

# Package ‘sNPLS’

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**Type** Package

**Title** NPLS Regression with L1 Penalization

**Version** 1.0.27

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**Depends** R (>= 2.10)

**Imports** clickR, future, future.apply, ggplot2, ggrepel, ks, MASS,  
Matrix, pbapply

**Description** Tools for performing variable selection in three-way data using N-PLS in combination with L1 penalization, Selectivity Ratio and VIP scores. The N-PLS model (Rasmus Bro, 1996 <[DOI:10.1002/\(SICI\)1099-128X\(199601\)10:1%3C47::AID-CEM400%3E3.0.CO;2-C](https://doi.org/10.1002/(SICI)1099-128X(199601)10:1%3C47::AID-CEM400%3E3.0.CO;2-C)>) is the natural extension of PLS (Partial Least Squares) to N-way structures, and tries to maximize the covariance between X and Y data arrays. The package also adds variable selection through L1 penalization, Selectivity Ratio and VIP scores.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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bread

*Bread data*


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### Description

Evaluation of ten bread with respect to eleven attributes by eight judges (Xbread). The outcome is the salt content of each bread (Ybread).

### Usage

```
data(bread)
```

### Format

An object of class `list` of length 2.

### References

Bro, R, Multi-way Analysis in the Food Industry. Models, Algorithms, and Applications. 1998. PhD thesis, University of Amsterdam (NL) & Royal Veterinary and Agricultural University (DK).

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coef.sNPLS	<i>Coefficients from a sNPLS model</i>
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**Description**

Extract coefficients from a sNPLS model

**Usage**

```
## S3 method for class 'sNPLS'  
coef(object, as.matrix = FALSE, ...)
```

**Arguments**

object	A sNPLS model fit
as.matrix	Should the coefficients be presented as matrix or vector?
...	Further arguments passed to coef

**Value**

A matrix (or vector) of coefficients

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cv_fit	<i>Internal function for cv_snp1s</i>
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---

**Description**

Internal function for cv\_snp1s

**Usage**

```
cv_fit(  
  xtrain,  
  ytrain,  
  xval,  
  yval,  
  ncomp,  
  threshold_j = NULL,  
  threshold_k = NULL,  
  keepJ = NULL,  
  keepK = NULL,  
  method,  
  ...  
)
```

**Arguments**

xtrain	A three-way training array
ytrain	A response training matrix
xval	A three-way test array
yval	A response test matrix
ncomp	Number of components for the sNPLS model
threshold_j	Threshold value on $W_j$ . Scaled between [0, 1)
threshold_k	Threshold value on $W_k$ . Scaled between [0, 1)
keepJ	Number of variables to keep for each component, ignored if threshold_j is provided
keepK	Number of 'times' to keep for each component, ignored if threshold_k is provided
method	Select between sNPLS, sNPLS-SR or sNPLS-VIP
...	Further arguments passed to sNPLS

**Value**

Returns the CV mean squared error

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 cv\_snpls
 

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---

*Cross-validation for a sNPLS model*


---

**Description**

Performs cross-validation for a sNPLS model

**Usage**

```
cv_snpls(
  X_npls,
  Y_npls,
  ncomp = 1:3,
  samples = 20,
  keepJ = NULL,
  keepK = NULL,
  nfold = 10,
  parallel = TRUE,
  method = "sNPLS",
  ...
)
```

**Arguments**

<code>X_npls</code>	A three-way array containing the predictors.
<code>Y_npls</code>	A matrix containing the response.
<code>ncomp</code>	A vector with the different number of components to test
<code>samples</code>	Number of samples for performing random search in continuous thresholding
<code>keepJ</code>	A vector with the different number of selected variables to test for discrete thresholding
<code>keepK</code>	A vector with the different number of selected 'times' to test for discrete thresholding
<code>nfold</code>	Number of folds for the cross-validation
<code>parallel</code>	Should the computations be performed in parallel? Set up strategy first with <code>future::plan()</code>
<code>method</code>	Select between sNPLS, sNPLS-SR or sNPLS-VIP
<code>...</code>	Further arguments passed to sNPLS

**Value**

A list with the best parameters for the model and the CV error

**Examples**

```
## Not run:
X_npls<-array(rpois(7500, 10), dim=c(50, 50, 3))

Y_npls<-matrix(2+0.4*X_npls[,5,1]+0.7*X_npls[,10,1]-0.9*X_npls[,15,1]+
0.6*X_npls[,20,1]-0.5*X_npls[,25,1]+rnorm(50), ncol=1)
#Grid search for discrete thresholding
cv1<- cv_snpls(X_npls, Y_npls, ncomp=1:2, keepJ = 1:3, keepK = 1:2, parallel = FALSE)
#Random search for continuous thresholding
cv2<- cv_snpls(X_npls, Y_npls, ncomp=1:2, samples=20, parallel = FALSE)

## End(Not run)
```

