins
plotMarkers(object = TCGA.block.spls, comp = 1, block = 'Y', group = group)
## only show boxplots
plotMarkers(object = TCGA.block.spls, comp = 1, block = 'Y', group = group, violin = FALSE)

## Not run:
network(TCGA.block.spls)
```

```
## End(Not run)
```

`block.splsda` *N-integration and feature selection with Projection to Latent Structures models (PLS) with sparse Discriminant Analysis*

Description

Integration of multiple data sets measured on the same samples or observations to classify a discrete outcome to classify a discrete outcome and select features from each data set, ie. N-integration with sparse Discriminant Analysis. The method is partly based on Generalised Canonical Correlation Analysis.

Usage

```
block.splsda(
  X,
  Y,
  indY,
  ncomp = 2,
  keepX,
  design,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)

wrapper.sgccda(
  X,
  Y,
  indY,
  ncomp = 2,
  keepX,
  design,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

`X`	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in matrices, samples x variables, with samples order matching in all data sets.
`Y`	a factor or a class vector for the discrete outcome.

indY	To supply if Y is missing, indicates the position of the matrix response in the list X.
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
keepX	A named list of same length as X. Each entry is the number of variables to select in each of the blocks of X for each component. By default all variables are kept in the model.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

block.splsda function fits a horizontal integration PLS-DA model with a specified number of components per block). A factor indicating the discrete outcome needs to be provided, either by Y or by its position indY in the list of blocks X.

X can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm block.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the impute.nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and ?pls for more details).

Note that our method is partly based on sparse Generalised Canonical Correlation Analysis and differs from the MB-PLS approaches proposed by Kowalski et al., 1989, J Chemom 3(1), Westerhuis et al., 1998, J Chemom, 12(5) and sparse variants Li et al., 2012, Bioinformatics 28(19); Karaman et al (2014), Metabolomics, 11(2); Kawaguchi et al., 2017, Biostatistics.

Variable selection is performed on each component for each block of X if specified, via input parameter keepX.

Value

`block.splsda` returns an object of class `"block.splsda"`,`"block.spls"`, a list that contains the following components:

`X`	the centered and standardized original predictor matrix.
`indY`	the position of the outcome Y in the output list X.
`ncomp`	the number of components included in the model for each block.
`mode`	the algorithm used to fit the model.
`keepX`	Number of variables used to build each component of each block
`variates`	list containing the variates of each block of X.
`loadings`	list containing the estimated loadings for the variates.
`names`	list containing the names to be used for individuals and variables.
`nzv`	list containing the zero- or near-zero predictors information.
`iter`	Number of iterations of the algorithm for each component
`weights`	Correlation between the variate of each block and the variate of the outcome. Used to weight predictions.
`prop_expl_var`	Percentage of explained variance for each component and each block
`call`	if `verbose.call = FALSE`, then just the function call is returned. If `verbose.call = TRUE` then all the inputted values are accessable via this component

Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

On multiple integration with sPLS-DA and 4 data blocks:

Singh A., Gautier B., Shannon C., Vacher M., Rohart F., Tebbutt S. and Lê Cao K.A. (2016). DIABLO: multi omics integration for biomarker discovery. BioRxiv available here: http://biorxiv.org/content/early/2016/08/03/067611

On data integration:

Tenenhaus A., Philippe C., Guillemot V, Lê Cao K.A., Grill J, Frouin V. Variable selection for generalized canonical correlation analysis. *Biostatistics*. kxu001

Gunther O., Shin H., Ng R. T. , McMaster W. R., McManus B. M. , Keown P. A. , Tebbutt S.J. , Lê Cao K-A. , (2014) Novel multivariate methods for integration of genomics and proteomics data: Applications in a kidney transplant rejection study, OMICS: A journal of integrative biology, 18(11), 682-95.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

`plotIndiv`, `plotArrow`, `plotLoadings`, `plotVar`, `predict`, `perf`, `selectVar`, `block.plsda`, `block.spls` and http://www.mixOmics.org/mixDIABLO for more details and examples.

Examples

```
# block.splsda
# -------------
data("breast.TCGA")
# this is the X data as a list of mRNA, miRNA and proteins
data = list(mrna = breast.TCGA$data.train$mrna, mirna = breast.TCGA$data.train$mirna,
protein = breast.TCGA$data.train$protein)
# set up a full design where every block is connected
design = matrix(1, ncol = length(data), nrow = length(data),
dimnames = list(names(data), names(data)))
diag(design) =  0
design
# set number of component per data set
ncomp = c(2)
# set number of variables to select, per component and per data set (this is set arbitrarily)
list.keepX = list(mrna = rep(8,2), mirna = rep(8,2), protein = rep(8,2))


TCGA.block.splsda = block.splsda(X = data, Y = breast.TCGA$data.train$subtype,
                                 ncomp = ncomp, keepX = list.keepX, design = design)
## use design = 'full'
TCGA.block.splsda = block.splsda(X = data, Y = breast.TCGA$data.train$subtype,
                                 ncomp = ncomp, keepX = list.keepX, design = 'full')
TCGA.block.splsda$design

plotIndiv(TCGA.block.splsda, ind.names = FALSE)
## use design = 'null'
TCGA.block.splsda = block.splsda(X = data, Y = breast.TCGA$data.train$subtype,
                                 ncomp = ncomp, keepX = list.keepX, design = 'null')
TCGA.block.splsda$design
## set all off-diagonal elements to 0.5
TCGA.block.splsda = block.splsda(X = data, Y = breast.TCGA$data.train$subtype,
                                 ncomp = ncomp, keepX = list.keepX, design = 0.5)
TCGA.block.splsda$design
# illustrates coefficient weights in each block
plotLoadings(TCGA.block.splsda, ncomp = 1, contrib = 'max')
plotVar(TCGA.block.splsda, style = 'graphics', legend = TRUE)

## plot markers (selected variables) for mrna and mirna
# mrna: show each selected feature separately
plotMarkers(object = TCGA.block.splsda, comp = 1, block = 'mrna')
# mrna: aggregate all selected features and separate by loadings signs
plotMarkers(object = TCGA.block.splsda, comp = 1, block = 'mrna', global = TRUE)
# proteins
plotMarkers(object = TCGA.block.splsda, comp = 1, block = 'protein')
## do not show violin plots
plotMarkers(object = TCGA.block.splsda, comp = 1, block = 'protein', violin = FALSE)
# show top 5 markers
plotMarkers(object = TCGA.block.splsda, comp = 1, block = 'protein', markers = 1:5)
# show specific markers
my.markers <- selectVar(TCGA.block.splsda, comp = 1)[['protein']]$name[c(1,3,5)]
my.markers
plotMarkers(object = TCGA.block.splsda, comp = 1, block = 'protein', markers = my.markers)
```

`breast.TCGA` *Breast Cancer multi omics data from TCGA*

Description

This data set is a small subset of the full data set from The Cancer Genome Atlas that can be analysed with the DIABLO framework. It contains the expression or abundance of three matching omics data sets: mRNA, miRNA and proteomics for 150 breast cancer samples (Basal, Her2, Luminal A) in the training set, and 70 samples in the test set. The test set is missing the proteomics data set.

Usage

```
data(breast.TCGA)
```

Format

A list containing two data sets, `data.train` and `data.test` which both include:

list("miRNA") data frame with 150 (70) rows and 184 columns in the training (test) data set. The expression levels of 184 miRNA.

list("mRNA") data frame with 150 (70) rows and 520 columns in the training (test) data set. The expression levels of 200 mRNA.

list("protein") data frame with 150 (70) rows and 142 columns in the training data set only. The abundance of 142 proteins.

list("subtype") a factor indicating the brerast cancer subtypes in the training (length of 150) and test (length of 70) sets.

Details

The data come from The Cancer Genome Atlas (TCGA, http://cancergenome.nih.gov/). We divided the data into a training (discovery) and test (validation) set. The protein dataset which had a limited number of subjects available was used to allocate subjects into the training set only, while the tes set included all remaining subject. Each data set was normalised and pre-processed. For illustrative purposes we drastically filtered the data here.

Value

none

Source

The raw data were downloaded from `http://cancergenome.nih.gov/`. The normalised and filtered data we analysed with DIABLO are available on `www.mixOmics.org/mixDIABLO`

References

Singh A., Shannon C., Gautier B., Rohart F., Vacher M., Tebbutt S. and Lê Cao K.A. (2019), DIABLO: an integrative approach for identifying key molecular drivers from multi-omics assays, Bioinformatics, Volume 35, Issue 17, 1 September 2019, Pages 3055–3062.

`breast.tumors` *Human Breast Tumors Data*

Description

This data set contains the expression of 1,000 genes in 47 surgical specimens of human breast tumours from 17 different individuals before and after chemotherapy treatment.

Usage

```
data(breast.tumors)
```

Format

A list containing the following components:

list("gene.exp") data matrix with 47 rows and 1000 columns. Each row represents an experimental sample, and each column a single gene.

list("sample") a list containing two character vector components: `name` the name of the samples, and `treatment` the treatment status.

list("genes") a list containing two character vector components: `name` the name of the genes, and `description` the description of each gene.

Details

This data consists of 47 breast cancer samples and 1753 cDNA clones pre-selected by Perez-Enciso *et al.* (2003) to draw their Fig. 1. The authors selected 47 samples for which there was information at least before or before and after chemotherapy treatment. There were 20 tumours that were microarrayed both before and after treatment. For illustrative purposes we then randomly selected 1000 cDNA clones for this data set.

Value

none

Source

The Human Breast Tumors dataset is a companion resource for the paper of Perou *et al.* (2000), and was downloaded from the Stanford Genomics Breast Cancer Consortium Portal `http://genome-www.stanford.edu/breast_cancer/molecularportraits/download.shtml`

References

Perez-Enciso, M. and Tenenhaus, M. (2003). Prediction of clinical outcome with microarray data: a partial least squares discriminant analysis (PLS-DA) approach. *Human Genetics* **112**, 581-592.

Perou, C. M., Sorlie, T., Eisen, M. B., van de Rijn, M., Jeffrey, S. S., Rees, C. A., Pollack, J. R., Ross, D. T., Johnsen, H., Akslen, L. A., Fluge, O., Pergamenschikov, A., Williams, C., Zhu, S. X., Lonning, P. E., Borresen-Dale, A. L., Brown, P. O. and Botstein, D. (2000). Molecular portraits of human breast tumours. *Nature* **406**, 747-752.

cim *Clustered Image Maps (CIMs) ("heat maps")*

Description

This function generates color-coded Clustered Image Maps (CIMs) ("heat maps") to represent "high-dimensional" data sets.

Usage

```
cim(
  mat = NULL,
  color = NULL,
  row.names = TRUE,
  col.names = TRUE,
  row.sideColors = NULL,
  col.sideColors = NULL,
  row.cex = NULL,
  col.cex = NULL,
  cutoff = 0,
  cluster = "both",
  dist.method = c("euclidean", "euclidean"),
  clust.method = c("complete", "complete"),
  cut.tree = c(0, 0),
  transpose = FALSE,
  symkey = TRUE,
  keysize = c(1, 1),
  keysize.label = 1,
  zoom = FALSE,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  margins = c(5, 5),
  lhei = NULL,
  lwid = NULL,
  comp = NULL,
  center = TRUE,
  scale = FALSE,
  mapping = "XY",
  legend = NULL,
  save = NULL,
  name.save = NULL,
  blocks = NULL
)
```

Arguments

mat	numeric matrix of values to be plotted. Alternatively, an object of class inheriting from "pca", "spca", "ipca", "sipca", "rcc", "pls", "spls", "plsda", "splsda", "mlspls", "mlsplsda", "block.pls" or "block.spls" (where "ml" stands for multilevel).

color — a character vector of colors such as that generated by terrain.colors, topo.colors, rainbow, color.jet or similar functions.

row.names, col.names — logical, should the name of rows and/or columns of mat be shown? If TRUE (defaults) rownames(mat) and/or colnames(mat) are used. Possible character vectors with row and/or column labels can be used.

row.sideColors — (optional) character vector of length nrow(mat) containing the color names for a vertical side bar that may be used to annotate the rows of mat.

col.sideColors — (optional) character vector of length ncol(mat) containing the color names for a horizontal side bar that may be used to annotate the columns of mat.

row.cex, col.cex — positive numbers, used as cex.axis in for the row or column axis labeling. The defaults currently only use number of rows or columns, respectively.

cutoff — numeric between 0 and 1. Variables with correlations below this threshold in absolute value are not plotted. To use only when mapping is "XY".

cluster — character string indicating whether to cluster "none", "row", "column" or "both". Defaults to "both".

dist.method — character vector of length two. The distance measure used in clustering rows and columns. Possible values are "correlation" for Pearson correlation and all the distances supported by dist, such as "euclidean", etc.

clust.method — character vector of length two. The agglomeration method to be used for rows and columns. Accepts the same values as in hclust such as "ward", "complete", etc.

cut.tree — numeric vector of length two with components in [0,1]. The height proportions where the trees should be cut for rows and columns, if these are clustered.

transpose — logical indicating if the matrix should be transposed for plotting. Defaults to FALSE.

symkey — Logical indicating whether the color key should be made symmetric about 0. Defaults to TRUE.

keysize — vector of length two, indicating the size of the color key.

keysize.label — vector of length 1, indicating the size of the labels and title of the color key.

zoom — logical. Whether to use zoom for interactive zoom. See Details.

title, xlab, ylab — title, x- and y-axis titles; default to none.

margins — numeric vector of length two containing the margins (see par(mar)) for column and row names respectively.

lhei, lwid — arguments passed to layout to divide the device up into two (or three if a side color is drawn) rows and two columns, with the row-heights lhei and the column-widths lwid.

comp — atomic or vector of positive integers. The components to adequately account for the data association. For a non sparse method, the similarity matrix is computed based on the variates and loading vectors of those specified components. For a sparse approach, the similarity matric is computed based on the variables selected on those specified components. See example. Defaults to comp = 1:object$ncomp.

center — either a logical value or a numeric vector of length equal to the number of columns of mat. See scale function.

scale	either a logical value or a numeric vector of length equal to the number of columns of mat. See scale function.
mapping	character string indicating whether to map "X", "Y" or "XY"-association matrix. Can also be "multiblock" when class(mat) == "block.pls" OR "block.spls". See Details.
legend	A list indicating the legend for each group, the color vector, title of the legend and cex.
save	should the plot be saved? If so, argument to be set to either 'jpeg', 'tiff', 'png' or 'pdf'.
name.save	character string for the name of the file to be saved.
blocks	integer or character vector. Used when class(mat) == "block.pls" OR "block.spls". Dictates which blocks will be visualised. See Details.

Details

One matrix Clustered Image Map (default method) is a 2-dimensional visualization of a real-valued matrix (basically image(t(mat))) with rows and/or columns reordered according to some hierarchical clustering method to identify interesting patterns. Generated dendrograms from clustering are added to the left side and to the top of the image. By default the used clustering method for rows and columns is the *complete linkage* method and the used distance measure is the distance *euclidean*.

In "pca", "spca", "ipca", "sipca", "plsda", "splsda" and multilevel variants methods the mat matrix is object$X.

For the remaining methods, if mapping = "X" or mapping = "Y" the mat matrix is object$X or object$Y respectively. If mapping = "XY":

- in rcc method, the matrix mat is created where element (j, k) is the scalar product value between every pairs of vectors in dimension length(comp) representing the variables X_j and Y_k on the axis defined by Z_i with i in comp, where Z_i is the equiangular vector between the i-th X and Y canonical variate.
- in pls, spls and multilevel spls methods, if object$mode is "regression", the element (j, k) of the matrix mat is given by the scalar product value between every pairs of vectors in dimension length(comp) representing the variables X_j and Y_k on the axis defined by U_i with i in comp, where U_i is the i-th X variate. If object$mode is "canonical" then X_j and Y_k are represented on the axis defined by U_i and V_i respectively.

The blocks parameter controls which blocks are to be included when class(mat) == "block.pls" OR "block.spls". This can be a character or a integer vector.

If using a multiblock object then mapping can be set to "multiblock". When done so, this will emulate the function of cimDiablo(), such that rows will denote each sample and all features included in blocks will be shown as columns, coloured by which block they inherit from. In this case, blocks can include any number of input blocks. If mapping = "X", "Y" OR "XY", then it functions similarly to if a mixo_pls object was being used. blocks has to be of length 2 in this scenario.

By default four components will be displayed in the plot. At the top left is the color key, top right is the column dendogram, bottom left is the row dendogram, bottom right is the image plot. When sideColors are provided, an additional row or column is inserted in the appropriate location. This layout can be overriden by specifiying appropriate values for lwid and lhei. lwid controls the column width, and lhei controls the row height. See the help page for layout for details on how to use these arguments.

For visualization of "high-dimensional" data sets, a nice zooming tool was created. `zoom = TRUE` open a new device, one for CIM, one for zoom-out region and define an interactive 'zoom' process: click two points at imagen map region by pressing the first mouse button. It then draws a rectangle around the selected region and zoom-out this at new device. The process can be repeated to zoom-out other regions of interest.

The zoom process is terminated by clicking the second button and selecting 'Stop' from the menu, or from the 'Stop' menu on the graphics window.

Value

A list containing the following components:

`M`	the mapped matrix used by `cim`.
`rowInd`, `colInd`	row and column index permutation vectors as returned by `order.dendrogram`.
`ddr`, `ddc`	object of class `"dendrogram"` which describes the row and column trees produced by `cim`.
`mat.cor`	the correlation matrix used for the heatmap. Available only when mapping = "XY".
`row.names`, `col.names`	character vectors with row and column labels used.
`row.sideColors`, `col.sideColors`	character vector containing the color names for vertical and horizontal side bars used to annotate the rows and columns.

Author(s)

Ignacio González, Francois Bartolo, Kim-Anh Lê Cao, Al J Abadi

References

Eisen, M. B., Spellman, P. T., Brown, P. O. and Botstein, D. (1998). Cluster analysis and display of genome-wide expression patterns. *Proceeding of the National Academy of Sciences of the USA* **95**, 14863-14868.

Weinstein, J. N., Myers, T. G., O'Connor, P. M., Friend, S. H., Fornace Jr., A. J., Kohn, K. W., Fojo, T., Bates, S. E., Rubinstein, L. V., Anderson, N. L., Buolamwini, J. K., van Osdol, W. W., Monks, A. P., Scudiero, D. A., Sausville, E. A., Zaharevitz, D. W., Bunow, B., Viswanadhan, V. N., Johnson, G. S., Wittes, R. E. and Paull, K. D. (1997). An information-intensive approach to the molecular pharmacology of cancer. *Science* **275**, 343-349.

González I., Lê Cao K.A., Davis M.J., Déjean S. (2012). Visualising associations between paired 'omics' data sets. *BioData Mining*; **5**(1).

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

`heatmap`, `hclust`, `plotVar`, `network` and

`http://mixomics.org/graphics/` for more details on all options available.

Examples

```
## default method: shows cross correlation between 2 data sets
#-----------------------------------------------------------------
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene

cim(cor(X, Y), cluster = "none")


## Not run:
## CIM representation for objects of class 'rcc'
#-----------------------------------------------------------------

nutri.rcc <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)

cim(nutri.rcc, xlab = "genes", ylab = "lipids", margins = c(5, 6))

#-- interactive 'zoom' available as below

cim(nutri.rcc, xlab = "genes", ylab = "lipids", margins = c(5, 6),
zoom = TRUE)
#-- select the region and "see" the zoom-out region


#-- cim from X matrix with a side bar to indicate the diet
diet.col <- palette()[as.numeric(nutrimouse$diet)]
cim(nutri.rcc, mapping = "X", row.names = nutrimouse$diet,
row.sideColors = diet.col, xlab = "lipids",
clust.method = c("ward", "ward"), margins = c(6, 4))

#-- cim from Y matrix with a side bar to indicate the genotype
geno.col = color.mixo(as.numeric(nutrimouse$genotype))
cim(nutri.rcc, mapping = "Y", row.names = nutrimouse$genotype,
row.sideColors = geno.col, xlab = "genes",
clust.method = c("ward", "ward"))

#-- save the result as a jpeg file
jpeg(filename = "test.jpeg", res = 600, width = 4000, height = 4000)
cim(nutri.rcc, xlab = "genes", ylab = "lipids", margins = c(5, 6))
dev.off()

## CIM representation for objects of class 'spca' (also works for sipca)
#-----------------------------------------------------------------

data(liver.toxicity)
X <- liver.toxicity$gene

liver.spca <- spca(X, ncomp = 2, keepX = c(30, 30), scale = FALSE)

dose.col <- color.mixo(as.numeric(as.factor(liver.toxicity$treatment[, 3])))

# side bar, no variable names shown
cim(liver.spca, row.sideColors = dose.col, col.names = FALSE,
row.names = liver.toxicity$treatment[, 3],
clust.method = c("ward", "ward"))
```

```
## CIM representation for objects of class '(s)pls'
#-----------------------------------------------------------------

data(liver.toxicity)

X <- liver.toxicity$gene
Y <- liver.toxicity$clinic
liver.spls <- spls(X, Y, ncomp = 3,
keepX = c(20, 50, 50), keepY = c(10, 10, 10))


# default
cim(liver.spls)


# transpose matrix, choose clustering method
cim(liver.spls, transpose = TRUE,
clust.method = c("ward", "ward"), margins = c(5, 7))

# Here we visualise only the X variables selected
cim(liver.spls, mapping="X")

# Here we should visualise only the Y variables selected
cim(liver.spls, mapping="Y")

# Here we only visualise the similarity matrix between the variables by spls
cim(liver.spls, cluster="none")

# plotting two data sets with the similarity matrix as input in the funciton
# (see our BioData Mining paper for more details)
# Only the variables selected by the sPLS model in X and Y are represented
cim(liver.spls, mapping="XY")

# on the X matrix only, side col var to indicate dose
dose.col <- color.mixo(as.numeric(as.factor(liver.toxicity$treatment[, 3])))
cim(liver.spls, mapping = "X", row.sideColors = dose.col,
row.names = liver.toxicity$treatment[, 3])

# CIM default representation includes the total of 120 genes selected, with the dose color
# with a sparse method, show only the variables selected on specific components
cim(liver.spls, comp = 1)
cim(liver.spls, comp = 2)
cim(liver.spls, comp = c(1,2))
cim(liver.spls, comp = c(1,3))


## CIM representation for objects of class '(s)plsda'
#-----------------------------------------------------------------
data(liver.toxicity)

X <- liver.toxicity$gene
# Setting up the Y outcome first
Y <- liver.toxicity$treatment[, 3]
#set up colors for cim
dose.col <- color.mixo(as.numeric(as.factor(liver.toxicity$treatment[, 3])))
```

```
liver.splsda <- splsda(X, Y, ncomp = 2, keepX = c(40, 30))

cim(liver.splsda, row.sideColors = dose.col, row.names = Y)


## CIM representation for objects of class splsda 'multilevel'
# with a two level factor (repeated sample and time)
#-----------------------------------------------------------------
data(vac18.simulated)
X <- vac18.simulated$genes
design <- data.frame(samp = vac18.simulated$sample)
Y = data.frame(time = vac18.simulated$time,
stim = vac18.simulated$stimulation)

res.2level <- splsda(X, Y = Y, ncomp = 2, multilevel = design,
keepX = c(120, 10))

#define colors for the levels: stimulation and time
stim.col <- c("darkblue", "purple", "green4","red3")
stim.col <- stim.col[as.numeric(Y$stim)]
time.col <- c("orange", "cyan")[as.numeric(Y$time)]


# The row side bar indicates the two levels of the facteor, stimulation and time.
# the sample names have been motified on the plot.
cim(res.2level, row.sideColors = cbind(stim.col, time.col),
row.names = paste(Y$time, Y$stim, sep = "_"),
col.names = FALSE,
#setting up legend:
legend=list(legend = c(levels(Y$time), levels(Y$stim)),
col = c("orange", "cyan", "darkblue", "purple", "green4","red3"),
title = "Condition", cex = 0.7)
)

## CIM representation for objects of class spls 'multilevel'
#-----------------------------------------------------------------

data(liver.toxicity)
repeat.indiv <- c(1, 2, 1, 2, 1, 2, 1, 2, 3, 3, 4, 3, 4, 3, 4, 4, 5, 6, 5, 5,
6, 5, 6, 7, 7, 8, 6, 7, 8, 7, 8, 8, 9, 10, 9, 10, 11, 9, 9,
10, 11, 12, 12, 10, 11, 12, 11, 12, 13, 14, 13, 14, 13, 14,
13, 14, 15, 16, 15, 16, 15, 16, 15, 16)

# sPLS is a non supervised technique, and so we only indicate the sample repetitions
# in the design (1 factor only here, sample)
# sPLS takes as an input 2 data sets, and the variables selected
design <- data.frame(sample = repeat.indiv)
res.spls.1level <- spls(X = liver.toxicity$gene,
Y=liver.toxicity$clinic,
multilevel = design,
ncomp = 2,
keepX = c(50, 50), keepY = c(5, 5),
mode = 'canonical')

stim.col <- c("darkblue", "purple", "green4","red3")
```

```
# showing only the Y variables, and only those selected in comp 1
cim(res.spls.1level, mapping="Y",
row.sideColors = stim.col[factor(liver.toxicity$treatment[,3])], comp = 1,
#setting up legend:
legend=list(legend = unique(liver.toxicity$treatment[,3]), col=stim.col,
title = "Dose", cex=0.9))


# showing only the X variables, for all selected on comp 1 and 2
cim(res.spls.1level, mapping="X",
row.sideColors = stim.col[factor(liver.toxicity$treatment[,3])],
#setting up legend:
legend=list(legend = unique(liver.toxicity$treatment[,3]), col=stim.col,
title = "Dose", cex=0.9))


# These are the cross correlations between the variables selected in X and Y.
# The similarity matrix is obtained as in our paper in Data Mining
cim(res.spls.1level, mapping="XY")


## End(Not run)
```

`cimDiablo` *Clustered Image Maps (CIMs) ("heat maps") for DIABLO*

Description

This function generates color-coded Clustered Image Maps (CIMs) ("heat maps") to represent "high-dimensional" data sets analysed with DIABLO.

Usage

```
cimDiablo(
  object,
  color = NULL,
  color.Y,
  color.blocks,
  comp = NULL,
  margins = c(2, 15),
  legend.position = "topright",
  transpose = FALSE,
  row.names = TRUE,
  col.names = TRUE,
  size.legend = 1.5,
  trim = TRUE,
  ...
)
```

Arguments

object	An object of class inheriting from "block.splsda".
color	a character vector of colors such as that generated by terrain.colors, topo.colors, rainbow, color.jet or similar functions.
color.Y	a character vector of colors to be used for the levels of the outcome
color.blocks	a character vector of colors to be used for the blocks
comp	positive integer. The similarity matrix is computed based on the variables selected on those specified components. See example. Defaults to comp = 1.
margins	numeric vector of length two containing the margins (see par(mar)) for column and row names respectively.
legend.position	position of the legend, one of "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center".
transpose	logical indicating if the matrix should be transposed for plotting. Defaults to FALSE.
row.names, col.names	logical, should the name of rows and/or columns of mat be shown? If TRUE (defaults) rownames(mat) and/or colnames(mat) are used. Possible character vectors with row and/or column labels can be used.
size.legend	size of the legend
trim	(Logical or numeric) If FALSE, values are not changed. If TRUE, the values are trimmed to 3 standard deviation range. If a numeric, values with absolute values greater than the provided values are trimmed.
...	Other valid arguments passed to cim.

Details

This function is a small wrapper of cim specific to the DIABLO framework.

Value

A list containing the following components:

M	the mapped matrix used by cim.
rowInd, colInd	row and column index permutation vectors as returned by order.dendrogram.
ddr, ddc	object of class "dendrogram" which describes the row and column trees produced by cim.
mat.cor	the correlation matrix used for the heatmap. Available only when mapping = "XY".
row.names, col.names	character vectors with row and column labels used.
row.sideColors, col.sideColors	character vector containing the color names for vertical and horizontal side bars used to annotate the rows and columns.

Author(s)

Amrit Singh, Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Singh A., Shannon C., Gautier B., Rohart F., Vacher M., Tebbutt S. and Lê Cao K.A. (2019), DIABLO: an integrative approach for identifying key molecular drivers from multi-omics assays, Bioinformatics, Volume 35, Issue 17, 1 September 2019, Pages 3055–3062.

Eisen, M. B., Spellman, P. T., Brown, P. O. and Botstein, D. (1998). Cluster analysis and display of genome-wide expression patterns. *Proceeding of the National Academy of Sciences of the USA* **95**, 14863-14868.

Weinstein, J. N., Myers, T. G., O'Connor, P. M., Friend, S. H., Fornace Jr., A. J., Kohn, K. W., Fojo, T., Bates, S. E., Rubinstein, L. V., Anderson, N. L., Buolamwini, J. K., van Osdol, W. W., Monks, A. P., Scudiero, D. A., Sausville, E. A., Zaharevitz, D. W., Bunow, B., Viswanadhan, V. N., Johnson, G. S., Wittes, R. E. and Paull, K. D. (1997). An information-intensive approach to the molecular pharmacology of cancer. *Science* **275**, 343-349.

González I., Lê Cao K.A., Davis M.J., Déjean S. (2012). Visualising associations between paired 'omics' data sets. *BioData Mining*; **5**(1).

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

`cim`, `heatmap`, `hclust`, `plotVar`, `network` and

http://mixomics.org/mixDIABLO/ for more details on all options available.

Examples

```
## default method: shows cross correlation between 2 data sets
#-----------------------------------------------------------------
data(nutrimouse)
Y = nutrimouse$diet
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid)

nutrimouse.sgccda <- block.splsda(X = data,
                                  Y = Y,
                                  design = "full",
                                  keepX = list(gene = c(10,10), lipid = c(15,15)),
                                  ncomp = 2)

cimDiablo(nutrimouse.sgccda, comp = c(1,2))
## change trim range
cimDiablo(nutrimouse.sgccda, comp = c(1,2), trim = 4)
## do not trim values
cimDiablo(nutrimouse.sgccda, comp = c(1,2), trim = FALSE)
```

---

circosPlot *circosPlot for DIABLO*

Description

Displays variable correlation among different blocks

Usage

```
## S3 method for class 'block.splsda'
circosPlot(
  object,
  comp = 1:min(object$ncomp),
  cutoff,
  color.Y,
  blocks = NULL,
  color.blocks,
  color.cor,
  var.names = NULL,
  showIntraLinks = FALSE,
  line = FALSE,
  size.legend = 0.8,
  ncol.legend = 1,
  size.variables = 0.25,
  size.labels = 1,
  legend = TRUE,
  legend.title = "Expression",
  linkWidth = 1,
  ...
)

## S3 method for class 'block.plsda'
circosPlot(
  object,
  comp = 1:min(object$ncomp),
  cutoff,
  color.Y,
  blocks = NULL,
  color.blocks,
  color.cor,
  var.names = NULL,
  showIntraLinks = FALSE,
  line = FALSE,
  size.legend = 0.8,
  ncol.legend = 1,
  size.variables = 0.25,
  size.labels = 1,
  legend = TRUE,
  legend.title = "Expression",
  linkWidth = 1,
  ...
)

## S3 method for class 'block.spls'
circosPlot(object, ..., group = NULL, Y.name = "Y")

## S3 method for class 'block.pls'
circosPlot(object, ..., group = NULL, Y.name = "Y")
```

Arguments

object	An object of class inheriting from "block.plsda", "block.splsda", "block.pls" or "blocks.spls".
comp	Numeric vector indicating which component to plot. Default to all
cutoff	Only shows links with a correlation higher than cutoff
color.Y	a character vector of colors to be used for the levels of the outcome
blocks	Character or integer vector indicating which blocks to show. Default to all
color.blocks	a character vector of colors to be used for the blocks
color.cor	a character vector of two colors. First one is for the negative correlation, second one is for the positive correlation
var.names	Optional parameter. A list of length the number of blocks in object$X, containing the names of the variables of each block. If NULL, the colnames of the data matrix are used.
showIntraLinks	if TRUE, shows the correlation higher than the threshold inside each block.
line	if TRUE, shows the overall expression of the selected variables. see examples.
size.legend	size of the legend
ncol.legend	number of columns for the legend
size.variables	size of the variable labels
size.labels	size of the block labels
legend	Logical. Whether the legend should be added. Default is TRUE.
legend.title	String. Name of the legend. Defaults to "Expression".
linkWidth	Numeric. Specifies the range of sizes used for lines linking the correlated variables (see details). Must be of length 2 or 1. Default to c(1). See details.
...	For object of class block.splsda, advanced plot parameters: • **var.adj** Numeric. Adjusts the radial location of variable names in units of the arc band width. Positive values push feature names radially outward. Default to -0.33. See examples. • **block.labels.adj** Numeric between -1 and 1. Adjusts the radial location of block names radially inward or outward. Default to 0. See examples. • **blocks.link** Character vector of blocks. If provided, only correlations from features of these blocks are shown using links. See examples. For object of class block.spls, all listed and advanced arguments passed to the block.splsda method.
group	The grouping factor used when line = TRUE
Y.name	Character, the name of the Y block

Details

circosPlot function depicts correlations of variables selected with block.splsda or block.spls among different blocks, using a generalisation of the method presented in González et al 2012. If ncomp is specified, then only the variables selected on that component are displayed.

The linkWidth argument specifies the width of the links drawn. If a vector of length 2 is provided, the smaller value will correspond to a similarity values designated by cutoff argument, while the larger value will be used for a link with perfect similarity (1), if any.

Value

If saved in an object, the circos plot will output the similarity matrix and the names of the variables displayed on the plot (see `attributes(object)`).

Author(s)

Michael Vacher, Amrit Singh, Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Singh A., Gautier B., Shannon C., Vacher M., Rohart F., Tebbutt S. and Lê Cao K.A. (2016). DIABLO: multi omics integration for biomarker discovery. BioRxiv available here: http://biorxiv.org/content/early/2016/08/03/067611

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

González I., Lê Cao K.A., Davis M.J., Déjean S. (2012). Visualising associations between paired 'omics' data sets. *BioData Mining*; **5**(1).

See Also

`block.splsda`, references and http://www.mixOmics.org/mixDIABLO for more details.

Examples

```
data(nutrimouse)
Y = nutrimouse$diet
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid)
design = matrix(c(0,1,1,1,0,1,1,1,0), ncol = 3, nrow = 3, byrow = TRUE)


nutrimouse.sgccda <- wrapper.sgccda(X=data,
Y = Y,
design = design,
keepX = list(gene=c(10,10), lipid=c(15,15)),
ncomp = 2)

circosPlot(nutrimouse.sgccda, cutoff = 0.7)
## links widths based on strength of their similarity
circosPlot(nutrimouse.sgccda, cutoff = 0.7, linkWidth = c(1, 10))
## custom legend
circosPlot(nutrimouse.sgccda, cutoff = 0.7, size.legend = 1.1)

## more customisation
circosPlot(nutrimouse.sgccda, cutoff = 0.7, size.legend = 1.1, color.Y = 1:5,
           color.blocks = c("green","brown"), color.cor = c("magenta", "purple"))

par(mfrow=c(2,2))

circosPlot(nutrimouse.sgccda, cutoff = 0.7, size.legend = 1.1)
## also show intra-block correlations
circosPlot(nutrimouse.sgccda, cutoff = 0.7,
           size.legend = 1.1, showIntraLinks = TRUE)
## show lines
```

```
circosPlot(nutrimouse.sgccda, cutoff = 0.7, line = TRUE, ncol.legend = 1,
           size.legend = 1.1, showIntraLinks = TRUE)
## custom line legends
circosPlot(nutrimouse.sgccda, cutoff = 0.7, line = TRUE, ncol.legend = 2,
           size.legend = 1.1, showIntraLinks = TRUE)
par(mfrow=c(1,1))

## adjust feature and block names radially
circosPlot(nutrimouse.sgccda, cutoff = 0.7, size.legend = 1.1)
circosPlot(nutrimouse.sgccda, cutoff = 0.7, size.legend = 1.1,
           var.adj = 0.8, block.labels.adj = -0.5)
## ---  example using breast.TCGA data
data("breast.TCGA")
data = list(mrna = breast.TCGA$data.train$mrna,
            mirna = breast.TCGA$data.train$mirna,
            protein = breast.TCGA$data.train$protein)
list.keepX = list(mrna = rep(20, 2), mirna = rep(10,2), protein = c(10, 2))

TCGA.block.splsda = block.splsda(X = data,
                            Y =breast.TCGA$data.train$subtype,
                            ncomp = 2, keepX = list.keepX,
                            design = 'full')
circosPlot(TCGA.block.splsda, cutoff = 0.7, line=TRUE)
## show only first 2 blocks
circosPlot(TCGA.block.splsda, cutoff = 0.7, line=TRUE, blocks = c(1,2))
## show only correlations including the mrna block features
circosPlot(TCGA.block.splsda, cutoff = 0.7, blocks.link = 'mrna')

data("breast.TCGA")
data = list(mrna = breast.TCGA$data.train$mrna, mirna = breast.TCGA$data.train$mirna)
list.keepX = list(mrna = rep(20, 2), mirna = rep(10,2))
list.keepY = c(rep(10, 2))

TCGA.block.spls = block.spls(X = data,
                            Y = breast.TCGA$data.train$protein,
                            ncomp = 2, keepX = list.keepX,
                            keepY = list.keepY, design = 'full')
circosPlot(TCGA.block.spls, group = breast.TCGA$data.train$subtype, cutoff = 0.7,
           Y.name = 'protein')
## only show links including mrna
circosPlot(TCGA.block.spls, group = breast.TCGA$data.train$subtype, cutoff = 0.7,
           Y.name = 'protein', blocks.link = 'mrna')
```

`colors` *Color Palette for mixOmics*

Description

The functions create a vector of `n` "contiguous" colors (except the `color.mixo` which are colors used internally to fit our logo colors).

Usage

```
color.mixo(num.vector)
```

```
color.GreenRed(n, alpha = 1)

color.jet(n, alpha = 1)

color.spectral(n, alpha = 1)
```

Arguments

num.vector	for color.mixo an integer vector specifying which colors to use in the mixOmics palette (there are only 10 colors available.
n	an integer, the number of colors (≥ 1) to be in the palette.
alpha	a numeric value between 0 and 1 for alpha channel (opacity).

Details

The function color.jet(n) create color scheme, beginning with dark blue, ranging through shades of blue, cyan, green, yellow and red, and ending with dark red. This colors palette is suitable for displaying ordered (symmetric) data, with n giving the number of colors desired.

Value

For color.jet(n), color.spectral(n), color.GreenRed(n) a character vector, cv, of color names. This can be used either to create a user-defined color palette for subsequent graphics by palette(cv), a col= specification in graphics functions or in par.

For color.mixo, a vector of colors matching the mixOmics logo (10 colors max.)

Author(s)

Ignacio Gonzalez, Kim-Anh Lê Cao, Benoit Gautier, Al J Abadi

See Also

colorRamp, palette, colors for the vector of built-in "named" colors; hsv, gray, rainbow, terrain.colors, ... to construct colors; and heat.colors, topo.colors for images.

Examples

```
# -----------------------
# jet colors
# ----------------------
par(mfrow = c(3, 1))
z <- seq(-1, 1, length = 125)
for (n in c(11, 33, 125)) {
image(matrix(z, ncol = 1), col = color.jet(n),
xaxt = 'n', yaxt = 'n', main = paste('n = ', n))
box()
par(usr = c(-1, 1, -1, 1))
axis(1, at = c(-1, 0, 1))
}

## Not run:
# -----------------------
# spectral colors
```

```
# ----------------------
par(mfrow = c(3, 1))
z <- seq(-1, 1, length = 125)
for (n in c(11, 33, 125)) {
image(matrix(z, ncol = 1), col = color.spectral(n),
xaxt = 'n', yaxt = 'n', main = paste('n = ', n))
box()
par(usr = c(-1, 1, -1, 1))
axis(1, at = c(-1, 0, 1))
}

# ----------------------
# GreenRed colors
# ----------------------
par(mfrow = c(3, 1))
z <- seq(-1, 1, length = 125)
for (n in c(11, 33, 125)) {
image(matrix(z, ncol = 1), col = color.GreenRed(n),
xaxt = 'n', yaxt = 'n', main = paste('n = ', n))
box()
par(usr = c(-1, 1, -1, 1))
axis(1, at = c(-1, 0, 1))
}

# # --------------------------------
# mixOmics colors
# # --------------------------------
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
nutri.res <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)

my.colors = color.mixo(1:5)
my.pch = ifelse(nutrimouse$genotype == 'wt', 16, 17)
#plotIndiv(nutri.res, ind.names = FALSE, group = my.colors, pch = my.pch, cex = 1.5)

## End(Not run)
```

`diverse.16S` *16S microbiome data: most diverse bodysites from HMP*

Description

The 16S data from the Human Microbiome Project includes only the most diverse bodysites: Antecubital fossa (skin), Stool and Subgingival plaque (oral) and can be analysed using a multilevel approach to account for repeated measurements using our module mixMC. The data include 162 samples (54 unique healthy individuals) measured on 1,674 OTUs.

Usage

```
data(diverse.16S)
```

Format

A list containing two data sets, `data.TSS` and `data.raw` and some meta data information:

list("data.TSS") data frame with 162 rows (samples) and 1674 columns (OTUs). The prefiltered normalised data using Total Sum Scaling normalisation.

list("data.raw") data frame with 162 rows (samples) and 1674 columns (OTUs). The prefiltered raw count OTU data which include a 1 offset (i.e. no 0 values).

list("taxonomy") data frame with 1674 rows (OTUs) and 6 columns indicating the taxonomy of each OTU.

list("indiv") data frame with 162 rows indicating sample meta data.

list("bodysite") factor of length 162 indicating the bodysite with levels "Antecubital_fossa", "Stool" and "Subgingival_plaque".

list("sample") vector of length 162 indicating the unique individual ID, useful for a multilevel approach to taken into account the repeated measured on each individual.

Details

The data were downloaded from the Human Microbiome Project (HMP, http://hmpdacc.org/HMQCP/all/ for the V1-3 variable region). The original data contained 43,146 OTU counts for 2,911 samples measured from 18 different body sites. We focused on the first visit of each healthy individual and focused on the three most diverse habitats. The prefiltered dataset included 1,674 OTU counts. We strongly recommend to use log ratio transformations on the `data.TSS` normalised data, as implemented in the PLS and PCA methods, see details on `www.mixOmics.org/mixMC`.

The `data.raw` include a 1 offset in order to be log ratios transformed after TSS normalisation. Consequently, the `data.TSS` are TSS normalisation of `data.raw`. The CSS normalisation was performed on the orignal data (including zero values)

Value

none

Source

The raw data were downloaded from `http://hmpdacc.org/HMQCP/all/`. Filtering and normalisation described in our website `www.mixOmics.org/mixMC`

References

Lê Cao K.-A., Costello ME, Lakis VA, Bartolo, F,Chua XY, Brazeilles R, Rondeau P. MixMC: Multivariate insights into Microbial Communities. PLoS ONE, 11(8): e0160169 (2016).

`estim.regul` *Estimate the parameters of regularization for Regularized CCA*

Description

This function has been renamed `tune.rcc`, see `tune.rcc`.

This function has been renamed 'image.tune.rcc', see `image.tune.rcc`.

This function has been renamed `tune.pca`.

Value

none

none

none

`explained_variance` *Calculates the proportion of explained variance of multivariate components*

Description

`explained_variance` calculates the proportion of variance explained by a set of *orthogonal* variates / components and divides by the total variance in `data` using the definition of 'redundancy'. This applies to any component-based approaches where components are orthogonal. It is worth noting that any missing values are set to zero (which is the column mean for the centered input data) prior to calculation of total variance in the data. Therefore, this function would underestimate the total variance in presence of abundant missing values. One can use `impute.nipals` function to impute the missing values to avoid such behaviour.

Usage

```
explained_variance(data, variates, ncomp)
```

Arguments

`data`	numeric matrix of predictors
`variates`	variates as obtained from a `pls` object for instance
`ncomp`	number of components. Should be lower than the number of columns of `variates`

Details

Variance explained by component t_h in X for dimension h:

$$Rd(X, t_h) = \frac{1}{p} \sum_{j=1}^{p} \text{cor}^2(X^j, t_h)$$

where X^j is the variable centered and scaled, p is the total number of variables.

Value

`explained_variance` returns a named numeric vector containing the proportion of explained variance for each variate after setting all missing values in the data to zero (see details).

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Tenenhaus, M., La Régression PLS théorie et pratique (1998). Technip, Paris, chap2.

See Also

spls, splsda, plotIndiv, plotVar, cim, network.

Examples

```
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic

toxicity.spls <- spls(X, Y, ncomp = 2, keepX = c(50, 50), keepY = c(10, 10))

ex = explained_variance(toxicity.spls$X, toxicity.spls$variates$X, ncomp =2)

# ex should be the same as
toxicity.spls$prop_expl_var$X
```

---

get.confusion_matrix *Create confusion table and calculate the Balanced Error Rate*

Description

Create confusion table between a vector of true classes and a vector of predicted classes, calculate the Balanced Error rate

Usage

```
get.confusion_matrix(truth, all.levels, predicted)

get.BER(confusion)
```

Arguments

truth	A factor vector indicating the true classes of the samples (typically Y from the training set).
all.levels	Levels of the 'truth' factor. Optional parameter if there are some missing levels in truth compared to the fitted predicted model
predicted	Vector of predicted classes (typically the prediction from the test set). Can contain NA.
confusion	result from a get.confusion_matrix to calculate the Balanced Error Rate

Details

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

Value

get.confusion_matrix returns a confusion matrix. get.BER returns the BER from a confusion matrix

Author(s)

Florian Rohart, Al J Abadi

References

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

predict.

