

Package ‘NPLStoolbox’

August 21, 2026

Title N-Way Partial Least Squares Modelling of Multi-Way Data

Version 1.1.1

Description Creation and selection of N-way Partial Least Squares (NPLS) models. Selection of the optimal number of components can be done using `ncrossreg()`. NPLS was originally described by Rasmus Bro, see <[doi:10.1002/%28SICI%291099-128X%28199601%2910%3A1%3C47%3A%3AAID-CEM400%3E3.0.CO%3B2-C](https://doi.org/10.1002/%28SICI%291099-128X%28199601%2910%3A1%3C47%3A%3AAID-CEM400%3E3.0.CO%3B2-C)>.

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Encoding UTF-8

RoxygenNote 7.3.2

Imports dplyr, parafac4microbiome, pracma, rTensor, stats

Depends R (>= 2.10)

LazyData true

Suggests ggpattern, ggplot2, ggpubr, knitr, readr, rmarkdown, scales, stringr, testthat (>= 3.0.0), tidyr

Config/testthat/edition 3

URL <https://github.com/GRvanderPloeg/NPLStoolbox>,
<https://grvanderploeg.com/NPLStoolbox/>

BugReports <https://github.com/GRvanderPloeg/NPLStoolbox/issues>

VignetteBuilder knitr

NeedsCompilation no

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Cornejo2025	<i>Cornejo2025 longitudinal dataset measured in transgender persons</i>
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Description

The Cornejo2025 longitudinal dataset as three-dimensional arrays, with subjects in mode 1, features in mode 2 and time in mode 3.

Usage

Cornejo2025

Format

- 'Cornejo2025':**
A list object with seven elements:
- Tongue_microbiome** List object of the tongue longitudinal microbiota data.
 - Salivary_microbiome** List object of the saliva longitudinal microbiota data.
 - Salivary_cytokines** List object of the longitudinal salivary cytokine data.
 - Salivary_biochemistry** List object of the longitudinal salivary biochemistry data.
 - Circulatory_hormones** List object of the longitudinal circulatory hormone data.
 - Clinical_measurements** List object of the longitudinal clinical outcome data.
 - Subject_metadata** Matrix with subject metadata.

Source

TBD

Jakobsen2025	<i>Jakobsen2025 longitudinal dataset measured in mother-infant dyads</i>
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Description

The Jakobsen2025 longitudinal dataset as three-dimensional arrays, with subjects in mode 1, features in mode 2 and time in mode 3.

Usage

```
Jakobsen2025
```

Format

'Jakobsen2025':

A list object with seven elements:

faeces List object of the longitudinal infant faecal microbiota data.

milkMicrobiome List object of the longitudinal HM microbiota data.

milkMetabolomics List object of the longitudinal salivary cytokine data.

Source

TBD

ncrossreg	<i>Cross-validation of NPLS by classical K-fold CV.</i>
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Description

This function runs ACMTF-R with cross-validation. A deterministic K-fold partition is used: the subjects are split in order into cvFolds groups. For each fold the training set consists of the other folds and the test set is the current fold.

Usage

```
ncrossreg(X, y, maxNumComponents = 5, maxIter = 120, cvFolds = dim(X)[1])
```

Arguments

X	Centered tensor of independent data
y	Centered dependent variable
maxNumComponents	Maximum number of components to investigate (default 5).
maxIter	Maximum number of iterations (default 100).

cvFolds Number of folds to use in the cross-validation. For example, if **cvFolds** is 5, then the subjects are deterministically partitioned into 5 groups (each CV iteration uses 4/5 for training and 1/5 for testing). Default: equal to the number of subjects (i.e. jack-knifing).

Value

A list with two elements: - **varExp**: a tibble with the variance–explained (for X and Y) per number of components. - **RMSE**: a tibble with the RMSE (computed over the unified CV prediction vector) per number of components.

Examples

```
set.seed(123)
X <- array(rnorm(25 * 5 * 4), dim = c(25, 5, 4))
y <- rnorm(25) # Random response variable
result = ncrossreg(X, y, cvFolds=2, maxNumComponents=2)
```

npred	<i>Predict Y for new data by projecting the data onto the latent space defined by an NPLS model.</i>
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Description

Predict Y for new data by projecting the data onto the latent space defined by an NPLS model.

Usage

```
npred(model, newX)
```

Arguments

model	NPLS model
newX	New data organized in a matrix of (Inew x J x K) with Inew new subjects

Value

Ypred: vector of the predicted value(s) of Y for the new data

Examples

```
Y = as.numeric(as.factor(Cornejo2025$Tongue$model$GenderID))
Ycnt = Y - mean(Y)
model = triPLS1(Cornejo2025$Tongue$data, Ycnt, numComponents=1)
npred(model, Cornejo2025$Tongue$data[1,,])
```

triPLS1	<i>Tri-PLS1: three-way PLS regressed onto a y vector</i>
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Description

Tri-PLS1: three-way PLS regressed onto a y vector

Usage

```
triPLS1(X, y, numComponents, tol = 1e-10, maxIter = 100)
```

Arguments

X	Centered tensor of independent data
y	Centered dependent variable
numComponents	Number of components to fit
tol	Relative change in loss for the model to converge (default 1e-10).
maxIter	Maximum number of iterations (default 100).

Value

Model

Examples

```
set.seed(123)
X <- array(rnorm(100 * 5 * 4), dim = c(100, 5, 4)) # Random tensor (100 samples, 5 vars, 4 vars)
y <- rnorm(100) # Random response variable
model <- triPLS1(X, y, numComponents = 2)
```

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