The pls Package

October 18, 2007

Version 2.1-0

Date 2007-10-17

Title Partial Least Squares Regression (PLSR) and Principal Component Regression (PCR)

Author Ron Wehrens and Bjørn-Helge Mevik

Maintainer Bjørn-Helge Mevik <pls@mevik.net>

Encoding latin1

Description Multivariate regression by partial least squares regression (PLSR) and principal component regression (PCR).

License GPL-2

URL http://mevik.net/work/software/pls.html

R topics documented:

biplot.mvr ................................................................. 2
coef.mvr ................................................................. 3
coefplot ................................................................. 5
crossval ................................................................. 8
cvsegments ............................................................. 10
delete.intercept ........................................................ 11
gasoline ................................................................. 12
jack.test ................................................................. 12
kernelpls.fit ........................................................... 14
msc ....................................................................... 16
mvr ....................................................................... 17
mvrCv ................................................................. 20
mvrVal ................................................................. 22
naExcludeMvr .......................................................... 24
oliveoil ................................................................. 25
oscorespls.fit ......................................................... 26
plot.mvr ............................................................... 27
Biplots of PLSR and PCR Models.

Description

Biplot method for \texttt{mvr} objects.

Usage

```r
## S3 method for class 'mvr':
biplot(x, comps = 1:2, which = c("x", "y", "scores", "loadings"),
      var.axes = FALSE, xlabs, ylabs, main, ...)
```

Arguments

- \texttt{x} an \texttt{mvr} object.
- \texttt{comps} integer vector of length two. The components to plot.
- \texttt{which} character. Which matrices to plot. One of "x" (X scores and loadings), "y" (Y scores and loadings), "scores" (X and Y scores) and "loadings" (X and Y loadings).
- \texttt{var.axes} logical. If \texttt{TRUE}, the second set of points have arrows representing them.
- \texttt{xlabs} either a character vector of labels for the first set of points, or \texttt{FALSE} for no labels. If missing, the row names of the first matrix is used as labels.
- \texttt{ylabs} either a character vector of labels for the second set of points, or \texttt{FALSE} for no labels. If missing, the row names of the second matrix is used as labels.
- \texttt{main} character. Title of plot. If missing, a title is constructed by \texttt{biplot.mvr}.
- ... Further arguments passed on to \texttt{biplot.default}.

Details

\texttt{biplot.mvr} can also be called through the \texttt{mvr} plot method by specifying \texttt{plottype = "biplot"}. 

Index

- \texttt{biplot.mvr}
Author(s)
Ron Wehrens and Bjørn-Helge Mevik

See Also
mvr, plot.mvr, biplot.default

Examples

data(oliveoil)
mod <- plsR(sensory ~ chemical, data = oliveoil)
## Not run:
## These are equivalent
biplot(mod)
plot(mod, plottype = "biplot")

## The four combinations of x and y points:
par(mfrow = c(2,2))
biplot(mod, which = "x") # Default
biplot(mod, which = "y")
biplot(mod, which = "scores")
biplot(mod, which = "loadings")
## End(Not run)

coef.mvr

Extract Information From a Fitted PLSR or PCR Model

Description
Functions to extract information from mvr objects: Regression coefficients, fitted values, residuals, the model frame, the model matrix, names of the variables and components, and the $X$ variance explained by the components.

Usage

## S3 method for class 'mvr':
coef(object, ncomp = object$ncomp, comps, intercept = FALSE, ...)
## S3 method for class 'mvr':
fitted(object, ...)
## S3 method for class 'mvr':
residuals(object, ...)
## S3 method for class 'mvr':
model.frame(formula, ...)
## S3 method for class 'mvr':
prednames(object, intercept = FALSE)
## S3 method for class 'mvr':
resnames(object)
## S3 method for class 'mvr':
comprnames(object, comps, explvar = FALSE, ...)
## S3 method for class 'mvr':
explvar(object)
Arguments

object, formula

an mvr object. The fitted model.

ncomp, comps

vector of positive integers. The components to include in the coefficients or to extract the names of. See below.

intercept

logical. Whether coefficients for the intercept should be included. Ignored if comps is specified. Defaults to FALSE.

explvar

logical. Whether the explained \( X \) variance should be appended to the component names.

... other arguments sent to underlying functions. Currently only used for model.frame.mvr and model.matrix.mvr.

Details

These functions are mostly used inside other functions. (Functions coef.mvr, fitted.mvr and residuals.mvr are usually called through their generic functions coef, fitted and residuals, respectively.)

coef.mvr is used to extract the regression coefficients of a model, i.e. the \( B \) in \( y = XB \) (for the \( Q \) in \( y = TQ \) where \( T \) is the scores, see Yloadings). An array of dimension \( c(nxvar, nyvar, \text{length}(ncomp)) \) or \( c(nxvar, nyvar, \text{length}(comps)) \) is returned.

If \( \text{comps} \) is missing (or is NULL), \( \text{coef}()[,,\text{ncomp}[i]] \) are the coefficients for models with \( \text{ncomp}[i] \) components, for \( i = 1,...,\text{length}(\text{ncomp}) \). Also, if \( \text{intercept} = \text{TRUE} \), the first dimension is \( nxvar + 1 \), with the intercept coefficients as the first row.

If \( \text{comps} \) is given, however, \( \text{coef}()[,,\text{comps}[i]] \) are the coefficients for a model with only the component \( \text{comps}[i] \), i.e. the contribution of the component \( \text{comps}[i] \) on the regression coefficients.

fitted.mvr and residuals.mvr return the fitted values and residuals, respectively. If the model was fitted with \( \text{na.action} = \text{na.exclude} \) (or after setting the default \( \text{na.action} \) to "na.exclude" with \( \text{options} \)), the fitted values (or residuals) corresponding to excluded observations are returned as NA; otherwise, they are omitted.

model.frame.mvr returns the model frame; i.e. a data frame with all variables necessary to generate the model matrix. See model.frame for details.

model.matrix.mvr returns the (possibly coded) matrix used as \( X \) in the fitting. See model.matrix for details.

prednames, respnames and compnames extract the names of the \( X \) variables, responses and components, respectively. With \( \text{intercept} = \text{TRUE} \) in prednames, the name of the intercept variable (i.e. "(Intercept) ") is returned as well. compnames can also extract component names from score and loading matrices. If explvar = TRUE in compnames, the explained variance for each component (if available) is appended to the component names. For optimal formatting of the explained variances when not all components are to be used, one should specify the desired components with the argument \( \text{comps} \).

explvar extracts the amount of \( X \) variance (in per cent) explained by for each component in the model. It can also handle score and loading matrices returned by scores and loadings.
Value

 coef.mvr returns an array of regression coefficients.
 fitted.mvr returns an array with fitted values.
 residuals.mvr returns an array with residuals.
 model.frame.mvr returns a data frame.
 model.matrix.mvr returns the X matrix.
 prednames, respnames and compnames return a character vector with the corresponding names.
 explvar returns a numeric vector with the explained variances, or NULL if not available.

Author(s)
Ron Wehrens and Bjørn-Helge Mevik

See Also
mvr, coef, fitted, residuals, model.frame, model.matrix, na.omit

Examples

data(yarn)
mod <- pcr(density ~ NIR, data = yarn[yarn$train,,] ncomp = 5)
B <- coef(mod, ncomp = 3, intercept = TRUE)
## A manual predict method:
stopifnot(drop(B[1,,] + yarn$NIR[!yarn$train,,] %*% B[-1,,]) ==
  drop(predict(mod, ncomp = 3, newdata = yarn[!yarn$train,,])))
## Note the difference in formatting:
mod2 <- pcr(density ~ NIR, data = yarn[yarn$train,,])
compnames(mod2, explvar = TRUE)[1:3]
compnames(mod2, comps = 1:3, explvar = TRUE)

coefplot

Plot Regression Coefficients of PLSR and PCR models

Description

Function to plot the regression coefficients of an mvr object.

Usage

ccoefplot(object, ncomp = object$ncomp, comps, intercept = FALSE, separate = FALSE, nCols, nRows, labels, type = "l", lty = 1:nLines, lwd = NULL, pch = 1:nLines, cex = NULL, col = 1:nLines, legendpos, xlab = "variable", ylab = "regression coefficient", main, pretty.xlabels = TRUE, xlim, ...)
Arguments

**object**
- an `mvr` object. The fitted model.

**ncomp, comps**
- vector of positive integers. The components to plot. See `coef.mvr` for details.

**separate**
- logical. If TRUE, coefficients for different model sizes are blotted in separate plots.

**intercept**
- logical. Whether coefficients for the intercept should be plotted. Ignored if `comps` is specified. Defaults to FALSE. See `coef.mvr` for details.

**nCols, nRows**
- integer. The number of columns and rows the plots will be laid out in. If not specified, `coefplot` tries to be intelligent.

**labels**
- optional. Alternative x axis labels. See Details.

**type**
- character. What type of plot to make. Defaults to "l" (lines). Alternative types include "p" (points) and "b" (both). See `plot` for a complete list of types.

**lty**
- vector of line types (recycled as necessary). Line types can be specified as integers or character strings (see `par` for the details).

**lwd**
- vector of positive numbers (recycled as necessary), giving the width of the lines.

**pch**
- plot character. A character string or a vector of single characters or integers (recycled as necessary). See `points` for all alternatives.

**cex**
- numeric vector of character expansion sizes (recycled as necessary) for the plotted symbols.

**col**
- character or integer vector of colors for plotted lines and symbols (recycled as necessary). See `par` for the details.

**legendpos**
- Legend position. Optional. Ignored if `separate` is TRUE. If present, a legend is drawn at the given position. The position can be specified symbolically (e.g., `legendpos = "topright"`). This requires R >= 2.1.0. Alternatively, the position can be specified explicitly (`legendpos = t(c(x,y))`) or interactively (`legendpos = locator()`). This only works well for plots of single-response models.

**xlab, ylab**
- titles for x and y axes. Typically character strings, but can be expressions (e.g., `expression(R^2)`) or lists. See `title` for details.

**main**
- optional main title for the plot. See Details.

**pretty.xlabels**
- logical. If TRUE, `coefplot` tries to plot the x labels more nicely. See Details.

**xlim**
- optional vector of length two, with the x limits of the plot.

**...**
- Further arguments sent to the underlying plot functions.

Details

`coefplot` handles multiple responses by making one plot for each response. If `separate` is TRUE, separate plots are made for each combination of model size and response. The plots are laid out in a rectangular fashion.