---

fitted.sNPLS

*Fitted method for sNPLS models*


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**Description**

Fitted method for sNPLS models

**Usage**

```
## S3 method for class 'sNPLS'
fitted(object, ...)
```

**Arguments**

object	A sNPLS model fit
...	Further arguments passed to fitted

**Value**

Fitted values for the sNPLS model

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plot.cvsNPLS	<i>Plot cross validation results for sNPLS objects</i>
--------------	--

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**Description**

Plot function for visualization of cross validation results for sNPLS models

**Usage**

```
## S3 method for class 'cvsNPLS'
plot(x, ...)
```

**Arguments**

x	A cv_sNPLS object
...	Not used

**Value**

A facet plot with the results of the cross validation

---

plot.repeatcv	<i>Density plot for repeat_cv results</i>
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**Description**

Plots a grid of slices from the 3-D kernel density estimates of the repeat\_cv function

**Usage**

```
## S3 method for class 'repeatcv'
plot(x, ...)
```

**Arguments**

x	A repeatcv object
...	Further arguments passed to plot

**Value**

A grid of slices from a 3-D density plot of the results of the repeated cross-validation

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plot.sNPLS	<i>Plots for sNPLS model fits</i>
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---

**Description**

Different plots for sNPLS model fits

**Usage**

```
## S3 method for class 'sNPLS'
plot(x, type = "T", comps = c(1, 2), labels = TRUE, group = NULL, ...)
```

**Arguments**

x	A sNPLS model fit
type	The type of plot. One of those: "T", "U", "Wj", "Wk", "time" or "variables"
comps	Vector with the components to plot. It can be of length ncomp for types "time" and "variables" and of length 2 otherwise.
labels	Should rownames be added as labels to the plot?
group	Vector with categorical variable defining groups (optional)
...	Not used

**Value**

A plot of the type specified in the type parameter

---

plot_T	<i>Internal function for plot.sNPLS</i>
--------	---

---

**Description**

Internal function for plot.sNPLS

**Usage**

```
plot_T(x, comps, labels, group = NULL)
```

**Arguments**

x	A sNPLS model fit
comps	A vector of length two with the components to plot
labels	Should rownames be added as labels to the plot?
group	Vector with categorical variable defining groups

**Value**

A plot of the T matrix of a sNPLS model fit

---

plot_time	<i>Internal function for plot.sNPLS</i>
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---

**Description**

Internal function for plot.sNPLS

**Usage**

```
plot_time(x, comps)
```

**Arguments**

x	A sNPLS model fit
comps	A vector with the components to plot

**Value**

A plot of Wk coefficients for each component

---

plot_U	<i>Internal function for plot.sNPLS</i>
--------	---

---

**Description**

Internal function for plot.sNPLS

**Usage**

```
plot_U(x, comps, labels, group = NULL)
```

**Arguments**

x	A sNPLS model fit
comps	A vector of length two with the components to plot
labels	Should rownames be added as labels to the plot?
group	Vector with categorical variable defining groups

**Value**

A plot of the U matrix of a sNPLS model fit

---

plot_variables	<i>Internal function for plot.sNPLS</i>
----------------	---

---

**Description**

Internal function for plot.sNPLS

**Usage**

```
plot_variables(x, comps)
```

**Arguments**

x	A sNPLS model fit
comps	A vector with the components to plot

**Value**

A plot of W<sub>j</sub> coefficients for each component

---

plot_Wj	<i>Internal function for plot.sNPLS</i>
---------	---

---

**Description**

Internal function for plot.sNPLS

**Usage**

```
plot_Wj(x, comps, labels)
```

**Arguments**

x	A sNPLS model fit
comps	A vector of length two with the components to plot
labels	Should rownames be added as labels to the plot?

**Value**

A plot of  $W_j$  coefficients

---

plot_Wk	<i>Internal function for plot.sNPLS</i>
---------	---

---

**Description**

Internal function for plot.sNPLS

**Usage**

```
plot_Wk(x, comps, labels)
```

**Arguments**

x	A sNPLS model fit
comps	A vector of length two with the components to plot
labels	Should rownames be added as labels to the plot?

**Value**

A plot of the  $W_k$  coefficients

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predict.sNPLS	<i>Predict for sNPLS models</i>
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**Description**

Predict function for sNPLS models

**Usage**

```
## S3 method for class 'sNPLS'
predict(object, newX, rescale = TRUE, ...)
```

**Arguments**

object	A sNPLS model fit
newX	A three-way array containing the new data
rescale	Should the prediction be rescaled to the original scale?
...	Further arguments passed to predict

**Value**

A matrix with the predictions

---

repeat_cv	<i>Repeated cross-validation for sNPLS models</i>
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---

**Description**

Performs repeated cross-validation and represents results in a plot

**Usage**

```
repeat_cv(
  X_npls,
  Y_npls,
  ncomp = 1:3,
  samples = 20,
  keepJ = NULL,
  keepK = NULL,
  nfold = 10,
  times = 30,
  parallel = TRUE,
  method = "sNPLS",
  ...
)
```