Examples

```
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- as.factor(liver.toxicity$treatment[, 4])

## if training is perfomed on 4/5th of the original data
samp <- sample(1:5, nrow(X), replace = TRUE)
test <- which(samp == 1)   # testing on the first fold
train <- setdiff(1:nrow(X), test)

plsda.train <- plsda(X[train, ], Y[train], ncomp = 2)
test.predict <- predict(plsda.train, X[test, ], dist = "max.dist")
Prediction <- test.predict$class$max.dist[, 2]

# the confusion table compares the real subtypes with the predicted subtypes for a 2 component model
confusion.mat = get.confusion_matrix(truth = Y[test],
predicted = Prediction)

get.BER(confusion.mat)
```

---

image.tune.rcc *Plot the cross-validation score.*

Description

This function provide a image map (checkerboard plot) of the cross-validation score obtained by the tune.rcc function.

Usage

```
## S3 method for class 'tune.rcc'
image(x, col = heat.colors, ...)

## S3 method for class 'tune.rcc'
plot(x, col = heat.colors, ...)
```

Arguments

x	object returned by tune.rcc.
col	a character string specifying the colors function to use: terrain.colors, topo.colors, rainbow or similar functions. Defaults to heat.colors.
...	not used currently.

Details

plot.tune.rcc creates an image map of the matrix object$mat containing the cross-validation score obtained by the tune.rcc function. Also a color scales strip is plotted.

Value

none

Author(s)

Sébastien Déjean, Ignacio González, Kim-Anh Le Cao, Al J Abadi

See Also

tune.rcc, image.

Examples

```
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene

## this can take some seconds
cv.score <- tune.rcc(X, Y, validation = "Mfold")
plot(cv.score)

# image(cv.score) # same result as plot()
```

---

imgCor *Image Maps of Correlation Matrices between two Data Sets*

Description

Display two-dimensional visualizations (image maps) of the correlation matrices within and between two data sets.

Usage

```
imgCor(
  X,
  Y,
  type = "combine",
  X.var.names = TRUE,
  Y.var.names = TRUE,
  sideColors = TRUE,
```

```
  interactive.dev = TRUE,
  title = TRUE,
  color,
  row.cex,
  col.cex,
  symkey,
  keysize,
  xlab,
  ylab,
  margins,
  lhei,
  lwid
)
```

Arguments

X	numeric matrix or data frame (n x p), the observations on the X variables. NAs are allowed.
Y	numeric matrix or data frame (n x q), the observations on the Y variables. NAs are allowed.
type	character string, (partially) maching one of "combine" or "separated", determining the kind of plots to be produced. See Details.
X.var.names, Y.var.names	logical, should the name of X- and/or Y-variables be shown? If TRUE (defaults) object$names$X and/or object$names$Y are used. Possible character vector with X- and/or Y-variable labels to use.
sideColors	character vector of length two. The color name for horizontal and vertical side bars that may be used to annotate the X and Y correlation matrices.
interactive.dev	Logical. The current graphics device that will be opened is interactive?
title	logical, should the main titles be shown?
color, xlab, ylab	arguments passed to cim.
row.cex, col.cex	positive numbers, used as cex.axis in for the row or column axis labeling. The defaults currently only use number of rows or columns, respectively.
symkey	Logical indicating whether the color key should be made symmetric about 0. Defaults to TRUE.
keysize	positive numeric value indicating the size of the color key.
margins	numeric vector of length two containing the margins (see par(mar)) for column and row names respectively.
lhei, lwid	arguments passed to layout to divide the device up into two rows and two columns, with the row-heights lhei and the column-widths lwid.

Details

If type="combine", the correlation matrix is computed of the combined matrices cbind(X, Y) and then plotted. If type="separate", three correlation matrices are computed, cor(X), cor(Y) and cor(X,Y) and plotted separately on a device. In both cases, a color correlation scales strip is plotted.

The correlation matrices are pre-processed before calling the image function in order to get, as in the numerical representation, the diagonal from upper-left corner to bottom-right one.

Missing values are handled by casewise deletion in the imgCor function.

If X.names = FALSE, the name of each X-variable is hidden. Default value is TRUE.

If Y.names = FALSE, the name of each Y-variable is hidden. Default value is TRUE.

Value

NULL (invisibly)

Author(s)

Ignacio González, Kim-Anh Lê Cao, Florian Rohart, Al J Abadi

See Also

cor, image, color.jet.

Examples

```
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene

## 'combine' type plot (default)
imgCor(X, Y)

## Not run:
## 'separate' type plot

imgCor(X, Y, type = "separate")

## 'separate' type plot without the name of datas
imgCor(X, Y, X.var.names = FALSE, Y.var.names = FALSE, type = "separate")

## End(Not run)
```

---

impute.nipals *Impute missing values using NIPALS algorithm*

Description

This function uses nipals function to decompose X into a set of components (t), (pseudo-) singular-values (eig), and feature loadings (p). The original matrix is then approximated/reconstituted using the following equation:

$$\hat{X} = t * diag(eig) * t(p)$$

The missing values from X are then approximated from this matrix. It is best to ensure enough number of components are used in order to best impute the missing values.

Usage

```
impute.nipals(X, ncomp, ...)
```

Arguments

X	A numeric matrix containing missing values
ncomp	Positive integer, the number of components to derive from X using the nipals function and reconstitute the original matrix
...	Optional arguments passed to nipals

Value

A numeric matrix with missing values imputed.

Author(s)

Al J Abadi

See Also

impute.nipals, pca

Examples

```
data("nutrimouse")
X <- data.matrix(nutrimouse$lipid)
## add missing values to X to impute and compare to actual values
set.seed(42)
na.ind <- sample(seq_along(X), size = 10)
true.values <- X[na.ind]
X[na.ind] <- NA
X.impute <- impute.nipals(X = X, ncomp = 5)
## compare
round(X.impute[na.ind], 2)
true.values
```

---

ipca *Independent Principal Component Analysis*

Description

Performs independent principal component analysis on the given data matrix, a combination of Principal Component Analysis and Independent Component Analysis.

Usage

```
ipca(
  X,
  ncomp = 2,
  mode = "deflation",
  fun = "logcosh",
  scale = FALSE,
  w.init = NULL,
  max.iter = 200,
  tol = 1e-04
)
```

Arguments

X	a numeric matrix (or data frame).
ncomp	integer, number of independent component to choose. Set by default to 3.
mode	character string. What type of algorithm to use when estimating the unmixing matrix, choose one of "deflation", "parallel". Default set to deflation.
fun	the function used in approximation to neg-entropy in the FastICA algorithm. Default set to logcosh, see details of FastICA.
scale	(Default=FALSE) Logical indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with prcomp function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of X can be supplied. The value is passed to scale.
w.init	initial un-mixing matrix (unlike fastICA, this matrix is fixed here).
max.iter	integer, the maximum number of iterations.
tol	a positive scalar giving the tolerance at which the un-mixing matrix is considered to have converged, see fastICA package.

Details

In PCA, the loading vectors indicate the importance of the variables in the principal components. In large biological data sets, the loading vectors should only assign large weights to important variables (genes, metabolites ...). That means the distribution of any loading vector should be super-Gaussian: most of the weights are very close to zero while only a few have large (absolute) values.

However, due to the existence of noise, the distribution of any loading vector is distorted and tends toward a Gaussian distribtion according to the Central Limit Theroem. By maximizing the non-Gaussianity of the loading vectors using FastICA, we obtain more noiseless loading vectors. We then project the original data matrix on these noiseless loading vectors, to obtain independent principal components, which should be also more noiseless and be able to better cluster the samples according to the biological treatment (note, IPCA is an unsupervised approach).

Algorithm 1. The original data matrix is centered.

2. PCA is used to reduce dimension and generate the loading vectors.

3. ICA (FastICA) is implemented on the loading vectors to generate independent loading vectors.

4. The centered data matrix is projected on the independent loading vectors to obtain the independent principal components.

Value

ipca returns a list with class "ipca" containing the following components:

ncomp	the number of independent principal components used.
unmixing	the unmixing matrix of size (ncomp x ncomp)
mixing	the mixing matrix of size (ncomp x ncomp)
X	the centered data matrix
x	the independent principal components
loadings	the independent loading vectors
kurtosis	the kurtosis measure of the independent loading vectors
prop_expl_var	Proportion of the explained variance of derived components, after setting possible missing values to zero.

Author(s)

Fangzhou Yao, Jeff Coquery, Kim-Anh Lê Cao, Florian Rohart, Al J Abadi

References

Yao, F., Coquery, J. and Lê Cao, K.-A. (2011) Principal component analysis with independent loadings: a combination of PCA and ICA. (in preparation)

A. Hyvarinen and E. Oja (2000) Independent Component Analysis: Algorithms and Applications, *Neural Networks*, **13(4-5)**:411-430

J L Marchini, C Heaton and B D Ripley (2010). fastICA: FastICA Algorithms to perform ICA and Projection Pursuit. R package version 1.1-13.

See Also

sipca, pca, plotIndiv, plotVar, and http://www.mixOmics.org for more details.

Examples

```
data(liver.toxicity)

# implement IPCA on a microarray dataset
ipca.res <- ipca(liver.toxicity$gene, ncomp = 3, mode="deflation")
ipca.res

# samples representation
plotIndiv(
    ipca.res,
    ind.names = as.character(liver.toxicity$treatment[, 4]),
    group = as.numeric(as.factor(liver.toxicity$treatment[, 4]))
)

## Not run:
    plotIndiv(ipca.res,
              cex = 0.01,
              col = as.numeric(as.factor(liver.toxicity$treatment[, 4])),
              style = "3d")

## End(Not run)
# variables representation
plotVar(ipca.res, cex = 0.5)

## Not run:
plotVar(ipca.res, rad.in = 0.5, cex = 0.5, style="3d")

## End(Not run)
```

Koren.16S *16S microbiome atherosclerosis study*

Description

The 16S data come from Koren et al. (2011) and compared the bodysites oral, gut and plaque microbial communities in patients with atherosclerosis. The data can be analysed with our mixMC module. The data include 43 samples measured on 980 OTUs.

Usage

```
data(Koren.16S)
```

Format

A list containing two data sets, `data.TSS` and `data.raw` and some meta data information:

list("data.TSS") data frame with 43 rows (samples) and 980 columns (OTUs). The prefiltered normalised data using Total Sum Scaling normalisation.

list("data.raw") data frame with 43 rows (samples) and 980 columns (OTUs). The prefiltered raw count OTU data which include a 1 offset (i.e. no 0 values).

list("taxonomy") data frame with 980 rows (OTUs) and 7 columns indicating the taxonomy of each OTU.

list("indiv") data frame with 43 rows indicating sample meta data.

list("bodysite") factor of length 43 indicating the bodysite with levels arterial plaque, saliva and stool.

Details

The data are from Koren et al. (2011) who examined the link between oral, gut and plaque microbial communities in patients with atherosclerosis and controls. Only healthy individuals were retained in the analysis. This study contained partially repeated measures from multiple sites including 15 unique patients samples from saliva and stool, and 13 unique patients only sampled from arterial plaque samples and we therefore considered a non multilevel analysis for that experimental design. After prefiltering, the data included 973 OTU for 43 samples. We strongly recommend to use log ratio transformations on the `data.TSS` normalisd data, as implemented in the PLS and PCA methods, see details on www.mixOmics.org/mixMC.

The `data.raw` include a 1 offset in order to be log ratios transformed after TSS normalisation. Consequently, the `data.TSS` are TSS normalisation of `data.raw`. The CSS normalisation was performed on the orignal data (including zero values)

Value

none

Source

The raw data were downloaded from the QIITA database. Filtering and normalisation described in our website www.mixOmics.org/mixMC

References

Lê Cao K.-A., Costello ME, Lakis VA, Bartolo, F,Chua XY, Brazeilles R, Rondeau P. MixMC: Multivariate insights into Microbial Communities. PLoS ONE, 11(8): e0160169 (2016).

Koren, O., Spor, A., Felin, J., Fak, F., Stombaugh, J., Tremaroli, V., et al.: Human oral, gut, and plaque microbiota in patients with atherosclerosis. Proceedings of the National Academy of Sciences 108(Supplement 1), 4592-4598 (2011)

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 list containing the following components:

list("exercise") data frame with 20 observations on 3 exercise variables.

list("physiological") data frame with 20 observations on 3 physiological variables.

Value

none

Source

Tenenhaus, M. (1998), Table 1, page 15.

References

Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

liver.toxicity *Liver Toxicity Data*

Description

This data set contains the expression measure of 3116 genes and 10 clinical measurements for 64 subjects (rats) that were exposed to non-toxic, moderately toxic or severely toxic doses of acetaminophen in a controlled experiment.

Usage

```
data(liver.toxicity)
```

Format

A list containing the following components:

list("gene") data frame with 64 rows and 3116 columns. The expression measure of 3116 genes for the 64 subjects (rats).

list("clinic") data frame with 64 rows and 10 columns, containing 10 clinical variables for the same 64 subjects.

list("treatment") data frame with 64 rows and 4 columns, containing the treatment information on the 64 subjects, such as doses of acetaminophen and times of necropsies.

list("gene.ID") data frame with 3116 rows and 2 columns, containing geneBank IDs and gene titles of the annotated genes

Details

The data come from a liver toxicity study (Bushel *et al*., 2007) in which 64 male rats of the inbred strain Fisher 344 were exposed to non-toxic (50 or 150 mg/kg), moderately toxic (1500 mg/kg) or severely toxic (2000 mg/kg) doses of acetaminophen (paracetamol) in a controlled experiment. Necropsies were performed at 6, 18, 24 and 48 hours after exposure and the mRNA from the liver was extracted. Ten clinical chemistry measurements of variables containing markers for liver injury are available for each subject and the serum enzymes levels are measured numerically. The data were further normalized and pre-processed by Bushel *et al*. (2007).

Value

none

Source

The two liver toxicity data sets are a companion resource for the paper of Bushel *et al.* (2007), and was downloaded from:

http://www.biomedcentral.com/1752-0509/1/15/additional/

References

Bushel, P., Wolfinger, R. D. and Gibson, G. (2007). Simultaneous clustering of gene expression data with clinical chemistry and pathological evaluations reveals phenotypic prototypes. *BMC Systems Biology* **1**, Number 15.

Lê Cao, K.-A., Rossouw, D., Robert-Granie, C. and Besse, P. (2008). A sparse PLS for variable selection when integrating Omics data. *Statistical Applications in Genetics and Molecular Biology* **7**, article 35.

---

logratio-transformations

Log-ratio transformation

Description

This function applies a log transformation to the data, either CLR or ILR

Usage

```
logratio.transfo(X, logratio = c("none", "CLR", "ILR"), offset = 0)
```

Arguments

X	numeric matrix of predictors
logratio	log-ratio transform to apply, one of "none", "CLR" or "ILR"
offset	Value that is added to X for CLR and ILR log transformation. Default to 0.

Details

logratio.transfo applies a log transformation to the data, either CLR (centered log ratio transformation) or ILR (Isometric Log Ratio transformation). In the case of CLR log-transformation, X needs to be a matrix of non-negative values and offset is used to shift the values away from 0, as commonly done with counts data.

Value

logratio.transfo simply returns the log-ratio transformed data.

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Kim-Anh Lê Cao, Mary-Ellen Costello, Vanessa Anne Lakis, Francois Bartolo, Xin-Yi Chua, Remi Brazeilles, Pascale Rondeau mixMC: a multivariate statistical framework to gain insight into Microbial Communities bioRxiv 044206; doi: http://dx.doi.org/10.1101/044206

John Aitchison. The statistical analysis of compositional data. Journal of the Royal Statistical Society. Series B (Methodological), pages 139-177, 1982.

Peter Filzmoser, Karel Hron, and Clemens Reimann. Principal component analysis for compositional data with outliers. Environmetrics, 20(6):621-632, 2009.

See Also

pca, pls, spls, plsda, splsda.

Examples

```
data(diverse.16S)
CLR = logratio.transfo(X = diverse.16S$data.TSS, logratio = 'CLR')
# no offset needed here as we have put it prior to the TSS, see www.mixOmics.org/mixMC
```

map *Classification given Probabilities*

Description

Converts a matrix in which each row sums to *1* into the nearest matrix of *(0,1)* indicator variables.

Usage

```
map(Y)
```

Arguments

Y	A matrix (for example a matrix of conditional probabilities in which each row sums to 1).

Value

A integer vector with one entry for each row of Y, in which the *i*-th value is the column index at which the *i*-th row of Y attains a maximum.

References

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association 97:611-631*.

C. Fraley, A. E. Raftery, T. B. Murphy and L. Scrucca (2012). mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. Technical Report No. 597, Department of Statistics, University of Washington.

See Also

unmap

Examples

```
data(nutrimouse)
Y = unmap(nutrimouse$diet)

map(Y)
```

mat.rank *Matrix Rank*

Description

This function estimate the rank of a matrix.

Usage

```
mat.rank(mat, tol)
```

Arguments

mat	a numeric matrix or data frame that can contain missing values.
tol	positive real, the tolerance for singular values, only those with values larger than tol are considered non-zero.

Details

mat.rank estimate the rank of a matrix by computing its singular values $d[i]$ (using nipals). The rank of the matrix can be defined as the number of singular values $d[i] > 0$.

If tol is missing, it is given by tol=max(dim(mat))*max(d)*.Machine$double.eps.

Value

The returned value is a list with components:

rank	a integer value, the matrix rank.
tol	the tolerance used for singular values.

Author(s)

Sébastien Déjean, Ignacio González, Al J Abadi

See Also

nipals

Examples

```
## Hilbert matrix
hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, "+") }
mat <- hilbert(16)
mat.rank(mat)

## Not run:
## Hilbert matrix with missing data
idx.na <- matrix(sample(c(0, 1, 1, 1, 1), 36, replace = TRUE), ncol = 6)
m.na <- m <- hilbert(9)[, 1:6]
m.na[idx.na == 0] <- NA
mat.rank(m)
mat.rank(m.na)

## End(Not run)
```

`mint.block.pls` *NP-integration*

Description

Function to integrate data sets measured on the same samples (N-integration) and to combine multiple independent studies measured on the same variables or predictors (P-integration) using variants of multi-group and generalised PLS (unsupervised analysis).

Usage

```
mint.block.pls(
  X,
  Y,
  indY,
  study,
  ncomp = 2,
  design,
  mode,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE
)
```

Arguments

`X`	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in samples x variables, with samples order matching in all data sets.
`Y`	Matrix or vector response for a multivariate regression framework. Data should be continuous variables (see `?mint.block.splsda` for supervised classification and factor response).
`indY`	To be supplied if Y is missing, indicates the position of the matrix / vector response in the list `X`
`study`	Factor, indicating the membership of each sample to each of the studies being combined
`ncomp`	the number of components to include in the model. Default to 2. Applies to all blocks.
`design`	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in `block.splsda`). If `Y` is provided instead of `indY`, the `design` matrix is changed to include relationships to `Y`.
`mode`	Character string indicating the type of PLS algorithm to use. One of `"regression"`, `"canonical"`, `"invariant"` or `"classic"`. See Details.

scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

The function fits multi-group generalised PLS models with a specified number of ncomp components. An outcome needs to be provided, either by Y or by its position indY in the list of blocks X.

Multi (continuous)response are supported. X and Y can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm block.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and more details in ?pls).

Value

mint.block.pls returns an object of class "mint.pls","block.pls", a list that contains the following components:

X	the centered and standardized original predictor matrix.
Y	the centered and standardized original response vector or matrix.
ncomp	the number of components included in the model for each block.
mode	the algorithm used to fit the model.
mat.c	matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by predict.
variates	list containing the X and Y variates.
loadings	list containing the estimated loadings for the variates.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
tol	the tolerance used in the iterative algorithm, used for subsequent S3 methods
max.iter	the maximum number of iterations, used for subsequent S3 methods
iter	Number of iterations of the algorithm for each component

Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

See Also

spls, summary, plotIndiv, plotVar, predict, perf, mint.block.spls, mint.block.plsda, mint.block.splsda and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(breast.TCGA)

# for the purpose of this example, we create data that fit in the context of
# this function.
# We consider the training set as study1 and the test set as another
# independent study2.

study = c(rep("study1",150), rep("study2",70))

# to put the data in the MINT format, we rbind the two studies
mrna = rbind(breast.TCGA$data.train$mrna, breast.TCGA$data.test$mrna)
mirna = rbind(breast.TCGA$data.train$mirna, breast.TCGA$data.test$mirna)

# For the purpose of this example, we create a continuous response by
# taking the first mrna variable, and removing it from the data
Y = mrna[,1]
mrna = mrna[,-1]

data = list(mrna = mrna, mirna = mirna)

# we can now apply the function
res = mint.block.plsda(data, Y, study=study, ncomp=2)

res
```

---

mint.block.plsda *NP-integration with Discriminant Analysis*

Description

Function to integrate data sets measured on the same samples (N-integration) and to combine multiple independent studies measured on the same variables or predictors (P-integration) using variants of multi-group and generalised PLS-DA for supervised classification.

Usage

```
mint.block.plsda(
  X,
  Y,
  indY,
  study,
  ncomp = 2,
  design,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in samples x variables, with samples order matching in all data sets.
Y	A factor or a class vector indicating the discrete outcome of each sample.
indY	To be supplied if Y is missing, indicates the position of the matrix / vector response in the list X
study	Factor, indicating the membership of each sample to each of the studies being combined
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

The function fits multi-group generalised PLS models with a specified number of ncomp components. A factor indicating the discrete outcome needs to be provided, either by Y or by its position indY in the list of blocks X.

X can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm block.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the impute.nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and more details in ?pls).

Value

mint.block.plsda returns an object of class "mint.plsda", "block.plsda", a list that contains the following components:

X	the centered and standardized original predictor matrix.
Y	the centered and standardized original response vector or matrix.
ncomp	the number of components included in the model for each block.
mode	the algorithm used to fit the model.
mat.c	matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by predict.
variates	list containing the X and Y variates.
loadings	list containing the estimated loadings for the variates.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
tol	the tolerance used in the iterative algorithm, used for subsequent S3 methods
max.iter	the maximum number of iterations, used for subsequent S3 methods
iter	Number of iterations of the algorithm for each component

Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

On multi-group PLS:

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

On multiple integration with PLSDA:

Singh A., Gautier B., Shannon C., Vacher M., Rohart F., Tebbutt S. and Lê Cao K.A. (2016). DIABLO: multi omics integration for biomarker discovery. BioRxiv available here: http://biorxiv.org/content/early/2016/08/03/067611 Tenenhaus A., Philippe C., Guillemot V, Lê Cao K.A., Grill J, Frouin V. Variable selection for generalized canonical correlation analysis. *Biostatistics*. kxu001

Gunther O., Shin H., Ng R. T. , McMaster W. R., McManus B. M. , Keown P. A. , Tebbutt S.J. , Lê Cao K-A. , (2014) Novel multivariate methods for integration of genomics and proteomics

data: Applications in a kidney transplant rejection study, OMICS: A journal of integrative biology, 18(11), 682-95.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

spls, summary, plotIndiv, plotVar, predict, perf, mint.block.spls, mint.block.plsda, mint.block.splsda and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(breast.TCGA)

# for the purpose of this example, we consider the training set as study1 and
# the test set as another independent study2.
study = c(rep("study1",150), rep("study2",70))

mrna = rbind(breast.TCGA$data.train$mrna, breast.TCGA$data.test$mrna)
mirna = rbind(breast.TCGA$data.train$mirna, breast.TCGA$data.test$mirna)
data = list(mrna = mrna, mirna = mirna)

Y = c(breast.TCGA$data.train$subtype, breast.TCGA$data.test$subtype)

res = mint.block.plsda(data,Y,study=study, ncomp=2)

res
```

---

mint.block.spls *NP-integration for integration with variable selection*

Description

Function to integrate data sets measured on the same samples (N-integration) and to combine multiple independent studies (P-integration) using variants of sparse multi-group and generalised PLS with variable selection (unsupervised analysis).

Usage

```
mint.block.spls(
  X,
  Y,
  indY,
  study,
  ncomp = 2,
  keepX,
  keepY,
  design,
  mode,
  scale = TRUE,
  tol = 1e-06,
```

```
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in samples x variables, with samples order matching in all data sets.
Y	Matrix or vector response for a multivariate regression framework. Data should be continuous variables (see ?mint.block.splsda for supervised classification and factor response).
indY	To be supplied if Y is missing, indicates the position of the matrix / vector response in the list X
study	Factor, indicating the membership of each sample to each of the studies being combined
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
keepX	A named list of same length as X. Each entry is the number of variables to select in each of the blocks of X for each component. By default all variables are kept in the model.
keepY	Only if Y is provided (and not indY). Each entry is the number of variables to select in each of the blocks of Y for each component.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

The function fits sparse multi-group generalised PLS models with a specified number of ncomp components. An outcome needs to be provided, either by Y or by its position indY in the list of blocks X.

Multi (continuous)response are supported. `X` and `Y` can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm `block.pls` without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the `nipals` function.

The type of algorithm to use is specified with the `mode` argument. Four PLS algorithms are available: PLS regression (`"regression"`), PLS canonical analysis (`"canonical"`), redundancy analysis (`"invariant"`) and the classical PLS algorithm (`"classic"`) (see References and more details in `?pls`).

Value

`mint.block.spls` returns an object of class `"mint.spls"`,`"block.spls"`, a list that contains the following components:

`X`	the centered and standardized original predictor matrix.
`Y`	the centered and standardized original response vector or matrix.
`ncomp`	the number of components included in the model for each block.
`mode`	the algorithm used to fit the model.
`mat.c`	matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by `predict`.
`variates`	list containing the X and Y variates.
`loadings`	list containing the estimated loadings for the variates.
`names`	list containing the names to be used for individuals and variables.
`nzv`	list containing the zero- or near-zero predictors information.
`tol`	the tolerance used in the iterative algorithm, used for subsequent S3 methods
`max.iter`	the maximum number of iterations, used for subsequent S3 methods
`iter`	Number of iterations of the algorithm for each component

Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

See Also

`spls`, `summary`, `plotIndiv`, `plotVar`, `predict`, `perf`, `mint.block.pls`, `mint.block.plsda`, `mint.block.splsda` and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(breast.TCGA)

# for the purpose of this example, we create data that fit in the context of
# this function.
# We consider the training set as study1 and the test set as another
# independent study2.

study = c(rep("study1",150), rep("study2",70))

# to put the data in the MINT format, we rbind the two studies
mrna = rbind(breast.TCGA$data.train$mrna, breast.TCGA$data.test$mrna)
mirna = rbind(breast.TCGA$data.train$mirna, breast.TCGA$data.test$mirna)

# For the purpose of this example, we create a continuous response by
# taking the first mrna variable, and removing it from the data
Y = mrna[,1]
mrna = mrna[,-1]

data = list(mrna = mrna, mirna = mirna)

# we can now apply the function
res = mint.block.splsda(data, Y, study=study, ncomp=2,
keepX = list(mrna=c(10,10), mirna=c(20,20)))

res
```

---

mint.block.splsda *NP-integration with Discriminant Analysis and variable selection*

Description

Function to integrate data sets measured on the same samples (N-integration) and to combine multiple independent studies measured on the same variables or predictors (P-integration) using variants of sparse multi-group and generalised PLS-DA for supervised classification and variable selection.

Usage

```
mint.block.splsda(
  X,
  Y,
  indY,
  study,
  ncomp = 2,
  keepX,
  design,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in samples x variables, with samples order matching in all data sets.
Y	A factor or a class vector indicating the discrete outcome of each sample.
indY	To be supplied if Y is missing, indicates the position of the matrix / vector response in the list X
study	Factor, indicating the membership of each sample to each of the studies being combined
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
keepX	A named list of same length as X. Each entry is the number of variables to select in each of the blocks of X for each component. By default all variables are kept in the model.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

The function fits sparse multi-group generalised PLS Discriminant Analysis models with a specified number of ncomp components. A factor indicating the discrete outcome needs to be provided, either by Y or by its position indY in the list of blocks X.

X can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm block.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the impute.nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and more details in ?pls).

Value

`mint.block.splsda` returns an object of class `"mint.splsda"`, `"block.splsda"`, a list that contains the following components:

`X`	the centered and standardized original predictor matrix.
`Y`	the centered and standardized original response vector or matrix.
`ncomp`	the number of components included in the model for each block.
`mode`	the algorithm used to fit the model.
`mat.c`	matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by `predict`.
`variates`	list containing the X and Y variates.
`loadings`	list containing the estimated loadings for the variates.
`names`	list containing the names to be used for individuals and variables.
`nzv`	list containing the zero- or near-zero predictors information.
`tol`	the tolerance used in the iterative algorithm, used for subsequent S3 methods
`max.iter`	the maximum number of iterations, used for subsequent S3 methods
`iter`	Number of iterations of the algorithm for each component

Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Author(s)

Florian Rohart, Benoit Gautier, Kim-Anh Lê Cao, Al J Abadi

References

On multi-group PLS: Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

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Tenenhaus A., Philippe C., Guillemot V, Lê Cao K.A., Grill J, Frouin V. Variable selection for generalized canonical correlation analysis. *Biostatistics*. kxu001

Gunther O., Shin H., Ng R. T. , McMaster W. R., McManus B. M. , Keown P. A. , Tebbutt S.J. , Lê Cao K-A. , (2014) Novel multivariate methods for integration of genomics and proteomics data: Applications in a kidney transplant rejection study, OMICS: A journal of integrative biology, 18(11), 682-95.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

`spls`, `summary`, `plotIndiv`, `plotVar`, `predict`, `perf`, `mint.block.spls`, `mint.block.plsda`, `mint.block.pls` and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(breast.TCGA)

# for the purpose of this example, we consider the training set as study1 and
# the test set as another independent study2.
study = c(rep("study1",150), rep("study2",70))

mrna = rbind(breast.TCGA$data.train$mrna, breast.TCGA$data.test$mrna)
mirna = rbind(breast.TCGA$data.train$mirna, breast.TCGA$data.test$mirna)
data = list(mrna = mrna, mirna = mirna)

Y = c(breast.TCGA$data.train$subtype, breast.TCGA$data.test$subtype)

res = mint.block.splsda(data,Y,study=study,
keepX = list(mrna=c(10,10), mirna=c(20,20)),ncomp=2)

res
```

`mint.pca` *P-integration with Principal Component Analysis*

Description

Function to integrate and combine multiple independent studies measured on the same variables or predictors (P-integration) using a multigroup Principal Component Analysis.

Usage

```
mint.pca(
  X,
  ncomp = 2,
  study,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  verbose.call = FALSE
)
```

Arguments

`X`	numeric matrix of predictors combining multiple independent studies on the same set of predictors. `NA`s are allowed.
`ncomp`	Number of components to include in the model (see Details). Default to 2
`study`	factor indicating the membership of each sample to each of the studies being combined
`scale`	Logical. If scale = TRUE, each block is standardized to zero means and unit variances. Default = `TRUE`.
`tol`	Convergence stopping value.
`max.iter`	integer, the maximum number of iterations.

verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

mint.pca fits a vertical PCA model with ncomp components in which several independent studies measured on the same variables are integrated. The study factor indicates the membership of each sample in each study. We advise to only combine studies with more than 3 samples as the function performs internal scaling per study.

Missing values are handled by being disregarded during the cross product computations in the algorithm without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the nipals function.

Useful graphical outputs are available, e.g. plotIndiv, plotLoadings, plotVar.

Value

mint.pca returns an object of class "mint.pca", "pca", a list that contains the following components:

X	the centered and standardized original predictor matrix.
ncomp	the number of components included in the model.
study	The study grouping factor
sdev	the eigenvalues of the covariance/correlation matrix, though the calculation is actually done with the singular values of the data matrix or by using NIPALS.
center, scale	the centering and scaling used, or FALSE.
rotation	the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors).
loadings	same as 'rotation' to keep the mixOmics spirit
x	the value of the rotated data (the centred (and scaled if requested) data multiplied by the rotation/loadings matrix), also called the principal components.
variates	same as 'x' to keep the mixOmics spirit
prop_expl_var	Proportion of the explained variance from the multivariate model after setting possible missing values to zero in the data.
names	list containing the names to be used for individuals and variables.
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

See Also

spls, summary, plotIndiv, plotVar, predict, perf, mint.spls, mint.plsda, mint.splsda and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(stemcells)

res = mint.pca(X = stemcells$gene, ncomp = 3,
study = stemcells$study)

plotIndiv(res, group = stemcells$celltype, legend=TRUE)
```

---

mint.pls *P-integration*

Description

Function to integrate and combine multiple independent studies measured on the same variables or predictors (P-integration) using variants of multi-group PLS (unsupervised analysis).

Usage

```
mint.pls(
  X,
  Y,
  ncomp = 2,
  mode = c("regression", "canonical", "invariant", "classic"),
  study,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

X	numeric matrix of predictors combining multiple independent studies on the same set of predictors. NAs are allowed.
Y	Matrix or vector response for a multivariate regression framework. Data should be continuous variables (see mint.plsda for supervised classification and factor response)
ncomp	Positive Integer. The number of components to include in the model. Default to 2.
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
study	Factor, indicating the membership of each sample to each of the studies being combined

scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

mint.pls fits a vertical PLS-DA models with ncomp components in which several independent studies measured on the same variables are integrated. The aim is to explain the continuous outcome Y. The study factor indicates the membership of each sample in each study. We advise to only combine studies with more than 3 samples as the function performs internal scaling per study.

Multi (continuous)response are supported. X and Y can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm mint.pls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and more details in ?pls).

Useful graphical outputs are available, e.g. plotIndiv, plotLoadings, plotVar.

Value

mint.pls returns an object of class "mint.pls", "pls", a list that contains the following components:

X	the centered and standardized original predictor matrix.
Y	the centered and standardized original response vector or matrix.
ncomp	the number of components included in the model.
study	The study grouping factor
mode	the algorithm used to fit the model.
variates	list containing the variates of X - global variates.
loadings	list containing the estimated loadings for the variates - global loadings.
variates.partial	list containing the variates of X relative to each study - partial variates.
loadings.partial	list containing the estimated loadings for the partial variates - partial loadings.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.

iter	Number of iterations of the algorithm for each component
prop_expl_var	Percentage of explained variance for each component and each study (note that contrary to PCA, this amount may not decrease as the aim of the method is not to maximise the variance, but the covariance between data sets).
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

See Also

spls, summary, plotIndiv, plotVar, predict, perf, mint.spls, mint.plsda, mint.splsda and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(stemcells)

# for the purpose of this example, we artificially
# create a continuous response Y by taking gene 1.

res = mint.pls(X = stemcells$gene[,-1], Y = stemcells$gene[,1], ncomp = 3,
study = stemcells$study)

plotIndiv(res)

#plot study-specific outputs for all studies
plotIndiv(res, study = "all.partial")

## Not run:
#plot study-specific outputs for study "2"
plotIndiv(res, study = "2", col = 1:3, legend = TRUE)

## End(Not run)
```

---

mint.plsda *P-integration with Projection to Latent Structures models (PLS) with Discriminant Analysis*

Description

Function to combine multiple independent studies measured on the same variables or predictors (P-integration) using variants of multi-group PLS-DA for supervised classification.

Usage

```
mint.plsda(
  X,
  Y,
  ncomp = 2,
  study,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

X	numeric matrix of predictors combining multiple independent studies on the same set of predictors. NAs are allowed.
Y	A factor or a class vector indicating the discrete outcome of each sample.
ncomp	Positive Integer. The number of components to include in the model. Default to 2.
study	Factor, indicating the membership of each sample to each of the studies being combined
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

mint.plsda function fits a vertical PLS-DA models with ncomp components in which several independent studies measured on the same variables are integrated. The aim is to classify the discrete outcome Y. The study factor indicates the membership of each sample in each study. We advise to only combine studies with more than 3 samples as the function performs internal scaling per study, and where all outcome categories are represented.

X can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm mint.plsda without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the impute.nipals function.

The type of deflation used is 'regression' for discriminant algorithms. i.e. no deflation is performed on Y.

Useful graphical outputs are available, e.g. plotIndiv, plotLoadings, plotVar.

Value

`mint.plsda` returns an object of class `"mint.plsda"`, `"plsda"`, a list that contains the following components:

`X`	the centered and standardized original predictor matrix.
`Y`	original factor
`ind.mat`	the centered and standardized original response vector or matrix.
`ncomp`	the number of components included in the model.
`study`	The study grouping factor
`mode`	the algorithm used to fit the model.
`variates`	list containing the variates of X - global variates.
`loadings`	list containing the estimated loadings for the variates - global loadings.
`variates.partial`	list containing the variates of X relative to each study - partial variates.
`loadings.partial`	list containing the estimated loadings for the partial variates - partial loadings.
`names`	list containing the names to be used for individuals and variables.
`nzv`	list containing the zero- or near-zero predictors information.
`iter`	Number of iterations of the algorithm for each component
`prop_expl_var`	Percentage of explained variance for each component and each study after setting possible missing values to zero (note that contrary to PCA, this amount may not decrease as the aim of the method is not to maximise the variance, but the covariance between X and the dummy matrix Y).
`call`	if `verbose.call = FALSE`, then just the function call is returned. If `verbose.call = TRUE` then all the inputted values are accessable via this component

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

`spls`, `summary`, `plotIndiv`, `plotVar`, `predict`, `perf`, `mint.pls`, `mint.spls`, `mint.splsda` and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(stemcells)

res = mint.plsda(X = stemcells$gene, Y = stemcells$celltype, ncomp = 3,
study = stemcells$study)

plotIndiv(res)

#plot study-specific outputs for all studies
plotIndiv(res, study = "all.partial")

## Not run:
#plot study-specific outputs for study "2"
plotIndiv(res, study = "2", col = 1:3, legend = TRUE)

## End(Not run)
```

`mint.spls` *P-integration with variable selection*

Description

Function to integrate and combine multiple independent studies measured on the same variables or predictors (P-integration) using variants of multi-group sparse PLS for variable selection (unsupervised analysis).

Usage

```
mint.spls(
  X,
  Y,
  ncomp = 2,
  mode = c("regression", "canonical", "invariant", "classic"),
  study,
  keepX = rep(ncol(X), ncomp),
  keepY = rep(ncol(Y), ncomp),
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

`X`	numeric matrix of predictors combining multiple independent studies on the same set of predictors. `NA`s are allowed.
`Y`	Matrix or vector response for a multivariate regression framework. Data should be continuous variables (see `mint.splsda` for supervised classification and factor response)

ncomp	Positive Integer. The number of components to include in the model. Default to 2.
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
study	Factor, indicating the membership of each sample to each of the studies being combined
keepX	numeric vector indicating the number of variables to select in X on each component. By default all variables are kept in the model.
keepY	numeric vector indicating the number of variables to select in Y on each component. By default all variables are kept in the model.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

mint.spls fits a vertical sparse PLS-DA models with ncomp components in which several independent studies measured on the same variables are integrated. The aim is to explain the continuous outcome Y and selecting correlated features between both data sets X and Y. The study factor indicates the membership of each sample in each study. We advise to only combine studies with more than 3 samples as the function performs internal scaling per study.

Multi (continuous)response are supported. X and Y can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm mint.spls without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the nipals function.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis ("invariant") and the classical PLS algorithm ("classic") (see References and more details in ?pls).

Variable selection is performed on each component for each block of X, and for Y if specified, via input parameter keepX and keepY.

Useful graphical outputs are available, e.g. plotIndiv, plotLoadings, plotVar.

Value

mint.spls returns an object of class "mint.spls","spls", a list that contains the following components:

X	numeric matrix of predictors combining multiple independent studies on the same set of predictors. NAs are allowed.
Y	the centered and standardized original response vector or matrix.
ncomp	the number of components included in the model.
study	The study grouping factor
mode	the algorithm used to fit the model.
keepX	Number of variables used to build each component of X
keepY	Number of variables used to build each component of Y
variates	list containing the variates of X - global variates.
loadings	list containing the estimated loadings for the variates - global loadings.
variates.partial	list containing the variates of X relative to each study - partial variates.
loadings.partial	list containing the estimated loadings for the partial variates - partial loadings.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
iter	Number of iterations of the algorithm for each component
prop_expl_var	The amount of the variance explained by each variate / component divided by the total variance in the data for each study (after removing the possible missing values) using the definition of 'redundancy'. Note that contrary to PCA, this amount may not decrease in the following components as the aim of the method is not to maximise the variance, but the covariance between data sets (including the dummy matrix representation of the outcome variable in case of the supervised approaches).
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

See Also

spls, summary, plotIndiv, plotVar, predict, perf, mint.pls, mint.plsda, mint.splsda and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(stemcells)

# for the purpose of this example, we artificially
# create a continuous response Y by taking gene 1.

res = mint.spls(X = stemcells$gene[,-1], Y = stemcells$gene[,1], ncomp = 3,
keepX = c(10, 5, 15), study = stemcells$study)

plotIndiv(res)

#plot study-specific outputs for all studies
plotIndiv(res, study = "all.partial")

## Not run:
#plot study-specific outputs for study "2"
plotIndiv(res, study = "2", col = 1:3, legend = TRUE)

## End(Not run)
```

`mint.splsda` *P-integration with Discriminant Analysis and variable selection*

Description

Function to combine multiple independent studies measured on the same variables or predictors (P-integration) using variants of multi-group sparse PLS-DA for supervised classification with variable selection.