If `legendpos` is given, a legend is drawn at the given position (unless `separate` is TRUE).
The argument \texttt{labels} can be a vector of labels or one of "names" and "numbers". The labels are used as x-axis labels. If \texttt{labels} is "names" or "numbers", the variable names are used as labels, the difference being that with "numbers", the variable names are converted to numbers, if possible. Variable names of the forms "number" or "number text" (where the space is optional), are handled.

The argument \texttt{main} can be used to specify the main title of the plot. It is handled in a non-standard way. If there is only on (sub) plot, \texttt{main} will be used as the main title of the plot. If there is more than one (sub) plot, however, the presence of \texttt{main} will produce a corresponding 'global' title on the page. Any graphical parameters, e.g., \texttt{cex.main}, supplied to \texttt{coefplot} will only affect the 'ordinary' plot titles, not the 'global' one. Its appearance can be changed by setting the parameters with \texttt{par}, which will affect both titles. (To have different settings for the two titles, one can override the \texttt{par} settings with arguments to \texttt{coefplot}.)

The argument \texttt{pretty.xlabels} is only used when \texttt{labels} is specified. If TRUE (default), the code tries to use a 'pretty' selection of labels. If \texttt{labels} is "numbers", it also uses the numerical values of the labels for horizontal spacing. If one has excluded parts of the spectral region, one might therefore want to use \texttt{pretty.xlabels = FALSE}.

The function can also be called through the \texttt{mvr} plot method by specifying \texttt{plottype = "coefficients"}.

\textbf{Note}

\texttt{legend} has many options. If you want greater control over the appearance of the legend, omit the \texttt{legendpos} argument and call \texttt{legend} manually.

The handling of \texttt{labels} and \texttt{pretty.xlabels} is experimental.

\textbf{Author(s)}

Ron Wehrens and Bjørn-Helge Mevik

\textbf{See Also}

\texttt{mvr, plot.mvr, coef.mvr, plot, legend}

\textbf{Examples}

\begin{verbatim}
data(yarn)
mod.nir <- pls(density ~ NIR, ncomp = 8, data = yarn)
  # Not run:
  coefplot(mod.nir, ncomp = 1:6)
plot(mod.nir, plottype = "coefficients", ncomp = 1:6)  # Equivalent to the previous
  # Plot with legend:
  coefplot(mod.nir, ncom = 1:6, legendpos = "bottomright")
  # End (Not run)
data(oliveoil)
mod.sens <- pls(sensory ~ chemical, ncomp = 4, data = oliveoil)
  # Not run: coefplot(mod.sens, ncomp = 2:4, separate = TRUE)
\end{verbatim}
Cross-validation of PLSR and PCR models

Description
A “stand alone” cross-validation function for mvr objects.

Usage
```r
crossval(object, segments = 10,
  segment.type = c("random", "consecutive", "interleaved"),
  length.seg, jackknife = FALSE, trace = 15, ...)
```

Arguments
- **object**: an mvr object; the regression to cross-validate.
- **segments**: the number of segments to use, or a list with segments (see below). Ignored if loo = TRUE.
- **segment.type**: the type of segments to use. Ignored if segments is a list.
- **length.seg**: Positive integer. The length of the segments to use. If specified, it overrides segments unless segments is a list.
- **jackknife**: logical. Whether jackknifing of regression coefficients should be performed.
- **trace**: if TRUE, tracing is turned on. If numeric, it denotes a time limit (in seconds). If the estimated total time of the cross-validation exceeds this limit, tracing is turned on.
- **...**: additional arguments, sent to the underlying fit function.

Details
This function performs cross-validation on a model fit by mvr. It can handle models such as plsr(y ~ msc(X), ...) or other models where the predictor variables need to be recalculated for each segment. When recalculation is not needed, the result of crossval(mvr(...)) is identical to mvr(..., validation = "CV"), but slower.

Note that to use crossval, the data must be specified with a data argument when fitting object. If segments is a list, the arguments segment.type and length.seg are ignored. The elements of the list should be integer vectors specifying the indices of the segments. See cvsegments for details.

Otherwise, segments of type segment.type are generated. How many segments to generate is selected by specifying the number of segments in segments, or giving the segment length in length.seg. If both are specified, segments is ignored.

If jackknife is TRUE, jackknifed regression coefficients are returned, which can be used for for variance estimation (var.jack) or hypothesis testing (jack.test).

When tracing is turned on, the segment number is printed for each segment.
Value

The supplied object is returned, with an additional component validation, which is a list with components

- **method**
  - euqals "CV" for cross-validation.
- **pred**
  - an array with the cross-validated predictions.
- **coefficients** (only if jackknife is TRUE) an array with the jackknifed regression coefficients. The dimensions correspond to the predictors, responses, number of components, and segments, respectively.
- **PRESS0**
  - a vector of PRESS values (one for each response variable) for a model with zero components, i.e., only the intercept.
- **PRESS**
  - a matrix of PRESS values for models with 1, ..., ncomp components. Each row corresponds to one response variable.
- **adj**
  - a matrix of adjustment values for calculating bias corrected MSEP. MSEP uses this.
- **segments**
  - the list of segments used in the cross-validation.
- **ncomp**
  - the number of components.

Note

The PRESS0 is always cross-validated using leave-one-out cross-validation. This usually makes little difference in practice, but should be fixed for correctness.

The current implementation of the jackknife stores all jackknife-replicates of the regression coefficients, which can be very costly for large matrices. This might change in a future version.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

References


See Also

- mvr
- mvrCv
- cvsegments
- MSEP
- var.jack
- jack.test

Examples

data(yarn)
yarn.pcr <- pcr(density ~ msc(NIR), 6, data = yarn)
yarn.cv <- crossval(yarn.pcr, segments = 10)
## Not run: plot(MSEP(yarn.cv))
cvsegments  

Generate segments for cross-validation

Description

The function generates a list of segments for cross-validation. Random, consecutive and interleaved segments can be produced.

Usage

```r
cvsegments(N, k, length.seg = ceiling(N/k),
            type = c("random", "consecutive", "interleaved"))
```

Arguments

- `N`  
  Integer. The number of objects in the data set.

- `k`  
  Integer. The number of segments to return.

- `length.seg`  
  Integer. The length of the segments. If given, it overrides `k`.

- `type`  
  One of "random", "consecutive" and "interleaved". The type of segments to generate. Default is "random".

Details

If `length.seg` is specified, it is used to calculate the number of segments to generate. Otherwise `k` must be specified. If `k * length.seg ≠ N`, the `k * length.seg - N` last segments will contain only `length.seg - 1` indices.

If `type` is "random", the indices are allocated to segments in random order. If it is "consecutive", the first segment will contain the first `length.seg` indices, and so on. If `type` is "interleaved", the first segment will contain the indices 1, `length.seg` + 1, 2 * `length.seg` + 1, . . . , (`k` - 1) * `length.seg` + 1, and so on.

Value

A list of vectors. Each vector contains the indices for one segment. The attribute "incomplete" contains the number of incomplete segments, and the attribute "type" contains the type of segments.

Author(s)

Bjørn-Helge Mevik and Ron Wehrens
**delete.intercept**  

Delete intercept from model matrix

### Description

A utility function to delete any intercept column from a model matrix, and adjust the "assign" attribute correspondingly. It is used by formula handling functions like `mvr` and `model.matrix.mvr`.

### Usage

```r
delete.intercept(mm)
```

### Arguments

- `mm`  
  Model matrix.

### Value

A model matrix without intercept column.

### Author(s)

Bjørn-Helge Mevik and Ron Wehrens

### See Also

- `mvr`
- `model.matrix.mvr`

---

**Examples**

```r
## Segments for 10-fold randomised cross-validation:
cvsegments(100, 10)

## Segments with four objects, taken consecutive:
cvsegments(60, length.seg = 4, type = "cons")

## Incomplete segments
segs <- cvsegments(50, length.seg = 3)
attr(segs, "incomplete")

## Leave-one-out cross-validation:
cvsegments(100, 100)

## Leave-one-out with variable/unknown data set size n:
n <- 50
cvsegments(n, length.seg = 1)
```
gasoline  

Octane numbers and NIR spectra of gasoline

Description
A data set with NIR spectra and octane numbers of 60 gasoline samples. The NIR spectra were measured using diffuse reflectance as \( \log(1/R) \) from 900 nm to 1700 nm in 2 nm intervals, giving 401 wavelengths. Many thanks to John H. Kalivas.

Usage
data(gasoline)

Format
A data frame with 60 observations on the following 2 variables.

octane  a numeric vector. The octane number.
NIR  a matrix with 401 columns. The NIR spectrum.

Source

Jackknife approximate t tests of regression coefficients

Description
Performes approximate t tests of regression coefficients based on jackknife variance estimates.

Usage
jack.test(object, ncomp = object$ncomp, use.mean = TRUE)
## S3 method for class 'jacktest':
print(x, P.values = TRUE, ...)

Arguments

- **object**: an `mvr` object. A cross-validated model fitted with `jackknife = TRUE`.
- **ncomp**: the number of components to use for estimating the variances.
- **use.mean**: logical. If `TRUE` (default), the mean coefficients are used when estimating the (co)variances; otherwise the coefficients from a model fitted to the entire data set. See `var.jack` for details.
- **x**: an `jacktest` object, the result of `jack.test`.
- **P.values**: logical. Whether to print \( p \)-values (default).
- **...**: Further arguments sent to the underlying print function `printCoefmat`.

Details

`jack.test` uses the variance estimates from `var.jack` to perform \( t \) tests of the regression coefficients. The resulting object has a print method, `print.jacktest`, which uses `printCoefmat` for the actual printing.

Value

`jack.test` returns an object of class "jacktest", with components:

- **coefficients**: The estimated regression coefficients
- **sd**: The square root of the jackknife variance estimates
- **tvalues**: The \( t \) statistics
- **df**: The `degrees of freedom` used for calculating \( p \) values
- **pvalues**: The calculated \( p \) values

`print.jacktest` returns the "jacktest" object (invisibly).

