

# Package ‘plsRglm’

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**Enhances** pls

**Suggests** MASS, plsdf, R.rsp, chemometrics, plsdepot

**Title** Partial Least Squares Regression for Generalized Linear Models

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## Description

Provides (weighted) Partial least squares Regression for generalized linear models and repeated k-fold cross-validation of such models using various criteria. It allows for missing data in the explanatory variables. Bootstrap confidence intervals constructions are also available.

**License** GPL-3

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aic.dof	<i>Akaike and Bayesian Information Criteria and Generalized minimum description length</i>
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**Description**

This function computes the Akaike and Bayesian Information Criteria and the Generalized minimum description length.

**Usage**

```
aic.dof(RSS, n, DoF, sigmahat)
bic.dof(RSS, n, DoF, sigmahat)
gmdl.dof(sigmahat, n, DoF, yhat)
```

**Arguments**

RSS	vector of residual sum of squares.
n	number of observations.
DoF	vector of Degrees of Freedom. The length of DoF is the same as the length of RSS.
sigmahat	Estimated model error. The length of sigmahat is the same as the length of RSS.
yhat	vector of squared norm of Yhat. The length of yhat is the same as the length of sigmahat.

**Details**

The gmdl criterion is defined as

$$gmdl = \frac{n}{2} \log(S) + \frac{DoF}{2} \log(F) + \frac{1}{2} \log(n)$$

with

$$S = \hat{\sigma}^2$$

**Value**

vector                    numerical values of the requested AIC, BIC or GMDL.

**Author(s)**

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**References**

- M. Hansen, B. Yu. (2001). Model Selection and Minimum Description Length Principle, *Journal of the American Statistical Association*, 96, 746-774.
- N. Kraemer, M. Sugiyama. (2011). The Degrees of Freedom of Partial Least Squares Regression. *Journal of the American Statistical Association*, 106(494), 697-705.
- N. Kraemer, M.L. Braun, Kernelizing PLS, Degrees of Freedom, and Efficient Model Selection, *Proceedings of the 24th International Conference on Machine Learning*, Omni Press, (2007) 441-448.

**See Also**

[plsR.dof](#) for degrees of freedom computation and [infcrit.dof](#) for computing information criteria directly from a previously fitted plsR model.

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsR(yCornell,XCornell,4)
dof.object <- plsR.dof(modpls)
aic.dof(modpls$RSS,modpls$nr,dof.object$DoF,dof.object$sigmahat)
bic.dof(modpls$RSS,modpls$nr,dof.object$DoF,dof.object$sigmahat)
gmdl.dof(dof.object$sigmahat,modpls$nr,dof.object$DoF,dof.object$yhat)
naive.object <- plsR.dof(modpls,naive=TRUE)
aic.dof(modpls$RSS,modpls$nr,naive.object$DoF,naive.object$sigmahat)
bic.dof(modpls$RSS,modpls$nr,naive.object$DoF,naive.object$sigmahat)
gmdl.dof(naive.object$sigmahat,modpls$nr,naive.object$DoF,naive.object$yhat)
```

---

AICpls

*AIC function for plsR models*

---

### Description

This function provides AIC computation for an univariate plsR model.

### Usage

```
AICpls(ncomp, residpls, weights=rep.int(1,length(residpls)))
```

### Arguments

ncomp	Number of components
residpls	Residuals of a fitted univariate plsR model
weights	Weights of observations

### Details

AIC function for plsR models with univariate response.

### Value

real	AIC value
------	-----------

### Author(s)

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### References

Baibing Li, Julian Morris, Elaine B. Martin, Model selection for partial least squares regression, *Chemometrics and Intelligent Laboratory Systems* 64 (2002) 79-89. [http://dx.doi.org/10.1016/S0169-7439\(02\)00051-5](http://dx.doi.org/10.1016/S0169-7439(02)00051-5)

### See Also

[loglikpls](#) for loglikelihood computations for plsR models and [AIC](#) for AIC computation for a linear models

## Examples