Usage

```
mint.splsda(
  X,
  Y,
  ncomp = 2,
  study,
  keepX = rep(ncol(X), ncomp),
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

`X`	numeric matrix of predictors combining multiple independent studies on the same set of predictors. `NA`s are allowed.
`Y`	A factor or a class vector indicating the discrete outcome of each sample.
`ncomp`	Positive Integer. The number of components to include in the model. Default to 2.

study	Factor, indicating the membership of each sample to each of the studies being combined
keepX	numeric vector indicating the number of variables to select in X on each component. By default all variables are kept in the model.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

mint.splsda function fits a vertical sparse PLS-DA models with ncomp components in which several independent studies measured on the same variables are integrated. The aim is to classify the discrete outcome Y and select variables that explain the outcome. The study factor indicates the membership of each sample in each study. We advise to only combine studies with more than 3 samples as the function performs internal scaling per study, and where all outcome categories are represented.

X can contain missing values. Missing values are handled by being disregarded during the cross product computations in the algorithm mint.splsda without having to delete rows with missing data. Alternatively, missing data can be imputed prior using the impute.nipals function.

The type of deflation used is 'regression' for discriminant algorithms. i.e. no deflation is performed on Y.

Variable selection is performed on each component for X via input parameter keepX.

Useful graphical outputs are available, e.g. plotIndiv, plotLoadings, plotVar.

Value

mint.splsda returns an object of class "mint.splsda","splsda", a list that contains the following components:

X	the centered and standardized original predictor matrix.
Y	the centered and standardized original response vector or matrix.
ind.mat	the centered and standardized original response vector or matrix.
ncomp	the number of components included in the model.
study	The study grouping factor
mode	the algorithm used to fit the model.
keepX	Number of variables used to build each component of X
variates	list containing the variates of X - global variates.

loadings	list containing the estimated loadings for the variates - global loadings.
variates.partial	list containing the variates of X relative to each study - partial variates.
loadings.partial	list containing the estimated loadings for the partial variates - partial loadings.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
iter	Number of iterations of the algorithm for each component
prop_expl_var	Percentage of explained variance for each component and each study (note that contrary to PCA, this amount may not decrease as the aim of the method is not to maximise the variance, but the covariance between X and the dummy matrix Y).
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2014). Algorithms for multi-group PLS. J. Chemometrics, 28(3), 192-201.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

spls, summary, plotIndiv, plotVar, predict, perf, mint.pls, mint.plsda, mint.plsda and http://www.mixOmics.org/mixMINT for more details.

Examples

```
data(stemcells)

# -- feature selection
res = mint.splsda(X = stemcells$gene, Y = stemcells$celltype, ncomp = 3, keepX = c(10, 5, 15),
study = stemcells$study)

plotIndiv(res)
#plot study-specific outputs for all studies
plotIndiv(res, study = "all.partial")

## Not run:
#plot study-specific outputs for study "2"
plotIndiv(res, study = "2")

#plot study-specific outputs for study "2", "3" and "4"
```

```
plotIndiv(res, study = c(2, 3, 4))

## End(Not run)
```

`mixOmics` *PLS-derived methods: one function to rule them all!*

Description

This is the documentation for mixOmics function from mixOmics package. For package documentation refer to `help(package='mixOmics')`

Usage

```
mixOmics(
  X,
  Y,
  indY,
  study,
  ncomp,
  keepX,
  keepY,
  design,
  tau = NULL,
  mode = c("regression", "canonical", "invariant", "classic"),
  scale,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE
)
```

Arguments

`X`	Input data. Either a matrix or a list of data sets (called 'blocks') matching on the same samples. Data should be arranged in samples x variables, with samples order matching in all data sets.
`Y`	Outcome. Either a numeric matrix of responses or a factor or a class vector for the discrete outcome.
`indY`	To supply if Y is missing, indicates the position of the outcome in the list X
`study`	grouping factor indicating which samples are from the same study
`ncomp`	If `X` is a data matrix, `ncomp` is a single value. If `X` is a list of data sets, `ncomp` is a numeric vector of length the number of blocks in `X`. The number of components to include in the model for each block (does not necessarily need to take the same value for each block).
`keepX`	Number of variables to keep in the X-loadings
`keepY`	Number of variables to keep in the Y-loadings
`design`	numeric matrix of size (number of blocks) x (number of blocks) with only 0 or 1 values. A value of 1 (0) indicates a relationship (no relationship) between the blocks to be modelled. If `Y` is provided instead of `indY`, the `design` matrix is changed to include relationships to `Y`.

tau	numeric vector of length the number of blocks in X. Each regularization parameter will be applied on each block and takes the value between 0 (no regularisation) and 1. If tau = "optimal" the shrinkage paramaters are estimated for each block and each dimension using the Schafer and Strimmer (2005) analytical formula.
mode	character string. What type of algorithm to use, (partially) matching one of "regression", "canonical", "invariant" or "classic". See Details.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE).
tol	Convergence stopping value.
max.iter	integer, the maximum number of iterations.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE

Details

This function performs one of the PLS derived methods included in the mixOmics package that is the most appropriate for your input data, one of (mint).(block).(s)pls(da) depending on your input data (single data, list of data, discrete outcome, ...)

This function performs one of the PLS derived methods included in the mixOmics package that is the most appropriate for your input data, one of (mint).(block).(s)pls(da).

If your input data X is a matrix, then the algorithm is directed towards one of (mint).(s)pls(da) depending on your input data Y (factor for the discrete outcome directs the algorithm to DA analysis) and whether you input a study parameter (MINT analysis) or a keepX parameter (sparse analysis).

If your input data X is a list of matrices, then the algorithm is directed towards one of (mint).block.(s)pls(da) depending on your input data Y (factor for the discrete outcome directs the algorithm to DA analysis) and whether you input a study parameter (MINT analysis) or a keepX parameter (sparse analysis).

More details about the PLS modes in ?pls.

Value

none

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

MINT models:

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

Eslami, A., Qannari, E. M., Kohler, A., and Bougeard, S. (2013). Multi-group PLS Regression: Application to Epidemiology. In New Perspectives in Partial Least Squares and Related Methods, pages 243-255. Springer.

Integration of omics data sets:

Singh A, Gautier B, Shannon C, Vacher M, Rohart F, Tebbutt S, Lê Cao K-A. DIABLO: an integrative, multi-omics, multivariate method for multi-group classification. http://biorxiv.org/content/early/2016/08/03/067611

Lê Cao, K.-A., Martin, P.G.P., Robert-Granie, C. and Besse, P. (2009). Sparse canonical methods for biological data integration: application to a cross-platform study. *BMC Bioinformatics* **10**:34.

Lê Cao, K.-A., Rossouw, D., Robert-Granie, C. and Besse, P. (2008). A sparse PLS for variable selection when integrating Omics data. *Statistical Applications in Genetics and Molecular Biology* **7**, article 35.

Tenenhaus A., Phillipe C., Guillemot V., Lê Cao K-A. , Grill J. , Frouin V. (2014), Variable selection for generalized canonical correlation analysis, *Biostatistics*, doi: 10.1093/biostatistics. PMID: 24550197.

Sparse SVD:

Shen, H. and Huang, J. Z. (2008). Sparse principal component analysis via regularized low rank matrix approximation. *Journal of Multivariate Analysis* **99**, 1015-1034.

PLS-DA:

Lê Cao K-A, Boitard S and Besse P (2011). Sparse PLS Discriminant Analysis: biologically relevant feature selection and graphical displays for multiclass problems. BMC Bioinformatics 12:253.

PLS:

Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

Wold H. (1966). Estimation of principal components and related models by iterative least squares. In: Krishnaiah, P. R. (editors), *Multivariate Analysis*. Academic Press, N.Y., 391-420.

Abdi H (2010). Partial least squares regression and projection on latent structure regression (PLS Regression). *Wiley Interdisciplinary Reviews: Computational Statistics*, 2(1), 97-106.

On multilevel analysis:

Liquet, B., Lê Cao, K.-A., Hocini, H. and Thiebaut, R. (2012) A novel approach for biomarker selection and the integration of repeated measures experiments from two platforms. *BMC Bioinformatics* **13**:325.

Westerhuis, J. A., van Velzen, E. J., Hoefsloot, H. C., and Smilde, A. K. (2010). Multivariate paired data analysis: multilevel PLSDA versus OPLSDA. *Metabolomics*, **6**(1), 119-128.

Visualisations:

González I., Lê Cao K.-A., Davis, M.D. and Déjean S. (2013) Insightful graphical outputs to explore relationships between two omics data sets. BioData Mining 5:19.

See Also

`pls`, `spls`, `plsda`, `splsda`, `mint.pls`, `mint.spls`, `mint.plsda`, `mint.splsda`, `block.pls`, `block.spls`, `block.plsda`, `block.splsda`, `mint.block.pls`, `mint.block.spls`, `mint.block.plsda`, `mint.block.splsda`

Examples

```
## -- directed towards PLS framework because X is a matrix and the study argument is missing
# ----------------------------------------------------
data(liver.toxicity)
X = liver.toxicity$gene
Y = liver.toxicity$clinic
Y.factor = as.factor(liver.toxicity$treatment[, 4])
```

```
# directed towards PLS
out = mixOmics(X, Y, ncomp = 2)

# directed towards sPLS because of keepX and/or keepY
out = mixOmics(X, Y, ncomp = 2, keepX = c(50, 50), keepY = c(10, 10))

# directed towards PLS-DA because Y is a factor
out = mixOmics(X, Y.factor, ncomp = 2)

# directed towards sPLS-DA because Y is a factor and there is a keepX
out = mixOmics(X, Y.factor, ncomp = 2, keepX = c(20, 20))


## Not run:
## -- directed towards block.pls framework because X is a list
# ----------------------------------------------------
data(nutrimouse)
Y = unmap(nutrimouse$diet)
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = Y)

# directed towards block PLS
out = mixOmics(X = data, Y = Y,ncomp = 3)

# directed towards block sPLS because of keepX and/or keepY
out = mixOmics(X = data, Y = Y,ncomp = 3,
keepX = list(gene = c(10,10), lipid = c(15,15)))

# directed towards block PLS-DA because Y is a factor
out = mixOmics(X = data, Y = nutrimouse$diet, ncomp = 3)

# directed towards block sPLS-DA because Y is a factor and there is a keepX
out = mixOmics(X = data, Y = nutrimouse$diet, ncomp = 3,
keepX = list(gene = c(10,10), lipid = c(15,15)))


## -- directed towards mint.pls framework because of the study factor
# ----------------------------------------------------
data(stemcells)
# directed towards PLS
out = mixOmics(X = stemcells$gene, Y = unmap(stemcells$celltype), ncomp = 2)

# directed towards mint.PLS
out = mixOmics(X = stemcells$gene, Y = unmap(stemcells$celltype),
ncomp = 2, study = stemcells$study)

# directed towards mint.sPLS because of keepX and/or keepY
out = mixOmics(X = stemcells$gene, Y = unmap(stemcells$celltype),
ncomp = 2, study = stemcells$study, keepX = c(10, 5, 15))

# directed towards mint.PLS-DA because Y is a factor
out = mixOmics(X = stemcells$gene, Y = stemcells$celltype, ncomp = 2,
study = stemcells$study)

# directed towards mint.sPLS-DA because Y is a factor and there is a keepX
out = mixOmics(X = stemcells$gene, Y = stemcells$celltype, ncomp = 2,
study = stemcells$study, keepX = c(10, 5, 15))
```

```
## End(Not run)
```

`multidrug` *Multidrug Resistence Data*

Description

This data set contains the expression of 48 known human ABC transporters with patterns of drug activity in 60 diverse cancer cell lines (the NCI-60) used by the National Cancer Institute to screen for anticancer activity.

Usage

```
data(multidrug)
```

Format

A list containing the following components:

list("ABC.trans") data matrix with 60 rows and 48 columns. The expression of the 48 human ABC transporters.

list("compound") data matrix with 60 rows and 1429 columns. The activity of 1429 drugs for the 60 cell lines.

list("comp.name") character vector. The names or the NSC No. of the 1429 compounds.

list("cell.line") a list containing two character vector components: `Sample` the names of the 60 cell line which were analysed, and `Class` the phenotypes of the 60 cell lines.

Details

The data come from a pharmacogenomic study (Szakacs *et al.*, 2004) in which two kinds of measurements acquired on the NCI-60 cancer cell lines are considered:

- the expression of the 48 human ABC transporters measured by real-time quantitative RT-PCR for each cell line;
- the activity of 1429 drugs expressed as GI_{50} which corresponds to the concentration at which the drug induces 50% inhibition of cellular growth for the cell line tested.

The NCI- 60 panel includes cell lines derived from cancers of colorectal (7 cell lines), renal(8), ovarian(6), breast(8), prostate(2), lung(9) and central nervous system origin(6), as well as leukemias(6) and melanomas(8). It was set up by the Developmental Therapeutics Program of the National Cancer Institute (NCI, one of the U.S. National Institutes of Health) to screen the toxicity of chemical compound repositories. The expressions of the 48 human ABC transporters is available as a supplement to the paper of Szak?cs *et al.* (2004).

The drug dataset consiste of 118 compounds whose mechanisms of action are putatively classifiable (Weinstein *et al.*, 1992) and a larger set of 1400 compounds that have been tested multiple times and whose screening data met quality control criteria described elsewhere (Scherf *et al.*, 2000). The two were combined to form a joint dataset that included 1429 compounds.

Value

none

Source

The NCI dataset was downloaded from The Genomics and Bioinformatics Group Supplemental Table S1 to the paper of Szakacs *et al.* (2004), http://discover.nci.nih.gov/abc/2004_cancercell_abstract.jsp#supplement

The two drug data sets are a companion resource for the paper of Scherf *et al.* (2000), and was downloaded from http://discover.nci.nih.gov/datasetsNature2000.jsp.

References

Scherf, U., Ross, D. T., Waltham, M., Smith, L. H., Lee, J. K., Tanabe, L., Kohn, K. W., Reinhold, W. C., Myers, T. G., Andrews, D. T., Scudiero, D. A., Eisen, M. B., Sausville, E. A., Pommier, Y., Botstein, D., Brown, P. O. and Weinstein, J. N. (2000). A Gene Expression Database for the Molecular Pharmacology of Cancer. *Nature Genetics*, **24**, 236-244.

Szakacs, G., Annereau, J.-P., Lababidi, S., Shankavaram, U., Arciello, A., Bussey, K. J., Reinhold, W., Guo, Y., Kruh, G. D., Reimers, M., Weinstein, J. N. and Gottesman, M. M. (2004). Predicting drug sensivity and resistance: Profiling ABC transporter genes in cancer cells. *Cancer Cell* **4**, 147-166.

Weinstein, J.N., Kohn, K.W., Grever, M.R., Viswanadhan, V.N., Rubinstein, L.V., Monks, A.P., Scudiero, D.A., Welch, L., Koutsoukos, A.D., Chiausa, A.J. et al. 1992. Neural computing in cancer drug development: Predicting mechanism of action. *Science* **258**, 447-451.

---

nearZeroVar *Identification of zero- or near-zero variance predictors*

Description

Borrowed from the **caret** package. It is used as an internal function in the PLS methods, but can also be used as an external function, in particular when the data contain a lot of zeroes values and need to be pre-filtered beforehand.

Usage

```
nearZeroVar(x, freqCut = 95/5, uniqueCut = 10)
```

Arguments

`x`	a numeric vector or matrix, or a data frame with all numeric data.
`freqCut`	the cutoff for the ratio of the most common value to the second most common value.
`uniqueCut`	the cutoff for the percentage of distinct values out of the number of total samples.

Details

This function diagnoses predictors that have one unique value (i.e. are zero variance predictors) or predictors that are have both of the following characteristics: they have very few unique values relative to the number of samples and the ratio of the frequency of the most common value to the frequency of the second most common value is large.

For example, an example of near zero variance predictor is one that, for 1000 samples, has two distinct values and 999 of them are a single value.

To be flagged, first the frequency of the most prevalent value over the second most frequent value (called the "frequency ratio") must be above `freqCut`. Secondly, the "percent of unique values," the number of unique values divided by the total number of samples (times 100), must also be below `uniqueCut`.

In the above example, the frequency ratio is 999 and the unique value percentage is 0.0001.

Value

`nearZeroVar` returns a list that contains the following components:

`Position`	a vector of integers corresponding to the column positions of the problematic predictors that will need to be removed.
`Metrics`	a data frame containing the zero- or near-zero predictors information with columns: `freqRatio`, the ratio of frequencies for the most common value over the second most common value and, `percentUnique`, the percentage of unique data points out of the total number of data points.

Author(s)

Max Kuhn, Allan Engelhardt, Florian Rohart, Benoit Gautier, AL J Abadi for mixOmics

See Also

`pls`, `spls`, `plsda`, `splsda`

Examples

```
data(diverse.16S)
nzv = nearZeroVar(diverse.16S$data.raw)
length(nzv$Position) # those would be removed for the default frequency cut
```

---

network *Relevance Network for (r)CCA and (s)PLS regression*

Description

Display relevance associations network for (regularized) canonical correlation analysis and (sparse) PLS regression. The function avoids the intensive computation of Pearson correlation matrices on large data set by calculating instead a pair-wise similarity matrix directly obtained from the latent components of our integrative approaches (CCA, PLS, block.pls methods). The similarity value between a pair of variables is obtained by calculating the sum of the correlations between the original variables and each of the latent components of the model. The values in the similarity matrix can be seen as a robust approximation of the Pearson correlation (see González et al. 2012 for a mathematical demonstration and exact formula). The advantage of relevance networks is their ability to simultaneously represent positive and negative correlations, which are missed by methods based on Euclidean distances or mutual information. Those networks are bipartite and thus only a link between two variables of different types can be represented. The network can be saved in a .glm format using the `igraph` package, the function `write.graph` and extracting the output `object$gR`, see details.

Usage

```
network(
  mat,
  comp = NULL,
  blocks = c(1, 2),
  cutoff = 0,
  row.names = TRUE,
  col.names = TRUE,
  block.var.names = TRUE,
  graph.scale = 0.5,
  size.node = 0.5,
  color.node = NULL,
  shape.node = NULL,
  alpha.node = 0.85,
  cex.node.name = NULL,
  color.edge = color.GreenRed(100),
  lty.edge = "solid",
  lwd.edge = 1,
  show.edge.labels = FALSE,
  cex.edge.label = 1,
  show.color.key = TRUE,
  symkey = TRUE,
  keysize = c(1, 1),
  keysize.label = 1,
  breaks,
  interactive = FALSE,
  layout.fun = NULL,
  save = NULL,
  name.save = NULL,
  plot.graph = TRUE
)
```

Arguments

mat	numeric matrix of values to be represented. Alternatively, an object from one of the following models: mix_pls, plsda, mixo_spls, splsda, rcc, sgcca, rgcca, sgccda.
comp	atomic or vector of positive integers. The components to adequately account for the data association. Defaults to comp = 1.
blocks	a vector indicating the block variables to display.
cutoff	numeric value between 0 and 1. The tuning threshold for the relevant associations network (see Details).
row.names, col.names	character vector containing the names of X- and Y-variables.
block.var.names	either a list of vector components for variable names in each block or FALSE for no names. If TRUE, the columns names of the blocks are used as names.
graph.scale	Numeric between 0 and 1 which alters the scale of the entire plot. Increasing the value decreases the size of nodes and increases their distance from one another. Defaults to 0.5.

size.node	Numeric between 0 and 1 which determines the relative size of nodes. Defaults to 0.5.
color.node	vector of length two, the colors of the X and Y nodes (see Details).
shape.node	character vector of length two, the shape of the X and Y nodes (see Details).
alpha.node	Numeric between 0 and 1 which determines the opacity of nodes. Only used in block objects.
cex.node.name	the font size for the node labels.
color.edge	vector of colors or character string specifying the colors function to using to color the edges, set to default to color.GreenRed(100) but other palettes can be chosen (see Details and Examples).
lty.edge	character vector of length two, the line type for the edges (see Details).
lwd.edge	vector of length two, the line width of the edges (see Details).
show.edge.labels	logical. If TRUE, plot association values as edge labels (defaults to FALSE).
cex.edge.label	the font size for the edge labels.
show.color.key	Logical. If TRUE a color key should be plotted.
symkey	Logical indicating whether the color key should be made symmetric about 0. Defaults to TRUE.
keysize	numeric value indicating the size of the color key.
keysize.label	vector of length 1, indicating the size of the labels and title of the color key.
breaks	(optional) either a numeric vector indicating the splitting points for binning mat into colors, or a integer number of break points to be used, in which case the break points will be spaced equally between min(mat) and max(mat).
interactive	logical. If TRUE, a scrollbar is created to change the cutoff value interactively (defaults to FALSE). See Details.
layout.fun	a function. It specifies how the vertices will be placed on the graph. See help(layout) in the igraph package. Defaults to layout.fruchterman.reingold.
save	should the plot be saved ? If so, argument to be set either to 'jpeg', 'tiff', 'png' or 'pdf'.
name.save	character string giving the name of the saved file.
plot.graph	logical. If TRUE (default), plotting window will be filled with network. If FALSE, then no graph will be plotted, though the return value of the function is the exact same.

Details

network allows to infer large-scale association networks between the X and Y datasets in rcc or spls. The output is a graph where each X- and Y-variable corresponds to a node and the edges included in the graph portray associations between them.

In rcc, to identify X-Y pairs showing relevant associations, network calculate a similarity measure between X and Y variables in a pair-wise manner: the scalar product value between every pairs of vectors in dimension length(comp) representing the variables X and Y on the axis defined by Z_i with i in comp, where Z_i is the equiangular vector between the i-th X and Y canonical variate.

In spls, if object$mode is regression, the similarity measure between X and Y variables is given by the scalar product value between every pairs of vectors in dimension length(comp) representing the variables X and Y on the axis defined by U_i with i in comp, where U_i is the i-th X variate.

If object$mode is canonical then X and Y are represented on the axis defined by U_i and V_i respectively.

Variable pairs with a high similarity measure (in absolute value) are considered as relevant. By changing the cut-off, one can tune the relevance of the associations to include or exclude relationships in the network.

interactive=TRUE open two device, one for association network, one for scrollbar, and define an interactive process: by clicking either at each end ($-$ or $+$) of the scrollbar or at middle portion of this. The position of the slider indicate which is the 'cutoff' value associated to the display network.

The network can be saved in a .glm format using the **igraph** package, the function write.graph and extracting the output obkect$gR.

The interactive process is terminated by clicking the second button and selecting Stop from the menu, or from the Stop menu on the graphics window.

The color.node is a vector of length two, of any of the three kind of R colors, i.e., either a color name (an element of colors()), a hexadecimal string of the form "#rrggbb", or an integer i meaning palette()[i]. color.node[1] and color.node[2] give the color for filled nodes of the X- and Y-variables respectively. Defaults to c("white", "white").

color.edge give the color to edges with colors corresponding to the values in mat. Defaults to color.GreenRed(100) for negative (green) and positive (red) correlations. We also propose other palettes of colors, such as color.jet and color.spectral, see help on those functions, and examples below. Other palette of colors from the stats package can be used too.

shape.node[1] and shape.node[2] provide the shape of the nodes associate to X- and Y-variables respectively. Current acceptable values are "circle" and "rectangle". Defaults to c("circle", "rectangle").

lty.edge[1] and lty.egde[2] give the line type to edges with positive and negative weight respectively. Can be one of "solid", "dashed", "dotted", "dotdash", "longdash" and "twodash". Defaults to c("solid", "solid").

lwd.edge[1] and lwd.edge[2] provide the line width to edges with positive and negative weight respectively. This attribute is of type double with a default of c(1, 1).

Value

network return a list containing the following components:

M	the correlation matrix used by network.
gR	a graph object to save the graph for cytoscape use (requires to load the **igraph** package).

Warning

If the number of variables is high, the generation of the network generation can take some time.

Author(s)

Ignacio González, Kim-Anh Lê Cao, AL J Abadi

References

Mathematical definition: González I., Lê Cao K-A., Davis, M.J. and Déjean, S. (2012). Visualising associations between paired omics data sets. J. Data Mining 5:19. http://www.biodatamining.org/content/5/1/19/abstract

Examples and illustrations:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

Relevance networks:

Butte, A. J., Tamayo, P., Slonim, D., Golub, T. R. and Kohane, I. S. (2000). Discovering functional relationships between RNA expression and chemotherapeutic susceptibility using relevance networks. *Proceedings of the National Academy of Sciences of the USA* **97**, 12182-12186.

Moriyama, M., Hoshida, Y., Otsuka, M., Nishimura, S., Kato, N., Goto, T., Taniguchi, H., Shiratori, Y., Seki, N. and Omata, M. (2003). Relevance Network between Chemosensitivity and Transcriptome in Human Hepatoma Cells. *Molecular Cancer Therapeutics* **2**, 199-205.

See Also

plotVar, cim, color.GreenRed, color.jet, color.spectral and http: //www.mixOmics.org for more details.

Examples

```
## network representation for objects of class 'rcc'
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
nutri.res <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)

## Not run:
# may not work on the Linux version, use Windows instead
# sometimes with Rstudio might not work because of margin issues,
# in that case save it as an image
jpeg('example1-network.jpeg', res = 600, width = 4000, height = 4000)
network(nutri.res, comp = 1:3, cutoff = 0.6)
dev.off()

## Changing the attributes of the network

# sometimes with Rstudio might not work because of margin issues,
# in that case save it as an image
jpeg('example2-network.jpeg')
network(nutri.res, comp = 1:3, cutoff = 0.45,
color.node = c("mistyrose", "lightcyan"),
shape.node = c("circle", "rectangle"),
color.edge = color.jet(100),
lty.edge = "solid", lwd.edge = 2,
show.edge.labels = FALSE)
dev.off()


## interactive 'cutoff' - select the 'cutoff' and "see" the new network
## only run this during an interactive session
if (interactive()) {
    network(nutri.res, comp = 1:3, cutoff = 0.55, interactive = TRUE)
}
dev.off()

## network representation for objects of class 'spls'
data(liver.toxicity)
```

```
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic
toxicity.spls <- spls(X, Y, ncomp = 3, keepX = c(50, 50, 50),
keepY = c(10, 10, 10))

# sometimes with Rstudio might not work because of margin issues,
# in that case save it as an image
jpeg('example3-network.jpeg')
network(toxicity.spls, comp = 1:3, cutoff = 0.8,
color.node = c("mistyrose", "lightcyan"),
shape.node = c("rectangle", "circle"),
color.edge = color.spectral(100),
lty.edge = "solid", lwd.edge =  1,
show.edge.labels = FALSE, interactive = FALSE)
dev.off()

## End(Not run)
```

`nipals` *Non-linear Iterative Partial Least Squares (NIPALS) algorithm*

Description

This function performs NIPALS algorithm, i.e. the singular-value decomposition (SVD) of a data table that can contain missing values.

Usage

```
nipals(X, ncomp = 2, max.iter = 500, tol = 1e-06)
```

Arguments

`X`	a numeric matrix (or data frame) which provides the data for the principal components analysis. It can contain missing values in which case `center = TRUE` is used as required by the `nipals` function.
`ncomp`	Integer, if data is complete `ncomp` decides the number of components and associated eigenvalues to display from the `pcasvd` algorithm and if the data has missing values, `ncomp` gives the number of components to keep to perform the reconstitution of the data using the NIPALS algorithm. If `NULL`, function sets `ncomp = min(nrow(X),ncol(X))`
`max.iter`	Integer, the maximum number of iterations in the NIPALS algorithm.
`tol`	Positive real, the tolerance used in the NIPALS algorithm.

Details

The NIPALS algorithm (Non-linear Iterative Partial Least Squares) has been developed by H. Wold at first for PCA and later-on for PLS. It is the most commonly used method for calculating the principal components of a data set. It gives more numerically accurate results when compared with the SVD of the covariance matrix, but is slower to calculate.

This algorithm allows to realize SVD with missing data, without having to delete the rows with missing data or to estimate the missing data.

Value

An object of class 'mixo_nipals' containing slots:

`eig`	Vector containing the pseudo-singular values of `X`, of length `ncomp`.
`t`	Matrix whose columns contain the left singular vectors of `X`. Note that for a complete data matrix X, the return values `eig`, `t` and `p` such that `X = t * diag(eig) * t(p)`.

Author(s)

Sébastien Déjean, Ignacio González, Kim-Anh Le Cao, Al J Abadi

References

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Wold H. (1966). Estimation of principal components and related models by iterative least squares. In: Krishnaiah, P. R. (editors), *Multivariate Analysis*. Academic Press, N.Y., 391-420.

Wold H. (1975). Path models with latent variables: The NIPALS approach. In: Blalock H. M. et al. (editors). *Quantitative Sociology: International perspectives on mathematical and statistical model building*. Academic Press, N.Y., 307-357.

See Also

`impute.nipals`, `svd`, `princomp`, `prcomp`, `eigen` and http://www.mixOmics.org for more details.

---

nutrimouse *Nutrimouse Dataset*

Description

The `nutrimouse` dataset contains the expression measure of 120 genes potentially involved in nutritional problems and the concentrations of 21 hepatic fatty acids for forty mice.

Usage

```
data(nutrimouse)
```

Format

A list containing the following components:

list("gene") data frame with 40 observations on 120 numerical variables.

list("lipid") data frame with 40 observations on 21 numerical variables.

list("diet") factor of 5 levels containing 40 labels for the diet factor.

list("genotype") factor of 2 levels containing 40 labels for the diet factor.

Details

The data sets come from a nutrigenomic study in the mouse (Martin *et al.*, 2007) in which the effects of five regimens with contrasted fatty acid compositions on liver lipids and hepatic gene expression in mice were considered. Two sets of variables were acquired on forty mice:

- gene: expressions of 120 genes measured in liver cells, selected (among about 30,000) as potentially relevant in the context of the nutrition study. These expressions come from a nylon macroarray with radioactive labelling;
- lipid: concentrations (in percentages) of 21 hepatic fatty acids measured by gas chromatography.

Biological units (mice) were cross-classified according to two factors experimental design (4 replicates):

- Genotype: 2-levels factor, wild-type (WT) and PPARα -/- (PPAR).
- Diet: 5-levels factor. Oils used for experimental diets preparation were corn and colza oils (50/50) for a reference diet (REF), hydrogenated coconut oil for a saturated fatty acid diet (COC), sunflower oil for an Omega6 fatty acid-rich diet (SUN), linseed oil for an Omega3-rich diet (LIN) and corn/colza/enriched fish oils for the FISH diet (43/43/14).

Value

none

Source

The `nutrimouse` dataset was provided by Pascal Martin from the Toxicology and Pharmacology Laboratory, National Institute for Agronomic Research, French.

References

Martin, P. G. P., Guillou, H., Lasserre, F., Déjean, S., Lan, A., Pascussi, J.-M., San Cristobal, M., Legrand, P., Besse, P. and Pineau, T. (2007). Novel aspects of PPARα-mediated regulation of lipid and xenobiotic metabolism revealed through a multrigenomic study. *Hepatology* **54**, 767-777.

`pca` *Principal Components Analysis*

Description

Performs a principal components analysis on the given data matrix that can contain missing values. If data are complete 'pca' uses Singular Value Decomposition, if there are some missing values, it uses the NIPALS algorithm.

Usage

```
pca(
  X,
  ncomp = 2,
  center = TRUE,
  scale = FALSE,
  max.iter = 500,
  tol = 1e-09,
  logratio = c("none", "CLR", "ILR"),
  ilr.offset = 0.001,
  V = NULL,
  multilevel = NULL,
  verbose.call = FALSE
)
```

Arguments

X	a numeric matrix (or data frame) which provides the data for the principal components analysis. It can contain missing values in which case center = TRUE is used as required by the nipals function.
ncomp	Integer, if data is complete ncomp decides the number of components and associated eigenvalues to display from the pcasvd algorithm and if the data has missing values, ncomp gives the number of components to keep to perform the reconstitution of the data using the NIPALS algorithm. If NULL, function sets ncomp = min(nrow(X),ncol(X))
center	(Default=TRUE) Logical, whether the variables should be shifted to be zero centered. Only set to FALSE if data have already been centered. Alternatively, a vector of length equal the number of columns of X can be supplied. The value is passed to scale. If the data contain missing values, columns should be centered for reliable results.
scale	(Default=FALSE) Logical indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with prcomp function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of X can be supplied. The value is passed to scale.
max.iter	Integer, the maximum number of iterations in the NIPALS algorithm.
tol	Positive real, the tolerance used in the NIPALS algorithm.
logratio	(Default='none') one of ('none','CLR','ILR'). Specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'
ilr.offset	(Default=0.001) When logratio is set to 'ILR', an offset must be input to avoid infinite value after the logratio transform.
V	Matrix used in the logratio transformation if provided.
multilevel	sample information for multilevel decomposition for repeated measurements.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

The calculation is done either by a singular value decomposition of the (possibly centered and scaled) data matrix, if the data is complete or by using the NIPALS algorithm if there is data missing. Unlike princomp, the print method for these objects prints the results in a nice format and the plot method produces a bar plot of the percentage of variance explained by the principal components (PCs).

When using NIPALS (missing values), we make the assumption that the first (min(ncol(X), nrow(X)) principal components will account for 100 % of the explained variance.

Note that scale = TRUE will throw an error if there are constant variables in the data, in which case it's best to filter these variables in advance.

According to Filzmoser et al., a ILR log ratio transformation is more appropriate for PCA with compositional data. Both CLR and ILR are valid.

Logratio transform and multilevel analysis are performed sequentially as internal pre-processing step, through logratio.transfo and withinVariation respectively.

Logratio can only be applied if the data do not contain any 0 value (for count data, we thus advise the normalise raw data with a 1 offset). For ILR transformation and additional offset might be needed.

Value

pca returns a list with class "pca" and "prcomp" containing the following components:

call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component
X	The input data matrix, possibly scaled and centered.
ncomp	The number of principal components used.
center	The centering used.
scale	The scaling used.
names	List of row and column names of data.
sdev	The eigenvalues of the covariance/correlation matrix, though the calculation is actually done with the singular values of the data matrix or by using NIPALS.
loadings	A length one list of matrix of variable loadings for X (i.e., a matrix whose columns contain the eigenvectors).
variates	Matrix containing the coordinate values corresponding to the projection of the samples in the space spanned by the principal components. These are the dimension-reduced representation of observations/samples.
var.tot	Total variance in the data.
prop_expl_var	Proportion of variance explained per component after setting possible missing values in the data to zero (note that contrary to PCA, this amount may not decrease as the aim of the method is not to maximise the variance, but the covariance between X and the dummy matrix Y).
cum.var	The cumulative explained variance for components.
Xw	If multilevel, the data matrix with within-group-variation removed.
design	If multilevel, the provided design.

Author(s)

Florian Rohart, Kim-Anh Lê Cao, Ignacio González, Al J Abadi

References

On log ratio transformations: Filzmoser, P., Hron, K., Reimann, C.: Principal component analysis for compositional data with outliers. Environmetrics 20(6), 621-632 (2009) Lê Cao K.-A., Costello ME, Lakis VA, Bartolo, F,Chua XY, Brazeilles R, Rondeau P. MixMC: Multivariate insights into Microbial Communities. PLoS ONE, 11(8): e0160169 (2016). On multilevel decomposition: Westerhuis, J.A., van Velzen, E.J., Hoefsloot, H.C., Smilde, A.K.: Multivariate paired data analysis: multilevel plsda versus oplsda. Metabolomics 6(1), 119-128 (2010) Liquet, B., Lê Cao, K.-A., Hocini, H., Thiebaut, R.: A novel approach for biomarker selection and the integration of repeated measures experiments from two assays. BMC bioinformatics 13(1), 325 (2012)

See Also

nipals, prcomp, biplot, plotIndiv, plotVar and http://www.mixOmics.org for more details.

Examples

```
# example with missing values where NIPALS is applied
# --------------------------------
data(multidrug)
X <- multidrug$ABC.trans
pca.res <- pca(X, ncomp = 4, scale = TRUE)
plot(pca.res)
print(pca.res)
biplot(pca.res, group = multidrug$cell.line$Class, legend.title = 'Class')

# samples representation
plotIndiv(pca.res, ind.names = multidrug$cell.line$Class,
    group = as.numeric(as.factor(multidrug$cell.line$Class)))

# variable representation
plotVar(pca.res, var.names = TRUE, cutoff = 0.4, pch = 16)

## Not run:
plotIndiv(pca.res, cex = 0.2,
    col = as.numeric(as.factor(multidrug$cell.line$Class)),style="3d")


plotVar(pca.res, rad.in = 0.5, cex = 0.5, style="3d")

## End(Not run)

# example with imputing the missing values using impute.nipals()
# --------------------------------
data("nutrimouse")
X <- data.matrix(nutrimouse$lipid)
X <- scale(X, center = TRUE, scale = TRUE)
## add missing values to X to impute and compare to actual values
set.seed(42)
na.ind <- sample(seq_along(X), size = 20)
true.values <- X[na.ind]
X[na.ind] <- NA
pca.no.impute <- pca(X, ncomp = 2)
plotIndiv(pca.no.impute, group = nutrimouse$diet, pch = 16)
X.impute <- impute.nipals(X, ncomp = 10)
## compare
cbind('imputed' = round(X.impute[na.ind], 2),
```

```
      'actual' = round(true.values, 2))
## run pca using imputed matrix
pca.impute <- pca(X.impute, ncomp = 2)
plotIndiv(pca.impute, group = nutrimouse$diet, pch = 16)
# example with multilevel decomposition and CLR log ratio transformation
# (ILR takes longer to run)
# ----------------
data("diverse.16S")
pca.res = pca(X = diverse.16S$data.TSS, ncomp = 3,
    logratio = 'CLR', multilevel = diverse.16S$sample)
plot(pca.res)
plotIndiv(pca.res, ind.names = FALSE,
          group = diverse.16S$bodysite,
          title = '16S diverse data',
          legend = TRUE,
          legend.title = 'Bodysite')
```

`perf` *Compute evaluation criteria for PLS, sPLS, PLS-DA, sPLS-DA, MINT and DIABLO*

Description

Function to evaluate the performance of the fitted PLS, sparse PLS, PLS-DA, sparse PLS-DA, MINT (mint.splsda) and DIABLO (block.splsda) models using various criteria.

Usage

```
perf(object, ...)

## S3 method for class 'mixo_pls'
perf(
  object,
  validation = c("Mfold", "loo"),
  folds,
  progressBar = FALSE,
  nrepeat = 1,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)

## S3 method for class 'mixo_spls'
perf(
  object,
  validation = c("Mfold", "loo"),
  folds,
  progressBar = FALSE,
  nrepeat = 1,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
```

```
)

## S3 method for class 'mixo_plsda'
perf(
  object,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  validation = c("Mfold", "loo"),
  folds = 10,
  nrepeat = 1,
  auc = FALSE,
  progressBar = FALSE,
  signif.threshold = 0.01,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)

## S3 method for class 'mixo_splsda'
perf(
  object,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  validation = c("Mfold", "loo"),
  folds = 10,
  nrepeat = 1,
  auc = FALSE,
  progressBar = FALSE,
  signif.threshold = 0.01,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)

## S3 method for class 'sgccda'
perf(
  object,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  validation = c("Mfold", "loo"),
  folds = 10,
  nrepeat = 1,
  auc = FALSE,
  progressBar = FALSE,
  signif.threshold = 0.01,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)

## S3 method for class 'mint.pls'
perf(
  object,
  validation = c("Mfold", "loo"),
  folds = 10,
```

```
  progressBar = FALSE,
  ...
)

## S3 method for class 'mint.spls'
perf(
  object,
  validation = c("Mfold", "loo"),
  folds = 10,
  progressBar = FALSE,
  ...
)

## S3 method for class 'mint.plsda'
perf(
  object,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  auc = FALSE,
  progressBar = FALSE,
  signif.threshold = 0.01,
  ...
)

## S3 method for class 'mint.splsda'
perf(
  object,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  auc = FALSE,
  progressBar = FALSE,
  signif.threshold = 0.01,
  ...
)
```

Arguments

object	object of class inherited from "pls", "plsda", "spls", "splsda" or "mint.splsda". The function will retrieve some key parameters stored in that object.
...	not used
validation	character. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (see below). Default is "Mfold".
folds	the folds in the Mfold cross-validation. See Details.
progressBar	by default set to FALSE to output the progress bar of the computation.
nrepeat	Number of times the Cross-Validation process is repeated. This is an important argument to ensure the estimation of the performance to be as accurate as possible.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples in ?tune.spca.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'. Note 'seed' is not required or used in perf.mint.plsda as this method uses loo cross-validation

dist — only applies to an object inheriting from "plsda", "splsda" or "mint.splsda" to evaluate the classification performance of the model. Should be a subset of "max.dist", "centroids.dist", "mahalanobis.dist". Default is "all". See predict.

auc — if TRUE calculate the Area Under the Curve (AUC) performance of the model.

signif.threshold — numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.

Details

Procedure. The process of evaluating the performance of a fitted model object is similar for all PLS-derived methods; a cross-validation approach is used to fit the method of object on folds-1 subsets of the data and then to predict on the subset left out. Different measures of performance are available depending on the model. Parameters such as logratio, multilevel, keepX or keepY are retrieved from object.

Parameters. If validation = "Mfold", M-fold cross-validation is performed. folds specifies the number of folds to generate. The folds also can be supplied as a list of vectors containing the indexes defining each fold as produced by split. When using validation = "Mfold", make sure that you repeat the process several times (as the results will be highly dependent on the random splits and the sample size).

If validation = "loo", leave-one-out cross-validation is performed (in that case, there is no need to repeat the process).

Measures of performance. For fitted PLS and sPLS regression models, perf estimates the mean squared error of prediction (MSEP), R^2, and Q^2 to assess the predictive perfity of the model using M-fold or leave-one-out cross-validation. Note that only the classic, regression and invariant modes can be applied. For sPLS, the MSEP, R^2, and Q^2 criteria are averaged across all folds. Note that for PLS and sPLS objects, perf is performed on the pre-processed data after log ratio transform and multilevel analysis, if any.

Sparse methods. The sPLS, sPLS-DA and sgccda functions are run on several and different subsets of data (the cross-folds) and will certainly lead to different subset of selected features. Those are summarised in the output features$stable (see output Value below) to assess how often the variables are selected across all folds. Note that for PLS-DA and sPLS-DA objects, perf is performed on the original data, i.e. before the pre-processing step of the log ratio transform and multilevel analysis, if any. In addition for these methods, the classification error rate is averaged across all folds.

The mint.sPLS-DA function estimates errors based on Leave-one-group-out cross validation (where each levels of object$study is left out (and predicted) once) and provides study-specific outputs (study.specific.error) as well as global outputs (global.error). Note the mint perf methods do not use seed or BPPARAM arguments.

AUROC. For PLS-DA, sPLS-DA, mint.PLS-DA, mint.sPLS-DA, and block.splsda methods: if auc=TRUE, Area Under the Curve (AUC) values are calculated from the predicted scores obtained from the predict function applied to the internal test sets in the cross-validation process, either for all samples or for study-specific samples (for mint models). Therefore we minimise the risk of overfitting. For block.splsda model, the calculated AUC is simply the blocks-combined AUC for each component calculated using auroc.sgccda. See auroc for more details. Our multivariate supervised methods already use a prediction threshold based on distances (see predict) that optimally determine class membership of the samples tested. As such AUC and ROC are not needed to estimate the performance of the model. We provide those outputs as complementary performance measures. See more details in our mixOmics article.

Prediction distances. See details from ?predict, and also our supplemental material in the mixOmics article.

Repeats of the CV-folds. Repeated cross-validation implies that the whole CV process is repeated a number of times (nrepeat) to reduce variability across the different subset partitions. In the case of Leave-One-Out CV (validation = 'loo'), each sample is left out once (folds = N is set internally) and therefore nrepeat is by default 1.

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

For sgccda objects, we provide weighted measures (e.g. error rate) in which the weights are simply the correlation of the derived components of a given block with the outcome variable Y.

More details about the PLS modes in ?pls.

Value

For PLS and sPLS models, perf produces a list with the following components for every repeat:

MSEP — Mean Square Error Prediction for each Y variable, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.

RMSEP — Root Mean Square Error Prediction for each Y variable, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.

R2 — a matrix of R^2 values of the Y-variables for models with $1, \ldots,$ncomp components, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.

Q2 — if Y contains one variable, a vector of Q^2 values else a list with a matrix of Q^2 values for each Y-variable. Note that in the specific case of an sPLS model, it is better to have a look at the Q2.total criterion, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.

Q2.total — a vector of Q^2-total values for models with $1, \ldots,$ncomp components, only applies to object inherited from "pls", and "spls". Available in both (s)PLS modes.

RSS — Residual Sum of Squares across all selected features and the components.

PRESS — Predicted Residual Error Sum of Squares across all selected features and the components.

features — a list of features selected across the folds ($stable.X and $stable.Y) for the keepX and keepY parameters from the input object. Note, this will be NULL if using standard (non-sparse) PLS.

cor.tpred, cor.upred — Correlation between the predicted and actual components for X (t) and Y (u)

RSS.tpred, RSS.upred — Residual Sum of Squares between the predicted and actual components for X (t) and Y (u)

For PLS-DA and sPLS-DA models, perf produces a matrix of classification error rate estimation. The dimensions correspond to the components in the model and to the prediction method used, respectively. Note that error rates reported in any component include the performance of the model in earlier components for the specified keepX parameters (e.g. error rate reported for component 3 for keepX = 20 already includes the fitted model on components 1 and 2 for keepX = 20).

error.rate — Prediction error rate for each dist and measure

auc	AUC values per component averaged over the nrepeat
auc.all	AUC values per component per repeat
predict	A list of length ncomp that os predicted values of each sample for each class
features	a list of features selected across the folds ($stable.X) for the keepX parameters from the input object.
choice.ncomp	Otimal number of components for the model for each prediction distance using one-sided t-tests that test for a significant difference in the mean error rate (gain in prediction) when components are added to the model.
class	A list which gives the predicted class of each sample for each dist and each of the ncomp components

For mint.splsda models, perf produces the following outputs:

study.specific.error	A list that gives BER, overall error rate and error rate per class, for each study
global.error	A list that gives BER, overall error rate and error rate per class for all samples
predict	A list of length ncomp that produces the predicted values of each sample for each class
class	A list which gives the predicted class of each sample for each dist and each of the ncomp components. Directly obtained from the predict output.
auc	AUC values
auc.study	AUC values for each study in mint models

For sgccda models (i.e. block (s)PLS-DA models), perf produces the following outputs:

error.rate	Prediction error rate for each block of object$X and each dist
error.rate.per.class	Prediction error rate for each block of object$X, each dist and each class
predict	Predicted values of each sample for each class, each block and each component
class	Predicted class of each sample for each block, each dist, each component and each nrepeat
features	a list of features selected across the folds ($stable.X and $stable.Y) for the keepX and keepY parameters from the input object.
AveragedPredict.class	if more than one block, returns the average predicted class over the blocks (averaged of the Predict output and prediction using the max.dist distance)
AveragedPredict.error.rate	if more than one block, returns the average predicted error rate over the blocks (using the AveragedPredict.class output)
WeightedPredict.class	if more than one block, returns the weighted predicted class over the blocks (weighted average of the Predict output and prediction using the max.dist distance). See details for more info on weights.
WeightedPredict.error.rate	if more than one block, returns the weighted average predicted error rate over the blocks (using the WeightedPredict.class output.)
MajorityVote	if more than one block, returns the majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`MajorityVote.error.rate`
: if more than one block, returns the error rate of the `MajorityVote` output

`WeightedVote`
: if more than one block, returns the weighted majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`WeightedVote.error.rate`
: if more than one block, returns the error rate of the `WeightedVote` output

`weights`
: Returns the weights of each block used for the weighted predictions, for each nrepeat and each fold

`choice.ncomp`
: For supervised models; returns the optimal number of components for the model for each prediction distance using one-sided t-tests that test for a significant difference in the mean error rate (gain in prediction) when components are added to the model. See more details in Rohart et al 2017 Suppl. For more than one block, an optimal ncomp is returned for each prediction framework.

Author(s)

Ignacio González, Amrit Singh, Kim-Anh Lê Cao, Benoit Gautier, Florian Rohart, Al J Abadi

References

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mixOmics article:

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Rohart F, Mason EA, Matigian N, Mosbergen R, Korn O, Chen T, Butcher S, Patel J, Atkinson K, Khosrotehrani K, Fisk NM, Lê Cao K-A&, Wells CA& (2016). A Molecular Classification of Human Mesenchymal Stromal Cells. PeerJ 4:e1845.

See Also

predict, nipals, plot.perf, auroc and www.mixOmics.org for more details.

Examples

```
## validation for objects of class 'pls' (regression)
# ----------------------------------------
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic

# try tune the number of component to choose
# --------------------
# first learn the full model
liver.pls <- pls(X, Y, ncomp = 5)

# with 5-fold cross validation: we use the same parameters as in model above
# but we perform cross validation to compute the MSEP, Q2 and R2 criteria
# ---------------------------
liver.val <- perf(liver.pls, validation = "Mfold", folds = 5)

# see available criteria
names(liver.val$measures)
# see values for all repeats
liver.val$measures$Q2.total$values
# see summary over repeats
liver.val$measures$Q2.total$summary
# Q2 total should decrease until it reaches a threshold
liver.val$measures$Q2.total

# ncomp = 2 is enough
plot(liver.val, criterion  = 'Q2.total')

## Not run:

# have a look at the other criteria
# ----------------------
# R2
plot(liver.val, criterion  = 'R2')
## correlation of components (see docs)
plot(liver.val, criterion  = 'cor.tpred')

# MSEP
plot(liver.val, criterion  = 'MSEP')
## validation for objects of class 'spls' (regression)
# ----------------------------------------
ncomp = 7
# first, learn the model on the whole data set
model.spls = spls(X, Y, ncomp = ncomp, mode = 'regression',
                  keepX = c(rep(10, ncomp)), keepY = c(rep(4,ncomp)))


# with leave-one-out cross validation
model.spls.val <- perf(model.spls, validation = "Mfold", folds = 5, seed = 45 )

#Q2 total
```

```
model.spls.val$measures$Q2$summary

# R2: we can see how the performance degrades when ncomp increases
plot(model.spls.val, criterion="R2")

## validation for objects of class 'splsda' (classification)
# ----------------------------------------
data(srbct)
X <- srbct$gene
Y <- srbct$class

ncomp = 2

srbct.splsda <- splsda(X, Y, ncomp = ncomp, keepX = rep(10, ncomp))

# with Mfold
# ---------
error <- perf(srbct.splsda, validation = "Mfold", folds = 8,
dist = "all", auc = TRUE, seed = 45)
error
error$auc

plot(error)

# parallel code
library(BiocParallel)
error <- perf(srbct.splsda, validation = "Mfold", folds = 8,
dist = "all", auc = TRUE, BPPARAM = SnowParam(workers = 2), seed = 45)

# with 5 components and nrepeat=5, to get a $choice.ncomp
ncomp = 5
srbct.splsda <- splsda(X, Y, ncomp = ncomp, keepX = rep(10, ncomp))

error <- perf(srbct.splsda, validation = "Mfold", folds = 8,
dist = "all", nrepeat = 5, seed = 45)
error$choice.ncomp

plot(error)


## validation for objects of class 'mint.splsda' (classification)
# ----------------------------------------

data(stemcells)
res = mint.splsda(X = stemcells$gene, Y = stemcells$celltype,
                  ncomp = 3, keepX = c(10, 5, 15),
                  study = stemcells$study)

out = perf(res, auc = TRUE)
out
plot(out)
out$auc
out$auc.study

## validation for objects of class 'sgccda' (classification)
# ----------------------------------------
```

```
data(nutrimouse)
Y = nutrimouse$diet
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid)

nutrimouse.sgccda <- block.splsda(X=data,
Y = Y,
design = 'full',
keepX = list(gene=c(10,10), lipid=c(15,15)),
ncomp = 2)

perf = perf(nutrimouse.sgccda)
perf
plot(perf)


# with 5 components and nrepeat=5 to get $choice.ncomp
nutrimouse.sgccda <- block.splsda(X=data,
Y = Y,
design = 'full',
keepX = list(gene=c(10,10), lipid=c(15,15)),
ncomp = 5)

perf = perf(nutrimouse.sgccda, folds = 5, nrepeat = 5)
perf
plot(perf)
perf$choice.ncomp

## End(Not run)
```

`perf.assess` *Compute evaluation criteria for PLS, sPLS, PLS-DA, sPLS-DA, MINT and DIABLO*

Description

Function to evaluate the performance of the fitted PLS, sparse PLS, PLS-DA, sparse PLS-DA, MINT (mint.splsda) and DIABLO (block.splsda) models using various criteria.

Usage

```
perf.assess(object, ...)