Warning

The jackknife variance estimates are known to be biased (see `var.jack`). Also, the distribution of the regression coefficient estimates and the jackknife variance estimates are unknown (at least in PLSR/PCR). Consequently, the distribution (and in particular, the degrees of freedom) of the resulting \( t \) statistics is unknown. The present code simply assumes a \( t \) distribution with \( m - 1 \) degrees of freedom, where \( m \) is the number of cross-validation segments.

Therefore, the resulting \( p \)-values should not be used uncritically, and should perhaps be regarded as mere indicator of (non-)significance.

Finally, also keep in mind that as the number of predictor variables increase, the problem of multiple tests increases correspondingly.

Author(s)

Bjørn-Helge Mevik
kernelpls.fit

References


See Also

`var.jack`, `mvrCv`

Examples

```r
data(oliveoil)
mod <- pcr(sensory ~ chemical, data = oliveoil, validation = "LOO", jackknife = TRUE)
jack.test(mod, ncomp = 2)
```

---

**kernelpls.fit**

*Kernel PLS (Dayal and MacGregor)*

Description

Fits a PLSR model with the kernel algorithm.

Usage

`kernelpls.fit(X, Y, ncomp, stripped = FALSE, ...)`

Arguments

- **X**: a matrix of observations. NAs and Infs are not allowed.
- **Y**: a vector or matrix of responses. NAs and Infs are not allowed.
- **ncomp**: the number of components to be used in the modelling.
- **stripped**: logical. If TRUE the calculations are stripped as much as possible for speed; this is meant for use with cross-validation or simulations when only the coefficients are needed. Defaults to FALSE.
- **...**: other arguments. Currently ignored.

Details

This function should not be called directly, but through the generic functions `plsr` or `mvr` with the argument `method="kernelpls"` (default). Kernel PLS is particularly efficient when the number of objects is (much) larger than the number of variables. The results are equal to the NIPALS algorithm. Several different forms of kernel PLS have been described in literature, e.g. by De Jong and Ter Braak, and two algorithms by Dayal and MacGregor. This function implements the fastest of the latter, not calculating the crossproduct matrix of X. In the Dyal & MacGregor paper, this is “algorithm 1”. 

**Value**

A list containing the following components is returned:

- **coefficients**: an array of regression coefficients for 1, ..., ncomp components. The dimensions of coefficients are $c(nvar, npred, ncomp)$ with $nvar$ the number of $X$ variables and $npred$ the number of variables to be predicted in $Y$.
- **scores**: a matrix of scores.
- **loadings**: a matrix of loadings.
- **loading.weights**: a matrix of loading weights.
- **Yscores**: a matrix of $Y$-scores.
- **Yloadings**: a matrix of $Y$-loadings.
- **projection**: the projection matrix used to convert $X$ to scores.
- **Xmeans**: a vector of means of the $X$ variables.
- **Ymeans**: a vector of means of the $Y$ variables.
- **fitted.values**: an array of fitted values. The dimensions of fitted.values are $c(nobj, npred, ncomp)$ with $nobj$ the number samples and $npred$ the number of $Y$ variables.
- **residuals**: an array of regression residuals. It has the same dimensions as fitted.values.
- **Xvar**: a vector with the amount of $X$-variance explained by each number of components.
- **Xtotvar**: Total variance in $X$.

If `stripped` is TRUE, only the components coefficients, Xmeans and Ymeans are returned.

**Author(s)**

Ron Wehrens and Bjørn-Helge Mevik

**References**


**See Also**

- `mvr`
- `plsr`
- `pcr`
- `widekernelpls.fit`
- `simpls.fit`
- `oscorespls.fit`
**Description**

Performs multiplicative scatter/signal correction on a data matrix.

**Usage**

```r
msc(X, reference = NULL)
## S3 method for class 'msc':
predict(object, newdata, ...)
## S3 method for class 'msc':
makepredictcall(var, call)
```

**Arguments**

- `X, newdata` numeric matrices. The data to scatter correct.
- `reference` numeric vector. Spectre to use as reference. If `NULL`, the column means of `X` are used.
- `object` an object inheriting from class "msc", normally the result of a call to `msc` with a single matrix argument.
- `var` A variable.
- `call` The term in the formula, as a call.
- `...` other arguments. Currently ignored.

**Details**

`makepredictcall.msc` is an internal utility function; it is not meant for interactive use. See `makepredictcall` for details.

**Value**

Both `msc` and `predict.msc` return a multiplicative scatter corrected matrix, with attribute "reference" the vector used as reference spectre. The matrix is given class c("msc", "matrix"). For `predict.msc`, the "reference" attribute of `object` is used as reference spectre.

**Author(s)**

Bjørn-Helge Mevik and Ron Wehrens

**References**

mvr

See Also

mvr, pcr, plsr, stdize

Examples

data(yarn)

## Direct correction:
Ztrain <- msc(yarn$NIR[yarn$train,])
Ztest <- predict(Ztrain, yarn$NIR[!yarn$train,])

## Used in formula:
mod <- plsr(density ~ msc(NIR), ncomp = 6, data = yarn[yarn$train,])
pred <- predict(mod, newdata = yarn[!yarn$train,]) # Automatically scatter corrected

mvr

Partial Least Squares and Principal Component Regression

Description

Functions to perform partial least squares regression (PLSR) or principal component regression (PCR), with a formula interface. Cross-validation can be used. Prediction, model extraction, plot, print and summary methods exist.

Usage

mvr(formula, ncomp, data, subset, na.action,
    method = pls.options()$mvralg,
    scale = FALSE, validation = c("none", "CV", "LOO"),
    model = TRUE, x = FALSE, y = FALSE, ...)
plsr(..., method = pls.options()$plsralg)
pcr(..., method = pls.options()$pcralg)

Arguments

formula a model formula. Most of the lm formula constructs are supported. See below.
ncomp the number of components to include in the model (see below).
data an optional data frame with the data to fit the model from.
subset an optional vector specifying a subset of observations to be used in the fitting process.
na.action a function which indicates what should happen when the data contain missing values.
method the multivariate regression method to be used. If "model.frame", the model frame is returned.
scale numeric vector, or logical. If numeric vector, X is scaled by dividing each variable with the corresponding element of scale. If scale is TRUE, X is scaled by dividing each variable by its sample standard deviation. If cross-validation is selected, scaling by the standard deviation is done for every segment.
validation character. What kind of (internal) validation to use. See below.
model a logical. If TRUE, the model frame is returned.
X a logical. If TRUE, the model matrix is returned.
y a logical. If TRUE, the response is returned.
... additional arguments, passed to the underlying fit functions, and mvrCv.

Details

The functions fit PLSR or PCR models with 1, \ldots, ncomp number of components. Multi-response models are fully supported.

The type of model to fit is specified with the method argument. Four PLSR algorithms are available: the kernel algorithm ("kernelpls"), the wide kernel algorithm ("widekernelpls"), SIMPLS ("simpls") and the classical orthogonal scores algorithm ("oscorespls"). One PCR algorithm is available: using the singular value decomposition ("svdpc"). If method is "model.frame", the model frame is returned. The functions pcr and plsr are wrappers for mvr, with different values for method.

The formula argument should be a symbolic formula of the form response ~ terms, where response is the name of the response vector or matrix (for multi-response models) and terms is the name of one or more predictor matrices, usually separated by +, e.g., water ~ FTIR or y ~ X + Z. See \texttt{lm} for a detailed description. The named variables should exist in the supplied data data frame or in the global environment. Note: Do not use mvr(mydata$y ~ mydata$X, ...), instead use mvr(y ~ X, data = mydata, ...). Otherwise, predict.mvr will not work properly. The chapter ‘Statistical models in R’ of the manual ‘An Introduction to R’ distributed with R is a good reference on formulas in R.

The number of components to fit is specified with the argument ncomp. It this is not supplied, the maximal number of components is used (taking account of any cross-validation).

If validation = "CV", cross-validation is performed. The number and type of cross-validation segments are specified with the arguments segments and segment.type. See mvrCv for details. If validation = "LOO", leave-one-out cross-validation is performed. It is an error to specify the segments when validation = "LOO" is specified.

Note that the cross-validation is optimised for speed, and some generality has been sacrificed. Especially, the model matrix is calculated only once for the complete cross-validation, so models like y ~ msc(X) will not be properly cross-validated. However, scaling requested by scale = TRUE is properly cross-validated. For proper cross-validation of models where the model matrix must be updated/regenerated for each segment, use the separate function crossval.

Value

If method = "model.frame", the model frame is returned. Otherwise, an object of class mvr is returned. The object contains all components returned by the underlying fit function. In addition, it contains the following components:

validation if validation was requested, the results of the cross-validation. See mvrCv for details.
na.action if observations with missing values were removed, na.action contains a vector with their indices. The class of this vector is used by functions like fitted to decide how to treat the observations.
ncomp

the number of components of the model.

method

the method used to fit the model. See the argument method for possible values.

scale

if scaling was requested (with scale), the scaling used.

call

the function call.

terms

the model terms.

model

if model = TRUE, the model frame.

x

if x = TRUE, the model matrix.

y

if y = TRUE, the model response.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

References


See Also

`kernelpls.fit`, `widekernelpls.fit`, `simpls.fit`, `oscorespls.fit`, `svdpc.fit`, `mvrCv`, `crossval`, `loadings`, `scores`, `loading.weights`, `coef.mvr`, `predict.mvr`, `R2`, `MSEP`, `RMSEP`, `plot.mvr`

Examples

data(yarn)
## Default methods:
yarn.pcr <- pcr(density ~ NIR, 6, data = yarn, validation = "CV")
yarn.pls <- plsr(density ~ NIR, 6, data = yarn, validation = "CV")

## Alternative methods:
yarn.oscorespls <- mvr(density ~ NIR, 6, data = yarn, validation = "CV",
                    method = "oscorespls")
yarn.simpls <- mvr(density ~ NIR, 6, data = yarn, validation = "CV",
                    method = "simpls")

data(oliveoil)
sens.pcr <- pcr(sensory ~ chemical, ncomp = 4, scale = TRUE, data = oliveoil)
sens.pls <- plsr(sensory ~ chemical, ncomp = 4, scale = TRUE, data = oliveoil)
Cross-validation

Description

Performs the cross-validation calculations for `mvr`.