```

data(pine)
ypine <- pine[,11]
Xpine <- pine[,1:10]
(Pinscaled <- as.data.frame(cbind(scale(ypine),scale(as.matrix(Xpine))))))
colnames(Pinscaled)[1] <- "yy"

lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)

modpls <- plsR(ypine,Xpine,10)
modpls$Std.Coeffs
lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)

AIC(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled))
print(logLik(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)))

sum(dnorm(modpls$RepY, modpls$Std.ValsPredictY, sqrt(mean(modpls$residY^2)), log=TRUE))
sum(dnorm(Pinscaled$yy,fitted(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled))),
sqrt(mean(residuals(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled))^2)), log=TRUE))
loglikpls(modpls$residY)
loglikpls(residuals(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)))
AICpls(10,residuals(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)))
AICpls(10,modpls$residY)

```

---

 aze

*Microsatellites Dataset*


---

## Description

This database was collected on patients carrying a colon adenocarcinoma. It has 104 observations on 33 binary qualitative explanatory variables and one response variable  $y$  representing the cancer stage according to the to Astler-Coller classification (Astler and Coller, 1954). This dataset has some missing data due to technical limits. A microsatellite is a non-coding DNA sequence.

## Usage

```
data(aze)
```

## Format

A data frame with 104 observations on the following 34 variables.

$y$  the response: a binary vector (Astler-Coller score).

D2S138 a binary vector that indicates whether this microsatellite is altered or not.

D18S61 a binary vector that indicates whether this microsatellite is altered or not.

D16S422 a binary vector that indicates whether this microsatellite is altered or not.

D17S794 a binary vector that indicates whether this microsatellite is altered or not.

D6S264 a binary vector that indicates whether this microsatellite is altered or not.  
D14S65 a binary vector that indicates whether this microsatellite is altered or not.  
D18S53 a binary vector that indicates whether this microsatellite is altered or not.  
D17S790 a binary vector that indicates whether this microsatellite is altered or not.  
D1S225 a binary vector that indicates whether this microsatellite is altered or not.  
D3S1282 a binary vector that indicates whether this microsatellite is altered or not.  
D9S179 a binary vector that indicates whether this microsatellite is altered or not.  
D5S430 a binary vector that indicates whether this microsatellite is altered or not.  
D8S283 a binary vector that indicates whether this microsatellite is altered or not.  
D11S916 a binary vector that indicates whether this microsatellite is altered or not.  
D2S159 a binary vector that indicates whether this microsatellite is altered or not.  
D16S408 a binary vector that indicates whether this microsatellite is altered or not.  
D5S346 a binary vector that indicates whether this microsatellite is altered or not.  
D10S191 a binary vector that indicates whether this microsatellite is altered or not.  
D13S173 a binary vector that indicates whether this microsatellite is altered or not.  
D6S275 a binary vector that indicates whether this microsatellite is altered or not.  
D15S127 a binary vector that indicates whether this microsatellite is altered or not.  
D1S305 a binary vector that indicates whether this microsatellite is altered or not.  
D4S394 a binary vector that indicates whether this microsatellite is altered or not.  
D20S107 a binary vector that indicates whether this microsatellite is altered or not.  
D1S197 a binary vector that indicates whether this microsatellite is altered or not.  
D1S207 a binary vector that indicates whether this microsatellite is altered or not.  
D10S192 a binary vector that indicates whether this microsatellite is altered or not.  
D3S1283 a binary vector that indicates whether this microsatellite is altered or not.  
D4S414 a binary vector that indicates whether this microsatellite is altered or not.  
D8S264 a binary vector that indicates whether this microsatellite is altered or not.  
D22S928 a binary vector that indicates whether this microsatellite is altered or not.  
TP53 a binary vector that indicates whether this microsatellite is altered or not.  
D9S171 a binary vector that indicates whether this microsatellite is altered or not.

### Source

Weber *et al.* (2007). Allelotyping analyzes of synchronous primary and metastasis CIN colon cancers identified different subtypes. *Int J Cancer*, 120(3), pages 524-32.

### References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18.

## Examples