**Arguments**

X_npls	A three-way array containing the predictors.
Y_npls	A matrix containing the response.
ncomp	A vector with the different number of components to test
samples	Number of samples for performing random search in continuous thresholding
keepJ	A vector with the different number of selected variables to test in discrete thresholding
keepK	A vector with the different number of selected 'times' to test in discrete thresholding
nfold	Number of folds for the cross-validation

<code>times</code>	Number of repetitions of the cross-validation
<code>parallel</code>	Should the computations be performed in parallel? Set up strategy first with <code>future::plan()</code>
<code>method</code>	Select between sNPLS, sNPLS-SR or sNPLS-VIP
<code>...</code>	Further arguments passed to <code>cv_snpls</code>

**Value**

A density plot with the results of the cross-validation and an (invisible) `data.frame` with these results

---

<code>Rmatrix</code>	<i>R-matrix from a sNPLS model fit</i>
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---

**Description**

Builds the R-matrix from a sNPLS model fit

**Usage**

```
Rmatrix(x)
```

**Arguments**

`x` A sNPLS model obtained from sNPLS

**Value**

Returns the R-matrix of the model, needed to compute the coefficients

---

<code>sNPLS</code>	<i>Fit a sNPLS model</i>
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---

**Description**

Fits a N-PLS regression model imposing sparsity on `wj` and `wk` matrices

**Usage**

```

sNPLS(
  XN,
  Y,
  ncomp = 2,
  threshold_j = 0.5,
  threshold_k = 0.5,
  keepJ = NULL,
  keepK = NULL,
  scale.X = TRUE,
  center.X = TRUE,
  scale.Y = TRUE,
  center.Y = TRUE,
  conver = 1e-16,
  max.iteration = 10000,
  silent = F,
  method = "sNPLS"
)

```

**Arguments**

XN	A three-way array containing the predictors.
Y	A matrix containing the response.
ncomp	Number of components in the projection
threshold_j	Threshold value on $W_j$ . Scaled between [0, 1)
threshold_k	Threshold value on $W_k$ . scaled between [0, 1)
keepJ	Number of variables to keep for each component, ignored if threshold_j is provided
keepK	Number of 'times' to keep for each component, ignored if threshold_k is provided
scale.X	Perform unit variance scaling on X?
center.X	Perform mean centering on X?
scale.Y	Perform unit variance scaling on Y?
center.Y	Perform mean centering on Y?
conver	Convergence criterion
max.iteration	Maximum number of iterations
silent	Show output?
method	Select between L1 penalization (sNPLS), variable selection with Selectivity Ratio (sNPLS-SR) or variable selection with VIP (sNPLS-VIP)

**Value**

A fitted sNPLS model

## References

C. A. Andersson and R. Bro. The N-way Toolbox for MATLAB Chemometrics & Intelligent Laboratory Systems. 52 (1):1-4, 2000.

Hervas, D. Prats-Montalban, J. M., Garcia-Cañaveras, J. C., Lahoz, A., & Ferrer, A. (2019). Sparse N-way partial least squares by L1-penalization. Chemometrics and Intelligent Laboratory Systems, 185, 85-91.

## Examples

```
X_npls<-array(rpois(7500, 10), dim=c(50, 50, 3))

Y_npls <- matrix(2+0.4*X_npls[,5,1]+0.7*X_npls[,10,1]-0.9*X_npls[,15,1]+
0.6*X_npls[,20,1]- 0.5*X_npls[,25,1]+rnorm(50), ncol=1)
#Discrete thresholding
fit <- sNPLS(X_npls, Y_npls, ncomp=3, keepJ = rep(2,3) , keepK = rep(1,3))
#Continuous thresholding
fit2 <- sNPLS(X_npls, Y_npls, ncomp=3, threshold_j=0.5, threshold_k=0.5)
#Use sNPLS-SR method
fit3 <- sNPLS(X_npls, Y_npls, ncomp=3, threshold_j=0.5, threshold_k=0.5, method="sNPLS-SR")
```

---

SR

*Compute Selectivity Ratio for a sNPLS model*

---

## Description

Estimates Selectivity Ratio for the different components of a sNPLS model fit

## Usage

```
SR(model)
```

## Arguments

model            A sNPLS model

## Value

A list of data.frames, each of them including the computed Selectivity Ratios for each variable

---

summary.sNPLS	<i>Summary for sNPLS models</i>
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---

**Description**

Summary of a sNPLS model fit

**Usage**

```
## S3 method for class 'sNPLS'  
summary(object, ...)
```

**Arguments**

object	A sNPLS object
...	Further arguments passed to summary.default

**Value**

A summary including number of components, squared error and coefficients of the fitted model

---

unfold3w	<i>Unfolding of three-way arrays</i>
----------	--------------------------------------

---

**Description**

Unfolds a three-way array into a matrix

**Usage**

```
unfold3w(x)
```

**Arguments**

x	A three-way array
---	-------------------

**Value**

Returns a matrix with dimensions  $\text{dim}(x)[1] \times \text{dim}(x)[2] * \text{dim}(x)[3]$

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