Usage

```r
mvrCv(X, Y, ncomp,
     method = pls.options()$mvralg, scale = FALSE,
     segments = 10, segment.type = c("random", "consecutive", "interleaved"),
     length.seg, jackknife = FALSE, trace = FALSE, ...)
```

Arguments

- **X**: a matrix of observations. NAs and Infs are not allowed.
- **Y**: a vector or matrix of responses. NAs and Infs are not allowed.
- **ncomp**: the number of components to be used in the modelling.
- **method**: the multivariate regression method to be used.
- **scale**: logical. If `TRUE`, the learning `X` data for each segment is scaled by dividing each variable by its sample standard deviation. The prediction data is scaled by the same amount.
- **segments**: the number of segments to use, or a list with segments (see below).
- **segment.type**: the type of segments to use. Ignored if `segments` is a list.
- **length.seg**: Positive integer. The length of the segments to use. If specified, it overrides `segments` unless `segments` is a list.
- **jackknife**: logical. Whether jackknifing of regression coefficients should be performed.
- **trace**: logical; if `TRUE`, the segment number is printed for each segment.
- **...**: additional arguments, sent to the underlying fit function.

Details

This function is not meant to be called directly, but through the generic functions `pcr`, `plsr` or `mvr` with the argument `validation` set to "CV" or "LOO". All arguments to `mvrCv` can be specified in the generic function call.

If `segments` is a list, the arguments `segment.type` and `length.seg` are ignored. The elements of the list should be integer vectors specifying the indices of the segments. See `cvsegments` for details.

Otherwise, segments of type `segment.type` are generated. How many segments to generate is selected by specifying the number of segments in `segments`, or giving the segment length in `length.seg`. If both are specified, `segments` is ignored.

If `jackknife` is `TRUE`, jackknifed regression coefficients are returned, which can be used for for variance estimation (`var.jack`) or hypothesis testing (`jack.test`).
X and Y do not need to be centered.

Note that this function cannot be used in situations where X needs to be recalculated for each segment (except for scaling by the standard deviation), for instance with msc or other preprocessing. For such models, use the more general (but slower) function crossval.

Also note that if needed, the function will silently(!) reduce ncomp to the maximal number of components that can be cross-validated, which is \( n - l - 1 \), where \( n \) is the number of observations and \( l \) is the length of the longest segment. The (possibly reduced) number of components is returned as the component ncomp.

Value

A list with the following components:

- **method**
  - equals "CV" for cross-validation.
- **pred**
  - an array with the cross-validated predictions.
- **coefficients** (only if jackknife is TRUE)
  - an array with the jackknifed regression coefficients. The dimensions correspond to the predictors, responses, number of components, and segments, respectively.
- **PRESS0**
  - a vector of PRESS values (one for each response variable) for a model with zero components, i.e., only the intercept.
- **PRESS**
  - a matrix of PRESS values for models with 1, ..., ncomp components. Each row corresponds to one response variable.
- **adj**
  - a matrix of adjustment values for calculating bias corrected MSEP. MSEP uses this.
- **segments**
  - the list of segments used in the cross-validation.
- **ncomp**
  - the actual number of components used.

Note

The PRESS0 is always cross-validated using leave-one-out cross-validation. This usually makes little difference in practice, but should be fixed for correctness.

The current implementation of the jackknife stores all jackknife-replicates of the regression coefficients, which can be very costly for large matrices. This might change in a future version.

Author(s)

Ron Wehrens and Björn-Helge Mevik

References


See Also

mvr, crossval, cvsegments, MSEP, var.jack, jack.test
Examples

```r
data(yarn)
yarn.pcr <- pcr(density ~ NIR, 6, data = yarn, validation = "CV", segments = 10)
## Not run: plot(MSEP(yarn.pcr))
```

---

### Description

Functions to estimate the mean squared error of prediction (MSEP), root mean squared error of prediction (RMSEP) and $R^2$ (A.K.A. coefficient of multiple determination) for fitted PCR and PLSR models. Test-set, cross-validation and calibration-set estimates are implemented.

### Usage

```r
MSEP(object, ...)  # S3 method for class 'mvr':
MSEP(object, estimate, newdata, ncomp = 1:object$ncomp, comps,
     intercept = cumulative, se = FALSE, ...)

RMSEP(object, ...)  # S3 method for class 'mvr':
RMSEP(object, ...)

R2(object, estimate, newdata, ncomp = 1:object$ncomp, comps,
    intercept = cumulative, se = FALSE, ...)

mvrValstats(object, estimate, newdata, ncomp = 1:object$ncomp, comps,
             intercept = cumulative, se = FALSE, ...)
```

### Arguments

- **object**: an mvr object
- **estimate**: a character vector. Which estimators to use. Should be a subset of c("all", "train", "CV", "adjCV", "test"). "adjCV" is only available for (R)MSEP. See below for how the estimators are chosen.
- **newdata**: a data frame with test set data.
- **ncomp, comps**: a vector of positive integers. The components or number of components to use. See below.
- **intercept**: logical. Whether estimates for a model with zero components should be returned as well.
- **se**: logical. Whether estimated standard errors of the estimates should be calculated. Not implemented yet.
- **...**: further arguments sent to underlying functions or (for RMSEP) to MSEP
Details

RMSEP simply calls MSEP and takes the square root of the estimates. It therefore accepts the same arguments as MSEP.

Several estimators can be used. "train" is the training or calibration data estimate, also called (R)MSEC. For R^2, this is the unadjusted R^2. It is overoptimistic and should not be used for assessing models. "CV" is the cross-validation estimate, and "adjCV" (for RMSEP and MSEP) is the bias-corrected cross-validation estimate. They can only be calculated if the model has been cross-validated. Finally, "test" is the test set estimate, using newdata as test set.

Which estimators to use is decided as follows (see below for mvrValstats). If estimate is not specified, the test set estimate is returned if newdata is specified, otherwise the CV and adjusted CV (for RMSEP and MSEP) estimates if the model has been cross-validated, otherwise the training data estimate. If estimate is "all", all possible estimates are calculated. Otherwise, the specified estimates are calculated.

Several model sizes can also be specified. If comps is missing (or is NULL), length(ncomp) models are used, with ncomp[1] components, ..., ncomp[length(ncomp)] components. Otherwise, a single model with the components comps[1], ..., comps[length(comps)] is used. If intercept is TRUE, a model with zero components is also used (in addition to the above).

The R^2 values returned by "R2" are calculated as 1 − SSE/SST, where SST is the (corrected) total sum of squares of the response, and SSE is the sum of squared errors for either the fitted values (i.e., the residual sum of squares), test set predictions or cross-validated predictions (i.e., the PRESS). For estimate = "train", this is equivalent to the squared correlation between the fitted values and the response. For estimate = "train", the estimate is often called the prediction R^2.

mvrValstats is a utility function that calculates the statistics needed by MSEP and R2. It is not intended to be used interactively. It accepts the same arguments as MSEP and R2. However, the estimate argument must be specified explicitly: no partial matching and no automatic choice is made. The function simply calculates the types of estimates it knows, and leaves the other untouched.

Value

mvrValstats returns a list with components

- **SSE**: three-dimensional array of SSE values. The first dimension is the different estimators, the second is the response variables and the third is the models.
- **SST**: matrix of SST values. The first dimension is the different estimators and the second is the response variables.
- **nobj**: a numeric vector giving the number of objects used for each estimator.
- **comps**: the components specified, with 0 prepended if intercept is TRUE.
- **cumulative**: TRUE if comps was NULL or not specified.

The other functions return an object of class "mvrVal", with components

- **val**: three-dimensional array of estimates. The first dimension is the different estimators, the second is the response variables and the third is the models.
naExcludeMvr

Adjust for Missing Values

Description
Use missing value information to adjust residuals and predictions. This is the ‘mvr equivalent’ of the naresid.exclude and napredict.exclude functions.

Usage
naExcludeMvr(omit, x, ...)

Arguments

omit an object produced by an na.action function, typically the "na.action" attribute of the result of na.omit or na.exclude.

x a three-dimensional array to be adjusted based upon the missing value information in omit.

... further arguments. Currently not used.

Examples
data(oliveoil)
mod <- plsr(sensory ~ chemical, ncomp = 4, data = oliveoil, validation = "LOO")
RMSEP(mod)
## Not run: plot(R2(mod))
Details

This is a utility function used to allow `predict.mvr` and `residuals.mvr` to compensate for the removal of NAs in the fitting process.

It is called only when the `na.action` is `na.exclude`, and pads `x` with NAs in the correct positions to have the same number of rows as the original data frame.

Value

`x`, padded with NAs along the first dimension (‘rows’).

Author(s)

Bjørn-Helge Mevik and Ron Wehrens

See Also

`predict.mvr`, `residuals.mvr`, `napredict`, `naresid`

---

**oliveoil**  
Sensory and physico-chemical data of olive oils

---

Description

A data set with scores on 6 attributes from a sensory panel and measurements of 5 physico-chemical quality parameters on 16 olive oil samples. The first five oils are Greek, the next five are Italian and the last six are Spanish.

Usage

`data(oliveoil)`

Format

A data frame with 16 observations on the following 2 variables.

- **chemical** a matrix with 5 columns. Measurements of acidity, peroxide, K232, K270, and DK.

Source

oscorespls.fit  

Orthogonal scores PLSR

Description

Fits a PLSR model with the orthogonal scores algorithm (aka the NIPALS algorithm).

Usage

oscorespls.fit(X, Y, ncomp, stripped = FALSE,
               tol = .Machine$double.eps^0.5, ...)

Arguments

X
a matrix of observations. NAs and Infs are not allowed.
Y
a vector or matrix of responses. NAs and Infs are not allowed.
ncomp
the number of components to be used in the modelling.
stripped
logical. If TRUE the calculations are stripped as much as possible for speed; this
is meant for use with cross-validation or simulations when only the coefficients
are needed. Defaults to FALSE.
tol
numeric. The tolerance used for determining convergence in multi-response
models.
... othe other arguments. Currently ignored.

Details

This function should not be called directly, but through the generic functions plsr or mvr with the
argument method = "oscorespls". It implements the orthogonal scores algorithm, as described
in Martens and Næs (1989). This is one of the two “classical” PLSR algorithms, the other being the
orthogonal loadings algorithm.