```
data(aze)
str(aze)
```

---

aze\_compl

*As aze without missing values*

---

## Description

This is a single imputation of the [aze](#) dataset which was collected on patients carrying a colon adenocarcinoma. It has 104 observations on 33 binary qualitative explanatory variables and one response variable *y* representing the cancer stage according to the to Astler-Coller classification (Astler and Coller, 1954). A microsatellite is a non-coding DNA sequence.

## Usage

```
data(aze_compl)
```

## Format

A data frame with 104 observations on the following 34 variables.

*y* the response: a binary vector (Astler-Coller score).

D2S138 a binary vector that indicates whether this microsatellite is altered or not.

D18S61 a binary vector that indicates whether this microsatellite is altered or not.

D16S422 a binary vector that indicates whether this microsatellite is altered or not.

D17S794 a binary vector that indicates whether this microsatellite is altered or not.

D6S264 a binary vector that indicates whether this microsatellite is altered or not.

D14S65 a binary vector that indicates whether this microsatellite is altered or not.

D18S53 a binary vector that indicates whether this microsatellite is altered or not.

D17S790 a binary vector that indicates whether this microsatellite is altered or not.

D1S225 a binary vector that indicates whether this microsatellite is altered or not.

D3S1282 a binary vector that indicates whether this microsatellite is altered or not.

D9S179 a binary vector that indicates whether this microsatellite is altered or not.

D5S430 a binary vector that indicates whether this microsatellite is altered or not.

D8S283 a binary vector that indicates whether this microsatellite is altered or not.

D11S916 a binary vector that indicates whether this microsatellite is altered or not.

D2S159 a binary vector that indicates whether this microsatellite is altered or not.

D16S408 a binary vector that indicates whether this microsatellite is altered or not.

D5S346 a binary vector that indicates whether this microsatellite is altered or not.

D10S191 a binary vector that indicates whether this microsatellite is altered or not.



D13S173 a binary vector that indicates whether this microsatellite is altered or not.  
D6S275 a binary vector that indicates whether this microsatellite is altered or not.  
D15S127 a binary vector that indicates whether this microsatellite is altered or not.  
D1S305 a binary vector that indicates whether this microsatellite is altered or not.  
D4S394 a binary vector that indicates whether this microsatellite is altered or not.  
D20S107 a binary vector that indicates whether this microsatellite is altered or not.  
D1S197 a binary vector that indicates whether this microsatellite is altered or not.  
D1S207 a binary vector that indicates whether this microsatellite is altered or not.  
D10S192 a binary vector that indicates whether this microsatellite is altered or not.  
D3S1283 a binary vector that indicates whether this microsatellite is altered or not.  
D4S414 a binary vector that indicates whether this microsatellite is altered or not.  
D8S264 a binary vector that indicates whether this microsatellite is altered or not.  
D22S928 a binary vector that indicates whether this microsatellite is altered or not.  
TP53 a binary vector that indicates whether this microsatellite is altered or not.  
D9S171 a binary vector that indicates whether this microsatellite is altered or not.

### Source

Weber *et al.* (2007). Allelotyping analyzes of synchronous primary and metastasis CIN colon cancers identified different subtypes. *Int J Cancer*, 120(3), pages 524-32.

### References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18.

### Examples

```
data(aze_compl)
str(aze_compl)
```

---

bootpls

*Non-parametric Bootstrap for PLS models*

---

### Description

Provides a wrapper for the bootstrap function `boot` from the `boot` R package.  
Implements non-parametric bootstraps for PLS Regression models by either (Y,X) or (Y,T) resampling.

**Usage**

