

Package ‘powerPLS’

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Type Package

Title Power Analysis for PLS Classification

Version 0.1.0

Description It estimates power and sample size for Partial Least Squares-based methods described in Andreella, et al., (2024) <[arXiv:2403.10289](https://arxiv.org/abs/2403.10289)>.

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BugReports <https://github.com/angeella/powerPLS/issues>

URL <https://github.com/angeella/powerPLS>

Depends R (>= 2.10)

NeedsCompilation no

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computePower*Power estimation*

Description

estimate power for a given sample size, alpha level and number of score components.

Usage

```
computePower(X, Y, A, n, seed = 123,
             Nsim = 100, nperm = 200, alpha = 0.05,
             test = "R2", Y.prob = FALSE, eps = 0.01, ...)
```

Arguments

X	data matrix where columns represent the p variables and rows the n observations.
Y	data matrix where columns represent the two classes and rows the n observations.
A	number of score components
n	sample size
seed	seed value
Nsim	number of simulations
nperm	number of permutations
alpha	type I error
test	type of test, one of c("score", "mcc", "R2").
Y.prob	Boolean value. Default @FALSE. IF @TRUE Y is a probability vector
eps	Default 0.01. eps is used when Y.prob = FALSE to transform Y in a probability vector. Default to "R2".
...	Futher parameters see PLSc

Value

Returns the corresponding estimated power

Author(s)

Angela Andreella

References

Andreella, A., Finos, L., Scarpa, B. and Stocchero, M. "Towards a power analysis for PLS-based methods" arXiv:2403.10289 stat.ME.

Examples

```
datas <- simulatePilotData(nvar = 10, clus.size = c(5,5), m = 6, nvar_rel = 5, A = 2)
out <- computePower(X = datas$X, Y = datas$Y, A = 3, n = 20)
```

computeSampleSize *sample size estimation*

Description

Compute optimal sample size calculation

Usage

```
computeSampleSize(n, X, Y, A, alpha, beta,
nperm, Nsim, seed, test = "R2", ...)
```

Arguments

<code>n</code>	vector of sample sizes to consider
<code>X</code>	data matrix where columns represent the p variables and rows the n observations.
<code>Y</code>	data matrix where columns represent the two classes and rows the n observations.
<code>A</code>	number of score components
<code>alpha</code>	level of type I error. Default 0.05
<code>beta</code>	level of type II error. Default 0.2.
<code>nperm</code>	number of permutations. Default 100.
<code>Nsim</code>	number of simulations. Default 100.
<code>seed</code>	seed value
<code>test</code>	type of test, one of c("score", "mcc", "R2"). Default to @R2.
<code>...</code>	Futher parameters.

Value

Returns a data frame that contains the estimated power for each sample size and number of components considered

Author(s)

Angela Andreella

References

Andreella, A., Finos, L., Scarpa, B. and Stocchero, M. "Towards a power analysis for PLS-based methods" arXiv:2403.10289 stat.ME.

Examples

```
datas <- simulatePilotData(nvar = 10, clus.size = c(5,5), m = 6, nvar_rel = 5, A = 2)
out <- computeSampleSize(X = datas$X, Y = datas$Y, A = 2, n = 20)
```

mccTest

MCC test

Description

Performs randomization test based on Matthews Correlation Coefficient

Usage

```
mccTest(X, Y, nperm = 100, A, randomization = FALSE, Y.prob = FALSE, eps = 0.01, ...)
```

Arguments

X	data matrix where columns represent the p variables and rows the n observations.
Y	data matrix where columns represent the two classes and rows the n observations.
nperm	number of permutations. Default 100.
A	number of score components
randomization	Boolean value. Default @FALSE. If @TRUE the permutation p-value is computed
Y.prob	Boolean value. Default @FALSE. IF @TRUE Y is a probability vector
eps	Default 0.01. eps is used when Y.prob = FALSE to transform Y in a probability vector
...	Futher parameters.

Value

Returns a list with the corresponding statistical tests, raw and adjusted p-values

List with the following objects: pv: raw p-value, pv_adj: adjusted p-value, test estimated statistical test.

Author(s)

Angela Andreella

References

For the general framework of power analysis for PLS-based methods see:

See Also

The type of tests implemented: [scoreTest](#) [R2Test](#).

Examples

```
datas <- simulatePilotData(nvar = 30, clus.size = c(5,5),m = 6,nvar_rel = 5,A = 2)
out <- mccTest(X = datas$X, Y = datas$Y, A = 1)
out
```

PLSc

PLS

Description

Performs Partial Least Squares two class

Usage

```
PLSc(X, Y, A, scaling = "auto-scaling", post.transformation = TRUE,
eps = 0.01, Y.prob = FALSE, transformation = "ilr")
```

Arguments

X	data matrix where columns represent the p variables and rows the n observations.
Y	data matrix where columns represent the two classes and rows the n observations.
A	number of score components
scaling	type of scaling, one of c("auto-scaling", "pareto-scaling", "mean-centering"). Default @auto-scaling
post.transformation	Boolean value. @TRUE if you want to apply post transformation. Default @TRUE
eps	Default 0.01. eps is used when Y.prob = FALSE to transform Y in a probability vector
Y.prob	Boolean value. Default @FALSE. IF @TRUE Y is a probability vector
transformation	transformation used to map Y in probability data vector. The options are @ilr and @clr. Default @ilr.