Value

A list containing the following components is returned:

coefficients  an array of regression coefficients for 1, ..., ncomp components. The dimen-
sions of coefficients are c(nvar, npred, ncomp) with nvar the
number of X variables and npred the number of variables to be predicted in Y.
scores     a matrix of scores.
loadings    a matrix of loadings.
loading.weights
a matrix of loading weights.
Yscores    a matrix of Y-scores.
Yloadings a matrix of Y-loadings.
plot.mvr

projection  the projection matrix used to convert X to scores.
Xmeans      a vector of means of the X variables.
Ymeans      a vector of means of the Y variables.
fitted.values an array of fitted values. The dimensions of fitted.values are c(nobj, npred, ncomp) with nobj the number samples and npred the number of Y variables.
residuals   an array of regression residuals. It has the same dimensions as fitted.values.
Xvar        a vector with the amount of X-variance explained by each number of components.
Xtotvar     Total variance in X.

If stripped is TRUE, only the components coefficients, Xmeans and Ymeans are returned.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

References


See Also

mvr plsr pcr kernelpls.fit widekernelpls.fit simpls.fit

---

plot.mvr  

Plot Method for MVR objects

Description

plot.mvr plots predictions, coefficients, scores, loadings, biplots, correlation loadings or validation plots (RMSEP curves, etc.).

Usage

```
## S3 method for class 'mvr':
plot(x, plottype = c("prediction", "validation", "coefficients", "scores", "loadings", "biplot", "correlation"), ...)
```

Arguments

- `x`  
an object of class mvr. The fitted model to plot.
- `plottype`  
character. What kind of plot to plot.
- `...`  
further arguments, sent to the underlying plot functions.
Details

The function is simply a wrapper for the underlying plot functions used to make the selected plots. See `predplot.mvr`, `validationplot`, `coefplot`, `scoreplot`, `loadingplot`, `biplot.mvr` or `corrplot` for details. Note that all arguments except `x` and `plottype` must be named.

Value

`plot.mvr` returns whatever the underlying plot function returns.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

See Also

`mvr`, `predplot.mvr`, `validationplot`, `coefplot`, `scoreplot`, `loadingplot`, `biplot.mvr`, `corrplot`

Examples

data(yarn)
nir.pcr <- pcr(density ~ NIR, ncomp = 9, data = yarn, validation = "CV")

## Not run:
plot(nir.pcr, ncomp = 5) # Plot of cross-validated predictions
plot(nir.pcr, "scores") # Score plot
plot(nir.pcr, "loadings", comps = 1:3) # The three first loadings
plot(nir.pcr, "coef", ncomp = 5) # Coefficients
plot(nir.pcr, "val") # RMSEP curves
plot(nir.pcr, "val", val.type = "MSEP", estimate = "CV") # CV MSEP

## End(Not run)

pls.options

Set or return options for the pls package

Description

A function to set options for the `pls` package, or to return the current options.

Usage

`pls.options(...)`

Arguments

... a single list, a single character vector, or any number of named arguments (name = value).
Details

If called with no arguments, or with an empty list as the single argument, pls.options returns the current options.

If called with a character vector as the single argument, a list with the arguments named in the vector are returned.

If called with a non-empty list as the single arguments, the list elements should be named, and are treated as named arguments to the function.

Otherwise, pls.options should be called with one or more named arguments name = value. For each argument, the option named name will be given the value value.

The options are saved in a variable .pls.Options in the global environment, and remain in effect until the end of the session. If the environment is saved upon exit, they will be remembered in the next session. The ‘factory defaults’ can be restored by removing .pls.Options from the global environment.

The recognised options are:

mvralg The fit method to use in mvr and mvrCv. The value should be one of the allowed methods. Defaults to "kernelpls". Can be overridden with the argument method in mvr and mvrCv.

pcralg The fit method to use in pcr. The value should be one of the allowed methods. Defaults to "svdpc". Can be overridden with the argument method in pcr.

plsralg The fit method to use in pls. The value should be one of the allowed methods. Defaults to "kernelpls". Can be overridden with the argument method in pls.

Value

A list with the (possibly changed) options. If any named argument (or list element) was provided, the list is returned invisibly.

Side Effects

If any named argument (or list element) was provided, pls.options updates the elements of the option list .pls.Options in the global environment.

Note

The function is a slight modification of the function sm.options from the package sm.

Author(s)

Bjørn-Helge Mevik and Ron Wehrens

Examples

```r
## Return current options:
pls.options()
pls.options("plsralg")
pls.options(c("plsralg", "pcralg"))
```
predict.mvr

Set options:
pls.options(plsrlalg = "simpls", mvralg = "simpls")
pls.options(list(plsrlalg = "simpls", mvralg = "simpls")) # Equivalent
pls.options()

## Restore 'factory settings':
rm(.pls.Options)
pls.options()

predict.mvr  Predict Method for PLSR and PCR

Description
Prediction for mvr (PCR, PLSR) models. New responses or scores are predicted using a fitted model and a new matrix of observations.

Usage
## S3 method for class 'mvr':
predict(object, newdata, ncomp = 1:object$ncomp, comps,
       type = c("response", "scores"), na.action = na.pass, ...)

Arguments
object  an mvr object. The fitted model
newdata a data frame. The new data. If missing, the training data is used.
comps, ncomp vector of positive integers. The components to use in the prediction. See below.
type character. Whether to predict scores or response values
na.action function determining what should be done with missing values in newdata. The default is to predict NA. See na.omit for alternatives.
... further arguments. Currently not used

Details
When type is "response" (default), predicted response values are returned. If comps is missing (or is NULL), predictions for length(ncomp) models with ncomp[1] components, ncomp[2] components, etc., are returned. Otherwise, predictions for a single model with the exact components in comps are returned. (Note that in both cases, the intercept is always included in the predictions. It can be removed by subtracting the Ymeans component of the fitted model.)

When type is "scores", predicted score values are returned for the components given in comps. If comps is missing or NULL, ncomps is used instead.

It is also possible to supply a matrix instead of a data frame as newdata, which is then assumed to be the X data matrix. Note that the usual checks for the type of the data are then omitted. Also note that this is only possible with predict; it will not work in functions like predplot, RMSEP or R2, because they also need the response variable of the new data.
**Value**

When `type` is "response", a three dimensional array of predicted response values is returned. The dimensions correspond to the observations, the response variables and the model sizes, respectively.

When `type` is "scores", a score matrix is returned.

**Note**

A warning message like ‘'newdata' had 10 rows but variable(s) found have 106 rows' means that not all variables were found in the `newdata` data frame. This (usually) happens if the formula contains terms like `yarn$NIR`. Do not use such terms; use the `data` argument instead. See `mvr` for details.

**Author(s)**

Ron Wehrens and Bjørn-Helge Mevik

**See Also**

`mvr`, `summary.mvr`, `coef.mvr`, `plot.mvr`

**Examples**

```r
data(yarn)
nir.mvr <- mvr(density ~ NIR, ncomp = 5, data = yarn[yarn$train,])

## Predicted responses for models with 1, 2, 3 and 4 components
pred.resp <- predict(nir.mvr, ncomp = 1:4, newdata = yarn[!yarn$train,])

## Predicted responses for a single model with components 1, 2, 3, 4
predict(nir.mvr, comps = 1:4, newdata = yarn[!yarn$train,])

## Predicted scores
predict(nir.mvr, comps = 1:3, type = "scores", newdata = yarn[!yarn$train,])
```

**Description**

Functions to plot predicted values against measured values for a fitted model.
**Usage**

```r
predplot(object, ...) # Default S3 method:
predplot(object, ...) # S3 method for class 'mvr':
predplot(object, ncomp = object$ncomp, which, newdata, nCols,
         nRows, xlab = "measured", ylab = "predicted", main,
         ..., font.main, cex.main)
predplotXy(x, y, line = FALSE, main = "Prediction plot",
          xlab = "measured response", ylab = "predicted response",
          line.col = par("col"), line.lty = NULL, line.lwd = NULL, ...)
```

**Arguments**

- **object**: a fitted model.
- **ncomp**: integer vector. The model sizes (numbers of components) to use for prediction.
- **which**: character vector. Which types of predictions to plot. Should be a subset of c("train", "validation", "test"). If not specified, `plot.mvr` selects test set predictions if `newdata` is supplied, otherwise cross-validated predictions if the model has been cross-validated, otherwise fitted values from the calibration data.
- **newdata**: data frame. New data to predict.
- **nCols, nRows**: integer. The number of columns and rows the plots will be laid out in. If not specified, `plot.mvr` tries to be intelligent.
- **xlab, ylab**: titles for x and y axes. Typically character strings, but can be expressions or lists. See `title` for details.
- **main**: optional main title for the plot. See Details.
- **font.main**: font to use for main titles. See `par` for details. Also see Details below.
- **cex.main**: numeric. The magnification to be used for main titles relative to the current size. Also see Details below.
- **x**: numeric vector. The observed response values.
- **y**: numeric vector. The predicted response values.
- **line**: logical. Whether a target line should be drawn.
- **line.col, line.lty, line.lwd**: character or numeric. The `col`, `lty` and `lwd` parameters for the target line. See `par` for details.
- **...**: further arguments sent to underlying plot functions.

**Details**

`predplot` is a generic function for plotting predicted versus measured response values, with default and `mvr` methods currently implemented. The default method is very simple, and doesn’t handle multiple responses or new data.
The `mvr` method, handles multiple responses, model sizes and types of predictions by making one plot for each combination. It can also be called through the plot method for `mvr`, by specifying `plottype = "prediction"` (the default).

The argument `main` can be used to specify the main title of the plot. It is handled in a non-standard way. If there is only one (sub) plot, `main` will be used as the main title of the plot. If there is more than one (sub) plot, however, the presence of `main` will produce a corresponding ‘global’ title on the page. Any graphical parameters, e.g., `cex.main`, supplied to `coefplot` will only affect the ‘ordinary’ plot titles, not the ‘global’ one. Its appearance can be changed by setting the parameters with `par`, which will affect both titles (with the exception of `font.main` and `cex.main`, which will only affect the ‘global’ title when there is more than one plot). (To have different settings for the two titles, one can override the `par` settings with arguments to `predplot`.)

`predplotXy` is an internal function and is not meant for interactive use. It is called by the `predplot` methods, and its arguments, e.g., `line`, can be given in the `predplot` call.