## S3 method for class 'sgccda'
perf.assess(
  object,
  validation = c("Mfold", "loo"),
  folds = 3,
  nrepeat = 1,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  auc = FALSE,
  progressBar = FALSE,
  BPPARAM = SerialParam(),
  seed = NULL,
```

```
  ...
)

## S3 method for class 'mint.plsda'
perf.assess(
  object,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  auc = FALSE,
  progressBar = FALSE,
  ...
)

## S3 method for class 'mint.splsda'
perf.assess(
  object,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  auc = FALSE,
  progressBar = FALSE,
  ...
)

## S3 method for class 'mixo_pls'
perf.assess(
  object,
  validation = c("Mfold", "loo"),
  folds,
  nrepeat = 1,
  progressBar = FALSE,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)

## S3 method for class 'mixo_spls'
perf.assess(
  object,
  validation = c("Mfold", "loo"),
  folds,
  nrepeat = 1,
  progressBar = FALSE,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)

## S3 method for class 'mixo_plsda'
perf.assess(
  object,
  validation = c("Mfold", "loo"),
  folds,
  nrepeat = 1,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
```

```
  auc = FALSE,
  progressBar = FALSE,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)

## S3 method for class 'mixo_splsda'
perf.assess(
  object,
  validation = c("Mfold", "loo"),
  folds,
  nrepeat = 1,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  auc = FALSE,
  progressBar = FALSE,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)
```

Arguments

object	object of class inherited from "pls", "plsda", "spls", "splsda". "sgccda" or "mint.splsda". The function will retrieve some key parameters stored in that object.
...	not used
validation	a character string. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (see below). Default is "Mfold". For MINT methods only "loo" will be used.
folds	numeric. Number of folds in the Mfold cross-validation. See Details.
nrepeat	numierc. Number of times the Cross-Validation process is repeated. This is an important argument to ensure the estimation of the performance to be as accurate as possible. Default it 1.
dist	only applies to an object inheriting from "plsda", "splsda" or "mint.splsda" to evaluate the classification performance of the model. Should be a subset of "max.dist", "centroids.dist", "mahalanobis.dist". Default is "all". See predict.
auc	if TRUE calculate the Area Under the Curve (AUC) performance of the model.
progressBar	by default set to FALSE to output the progress bar of the computation.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples in ?tune.spca.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'. Note 'seed' is not required or used in perf.mint.plsda as this method uses loo cross-validation

Details

This function is built upon 'perf()' but instead of assessing model performance across components 1:ncomp only assesses performance of the given model

Procedure. The process of evaluating the performance of a fitted model `object` is similar for all PLS-derived methods; a cross-validation approach is used to fit the method of `object` on `folds-1` subsets of the data and then to predict on the subset left out. Different measures of performance are available depending on the model. Parameters such as `logratio`, `multilevel`, `keepX` or `keepY` are retrieved from `object`.

Parameters. If `validation = "Mfold"`, M-fold cross-validation is performed. `folds` specifies the number of folds to generate. The folds also can be supplied as a list of vectors containing the indexes defining each fold as produced by `split`. When using `validation = "Mfold"`, make sure that you repeat the process several times (as the results will be highly dependent on the random splits and the sample size).

If `validation = "loo"`, leave-one-out cross-validation is performed (in that case, there is no need to repeat the process).

Measures of performance. For fitted PLS and sPLS regression models, `perf` estimates the mean squared error of prediction (MSEP), R^2, and Q^2 to assess the predictive perfity of the model using M-fold or leave-one-out cross-validation. Note that only the `classic`, `regression` and `invariant` modes can be applied. For sPLS, the MSEP, R^2, and Q^2 criteria are averaged across all folds. Note that for PLS and sPLS objects, perf is performed on the pre-processed data after log ratio transform and multilevel analysis, if any.

The mint.sPLS-DA function estimates errors based on Leave-one-group-out cross validation (where each levels of object$study is left out (and predicted) once) and provides study-specific outputs (`study.specific.error`) as well as global outputs (`global.error`). Note the mint perf methods do not use `seed` or `BPPARAM` arguments.

AUROC. For PLS-DA, sPLS-DA, mint.PLS-DA, mint.sPLS-DA, and block.splsda methods: if `auc=TRUE`, Area Under the Curve (AUC) values are calculated from the predicted scores obtained from the `predict` function applied to the internal test sets in the cross-validation process, either for all samples or for study-specific samples (for mint models). Therefore we minimise the risk of over-fitting. For block.splsda model, the calculated AUC is simply the blocks-combined AUC calculated using `auroc.sgccda`. See `auroc` for more details. Our multivariate supervised methods already use a prediction threshold based on distances (see `predict`) that optimally determine class membership of the samples tested. As such AUC and ROC are not needed to estimate the performance of the model. We provide those outputs as complementary performance measures.

Prediction distances. See details from ?`predict`, and also our supplemental material in the mixOmics article.

Repeats of the CV-folds. Repeated cross-validation implies that the whole CV process is repeated a number of times (`nrepeat`) to reduce variability across the different subset partitions. In the case of Leave-One-Out CV (`validation = 'loo'`), each sample is left out once (`folds = N` is set internally) and therefore nrepeat is by default 1.

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

For `sgccda` objects, we provide weighted measures (e.g. error rate) in which the weights are simply the correlation of the derived components of a given block with the outcome variable Y.

More details about the PLS modes in ?`pls`.

Value

For PLS and sPLS models:

`MSEP` Mean Square Error Prediction for each Y variable, only applies to object inherited from `"pls"`, and `"spls"`. Only available when in regression (s)PLS.

`RMSEP` Root Mean Square Error Prediction for each Y variable, only applies to object inherited from `"pls"`, and `"spls"`. Only available when in regression (s)PLS.

`R2` a matrix of R^2 values of the Y-variables for models with $1, \ldots,$`ncomp` components, only applies to object inherited from `"pls"`, and `"spls"`. Only available when in regression (s)PLS.

`Q2` if Y contains one variable, a vector of Q^2 values else a list with a matrix of Q^2 values for each Y-variable. Note that in the specific case of an sPLS model, it is better to have a look at the Q2.total criterion, only applies to object inherited from `"pls"`, and `"spls"`. Only available when in regression (s)PLS.

`Q2.total` a vector of Q^2-total values for models with $1, \ldots,$`ncomp` components, only applies to object inherited from `"pls"`, and `"spls"`. Available in both (s)PLS modes.

`RSS` Residual Sum of Squares across all selected features

`PRESS` Predicted Residual Error Sum of Squares across all selected features

`cor.tpred`, `cor.upred`
Correlation between the predicted and actual components for X (t) and Y (u)

`RSS.tpred`, `RSS.upred`
Residual Sum of Squares between the predicted and actual components for X (t) and Y (u)

For PLS-DA and sPLS-DA models:

`error.rate` Prediction error rate for each dist and measure

`auc` AUC value averaged over the `nrepeat`

`auc.all` AUC values per repeat

`predict` Predicted values of each sample for each class

`class` A list which gives the predicted class of each sample for each dist and each of the ncomp components

For mint.splsda models:

`study.specific.error`
A list that gives BER, overall error rate and error rate per class, for each study

`global.error` A list that gives BER, overall error rate and error rate per class for all samples

`predict` A list of length `ncomp` that produces the predicted values of each sample for each class

`class` A list which gives the predicted class of each sample for each `dist`.

`auc` AUC values

`auc.study` AUC values for each study in mint models

For sgccda models (i.e. block (s)PLS-DA models):

`error.rate` Prediction error rate for each block of `object$X` and each `dist`

`error.rate.per.class`
Prediction error rate for each block of `object$X`, each `dist` and each class

`predict` Predicted values of each sample for each class and each block

`class` Predicted class of each sample for each block, each `dist`, and each nrepeat

`AveragedPredict.class`
if more than one block, returns the average predicted class over the blocks (averaged of the `Predict` output and prediction using the `max.dist` distance)

`AveragedPredict.error.rate`
: if more than one block, returns the average predicted error rate over the blocks (using the `AveragedPredict.class` output)

`WeightedPredict.class`
: if more than one block, returns the weighted predicted class over the blocks (weighted average of the `Predict` output and prediction using the `max.dist` distance). See details for more info on weights.

`WeightedPredict.error.rate`
: if more than one block, returns the weighted average predicted error rate over the blocks (using the `WeightedPredict.class` output.)

`MajorityVote`
: if more than one block, returns the majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`MajorityVote.error.rate`
: if more than one block, returns the error rate of the `MajorityVote` output

`WeightedVote`
: if more than one block, returns the weighted majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`WeightedVote.error.rate`
: if more than one block, returns the error rate of the `WeightedVote` output

`weights`
: Returns the weights of each block used for the weighted predictions, for each nrepeat and each fold

Author(s)

Ignacio González, Amrit Singh, Kim-Anh Lê Cao, Benoit Gautier, Florian Rohart, Al J Abadi

References

Singh A., Shannon C., Gautier B., Rohart F., Vacher M., Tebbutt S. and Lê Cao K.A. (2019), DIABLO: an integrative approach for identifying key molecular drivers from multi-omics assays, Bioinformatics, Volume 35, Issue 17, 1 September 2019, Pages 3055–3062.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

MINT:

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

PLS and PLS citeria for PLS regression: Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

Chavent, Marie and Patouille, Brigitte (2003). Calcul des coefficients de regression et du PRESS en regression PLS1. *Modulad n*, **30** 1-11. (this is the formula we use to calculate the Q2 in perf.pls and perf.spls)

Mevik, B.-H., Cederkvist, H. R. (2004). Mean Squared Error of Prediction (MSEP) Estimates for Principal Component Regression (PCR) and Partial Least Squares Regression (PLSR). *Journal of Chemometrics* **18**(9), 422-429.

sparse PLS regression mode:

Lê Cao, K. A., Rossouw D., Robert-Granie, C. and Besse, P. (2008). A sparse PLS for variable selection when integrating Omics data. *Statistical Applications in Genetics and Molecular Biology* **7**, article 35.

One-sided t-tests (suppl material):

Rohart F, Mason EA, Matigian N, Mosbergen R, Korn O, Chen T, Butcher S, Patel J, Atkinson K, Khosrotehrani K, Fisk NM, Lê Cao K-A&, Wells CA& (2016). A Molecular Classification of Human Mesenchymal Stromal Cells. PeerJ 4:e1845.

See Also

predict, nipals, plot.perf, auroc and www.mixOmics.org for more details.

Examples

```
## PLS-DA example

data(liver.toxicity) # rats gex and clinical measurements/treatments
unique(liver.toxicity$treatment$Treatment.Group) # 16 groups
length(liver.toxicity$treatment$Treatment.Group) # 64 samples

plsda.res <- plsda(liver.toxicity$gene, liver.toxicity$treatment$Treatment.Group, ncomp = 2)

performance <- perf.assess(plsda.res,
                        # to make sure each fold has all classes represented
                           validation = "Mfold", folds = 3, nrepeat = 10,
                           seed = 12) # for reproducibility, remove for analysis

performance$error.rate$BER

## sPLS-DA example

splsda.res <- splsda(liver.toxicity$gene, liver.toxicity$treatment$Treatment.Group,
                     keepX = c(25, 25), ncomp = 2)

performance <- perf.assess(splsda.res,
                           validation = "Mfold", folds = 3, nrepeat = 10,
                           seed = 12)

performance$error.rate$BER # can see slight improvement in error rate over PLS-DA example

## PLS example

ncol(liver.toxicity$clinic) # 10 Y variables as output of PLS model

pls.res <- pls(liver.toxicity$gene, liver.toxicity$clinic, ncomp = 2)

performance <- perf.assess(pls.res,
                           validation = "Mfold", folds = 3, nrepeat = 10,
                           seed = 12)

# see Q2 which gives indication of predictive ability for each of the 10 Y outputs
performance$measures$Q2$summary

## sPLS example

spls.res <- spls(liver.toxicity$gene, liver.toxicity$clinic, ncomp = 2, keepX = c(50, 50))
```

```
performance <- perf.assess(spls.res,
                           validation = "Mfold", folds = 3, nrepeat = 10,
                           seed = 12)

# see Q2 which gives indication of predictive ability for each of the 10 Y outputs
performance$measures$Q2$summary


## block PLS-DA example

data("breast.TCGA")
mrna <- breast.TCGA$data.train$mrna
mirna <- breast.TCGA$data.train$mirna
data <- list(mrna = mrna, mirna = mirna)
design <- matrix(1,
   ncol = length(data),
   nrow = length(data),
   dimnames = list(names(data), names(data)))
diag(design) <-  0

block.plsda.res <- block.plsda(X = data, Y = breast.TCGA$data.train$subtype,
                               ncomp = 2, design = design)

performance <- perf.assess(block.plsda.res)

performance$error.rate.per.class # error rate per class per distance metric

## block sPLS-DA example

block.splsda.res <- block.splsda(X = data, Y = breast.TCGA$data.train$subtype,
                                 ncomp = 2, design = design,
                                 keepX = list(mrna = c(8,8), mirna = c(8,8)))

performance <- perf.assess(block.splsda.res)

performance$error.rate.per.class

## MINT PLS-DA example

data("stemcells")

mint.plsda.res <- mint.plsda(X = stemcells$gene, Y = stemcells$celltype, ncomp = 3,
                             study = stemcells$study)

performance <- perf.assess(mint.plsda.res)

performance$global.error$BER # global error per distance metric

## MINT sPLS-DA example

mint.splsda.res <- mint.splsda(X = stemcells$gene, Y = stemcells$celltype, ncomp = 3,
                               keepX = c(10, 5, 15), study = stemcells$study)

performance <- perf.assess(mint.splsda.res)

performance$global.error$BER # error slightly higher in this sparse model verses non-sparse
```

plot.pca *Show (s)pca explained variance plots*

Description

Show (s)pca explained variance plots

Usage

```
## S3 method for class 'pca'
plot(x, ncomp = NULL, type = "barplot", ...)
```

Arguments

x	A (s)pca object
ncomp	Integer, the number of components
type	Character, default "barplot" or any other type available in plot, as "l","b","p",..
...	Not used

Author(s)

Kim-Anh Lê Cao, Florian Rohart, Leigh Coonan, Al J Abadi

plot.perf *Plot for model performance for PSLDA analyses*

Description

Function to plot classification performance for supervised methods, as a function of the number of components.

Usage

```
## S3 method for class 'perf.plsda.mthd'
plot(
  x,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  measure = c("all", "overall", "BER"),
  col,
  xlab = NULL,
  ylab = NULL,
  overlay = c("all", "measure", "dist"),
  legend.position = c("vertical", "horizontal"),
  sd = TRUE,
  ...
)

## S3 method for class 'perf.splsda.mthd'
plot(
```

```
  x,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  measure = c("all", "overall", "BER"),
  col,
  xlab = NULL,
  ylab = NULL,
  overlay = c("all", "measure", "dist"),
  legend.position = c("vertical", "horizontal"),
  sd = TRUE,
  ...
)

## S3 method for class 'perf.mint.plsda.mthd'
plot(
  x,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  measure = c("all", "overall", "BER"),
  col,
  xlab = NULL,
  ylab = NULL,
  study = "global",
  overlay = c("all", "measure", "dist"),
  legend.position = c("vertical", "horizontal"),
  ...
)

## S3 method for class 'perf.mint.splsda.mthd'
plot(
  x,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  measure = c("all", "overall", "BER"),
  col,
  xlab = NULL,
  ylab = NULL,
  study = "global",
  overlay = c("all", "measure", "dist"),
  legend.position = c("vertical", "horizontal"),
  ...
)

## S3 method for class 'perf.sgccda.mthd'
plot(
  x,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  measure = c("all", "overall", "BER"),
  col,
  weighted = TRUE,
  xlab = NULL,
  ylab = NULL,
  overlay = c("all", "measure", "dist"),
  legend.position = c("vertical", "horizontal"),
  sd = TRUE,
```

```
  ...
)
```

Arguments

x	an perf.plsda object.
dist	prediction method applied in perf for plsda or splsda. See perf.
measure	Two misclassification measure are available: overall misclassification error overall or the Balanced Error Rate BER
col	character (or symbol) colour to be used, possibly vector. One color per distance dist.
xlab, ylab	titles for x and y axes. Typically character strings, but can be expressions (e.g., expression(R^2)).
overlay	parameter to overlay graphs; if 'all', only one graph is shown with all outputs; if 'measure', a graph is shown per distance; if 'dist', a graph is shown per measure.
legend.position	position of the legend, one of "vertical" (only one column) or "horizontal" (two columns).
sd	If 'nrepeat' was used in the call to 'perf', error bar shows the standard deviation if sd=TRUE. For mint objects sd is set to FALSE as the number of repeats is 1.
...	Not used.
study	Indicates which study-specific outputs to plot. A character vector containing some levels of object$study, "all.partial" to plot all studies or "global" is expected. Default to "global".
weighted	plot either the performance of the Majority vote or the Weighted vote.

Details

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017). See ?perf for examples.

Value

none

Author(s)

Ignacio González, Florian Rohart, Francois Bartolo, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

pls, spls, plsda, splsda, perf.

`plot.perf.pls` *Plot for model performance for PLS analyses*

Description

Function to plot performance criteria, such as MSEP, RMSEP, R^2, Q^2 for s/PLS methods as a function of the number of components.

Usage

```
## S3 method for class 'perf.pls.mthd'
plot(
  x,
  criterion = "MSEP",
  xlab = "Number of components",
  ylab = NULL,
  LimQ2 = 0.0975,
  LimQ2.col = "grey30",
  sd = NULL,
  pch = 1,
  pch.size = 3,
  cex = 1.2,
  col = color.mixo(1),
  title = NULL,
  ...
)

## S3 method for class 'perf.spls.mthd'
plot(
  x,
  criterion = "MSEP",
  xlab = "Number of components",
  ylab = NULL,
  LimQ2 = 0.0975,
  LimQ2.col = "grey30",
  sd = NULL,
  pch = 1,
  pch.size = 3,
  cex = 1.2,
  col = color.mixo(1),
  title = NULL,
  ...
)
```

Arguments

`x`	an `perf.pls` object.
`criterion`	character string. What type of validation criterion to plot for `pls` or `spls`. One of `"MSEP"`, `"RMSEP"`, `"R2"` or `"Q2"`. More measures available for pls2 methods. See `perf`.

xlab, ylab	titles for x and y axes. Typically character strings, but can be expressions (e.g., expression(R^2)).
LimQ2	numeric value. Signification limit for the components in the model. Default is LimQ2 = 0.0975.
LimQ2.col	character string specifying the color for the LimQ2 line to be plotted. If "none" the line will not be plotted.
sd	If 'nrepeat' was used in the call to 'perf', error bar shows the standard deviation if sd=TRUE. For mint objects sd is set to FALSE as the number of repeats is 1.
pch	Plot character to use.
pch.size	Plot character size to use.
cex	A numeric which adjusts the font size in the plot.
col	Character. Colour to be used for data points.
title	Character, Plot title. Not used by PLS2 feature-wise measure plots.
...	Not used.

Details

plot.perf creates one plot for each response variable in the model, laid out in a multi-panel display. See ?perf for examples.

Value

none

Author(s)

Al J Abadi

References

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

pls, spls, plsda, splsda, perf.

---

plot.rcc *Canonical Correlations Plot*

Description

This function provides scree plot of the canonical correlations.

Usage

```
## S3 method for class 'rcc'
plot(x, type = "barplot", ...)
```

Arguments

x	object of class inheriting from "rcc".
type	Character, default "barplot" or any other type available in plot, as "l","b","p",..
...	Not used

Value

none

Author(s)

Sébastien Déjean, Ignacio González, Al J Abadi

See Also

points, barplot, par.

Examples

```
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
nutri.res <- rcc(X, Y, lambda1 = 0.064, lambda2 = 0.008)

## 'pointplot' type scree
plot(nutri.res, type = "point") #(default)

## Not run:
plot(nutri.res, type = "point", pch = 19, cex = 1.2,
col = c(rep("red", 3), rep("darkblue", 18)))

## 'barplot' type scree
plot(nutri.res, type = "barplot")

plot(nutri.res, type = "barplot", density = 20, col = "black")

## End(Not run)
```

---

plot.tune *Plot model performance*

Description

Function to plot performance criteria, such as classification error rate or correlation of cross-validated components for different models.

Function to plot performance criteria, such as classification error rate or balanced error rate on a tune.splsda result.

Usage

```
## S3 method for class 'tune.spls'
plot(
  x,
  measure = NULL,
  comp = c(1, 2),
  pch = 16,
  cex = 1.2,
  title = NULL,
  size.range = c(3, 10),
  sd = NULL,
  ...
)

## S3 method for class 'tune.block.splsda'
plot(x, sd = NULL, col, ...)

## S3 method for class 'tune.spca'
plot(x, optimal = TRUE, sd = NULL, col = NULL, ...)

## S3 method for class 'tune.spls1'
plot(x, optimal = TRUE, sd = NULL, col, ...)

## S3 method for class 'tune.splsda'
plot(x, optimal = TRUE, sd = NULL, col, ...)
```

Arguments

x	an tune.splsda object.
measure	Character. Measure used for plotting a tune.spls object. One of c('cor', 'RSS').
comp	Integer of length 2 denoting the components to plot.
pch	value or vector, controls shape of points to be plotted. Can be used to control the shape of the points directly or to create a second group membership and legend. See details.
cex	numeric character (or symbol) expansion, possibly vector.
title	Plot title.
size.range	Numeric vector of length 2. Range of sizes used in plot.
sd	If 'nrepeat' was used in the call to 'tune.splsda', error bar shows the standard deviation if sd=TRUE
...	Not currently used.
col	character (or symbol) color to be used, possibly vector. One colour per component.
optimal	If TRUE, highlights the optimal keepX per component

Details

plot.tune.splsda plots the classification error rate or the balanced error rate from x$error.rate, for each component of the model. A lozenge highlights the optimal number of variables on each component.

`plot.tune.block.splsda` plots the classification error rate or the balanced error rate from x$error.rate, for each component of the model. The error rate is ordered by increasing value, the yaxis shows the optimal combination of keepX at the top (e.g. 'keepX on block 1'_'keepX on block 2'_'keepX on block 3')

`plot.tune.spls` plots either the correlation of cross-validated components or the Residual Sum of Square (RSS) values for these components against those from the full model for both `t` (X components) and `u` (Y components). The optimal number of features chosen are indicated by squares.

If neither of the `object$test.keepX` or `object$test.keepY` are fixed, a dot plot is produced where a larger size indicates the strength of the measure (higher correlation or lower RSS). Otherwise, the measures are plotted against the number of features selected. In both cases, the colour shows the dispersion of the values across repeated cross validations.

`plot.tune.spca` plots the correlation of cross-validated components from the `tune.spca` function with respect to the full model.

`plot.tune.splsda` plots the classification error rate or the balanced error rate from x$error.rate, for each component of the model. A lozenge highlights the optimal number of variables on each component.

`plot.tune.block.splsda` plots the classification error rate or the balanced error rate from x$error.rate, for each component of the model. The error rate is ordered by increasing value, the yaxis shows the optimal combination of keepX at the top (e.g. 'keepX on block 1'_'keepX on block 2'_'keepX on block 3')

Value

none

none

plot arguments for pls2 tuning

For tune.spls objects where tuning is performed on both X and Y, arguments 'col.low.sd' and 'col.high.sd' can be used to indicate a low and high sd, respectively. Default to 'blue' & 'red'.

Author(s)

Kim-Anh Lê Cao, Florian Rohart, Francois Bartolo, Al J Abadi

Kim-Anh Lê Cao, Florian Rohart, Francois Bartolo, AL J Abadi

See Also

`tune.mint.splsda`, `tune.splsda`, `tune.block.splsda`, `tune.spca` and http://www.mixOmics.org for more details.

`tune.mint.splsda`, `tune.splsda` `tune.block.splsda` and http://www.mixOmics.org for more details.

Examples

```
## Not run:
## validation for objects of class 'splsda'

data(breast.tumors)
X = breast.tumors$gene.exp
Y = as.factor(breast.tumors$sample$treatment)
out = tune.splsda(X, Y, ncomp = 3, nrepeat = 5, logratio = "none",
```

```
test.keepX = c(5, 10, 15), folds = 10, dist = "max.dist",
progressBar = TRUE)


plot(out, sd=TRUE)

## End(Not run)
## Not run:
## validation for objects of class 'mint.splsda'

data(stemcells)
data = stemcells$gene
type.id = stemcells$celltype
exp = stemcells$study

out = tune(method="mint.splsda", X=data,Y=type.id, ncomp=2, study=exp, test.keepX=seq(1,10,1))
out$choice.keepX

plot(out)

## validation for objects of class 'mint.splsda'

data("breast.TCGA")
# this is the X data as a list of mRNA and miRNA; the Y data set is a single data set of proteins
data = with(breast.TCGA$data.train, list(mrna = mrna,
            mirna = mirna,
            protein = protein,
            Y = subtype))
# set number of component per data set
ncomp = 5

# Tuning the first two components
# -------------

# definition of the keepX value to be tested for each block mRNA miRNA and protein
# names of test.keepX must match the names of 'data'
test.keepX = list(mrna = seq(10,40,20), mirna = seq(10,30,10), protein = seq(1,10,5))

# the following may take some time to run, note that for through tuning
# nrepeat should be > 1
tune = tune.block.splsda(X = data, indY = 4,
ncomp = ncomp, test.keepX = test.keepX, design = 'full', nrepeat = 3)

tune$choice.ncomp
tune$choice.keepX

plot(tune)
## --- spls model
data(nutrimouse)
X <- nutrimouse$gene
Y <- nutrimouse$lipid
list.keepX <- c(2:10, 15, 20)
# tuning based on correlations
set.seed(30)
## tune X only
tune.spls.cor.X <- tune.spls(X, Y, ncomp = 3,
                             test.keepX = list.keepX,
```

```
                            validation = "Mfold", folds = 5,
                            nrepeat = 3, progressBar = FALSE,
                            measure = 'cor')

plot(tune.spls.cor.X)
plot(tune.spls.cor.X, measure = 'RSS')

## tune Y only
tune.spls.cor.Y <- tune.spls(X, Y, ncomp = 3,
                            test.keepY = list.keepX,
                            validation = "Mfold", folds = 5,
                            nrepeat = 3, progressBar = FALSE,
                            measure = 'cor')

plot(tune.spls.cor.Y)
plot(tune.spls.cor.Y, sd = FALSE)
plot(tune.spls.cor.Y, measure = 'RSS')

## tune Y and X
tune.spls.cor.XY <- tune.spls(X, Y, ncomp = 3,
                              test.keepY = c(8, 15, 20),
                              test.keepX = c(8, 15, 20),
                              validation = "Mfold", folds = 5,
                              nrepeat = 3, progressBar = FALSE,
                              measure = 'cor')

plot(tune.spls.cor.XY)
## show RSS
plot(tune.spls.cor.XY, measure = 'RSS')
## customise point sizes
plot(tune.spls.cor.XY, size.range = c(6,12))

## End(Not run)
```

`plotArrow` *Arrow sample plot*

Description

Represents samples from multiple coordinates to assess the alignment in the latent space.

Usage

```
plotArrow(
  object,
  comp = c(1, 2),
  ind.names = TRUE,
  group = NULL,
  col = NULL,
  ind.names.position = c("start", "end"),
  ind.names.size = 2,
  pch = NULL,
  pch.size = 2,
  arrow.alpha = 0.6,
```

```
  arrow.size = 0.5,
  arrow.length = 0.2,
  legend = if (is.null(group)) FALSE else TRUE,
  legend.title = NULL,
  ...
)
```

Arguments

object	object of class inheriting from **mixOmics**: PLS, sPLS, rCC, rGCCA, sGCCA, sGCCDA
comp	integer vector of length two (or three to 3d). The components that will be used on the horizontal and the vertical axis respectively to project the individuals.
ind.names	either a character vector of names for the individuals to be plotted, or FALSE for no names. If TRUE, the row names of the first (or second) data matrix is used as names (see Details). If 'pch' is set this will overwrite the names as shapes. Default is TRUE. Not avaliable for MINT objects.
group	Factor indicating the group membership for each sample.
col	character (or symbol) color to be used. If group provided, should be a vector of the same length as groups, order of colours will be respected to correspond to order of group levels.
ind.names.position	One of c('start', 'end') indicating where to show the ind.names . Not used in block analyses, where centroids are used.
ind.names.size	Numeric, sample name size.
pch	plot character. A character string or a named vector of single characters or integers whose names match those of object$variates.
pch.size	Numeric, sample point character size.
arrow.alpha	Numeric between 0 and 1 determining the opacity of arrows.
arrow.size	Numeric, variable arrow head size.
arrow.length	Numeric, length of the arrow head in 'cm'.
legend	Logical, whether to show the legend if group != NULL.
legend.title	Character, the legend title if group != NULL.
...	Not currently used. sample size to display sample names.

Details

Graphical of the samples (individuals) is displayed in a superimposed manner where each sample will be indicated using an arrow. The start of the arrow indicates the location of the sample in X in one plot, and the tip the location of the sample in Y in the other plot. Short arrows indicate a strong agreement between the matching data sets, long arrows a disagreement between the matching data sets. The representation space is scaled using the range of coordinates so minimum and maximum values are equal for all blocks. Since the algorithm maximises the covariance of these components, the absolute values do not affect the alignment.

For objects of class "GCCA" and if there are more than 2 blocks, the start of the arrow indicates the centroid between all data sets for a given individual and the tips of the arrows the location of that individual in each block.

Value

A ggplot object

Author(s)

Al J Abadi

References

Lê Cao, K.-A., Martin, P.G.P., Robert-Granie, C. and Besse, P. (2009). Sparse canonical methods for biological data integration: application to a cross-platform study. *BMC Bioinformatics* **10**:34.

See Also

arrows, text, points and http://mixOmics.org/graphics for more details.

Examples

```
## 'spls' class - examples demonstrate how to control sample colours with sample names shown
# ------------------------------------------------------
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic
spls.obj <- spls(X, Y, ncomp = 3, keepX = c(50, 50, 50),
                 keepY = c(10, 10, 10))

# colors indicate time of necropsy, text is the dose, label at start of arrow
plotArrow(spls.obj,  group = as.factor(liver.toxicity$treatment[, 'Time.Group']),
          col = c("red", "blue", "purple", "darkgreen"),
          ind.names  = liver.toxicity$treatment[, 'Dose.Group'],
          legend = TRUE, position.names = 'start', legend.title = 'Time.Group')


## 'rcc' class - examples demonstrate how to control shape of all samples
# ------------------------------------------------------------------------------

# create model
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
rcc.obj <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)

primary_groups <- nutrimouse$diet

# plot samples coloured by primary groups, by default shapes are all circles
plotArrow(rcc.obj, ind.names = FALSE,
          group = primary_groups, legend = TRUE)

# plot samples coloured by primary groups, force all samples to have
# a different shape (2 = triangle)
plotArrow(rcc.obj, ind.names = FALSE,
          group = primary_groups, legend = TRUE,
          pch = 2)


## 'sgccda' class - examples demonstrate how to control shape of different blocks
```

```
# ----------------------------------------------------------------------------

data(breast.TCGA)
idx = seq(1, length(breast.TCGA$data.train$subtype), 10)
X <- list(mRNA = breast.TCGA$data.train$mrna[idx,],
          miRNA = breast.TCGA$data.train$mirna[idx,],
          protein = breast.TCGA$data.train$protein[idx,])
Y <- breast.TCGA$data.train$subtype[idx] # set the response variable

diablo.obj <- block.splsda(X, Y, ncomp = 2) # undergo multiblock sPLS-DA

# plot the samples using an arrow plot -
plotArrow(diablo.obj,
          ind.names = FALSE,
          legend = TRUE,
          title = 'TCGA, DIABLO comp 1 - 2')

pchs <- c(3, 2, 1)
names(pchs) <- c("miRNA", "mRNA", "protein")

# plot the samples using an arrow plot changed shapes of data blocks
plotArrow(diablo.obj,
          ind.names = FALSE,
          legend = TRUE,
          title = 'TCGA, DIABLO comp 1 - 2',
          pch = pchs)
```

`plotDiablo` *Graphical output for the DIABLO framework*

Description

Function to visualise correlation between components from different data sets

Usage

```
plotDiablo(
  object,
  ncomp = 1,
  legend = TRUE,
  legend.ncol,
  col.per.group = NULL,
  ...
)

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

Arguments

`object`, `x`	object of class inheriting from `"block.splsda"`.
`ncomp`	Which component to plot calculated from each data set. Has to be lower than the minimum of `object$ncomp`.

legend	Logical. Whether the legend should be added. Default is TRUE.
legend.ncol	Number of columns for the legend. Default to min(5,nlevels(x$Y)).
col.per.group	A named character of colours for each group class representation. Its names must match the levels of object$Y.
...	not used

Details

The function uses a plot.data.frame to plot the component ncomp calculated from each data set to visualise whether DIABLO (block.splsda) is successful at maximising the correlation between each data sets' component. The lower triangular panel indicated the Pearson's correlation coefficient, the upper triangular panel the scatter plot.

Value

none

Author(s)

Amrit Singh, Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Singh A., Shannon C., Gautier B., Rohart F., Vacher M., Tebbutt S. and Lê Cao K.A. (2019), DIABLO: an integrative approach for identifying key molecular drivers from multi-omics assays, Bioinformatics, Volume 35, Issue 17, 1 September 2019, Pages 3055–3062.

See Also

block.splsda and http://www.mixOmics.org/mixDIABLO for more details.

Examples

```
data('breast.TCGA')
Y = breast.TCGA$data.train$subtype

data = list(mrna =  breast.TCGA$data.train$mrna,
mirna =  breast.TCGA$data.train$mirna, prot =  breast.TCGA$data.train$protein)

# set number of component per data set
ncomp = 3
# set number of variables to select, per component and per data set (arbitrarily set)
list.keepX = list(mrna = rep(20, 3), mirna = rep(10,3), prot = rep(10,3))

# DIABLO using a full design where every block is connected
BC.diablo = block.splsda(X = data, Y = Y, ncomp = ncomp, keepX = list.keepX, design = 'full')
## default col.per.group
plotDiablo(BC.diablo, ncomp = 1, legend = TRUE, col.per.group = NULL)
## custom col.per.group
col.per.group <- color.mixo(1:3)
names(col.per.group) <- levels(Y)
plotDiablo(BC.diablo, ncomp = 1, legend = TRUE, col.per.group = col.per.group)
```

plotIndiv *Plot of Individuals (Experimental Units)*

Description

This function provides scatter plots for individuals (observations) representation in (s)(I)PCA, (r)CCA, (s)PLS(DA), multiblock (s)PLS(DA) and MINT models.

Usage

```
plotIndiv(object, ...)

## S3 method for class 'mint.pls'
plotIndiv(
  object,
  comp = NULL,
  rep.space = NULL,
  study = "global",
  layout = NULL,
  style = "ggplot2",
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  background = NULL,
  pch,
  title = NULL,
  subtitle,
  legend = FALSE,
  legend.title = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  xlim = NULL,
  ylim = NULL,
  abline = FALSE,
  point.lwd = 1,
  cex,
  size.title = rel(2),
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)

## S3 method for class 'mint.spls'
```

```
plotIndiv(
  object,
  comp = NULL,
  rep.space = NULL,
  study = "global",
  layout = NULL,
  style = "ggplot2",
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  background = NULL,
  pch,
  title = NULL,
  subtitle,
  legend = FALSE,
  legend.title = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  xlim = NULL,
  ylim = NULL,
  abline = FALSE,
  point.lwd = 1,
  cex,
  size.title = rel(2),
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)

## S3 method for class 'mint.plsda'
plotIndiv(
  object,
  comp = NULL,
  rep.space = NULL,
  study = "global",
  layout = NULL,
  style = "ggplot2",
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  background = NULL,
```

```
  pch,
  title = NULL,
  subtitle,
  legend = FALSE,
  legend.title = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  xlim = NULL,
  ylim = NULL,
  abline = FALSE,
  point.lwd = 1,
  cex,
  size.title = rel(2),
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)

## S3 method for class 'mint.splsda'
plotIndiv(
  object,
  comp = NULL,
  rep.space = NULL,
  study = "global",
  layout = NULL,
  style = "ggplot2",
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  background = NULL,
  pch,
  title = NULL,
  subtitle,
  legend = FALSE,
  legend.title = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  xlim = NULL,
  ylim = NULL,
  abline = FALSE,
  point.lwd = 1,
  cex,
  size.title = rel(2),
```

```
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)

## S3 method for class 'pca'
plotIndiv(
  object,
  comp = NULL,
  style = "ggplot2",
  ind.names = TRUE,
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  pch,
  title = NULL,
  legend = FALSE,
  legend.title.pch = "Legend",
  legend.title = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  Z.label = NULL,
  xlim = NULL,
  ylim = NULL,
  axes.box = "box",
  abline = FALSE,
  cex,
  alpha = 0.2,
  point.lwd = 1,
  size.title = rel(2),
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)

## S3 method for class 'mixo_pls'
plotIndiv(
  object,
  comp = NULL,
  rep.space = NULL,
```

```
  style = "ggplot2",
  ind.names = TRUE,
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  background = NULL,
  pch,
  title = NULL,
  subtitle,
  legend = FALSE,
  legend.title = "Legend",
  legend.title.pch = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  Z.label = NULL,
  abline = FALSE,
  xlim = NULL,
  ylim = NULL,
  axes.box = "box",
  cex,
  alpha = 0.2,
  point.lwd = 1,
  size.title = rel(2),
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)

## S3 method for class 'sgcca'
plotIndiv(
  object,
  comp = NULL,
  blocks = NULL,
  style = "ggplot2",
  ind.names = TRUE,
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  pch,
  title = NULL,
  subtitle,
```

```
  legend = FALSE,
  legend.title = "Legend",
  legend.title.pch = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  Z.label = NULL,
  abline = FALSE,
  xlim = NULL,
  ylim = NULL,
  axes.box = "box",
  cex,
  alpha = 0.2,
  point.lwd = 1,
  size.title = rel(2),
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)

## S3 method for class 'rgcca'
plotIndiv(
  object,
  comp = NULL,
  blocks = NULL,
  style = "ggplot2",
  ind.names = TRUE,
  group,
  col,
  ellipse = FALSE,
  ellipse.level = 0.95,
  centroid = FALSE,
  star = FALSE,
  pch,
  title = NULL,
  subtitle,
  legend = FALSE,
  legend.title = "Legend",
  legend.title.pch = "Legend",
  legend.position = "right",
  X.label = NULL,
  Y.label = NULL,
  Z.label = NULL,
  abline = FALSE,
  xlim = NULL,
  ylim = NULL,
  axes.box = "box",
  cex,
```

```
  alpha = 0.2,
  point.lwd = 1,
  size.title = rel(2),
  size.subtitle = rel(1.5),
  size.xlabel = rel(1),
  size.ylabel = rel(1),
  size.axis = rel(0.8),
  size.legend = rel(1),
  size.legend.title = rel(1.1),
  ...
)
```

Arguments

object	object of class inherited from any **mixOmics**: PLS, sPLS, PLS-DA, SPLS-DA, rCC, PCA, sPCA, IPCA, sIPCA, rGCCA, sGCCA, sGCCDA, MINT
...	Optional arguments or type par can be added with style = 'graphics'
comp	integer vector of length two (or three to 3d). The components that will be used on the horizontal and the vertical axis respectively to project the individuals.
rep.space	- only for objects of class "pca", "plsda", "plsda", "rcc". Can be "X-variate", "Y-variate", "XY-variate", "multi".
study	- only for MINT models. Indicates whether to plot all studies together "global" or separately "all.partial". Default is "global".
layout	layout parameter passed to mfrow. Only for MINT model and only used when study is "all.partial"
style	argument to be set to either 'graphics', 'lattice', 'ggplot2' or '3d' for a style of plotting. Default set to 'ggplot2'. See details. 3d is not available for MINT objects.
group	factor indicating the group membership for each sample, useful for colouring samples by groups, adding ellipses, centroids and stars. Coded as default for the supervised methods PLS-DA, SPLS-DA, sGCCDA, but needs to be input for the unsupervised methods PCA, sPCA, IPCA, sIPCA, PLS, sPLS, rCC, rGCCA, sGCCA. Order of levels will reflect the order the groups appear in legends and correspond to the order of set colours in col.
col	character (or symbol) color to be used. If group provided, should be a vector of the same length as groups, order of colours will be respected to correspond to order of group levels.
ellipse	Logical indicating if ellipse plots should be plotted. See details.
ellipse.level	Numerical value indicating the confidence level of ellipse being plotted when ellipse =TRUE (i.e. the size of the ellipse). The default is set to 0.95, for a 95% region. See details.
centroid	Logical indicating whether centroid points should be plotted. See details.
star	Logical indicating whether a star plot should be plotted, with arrows starting from the centroid (see argument centroid, and ending for each sample belonging to each group or outcome. See details.
background	color the background by the predicted class, see background.predict
pch	value or vector, controls shape of points to be plotted. Can be used to control the shape of the points directly or to create a second group membership and legend. See details.

title	set of characters indicating the title plot.
subtitle	subtitle for each plot, only used when several block or study are plotted.
legend	Logical. Whether the legend should be added. Default is FALSE.
legend.title	title of the legend
legend.position	position of the legend, one of "bottom", "left", "top" and "right".
X.label	x axis titles.
Y.label	y axis titles.
xlim, ylim	numeric list of vectors of length 2 and length =length(blocks), giving the x and y coordinates ranges.
abline	should the vertical and horizontal line through the center be plotted? Default set to FALSE
point.lwd	lwd of the points, used when ind.names = FALSE
cex	numeric character (or symbol) expansion, possibly vector.
size.title	size of the title
size.subtitle	size of the subtitle
size.xlabel	size of xlabel
size.ylabel	size of ylabel
size.axis	size of the axis
size.legend	size of the legend
size.legend.title	size of the legend title
ind.names	either a character vector of names for the individuals to be plotted, or FALSE for no names. If TRUE, the row names of the first (or second) data matrix is used as names (see Details). If 'pch' is set this will overwrite the names as shapes. Default is TRUE. Not avaliable for MINT objects.
legend.title.pch	title of the second legend created by pch, if any.
Z.label	z axis titles (when style = '3d').
axes.box	for style '3d', argument to be set to either 'axes', 'box', 'bbox' or 'all', defining the shape of the box.
alpha	Semi-transparent colors (0 < 'alpha' < 1)
blocks	- only for multiblock objects. Integer value or name(s) of block(s) to be plotted OR "average" (averages the components from all blocks to produce a consensus plot) OR "weighted.average" (weighted average of the components according to their correlation with the outcome Y). See examples.