Value

Returns a list with the following objects: - W: matrix of weights - X_loading: matrix of X loading - Y_loading: matrix of Y loading - X: matrix of X data - Y: matrix of Y data - T_score: matrix of scores - Y_fitted: fitted Y matrix - B: Matrix regression coefficients - M: number of orthogonal components if post transformation is applied.

Author(s)

Angela Andreella

References

Stocchero, M., De Nardi, M., & Scarpa, B. (2021). PLS for classification. *Chemometrics and Intelligent Laboratory Systems*, 216, 104374.

Examples

```
datas <- simulatePilotData(nvar = 30, clus.size = c(5,5), m = 6, nvar_rel = 5, A = 2)
out <- PLSc(X = datas$X, Y = datas$Y, A = 3)
```

R2Test

R2 test

Description

Performs randomization test based on R2

Usage

```
R2Test(X, Y, nperm = 100, A, randomization = FALSE, Y.prob = FALSE, eps = 0.01, ...)
```

Arguments

X	data matrix where columns represent the p variables and rows the n observations.
Y	data matrix where columns represent the two classes and rows the n observations.
nperm	number of permutations. Default 100.
A	number of score components
randomization	Boolean value. Default @FALSE. If @TRUE the permutation p-value is computed
Y.prob	Boolean value. Default @FALSE. IF @TRUE Y is a probability vector
eps	Default 0.01. eps is used when Y.prob = FALSE to transform Y in a probability vector
...	Futher parameters.

Value

Returns a list with the corresponding statistical tests, raw and adjusted p-values
List with the following objects: pv: raw p-value, pv_adj: adjusted p-value, test estimated statistical test.

Author(s)

Angela Andreella

References

For the general framework of power analysis for PLS-based methods see:

See Also

The type of tests implemented: [scoreTest](#) [mccTest](#).

Examples

```
datas <- simulatePilotData(nvar = 30, clus.size = c(5,5), m = 6, nvar_rel = 5, A = 2)
out <- R2Test(X = datas$X, Y = datas$Y, A = 1)
out
```

scoreTest

Score test

Description

Performs randomization test based on predictive score vector

Usage

```
scoreTest(X, Y, nperm = 100, A, randomization = FALSE, Y.prob = FALSE, eps = 0.01, ...)
```

Arguments

X	data matrix where columns represent the p variables and rows the n observations.
Y	data matrix where columns represent the two classes and rows the n observations.
nperm	number of permutations. Default 100.
A	number of score components
randomization	Boolean value. Default @FALSE. If @TRUE the permutation p-value is computed
Y.prob	Boolean value. Default @FALSE. IF @TRUE Y is a probability vector
eps	Default 0.01. eps is used when Y.prob = FALSE to transform Y in a probability vector
...	Further parameters.

Value

Returns a list with the corresponding statistical tests, raw and adjusted p-values

List with the following objects: `pv`: raw p-value, `pv_adj`: adjusted p-value, `test` estimated statistical test.

Author(s)

Angela Andreella

References

For the general framework of power analysis for PLS-based methods see:

See Also

The type of tests implemented: [mccTest](#) [R2Test](#).

Examples

```
datas <- simulatePilotData(nvar = 30, clus.size = c(5,5), m = 6, nvar_rel = 5, A = 2)
out <- scoreTest(X = datas$X, Y = datas$Y, A = 1)
out
```

simulatePilotData *simulate pilot data*

Description

simulate cluster pilot data

Usage

```
simulatePilotData(seed = 123, nvar, clus.size, nvar_rel, m, A = 2, S1 = NULL, S2 = NULL)
```

Arguments

<code>seed</code>	seed value
<code>nvar</code>	number of variables
<code>clus.size</code>	Vector of two elements, specifying the size of classes (only two classes are considered)
<code>nvar_rel</code>	number of variables relevant to predict Y
<code>m</code>	separation between classes
<code>A</code>	oracle number of score components
<code>S1</code>	covariance matrix for the first class. Default @NULL i.e., the identity is considered.
<code>S2</code>	covariance matrix for the second class. Default @NULL i.e., the identity is considered.

Value

Returns list of X and Y simulated data

Author(s)

Angela Andreella

Examples

```
datas <- simulatePilotData(nvar = 10, clus.size = c(5,5),m = 6,nvar_rel = 5,A = 2)
```

sim_XY

simulate data matrix under the alternative hypothesis

Description

simulate data matrix under the alternative hypothesis

Usage

```
sim_XY(out, n, seed = 123, post.transformation = TRUE, A)
```

Arguments

out	output from PLSc
n	number of observations to simulate
seed	seed value
post.transformation	Boolean value. Default @TRUE i.e., post transformation is applied.
A	number of score components used in PLSc.

Value

Returns a simulated matrix under the alternative hypothesis.

Author(s)

Angela Andreella

Examples

```
datas <- simulatePilotData(nvar = 10, clus.size = c(5,5),m = 6,nvar_rel = 5,A = 2)
out <- PLSc(X = datas$X, Y = datas$Y, A = 2)
out_sim <- sim_XY(out = out, n = 10, A = 2)
```

umor_acqueo

This is data to be included in my package

Description

This is data to be included in my package

Usage

umor_acqueo

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 59 rows and 45 columns.

Author(s)

Angela Andreella <angela.andreella@unive.it>

References

<https://pubmed.ncbi.nlm.nih.gov/31069551/>

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