**Value**

The functions invisibly return a matrix with the (last) plotted data.

**Note**

The `font.main` and `cex.main` must be (completely) named. This is to avoid that any argument `cex` or `font` matches them.

**Author(s)**

Ron Wehrens and Bjørn-Helge Mevik

**See Also**

`mvr`, `plot.mvr`

**Examples**

data(yarn)
mod <- plsr(density ~ NIR, ncomp = 10, data = yarn[yarn$train,], validation = "CV")
## Not run:
predplot(mod, ncomp = 1:6)
plot(mod, ncomp = 1:6) # Equivalent to the previous
## Both cross-validated and test set predictions:
predplot(mod, ncomp = 4:6, which = c("validation", "test"),
       newdata = yarn[!yarn$train,])
## End(Not run)

data(oliveoil)
mod.sens <- plsr(sensory ~ chemical, ncomp = 4, data = oliveoil)
## Not run: plot(mod.sens, ncomp = 2:4) # Several responses gives several plots
Plots of Scores, Loadings and Correlation Loadings

Description

Functions to make scatter plots of scores or correlation loadings, and scatter or line plots of loadings.

Usage

scoreplot(object, ...)
## Default S3 method:
scoreplot(object, comps = 1:2, labels, identify = FALSE, type = "p",
xlab, ylab, ...)
## S3 method for class 'scores':
plot(x, ...)

loadingplot(object, ...)
## Default S3 method:
loadingplot(object, comps = 1:2, scatter = FALSE, labels,
    identify = FALSE, type, lty, lwd = NULL, pch, cex = NULL,
    col, legendpos, xlab, ylab, pretty.xlabels = TRUE, xlim, ...)
## S3 method for class 'loadings':
plot(x, ...)

corrplot(object, comps = 1:2, labels, radii = c(sqrt(1/2), 1),
    identify = FALSE, type = "p", xlab, ylab, ...)

Arguments

object an R object. The fitted model.
comps integer vector. The components to plot.
scatter logical. Whether the loadings should be plotted as a scatter instead of as lines.
labels optional. Alternative plot labels or x axis labels. See Details.
radii numeric vector, giving the radii of the circles drawn in corrplot. The default radii represent 50% and 100% explained variance of the X variables by the chosen components.
identify logical. Whether to use identify to interactively identify points. See below.
type character. What type of plot to make. Defaults to "p" (points) for scatter plots and "l" (lines) for line plots. See plot for a complete list of types (not all types are possible/meaningful for all plots).
lty vector of line types (recycled as neccessary). Line types can be specified as integers or character strings (see par for the details).
lwd vector of positive numbers (recycled as neccessary), giving the width of the lines.
scoreplot

**pch**  
plot character. A character string or a vector of single characters or integers (recycled as necessary). See **points** for all alternatives.

**cex**  
numeric vector of character expansion sizes (recycled as necessary) for the plotted symbols.

**col**  
character or integer vector of colors for plotted lines and symbols (recycled as necessary). See **par** for the details.

**legendpos**  
Legend position. Optional. Ignored if **scatter** is TRUE. If present, a legend is drawn at the given position. The position can be specified symbolically (e.g., `legendpos = "topright"`). This requires R >= 2.1.0. Alternatively, the position can be specified explicitly (`legendpos = t(c(x, y))`) or interactively (`legendpos = locator()`).

**xlab, ylab**  
titles for x and y axes. Typically character strings, but can be expressions or lists. See **title** for details.

**pretty.xlabels**  
logical. If TRUE, **loadingplot** tries to plot the x labels more nicely. See Details.

**xlim**  
optional vector of length two, with the x limits of the plot.

**x**  
a **scores** or **loadings** object. The scores or loadings to plot.

**...**  
further arguments sent to the underlying plot function(s).

**Details**

**plot.scores** is simply a wrapper calling **scoreplot**, passing all arguments. Similarly for **plot.loadings**.

**scoreplot** is generic, currently with a default method that works for matrices and any object for which **scores** returns a matrix. The default **scoreplot** method makes one or more scatter plots of the scores, depending on how many components are selected. If one or two components are selected, and **identify** is TRUE, the function **identify** is used to interactively identify points.

Also **loadingplot** is generic, with a default method that works for matrices and any object where **loadings** returns a matrix. If **scatter** is TRUE, the default method works exactly like the default **scoreplot** method. Otherwise, it makes a lineplot of the selected loading vectors, and if **identify** is TRUE, uses **identify** to interactively identify points. Also, if **legendpos** is given, a legend is drawn at the position indicated.

**corrplot** works exactly like the default **scoreplot** method, except that at least two components must be selected. The “correlation loadings”, i.e. the correlations between each variable and the selected components (see References), are plotted as pairwise scatter plots, with concentric circles of radii given by **radii**. Each point corresponds to an X variable. The squared distance between the point and origin equals the fraction of the variance of the variable explained by the components in the panel. The default radii corresponds to 50% and 100% explained variance.

**scoreplot**, **loadingplot** and **corrplot** can also be called through the plot method for **mvr** objects, by specifying **plottype** as "scores", "loadings" or "correlation", respectively. See **plot.mvr**.

The argument **labels** can be a vector of labels or one of "names" and "numbers".

If a scatter plot is produced (i.e., **scoreplot**, **corrplot**, or **loadingplot** with **scatter** = TRUE), the labels are used instead of plot symbols for the points plotted. If **labels** is "names"
or "numbers", the row names or row numbers of the matrix (scores, loadings or correlation loadings) are used.

If a line plot is produced (i.e., loadingplot), the labels are used as x axis labels. If labels is "names" or "numbers", the variable names are used as labels, the difference being that with "numbers", the variable names are converted to numbers, if possible. Variable names of the forms '"number"' or '"number text"' (where the space is optional), are handled.

The argument pretty.xlabels is only used when labels is specified for a line plot. If TRUE (default), the code tries to use a ‘pretty’ selection of labels. If labels is "numbers", it also uses the numerical values of the labels for horizontal spacing. If one has excluded parts of the spectral region, one might therefore want to use pretty.xlabels = FALSE.

Value

The functions return whatever the underlying plot function (or identify) returns.

Note

legend has many options. If you want greater control over the appearance of the legend, omit the legendpos argument and call legend manually.

Graphical parameters (such as pch and cex) can also be used with scoreplot and corrplot. They are not listed in the argument list simply because they are not handled specifically in the function (unlike in loadingplot), but passed directly to the underlying plot functions by ....

The handling of labels and pretty.xlabels in coefplot is experimental.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

References


See Also

mvr, plot.mvr, scores, loadings, identify, legend

Examples

data(yarn)
mod <- plsR(density ~ NIR, ncomp = 10, data = yarn)
## These three are equivalent:
## Not run:
scoreplot(mod, comps = 1:5)
plot(scores(mod), comps = 1:5)
plot(mod, plottype = "scores", comps = 1:5)

loadingplot(mod, comps = 1:5)
These functions extract score and loading matrices from fitted mvr models.

**Usage**

```r
scores(object, ...)  
## Default S3 method:
scores(object, ...)
```

```r
loadings(object, ...)  
## Default S3 method:
loadings(object, ...)
```

```r
loading.weights(object)
```

```r
Yscores(object)
```

```r
Yloadings(object)
```

**Arguments**

- `object` a fitted model to extract from.
- `...` extra arguments, currently not used.

**Details**

All functions extract the indicated matrix from the fitted model, and will work with any object having a suitably named component.

The default `scores` and `loadings` methods also handle `prcomp` objects (their scores and loadings components are called `x` and `rotation`, resp.), and add an attribute "explvar" with the variance explained by each component, if this is available. (See `explvar` for details.)

**Value**

A matrix with scores or loadings.
Note

There is a loadings function in package stats. It simply returns any element named "loadings". See loadings for details. The function can be accessed as stats::loadings(...).

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

See Also

mvr, coef.mvr

Examples

data(yarn)
plsmod <- plsr(density ~ NIR, 6, data = yarn)
scores(plsmod)
loadings(plsmod)[,1:4]

simpls.fit  Sijmen de Jong's SIMPLS

Description

Fits a PLSR model with the SIMPLS algorithm.

Usage

simpls.fit(X, Y, ncomp, stripped = FALSE, ...)

Arguments

X a matrix of observations. NAs and Infs are not allowed.
Y a vector or matrix of responses. NAs and Infs are not allowed.
ncomp the number of components to be used in the modelling.
stripped logical. If TRUE the calculations are stripped as much as possible for speed; this is meant for use with cross-validation or simulations when only the coefficients are needed. Defaults to FALSE.
... other arguments. Currently ignored.

Details

This function should not be called directly, but through the generic functions plsr or mvr with the argument method="simpls". SIMPLS is much faster than the NIPALS algorithm, especially when the number of X variables increases, but gives slightly different results in the case of multivariate Y. SIMPLS truly maximises the covariance criterion. According to de Jong, the standard PLS2 algorithms lie closer to ordinary least-squares regression where a precise fit is sought; SIMPLS lies closer to PCR with stable predictions.
Value

A list containing the following components is returned:

- **coefficients**: an array of regression coefficients for 1, ..., ncomp components. The dimensions of coefficients are c(nvar, npred, ncomp) with nvar the number of X variables and npred the number of variables to be predicted in Y.
- **scores**: a matrix of scores.
- **loadings**: a matrix of loadings.
- **Yscores**: a matrix of Y-scores.
- **Yloadings**: a matrix of Y-loadings.
- **projection**: the projection matrix used to convert X to scores.
- **Xmeans**: a vector of means of the X variables.
- **Ymeans**: a vector of means of the Y variables.
- **fitted.values**: an array of fitted values. The dimensions of fitted.values are c(nobj, npred, ncomp) with nobj the number samples and npred the number of Y variables.
- **residuals**: an array of regression residuals. It has the same dimensions as fitted.values.
- **Xvar**: a vector with the amount of X-variance explained by each number of components.
- **Xtotvar**: Total variance in X.

If stripped is TRUE, only the components coefficients, Xmeans and Ymeans are returned.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

References


See Also

- mvr
- plsr
- pcr
- kernelpls.fit
- widekernelpls.fit
- oscorespls.fit
stdize  Standardization of Data Matrices

Description
Perform standardization (centering and scaling) of a data matrix.