Details

plotIndiv method makes scatter plot for individuals representation depending on the subspace of projection. Each point corresponds to an individual.

If ind.names=TRUE and row names is NULL, then ind.names=1:n, where n is the number of individuals. Also, if pch is an input, then ind.names is set to FALSE as we do not show both names and shapes.

The outputs of "ellipse", "ellipse.level", "centroid", "star" are: 1) based on the sample group membership (specified with the group) for unsupervised models such as PCA, sPCA, IPCA,

sIPCA, PLS, sPLS, rCC, rGCCA, sGCCA or 2) based on the outcome Y for supervised models such as PLS-DA, SPLS-DA, sGCCDA

#' In the specific case of a single 'omics supervised model (plsda, splsda), users can overlay prediction results to sample plots in order to visualise the prediction areas of each class, via the background input parameter. Note that this functionality is only available for models with less than 2 components as the surfaces obtained for higher order components cannot be projected onto a 2D representation in a meaningful way. For more details, see background.predict

The group parameter is used to colour the samples by group membership, and by default the shape of samples will also correspond to these groups. Sample shapes can be further customised using the pch parameter. This can be done in 3 ways: 1) If pch is one numeric value, shape of all points will be this. 2) If pch is a vector of numeric values length equal to the number of groups set in group, then each group will have the given different shape. 3) If pch is a character vector of length equal to the number of samples, then the shape of each sample will correspond to this grouping, i.e. this allows users to visualise second group membership. In case 3), the elements of the vector should be the names of the second group membership, as these will appear in the legend. The shapes of the second group membership will be 1, 2, 3, etc by default, control of the shape is only possible by reordering the levels of the second group membership. See examples.

For customized plots (i.e. adding points, text), use the style = 'graphics' (default is ggplot2).

Note: the ellipse options were borrowed from the **ellipse**.

Value

none

Author(s)

Ignacio González, Benoit Gautier, Francois Bartolo, Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

See Also

text, background.predict, points and http://mixOmics.org/graphics for more details.

Examples

```
## 'pca' class - examples demonstrate how to control sample colours and shapes
# ------------------------------------------------------------------------------

# subset data and create model
data("srbct")
X <- srbct$gene[1:6, ]
rownames(X) <- c(paste0("Sample_", 1:6))
pca.obj <- pca(X, ncomp = 3)

primary_groups <- as.factor(c(rep("Group_1", 2), rep("Group_2", 2), rep("Group_3", 2)))
# [1] Group_1 Group_1 Group_2 Group_2 Group_3 Group_3
# Levels: Group_1 Group_2 Group_3
secondary_groups <- as.factor(c(rep("A", 3), rep("B", 2), rep("C", 1)))
# [1] A A A B B C
# Levels: A B C

# plot samples coloured by primary groups, show sample names
plotIndiv(pca.obj, ind.names = TRUE,
          group = primary_groups, legend = TRUE)
```

```
# plot samples coloured using custom colours by primary groups, show sample names
plotIndiv(pca.obj, ind.names = TRUE,
          group = primary_groups, legend = TRUE,
          col = c("red", "pink", "blue"))

# plot samples coloured by primary groups, by default shapes match primary groups
plotIndiv(pca.obj, ind.names = FALSE,
          group = primary_groups, legend = TRUE)

# plot samples coloured by primary groups, force all samples to have the same shape (2 = triangle)
plotIndiv(pca.obj, ind.names = FALSE,
          group = primary_groups, legend = TRUE,
          pch = 2)

# plot samples coloured by primary groups, use shapes to visualise secondary grouping
plotIndiv(pca.obj, ind.names = FALSE,
          group = primary_groups, legend = TRUE,
          pch = secondary_groups)

# plot samples coloured by primary groups, use shapes to visualise secondary grouping
# and change order of secondary groups
plotIndiv(pca.obj, ind.names = FALSE,
          group = primary_groups, legend = TRUE,
          pch = factor(secondary_groups, levels = c("B", "C", "A")))


## 'rcc' class - examples demonstrate how to control rep.space
# ------------------------------------------------------------

# create model
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
rcc.obj <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)

# plot samples, by default makes a panel plot for X and Y subspaces (multi)
plotIndiv(rcc.obj)

# plot samples only on X-variate subspace
plotIndiv(rcc.obj, rep.space = "X-variate")

# plot samples only on XY-variate subspace
plotIndiv(rcc.obj, rep.space = "XY-variate")


## 'spls' class - examples demonstrate how to add ellipses and centroids/stars on groups
# ------------------------------------------------------------------------------------

# create model
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic
spls.obj <- spls(X, Y, ncomp = 3, keepX = c(50, 50, 50),
                      keepY = c(10, 10, 10))

# plot samples with ellipse on groups
plotIndiv(spls.obj, group = liver.toxicity$treatment$Time.Group, ellipse = TRUE)
```

```
# plot samples with centroids on groups
plotIndiv(spls.obj, group = liver.toxicity$treatment$Time.Group, centroid = TRUE)

# plot samples with centroids and stars on groups
plotIndiv(spls.obj, group = liver.toxicity$treatment$Time.Group, centroid = TRUE, star = TRUE)



## 'splsda' class - examples demonstrate how to add ellipses and backgrounds based on
# predicted classes
# ------------------------------------------------------------------------------------

# create model
data(breast.tumors)
X <- breast.tumors$gene.exp
Y <- breast.tumors$sample$treatment
splsda.obj <- splsda(X, Y,keepX=c(10,10),ncomp=2)

# plot samples with ellipse on groups, note groups do not have to be defined
plotIndiv(splsda.obj, ellipse = TRUE, ellipse.level = 0.8)

# plot samples with background coloured by predicted classes
background <- background.predict(splsda.obj, comp.predicted = 2, dist = "max.dist")
plotIndiv(splsda.obj, background = background)



## 'sgccda' class - examples demonstrate how to control which data blocks are plotted
# ------------------------------------------------------------------------------------

# create model
data(nutrimouse)
Y <- nutrimouse$diet
data <- list(gene = nutrimouse$gene, lipid = nutrimouse$lipid)
design <- matrix(c(0,1,0,1), ncol = 2, nrow = 2, byrow = TRUE)
sgccda.obj <- wrapper.sgccda(X = data, Y = Y, design = design, ncomp = 2,
                             keepX = list(gene = c(10,10), lipid = c(15,15)))

# plot samples, by default one data block for each plot
plotIndiv(sgccda.obj)

# plot samples for just the gene data block
plotIndiv(sgccda.obj, blocks = 1)
plotIndiv(sgccda.obj, blocks = "gene")

# plot samples by averaging components from all blocks
plotIndiv(sgccda.obj, blocks = "average")

# plot samples by the weighted average of the components according to their correlation
# with Y
plotIndiv(sgccda.obj, blocks = "weighted.average")



## 'mint.splsda' class - examples demonstrate how to control which studies are plotted
# ------------------------------------------------------------------------------------
```

```
# create model
data(stemcells)
mint.obj <- mint.splsda(X = stemcells$gene, Y = stemcells$celltype, ncomp = 2,
                  keepX = c(10, 5), study = stemcells$study)

# plot samples, by default samples are plotted together coloured by groups and pch by study
plotIndiv(mint.obj, legend = TRUE)

# plot samples separated by study, can control layout
plotIndiv(mint.obj, legend = TRUE, study = "all.partial")
plotIndiv(mint.obj, legend = TRUE, study = "all.partial", layout = c(1,1))
```

---

plotLoadings *Plot of Loading vectors*

Description

This function provides a horizontal bar plot to visualise loading vectors. For discriminant analysis, it provides visualisation of highest or lowest mean/median value of the variables with color code corresponding to the outcome of interest.

Usage

```
plotLoadings(object, ...)

## S3 method for class 'mint.pls'
plotLoadings(
  object,
  style = "graphics",
  comp = 1,
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = 1.7,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  study = "global",
  ...
)

## S3 method for class 'mint.spls'
```

```
plotLoadings(
  object,
  style = "graphics",
  comp = 1,
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = 1.7,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  study = "global",
  ...
)

## S3 method for class 'mint.plsda'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = 1.7,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  contrib = NULL,
  method = "mean",
  show.ties = TRUE,
  col.ties = "white",
  legend = TRUE,
  legend.color = NULL,
  legend.title = "Outcome",
  size.legend = 0.8,
  study = "global",
```

```
  ...
)

## S3 method for class 'mint.splsda'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = 1.7,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  contrib = NULL,
  method = "mean",
  show.ties = TRUE,
  col.ties = "white",
  legend = TRUE,
  legend.color = NULL,
  legend.title = "Outcome",
  size.legend = 0.8,
  study = "global",
  ...
)

## S3 method for class 'pca'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  size.title = 2,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
```

```
  ...
)

## S3 method for class 'mixo_pls'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = rel(1.5),
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  ...
)

## S3 method for class 'mixo_spls'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = rel(1.5),
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  ...
)

## S3 method for class 'rcc'
```

```
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = rel(1.5),
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  ...
)

## S3 method for class 'sgcca'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = rel(1.5),
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  ...
)

## S3 method for class 'rgcca'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
```

```
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  col = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = rel(1.5),
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  ...
)

## S3 method for class 'mixo_plsda'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = 1.6,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  contrib = NULL,
  method = "mean",
  show.ties = TRUE,
  col.ties = "white",
  legend = TRUE,
  legend.color = NULL,
  legend.title = "Outcome",
  size.legend = 0.8,
  ...
)

## S3 method for class 'mixo_splsda'
plotLoadings(
```

```
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = 1.6,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  contrib = NULL,
  method = "mean",
  show.ties = TRUE,
  col.ties = "white",
  legend = TRUE,
  legend.color = NULL,
  legend.title = "Outcome",
  size.legend = 0.8,
  ...
)

## S3 method for class 'sgccda'
plotLoadings(
  object,
  comp = 1,
  style = "graphics",
  ndisplay = NULL,
  xlim = NULL,
  layout = NULL,
  border = NA,
  name.var = NULL,
  size.name = 0.7,
  title = NULL,
  subtitle,
  size.title = 2,
  size.subtitle = 1.6,
  size.axis = 0.7,
  X.label = NULL,
  Y.label = NULL,
  size.labs = 1,
  block,
  contrib = NULL,
  method = "mean",
  show.ties = TRUE,
```

```
  col.ties = "white",
  legend = TRUE,
  legend.color = NULL,
  legend.title = "Outcome",
  size.legend = 0.8,
  ...
)
```

Arguments

object	object
...	not used.
style	argument to be set to either 'graphics' or 'ggplot2' to indicate the style of the plot. Default is 'graphics'.
comp	integer value, which component to plot. Default is 1.
ndisplay	integer indicating how many of the most important variables are to be plotted (ranked by decreasing weights in each component). Useful to lighten a graph.
xlim	Limit of the x-axis, vector of length 2.
layout	Vector of two values (rows,cols) that indicates the layout of the plot. If layout is provided, the remaining empty subplots are still active. See details and examples.
col	color of barplot, only for non-DA methods.
border	Argument from barplot: indicates whether to draw a border on the barplot and in which colour. Note that for -DA methods, when contrib is not provided, the colour is set to white and border black.
name.var	A character vector or list indicating the names of the variables. For single block analysis or when study="all.partial", a vector of length equal to the number of variables in the block. For multi-block analysis, a list where each element is a vector of length equal to the number of variables in the corresponding block. The names of the vector should match the names of the input data, see example.
size.name	A numerical value giving the amount by which plotting the variable name text should be magnified or reduced relative to the default.
title	Title of the plot. Default is NULL.
subtitle	subtitle for each plot, only used when several block or study are plotted.
size.title	size of the title
size.subtitle	size of the subtitle
size.axis	size of text on the X axis
X.label	X axis label. Default is NULL.
Y.label	Y axis label. Default is NULL.
size.labs	size of the axis labels.
block	A single value or vector indicating which block to plot. See details for behavior depending on object type.
study	Indicates which study are to be plotted. A character vector containing some levels of object$study, "all.partial" to plot all studies or "global" is expected.
contrib	a character set to 'max' or 'min' indicating if the color of the bar should correspond to the group with the maximal or minimal expression levels / abundance.

method	a character set to 'mean' or 'median' indicating the criterion to assess the contribution. We recommend using median in the case of count or skewed data.
show.ties	Logical. If TRUE then tie groups appear in the color set by col.ties, which will appear in the legend. Ties can happen when dealing with count data type. By default set to TRUE.
col.ties	Color corresponding to ties, only used if show.ties=TRUE and ties are present.
legend	Logical indicating if the legend indicating the group outcomes should be added to the plot. Default value is TRUE.
legend.color	A color vector of length the number of group outcomes. See examples.
legend.title	A set of characters to indicate the title of the legend. Default value is NULL.
size.legend	A numerical value giving the amount by which plotting the legend text should be magnified or reduced relative to the default.

Details

The contribution of each variable for each component (depending on the object) is represented in a barplot where each bar length corresponds to the loading weight (importance) of the feature. The loading weight can be positive or negative.

For discriminant analysis, the color corresponds to the group in which the feature is most 'abundant'. Note that this type of graphical output is particularly insightful for count microbial data - in that latter case using the method = 'median' is advised. Note also that if the parameter contrib is not provided, plots are white.

For MINT analysis, study="global" plots the global loadings while partial loadings are plotted when study is a level of object$study. Since variable selection in MINT is performed at the global level, only the selected variables are plotted for the partial loadings even if the partial loadings are not sparse. See references. Importantly for multi plots, the legend accounts for one subplot in the layout design.

The block argument behavior varies depending on the object type. For mixo_pls, mixo_spls, rcc, rgcca, sgcca, block can be any number of blocks from object$names$blocks. For codemint.pls, mint.spls: when study="all.partial", can only be one block from object$names$blocks.

Value

Invisibly returns a data.frame containing the contribution of features on each component. For supervised models the contributions for each class is also specified. See details.

Author(s)

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See Also

pls, spls, plsda, splsda, mint.pls, mint.spls, mint.plsda, mint.splsda, block.pls, block.spls, block.plsda, block.splsda, mint.block.pls, mint.block.spls, mint.block.plsda, mint.block.splsda

Examples

```
## object of class 'spls'
# -------------------------
data(liver.toxicity)
X = liver.toxicity$gene
Y = liver.toxicity$clinic

toxicity.spls = spls(X, Y, ncomp = 2, keepX = c(50, 50),
keepY = c(10, 10))

plotLoadings(toxicity.spls)

# with xlim
xlim = c(-0.5, 0.5)
plotLoadings(toxicity.spls, xlim = xlim)


## Not run:
## object of class 'splsda'
# -------------------------
data(liver.toxicity)
X = as.matrix(liver.toxicity$gene)
Y = as.factor(paste0('treatment_' ,liver.toxicity$treatment[, 4]))

splsda.liver = splsda(X, Y, ncomp = 2, keepX = c(20, 20))

# contribution on comp 1, based on the median.
# Colors indicate the group in which the median expression is maximal
plotLoadings(splsda.liver, comp = 1, method = 'median')
plotLoadings(splsda.liver, comp = 1, method = 'median', contrib = "max")

# contribution on comp 2, based on median.
#Colors indicate the group in which the median expression is maximal
plotLoadings(splsda.liver, comp = 2, method = 'median', contrib = "max")

# contribution on comp 2, based on median.
# Colors indicate the group in which the median expression is minimal
plotLoadings(splsda.liver, comp = 2, method = 'median', contrib = 'min')

# look at the contribution (median) for each variable
plot.contrib = plotLoadings(splsda.liver, comp = 2, method = 'median', plot = FALSE,
contrib = "max")
head(plot.contrib[[1]][,1:4])
# change the title of the legend and title name
```

```
plotLoadings(splsda.liver, comp = 2, method = 'median', legend.title = 'Time',
title = 'Contribution plot', contrib = "max")

# no legend
plotLoadings(splsda.liver, comp = 2, method = 'median', legend = FALSE, contrib = "max")

# change the color of the legend
plotLoadings(splsda.liver, comp = 2, method = 'median', legend.color = c(1:4), contrib = "max")


# object 'splsda multilevel'
# -----------------

data(vac18)
X = vac18$genes
Y = vac18$stimulation
# sample indicates the repeated measurements
sample = vac18$sample
stimul = vac18$stimulation

# multilevel sPLS-DA model
res.1level = splsda(X, Y = stimul, ncomp = 3, multilevel = sample,
keepX = c(30, 137, 123))


name.var = vac18$tab.prob.gene[, 'Gene']
names(name.var) = colnames(X)

plotLoadings(res.1level, comp = 2, method = 'median', legend.title = 'Stimu',
name.var = name.var, size.name = 0.2, contrib = "max")

# too many transcripts? only output the top ones
plotLoadings(res.1level, comp = 2, method = 'median', legend.title = 'Stimu',
name.var = name.var, size.name = 0.5, ndisplay = 60, contrib = "max")



# object 'plsda'
# ----------------

# breast tumors
# ---
data(breast.tumors)
X = breast.tumors$gene.exp
Y = breast.tumors$sample$treatment

plsda.breast = plsda(X, Y, ncomp = 2)

name.var = as.character(breast.tumors$genes$name)
names(name.var) = colnames(X)

# with gene IDs, showing the top 60
plotLoadings(plsda.breast, contrib = 'max', comp = 1, method = 'median',
ndisplay = 60,
name.var = name.var,
size.name = 0.6,
legend.color = color.mixo(1:2))
```

```
# liver toxicity
# ---

data(liver.toxicity)
X = liver.toxicity$gene
Y = liver.toxicity$treatment[, 4]

plsda.liver = plsda(X, Y, ncomp = 2)

name.var = liver.toxicity$gene.ID[, 'geneBank']
names(name.var) = rownames(liver.toxicity$gene.ID)

plotLoadings(plsda.liver, contrib = 'max', comp = 1, method = 'median', ndisplay = 100,
name.var = name.var, size.name = 0.4,
legend.color = color.mixo(1:4))


# object 'sgccda'
# ----------------

data(nutrimouse)
Y = nutrimouse$diet
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid)
design = matrix(c(0,1,1,1,0,1,1,1,0), ncol = 3, nrow = 3, byrow = TRUE)

nutrimouse.sgccda = wrapper.sgccda(X = data,
Y = Y,
design = design,
keepX = list(gene = c(10,10), lipid = c(15,15)),
ncomp = 2)

plotLoadings(nutrimouse.sgccda,block=2)
plotLoadings(nutrimouse.sgccda,block="gene")


## End(Not run)


#' PCA example
#' -----------
data(liver.toxicity)
X = liver.toxicity$gene
Y = liver.toxicity$clinic

#' Simple PCA plot
pca.liver = pca(X, ncomp = 2)
plotLoadings(pca.liver)

#' Customize PCA plot
plotLoadings(pca.liver,
    comp = 2,
    ndisplay = 20,  # Show top 20 variables
    col = "steelblue",
    border = "black",
    size.name = 0.8,
```

```
    title = "PCA Loadings - Component 2",
    X.label = "Loading value",
    Y.label = "Variables")

#' PLS/SPLS example
#' ----------------
toxicity.spls = spls(X, Y, ncomp = 2, keepX = c(50, 50), keepY = c(10, 10))

#' Plot both blocks with custom layout
plotLoadings(toxicity.spls,
    comp = 2,
    block = c("X", "Y"),
    layout = c(2, 2),
    title = "PLS Loadings - Component 2",
    subtitle = c("Gene Block", "Clinical Block"))

#' PLSDA/SPLSDA example
#' --------------------
X = as.matrix(liver.toxicity$gene)
Y = as.factor(paste0('treatment_', liver.toxicity$treatment[, 4]))
splsda.liver = splsda(X, Y, ncomp = 2, keepX = c(20, 20))

#' Show contribution with gene names
name.var = liver.toxicity$gene.ID[, 'geneBank']
names(name.var) = rownames(liver.toxicity$gene.ID)

plotLoadings(splsda.liver,
    comp = 2,
    method = 'median',
    contrib = "max",
    name.var = name.var,
    size.name = 0.5,
    title = "Liver Treatment - Component 2",
    legend.title = "Treatment",
    legend.color = color.mixo(1:4))


#' MINT PLSDA example
#' ------------------
data(stemcells)
X = stemcells$gene
Y = stemcells$celltype
study = stemcells$study
mint.splsda = mint.splsda(X = X, Y = Y, ncomp = 3, keepX = c(10, 5, 15), study = study)

#' All partial loadings with custom layout
plotLoadings(mint.splsda,
    comp = 2,
    study = "all.partial",
    contrib = "max",
    method = "median",
    layout = c(2, 4),
    legend.color = color.mixo(1:3),
    subtitle = paste("Study", 1:4),
    show.ties = TRUE,
    col.ties = "gray")
```

```
#' Advanced customization examples
#' ------------------------------

#' Custom variable names and sizes
plotLoadings(splsda.liver,
    comp = 2,
    method = 'median',
    contrib = "max",
    name.var = name.var,
    size.name = 0.8,
    title = "Custom Variable Names",
    size.title = 1.2,
    size.axis = 0.8,
    size.labs = 1.0)

#' No legend
plotLoadings(splsda.liver,
    comp = 2,
    method = 'median',
    contrib = "max",
    legend = FALSE)

#' Custom legend
plotLoadings(splsda.liver,
    comp = 2,
    method = 'median',
    contrib = "max",
    legend.title = "Treatment Groups",
    legend.color = c("red", "blue", "green", "purple"),
    size.legend = 0.8)

#' Minimal display with top variables
plotLoadings(splsda.liver,
    comp = 2,
    method = 'median',
    contrib = "max",
    ndisplay = 20,  # Show only top 20 variables
    title = "Top 20 Contributing Variables")
```

`plotMarkers` *Plot the values for multivariate markers in block analyses*

Description

Plots the standardised values (after centring and/or scaling) for the selected variables for a given block on a given component. Only applies to `block.splsda` or `block.spls`.

Usage

```
plotMarkers(
  object,
  block,
  markers = NULL,
```

```
  comp = 1,
  group = NULL,
  col.per.group = NULL,
  global = FALSE,
  title = NULL,
  violin = TRUE,
  boxplot.width = NULL,
  violin.width = 0.9
)
```

Arguments

object	An object of class block.splsda or block.spls
block	Name or index of the block to use
markers	Character or integer, only include these markers. If integer, the top 'markers' features are shown
comp	Integer, the component to use
group	Factor, the grouping variable (only required for block.spls objects)
col.per.group	character (or symbol) color to be used when 'group' is defined. Vector of the same length as the number of groups.
global	Logical indicating whether to show the global plots (TRUE) or segregate by feature (FALSE). Only available when object$scale=TRUE
title	The plot title
violin	(if global = FALSE) Logical indicating whether violin plots should also be shown
boxplot.width	Numeric, adjusts the width of the box plots
violin.width	Numeric, adjusts the width of the violin plots

Value

A ggplot object

See Also

plotLoadings, block.splsda, block.spls

Examples

```
# see ?block.splsda and ?block.spls
```

---

plotVar *Plot of Variables*

Description

This function provides variables representation for (regularized) CCA, (sparse) PLS regression, PCA and (sparse) Regularized generalised CCA.

Usage

```
plotVar(
  object,
  comp = NULL,
  comp.select = comp,
  plot = TRUE,
  var.names = NULL,
  blocks = NULL,
  X.label = NULL,
  Y.label = NULL,
  Z.label = NULL,
  abline = TRUE,
  col,
  cex,
  pch,
  font,
  cutoff = 0,
  rad.in = 0.5,
  title = "Correlation Circle Plot",
  legend = FALSE,
  legend.title = "Block",
  style = "ggplot2",
  overlap = TRUE,
  axes.box = "all",
  label.axes.box = "both"
)
```

Arguments

object	object of class inheriting from "rcc", "pls", "plsda", "spls", "splsda", "pca" or "spca".
comp	integer vector of length two. The components that will be used on the horizontal and the vertical axis respectively to project the variables. By default, comp=c(1,2) except when style='3d', comp=c(1:3)
comp.select	for the sparse versions, an input vector indicating the components on which the variables were selected. Only those selected variables are displayed. By default, comp.select=comp
plot	if TRUE (the default) then a plot is produced. If not, the summaries which the plots are based on are returned.
var.names	either a character vector of names for the variables to be plotted, or FALSE for no names. If TRUE, the col names of the first (or second) data matrix is used as names.
blocks	for an object of class "rgcca" or "sgcca", a numerical vector indicating the block variables to display.
X.label	x axis titles.
Y.label	y axis titles.
Z.label	z axis titles (when style = '3d').
abline	should the vertical and horizontal line through the center be plotted? Default set to FALSE

col	character or integer vector of colors for plotted character and symbols, can be of length 2 (one for each data set) or of length (p+q) (i.e. the total number of variables). See Details.
cex	numeric vector of character expansion sizes for the plotted character and symbols, can be of length 2 (one for each data set) or of length (p+q) (i.e. the total number of variables).
pch	plot character. A vector of single characters or integers, can be of length 2 (one for each data set) or of length (p+q) (i.e. the total number of variables). See points for all alternatives.
font	numeric vector of font to be used, can be of length 2 (one for each data set) or of length (p+q) (i.e. the total number of variables). See par for details.
cutoff	numeric between 0 and 1. Variables with correlations below this cutoff in absolute value are not plotted (see Details).
rad.in	numeric between 0 and 1, the radius of the inner circle. Defaults to 0.5.
title	character indicating the title plot.
legend	Logical when more than 3 blocks. Can be a character vector when one or 2 blocks to customize the legend. See examples. Default is FALSE.
legend.title	title of the legend
style	argument to be set to either 'graphics', 'lattice', 'ggplot2' or '3d' for a style of plotting.
overlap	Logical. Whether the variables should be plotted in one single figure. Default is TRUE.
axes.box	for style '3d', argument to be set to either 'axes', 'box', 'bbox' or 'all', defining the shape of the box.
label.axes.box	for style '3d', argument to be set to either 'axes', 'box', 'both', indicating which labels to print.

Details

plotVar produce a "correlation circle", i.e. the correlations between each variable and the selected components are plotted as scatter plot, with concentric circles of radius one et radius given by rad.in. Each point corresponds to a variable. For (regularized) CCA the components correspond to the equiangular vector between X- and Y-variates. For (sparse) PLS regression mode the components correspond to the X-variates. If mode is canonical, the components for X and Y variables correspond to the X- and Y-variates respectively.

For plsda and splsda objects, only the X variables are represented.

For spls and splsda objects, only the X and Y variables selected on dimensions comp are represented.

The arguments col, pch, cex and font can be either vectors of length two or a list with two vector components of length p and q respectively, where p is the number of X-variables and q is the number of Y-variables. In the first case, the first and second component of the vector determine the graphics attributes for the X- and Y-variables respectively. Otherwise, multiple arguments values can be specified so that each point (variable) can be given its own graphic attributes. In this case, the first component of the list correspond to the X attributs and the second component correspond to the Y attributs. Default values exist for this arguments.

Value

A list containing the following components:

x	a vector of coordinates of the variables on the x-axis.
y	a vector of coordinates of the variables on the y-axis.
Block	the data block name each variable belongs to.
names	the name of each variable, matching their coordinates values.

Author(s)

Ignacio González, Benoit Gautier, Francois Bartolo, Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

González I., Lê Cao K-A., Davis, M.J. and Déjean, S. (2012). Visualising associations between paired 'omics data sets. J. Data Mining 5:19. http://www.biodatamining.org/content/5/1/19/abstract

See Also

cim, network, par and http://www.mixOmics.org for more details.

Examples

```
## variable representation for objects of class 'rcc'
# ----------------------------------------------------
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
nutri.res <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)

plotVar(nutri.res) #(default)


plotVar(nutri.res, comp = c(1,3), cutoff = 0.5)

## Not run:
## variable representation for objects of class 'pls' or 'spls'
# ----------------------------------------------------
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic
toxicity.spls <- spls(X, Y, ncomp = 3, keepX = c(50, 50, 50),
keepY = c(10, 10, 10))

plotVar(toxicity.spls, cex = c(1,0.8))

# with a customized legend
plotVar(toxicity.spls, legend = c("block 1", "my block 2"),
legend.title="my legend")

## variable representation for objects of class 'splsda'
# ----------------------------------------------------

data(liver.toxicity)
```

```
X <- liver.toxicity$gene
Y <- as.factor(liver.toxicity$treatment[, 4])

ncomp <- 2
keepX <- rep(20, ncomp)

splsda.liver <- splsda(X, Y, ncomp = ncomp, keepX = keepX)
plotVar(splsda.liver)

## variable representation for objects of class 'sgcca' (or 'rgcca')
# ----------------------------------------------------
## see example in ??wrapper.sgcca
data(nutrimouse)
# need to unmap the Y factor diet
Y = unmap(nutrimouse$diet)
# set up the data as list
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = Y)

# set up the design matrix:
# with this design, gene expression and lipids are connected to the diet factor
# design = matrix(c(0,0,1,
#                   0,0,1,
#                   1,1,0), ncol = 3, nrow = 3, byrow = TRUE)

# with this design, gene expression and lipids are connected to the diet factor
# and gene expression and lipids are also connected
design = matrix(c(0,1,1,
1,0,1,
1,1,0), ncol = 3, nrow = 3, byrow = TRUE)


#note: the penalty parameters will need to be tuned
wrap.result.sgcca = wrapper.sgcca(X = data, design = design, penalty = c(.3,.3, 1),
ncomp = 2)
wrap.result.sgcca

#variables selected on component 1 for each block
selectVar(wrap.result.sgcca, comp = 1, block = c(1,2))$'gene'$name
selectVar(wrap.result.sgcca, comp = 1, block = c(1,2))$'lipid'$name

#variables selected on component 2 for each block
selectVar(wrap.result.sgcca, comp = 2, block = c(1,2))$'gene'$name
selectVar(wrap.result.sgcca, comp = 2, block = c(1,2))$'lipid'$name

plotVar(wrap.result.sgcca, comp = c(1,2), block = c(1,2), comp.select = c(1,1),
title = c('Variables selected on component 1 only'))


plotVar(wrap.result.sgcca, comp = c(1,2), block = c(1,2), comp.select = c(2,2),
title = c('Variables selected on component 2 only'))

# -> this one shows the variables selected on both components
plotVar(wrap.result.sgcca, comp = c(1,2), block = c(1,2),
title = c('Variables selected on components 1 and 2'))

## variable representation for objects of class 'rgcca'
# ----------------------------------------------------
```

```
data(nutrimouse)
# need to unmap Y for an unsupervised analysis, where Y is included as a data block in data
Y = unmap(nutrimouse$diet)

data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = Y)
# with this design, all blocks are connected
design = matrix(c(0,1,1,1,0,1,1,1,0), ncol = 3, nrow = 3,
byrow = TRUE, dimnames = list(names(data), names(data)))

nutrimouse.rgcca <- wrapper.rgcca(X = data,
design = design,
tau = "optimal",
ncomp = 2)

plotVar(nutrimouse.rgcca, comp = c(1,2), block = c(1,2), cex = c(1.5, 1.5))


plotVar(nutrimouse.rgcca, comp = c(1,2), block = c(1,2))


# set up the data as list
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y =Y)
# with this design, gene expression and lipids are connected to the diet factor
# design = matrix(c(0,0,1,
#                   0,0,1,
#                   1,1,0), ncol = 3, nrow = 3, byrow = TRUE)

# with this design, gene expression and lipids are connected to the diet factor
# and gene expression and lipids are also connected
design = matrix(c(0,1,1,
1,0,1,
1,1,0), ncol = 3, nrow = 3, byrow = TRUE)
#note: the tau parameter is the regularization parameter
wrap.result.rgcca = wrapper.rgcca(X = data, design = design, tau = c(1, 1, 0),
ncomp = 2)
#wrap.result.rgcca
plotVar(wrap.result.rgcca, comp = c(1,2), block = c(1,2))


## End(Not run)
```

`pls` *Partial Least Squares (PLS) Regression*

Description

Function to perform Partial Least Squares (PLS) regression.

Usage

```
pls(
  X,
  Y,
```

```
  ncomp = 2,
  scale = TRUE,
  mode = c("regression", "canonical", "invariant", "classic"),
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  logratio = "none",
  multilevel = NULL,
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

X	numeric matrix of predictors with the rows as individual observations. missing values (NAs) are allowed.
Y	numeric matrix of response(s) with the rows as individual observations matching X. missing values (NAs) are allowed.
ncomp	Positive Integer. The number of components to include in the model. Default to 2.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
logratio	Character, one of ('none','CLR') specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'. See ?logratio.transfo for details.
multilevel	Numeric, design matrix for repeated measurement analysis, where multilevel decomposition is required. For a one factor decomposition, the repeated measures on each individual, i.e. the individuals ID is input as the first column. For a 2 level factor decomposition then 2nd AND 3rd columns indicate those factors. See examplesin ?spls.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

pls function fit PLS models with $1, \ldots,$ncomp components. Multi-response models are fully supported. The X and Y datasets can contain missing values.

The type of algorithm to use is specified with the mode argument. Four PLS algorithms are available: PLS regression ("regression"), PLS canonical analysis ("canonical"), redundancy analysis

("invariant") and the classical PLS algorithm ("classic") (see References). Different modes relate on how the Y matrix is deflated across the iterations of the algorithms - i.e. the different components.

- Regression mode: the Y matrix is deflated with respect to the information extracted/modelled from the local regression on X. Here the goal is to predict Y from X (Y and X play an asymmetric role). Consequently the latent variables computed to predict Y from X are different from those computed to predict X from Y.

- Canonical mode: the Y matrix is deflated to the information extracted/modelled from the local regression on Y. Here X and Y play a symmetric role and the goal is similar to a Canonical Correlation type of analysis.

- Invariant mode: the Y matrix is not deflated

- Classic mode: is similar to a regression mode. It gives identical results for the variates and loadings associated to the X data set, but differences for the loadings vectors associated to the Y data set (different normalisations are used). Classic mode is the PLS2 model as defined by Tenenhaus (1998), Chap 9.

Note that in all cases the results are the same on the first component as deflation only starts after component 1.

Value

pls returns an object of class "pls", a list that contains the following components:

call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component
X	the centered and standardized original predictor matrix.
Y	the centered and standardized original response vector or matrix.
ncomp	the number of components included in the model.
mode	the algorithm used to fit the model.
variates	list containing the variates.
loadings	list containing the estimated loadings for the X and Y variates. The loading weights multiplied with their associated deflated (residual) matrix gives the variate.
loadings.stars	list containing the estimated weighted loadings for the X and Y variates. The loading weights are projected so that when multiplied with their associated original matrix we obtain the variate.
names	list containing the names to be used for individuals and variables.
tol	the tolerance used in the iterative algorithm, used for subsequent S3 methods
iter	Number of iterations of the algorithm for each component
max.iter	the maximum number of iterations, used for subsequent S3 methods
nzv	list containing the zero- or near-zero predictors information.
scale	whether scaling was applied per predictor.
logratio	whether log ratio transformation for relative proportion data was applied, and if so, which type of transformation.
prop_expl_var	The proportion of the variance explained by each variate / component divided by the total variance in the data (after removing the possible missing values) using the definition of 'redundancy'. Note that contrary to PCA, this amount may not decrease in the following components as the aim of the method is not

to maximise the variance, but the covariance between data sets (including the dummy matrix representation of the outcome variable in case of the supervised approaches).

`input.X` numeric matrix of predictors in X that was input, before any scaling / logratio / multilevel transformation.

`mat.c` matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by `predict`.

`defl.matrix` residual matrices X for each dimension.

missing values

The estimation of the missing values can be performed using the `impute.nipals` function. Otherwise, missing values are handled by element-wise deletion in the `pls` function without having to delete the rows with missing data.

multilevel

Multilevel (s)PLS enables the integration of data measured on two different data sets on the same individuals. This approach differs from multilevel sPLS-DA as the aim is to select subsets of variables from both data sets that are highly positively or negatively correlated across samples. The approach is unsupervised, i.e. no prior knowledge about the sample groups is included.

logratio and multilevel

logratio transform and multilevel analysis are performed sequentially as internal pre-processing step, through `logratio.transfo` and `withinVariation` respectively.

Author(s)

Sébastien Déjean, Ignacio González, Florian Rohart, Kim-Anh Lê Cao, Al J Abadi

References

Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

Wold H. (1966). Estimation of principal components and related models by iterative least squares. In: Krishnaiah, P. R. (editors), *Multivariate Analysis*. Academic Press, N.Y., 391-420.

Abdi H (2010). Partial least squares regression and projection on latent structure regression (PLS Regression). *Wiley Interdisciplinary Reviews: Computational Statistics*, 2(1), 97-106.

See Also

`spls`, `summary`, `plotIndiv`, `plotVar`, `predict`, `perf` and http://www.mixOmics.org for more details.

Examples

```
data(linnerud)
X <- linnerud$exercise
Y <- linnerud$physiological
linn.pls <- pls(X, Y, mode = "classic")

## Not run:
data(liver.toxicity)
```

```
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic
toxicity.pls <- pls(X, Y, ncomp = 3)

## End(Not run)
```

---

plsda *Partial Least Squares Discriminant Analysis (PLS-DA).*

Description

Function to perform standard Partial Least Squares regression to classify samples.

Usage

```
plsda(
  X,
  Y,
  ncomp = 2,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  logratio = c("none", "CLR"),
  multilevel = NULL,
  all.outputs = TRUE
)
```

Arguments

X	numeric matrix of predictors with the rows as individual observations. missing values (NAs) are allowed.
Y	a factor or a class vector for the discrete outcome.
ncomp	Positive Integer. The number of components to include in the model. Default to 2.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
logratio	Character, one of ('none','CLR') specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'. See ?logratio.transfo for details.
multilevel	sample information for multilevel decomposition for repeated measurements. A numeric matrix or data frame indicating the repeated measures on each individual, i.e. the individuals ID. See examples in ?splsda.

all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

plsda function fit PLS models with $1, \ldots,$ncomp components to the factor or class vector Y. The appropriate indicator matrix is created.

Logratio transformation and multilevel analysis are performed sequentially as internal pre-processing step, through logratio.transfo and withinVariation respectively. Logratio can only be applied if the data do not contain any 0 value (for count data, we thus advise the normalise raw data with a 1 offset).

The type of deflation used is 'regression' for discriminant algorithms. i.e. no deflation is performed on Y.

Value

plsda returns an object of class "plsda", a list that contains the following components:

X	the centered and standardized original predictor matrix.
Y	the centered and standardized indicator response vector or matrix.
ind.mat	the indicator matrix.
ncomp	the number of components included in the model.
variates	list containing the X and Y variates.
loadings	list containing the estimated loadings associated to each component/variate. The loading weights multiplied with the deflated (residual) matrix gives the variate.
loadings.stars	list containing the estimated loadings associated to each component/variate. The loading weights are projected so that when multiplied with the original matrix we obtain the variate.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
tol	the tolerance used in the iterative algorithm, used for subsequent S3 methods
max.iter	the maximum number of iterations, used for subsequent S3 methods
iter	Number of iterations of the algorithm for each component
prop_expl_var	The proportion of the variance explained by each variate / component divided by the total variance in the data (after removing the possible missing values) using the definition of 'redundancy'. Note that contrary to PCA, this amount may not decrease in the following components as the aim of the method is not to maximise the variance, but the covariance between data sets (including the dummy matrix representation of the outcome variable in case of the supervised approaches).
mat.c	matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by predict.
defl.matrix	residual matrices X for each dimension.

Author(s)

Ignacio González, Kim-Anh Lê Cao, Florian Rohart, Al J Abadi

References

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See Also

splsda, summary, plotIndiv, plotVar, predict, perf, mint.block.plsda, block.plsda and http://mixOmics.org for more details.

Examples

```
## First example
data(breast.tumors)
X <- breast.tumors$gene.exp
Y <- breast.tumors$sample$treatment

plsda.breast <- plsda(X, Y, ncomp = 2)
plotIndiv(plsda.breast, ind.names = TRUE, ellipse = TRUE, legend = TRUE)


## Not run:
## Second example
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$treatment[, 4]

plsda.liver <- plsda(X, Y, ncomp = 2)
plotIndiv(plsda.liver, ind.names = Y, ellipse = TRUE, legend =TRUE)

## End(Not run)
```

---

predict *Predict Method for (mint).(block).(s)pls(da) methods*

Description

Predicted values based on PLS models. New responses and variates are predicted using a fitted model and a new matrix of observations.

Usage

```
## S3 method for class 'mixo_pls'
predict(
  object,
  newdata,
  study.test,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  multilevel = NULL,
  ...
)

## S3 method for class 'mixo_spls'
predict(
  object,
  newdata,
  study.test,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  multilevel = NULL,
  ...
)

## S3 method for class 'mint.splsda'
predict(
  object,
  newdata,
  study.test,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  multilevel = NULL,
  ...
)

## S3 method for class 'block.pls'
predict(
  object,
  newdata,
  study.test,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  multilevel = NULL,
  ...
)

## S3 method for class 'block.spls'
predict(
  object,
  newdata,
  study.test,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  multilevel = NULL,
  ...
)
```

Arguments

object	object of class inheriting from "(mint).(block).(s)pls(da)".
newdata	data matrix in which to look for for explanatory variables to be used for prediction. Please note that this method does not perform multilevel decomposition or log ratio transformations, which need to be processed beforehand.
study.test	For MINT objects, grouping factor indicating which samples of newdata are from the same study. Overlap with object$study are allowed.
dist	distance to be applied for discriminant methods to predict the class of new data, should be a subset of "centroids.dist", "mahalanobis.dist" or "max.dist" (see Details). Defaults to "all".
multilevel	Design matrix for multilevel analysis (for repeated measurements). A numeric matrix or data frame. For a one level factor decomposition, the input is a vector indicating the repeated measures on each individual, i.e. the individuals ID. For a two level decomposition with splsda models, the two factors are included in Y. Finally for a two level decomposition with spls models, 2nd AND 3rd columns in design indicate those factors (see example in ?splsda and ?spls).
...	not used currently.

Details

predict produces predicted values, obtained by evaluating the PLS-derived methods, returned by (mint).(block).(s)pls(da) in the frame newdata. Variates for newdata are also returned. Please note that this method performs multilevel decomposition and/or log ratio transformations if needed (multilevel is an input parameter while logratio is extracted from object).

Different prediction distances are proposed for discriminant analysis. The reason is that our supervised models work with a dummy indicator matrix of Y to indicate the class membership of each sample. The prediction of a new observation results in either a predicted dummy variable (output object$predict), or a predicted variate (output object$variates). Therefore, an appropriate distance needs to be applied to those predicted values to assign the predicted class. We propose distances such as 'maximum distance' for the predicted dummy variables, 'Mahalanobis distance' and 'Centroids distance' for the predicted variates.

"max.dist" is the simplest method to predict the class of a test sample. For each new individual, the class with the largest predicted dummy variable is the predicted class. This distance performs well in single data set analysis with multiclass problems (PLS-DA).

"centroids.dist" allocates to the new observation the class that mimimises the distance between the predicted score and the centroids of the classes calculated on the latent components or variates of the trained model.

"mahalanobis.dist" allocates the new sample the class defined as the centroid distance, but using the Mahalanobis metric in the calculation of the distance.

In practice we found that the centroid-based distances ("centroids.dist" and "mahalanobis.dist"), and specifically the Mahalanobis distance led to more accurate predictions than the maximum distance for complex classification problems and N-integration problems (block.splsda). The centroid distances consider the prediction in dimensional space spanned by the predicted variates, while the maximum distance considers a single point estimate using the predicted scores on the last dimension of the model. The user can assess the different distances, and choose the prediction distance that leads to the best performance of the model, as highlighted from the tune and perf outputs

More (mathematical) details about the prediction distances are available in the supplemental of the mixOmics article (Rohart et al 2017).

For a visualisation of those prediction distances, see background.predict that overlays the prediction area in plotIndiv for a sPLS-DA object.

Allocates the individual x to the class of Y minimizing $dist(\texttt{x-variate}, G_l)$, where $G_l, l = 1, ..., L$ are the centroids of the classes calculated on the X-variates of the model. "mahalanobis.dist" allocates the individual x to the class of Y as in "centroids.dist" but by using the Mahalanobis metric in the calculation of the distance.

For MINT objects, the study.test argument is required and provides the grouping factor of newdata.

For multi block analysis (thus block objects), newdata is a list of matrices whose names are a subset of names(object$X) and missing blocks are allowed. Several predictions are returned, either for each block or for all blocks. For non discriminant analysis, the predicted values (predict) are returned for each block and these values are combined by average (AveragedPredict) or weighted average (WeightedPredict), using the weights of the blocks that are calculated as the correlation between a block's components and the outcome's components.

For discriminant analysis, the predicted class is returned for each block (class) and each distance (dist) and these predictions are combined by majority vote (MajorityVote) or weighted majority vote (WeightedVote), using the weights of the blocks that are calculated as the correlation between a block's components and the outcome's components. NA means that there is no consensus among the block. For PLS-DA and sPLS-DA objects, the prediction area can be visualised in plotIndiv via the background.predict function.

Value

predict produces a list with the following components:

predict	predicted response values. The dimensions correspond to the observations, the response variables and the model dimension, respectively. For a supervised model, it corresponds to the predicted dummy variables.
variates	matrix of predicted variates.
B.hat	matrix of regression coefficients (without the intercept).
AveragedPredict	if more than one block, returns the average predicted values over the blocks (using the predict output)
WeightedPredict	if more than one block, returns the weighted average of the predicted values over the blocks (using the predict and weights outputs)
class	predicted class of newdata for each $1, ...,$ncomp components.
MajorityVote	if more than one block, returns the majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.
WeightedVote	if more than one block, returns the weighted majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.
weights	Returns the weights of each block used for the weighted predictions, for each nrepeat and each fold
centroids	matrix of coordinates for centroids.
dist	type of distance requested.
vote	majority vote result for multi block analysis (see details above).

Author(s)

Florian Rohart, Sébastien Déjean, Ignacio González, Kim-Anh Lê Cao, Al J Abadi

References

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See Also

pls, spls, plsda, splsda, mint.pls, mint.spls, mint.plsda, mint.splsda, block.pls, block.spls, block.plsda, block.splsda, mint.block.pls, mint.block.spls, mint.block.plsda, mint.block.splsda and visualisation with background.predict and http://www.mixOmics.org for more details.

Examples

```
data(linnerud)
X <- linnerud$exercise
Y <- linnerud$physiological
linn.pls <- pls(X, Y, ncomp = 2, mode = "classic")

indiv1 <- c(200, 40, 60)
indiv2 <- c(190, 45, 45)
newdata <- rbind(indiv1, indiv2)
colnames(newdata) <- colnames(X)
newdata

pred <- predict(linn.pls, newdata)

plotIndiv(linn.pls, comp = 1:2, rep.space = "X-variate",style="graphics",ind.names=FALSE)
points(pred$variates[, 1], pred$variates[, 2], pch = 19, cex = 1.2)
text(pred$variates[, 1], pred$variates[, 2],
c("new ind.1", "new ind.2"), pos = 3)

## First example with plsda
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- as.factor(liver.toxicity$treatment[, 4])


## if training is perfomed on 4/5th of the original data
samp <- sample(1:5, nrow(X), replace = TRUE)
test <- which(samp == 1)   # testing on the first fold
train <- setdiff(1:nrow(X), test)

plsda.train <- plsda(X[train, ], Y[train], ncomp = 2)
test.predict <- predict(plsda.train, X[test, ], dist = "max.dist")
Prediction <- test.predict$class$max.dist[, 2]
cbind(Y = as.character(Y[test]), Prediction)

## Not run:
## Second example with splsda
splsda.train <- splsda(X[train, ], Y[train], ncomp = 2, keepX = c(30, 30))
test.predict <- predict(splsda.train, X[test, ], dist = "max.dist")
```

```
Prediction <- test.predict$class$max.dist[, 2]
cbind(Y = as.character(Y[test]), Prediction)


## example with block.splsda=diablo=sgccda and a missing block
data(nutrimouse)
# need to unmap Y for an unsupervised analysis, where Y is included as a data block in data
Y.mat = unmap(nutrimouse$diet)
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = Y.mat)
# with this design, all blocks are connected
design = matrix(c(0,1,1,1,0,1,1,1,0), ncol = 3, nrow = 3,
byrow = TRUE, dimnames = list(names(data), names(data)))

# train on 75% of the data
ind.train=NULL
for(i in 1:nlevels(nutrimouse$diet))
ind.train=c(ind.train,which(nutrimouse$diet==levels(nutrimouse$diet)[i])[1:6])

#training set
gene.train=nutrimouse$gene[ind.train,]
lipid.train=nutrimouse$lipid[ind.train,]
Y.mat.train=Y.mat[ind.train,]
Y.train=nutrimouse$diet[ind.train]
data.train=list(gene=gene.train,lipid=lipid.train,Y=Y.mat.train)

#test set
gene.test=nutrimouse$gene[-ind.train,]
lipid.test=nutrimouse$lipid[-ind.train,]
Y.mat.test=Y.mat[-ind.train,]
Y.test=nutrimouse$diet[-ind.train]
data.test=list(gene=gene.test,lipid=lipid.test)

# example with block.splsda=diablo=sgccda and a missing block
res.train = block.splsda(X=list(gene=gene.train,lipid=lipid.train),Y=Y.train,
ncomp=3,keepX=list(gene=c(10,10,10),lipid=c(5,5,5)))
test.predict = predict(res.train, newdata=data.test[2], method = "max.dist")


## example with mint.splsda
data(stemcells)

#training set
ind.test = which(stemcells$study == "3")
gene.train = stemcells$gene[-ind.test,]
Y.train = stemcells$celltype[-ind.test]
study.train = factor(stemcells$study[-ind.test])

#test set
gene.test = stemcells$gene[ind.test,]
Y.test = stemcells$celltype[ind.test]
study.test = factor(stemcells$study[ind.test])

res = mint.splsda(X = gene.train, Y = Y.train, ncomp = 3, keepX = c(10, 5, 15),
study = study.train)

pred = predict(res, newdata = gene.test, study.test = study.test)
```

```
data.frame(Truth = Y.test, prediction = pred$class$max.dist)


## End(Not run)
```

---

print *Print Methods for CCA, (s)PLS, PCA and Summary objects*

Description

Produce `print` methods for class `"rcc"`, `"pls"`, `"spls"`, `"pca"`, `"rgcca"`, `"sgcca"` and `"summary"`.

Usage

```
## S3 method for class 'mixo_pls'
print(x, ...)

## S3 method for class 'mint.pls'
print(x, ...)

## S3 method for class 'mixo_plsda'
print(x, ...)

## S3 method for class 'mint.plsda'
print(x, ...)

## S3 method for class 'mixo_spls'
print(x, ...)

## S3 method for class 'mint.spls'
print(x, ...)

## S3 method for class 'mixo_splsda'
print(x, ...)

## S3 method for class 'mint.splsda'
print(x, ...)

## S3 method for class 'rcc'
print(x, ...)

## S3 method for class 'pca'
print(x, ...)

## S3 method for class 'ipca'
print(x, ...)

## S3 method for class 'sipca'
print(x, ...)

## S3 method for class 'rgcca'
```

```
print(x, ...)

## S3 method for class 'sgcca'
print(x, ...)

## S3 method for class 'sgccda'
print(x, ...)

## S3 method for class 'summary'
print(x, ...)

## S3 method for class 'perf.pls.mthd'
print(x, ...)

## S3 method for class 'perf.plsda.mthd'
print(x, ...)

## S3 method for class 'perf.splsda.mthd'
print(x, ...)

## S3 method for class 'perf.mint.splsda.mthd'
print(x, ...)

## S3 method for class 'perf.sgccda.mthd'
print(x, ...)

## S3 method for class 'tune.pca'
print(x, ...)

## S3 method for class 'tune.spca'
print(x, ...)

## S3 method for class 'tune.rcc'
print(x, ...)

## S3 method for class 'tune.splsda'
print(x, ...)

## S3 method for class 'tune.pls'
print(x, ...)

## S3 method for class 'tune.spls1'
print(x, ...)

## S3 method for class 'tune.mint.splsda'
print(x, ...)

## S3 method for class 'tune.block.splsda'
print(x, ...)

## S3 method for class 'predict'
print(x, ...)
```

Arguments

x	object of class inherited from "rcc", "pls", "spls", "pca", "spca", "rgcca", "sgcca" or "summary".
...	not used currently.

Details

print method for "rcc", "pls", "spls" "pca", "rgcca", "sgcca" class, returns a description of the x object including: the function used, the regularization parameters (if x of class "rcc"), the (s)PLS algorithm used (if x of class "pls" or "spls"), the samples size, the number of variables selected on each of the sPLS components (if x of class "spls") and the available components of the object.

print method for "summary" class, gives the (s)PLS algorithm used (if x of class "pls" or "spls"), the number of variates considered, the canonical correlations (if x of class "rcc"), the number of variables selected on each of the sPLS components (if x of class "spls") and the available components for Communalities Analysis, Redundancy Analysis and Variable Importance in the Projection (VIP).

Value

none

Author(s)

Sébastien Déjean, Ignacio González, Kim-Anh Lê Cao, Fangzhou Yao, Jeff Coquery, Al J Abadi.

See Also

rcc, pls, spls, vip.

Examples

```
## print for objects of class 'rcc'
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
nutri.res <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)
print(nutri.res)

## Not run:
## print for objects of class 'summary'
more <- summary(nutri.res, cutoff = 0.65)
print(more)

## print for objects of class 'pls'
data(linnerud)
X <- linnerud$exercise
Y <- linnerud$physiological
linn.pls <- pls(X, Y)
print(linn.pls)

## print for objects of class 'spls'
data(liver.toxicity)
X <- liver.toxicity$gene
```

```
Y <- liver.toxicity$clinic
toxicity.spls <- spls(X, Y, ncomp = 3, keepX = c(50, 50, 50),
keepY = c(10, 10, 10))
print(toxicity.spls)

## End(Not run)
```

`rcc` *Regularized Canonical Correlation Analysis*

Description

The function performs the regularized extension of the Canonical Correlation Analysis to seek correlations between two data matrices.

Usage

```
rcc(
  X,
  Y,
  ncomp = 2,
  method = c("ridge", "shrinkage"),
  lambda1 = 0,
  lambda2 = 0,
  verbose.call = FALSE
)
```

Arguments

`X`	numeric matrix or data frame $(n \times p)$, the observations on the X variables. `NA`s are allowed.
`Y`	numeric matrix or data frame $(n \times q)$, the observations on the Y variables. `NA`s are allowed.
`ncomp`	the number of components to include in the model. Default to 2.
`method`	One of "ridge" or "shrinkage". If "ridge", `lambda1` and `lambda2` need to be supplied (see also our function tune.rcc); if "shrinkage", parameters are directly estimated with Strimmer's formula, see below and reference.
`lambda1`, `lambda2`	a non-negative real. The regularization parameter for the *X* and *Y* data. Defaults to `lambda1=lambda2=0`. Only used if `method="ridge"`
`verbose.call`	Logical (Default=FALSE), if set to TRUE then the `$call` component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

The main purpose of Canonical Correlations Analysis (CCA) is the exploration of sample correlations between two sets of variables X and Y observed on the same individuals (experimental units) whose roles in the analysis are strictly symmetric.

The cancor function performs the core of computations but additional tools are required to deal with data sets highly correlated (nearly collinear), data sets with more variables than units by example.

The rcc function, the regularized version of CCA, is one way to deal with this problem by including a regularization step in the computations of CCA. Such a regularization in this context was first proposed by Vinod (1976), then developped by Leurgans *et al.* (1993). It consists in the regularization of the empirical covariances matrices of X and Y by adding a multiple of the matrix identity, that is, $\text{Cov}(X) + \lambda_1 I$ and $\text{Cov}(Y) + \lambda_2 I$.

When lambda1=0 and lambda2=0, rcc performs a classical CCA, if possible (i.e. when $n > p + q$.

The shrinkage estimates method = "shrinkage" can be used to bypass tune.rcc to choose the shrinkage parameters - which can be long and costly to compute with very large data sets. Note that both functions tune.rcc (which uses cross-validation) and the shrinkage parameters (which uses the formula from Schafer and Strimmer, see the corpcor package estimate.lambda) may output different results.

Note: when method = "shrinkage" the parameters are estimated using estimate.lambda from the corpcor package. Data are then centered to calculate the regularised variance-covariance matrices in rcc.

Missing values are handled in the function, except when using method = "shrinkage". In that case the estimation of the missing values can be performed by the reconstitution of the data matrix using the nipals function.

Value

rcc returns a object of class "rcc", a list that contains the following components:

X	the original X data.
Y	the original Y data.
cor	a vector containing the canonical correlations.
lambda	a vector containing the regularization parameters whether those were input if ridge method or directly estimated with the shrinkage method.
loadings	list containing the estimated coefficients used to calculate the canonical variates in X and Y.
variates	list containing the canonical variates.
names	list containing the names to be used for individuals and variables.
prop_expl_var	Proportion of the explained variance of derived components, after setting possible missing values to zero.
call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

Author(s)

Sébastien Déjean, Ignacio González, Francois Bartolo, Kim-Anh Lê Cao, Florian Rohart, Al J Abadi

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Sch"afer, J., and K. Strimmer. 2005. A shrinkage approach to large-scale covariance estimation and implications for functional genomics. Statist. emphAppl. Genet. Mol. Biol. **4**:32. (http://www.bepress.com/sagmb/vol4/iss1/art32/)

See Also

summary, tune.rcc, plot.rcc, plotIndiv, plotVar, cim, network and http://www.mixOmics.org for more details.

Examples

```
## Classic CCA
data(linnerud)
X <- linnerud$exercise
Y <- linnerud$physiological
linn.res <- rcc(X, Y)

## Not run:
## Regularized CCA
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
nutri.res1 <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)

## using shrinkage parameters
nutri.res2 <- rcc(X, Y, ncomp = 3, method = 'shrinkage')
nutri.res2$lambda # the shrinkage parameters

## End(Not run)
```

---

selectVar *Output of selected variables*

Description

This function outputs the selected variables on each component for the sparse versions of the approaches (was also generalised to the non sparse versions for our internal functions).

Usage

```
selectVar(...)

## S3 method for class 'mixo_pls'
selectVar(object, comp = 1, block = NULL, ...)

## S3 method for class 'mixo_spls'
```

```
selectVar(object, comp = 1, block = NULL, ...)

## S3 method for class 'pca'
selectVar(object, comp = 1, block = NULL, ...)

## S3 method for class 'sgcca'
selectVar(object, comp = 1, block = NULL, ...)

## S3 method for class 'rgcca'
selectVar(object, comp = 1, block = NULL, ...)
```

Arguments

...	other arguments.
object	object of class inherited from "pls", "spls", "plsda","splsda","sgcca", "rgcca", "pca", "spca", "sipca".
comp	integer value indicating the component of interest.
block	for an object of class "sgcca", the block data sets can be specified as an input vector, for example c(1,2) for the first two blocks. Default to NULL (all block data sets)

Details

selectVar provides the variables selected on a given component. \

list("name") outputs the name of the selected variables (provided that the input data have column names) ranked in decreasing order of importance.

list("value") outputs the loading value for each selected variable, the loadings are ranked according to their absolute value.

These functions are only implemented for the sparse versions.

Value

none

Author(s)

Kim-Anh Lê Cao, Florian Rohart, Al J Abadi

Examples

```
data(liver.toxicity)
X = liver.toxicity$gene
Y = liver.toxicity$clinic

# example with sPCA
# ------------------
liver.spca <- spca(X, ncomp = 1, keepX = 10)
selectVar(liver.spca, comp = 1)$name
selectVar(liver.spca, comp = 1)$value

## Not run:
#example with sIPCA
```

```
# -----------------

liver.sipca <- sipca(X, ncomp = 3, keepX = rep(10, 3))
selectVar(liver.sipca, comp = 1)

# example with sPLS
# -----------------

liver.spls = spls(X, Y, ncomp = 2, keepX = c(20, 40),keepY = c(5, 5))
selectVar(liver.spls, comp = 2)

# example with sPLS-DA
data(srbct)   # an example with no gene name in the data
X = srbct$gene
Y = srbct$class

srbct.splsda = splsda(X, Y, ncomp = 2, keepX = c(5, 10))
select = selectVar(srbct.splsda, comp = 2)
select
# this is a very specific case where a data set has no rownames.
srbct$gene.name[substr(select$select, 2,5),]


# example with sGCCA
# -----------------

data(nutrimouse)

# ! need to unmap the Y factor
Y = unmap(nutrimouse$diet)
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid,Y)
# in this design, gene expression and lipids are connected to the diet factor
# and gene expression and lipids are also connected
design = matrix(c(0,1,1,
1,0,1,
1,1,0), ncol = 3, nrow = 3, byrow = TRUE)
#note: the penalty parameters need to be tuned
wrap.result.sgcca = wrapper.sgcca(X = data, design = design, penalty = c(.3,.3, 1),
ncomp = 2)

#variables selected and loadings values on component 1 for the two blocs
selectVar(wrap.result.sgcca, comp = 1, block = c(1,2))

#variables selected on component 1 for each block
selectVar(wrap.result.sgcca, comp = 1, block = c(1,2))$'gene'$name
selectVar(wrap.result.sgcca, comp = 1, block = c(1,2))$'lipid'$name

#variables selected on component 2 for each block
selectVar(wrap.result.sgcca, comp = 2, block = c(1,2))$'gene'$name
selectVar(wrap.result.sgcca, comp = 2, block = c(1,2))$'lipid'$name

# loading value of the variables selected on the first block
selectVar(wrap.result.sgcca, comp = 1, block = 1)$'gene'$value

## End(Not run)
```

`sipca` *Independent Principal Component Analysis*

Description

Performs sparse independent principal component analysis on the given data matrix to enable variable selection.

Usage

```
sipca(
  X,
  ncomp = 3,
  mode = c("deflation", "parallel"),
  fun = c("logcosh", "exp"),
  scale = FALSE,
  max.iter = 200,
  tol = 1e-04,
  keepX = rep(50, ncomp),
  w.init = NULL
)
```

Arguments

`X`	a numeric matrix (or data frame).
`ncomp`	integer, number of independent component to choose. Set by default to 3.
`mode`	character string. What type of algorithm to use when estimating the unmixing matrix, choose one of `"deflation"`, `"parallel"`. Default set to `deflation`.
`fun`	the function used in approximation to neg-entropy in the FastICA algorithm. Default set to `logcosh`, see details of FastICA.
`scale`	(Default=FALSE) Logical indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is `FALSE` for consistency with `prcomp` function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of `X` can be supplied. The value is passed to `scale`.
`max.iter`	integer, the maximum number of iterations.
`tol`	a positive scalar giving the tolerance at which the un-mixing matrix is considered to have converged, see fastICA package.
`keepX`	the number of variable to keep on each dimensions.
`w.init`	initial un-mixing matrix (unlike fastICA, this matrix is fixed here).

Details

See Details of ipca.

Soft thresholding is implemented on the independent loading vectors to obtain sparse loading vectors and enable variable selection.

Value

pca returns a list with class "ipca" containing the following components:

ncomp	the number of principal components used.
unmixing	the unmixing matrix of size (ncomp x ncomp)
mixing	the mixing matrix of size (ncomp x ncomp
X	the centered data matrix
x	the principal components (with sparse independent loadings)
loadings	the sparse independent loading vectors
kurtosis	the kurtosis measure of the independent loading vectors
prop_expl_var	Proportion of the explained variance of derived components, after setting possible missing values to zero.

Author(s)

Fangzhou Yao, Jeff Coquery, Francois Bartolo, Kim-Anh Lê Cao, Al J Abadi

References

Yao, F., Coquery, J. and Lê Cao, K.-A. (2011) Principal component analysis with independent loadings: a combination of PCA and ICA. (in preparation)

A. Hyvarinen and E. Oja (2000) Independent Component Analysis: Algorithms and Applications, *Neural Networks*, **13(4-5)**:411-430

J L Marchini, C Heaton and B D Ripley (2010). fastICA: FastICA Algorithms to perform ICA and Projection Pursuit. R package version 1.1-13.

See Also

ipca, pca, plotIndiv, plotVar and http://www.mixOmics.org for more details.

Examples

```
data(liver.toxicity)

# implement IPCA on a microarray dataset
sipca.res <- sipca(liver.toxicity$gene, ncomp = 3, mode="deflation", keepX=c(50,50,50))
sipca.res

# samples representation
plotIndiv(sipca.res, ind.names = liver.toxicity$treatment[, 4],
group = as.numeric(as.factor(liver.toxicity$treatment[, 4])))

## Not run:
plotIndiv(sipca.res, cex = 0.01,
          col = as.numeric(as.factor(liver.toxicity$treatment[, 4])),
          style="3d")

# variables representation
plotVar(sipca.res, cex = 2.5)

plotVar(sipca.res, rad.in = 0.5, cex = .6, style="3d")

## End(Not run)
```

spca *Sparse Principal Components Analysis*

Description

Performs a sparse principal component analysis for variable selection using singular value decomposition and lasso penalisation on the loading vectors.

Usage

```
spca(
  X,
  ncomp = 2,
  center = TRUE,
  scale = TRUE,
  keepX = rep(ncol(X), ncomp),
  max.iter = 500,
  tol = 1e-06,
  logratio = c("none", "CLR"),
  multilevel = NULL,
  verbose.call = FALSE
)
```

Arguments

X	a numeric matrix (or data frame) which provides the data for the sparse principal components analysis. It should not contain missing values.
ncomp	Integer, if data is complete ncomp decides the number of components and associated eigenvalues to display from the pcasvd algorithm and if the data has missing values, ncomp gives the number of components to keep to perform the reconstitution of the data using the NIPALS algorithm. If NULL, function sets ncomp = min(nrow(X),ncol(X))
center	(Default=TRUE) Logical, whether the variables should be shifted to be zero centered. Only set to FALSE if data have already been centered. Alternatively, a vector of length equal the number of columns of X can be supplied. The value is passed to scale. If the data contain missing values, columns should be centered for reliable results.
scale	(Default=TRUE) Logical indicating whether the variables should be scaled to have unit variance before the analysis takes place.
keepX	numeric vector of length ncomp, the number of variables to keep in loading vectors. By default all variables are kept in the model. See details.
max.iter	Integer, the maximum number of iterations in the NIPALS algorithm.
tol	Positive real, the tolerance used in the NIPALS algorithm.
logratio	one of ('none','CLR'). Specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'
multilevel	sample information for multilevel decomposition for repeated measurements.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

scale= TRUE is highly recommended as it will help obtaining orthogonal sparse loading vectors.

keepX is the number of variables to select in each loading vector, i.e. the number of variables with non zero coefficient in each loading vector.

Note that data can contain missing values only when logratio = 'none' is used. In this case, center=TRUE should be used to center the data in order to effectively ignore the missing values. This is the default behaviour in spca.

According to Filzmoser et al., a ILR log ratio transformation is more appropriate for PCA with compositional data. Both CLR and ILR are valid.

Logratio transform and multilevel analysis are performed sequentially as internal pre-processing step, through logratio.transfo and withinVariation respectively.

Logratio can only be applied if the data do not contain any 0 value (for count data, we thus advise the normalise raw data with a 1 offset). For ILR transformation and additional offset might be needed.

The principal components are not guaranteed to be orthogonal in sPCA. We adopt the approach of Shen and Huang 2008 (Section 2.3) to estimate the explained variance in the case where the sparse loading vectors (and principal components) are not orthogonal. The data are projected onto the space spanned by the first loading vectors and the variance explained is then adjusted for potential correlation between PCs. Note that in practice, the loading vectors tend to be orthogonal if the data are centered and scaled in sPCA.

Value

spca returns a list with class "spca" containing the following components:

call if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

ncomp the number of components to keep in the calculation.

prop_expl_var the adjusted percentage of variance explained for each component.

cum.var the adjusted cumulative percentage of variances explained.

keepX the number of variables kept in each loading vector.

iter the number of iterations needed to reach convergence for each component.

rotation the matrix containing the sparse loading vectors.

x the matrix containing the principal components.

Author(s)

Kim-Anh Lê Cao, Fangzhou Yao, Leigh Coonan, Ignacio Gonzalez, Al J Abadi

References

Shen, H. and Huang, J. Z. (2008). Sparse principal component analysis via regularized low rank matrix approximation. *Journal of Multivariate Analysis* **99**, 1015-1034.

See Also

pca and http://www.mixOmics.org for more details.

Examples

```
data(liver.toxicity)
spca.rat <- spca(liver.toxicity$gene, ncomp = 3, keepX = rep(50, 3))
spca.rat

## variable representation
plotVar(spca.rat, cex = 1)
## Not run:
plotVar(spca.rat,style="3d")

## End(Not run)

## samples representation
plotIndiv(spca.rat, ind.names = liver.toxicity$treatment[, 3],
          group = as.numeric(liver.toxicity$treatment[, 3]))

## Not run:
plotIndiv(spca.rat, cex = 0.01,
col = as.numeric(liver.toxicity$treatment[, 3]),style="3d")

## End(Not run)

## example with multilevel decomposition and CLR log ratio transformation
data("diverse.16S")
spca.res = spca(X = diverse.16S$data.TSS, ncomp = 5,
logratio = 'CLR', multilevel = diverse.16S$sample)
plot(spca.res)
plotIndiv(spca.res, ind.names = FALSE, group = diverse.16S$bodysite, title = '16S diverse data',
legend=TRUE)
```

---

spls *Sparse Partial Least Squares (sPLS)*

Description

Function to perform sparse Partial Least Squares (sPLS). The sPLS approach combines both integration and variable selection simultaneously on two data sets in a one-step strategy.

Usage

```
spls(
  X,
  Y,
  ncomp = 2,
  mode = c("regression", "canonical", "invariant", "classic"),
  keepX,
  keepY,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  logratio = "none",
  multilevel = NULL,
```

```
  all.outputs = TRUE,
  verbose.call = FALSE
)
```

Arguments

X	numeric matrix of predictors with the rows as individual observations. missing values (NAs) are allowed.
Y	numeric matrix of response(s) with the rows as individual observations matching X. missing values (NAs) are allowed.
ncomp	Positive Integer. The number of components to include in the model. Default to 2.
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
keepX	numeric vector of length ncomp, the number of variables to keep in X-loadings. By default all variables are kept in the model.
keepY	numeric vector of length ncomp, the number of variables
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
logratio	Character, one of ('none','CLR') specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'. See ?logratio.transfo for details.
multilevel	Numeric, design matrix for repeated measurement analysis, where multilevel decomposition is required. For a one factor decomposition, the repeated measures on each individual, i.e. the individuals ID is input as the first column. For a 2 level factor decomposition then 2nd AND 3rd columns indicate those factors. See examples.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.
verbose.call	Logical (Default=FALSE), if set to TRUE then the $call component of the returned object will contain the variable values for all parameters. Note that this may cause large memory usage.

Details

spls function fit sPLS models with $1, \ldots,$ncomp components. Multi-response models are fully supported. The X and Y datasets can contain missing values.

Value

spls returns an object of class "spls", a list that contains the following components:

call	if verbose.call = FALSE, then just the function call is returned. If verbose.call = TRUE then all the inputted values are accessable via this component

X	the centered and standardized original predictor matrix.
Y	the centered and standardized original response vector or matrix.
ncomp	the number of components included in the model.
mode	the algorithm used to fit the model.
keepX	number of X variables kept in the model on each component.
keepY	number of Y variables kept in the model on each component.
variates	list containing the variates.
loadings	list containing the estimated loadings for the X and Y variates.
names	list containing the names to be used for individuals and variables.
tol	the tolerance used in the iterative algorithm, used for subsequent S3 methods
iter	Number of iterations of the algorithm for each component
max.iter	the maximum number of iterations, used for subsequent S3 methods
nzv	list containing the zero- or near-zero predictors information.
scale	whether scaling was applied per predictor.
logratio	whether log ratio transformation for relative proportion data was applied, and if so, which type of transformation.
prop_expl_var	Proportion of variance explained per component (note that contrary to PCA, this amount may not decrease as the aim of the method is not to maximise the variance, but the covariance between data sets).
input.X	numeric matrix of predictors in X that was input, before any saling / logratio / multilevel transformation.
mat.c	matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by `predict`.
defl.matrix	residual matrices X for each dimension.

missing values

The estimation of the missing values can be performed using the `impute.nipals` function. Otherwise, missing values are handled by element-wise deletion in the `pls` function without having to delete the rows with missing data.

multilevel

Multilevel (s)PLS enables the integration of data measured on two different data sets on the same individuals. This approach differs from multilevel sPLS-DA as the aim is to select subsets of variables from both data sets that are highly positively or negatively correlated across samples. The approach is unsupervised, i.e. no prior knowledge about the sample groups is included.

logratio and multilevel

logratio transform and multilevel analysis are performed sequentially as internal pre-processing step, through `logratio.transfo` and `withinVariation` respectively.

Author(s)

Sébastien Déjean, Ignacio González, Florian Rohart, Kim-Anh Lê Cao, Al J abadi

References

Sparse PLS: canonical and regression modes:

Lê Cao, K.-A., Martin, P.G.P., Robert-Granie, C. and Besse, P. (2009). Sparse canonical methods for biological data integration: application to a cross-platform study. *BMC Bioinformatics* **10**:34.

Lê Cao, K.-A., Rossouw, D., Robert-Granie, C. and Besse, P. (2008). A sparse PLS for variable selection when integrating Omics data. *Statistical Applications in Genetics and Molecular Biology* **7**, article 35.

Sparse SVD: Shen, H. and Huang, J. Z. (2008). Sparse principal component analysis via regularized low rank matrix approximation. *Journal of Multivariate Analysis* **99**, 1015-1034.

PLS methods: Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic. Chapters 9 and 11.

Abdi H (2010). Partial least squares regression and projection on latent structure regression (PLS Regression). *Wiley Interdisciplinary Reviews: Computational Statistics*, 2(1), 97-106.

Wold H. (1966). Estimation of principal components and related models by iterative least squares. In: Krishnaiah, P. R. (editors), *Multivariate Analysis*. Academic Press, N.Y., 391-420.

On multilevel analysis:

Liquet, B., Lê Cao, K.-A., Hocini, H. and Thiebaut, R. (2012) A novel approach for biomarker selection and the integration of repeated measures experiments from two platforms. *BMC Bioinformatics* **13**:325.

Westerhuis, J. A., van Velzen, E. J., Hoefsloot, H. C., and Smilde, A. K. (2010). Multivariate paired data analysis: multilevel PLSDA versus OPLSDA. *Metabolomics*, **6**(1), 119-128.

See Also

`pls`, `summary`, `plotIndiv`, `plotVar`, `cim`, `network`, `predict`, `perf` and http://www.mixOmics.org for more details.

Examples

```
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic

toxicity.spls <- spls(X, Y, ncomp = 2, keepX = c(50, 50),
keepY = c(10, 10))

toxicity.spls <- spls(X, Y[,1:2,drop=FALSE], ncomp = 5, keepX = c(50, 50))#, mode="canonical")

## Not run:

## Second example: one-factor multilevel analysis with sPLS, selecting a subset of variables
#-----------------------------------------------------------------

data(liver.toxicity)
# note: we made up those data, pretending they are repeated measurements
repeat.indiv <- c(1, 2, 1, 2, 1, 2, 1, 2, 3, 3, 4, 3, 4, 3, 4, 4, 5, 6, 5, 5,
6, 5, 6, 7, 7, 8, 6, 7, 8, 7, 8, 8, 9, 10, 9, 10, 11, 9, 9,
10, 11, 12, 12, 10, 11, 12, 11, 12, 13, 14, 13, 14, 13, 14,
13, 14, 15, 16, 15, 16, 15, 16, 15, 16)
summary(as.factor(repeat.indiv)) # 16 rats, 4 measurements each
```

```
# this is a spls (unsupervised analysis) so no need to mention any factor in design
# we only perform a one level variation split
design <- data.frame(sample = repeat.indiv)
res.spls.1level <- spls(X = liver.toxicity$gene,
Y=liver.toxicity$clinic,
multilevel = design,
ncomp = 3,
keepX = c(50, 50, 50), keepY = c(5, 5, 5),
mode = 'canonical')

# set up colors and pch for plotIndiv
col.stimu <- 1:nlevels(design$stimu)

plotIndiv(res.spls.1level, rep.space = 'X-variate', ind.names = FALSE,
group = liver.toxicity$treatment$Dose.Group,
pch = 20, main = 'Gene expression subspace',
legend = TRUE)


plotIndiv(res.spls.1level, rep.space = 'Y-variate', ind.names = FALSE,
group = liver.toxicity$treatment$Dose.Group,
pch = 20, main = 'Clinical measurements ssubpace',
legend = TRUE)

plotIndiv(res.spls.1level, rep.space = 'XY-variate', ind.names = FALSE,
group = liver.toxicity$treatment$Dose.Group,
pch = 20, main = 'Both Gene expression and Clinical subspaces',
legend = TRUE)

## Third example: two-factor multilevel analysis with sPLS, selecting a subset of variables
#-------------------------------------------------------------

data(liver.toxicity)
dose <- as.factor(liver.toxicity$treatment$Dose.Group)
time <- as.factor(liver.toxicity$treatment$Time.Group)
# note: we made up those data, pretending they are repeated measurements
repeat.indiv <- c(1, 2, 1, 2, 1, 2, 1, 2, 3, 3, 4, 3, 4, 3, 4, 4, 5, 6, 5, 5,
6, 5, 6, 7, 7, 8, 6, 7, 8, 7, 8, 8, 9, 10, 9, 10, 11, 9, 9,
10, 11, 12, 12, 10, 11, 12, 11, 12, 13, 14, 13, 14, 13, 14,
13, 14, 15, 16, 15, 16, 15, 16, 15, 16)
summary(as.factor(repeat.indiv)) # 16 rats, 4 measurements each
design <- data.frame(sample = repeat.indiv, dose = dose, time = time)

res.spls.2level = spls(liver.toxicity$gene,
Y = liver.toxicity$clinic,
multilevel = design,
ncomp=2,
keepX = c(10,10), keepY = c(5,5))

## End(Not run)
```

---

splsda *Sparse Partial Least Squares Discriminant Analysis (sPLS-DA)*

Description

Function to perform sparse Partial Least Squares to classify samples (supervised analysis) and select variables.

Usage

```
splsda(
  X,
  Y,
  ncomp = 2,
  keepX,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  logratio = "none",
  multilevel = NULL,
  all.outputs = TRUE
)
```

Arguments

X	numeric matrix of predictors with the rows as individual observations. missing values (NAs) are allowed.
Y	a factor or a class vector for the discrete outcome.
ncomp	Positive Integer. The number of components to include in the model. Default to 2.
keepX	numeric vector of length ncomp, the number of variables to keep in X-loadings. By default all variables are kept in the model.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
logratio	Character, one of ('none','CLR') specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'. See ?logratio.transfo for details.
multilevel	sample information for multilevel decomposition for repeated measurements. A numeric matrix or data frame indicating the repeated measures on each individual, i.e. the individuals ID. See examples in ?splsda.
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

splsda function fits an sPLS model with $1, \ldots,$ncomp components to the factor or class vector Y. The appropriate indicator (dummy) matrix is created.

Logratio transformation and multilevel analysis are performed sequentially as internal pre-processing step, through logratio.transfo and withinVariation respectively. Logratio can only be applied if the data do not contain any 0 value (for count data, we thus advise the normalise raw data with a 1 offset).

The type of deflation used is 'regression' for discriminant algorithms. i.e. no deflation is performed on Y.

Value

splsda returns an object of class "splsda", a list that contains the following components:

X	the centered and standardized original predictor matrix.
Y	the centered and standardized indicator response vector or matrix.
ind.mat	the indicator matrix.
ncomp	the number of components included in the model.
keepX	number of X variables kept in the model on each component.
variates	list containing the variates.
loadings	list containing the estimated loadings for the X and Y variates.
names	list containing the names to be used for individuals and variables.
nzv	list containing the zero- or near-zero predictors information.
tol	the tolerance used in the iterative algorithm, used for subsequent S3 methods
iter	Number of iterations of the algorithm for each component
max.iter	the maximum number of iterations, used for subsequent S3 methods
scale	Logical indicating whether the data were scaled in MINT S3 methods
logratio	whether logratio transformations were used for compositional data
prop_expl_var	Proportion of variance explained per component after setting possible missing values in the data to zero (note that contrary to PCA, this amount may not decrease as the aim of the method is not to maximise the variance, but the covariance between X and the dummy matrix Y).
mat.c	matrix of coefficients from the regression of X / residual matrices X on the X-variates, to be used internally by predict.
defl.matrix	residual matrices X for each dimension.

Author(s)

Florian Rohart, Ignacio González, Kim-Anh Lê Cao, Al J abadi

References

On sPLS-DA: Lê Cao, K.-A., Boitard, S. and Besse, P. (2011). Sparse PLS Discriminant Analysis: biologically relevant feature selection and graphical displays for multiclass problems. *BMC Bioinformatics* **12**:253. On log ratio transformations: Filzmoser, P., Hron, K., Reimann, C.: Principal component analysis for compositional data with outliers. Environmetrics 20(6), 621-632 (2009) Lê

Cao K.-A., Costello ME, Lakis VA, Bartolo, F,Chua XY, Brazeilles R, Rondeau P. MixMC: Multivariate insights into Microbial Communities. PLoS ONE, 11(8): e0160169 (2016). On multilevel decomposition: Westerhuis, J.A., van Velzen, E.J., Hoefsloot, H.C., Smilde, A.K.: Multivariate paired data analysis: multilevel plsda versus oplsda. Metabolomics 6(1), 119-128 (2010) Liquet, B., Lê Cao K.-A., Hocini, H., Thiebaut, R.: A novel approach for biomarker selection and the integration of repeated measures experiments from two assays. BMC bioinformatics 13(1), 325 (2012)

See Also

spls, summary, plotIndiv, plotVar, cim, network, predict, perf, mint.block.splsda, block.splsda and http://www.mixOmics.org for more details.

Examples

```
## First example
data(breast.tumors)
X <- breast.tumors$gene.exp
# Y will be transformed as a factor in the function,
# but we set it as a factor to set up the colors.
Y <- as.factor(breast.tumors$sample$treatment)

res <- splsda(X, Y, ncomp = 2, keepX = c(25, 25))


# individual names appear
plotIndiv(res, ind.names = Y, legend = TRUE, ellipse =TRUE)

## Not run:
## Second example: one-factor analysis with sPLS-DA, selecting a subset of variables
# as in the paper Liquet et al.
#-----------------------------------------------------------------
data(vac18)
X <- vac18$genes
Y <- vac18$stimulation
# sample indicates the repeated measurements
design <- data.frame(sample = vac18$sample)
Y = data.frame(stimul = vac18$stimulation)

# multilevel sPLS-DA model
res.1level <- splsda(X, Y = Y, ncomp = 3, multilevel = design,
keepX = c(30, 137, 123))

# set up colors for plotIndiv
col.stim <- c("darkblue", "purple", "green4","red3")
plotIndiv(res.1level, ind.names = Y, col = col.stim)

## Third example: two-factor analysis with sPLS-DA, selecting a subset of variables
# as in the paper Liquet et al.
#-----------------------------------------------------------------

data(vac18.simulated) # simulated data

X <- vac18.simulated$genes
design <- data.frame(sample = vac18.simulated$sample)
Y = data.frame( stimu = vac18.simulated$stimulation,
```

```
time = vac18.simulated$time)

res.2level <- splsda(X, Y = Y, ncomp = 2, multilevel = design,
keepX = c(200, 200))

plotIndiv(res.2level, group = Y$stimu, ind.names = vac18.simulated$time,
legend = TRUE, style = 'lattice')



## Fourth example: with more than two classes
# ------------------------------------------------

data(liver.toxicity)
X <- as.matrix(liver.toxicity$gene)
# Y will be transformed as a factor in the function,
# but we set it as a factor to set up the colors.
Y <- as.factor(liver.toxicity$treatment[, 4])

splsda.liver <- splsda(X, Y, ncomp = 2, keepX = c(20, 20))

# individual name is set to the treatment
plotIndiv(splsda.liver, ind.names = Y, ellipse = TRUE, legend = TRUE)


## Fifth example: 16S data with multilevel decomposion and log ratio transformation
# ------------------------------------------------

data(diverse.16S)
splsda.16S = splsda(
X = diverse.16S$data.TSS,  # TSS normalised data
Y =  diverse.16S$bodysite,
multilevel = diverse.16S$sample, # multilevel decomposition
ncomp = 2,
keepX =  c(10, 150),
logratio= 'CLR')  # CLR log ratio transformation


plotIndiv(splsda.16S, ind.names = FALSE, pch = 16, ellipse = TRUE, legend = TRUE)
#OTUs selected at the family level
diverse.16S$taxonomy[selectVar(splsda.16S, comp = 1)$name,'Family']

## End(Not run)
```

---

srbct *Small version of the small round blue cell tumors of childhood data*

Description

This data set from Khan *et al.*, (2001) gives the expression measure of 2308 genes measured on 63 samples.

Usage

```
data(srbct)
```

Format

A list containing the following components:

list("gene") data frame with 63 rows and 2308 columns. The expression measure of 2308 genes for the 63 subjects.

list("class") A class vector containing the class tumour of each case (4 classes in total).

list("gene.name") data frame with 2308 rows and 2 columns containing further information on the genes.

Value

none

Source

https://www.research.nhgri.nih.gov/projects/Microarray/Supplement/index.html

References

Khan et al. (2001). Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. *Nature Medicine* **7**, Number 6, June.

---

stemcells *Human Stem Cells Data*

Description

This data set contains the expression of a random subset of 400 genes in 125 samples from 4 independent studies and 3 cell types.

Usage

```
data(stemcells)
```

Format

A list containing the following components:

list("gene") data matrix with 125 rows and 400 columns. Each row represents an experimental sample, and each column a single gene.

list("celltype") a factor indicating the cell type of each sample.

list("study") a factor indicating the study from which the sample was extracted.

Details

This data set contains the expression of a random subset of 400 genes in 125 samples from 4 independent studies and 3 cell types. Those studies can be combined and analysed using the MINT procedure.

Value

none

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

`study_split` *divides a data matrix in a list of matrices defined by a factor*

Description

`study_split` divides a data matrix in a list of matrices defined by a `study` input.

Usage

```
study_split(data, study)
```

Arguments

`data`	numeric matrix of predictors
`study`	grouping factor indicating which samples are from the same study

Value

`study_split` simply returns a list of the same length as the number of levels of `study` that contains sub-matrices of `data`.

Author(s)

Florian Rohart, Al J Abadi

See Also

`mint.pls`, `mint.spls`, `mint.plsda`, `mint.splsda`.

Examples

```
data(stemcells)
data = stemcells$gene
exp = stemcells$study

data.list = study_split(data, exp)

names(data.list)
lapply(data.list, dim)
table(exp)
```

summary *Summary Methods for CCA and PLS objects*

Description

Produce summary methods for class "rcc", "pls" and "spls".

Usage

```
## S3 method for class 'mixo_pls'
summary(
  object,
  what = c("all", "communalities", "redundancy", "VIP"),
  digits = 4,
  keep.var = FALSE,
  ...
)

## S3 method for class 'mixo_spls'
summary(
  object,
  what = c("all", "communalities", "redundancy", "VIP"),
  digits = 4,
  keep.var = FALSE,
  ...
)

## S3 method for class 'rcc'
summary(
  object,
  what = c("all", "communalities", "redundancy"),
  cutoff = NULL,
  digits = 4,
  ...
)

## S3 method for class 'pca'
summary(object, ...)
```

Arguments

object	object of class inherited from "rcc", "pls" or "spls".
what	character string or vector. Should be a subset of c("all", "summarised", "communalities", "redundancy", "VIP"). "VIP" is only available for (s)PLS. See Details.
digits	integer, the number of significant digits to use when printing. Defaults to 4.
keep.var	Logical. If TRUE only the variables with loadings not zero (as selected by spls) are showed. Defaults to FALSE.
...	not used currently.
cutoff	real between 0 and 1. Variables with all correlations components below this cut-off in absolute value are not showed (see Details).

Details

The information in the rcc, pls or spls object is summarised, it includes: the dimensions of X and Y data, the number of variates considered, the canonical correlations (if object of class "rcc") and the (s)PLS algorithm used (if object of class "pls" or "spls") and the number of variables selected on each of the sPLS components (if x of class "spls").

"communalities" in what gives Communalities Analysis. "redundancy" display Redundancy Analysis. "VIP" gives the Variable Importance in the Projection (VIP) coefficients fit by pls or spls. If what is "all", all are given.

For class "rcc", when a value to cutoff is specified, the correlations between each variable and the equiangular vector between X- and Y-variates are computed. Variables with at least one correlation componente bigger than cutoff are showed. The defaults is cutoff=NULL all the variables are given.

Value

The function summary returns a list with components:

ncomp	the number of components in the model.
cor	the canonical correlations.
cutoff	the cutoff used.
keep.var	list containing the name of the variables selected.
mode	the algorithm used in pls or spls.
Cm	list containing the communalities.
Rd	list containing the redundancy.
VIP	matrix of VIP coefficients.
what	subset of c("all", "communalities", "redundancy", "VIP").
digits	the number of significant digits to use when printing.
method	method used: rcc, pls or spls.

Author(s)

Sébastien Déjean, Ignacio González, Kim-Anh Lê Cao, Al J Abadi

See Also

rcc, pls, spls, vip.

Examples