Usage
stdize(x, center = TRUE, scale = TRUE)
## S3 method for class 'stdized':
predict(object, newdata, ...)
## S3 method for class 'stdized':
makepredictcall(var, call)

Arguments
- x, newdata: numeric matrix. The data to standardize.
- center: logical value or numeric vector of length equal to the number of columnns of x.
- scale: logical value or numeric vector of length equal to the number of columnns of x.
- object: an object inheriting from class "stdized", normally the result of a call to stdize.
- var: A variable.
- call: The term in the formula, as a call.
- ...: other arguments. Currently ignored.

Details
makepredictcall.stdized is an internal utility function; it is not meant for interactive use. See makepredictcall for details.

If center is TRUE, x is centered by subtracting the column mean from each column. If center is a numeric vector, it is used in place of the column means.

If scale is TRUE, x is scaled by dividing each column by its sample standard deviation. If scale is a numeric vector, it is used in place of the standard deviations.

Value
Both stdize and predict.stdized return a scaled and/or centered matrix, with attributes "stdized:center" and/or "stdized:scale" the vector used for centering and/or scaling. The matrix is given class c("stdized", "matrix").

Note
stdize is very similar to scale. The difference is that when scale = TRUE, stdize divides the columns by their standard deviation, while scale uses the root-mean-square of the columns. If center is TRUE, this is equivalent, but in general it is not.
**Author(s)**

Bjørn-Helge Mevik and Ron Wehrens

**See Also**

`mvr`, `pcr`, `plsr`, `msc`, `scale`

**Examples**

```r
data(yarn)
## Direct standardization:
Ztrain <- stdize(yarn$NIR[yarn$train,])
Ztest <- predict(Ztrain, yarn$NIR[!yarn$train,])

## Used in formula:
mod <- plsr(density ~ stdize(NIR), ncomp = 6, data = yarn[yarn$train,])
pred <- predict(mod, newdata = yarn[!yarn$train,]) # Automatically standardized
```

---

**Description**

Summary and print methods for `mvr` and `mvrVal` objects.

**Usage**

```r
## S3 method for class 'mvr':
summary(object, what = c("all", "validation", "training"),
digits = 4, print.gap = 2, ...)  # S3 method for class 'mvr':
print(x, ...)  # S3 method for class 'mvrVal':
print(x, digits = 4, print.gap = 2, ...)
```

**Arguments**

- `x, object`: an `mvr` object
- `what`: one of "all", "validation" or "training"
- `digits`: integer. Minimum number of significant digits in the output. Default is 4.
- `print.gap`: Integer. Gap between columns of the printed tables.
- `...`: Other arguments sent to underlying methods.

**Details**

If `what` is "training", the explained variances are given; if it is "validation", the cross-validated RMSEPs (if available) are given; if it is "all", both are given.
svdpc.fit

Principal Component Regression

Description

Fits a PCR model using the singular value decomposition.

Usage

svdpc.fit(X, Y, ncomp, stripped = FALSE, ...)

Arguments

X  a matrix of observations. NAs and Infs are not allowed.
Y  a vector or matrix of responses. NAs and Infs are not allowed.
ncomp  the number of components to be used in the modelling.
stripped  logical. If TRUE the calculations are stripped as much as possible for speed; this is meant for use with cross-validation or simulations when only the coefficients are needed. Defaults to FALSE.
...  other arguments. Currently ignored.

Details

This function should not be called directly, but through the generic functions pcr or mvr with the argument method="svdpc". The singular value decomposition is used to calculate the principal components.
svdpc.fit

Value

A list containing the following components is returned:

- **coefficients**: an array of regression coefficients for 1, ..., ncomp components. The dimensions of coefficients are c(nvar, npred, ncomp) with nvar the number of X variables and npred the number of variables to be predicted in Y.
- **scores**: a matrix of scores.
- **loadings**: a matrix of loadings.
- **Yloadings**: a matrix of Y-loadings.
- **projection**: the projection matrix used to convert X to scores.
- **Xmeans**: a vector of means of the X variables.
- **Ymeans**: a vector of means of the Y variables.
- **fitted.values**: an array of fitted values. The dimensions of fitted.values are c(nobj, npred, ncomp) with nobj the number samples and npred the number of Y variables.
- **residuals**: an array of regression residuals. It has the same dimensions as fitted.values.
- **Xvar**: a vector with the amount of X-variance explained by each number of components.
- **Xtotvar**: Total variance in X.

If stripped is TRUE, only the components coefficients, Xmeans and Ymeans are returned.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

References


See Also

- mvr
- plsr
- pcr
validationplot  Validation Plots

Description
Functions to plot validation statistics, such as RMSEP or $R^2$, as a function of the number of components.

Usage
validationplot(object, val.type = c("RMSEP", "MSEP", "R2"), estimate, newdata, ncomp, comps, intercept, ...)
## S3 method for class 'mvrVal':
plot(x, nCols, nRows, type = "l", lty = 1:nEst, lwd = NULL, pch = 1:nEst, cex = NULL, col = 1:nEst, legendpos, xlab = "number of components", ylab = x$type, main, ...)

Arguments
object an mvr object.
val.type character. What type of validation statistic to plot.
estimate character. Which estimates of the statistic to calculate. See RMSEP.
newdata data frame. Optional new data used to calculate statistic.
ncomp, comps integer vector. The model sizes to compute the statistic for. See RMSEP.
intercept logical. Whether estimates for a model with zero components should be calculated as well.
x an mvrVal object. Usually the result of a RMSEP, MSEP or R2 call.
nCols, nRows integers. The number of columns and rows the plots will be laid out in. If not specified, plot.mvrVal tries to be intelligent.
type character. What type of plots to create. Defaults to "l" (lines). Alternative types include "p" (points) and "b" (both). See plot for a complete list of types.
lty vector of line types (recycled as necessary). Line types can be specified as integers or character strings (see par for the details).
lwd vector of positive numbers (recycled as necessary), giving the width of the lines.
pch plot character. A character string or a vector of single characters or integers (recycled as necessary). See points for all alternatives.
cex numeric vector of character expansion sizes (recycled as necessary) for the plotted symbols.
col character or integer vector of colors for plotted lines and symbols (recycled as necessary). See par for the details.
legendpos  Legend position. Optional. If present, a legend is drawn at the given position. The position can be specified symbolically (e.g., `legendpos = "topright"`). This requires R >= 2.1.0. Alternatively, the position can be specified explicitly (`legendpos = t(c(x,y))`) or interactively (`legendpos = locator()`). This only works well for plots of single-response models.

xlab, ylab  titles for x and y axes. Typically character strings, but can be expressions (e.g., `expression(R^2)`) or lists. See `title` for details.

main  optional main title for the plot. See Details.

...  Further arguments sent to underlying plot functions.

Details

`validationplot` calls the proper validation function (currently `MSEP`, `RMSEP` or `R2`) and plots the results with `plot.mvrVal`. `validationplot` can be called through the `mvr` plot method, by specifying `plottype = "validation"`.

`plot.mvrVal` creates one plot for each response variable in the model, laid out in a rectangle. It uses `matplot` for performing the actual plotting. If `legendpos` is given, a legend is drawn at the given position.

The argument `main` can be used to specify the main title of the plot. It is handled in a non-standard way. If there is only on (sub) plot, `main` will be used as the main title of the plot. If there is more than one (sub) plot, however, the presence of `main` will produce a corresponding ‘global’ title on the page. Any graphical parameters, e.g., `cex.main`, supplied to `coefplot` will only affect the ‘ordinary’ plot titles, not the ‘global’ one. Its appearance can be changed by setting the parameters with `par`, which will affect both titles. (To have different settings for the two titles, one can override the `par` settings with arguments to the plot function.)

Note

`legend` has many options. If you want greater control over the appearance of the legend, omit the `legendpos` argument and call `legend` manually.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

See Also

`mvr`, `plot.mvr`, `RMSEP`, `MSEP`, `R2`, `matplot`, `legend`

Examples

data(oliveoil)
mod <- plsr(sensory ~ chemical, data = oliveoil, validation = "LOO")
## Not run:
## These three are equivalent:
validationplot(mod, estimate = "all")
plot(mod, "validation", estimate = "all")
plot(RMSEP(mod, estimate = "all"))
## Plot R2:
plot(mod, "validation", val.type = "R2")
## Plot R2, with a legend:
plot(mod, "validation", val.type = "MSEP", legendpos = "top") # R >= 2.1.0
## End(Not run)

---

### var.jack

**Jackknife Variance Estimates of Regression Coefficients**

**Description**

Calculates jackknife variance or covariance estimates of regression coefficients.

**Usage**

```r
var.jack(object, ncomp = object$ncomp, covariance = FALSE, use.mean = TRUE)
```

**Arguments**

- **object**: an `mvr` object. A cross-validated model fitted with `jackknife = TRUE`.
- **ncomp**: the number of components to use for estimating the (co)variances
- **covariance**: logical. If `TRUE`, covariances are calculated; otherwise only variances. The default is `FALSE`.
- **use.mean**: logical. If `TRUE` (default), the mean coefficients are used when estimating the (co)variances; otherwise the coefficients from a model fitted to the entire data set. See Details.

**Details**

The original (Tukey) jackknife variance estimator is defined as \((g - 1)/g \sum_{i=1}^{g} (\hat{\beta}_i - \bar{\beta})^2\), where \(g\) is the number of segments, \(\hat{\beta}_i\) is the estimated coefficient when segment \(i\) is left out (called the jackknife replicates), and \(\bar{\beta}\) is the mean of the \(\hat{\beta}_i\). The most common case is delete-one jackknife, with \(g = n\), the number of observations.

This is the definition `var.jack` uses by default.

However, Martens and Martens (2000) defined the estimator as \((g - 1)/g \sum_{i=1}^{g} (\hat{\beta}_i - \hat{\beta})^2\), where \(\hat{\beta}\) is the coefficient estimate using the entire data set. I.e., they use the original fitted coefficients instead of the mean of the jackknife replicates. Most (all?) other jackknife implementations for PLSR use this estimator. `var.jack` can be made to use this definition with `use.mean = FALSE`. In practice, the difference should be small if the number of observations is sufficiently large. Note, however, that all theoretical results about the jackknife refer to the ‘proper’ definition. (Also note that this option might disappear in a future version.)