```
## summary for objects of class 'rcc'
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene
nutri.res <- rcc(X, Y, ncomp = 3, lambda1 = 0.064, lambda2 = 0.008)
more <- summary(nutri.res, cutoff = 0.65)

## Not run:
## summary for objects of class 'pls'
data(linnerud)
X <- linnerud$exercise
```

```
Y <- linnerud$physiological
linn.pls <- pls(X, Y)
more <- summary(linn.pls)

## summary for objects of class 'spls'
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic
toxicity.spls <- spls(X, Y, ncomp = 3, keepX = c(50, 50, 50),
keepY = c(10, 10, 10))
more <- summary(toxicity.spls, what = "redundancy", keep.var = TRUE)

## End(Not run)
```

---

tune *Wrapper function to tune pls-derived methods.*

Description

This function uses repeated cross-validation to tune hyperparameters such as the number of features to select and possibly the number of components to extract.

Usage

```
tune(
  method = c("pls", "spls", "plsda", "splsda", "block.plsda", "block.splsda",
    "mint.plsda", "mint.splsda", "rcc", "pca", "spca"),
  X,
  Y,
  test.keepX = c(5, 10, 15),
  test.keepY = NULL,
  already.tested.X,
  already.tested.Y,
  ncomp,
  V,
  center = TRUE,
  grid1 = seq(0.001, 1, length = 5),
  grid2 = seq(0.001, 1, length = 5),
  mode = c("regression", "canonical", "invariant", "classic"),
  indY,
  weighted = TRUE,
  design,
  study,
  tol = 1e-09,
  scale = TRUE,
  logratio = c("none", "CLR"),
  near.zero.var = FALSE,
  max.iter = 100,
  multilevel = NULL,
  validation = "Mfold",
  nrepeat = 1,
```

```
  folds = 10,
  signif.threshold = 0.01,
  dist = "max.dist",
  measure = ifelse(method == "spls", "cor", "BER"),
  auc = FALSE,
  seed = NULL,
  BPPARAM = SerialParam(),
  progressBar = FALSE,
  light.output = TRUE
)
```

Arguments

method	This parameter is used to pass all other argument to the suitable function. method has to be one of the following: "spls", "splsda", "block.splsda", "mint.splsda", "rcc", "pca", "spca" or "pls".
X	numeric matrix of predictors. NAs are allowed.
Y	Either a factor or a class vector for the discrete outcome, or a numeric vector or matrix of continuous responses (for multi-response models).
test.keepX	numeric vector for the different number of variables to test from the X data set
test.keepY	If method = 'spls', numeric vector for the different number of variables to test from the Y data set
already.tested.X	Optional, if ncomp > 1 A numeric vector indicating the number of variables to select from the X data set on the firsts components.
already.tested.Y	if method = 'spls' and if(ncomp > 1) numeric vector indicating the number of variables to select from the Y data set on the first components
ncomp	the number of components to include in the model.
V	Matrix used in the logratio transformation id provided (for tune.pca)
center	a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of X can be supplied. The value is passed to scale.
grid1, grid2	vector numeric defining the values of lambda1 and lambda2 at which cross-validation score should be computed. Defaults to grid1=grid2=seq(0.001, 1, length=5).
mode	character string. What type of algorithm to use, (partially) matching one of "regression", "canonical", "invariant" or "classic". See Details.
indY	To supply if Y is missing, indicates the position of the matrix response in the list X.
weighted	tune using either the performance of the Majority vote or the Weighted vote.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.

study	grouping factor indicating which samples are from the same study
tol	Numeric, convergence tolerance criteria.
scale	a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with prcomp function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of X can be supplied. The value is passed to scale.
logratio	one of ('none','CLR'). Default to 'none'
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Default value is FALSE
max.iter	Integer, the maximum number of iterations.
multilevel	Design matrix for multilevel analysis (for repeated measurements) that indicates the repeated measures on each individual, i.e. the individuals ID. See Details.
validation	character. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (see below). Default is "Mfold".
nrepeat	Number of times the Cross-Validation process is repeated.
folds	the folds in the Mfold cross-validation. See Details.
signif.threshold	numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.
dist	distance metric to estimate the classification error rate, should be a subset of "centroids.dist", "mahalanobis.dist" or "max.dist" (see Details).
measure	The tuning measure used for different methods. See details.
auc	if TRUE calculate the Area Under the Curve (AUC) performance of the model.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples.
progressBar	by default set to TRUE to output the progress bar of the computation.
light.output	if set to FALSE, the prediction/classification of each sample for each of test.keepX and each comp is returned.

Details

See the help file corresponding to the corresponding method, e.g. tune.splsda for further details. Note that only the arguments used in the tune function corresponding to method are passed on.

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017). More details about the PLS modes are in ?pls.

Value

Depending on the type of analysis performed and the input arguments, a list that may contain:

error.rate	returns the prediction error for each test.keepX on each component, averaged across all repeats and subsampling folds. Standard deviation is also output. All error rates are also available as a list.
choice.keepX	returns the number of variables selected (optimal keepX) on each component.

`choice.ncomp` For supervised models; returns the optimal number of components for the model for each prediction distance using one-sided t-tests that test for a significant difference in the mean error rate (gain in prediction) when components are added to the model. See more details in Rohart et al 2017 Suppl. For more than one block, an optimal ncomp is returned for each prediction framework.

`error.rate.class` returns the error rate for each level of `Y` and for each component computed with the optimal keepX

`predict` Prediction values for each sample, each `test.keepX`, each comp and each repeat. Only if light.output=FALSE

`class` Predicted class for each sample, each `test.keepX`, each comp and each repeat. Only if light.output=FALSE

`auc` AUC mean and standard deviation if the number of categories in `Y` is greater than 2, see details above. Only if auc = TRUE

`cor.value` only if multilevel analysis with 2 factors: correlation between latent variables.

Author(s)

Florian Rohart, Francois Bartolo, Kim-Anh Lê Cao, Al J Abadi

References

Singh A., Shannon C., Gautier B., Rohart F., Vacher M., Tebbutt S. and Lê Cao K.A. (2019), DIABLO: an integrative approach for identifying key molecular drivers from multi-omics assays, Bioinformatics, Volume 35, Issue 17, 1 September 2019, Pages 3055–3062.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

MINT:

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

PLS and PLS citeria for PLS regression: Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

Chavent, Marie and Patouille, Brigitte (2003). Calcul des coefficients de regression et du PRESS en regression PLS1. *Modulad n*, **30** 1-11. (this is the formula we use to calculate the Q2 in perf.pls and perf.spls)

Mevik, B.-H., Cederkvist, H. R. (2004). Mean Squared Error of Prediction (MSEP) Estimates for Principal Component Regression (PCR) and Partial Least Squares Regression (PLSR). *Journal of Chemometrics* **18**(9), 422-429.

sparse PLS regression mode:

Lê Cao, K. A., Rossouw D., Robert-Granie, C. and Besse, P. (2008). A sparse PLS for variable selection when integrating Omics data. *Statistical Applications in Genetics and Molecular Biology* **7**, article 35.

One-sided t-tests (suppl material):

Rohart F, Mason EA, Matigian N, Mosbergen R, Korn O, Chen T, Butcher S, Patel J, Atkinson K, Khosrotehrani K, Fisk NM, Lê Cao K-A&, Wells CA& (2016). A Molecular Classification of Human Mesenchymal Stromal Cells. PeerJ 4:e1845.

See Also

tune.rcc, tune.mint.splsda, tune.pca, tune.splsda, tune.splslevel and http://www.mixOmics.org for more details.

Examples

```
## sPLS-DA
data(breast.tumors)
X <- breast.tumors$gene.exp
Y <- as.factor(breast.tumors$sample$treatment)
tune= tune(method = "splsda", X, Y, ncomp=1, nrepeat=10, logratio="none",
test.keepX = c(5, 10, 15), folds=10, dist="max.dist", progressBar = TRUE)

plot(tune)

## Not run:
## mint.splsda

data(stemcells)
data = stemcells$gene
type.id = stemcells$celltype
exp = stemcells$study

out = tune(method="mint.splsda", X=data,Y=type.id, ncomp=2, study=exp, test.keepX=seq(1,10,1))
out$choice.keepX

plot(out)

## End(Not run)
```

---

tune.block.plsda *Tuning function for block.plsda method (N-integration with Discriminant Analysis)*

Description

Computes M-fold or Leave-One-Out Cross-Validation scores based on a user-input grid to determine the optimal parameters for method block.plsda.

Usage

```
tune.block.plsda(
  X,
  Y,
  indY,
  ncomp = 2,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  design,
  scale = TRUE,
  validation = "Mfold",
  folds = 10,
```

```
  nrepeat = 1,
  signif.threshold = 0.01,
  dist = "all",
  weighted = TRUE,
  progressBar = FALSE,
  light.output = TRUE,
  BPPARAM = SerialParam(),
  seed = NULL,
  ...
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in matrices, samples x variables, with samples order matching in all data sets.
Y	a factor or a class vector for the discrete outcome.
indY	To supply if Y is missing, indicates the position of the matrix response in the list X.
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
validation	character. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (see below). Default is "Mfold".
folds	the folds in the Mfold cross-validation. See Details.
nrepeat	Number of times the Cross-Validation process is repeated.
signif.threshold	numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.
dist	Distance metric. Should be a subset of "max.dist", "centroids.dist", "mahalanobis.dist" or "all". Default is "all"
weighted	tune using either the performance of the Majority vote or the Weighted vote.
progressBar	by default set to TRUE to output the progress bar of the computation.

light.output	if set to FALSE, the prediction/classification of each sample for each of test.keepX and each comp is returned.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.
...	Optional arguments: • **seed** Integer. Seed number for reproducible parallel code. Default is NULL. run in parallel when repeating the cross-validation, which is usually the most computationally intensive process. If there is excess CPU, the cross-vaidation is also parallelised on *nix-based OS which support mclapply. Note that the argument 'scheme' has now been hardcoded to 'horst' and 'init' to 'svd.single'.

Details

This tuning function should be used to tune the number of components in the block.plsda function (N-integration with Discriminant Analysis).

M-fold or LOO cross-validation is performed with stratified subsampling where all classes are represented in each fold.

If validation = "Mfold", M-fold cross-validation is performed. The number of folds to generate is to be specified in the argument folds.

If validation = "loo", leave-one-out cross-validation is performed. By default folds is set to the number of unique individuals.

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017). Details about the PLS modes are in ?pls.

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

Value

returns:

error.rate	Prediction error rate for each block of object$X and each dist
error.rate.per.class	Prediction error rate for each block of object$X, each dist and each class
predict	Predicted values of each sample for each class, each block and each component
class	Predicted class of each sample for each block, each dist, each component and each nrepeat
features	a list of features selected across the folds ($stable.X and $stable.Y) for the keepX and keepY parameters from the input object.
AveragedPredict.class	if more than one block, returns the average predicted class over the blocks (averaged of the Predict output and prediction using the max.dist distance)
AveragedPredict.error.rate	if more than one block, returns the average predicted error rate over the blocks (using the AveragedPredict.class output)

`WeightedPredict.class`
: if more than one block, returns the weighted predicted class over the blocks (weighted average of the `Predict` output and prediction using the `max.dist` distance). See details for more info on weights.

`WeightedPredict.error.rate`
: if more than one block, returns the weighted average predicted error rate over the blocks (using the `WeightedPredict.class` output.)

`MajorityVote`
: if more than one block, returns the majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`MajorityVote.error.rate`
: if more than one block, returns the error rate of the `MajorityVote` output

`WeightedVote`
: if more than one block, returns the weighted majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`WeightedVote.error.rate`
: if more than one block, returns the error rate of the `WeightedVote` output

`weights`
: Returns the weights of each block used for the weighted predictions, for each nrepeat and each fold

`choice.ncomp`
: For supervised models; returns the optimal number of components for the model for each prediction distance using one-sided t-tests that test for a significant difference in the mean error rate (gain in prediction) when components are added to the model. See more details in Rohart et al 2017 Suppl. For more than one block, an optimal ncomp is returned for each prediction framework.

Author(s)

Florian Rohart, Amrit Singh, Kim-Anh Lê Cao, AL J Abadi

References

Method:

Singh A., Gautier B., Shannon C., Vacher M., Rohart F., Tebbutt S. and Lê Cao K.A. (2016). DIABLO: multi omics integration for biomarker discovery.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

`block.splsda` and http://www.mixOmics.org for more details.

Examples

```
data("breast.TCGA")

# X data - list of mRNA and miRNA
X <- list(mrna = breast.TCGA$data.train$mrna, mirna = breast.TCGA$data.train$mirna,
          protein = breast.TCGA$data.train$protein)

# Y data - single data set of proteins
```

```
Y <- breast.TCGA$data.train$subtype

# subset the X and Y data to speed up computation in this example
set.seed(100)
subset <- mixOmics:::stratified.subsampling(breast.TCGA$data.train$subtype, folds = 3)[[1]][[1]]
X <- lapply(X, function(omic) omic[subset,])
Y <- Y[subset]

# set up a full design where every block is connected
# could also consider other weights, see our mixOmics manuscript
design = matrix(1, ncol = length(X), nrow = length(X),
                dimnames = list(names(X), names(X)))
diag(design) =  0
design

## Tune number of components to keep - use all distance metrics
tune_res <- tune.block.plsda(X, Y, design = design,
                             ncomp = 5,
                             nrepeat = 3,
                             seed = 13,
                             dist = c("all"))

plot(tune_res)
tune_res$choice.ncomp # 3 components best for max.dist, 1 for centroids.dist


## Tune number of components to keep - use weighted vote rather than majority vote
tune_res <- tune.block.plsda(X, Y, design = design,
                             ncomp = 5,
                             nrepeat = 3,
                             seed = 13,
                             dist = c("all"),
                             weighted = FALSE)
tune_res$weights

## Tune number of components to keep - plot just max.dist
tune_res <- tune.block.plsda(X, Y, design = design,
                             ncomp = 5,
                             nrepeat = 3,
                             seed = 13,
                             dist = c("max.dist"))
plot(tune_res)
```

`tune.block.splsda` *Tuning function for block.splsda method (N-integration with sparse Discriminant Analysis)*

Description

Computes M-fold or Leave-One-Out Cross-Validation scores based on a user-input grid to determine the optimal parameters for method `block.splsda`.

Usage

```
tune.block.splsda(
  X,
  Y,
  indY,
  ncomp = 2,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  design,
  scale = TRUE,
  test.keepX,
  already.tested.X,
  validation = "Mfold",
  folds = 10,
  nrepeat = 1,
  signif.threshold = 0.01,
  dist = "max.dist",
  measure = "BER",
  weighted = TRUE,
  progressBar = FALSE,
  light.output = TRUE,
  BPPARAM = SerialParam(),
  seed = NULL
)
```

Arguments

X	A named list of data sets (called 'blocks') measured on the same samples. Data in the list should be arranged in matrices, samples x variables, with samples order matching in all data sets.
Y	a factor or a class vector for the discrete outcome.
indY	To supply if Y is missing, indicates the position of the matrix response in the list X.
ncomp	the number of components to include in the model. Default to 2. Applies to all blocks.
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks; a value of 0 indicates no relationship, 1 is the maximum value. Alternatively, one of c('null', 'full') indicating a disconnected or fully connected design, respecively, or a numeric between 0 and 1 which will designate all off-diagonal elements of a fully connected design (see examples in block.splsda). If Y is provided instead of indY, the design matrix is changed to include relationships to Y.

scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
test.keepX	A named list with the same length and names as X (without the outcome Y, if it is provided in X and designated using indY). Each entry of this list is a numeric vector for the different keepX values to test for that specific block. If set to NULL, ncomp is tuned.
already.tested.X	Optional, if ncomp > 1 A named list of numeric vectors each of length n_tested indicating the number of variables to select from the X data set on the first n_tested components.
validation	character. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (see below). Default is "Mfold".
folds	the folds in the Mfold cross-validation. See Details.
nrepeat	Number of times the Cross-Validation process is repeated.
signif.threshold	numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.
dist	distance metric to estimate the classification error rate, should be one of "centroids.dist", "mahalanobis.dist" or "max.dist" (see Details). If test.keepX = NULL, can also input "all" or more than one distance metric
measure	only used when test.keepX is not NULL. Measure used when plotting, should be 'BER' or 'overall'
weighted	tune using either the performance of the Majority vote or the Weighted vote.
progressBar	by default set to TRUE to output the progress bar of the computation.
light.output	if set to FALSE, the prediction/classification of each sample for each of test.keepX and each comp is returned.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.

Details

This tuning function should be used to tune the number of components and the keepX parameters in the block.splsda function (N-integration with sparse Discriminant Analysis).

M-fold or LOO cross-validation is performed with stratified subsampling where all classes are represented in each fold.

If validation = "Mfold", M-fold cross-validation is performed. The number of folds to generate is to be specified in the argument folds.

If validation = "loo", leave-one-out cross-validation is performed. By default folds is set to the number of unique individuals.

All combination of test.keepX values are tested. A message informs how many will be fitted on each component for a given test.keepX.

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017). Details about the PLS modes are in ?pls.

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

Value

A list that contains:

`error.rate` returns the prediction error for each `test.keepX` on each component, averaged across all repeats and subsampling folds. Standard deviation is also output. All error rates are also available as a list.

`choice.keepX` returns the number of variables selected (optimal keepX) on each component, for each block.

`choice.ncomp` returns the optimal number of components for the model fitted with `$choice.keepX`.

`error.rate.class` returns the error rate for each level of `Y` and for each component computed with the optimal keepX

`predict` Prediction values for each sample, each `test.keepX`, each comp and each repeat. Only if light.output=FALSE

`class` Predicted class for each sample, each `test.keepX`, each comp and each repeat. Only if light.output=FALSE

`cor.value` compute the correlation between latent variables for two-factor sPLS-DA analysis.

If `test.keepX = NULL`, returns:

`error.rate` Prediction error rate for each block of `object$X` and each `dist`

`error.rate.per.class` Prediction error rate for each block of `object$X`, each `dist` and each class

`predict` Predicted values of each sample for each class, each block and each component

`class` Predicted class of each sample for each block, each `dist`, each component and each nrepeat

`features` a list of features selected across the folds (`$stable.X` and `$stable.Y`) for the `keepX` and `keepY` parameters from the input object.

`AveragedPredict.class` if more than one block, returns the average predicted class over the blocks (averaged of the `Predict` output and prediction using the `max.dist` distance)

`AveragedPredict.error.rate` if more than one block, returns the average predicted error rate over the blocks (using the `AveragedPredict.class` output)

`WeightedPredict.class` if more than one block, returns the weighted predicted class over the blocks (weighted average of the `Predict` output and prediction using the `max.dist` distance). See details for more info on weights.

`WeightedPredict.error.rate` if more than one block, returns the weighted average predicted error rate over the blocks (using the `WeightedPredict.class` output.)

`MajorityVote` if more than one block, returns the majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`MajorityVote.error.rate` if more than one block, returns the error rate of the `MajorityVote` output

`WeightedVote` if more than one block, returns the weighted majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.

`WeightedVote.error.rate` if more than one block, returns the error rate of the `WeightedVote` output

`weights` Returns the weights of each block used for the weighted predictions, for each nrepeat and each fold

`choice.ncomp` For supervised models; returns the optimal number of components for the model for each prediction distance using one-sided t-tests that test for a significant difference in the mean error rate (gain in prediction) when components are added to the model. See more details in Rohart et al 2017 Suppl. For more than one block, an optimal ncomp is returned for each prediction framework.

Author(s)

Florian Rohart, Amrit Singh, Kim-Anh Lê Cao, AL J Abadi

References

Method:

Singh A., Gautier B., Shannon C., Vacher M., Rohart F., Tebbutt S. and Lê Cao K.A. (2016). DIABLO: multi omics integration for biomarker discovery.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

`block.splsda` and http://www.mixOmics.org for more details.

Examples

```
## Set up data

# load data
data("breast.TCGA")

# X data - list of mRNA and miRNA
X <- list(mrna = breast.TCGA$data.train$mrna, mirna = breast.TCGA$data.train$mirna,
          protein = breast.TCGA$data.train$protein)

# Y data - single data set of proteins
Y <- breast.TCGA$data.train$subtype

# subset the X and Y data to speed up computation in this example
set.seed(100)
subset <- mixOmics:::stratified.subsampling(breast.TCGA$data.train$subtype, folds = 3)[[1]][[1]]
X <- lapply(X, function(omic) omic[subset,])
Y <- Y[subset]

# set up a full design where every block is connected
# could also consider other weights, see our mixOmics manuscript
design = matrix(1, ncol = length(X), nrow = length(X),
```

```
                dimnames = list(names(X), names(X)))
diag(design) =  0
design

## Tune number of components to keep
tune_res <- tune.block.splsda(X, Y, design = design,
                              ncomp = 5,
                              test.keepX = NULL,
                              validation = "Mfold", nrepeat = 3,
                              dist = "all", measure = "BER",
                              seed = 13)

plot(tune_res)

tune_res$choice.ncomp # 3 components best

## Tune number of variables to keep

# definition of the keepX value to be tested for each block mRNA miRNA and protein
# names of test.keepX must match the names of 'data'
test.keepX = list(mrna = c(10, 30), mirna = c(15, 25), protein = c(4, 8))

# load parallel package
library(BiocParallel)

# run tuning in parallel on 2 cores, output plot on overall error
tune_res <- tune.block.splsda(X, Y, design = design,
                              ncomp = 2,
                              test.keepX = test.keepX,
                              validation = "Mfold", nrepeat = 3,
                              measure = "overall",
                              seed = 13, BPPARAM = SnowParam(workers = 2))

plot(tune_res)
tune_res$choice.keepX

# Now tuning a new component given previous tuned keepX
already.tested.X <- tune_res$choice.keepX
tune_res <- tune.block.splsda(X, Y, design = design,
                              ncomp = 3,
                              test.keepX = test.keepX,
                              validation = "Mfold", nrepeat = 3,
                              measure = "overall",
                              seed = 13, BPPARAM = SnowParam(workers = 2),
                              already.tested.X = already.tested.X)
tune_res$choice.keepX
```

`tune.mint.plsda` *Estimate the parameters of mint.plsda method*

Description

Computes Leave-One-Group-Out-Cross-Validation (LOGOCV) scores on a user-input grid to determine optimal values for the parameters in `mint.plsda`.

Usage

```
tune.mint.plsda(
  X,
  Y,
  ncomp = 1,
  study,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  signif.threshold = 0.01,
  dist = c("max.dist", "centroids.dist", "mahalanobis.dist"),
  auc = FALSE,
  progressBar = FALSE,
  light.output = TRUE
)
```

Arguments

X	numeric matrix of predictors. NAs are allowed.
Y	Outcome. Numeric vector or matrix of responses (for multi-response models)
ncomp	Number of components to include in the model (see Details). Default to 1
study	grouping factor indicating which samples are from the same study
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Convergence stopping value.
max.iter	integer, the maximum number of iterations.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Default value is FALSE
signif.threshold	numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.
dist	only applies to an object inheriting from "plsda" or "splsda" to evaluate the classification performance of the model. Should be a subset of "max.dist", "centroids.dist", "mahalanobis.dist". Default is "all". See predict.
auc	if TRUE calculate the Area Under the Curve (AUC) performance of the model.
progressBar	by default set to TRUE to output the progress bar of the computation.
light.output	if set to FALSE, the prediction/classification of each sample for each of test.keepX and each comp is returned.

Details

This function performs a Leave-One-Group-Out-Cross-Validation (LOGOCV), where each of study is left out once.

The function outputs the optimal number of components that achieve the best performance based on the overall error rate or BER. The assessment is data-driven and similar to the process detailed in (Rohart et al., 2016), where one-sided t-tests assess whether there is a gain in performance when adding a component to the model. Our experience has shown that in most case, the optimal number

of components is the number of categories in Y - 1, but it is worth tuning a few extra components to check (see our website and case studies for more details).

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017).

Value

The returned value is a list with components:

study.specific.error	A list that gives BER, overall error rate and error rate per class, for each study
global.error	A list that gives BER, overall error rate and error rate per class for all samples
predict	A list of length ncomp that produces the predicted values of each sample for each class
class	A list which gives the predicted class of each sample for each dist and each of the ncomp components. Directly obtained from the predict output.
auc	AUC values
auc.study	AUC values for each study in mint models

.

Author(s)

Florian Rohart, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

mint.plsda and http://www.mixOmics.org for more details.

Examples

```
# set up data
data(stemcells)
data <- stemcells$gene
type.id <- stemcells$celltype
exp <- stemcells$study

# tune number of components
tune_res <- tune.mint.plsda(X = data,Y = type.id, ncomp=5,
                            near.zero.var=FALSE,
```

```
                              study=exp)

plot(tune_res)
tune_res$choice.ncomp # 1 component
```

`tune.mint.splsda` *Estimate the parameters of mint.splsda method*

Description

Computes Leave-One-Group-Out-Cross-Validation (LOGOCV) scores on a user-input grid to determine optimal values for the parameters in `mint.splsda`.

Usage

```
tune.mint.splsda(
  X,
  Y,
  ncomp = 1,
  study,
  test.keepX = NULL,
  already.tested.X,
  scale = TRUE,
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  signif.threshold = 0.01,
  dist = c("max.dist", "centroids.dist", "mahalanobis.dist"),
  measure = c("BER", "overall"),
  auc = FALSE,
  progressBar = FALSE,
  light.output = TRUE
)
```

Arguments

`X`	numeric matrix of predictors. `NA`s are allowed.
`Y`	Outcome. Numeric vector or matrix of responses (for multi-response models)
`ncomp`	Number of components to include in the model (see Details). Default to 1
`study`	grouping factor indicating which samples are from the same study
`test.keepX`	numeric vector for the different number of variables to test from the X data set. If set to NULL only number of components will be tuned.
`already.tested.X`	if `ncomp` > 1 Numeric vector indicating the number of variables to select from the X data set on the firsts components
`scale`	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
`tol`	Convergence stopping value.
`max.iter`	integer, the maximum number of iterations.

near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Default value is FALSE
signif.threshold	numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.
dist	only applies to an object inheriting from "plsda" or "splsda" to evaluate the classification performance of the model. Should be a subset of "max.dist", "centroids.dist", "mahalanobis.dist". Default is "all". See predict.
measure	Two misclassification measure are available: overall misclassification error overall or the Balanced Error Rate BER. Only used when test.keepX = NULL.
auc	if TRUE calculate the Area Under the Curve (AUC) performance of the model.
progressBar	by default set to TRUE to output the progress bar of the computation.
light.output	if set to FALSE, the prediction/classification of each sample for each of test.keepX and each comp is returned.

Details

This function performs a Leave-One-Group-Out-Cross-Validation (LOGOCV), where each of study is left out once.

When test.keepX is not NULL, all component 1 : ncomp are tuned to identify number of variables to keep, except the first ones for which a already.tested.X is provided. See examples below.

The function outputs the optimal number of components that achieve the best performance based on the overall error rate or BER. The assessment is data-driven and similar to the process detailed in (Rohart et al., 2016), where one-sided t-tests assess whether there is a gain in performance when adding a component to the model. Our experience has shown that in most case, the optimal number of components is the number of categories in Y - 1, but it is worth tuning a few extra components to check (see our website and case studies for more details).

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017).

Value

The returned value is a list with components:

error.rate	returns the prediction error for each test.keepX on each component, averaged across all repeats and subsampling folds. Standard deviation is also output. All error rates are also available as a list.
choice.keepX	returns the number of variables selected (optimal keepX) on each component.
choice.ncomp	returns the optimal number of components for the model fitted with $choice.keepX
error.rate.class	returns the error rate for each level of Y and for each component computed with the optimal keepX
predict	Prediction values for each sample, each test.keepX and each comp.
class	Predicted class for each sample, each test.keepX and each comp.

If test.keepX = NULL, returns:

study.specific.error	A list that gives BER, overall error rate and error rate per class, for each study
global.error	A list that gives BER, overall error rate and error rate per class for all samples
predict	A list of length ncomp that produces the predicted values of each sample for each class
class	A list which gives the predicted class of each sample for each dist and each of the ncomp components. Directly obtained from the predict output.
auc	AUC values
auc.study	AUC values for each study in mint models

.

Author(s)

Florian Rohart, Al J Abadi

References

Rohart F, Eslami A, Matigian, N, Bougeard S, Lê Cao K-A (2017). MINT: A multivariate integrative approach to identify a reproducible biomarker signature across multiple experiments and platforms. BMC Bioinformatics 18:128.

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

mint.splsda and http://www.mixOmics.org for more details.

Examples

```
# set up data
data(stemcells)
data <- stemcells$gene
type.id <- stemcells$celltype
exp <- stemcells$study

# tune number of components
tune_res <- tune.mint.splsda(X = data,Y = type.id, ncomp=5,
                             near.zero.var=FALSE,
                             study=exp,
                             test.keepX = NULL)

plot(tune_res)
tune_res$choice.ncomp # 1 component

## tune number of variables to keep
tune_res <- tune.mint.splsda(X = data,Y = type.id, ncomp = 1,
                             near.zero.var = FALSE,
                             study=exp,
                             test.keepX=seq(1,10,1))

plot(tune_res)
tune_res$choice.keepX # 9 variables to keep on component 1
```

```
## only tune component 3 and keeping 10 genes on comp1
tune_res <- tune.mint.splsda(X = data, Y = type.id, ncomp = 2, study = exp,
                             already.tested.X = c(9),
                             test.keepX = seq(1,10,1))
plot(tune_res)
tune_res$choice.keepX # 10 variables to keep on comp2
```

`tune.pca` *Tune the number of principal components in PCA*

Description

`tune.pca` can be used to quickly visualise the proportion of explained variance for a large number of principal components in PCA.

Usage

```
tune.pca(
  X,
  ncomp = NULL,
  center = TRUE,
  scale = TRUE,
  max.iter = 100,
  tol = 1e-09,
  logratio = c("none", "CLR", "ILR"),
  V = NULL,
  multilevel = NULL
)
```

Arguments

`X`	numeric matrix of predictors. `NA`s are allowed.
`ncomp`	integer, the number of components to initially analyse in `tune.pca` to choose a final `ncomp` for `pca`. If `NULL`, function sets `ncomp = min(nrow(X), ncol(X))`
`center`	a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of `X` can be supplied. The value is passed to `scale`.
`scale`	a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is `FALSE` for consistency with `prcomp` function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of `X` can be supplied. The value is passed to `scale`.
`max.iter`	Integer, the maximum number of iterations.
`tol`	Numeric, convergence tolerance criteria.
`logratio`	one of ('none','CLR','ILR'). Default to 'none'
`V`	Matrix used in the logratio transformation id provided.
`multilevel`	Design matrix for multilevel analysis (for repeated measurements).

Details

The calculation is done either by a singular value decomposition of the (possibly centered and scaled) data matrix, if the data is complete or by using the NIPALS algorithm if there is data missing. Unlike princomp, the print method for these objects prints the results in a nice format and the plot method produces a bar plot of the percentage of variance explaned by the principal components (PCs).

When using NIPALS (missing values), we make the assumption that the first (min(ncol(X), nrow(X)) principal components will account for 100 % of the explained variance.

Note that scale= TRUE cannot be used if there are zero or constant (for center = TRUE) variables.

Components are omitted if their standard deviations are less than or equal to comp.tol times the standard deviation of the first component. With the default null setting, no components are omitted. Other settings for comp.tol could be comp.tol = sqrt(.Machine$double.eps), which would omit essentially constant components, or comp.tol = 0.

logratio transform and multilevel analysis are performed sequentially as internal pre-processing step, through logratio.transfo and withinVariation respectively.

Value

tune.pca returns a list with class "tune.pca" containing the following components:

sdev	the square root of the eigenvalues of the covariance/correlation matrix, though the calculation is actually done with the singular values of the data matrix).
prop_expl_var	The proportion of explained variance accounted for by each principal component.
cum.var	the cumulative proportion of explained variance accounted for by the sequential accumulation of principal components is calculated using the sum of the proportion of explained variance

Author(s)

Ignacio González, Leigh Coonan, Kim-Anh Le Cao, Fangzhou Yao, Florian Rohart, Al J Abadi

See Also

nipals, biplot, plotIndiv, plotVar and http://www.mixOmics.org for more details.

Examples

```
# load data
data(liver.toxicity)

# run tuning
tune <- tune.pca(liver.toxicity$gene, center = TRUE, scale = TRUE)
plot(tune)

# set up multilevel dataset
repeat.indiv <- c(1, 2, 1, 2, 1, 2, 1, 2, 3, 3, 4, 3, 4, 3, 4, 4, 5, 6, 5, 5,
                  6, 5, 6, 7, 7, 8, 6, 7, 8, 7, 8, 8, 9, 10, 9, 10, 11, 9, 9,
                  10, 11, 12, 12, 10, 11, 12, 11, 12, 13, 14, 13, 14, 13, 14,
                  13, 14, 15, 16, 15, 16, 15, 16, 15, 16)
design <- data.frame(sample = repeat.indiv)
```

```
# run tuning
tune <- tune.pca(liver.toxicity$gene, center = TRUE, scale = TRUE, multilevel = design)
plot(tune)
```

`tune.pls` *Tuning functions for PLS method*

Description

Computes M-fold or Leave-One-Out Cross-Validation scores on a user-input grid to determine optimal values for the parameters in `spls`.

Usage

```
tune.pls(
  X,
  Y,
  ncomp,
  validation = c("Mfold", "loo"),
  nrepeat = 1,
  folds,
  measure = NULL,
  mode = c("regression", "canonical", "classic"),
  scale = TRUE,
  logratio = "none",
  tol = 1e-06,
  max.iter = 100,
  near.zero.var = FALSE,
  multilevel = NULL,
  BPPARAM = SerialParam(),
  seed = NULL,
  progressBar = FALSE,
  ...
)
```

Arguments

`X`	numeric matrix of predictors with the rows as individual observations.
`Y`	numeric matrix of response(s) with the rows as individual observations matching `X`.
`ncomp`	Positive Integer. The number of components to include in the model. Default to 2.
`validation`	character. What kind of (internal) validation to use, matching one of `"Mfold"` or `"loo"` (Leave-One-out). Default is `"Mfold"`.
`nrepeat`	Positive integer. Number of times the Cross-Validation process should be repeated. `nrepeat` > 2 is required for robust tuning. See details.
`folds`	Positive Integer, The folds in the Mfold cross-validation.
`measure`	The tuning measure to use. Cannot be NULL when applied to sPLS1 object. See details.

mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE
logratio	Character, one of ('none','CLR') specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'. See ?logratio.transfo for details.
tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
multilevel	Numeric, design matrix for repeated measurement analysis, where multilevel decomposition is required. For a one factor decomposition, the repeated measures on each individual, i.e. the individuals ID is input as the first column. For a 2 level factor decomposition then 2nd AND 3rd columns indicate those factors. See examples.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples in ?tune.spca.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.
progressBar	Logical. If TRUE a progress bar is shown as the computation completes. Default to FALSE.
...	Optional parameters passed to pls

Details

This tuning function should be used to tune the number of components to select for spls models.

Value

Returns a list with the following components for every repeat:

MSEP	Mean Square Error Prediction for each Y variable, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
RMSEP	Root Mean Square Error Prediction for each Y variable, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
R2	a matrix of R^2 values of the Y-variables for models with $1, \ldots,$ncomp components, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
Q2	if Y contains one variable, a vector of Q^2 values else a list with a matrix of Q^2 values for each Y-variable. Note that in the specific case of an sPLS model, it is better to have a look at the Q2.total criterion, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
Q2.total	a vector of Q^2-total values for models with $1, \ldots,$ncomp components, only applies to object inherited from "pls", and "spls". Available in both (s)PLS modes.

RSS	Residual Sum of Squares across all selected features and the components.
PRESS	Predicted Residual Error Sum of Squares across all selected features and the components.
features	a list of features selected across the folds ($stable.X and $stable.Y) for the keepX and keepY parameters from the input object. Note, this will be NULL if using standard (non-sparse) PLS.
cor.tpred, cor.upred	Correlation between the predicted and actual components for X (t) and Y (u)
RSS.tpred, RSS.upred	Residual Sum of Squares between the predicted and actual components for X (t) and Y (u)

folds

During a cross-validation (CV), data are randomly split into M subgroups (folds). M-1 subgroups are then used to train submodels which would be used to predict prediction accuracy statistics for the held-out (test) data. All subgroups are used as the test data exactly once. If validation = "loo", leave-one-out CV is used where each group consists of exactly one sample and hence M == N where N is the number of samples.

nrepeat

The cross-validation process is repeated nrepeat times and the accuracy measures are averaged across repeats. If validation = "loo", the process does not need to be repeated as there is only one way to split N samples into N groups and hence nrepeat is forced to be 1.

measure

- **For PLS2** Two measures of accuracy are available: Correlation (cor, used as default), as well as the Residual Sum of Squares (RSS). For cor, the parameters which would maximise the correlation between the predicted and the actual components are chosen. The RSS measure tries to predict the held-out data by matrix reconstruction and seeks to minimise the error between actual and predicted values. For mode='canonical', The X matrix is used to calculate the RSS, while for others modes the Y matrix is used. This measure gives more weight to any large errors and is thus sensitive to outliers. It also intrinsically selects less number of features on the Y block compared to measure='cor'.
- **For PLS1** Four measures of accuracy are available: Mean Absolute Error (MAE), Mean Square Error (MSE, used as default), Bias and R2. Both MAE and MSE average the model prediction error. MAE measures the average magnitude of the errors without considering their direction. It is the average over the fold test samples of the absolute differences between the Y predictions and the actual Y observations. The MSE also measures the average magnitude of the error. Since the errors are squared before they are averaged, the MSE tends to give a relatively high weight to large errors. The Bias is the average of the differences between the Y predictions and the actual Y observations and the R2 is the correlation between the predictions and the observations.

Optimisation Process

The optimisation process is data-driven and similar to the process detailed in (Rohart et al., 2016), where one-sided t-tests assess whether there is a gain in performance when incrementing the number of features or components in the model. However, it will assess all the provided grid through pairwise comparisons as the performance criteria do not always change linearly with respect to the added number of features or components.

more

See also `?perf` for more details.

Author(s)

Kim-Anh Lê Cao, Al J Abadi, Benoit Gautier, Francois Bartolo and Florian Rohart.

References

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

PLS and PLS citeria for PLS regression: Tenenhaus, M. (1998). La regression PLS: theorie et pratique. Paris: Editions Technic.

Chavent, Marie and Patouille, Brigitte (2003). Calcul des coefficients de regression et du PRESS en regression PLS1. Modulad n, 30 1-11. (this is the formula we use to calculate the Q2 in perf.pls and perf.spls)

Mevik, B.-H., Cederkvist, H. R. (2004). Mean Squared Error of Prediction (MSEP) Estimates for Principal Component Regression (PCR) and Partial Least Squares Regression (PLSR). Journal of Chemometrics 18(9), 422-429.

Sparse PLS regression mode:

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One-sided t-tests (suppl material):

Rohart F, Mason EA, Matigian N, Mosbergen R, Korn O, Chen T, Butcher S, Patel J, Atkinson K, Khosrotehrani K, Fisk NM, Lê Cao K-A&, Wells CA& (2016). A Molecular Classification of Human Mesenchymal Stromal Cells. PeerJ 4:e1845.

See Also

`splsda`, `predict.splsda`, and http://www.mixOmics.org for more details.

Examples

```
# set up data
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic

# tune PLS2 model to find optimal number of components
tune.res <- tune.pls(X, Y, ncomp = 10, measure = "cor",
                    folds = 5, nrepeat = 3, progressBar = TRUE)
plot(tune.res) # plot outputs

# PLS1 model example
Y1 <- liver.toxicity$clinic[,1]

tune.res <- tune.pls(X, Y1, ncomp = 10, measure = "cor",
                    folds = 5, nrepeat = 3, progressBar = TRUE)

plot(tune.res)
```

```
# Multilevel PLS2 model
repeat.indiv <- c(1, 2, 1, 2, 1, 2, 1, 2, 3, 3, 4, 3, 4, 3, 4, 4, 5, 6, 5, 5,
                  6, 5, 6, 7, 7, 8, 6, 7, 8, 7, 8, 8, 9, 10, 9, 10, 11, 9, 9,
                  10, 11, 12, 12, 10, 11, 12, 11, 12, 13, 14, 13, 14, 13, 14,
                  13, 14, 15, 16, 15, 16, 15, 16, 15, 16)
design <- data.frame(sample = repeat.indiv)

tune.res <- tune.pls(X, Y1, ncomp = 10, measure = "cor", multilevel = design,
                     folds = 5, nrepeat = 3, progressBar = TRUE)

plot(tune.res)
```

`tune.plsda` *Tuning functions for PLS-DA method*

Description

Computes M-fold or Leave-One-Out Cross-Validation scores on a user-input grid to determine optimal values for the parameters in `plsda`.

Usage

```
tune.plsda(
  X,
  Y,
  ncomp = 1,
  scale = TRUE,
  logratio = c("none", "CLR"),
  max.iter = 100,
  tol = 1e-06,
  near.zero.var = FALSE,
  multilevel = NULL,
  validation = "Mfold",
  folds = 10,
  nrepeat = 1,
  signif.threshold = 0.01,
  dist = "all",
  auc = FALSE,
  progressBar = FALSE,
  light.output = TRUE,
  BPPARAM = SerialParam(),
  seed = NULL
)
```

Arguments

`X`	numeric matrix of predictors. `NA`s are allowed.
`Y`	`if(method = 'spls')` numeric vector or matrix of continuous responses (for multi-response models) `NA`s are allowed.
`ncomp`	the number of components to include in the model.

scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
logratio	one of ('none','CLR'). Default to 'none'
max.iter	integer, the maximum number of iterations.
tol	Convergence stopping value.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Default value is FALSE
multilevel	Design matrix for multilevel analysis (for repeated measurements) that indicates the repeated measures on each individual, i.e. the individuals ID. See Details.
validation	character. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (short for 'leave-one-out'). Default is "Mfold".
folds	the folds in the Mfold cross-validation. See Details.
nrepeat	Number of times the Cross-Validation process is repeated.
signif.threshold	numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.
dist	distance metric to use for splsda to estimate the classification error rate, should be a subset of "centroids.dist", "mahalanobis.dist" or "max.dist" (see Details).
auc	if TRUE calculate the Area Under the Curve (AUC)
progressBar	by default set to TRUE to output the progress bar of the computation.
light.output	if set to FALSE, the prediction/classification of each sample for each of test.keepX and each comp is returned.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples in ?tune.spca.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.

Details

This tuning function should be used to tune the parameters in the plsda function (number of components and distance metric to select).

For a PLS-DA, M-fold or LOO cross-validation is performed with stratified subsampling where all classes are represented in each fold.

If validation = "loo", leave-one-out cross-validation is performed. By default folds is set to the number of unique individuals.

The function outputs the optimal number of components that achieve the best performance based on the overall error rate or BER. The assessment is data-driven and similar to the process detailed in (Rohart et al., 2016), where one-sided t-tests assess whether there is a gain in performance when adding a component to the model. Our experience has shown that in most case, the optimal number of components is the number of categories in Y - 1, but it is worth tuning a few extra components to check (see our website and case studies for more details).

For PLS-DA multilevel one-factor analysis, M-fold or LOO cross-validation is performed where all repeated measurements of one sample are in the same fold. Note that logratio transform and the multilevel analysis are performed internally and independently on the training and test set.

For a PLS-DA multilevel two-factor analysis, the correlation between components from the within-subject variation of X and the cond matrix is computed on the whole data set. The reason why we cannot obtain a cross-validation error rate as for the pls-DA one-factor analysis is because of the difficulty to decompose and predict the within matrices within each fold.

For a PLS two-factor analysis a PLS canonical mode is run, and the correlation between components from the within-subject variation of X and Y is computed on the whole data set.

If validation = "Mfold", M-fold cross-validation is performed. How many folds to generate is selected by specifying the number of folds in folds.

If auc = TRUE and there are more than 2 categories in Y, the Area Under the Curve is averaged using one-vs-all comparison. Note however that the AUC criteria may not be particularly insightful as the prediction threshold we use in PLS-DA differs from an AUC threshold (PLS-DA relies on prediction distances for predictions, see ?predict.plsda for more details) and the supplemental material of the mixOmics article (Rohart et al. 2017).

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

More details about the prediction distances in ?predict and the supplemental material of the mixOmics article (Rohart et al. 2017).

The tune.plsda() function calls older function perf() to perform this cross-validation, for more details see the perf() help pages.

Value

matrix of classification error rate estimation. The dimensions correspond to the components in the model and to the prediction method used, respectively.

auc	Averaged AUC values over the nrepeat
cor.value	only if multilevel analysis with 2 factors: correlation between latent variables.

Author(s)

Kim-Anh Lê Cao, Benoit Gautier, Francois Bartolo, Florian Rohart, Al J Abadi

References

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

splsda, predict.splsda and http://www.mixOmics.org for more details.