**Value**

If `covariance` is `FALSE`, an \(p \times q \times c\) array of variance estimates, where \(p\) is the number of predictors, \(q\) is the number of responses, and \(c\) is the number of components.

If `covariance` is `TRUE`, an \(pq \times pq \times c\) array of variance-covariance estimates.
Warning

Note that the Tukey jackknife variance estimator is not unbiased for the variance of regression coefficients (Hinkley 1977). The bias depends on the X matrix. For ordinary least squares regression (OLSR), the bias can be calculated, and depends on the number of observations \( n \) and the number of parameters \( k \) in the mode. For the common case of an orthogonal design matrix with \( \pm 1 \) levels, the delete-one jackknife estimate equals \( (n - 1)/(n - k) \) times the classical variance estimate for the regression coefficients in OLSR. Similar expressions hold for delete-d estimates. Modifications have been proposed to reduce or eliminate the bias for the OLSR case, however, they depend on the number of parameters used in the model. See e.g. Hinkley (1977) or Wu (1986).

Thus, the results of \texttt{var.jack} should be used with caution.

Author(s)

Bjørn-Helge Mevik

References


See Also

\texttt{mvrCv, jack.test}

Examples

```r
data(oliveoil)
mod <- pcr(sensory ~ chemical, data = oliveoil, validation = "LOO",
          jackknife = TRUE)
var.jack(mod, ncomp = 2)
```

Description

Fits a PLSR model with the wide kernel algorithm.
Usage

widekernelpls.fit(X, Y, ncomp, stripped = FALSE,
                   tol = .Machine$double.eps^0.5, maxit = 100, ...)

Arguments

X  a matrix of observations. NAs and Infs are not allowed.
Y  a vector or matrix of responses. NAs and Infs are not allowed.
ncomp the number of components to be used in the modelling.
stripped logical. If TRUE the calculations are stripped as much as possible for speed; this
     is meant for use with cross-validation or simulations when only the coefficients
     are needed. Defaults to FALSE.
tol numeric. The tolerance used for determining convergence in the algorithm.
maxit positive integer. The maximal number of iterations used in the internal Eigen-
        vector calculation.
... other arguments. Currently ignored.

Details

This function should not be called directly, but through the generic functions plsr or mvr with the
argument method="widekernelpls". The wide kernel PLS algorithm is efficient when the
number of variables is (much) larger than the number of observations. For very wide X, for instance
12x18000, it can be twice as fast as kernelpls.fit and simpls.fit. For other matrices,
however, it can be much slower. The results are equal to the results of the NIPALS algorithm.

Value

A list containing the following components is returned:

coefficients an array of regression coefficients for 1, ..., ncomp components. The dimensions of coefficients are c(nvar, npred, ncomp) with nvar the
number of X variables and npred the number of variables to be predicted in Y.
scores    a matrix of scores.
loadings  a matrix of loadings.
loading.weights a matrix of loading weights.
Yscores   a matrix of Y-scores.
Yloadings a matrix of Y-loadings.
projection the projection matrix used to convert X to scores.
Xmeans    a vector of means of the X variables.
Ymeans    a vector of means of the Y variables.
fitted.values an array of fitted values. The dimensions of fitted.values are c(nobj, npred, ncomp) with nobj the number samples and npred the number of Y variables.
residuals    an array of regression residuals. It has the same dimensions as fitted.values.
Xvar         a vector with the amount of X-variance explained by each number of components.
Xtotvar      Total variance in X.

If stripped is TRUE, only the components coefficients, Xmeans and Ymeans are returned.

Note

The current implementation has not undergone extensive testing yet, and should perhaps be regarded as experimental. Specifically, the internal Eigenvector calculation does not always converge in extreme cases where the Eigenvalue is close to zero. However, when it does converge, it always converges to the same results as kernelpls.fit, up to numerical inaccuracies.

The algorithm also has a bit of overhead, so when the number of observations is moderately high, kernelpls.fit can be faster even if the number of predictors is much higher. The relative speed of the algorithms can also depend greatly on which BLAS and/or LAPACK library R is linked against.

Author(s)

Bjørn-Helge Mevik

References


See Also

mvr plsr pcr kernelpls.fit simpls.fit oscorespls.fit

yarn         NIR spectra and density measurements of PET yarns

Description

A training set consisting of 21 NIR spectra of PET yarns, measured at 268 wavelengths, and 21 corresponding densities. A test set of 7 samples is also provided. Many thanks to Erik Swierenga.

Usage

data(yarn)
Format

A data frame with components

- **NIR** Numeric matrix of NIR measurements
- **density** Numeric vector of densities
- **train** Logical vector with `TRUE` for the training samples and `FALSE` for the test samples

Source

Index

*Topic datasets
  gasoline, 11
  oliveoil, 25
  yarn, 49

*Topic hplot
  biplot.mvr, 1
  coefplot, 5
  plot.mvr, 27
  predplot, 31
  scoreplot, 33
  validationplot, 43

*Topic htest
  jack.test, 12

*Topic internal
  delete.intercept, 10
  naExcludeMvr, 24

*Topic models
  cvsegments, 9

*Topic multivariate
  biplot.mvr, 1
  coef.mvr, 3
  coefplot, 5
  crossval, 7
  kernelpls.fit, 13
  msc, 15
  mvr, 16
  mvrCv, 19
  mvrVal, 21
  naExcludeMvr, 24
  oscorespls.fit, 25
  plot.mvr, 27
  pls.options, 28
  predict.mvr, 30
  predplot, 31
  scoreplot, 33
  scores, 36
  simpls.fit, 38
  stdize, 39
  summary.mvr, 41
  svdpc.fit, 42
  validationplot, 43
  widekernelpls.fit, 47

*Topic regression
  biplot.mvr, 1
  coef.mvr, 3
  coefplot, 5
  crossval, 7
  kernelpls.fit, 13
  msc, 15
  mvr, 16
  mvrCv, 19
  mvrVal, 21
  naExcludeMvr, 24
  oscorespls.fit, 25
  plot.mvr, 27
  pls.options, 28
  predict.mvr, 30
  predplot, 31
  scoreplot, 33
  scores, 36
  simpls.fit, 38
  stdize, 39
  summary.mvr, 41
  svdpc.fit, 42
  validationplot, 43
  widekernelpls.fit, 47

*Topic univar
  var.jack, 45

biplot.default, 2
biplot.mvr, 1, 27, 28

coef, 3, 4
coef.mvr, 3, 5, 7, 18, 31, 37
coefplot, 5, 27, 28
compnames (coef.mvr), 3
corrplot, 27, 28
corrplot (scoreplot), 33
crossval, 7, 18, 20, 21, 23
cvsegments, 8, 9, 20, 21

delete.intercept, 10

eplvar, 37
eplvar(coef.mvr), 3

fitted, 3, 4
fitted.mvr(coef.mvr), 3

gasoline, 11

identify, 35, 36

jack.test, 8, 9, 12, 20, 21, 47

kernelpls.fit, 13, 18, 27, 39, 48, 49

legend, 7, 36, 45

lm, 17

loading.weights, 18
loading.weights(scores), 36
loadingplot, 27, 28
loadingplot(scoreplot), 33
loadings, 4, 18, 35–37
loadings(scores), 36

locator, 6, 34, 44

makepredictcall, 15, 40
makepredictcall.msc(msc), 15
makepredictcall.stdized(stdize), 39

matplot, 44, 45
model.frame, 4
model.frame.mvr(coef.mvr), 3
model.matrix, 4
model.matrix.mvr, 11
model.matrix.mvr(coef.mvr), 3
msc, 15, 40
MSEP, 9, 18, 21, 41, 44, 45
MSEP(mvrVal), 21

mvr, 2, 4, 7, 9, 11, 15, 16, 21, 23, 27–29, 31, 33, 36, 37, 39–41, 43, 45, 49
mvrCv, 9, 13, 17, 18, 19, 23, 29, 47
mvrVal, 21
mvrValstats(mvrVal), 21

na.omit, 4, 30
na ExcludeMvr, 24
napredict, 24

naresid, 24

oliveoil, 25
options, 4
oscorespls.fit, 15, 18, 25, 39, 49

par, 5, 6, 32, 14, 44, 45
pcc, 15, 16, 27, 29, 39–41, 43, 49
pcc(mvr), 16
plot, 5, 7, 34, 44
plot.loadings(scoreplot), 33
plot.mvr, 2, 7, 18, 27, 31, 33, 35, 36, 45
plot.mvrVal, 23
plot.mvrVal(validationplot), 43
plot.scores(scoreplot), 33

plsr, 15, 16, 27, 29, 39–41, 43, 49
plsr(mvr), 16
points, 6, 34, 44
predict.msc(msc), 15
predict.mvr, 15, 17, 18, 24, 30
predict.stdized(stdize), 39
predictnames(coef.mvr), 3

predplot, 30, 31
predplot.mvr, 27, 28
predplotXY(predplot), 31
print.jacktest(jack.test), 12
print.mvr(summary.mvr), 41
print.mvrVal(summary.mvr), 41
printCoefmat, 12

R2, 18, 30, 44, 45
R2(mvrVal), 21
residuals, 3, 4
residuals.mvr, 24
residuals.mvr(coef.mvr), 3
responames(coef.mvr), 3
RMSEP, 18, 30, 41, 44, 45
RMSEP(mvrVal), 21

scale, 40
scoreplot, 27, 28, 33
scores, 4, 18, 35, 36, 39, 48, 49
sm.options, 29
stdize, 16, 39
summary.mvr, 31, 41
svdpc.fit, 18, 42

title, 6, 32, 34, 44
<table>
<thead>
<tr>
<th>Index</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>validationplot</td>
<td>23, 27, 28, 43</td>
</tr>
<tr>
<td>var.jack</td>
<td>8, 9, 12, 13, 20, 21, 45</td>
</tr>
<tr>
<td>widekernelpls.fit</td>
<td>15, 18, 27, 39, 47</td>
</tr>
<tr>
<td>yarn</td>
<td>49</td>
</tr>
<tr>
<td>Yloadings</td>
<td>4</td>
</tr>
<tr>
<td>Yloadings (scores)</td>
<td>36</td>
</tr>
<tr>
<td>Yscores (scores)</td>
<td>36</td>
</tr>
</tbody>
</table>