Examples

```
## Example: analysis with PLS-DA
data(breast.tumors)

# tune components and distance
tune = tune.plsda(breast.tumors$gene.exp, as.factor(breast.tumors$sample$treatment),
                  ncomp = 5, logratio = "none",
                  nrepeat = 10, folds = 10,
```

```
                  progressBar = TRUE,
                  seed = 20) # set for reproducibility of example only
plot(tune) # optimal distance = centroids.dist
tune$choice.ncomp # optimal component number = 3

## Example: multilevel PLS-DA
data(vac18)
design <- data.frame(sample = vac18$sample) # set the multilevel design

tune1 <- tune.plsda(vac18$genes, vac18$stimulation,
                    ncomp = 5, multilevel = design,
                   nrepeat = 10, folds = 10,
                   seed = 20)
plot(tune1)
```

`tune.rcc` *Estimate the parameters of regularization for Regularized CCA*

Description

Computes leave-one-out or M-fold cross-validation scores on a two-dimensional grid to determine optimal values for the parameters of regularization in `rcc`.

Usage

```
tune.rcc(
  X,
  Y,
  grid1 = seq(0.001, 1, length = 5),
  grid2 = seq(0.001, 1, length = 5),
  validation = c("loo", "Mfold"),
  folds = 10,
  BPPARAM = SerialParam(),
  seed = NULL
)
```

Arguments

`X`	numeric matrix or data frame $(n \times p)$, the observations on the X variables. `NA`s are allowed.
`Y`	numeric matrix or data frame $(n \times q)$, the observations on the Y variables. `NA`s are allowed.
`grid1, grid2`	vector numeric defining the values of `lambda1` and `lambda2` at which cross-validation score should be computed. Defaults to `grid1=grid2=seq(0.001, 1, length=5)`.
`validation`	character string. What kind of (internal) cross-validation method to use, (partially) matching one of `"loo"` (leave-one-out) or `"Mfolds"` (M-folds). See Details.
`folds`	positive integer. Number of folds to use if `validation="Mfold"`. Defaults to `folds=10`.

BPPARAM	a BiocParallel parameter object; see BiocParallel::bpparam for details. Default is MulticoreParam() for parallel processing.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.

Details

If validation="Mfolds", M-fold cross-validation is performed by calling Mfold. When folds is given, the elements of folds should be integer vectors specifying the indices of the validation sample and the argument M is ignored. Otherwise, the folds are generated. The number of cross-validation folds is specified with the argument M.

If validation="loo", leave-one-out cross-validation is performed by calling the loo function. In this case the arguments folds and M are ignored.

The estimation of the missing values can be performed by the reconstitution of the data matrix using the nipals function. Otherwise, missing values are handled by casewise deletion in the rcc function.

Value

The returned value is a list with components:

opt.lambda1	
opt.lambda2	value of the parameters of regularization on which the cross-validation method reached its optimal.
opt.score	the optimal cross-validation score reached on the grid.
grid1, grid2	original vectors grid1 and grid2.
mat	matrix containing the cross-validation score computed on the grid.

Author(s)

Sébastien Déjean, Ignacio González, Kim-Anh Lê Cao, Al J Abadi

See Also

image.tune.rcc and http://www.mixOmics.org for more details.

Examples

```
#load data
data(nutrimouse)
X <- nutrimouse$lipid
Y <- nutrimouse$gene

# run tuning
tune_res <- tune.rcc(X, Y, validation = "Mfold")

# plot output
plot(tune_res)
```

tune.spca *Tune number of selected variables for spca*

Description

This function performs sparse pca and optimises the number of variables to keep on each component using repeated cross-validation.

Usage

```
tune.spca(
  X,
  ncomp = 2,
  nrepeat = 1,
  folds,
  test.keepX,
  center = TRUE,
  scale = TRUE,
  BPPARAM = SerialParam(),
  seed = NULL
)
```

Arguments

X	a numeric matrix (or data frame) which provides the data for the sparse principal components analysis. It should not contain missing values.
ncomp	Integer, if data is complete ncomp decides the number of components and associated eigenvalues to display from the pcasvd algorithm and if the data has missing values, ncomp gives the number of components to keep to perform the reconstitution of the data using the NIPALS algorithm. If NULL, function sets ncomp = min(nrow(X),ncol(X))
nrepeat	Number of times the Cross-Validation process is repeated.
folds	Number of folds in 'Mfold' cross-validation. See details.
test.keepX	numeric vector for the different number of variables to test from the X data set.
center	(Default=TRUE) Logical, whether the variables should be shifted to be zero centered. Only set to FALSE if data have already been centered. Alternatively, a vector of length equal the number of columns of X can be supplied. The value is passed to scale. If the data contain missing values, columns should be centered for reliable results.
scale	(Default=TRUE) Logical indicating whether the variables should be scaled to have unit variance before the analysis takes place.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.

Details

Essentially, for the first component, and for a grid of the number of variables to select (`keepX`), a number of repeats and folds, data are split to train and test and the extracted components are compared against those from a spca model with all the data to ascertain the optimal `keepX`. In order to keep at least 3 samples in each test set for reliable scaling of the test data for comparison, `folds` must be <= `floor(nrow(X)/3)`

The number of selected variables for the following components will then be sequentially optimised. If the number of observations are small (e.g. < 30), it is recommended to use Leave-One-Out Cross-Validation which can be achieved by setting `folds = nrow(X)`.

Value

A `tune.spca` object containing:

call The function call

choice.keepX The selected number of components on each component

cor.comp The correlations between the components from the cross-validated studies and those from the study which used all of the data in training.

Examples

```
data("nutrimouse")
nrepeat <- 5
tune.spca.res <- tune.spca(
    X = nutrimouse$lipid,
    ncomp = 2,
    nrepeat = nrepeat,
    folds = 3,
    test.keepX = seq(5, 15, 5),
    seed = 42
)
tune.spca.res
plot(tune.spca.res)
## Not run:
## parallel processing using BiocParallel on repeats with more workers (cpus)
# Check if the environment variable exists (during R CMD check) and limit cores accordingly
max_cores <- if (Sys.getenv("_R_CHECK_LIMIT_CORES_") != "") 2 else parallel::detectCores() - 1
# Setup the parallel backend with the appropriate number of workers
BPPARAM <- BiocParallel::MulticoreParam(workers = max_cores)
tune.spca.res <- tune.spca(
    X = nutrimouse$lipid,
    ncomp = 2,
    nrepeat = nrepeat,
    folds = 3,
    test.keepX = seq(5, 15, 5),
    BPPARAM = BPPARAM
)
plot(tune.spca.res)

## End(Not run)
```

tune.spls *Tuning functions for sPLS method*

Description

Computes M-fold or Leave-One-Out Cross-Validation scores on a user-input grid to determine optimal values for the parameters in spls.

Usage

```
tune.spls(
  X,
  Y,
  test.keepX = NULL,
  test.keepY = NULL,
  ncomp,
  mode = c("regression", "canonical", "classic"),
  scale = TRUE,
  logratio = "none",
  tol = 1e-09,
  max.iter = 100,
  near.zero.var = FALSE,
  multilevel = NULL,
  validation = c("Mfold", "loo"),
  nrepeat = 1,
  folds,
  measure = NULL,
  BPPARAM = SerialParam(),
  seed = NULL,
  progressBar = FALSE,
  ...
)
```

Arguments

X	numeric matrix of predictors with the rows as individual observations.
Y	numeric matrix of response(s) with the rows as individual observations matching X.
test.keepX	numeric vector for the different number of variables to test from the X data set.
test.keepY	numeric vector for the different number of variables to test from the Y data set. Default to ncol(Y).
ncomp	Positive Integer. The number of components to include in the model. Default to 2.
mode	Character string indicating the type of PLS algorithm to use. One of "regression", "canonical", "invariant" or "classic". See Details.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE
logratio	Character, one of ('none','CLR') specifies the log ratio transformation to deal with compositional values that may arise from specific normalisation in sequencing data. Default to 'none'. See ?logratio.transfo for details.

tol	Positive numeric used as convergence criteria/tolerance during the iterative process. Default to 1e-06.
max.iter	Integer, the maximum number of iterations. Default to 100.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE.
multilevel	Numeric, design matrix for repeated measurement analysis, where multilevel decomposition is required. For a one factor decomposition, the repeated measures on each individual, i.e. the individuals ID is input as the first column. For a 2 level factor decomposition then 2nd AND 3rd columns indicate those factors. See examples.
validation	character. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (Leave-One-out). Default is "Mfold".
nrepeat	Positive integer. Number of times the Cross-Validation process should be repeated. nrepeat > 2 is required for robust tuning. See details.
folds	Positive Integer, The folds in the Mfold cross-validation.
measure	The tuning measure to use. Cannot be NULL when applied to sPLS1 object. See details.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples in ?tune.spca.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.
progressBar	Logical. If TRUE a progress bar is shown as the computation completes. Default to FALSE.
...	Optional parameters passed to spls

Details

This tuning function should be used to tune the parameters in the spls function (number of components and number of variables to select).

Value

If test.keepX != NULL and test.keepY != NULL returns a list that contains:

cor.pred	The correlation of predicted vs actual components from X (t) and Y (u) for each component
RSS.pred	The Residual Sum of Squares of predicted vs actual components from X (t) and Y (u) for each component
choice.keepX	returns the number of variables selected for X (optimal keepX) on each component.
choice.keepY	returns the number of variables selected for Y (optimal keepY) on each component.
choice.ncomp	returns the optimal number of components for the model fitted with $choice.keepX and $choice.keepY
call	The functioncal call including the parameteres used.

If test.keepX = NULL and test.keepY = NULL returns a list with the following components for every repeat:

MSEP	Mean Square Error Prediction for each Y variable, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
RMSEP	Root Mean Square Error Prediction for each Y variable, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
R2	a matrix of R^2 values of the Y-variables for models with $1, \ldots,$ncomp components, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
Q2	if Y contains one variable, a vector of Q^2 values else a list with a matrix of Q^2 values for each Y-variable. Note that in the specific case of an sPLS model, it is better to have a look at the Q2.total criterion, only applies to object inherited from "pls", and "spls". Only available when in regression (s)PLS.
Q2.total	a vector of Q^2-total values for models with $1, \ldots,$ncomp components, only applies to object inherited from "pls", and "spls". Available in both (s)PLS modes.
RSS	Residual Sum of Squares across all selected features and the components.
PRESS	Predicted Residual Error Sum of Squares across all selected features and the components.
features	a list of features selected across the folds ($stable.X and $stable.Y) for the keepX and keepY parameters from the input object. Note, this will be NULL if using standard (non-sparse) PLS.
cor.tpred, cor.upred	Correlation between the predicted and actual components for X (t) and Y (u)
RSS.tpred, RSS.upred	Residual Sum of Squares between the predicted and actual components for X (t) and Y (u)

folds

During a cross-validation (CV), data are randomly split into M subgroups (folds). M-1 subgroups are then used to train submodels which would be used to predict prediction accuracy statistics for the held-out (test) data. All subgroups are used as the test data exactly once. If validation = "loo", leave-one-out CV is used where each group consists of exactly one sample and hence M == N where N is the number of samples.

nrepeat

The cross-validation process is repeated nrepeat times and the accuracy measures are averaged across repeats. If validation = "loo", the process does not need to be repeated as there is only one way to split N samples into N groups and hence nrepeat is forced to be 1.

measure

- **For PLS2** Two measures of accuracy are available: Correlation (cor, used as default), as well as the Residual Sum of Squares (RSS). For cor, the parameters which would maximise the correlation between the predicted and the actual components are chosen. The RSS measure tries to predict the held-out data by matrix reconstruction and seeks to minimise the error between actual and predicted values. For mode='canonical', The X matrix is used to calculate the RSS, while for others modes the Y matrix is used. This measure gives more weight to any

large errors and is thus sensitive to outliers. It also intrinsically selects less number of features on the `Y` block compared to `measure='cor'`.

- **For PLS1** Four measures of accuracy are available: Mean Absolute Error (`MAE`), Mean Square Error (`MSE`, used as default), `Bias` and `R2`. Both MAE and MSE average the model prediction error. MAE measures the average magnitude of the errors without considering their direction. It is the average over the fold test samples of the absolute differences between the Y predictions and the actual Y observations. The MSE also measures the average magnitude of the error. Since the errors are squared before they are averaged, the MSE tends to give a relatively high weight to large errors. The Bias is the average of the differences between the Y predictions and the actual Y observations and the R2 is the correlation between the predictions and the observations.

Optimisation Process

The optimisation process is data-driven and similar to the process detailed in (Rohart et al., 2016), where one-sided t-tests assess whether there is a gain in performance when incrementing the number of features or components in the model. However, it will assess all the provided grid through pairwise comparisons as the performance criteria do not always change linearly with respect to the added number of features or components.

more

See also `?perf` for more details.

Author(s)

Kim-Anh Lê Cao, Al J Abadi, Benoit Gautier, Francois Bartolo, Florian Rohart,

References

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

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Chavent, Marie and Patouille, Brigitte (2003). Calcul des coefficients de regression et du PRESS en regression PLS1. Modulad n, 30 1-11. (this is the formula we use to calculate the Q2 in perf.pls and perf.spls)

Mevik, B.-H., Cederkvist, H. R. (2004). Mean Squared Error of Prediction (MSEP) Estimates for Principal Component Regression (PCR) and Partial Least Squares Regression (PLSR). Journal of Chemometrics 18(9), 422-429.

sparse PLS regression mode:

Lê Cao, K. A., Rossouw D., Robert-Granie, C. and Besse, P. (2008). A sparse PLS for variable selection when integrating Omics data. Statistical Applications in Genetics and Molecular Biology 7, article 35.

One-sided t-tests (suppl material):

Rohart F, Mason EA, Matigian N, Mosbergen R, Korn O, Chen T, Butcher S, Patel J, Atkinson K, Khosrotehrani K, Fisk NM, Lê Cao K-A&, Wells CA& (2016). A Molecular Classification of Human Mesenchymal Stromal Cells. PeerJ 4:e1845.

See Also

splsda, predict.splsda and http://www.mixOmics.org for more details.

Examples

```
## sPLS2 model example (more than one Y outcome variable)

# set up data
data(liver.toxicity)
X <- liver.toxicity$gene
Y <- liver.toxicity$clinic

# tune spls model for components only
tune.res.ncomp <- tune.spls( X, Y, ncomp = 5,
                             test.keepX = NULL,
                             test.keepY = NULL, measure = "cor",
                             folds = 5, nrepeat = 3, progressBar = TRUE)
plot(tune.res.ncomp) # plot outputs

# tune spls model for number of X and Y variables to keep
tune.res <- tune.spls( X, Y, ncomp = 3,
                       test.keepX = c(5, 10, 15),
                       test.keepY = c(3, 6, 8), measure = "cor",
                       folds = 5, nrepeat = 3, progressBar = TRUE)
plot(tune.res) # plot outputs

## sPLS1 model example (only one Y outcome variable)

# set up data
Y1 <- liver.toxicity$clinic[,1]

# tune spls model for components only
plot(tune.spls(X, Y1, ncomp = 3,
               folds = 3,
               test.keepX = NULL, test.keepY = NULL))

# tune spls model for number of X variables to keep, note for sPLS1 models 'measure' needs to be set
plot(tune.spls(X, Y1, ncomp = 3,
               folds = 3, measure = "MSE",
               test.keepX = c(5, 10, 15), test.keepY = c(3, 6, 8)))


## sPLS2 multilevel model example

# set up multilevel design
repeat.indiv <- c(1, 2, 1, 2, 1, 2, 1, 2, 3, 3, 4, 3, 4, 3, 4, 4, 5, 6, 5, 5,
                  6, 5, 6, 7, 7, 8, 6, 7, 8, 7, 8, 8, 9, 10, 9, 10, 11, 9, 9,
                  10, 11, 12, 12, 10, 11, 12, 11, 12, 13, 14, 13, 14, 13, 14,
                  13, 14, 15, 16, 15, 16, 15, 16, 15, 16)
design <- data.frame(sample = repeat.indiv)

# tune spls model for components only
tune.res.ncomp <- tune.spls( X, Y, ncomp = 5,
                             test.keepX = NULL,
                             test.keepY = NULL, measure = "cor", multilevel = design,
                             folds = 5, nrepeat = 3, progressBar = TRUE)
```

```
plot(tune.res.ncomp) # plot outputs

# tune spls model for number of X and Y variables to keep
tune.res <- tune.spls( X, Y, ncomp = 3,
                       test.keepX = c(5, 10, 15),
                       test.keepY = c(3, 6, 8), measure = "cor", multilevel = design,
                       folds = 5, nrepeat = 3, progressBar = TRUE)
plot(tune.res) # plot outputs
```

`tune.splsda` *Tuning functions for sPLS-DA method*

Description

Computes M-fold or Leave-One-Out Cross-Validation scores on a user-input grid to determine optimal values for the parameters in `splsda`.

Usage

```
tune.splsda(
  X,
  Y,
  ncomp = 1,
  test.keepX = NULL,
  already.tested.X,
  scale = TRUE,
  logratio = c("none", "CLR"),
  max.iter = 100,
  tol = 1e-06,
  near.zero.var = FALSE,
  multilevel = NULL,
  validation = "Mfold",
  folds = 10,
  nrepeat = 1,
  signif.threshold = 0.01,
  dist = "max.dist",
  measure = "BER",
  auc = FALSE,
  progressBar = FALSE,
  light.output = TRUE,
  BPPARAM = SerialParam(),
  seed = NULL
)
```

Arguments

`X`	numeric matrix of predictors. `NA`s are allowed.
`Y`	`if(method = 'spls')` numeric vector or matrix of continuous responses (for multi-response models) `NA`s are allowed.
`ncomp`	the number of components to include in the model.

test.keepX	numeric vector for the different number of variables to test from the X data set. If set to NULL, tuning will be performed on ncomp using all variables in the X data set.
already.tested.X	Optional, if ncomp > 1 A numeric vector indicating the number of variables to select from the X data set on the firsts components.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
logratio	one of ('none','CLR'). Default to 'none'
max.iter	integer, the maximum number of iterations.
tol	Convergence stopping value.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Default value is FALSE
multilevel	Design matrix for multilevel analysis (for repeated measurements) that indicates the repeated measures on each individual, i.e. the individuals ID. See Details.
validation	character. What kind of (internal) validation to use, matching one of "Mfold" or "loo" (short for 'leave-one-out'). Default is "Mfold".
folds	the folds in the Mfold cross-validation. See Details.
nrepeat	Number of times the Cross-Validation process is repeated.
signif.threshold	numeric between 0 and 1 indicating the significance threshold required for improvement in error rate of the components. Default to 0.01.
dist	distance metric to use for splsda to estimate the classification error rate, should one of "centroids.dist", "mahalanobis.dist" or "max.dist" (see Details). If test.keepX = NULL multiple distances can be inputted or "all".
measure	Three misclassification measure are available: overall misclassification error overall, the Balanced Error Rate BER or the Area Under the Curve AUC. Only used when test.keepX is not NULL.
auc	if TRUE calculate the Area Under the Curve (AUC) performance of the model based on the optimisation measure measure.
progressBar	by default set to TRUE to output the progress bar of the computation.
light.output	if set to FALSE, the prediction/classification of each sample for each of test.keepX and each comp is returned.
BPPARAM	A BiocParallelParam object indicating the type of parallelisation. See examples in ?tune.spca.
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.

Details

This tuning function should be used to tune the parameters in the splsda function (number of components and number of variables in keepX to select).

For a sPLS-DA, M-fold or LOO cross-validation is performed with stratified subsampling where all classes are represented in each fold.

If validation = "loo", leave-one-out cross-validation is performed. By default folds is set to the number of unique individuals.

The function outputs the optimal number of components that achieve the best performance based on the overall error rate or BER. The assessment is data-driven and similar to the process detailed in (Rohart et al., 2016), where one-sided t-tests assess whether there is a gain in performance when adding a component to the model. Our experience has shown that in most case, the optimal number of components is the number of categories in `Y` - 1, but it is worth tuning a few extra components to check (see our website and case studies for more details).

For sPLS-DA multilevel one-factor analysis, M-fold or LOO cross-validation is performed where all repeated measurements of one sample are in the same fold. Note that logratio transform and the multilevel analysis are performed internally and independently on the training and test set.

For a sPLS-DA multilevel two-factor analysis, the correlation between components from the within-subject variation of X and the `cond` matrix is computed on the whole data set. The reason why we cannot obtain a cross-validation error rate as for the spls-DA one-factor analysis is because of the difficulty to decompose and predict the within matrices within each fold.

For a sPLS two-factor analysis a sPLS canonical mode is run, and the correlation between components from the within-subject variation of X and Y is computed on the whole data set.

If `validation = "Mfold"`, M-fold cross-validation is performed. How many folds to generate is selected by specifying the number of folds in `folds`.

If `auc = TRUE` and there are more than 2 categories in `Y`, the Area Under the Curve is averaged using one-vs-all comparison. Note however that the AUC criteria may not be particularly insightful as the prediction threshold we use in sPLS-DA differs from an AUC threshold (sPLS-DA relies on prediction distances for predictions, see `?predict.splsda` for more details) and the supplemental material of the mixOmics article (Rohart et al. 2017). If you want the AUC criterion to be insightful, you should use `measure==AUC` as this will output the number of variable that maximises the AUC; in this case there is no prediction threshold from sPLS-DA (`dist` is not used). If `measure==AUC`, we do not output SD as this measure can be a mean (over `nrepeat`) of means (over the categories).

BER is appropriate in case of an unbalanced number of samples per class as it calculates the average proportion of wrongly classified samples in each class, weighted by the number of samples in each class. BER is less biased towards majority classes during the performance assessment.

More details about the prediction distances in `?predict` and the supplemental material of the mixOmics article (Rohart et al. 2017).

If test.keepX is set to NULL, the `perf()` function will be run internally, which performs cross-validation to identify optimal number of components and distance measure. Running tuning initially using `test.keepX = NULL` speeds up the parameter tuning workflow, as then a lower ncomp value can be used for variable selection tuning.

Value

Depending on the type of analysis performed, a list that contains:

`error.rate`	returns the prediction error for each `test.keepX` on each component, averaged across all repeats and subsampling folds. Standard deviation is also output. All error rates are also available as a list.
`choice.keepX`	returns the number of variables selected (optimal keepX) on each component.
`choice.ncomp`	returns the optimal number of components for the model fitted with `$choice.keepX`
`error.rate.class`	returns the error rate for each level of `Y` and for each component computed with the optimal keepX

If test.keepX = FALSE,produces a matrix of classification error rate estimation. The dimensions correspond to the components in the model and to the prediction method used, respectively. Note

that error rates reported in any component include the performance of the model in earlier components for the specified keepX parameters (e.g. error rate reported for component 3 for keepX = 20 already includes the fitted model on components 1 and 2 for keepX = 20).

predict	Prediction values for each sample, each test.keepX, each comp and each repeat. Only if light.output=FALSE
class	Predicted class for each sample, each test.keepX, each comp and each repeat. Only if light.output=FALSE
auc	AUC mean and standard deviation if the number of categories in Y is greater than 2, see details above. Only if auc = TRUE
cor.value	only if multilevel analysis with 2 factors: correlation between latent variables.

Author(s)

Kim-Anh Lê Cao, Benoit Gautier, Francois Bartolo, Florian Rohart, Al J Abadi

References

mixOmics article:

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

See Also

splsda, predict.splsda and http://www.mixOmics.org for more details.

Examples

```
## First example: analysis with sPLS-DA
data(breast.tumors)
X = breast.tumors$gene.exp
Y = as.factor(breast.tumors$sample$treatment)

# first tune on components only
tune = tune.splsda(X, Y, ncomp = 5, logratio = "none",
                   nrepeat = 10, folds = 10,
                   test.keepX = NULL,
                   dist = "all",
                   progressBar = TRUE,
                   seed = 20) # set for reproducibility of example only
plot(tune) # optimal distance = centroids.dist
tune$choice.ncomp # optimal component number = 3

# then tune optimal keepX for each component
tune = tune.splsda(X, Y, ncomp = 3, logratio = "none",
                   nrepeat = 10, folds = 10,
                   test.keepX = c(5, 10, 15), dist = "centroids.dist",
                   progressBar = TRUE,
                   seed = 20)

plot(tune)
tune$choice.keepX # optimal number of variables to keep c(15, 5, 15)

## With already tested variables:
tune = tune.splsda(X, Y, ncomp = 3, logratio = "none",
```

```
                    nrepeat = 10, folds = 10,
                    test.keepX = c(5, 10, 15), already.tested.X = c(5, 10),
                    dist = "centroids.dist",
                    progressBar = TRUE,
                    seed = 20)
plot(tune)

## Second example: multilevel one-factor analysis with sPLS-DA

data(vac18)
X = vac18$genes
Y = vac18$stimulation
# sample indicates the repeated measurements
design = data.frame(sample = vac18$sample)

# tune on components
tune = tune.splsda(X, Y = Y, ncomp = 5, nrepeat = 10, logratio = "none",
                   test.keepX = NULL, folds = 10, dist = "max.dist", multilevel = design)

plot(tune)

# tune on variables
tune = tune.splsda(X, Y = Y, ncomp = 3, nrepeat = 10, logratio = "none",
                test.keepX = c(5,50,100),folds = 10, dist = "max.dist", multilevel = design)

plot(tune)
```

`tune.splslevel` *Parallelized Tuning function for multilevel sPLS method using BiocParallel*

Description

For a multilevel spls analysis, the tuning criterion is based on the maximisation of the correlation between the components from both data sets

Usage

```
tune.splslevel(
  X,
  Y,
  multilevel,
  ncomp = NULL,
  mode = "regression",
  test.keepX = rep(ncol(X), ncomp),
  test.keepY = rep(ncol(Y), ncomp),
  already.tested.X = NULL,
  already.tested.Y = NULL,
  BPPARAM = BiocParallel::SerialParam(),
  seed = NULL
)
```

Arguments

X	numeric matrix of predictors. NAs are allowed.
Y	if(method = 'spls') numeric vector or matrix of continuous responses (for multi-response models) NAs are allowed.
multilevel	Design matrix for multilevel analysis (for repeated measurements) that indicates the repeated measures on each individual, i.e. the individuals ID. See Details.
ncomp	the number of components to include in the model.
mode	character string. What type of algorithm to use, (partially) matching one of "regression", "canonical", "invariant" or "classic".
test.keepX	numeric vector for the different number of variables to test from the X data set
test.keepY	numeric vector for the different number of variables to test from the Y data set
already.tested.X	Optional, if ncomp > 1 A numeric vector indicating the number of variables to select from the X data set on the firsts components.
already.tested.Y	Optional, if ncomp > 1 A numeric vector indicating the number of variables to select from the Y data set on the firsts components.
BPPARAM	BiocParallelParam object to manage parallelization
seed	set a number here if you want the function to give reproducible outputs. Not recommended during exploratory analysis. Note if RNGseed is set in 'BPPARAM', this will be overwritten by 'seed'.

Value

cor.value	correlation between latent variables

---

unmap *Dummy matrix for an outcome factor*

Description

Converts a class or group vector or factor into a matrix of indicator variables.

Usage

```
unmap(classification, groups = NULL, noise = NULL)
```

Arguments

classification	A numeric or character vector or factor. Typically the distinct entries of this vector would represent a classification of observations in a data set.
groups	A numeric or character vector indicating the groups from which classification is drawn. If not supplied, the default is to assumed to be the unique entries of classification.
noise	A single numeric or character value used to indicate the value of groups corresponding to noise.

Value

An *n* by *K* matrix of *(0,1)* indicator variables, where *n* is the length of samples and *K* the number of classes in the outcome.

If a `noise` value of symbol is designated, the corresponding indicator variables are relocated to the last column of the matrix.

Note: - you can remap an unmap vector using the function `map` from the package **mclust**. - this function should be used to unmap an outcome vector as in the non-supervised methods of mixOmics. For other supervised analyses such as (s)PLS-DA, (s)gccaDA this function is used internally.

Author(s)

Ignacio Gonzalez, Kim-Anh Le Cao, Pierre Monget, AL J Abadi

References

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association 97:611-631*.

C. Fraley, A. E. Raftery, T. B. Murphy and L. Scrucca (2012). mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. Technical Report No. 597, Department of Statistics, University of Washington.

Examples

```
data(nutrimouse)
Y = unmap(nutrimouse$diet)
Y
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = Y)
# data could then used as an input in wrapper.rgcca, which is not, technically,
# a supervised method, see ??wrapper.rgcca
```

---

vac18 *Vaccine study Data*

Description

The data come from a trial evaluating a vaccine based on HIV-1 lipopeptides in HIV-negative volunteers. The vaccine (HIV-1 LIPO-5 ANRS vaccine) contains five HIV-1 amino acid sequences coding for Gag, Pol and Nef proteins. This data set contains the expression measure of a subset of 1000 genes from purified in vitro stimulated Peripheral Blood Mononuclear Cells from 42 repeated samples (12 unique vaccinated participants) 14 weeks after vaccination, , 6 hours after in vitro stimulation by either (1) all the peptides included in the vaccine (LIPO-5), or (2) the Gag peptides included in the vaccine (GAG+) or (3) the Gag peptides not included in the vaccine (GAG-) or (4) without any stimulation (NS).

Usage

```
data(vac18)
```

Format

A list containing the following components:

list("gene") data frame with 42 rows and 1000 columns. The expression measure of 1000 genes for the 42 samples (PBMC cells from 12 unique subjects).

list("stimulation") is a fctor of 42 elements indicating the type of in vitro simulation for each sample.

list("sample") is a vector of 42 elements indicating the unique subjects (for example the value '1' correspond to the first patient PBMC cells). Note that the design of this study is unbalanced.

list("tab.prob.gene") is a data frame with 1000 rows and 2 columns, indicating the Illumina probe ID and the gene name of the annotated genes.

Details

This is a subset of the original study for illustrative purposes.

Value

none

References

Salmon-Ceron D, Durier C, Desaint C, Cuzin L, Surenaud M, Hamouda N, Lelievre J, Bonnet B, Pialoux G, Poizot-Martin I, Aboulker J, Levy Y, Launay O, trial group AV: Immunogenicity and safety of an HIV-1 lipopeptide vaccine in healthy adults: a phase 2 placebo-controlled ANRS trial. AIDS 2010, 24(14):2211-2223.

`vac18.simulated` *Simulated data based on the vac18 study for multilevel analysis*

Description

Simulated data based on the vac18 study to illustrate the use of the multilevel analysis for one and two-factor analysis with sPLS-DA. This data set contains the expression simulated of 500 genes.

Usage

```
data(vac18.simulated)
```

Format

A list containing the following components:

list("genes") data frame with 48 rows and 500 columns. The simulated expression of 500 genes for 48 subjects.

list("sample") a vector indicating the repeated measurements on each unique subject. See Details.

list("stimulation") a factor indicating the stimulation condition on each sample.

list("time") a factor indicating the time condition on each sample.

Details

In this cross-over design, repeated measurements are performed 12 experiments units (or unique subjects) for each of the 4 stimulations.

The simulation study was based on a mixed effects model (see reference for details). Ten clusters of 100 genes were generated. Amongt those, 4 clusters of genes discriminate the 4 stimulations (denoted LIPO5, GAG+, GAG- and NS) as follows: \ -2 gene clusters discriminate (LIPO5, GAG+) versus (GAG-, NS) \ -2 gene clusters discriminate LIPO5 versus GAG+, while GAG+ and NS have the same effect \ -2 gene clusters discriminate GAG- versus NS, while LIPO5 and GAG+ have the same effect \ -the 4 remaining clusters represent noisy signal (no stimulation effect) \

Only a subset of those genes are presented here (to save memory space).

Value

none

References

Liquet, B., Lê Cao, K.-A., Hocini, H. and Thiebaut, R. (2012). A novel approach for biomarker selection and the integration of repeated measures experiments from two platforms. *BMC Bioinformatics* **13**:325.

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

Description

The function `vip` computes the influence on the Y-responses of every predictor X in the model.

Usage

```
vip(object)
```

Arguments

`object`	object of class inheriting from `"pls"`, `"plsda"`, `"spls"` or `"splsda"`.

Details

Variable importance in projection (VIP) coefficients reflect the relative importance of each X variable for each X variate in the prediction model. VIP coefficients thus represent the importance of each X variable in fitting both the X- and Y-variates, since the Y-variates are predicted from the X-variates.

VIP allows to classify the X-variables according to their explanatory power of Y. Predictors with large VIP, larger than 1, are the most relevant for explaining Y.

Value

`vip` produces a matrix of VIP coefficients for each X variable (rows) on each variate component (columns).

Author(s)

Sébastien Déjean, Ignacio Gonzalez, Florian Rohart, Al J Abadi

References

Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

See Also

pls, spls, summary.

Examples

```
data(linnerud)
X <- linnerud$exercise
Y <- linnerud$physiological
linn.pls <- pls(X, Y)

linn.vip <- vip(linn.pls)

barplot(linn.vip,
beside = TRUE, col = c("lightblue", "mistyrose", "lightcyan"),
ylim = c(0, 1.7), legend = rownames(linn.vip),
main = "Variable Importance in the Projection", font.main = 4)
```

---

withinVariation *Within matrix decomposition for repeated measurements (cross-over design)*

Description

This function is internally called by pca, pls, spls, plsda and splsda functions for cross-over design data, but can be called independently prior to any kind of multivariate analyses.

Usage

```
withinVariation(X, design)
```

Arguments

X	numeric matrix of predictors. NAs are allowed.
design	a numeric matrix or data frame. The first column indicates the repeated measures on each individual, i.e. the individuals ID. The 2nd and 3rd columns are to split the variation for a 2 level factor.

Details

withinVariation function decomposes the Within variation in the X data set. The resulting Xw matrix is then input in the multilevel function.

One or two-factor analyses are available.

Value

withinVariation simply returns the Xw within matrix, which can be input in the other multivariate approaches already implemented in mixOmics (i.e. spls or splsda, see multilevel, but also pca or ipca).

Author(s)

Benoit Liquet, Kim-Anh Lê Cao, Benoit Gautier, Ignacio González, Florian Rohart, AL J Abadi

References

On multilevel analysis:

Liquet, B., Lê Cao, K.-A., Hocini, H. and Thiebaut, R. (2012) A novel approach for biomarker selection and the integration of repeated measures experiments from two platforms. *BMC Bioinformatics* **13**:325.

Westerhuis, J. A., van Velzen, E. J., Hoefsloot, H. C., and Smilde, A. K. (2010). Multivariate paired data analysis: multilevel PLSDA versus OPLSDA. *Metabolomics*, **6**(1), 119-128.

See Also

spls, splsda, plotIndiv, plotVar, cim, network.

Examples

```
## Example: one-factor analysis matrix decomposition
#-----------------------------------------------------------------
data(vac18)
X <- vac18$genes
# in design we only need to mention the repeated measurements to split the one level variation
design <- data.frame(sample = vac18$sample)

Xw <- withinVariation(X = X, design = design)
# multilevel PCA
res.pca.1level <- pca(Xw, ncomp = 3)

# compare a normal PCA with a multilevel PCA for repeated measurements.
# note: PCA makes the assumptions that all samples are independent,
# so this analysis is flawed and you should use a multilevel PCA instead
res.pca <- pca(X, ncomp = 3)

# set up colors for plotIndiv
col.stim <- c("darkblue", "purple", "green4","red3")
col.stim <- col.stim[as.numeric(vac18$stimulation)]

# plotIndiv comparing both PCA and PCA multilevel
plotIndiv(res.pca, ind.names = vac18$stimulation, group = col.stim)
title(main = 'PCA ')
plotIndiv(res.pca.1level, ind.names = vac18$stimulation, group = col.stim)
title(main = 'PCA multilevel')
```

`wrapper.rgcca` *mixOmics wrapper for Regularised Generalised Canonical Correlation Analysis (rgcca)*

Description

Wrapper function to perform Regularized Generalised Canonical Correlation Analysis (rGCCA), a generalised approach for the integration of multiple datasets. For more details, see the `help(rgcca)` from the **RGCCA** package.

Usage

```
wrapper.rgcca(
  X,
  design = 1 - diag(length(X)),
  tau = rep(1, length(X)),
  ncomp = 1,
  keepX,
  scale = TRUE,
  tol = .Machine$double.eps,
  max.iter = 1000,
  near.zero.var = FALSE,
  all.outputs = TRUE
)
```

Arguments

`X`	a list of data sets (called 'blocks') matching on the same samples. Data in the list should be arranged in samples x variables. `NA`s are not allowed.
`design`	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks using sGCCA; a value of 0 indicates no relationship, 1 is the maximum value. If `Y` is provided instead of `indY`, the `design` matrix is changed to include relationships to `Y`.
`tau`	numeric vector of length the number of blocks in `X`. Each regularization parameter will be applied on each block and takes the value between 0 (no regularisation) and 1. If tau = "optimal" the shrinkage paramaters are estimated for each block and each dimension using the Schafer and Strimmer (2005) analytical formula.
`ncomp`	the number of components to include in the model. Default to 1.
`keepX`	A vector of same length as X. Each entry keepX[i] is the number of X[[i]]-variables kept in the model.
`scale`	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
`tol`	Convergence stopping value.
`max.iter`	integer, the maximum number of iterations.
`near.zero.var`	Logical, see the internal `nearZeroVar` function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE

all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

This wrapper function performs rGCCA (see **RGCCA**) with $1, \ldots,$ ncomp components on each block data set. A supervised or unsupervised model can be run. For a supervised model, the unmap function should be used as an input data set. More details can be found on the package **RGCCA**.

Value

wrapper.rgcca returns an object of class "rgcca", a list that contains the following components:

data	the input data set (as a list).
design	the input design.
variates	the sgcca components.
loadings	the loadings for each block data set (outer wieght vector).
loadings.star	the laodings, standardised.
tau	the input tau parameter.
ncomp	the number of components included in the model for each block.
crit	the convergence criterion.
AVE	Indicators of model quality based on the Average Variance Explained (AVE): AVE(for one block), AVE(outer model), AVE(inner model)..
names	list containing the names to be used for individuals and variables.

More details can be found in the references. Note that the argument 'scheme' has now been hard-coded to 'horst' and 'init' to 'svd.single'.

Author(s)

Arthur Tenenhaus, Vincent Guillemot, Kim-Anh Lê Cao, Florian Rohart, Benoit Gautier

References

Tenenhaus A. and Tenenhaus M., (2011), Regularized Generalized Canonical Correlation Analysis, Psychometrika, Vol. 76, Nr 2, pp 257-284.

Schafer J. and Strimmer K., (2005), A shrinkage approach to large-scale covariance matrix estimation and implications for functional genomics. Statist. Appl. Genet. Mol. Biol. 4:32.

See Also

wrapper.rgcca, plotIndiv, plotVar, wrapper.sgcca and http://www.mixOmics.org for more details.

Examples

```
data(nutrimouse)
# need to unmap the Y factor diet
Y = unmap(nutrimouse$diet)
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = Y)
# with this design, gene expression and lipids are connected to the diet factor
# design = matrix(c(0,0,1,
#                   0,0,1,
#                   1,1,0), ncol = 3, nrow = 3, byrow = TRUE)

# with this design, gene expression and lipids are connected to the diet factor
# and gene expression and lipids are also connected
design = matrix(c(0,1,1,
1,0,1,
1,1,0), ncol = 3, nrow = 3, byrow = TRUE)
#note: the tau parameter is the regularization parameter
wrap.result.rgcca = wrapper.rgcca(X = data, design = design, tau = c(1, 1, 0),
ncomp = 2)
#wrap.result.rgcca
```

`wrapper.sgcca` *mixOmics wrapper for Sparse Generalised Canonical Correlation Analysis (sgcca)*

Description

Wrapper function to perform Sparse Generalised Canonical Correlation Analysis (sGCCA), a generalised approach for the integration of multiple datasets. For more details, see the `help(sgcca)` from the **RGCCA** package.

Usage

```
wrapper.sgcca(
  X,
  design = 1 - diag(length(X)),
  penalty = NULL,
  ncomp = 1,
  keepX,
  mode = "canonical",
  scale = TRUE,
  tol = .Machine$double.eps,
  max.iter = 1000,
  near.zero.var = FALSE,
  all.outputs = TRUE
)
```

Arguments

`X`	a list of data sets (called 'blocks') matching on the same samples. Data in the list should be arranged in samples x variables. `NA`s are not allowed.

design	numeric matrix of size (number of blocks in X) x (number of blocks in X) with values between 0 and 1. Each value indicates the strenght of the relationship to be modelled between two blocks using sGCCA; a value of 0 indicates no relationship, 1 is the maximum value. If Y is provided instead of indY, the design matrix is changed to include relationships to Y.
penalty	numeric vector of length the number of blocks in X. Each penalty parameter will be applied on each block and takes the value between 0 (no variable selected) and 1 (all variables included).
ncomp	the number of components to include in the model. Default to 1.
keepX	A vector of same length as X. Each entry keepX[i] is the number of X[[i]]-variables kept in the model.
mode	character string. What type of algorithm to use, (partially) matching one of "regression", "canonical", "invariant" or "classic". See Details.
scale	Logical. If scale = TRUE, each block is standardized to zero means and unit variances (default: TRUE)
tol	Convergence stopping value.
max.iter	integer, the maximum number of iterations.
near.zero.var	Logical, see the internal nearZeroVar function (should be set to TRUE in particular for data with many zero values). Setting this argument to FALSE (when appropriate) will speed up the computations. Default value is FALSE
all.outputs	Logical. Computation can be faster when some specific (and non-essential) outputs are not calculated. Default = TRUE.

Details

This wrapper function performs sGCCA (see **RGCCA**) with $1, \ldots,$ncomp components on each block data set. A supervised or unsupervised model can be run. For a supervised model, the unmap function should be used as an input data set. More details can be found on the package **RGCCA**.

Note that this function is the same as block.spls with different default arguments.

More details about the PLS modes in ?pls.

Value

wrapper.sgcca returns an object of class "sgcca", a list that contains the following components:

data	the input data set (as a list).
design	the input design.
variates	the sgcca components.
loadings	the loadings for each block data set (outer wieght vector).
loadings.star	the laodings, standardised.
penalty	the input penalty parameter.
scheme	the input schme.
ncomp	the number of components included in the model for each block.
crit	the convergence criterion.
AVE	Indicators of model quality based on the Average Variance Explained (AVE): AVE(for one block), AVE(outer model), AVE(inner model)..
names	list containing the names to be used for individuals and variables.

More details can be found in the references. Note that the argument 'scheme' has now been hard-coded to 'horst' and 'init' to 'svd.single'.

Author(s)

Arthur Tenenhaus, Vincent Guillemot, Kim-Anh Lê Cao, Florian Rohart, Benoit Gautier, Al J Abadi

References

Tenenhaus A. and Tenenhaus M., (2011), Regularized Generalized Canonical Correlation Analysis, Psychometrika, Vol. 76, Nr 2, pp 257-284.

Tenenhaus A., Phillipe C., Guillemot, V., Lê Cao K-A., Grill J., Frouin, V. Variable Selection For Generalized Canonical Correlation Analysis. 2013. (in revision)

See Also

wrapper.sgcca, plotIndiv, plotVar, wrapper.rgcca and http://www.mixOmics.org for more details.

Examples

```
data(nutrimouse)
# need to unmap the Y factor diet if you pretend this is not a classification pb.
# see also the function block.splsda for discriminant analysis  where you dont
# need to unmap Y.
Y = unmap(nutrimouse$diet)
data = list(gene = nutrimouse$gene, lipid = nutrimouse$lipid, Y = Y)
# with this design, gene expression and lipids are connected to the diet factor
# design = matrix(c(0,0,1,
#                   0,0,1,
#                   1,1,0), ncol = 3, nrow = 3, byrow = TRUE)

# with this design, gene expression and lipids are connected to the diet factor
# and gene expression and lipids are also connected
design = matrix(c(0,1,1,
1,0,1,
1,1,0), ncol = 3, nrow = 3, byrow = TRUE)

#note: the penalty parameters will need to be tuned
wrap.result.sgcca = wrapper.sgcca(X = data, design = design, penalty = c(.3,.5, 1),
ncomp = 2)
wrap.result.sgcca
#did the algo converge?
wrap.result.sgcca$crit  # yes
```

---

yeast *Yeast metabolomic study*

Description

Two Saccharomyces Cerevisiae strains were compared under two different environmental conditions, 37 metabolites expression are measured.

Usage

```
data(yeast)
```

Format

A list containing the following components:

list("data") data matrix with 55 rows and 37 columns. Each row represents an experimental sample, and each column a single metabolite.

list("strain") a factor containing the type of strain (MT or WT).

list("condition") a factor containing the type of environmental condition (AER or ANA).

list("strain.condition") a crossed factor between `strain` and `condition`.

Details

In this study, two Saccharomyces cerevisiae strains were used - wild-type (WT) and mutant (MT), and were carried out in batch cultures under two different environmental conditions, aerobic (AER) and anaerobic (ANA) in standard mineral media with glucose as the sole carbon source. After normalization and pre processing, the metabolomic data results in 37 metabolites and 55 samples which include 13 MT-AER, 14 MT-ANA, 15 WT-AER and 13 WT-ANA samples

Value

none

References

Villas-Boas S, Moxley J, Akesson M, Stephanopoulos G, Nielsen J: High-throughput metabolic state analysis (2005). The missing link in integrated functional genomics. *Biochemical Journal*, **388**:669–677.

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