```
bootpls(object, typeboot="plsmodel", R=250, statistic=coefs.plsR, sim="ordinary",
styp="i", stabvalue=1e6, verbose=TRUE,...)
```

**Arguments**

object	An object of class <code>plsRmodel</code> to bootstrap
typeboot	The type of bootstrap. Either (Y,X) bootstrap ( <code>typeboot="plsmodel"</code> ) or (Y,T) bootstrap ( <code>typeboot="fmodel_np"</code> ). Defaults to (Y,X) resampling.
R	The number of bootstrap replicates. Usually this will be a single positive integer. For importance resampling, some resamples may use one set of weights and others use a different set of weights. In this case R would be a vector of integers where each component gives the number of resamples from each of the rows of weights.
statistic	A function which when applied to data returns a vector containing the statistic(s) of interest. <code>statistic</code> must take at least two arguments. The first argument passed will always be the original data. The second will be a vector of indices, frequencies or weights which define the bootstrap sample. Further, if predictions are required, then a third argument is required which would be a vector of the random indices used to generate the bootstrap predictions. Any further arguments can be passed to <code>statistic</code> through the <code>...</code> argument.
sim	A character string indicating the type of simulation required. Possible values are "ordinary" (the default), "balanced", "permutation", or "antithetic".
styp	A character string indicating what the second argument of <code>statistic</code> represents. Possible values of <code>styp</code> are "i" (indices - the default), "f" (frequencies), or "w" (weights).
stabvalue	A value to hard threshold bootstrap estimates computed from atypical resamplings. Especially useful for Generalized Linear Models.
verbose	should info messages be displayed ?
...	Other named arguments for <code>statistic</code> which are passed unchanged each time it is called. Any such arguments to <code>statistic</code> should follow the arguments which <code>statistic</code> is required to have for the simulation. Beware of partial matching to arguments of <code>boot</code> listed above.

**Details**

More details on bootstrap techniques are available in the help of the [boot](#) function.

**Value**

An object of class "boot". See the Value part of the help of the function [boot](#).

**Author(s)**

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<http://www-irma.u-strasbg.fr/~fbertran/>

## References

- A. Lazraq, R. Cleroux, and J.-P. Gauchi. (2003). Selecting both latent and explanatory variables in the PLS1 regression model. *Chemometrics and Intelligent Laboratory Systems*, 66(2):117-126.
- P. Bastien, V. Esposito-Vinzi, and M. Tenenhaus. (2005). PLS generalised linear regression. *Computational Statistics & Data Analysis*, 48(1):17-46.
- A. C. Davison and D. V. Hinkley. (1997). *Bootstrap Methods and Their Applications*. Cambridge University Press, Cambridge.

## See Also

[boot](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

# Lazraq-Cleroux PLS ordinary bootstrap
set.seed(250)
modpls <- plsR(yCornell,XCornell,3)

#(Y,X) resampling
Cornell.bootYX <- bootpls(modpls, R=250)

#(Y,T) resampling
Cornell.bootYT <- bootpls(modpls, typeboot="fmodel_np", R=250)

# Using the boxplots.bootpls function
boxplots.bootpls(Cornell.bootYX,indices=2:8)
# Confidence intervals plotting
confints.bootpls(Cornell.bootYX,indices=2:8)
plots.confints.bootpls(confints.bootpls(Cornell.bootYX,indices=2:8))
# Graph similar to the one of Bastien et al. in CSDA 2005
boxplot(as.vector(Cornell.bootYX$t[,-1])~factor(rep(1:7,rep(250,7))),
main="Bootstrap distributions of standardised bj (j = 1, ..., 7).")
points(c(1:7),Cornell.bootYX$t0[-1],col="red",pch=19)

library(boot)
boot.ci(Cornell.bootYX, conf = c(0.90,0.95), type = c("norm","basic","perc","bca"), index=2)
plot(Cornell.bootYX,index=2)
jack.after.boot(Cornell.bootYX, index=2, useJ=TRUE, nt=3)
plot(Cornell.bootYX,index=2,jack=TRUE)

car::dataEllipse(Cornell.bootYX$t[,2], Cornell.bootYX$t[,3], cex=.3,
levels=c(.5, .95, .99), robust=TRUE)
rm(Cornell.bootYX)
```

```

# PLS balanced bootstrap

set.seed(225)
Cornell.bootYX <- bootpls(modpls, sim="balanced", R=250)
boot.array(Cornell.bootYX, indices=TRUE)

# Using the boxplots.bootpls function
boxplots.bootpls(Cornell.bootYX,indices=2:8)
# Confidence intervals plotting
confints.bootpls(Cornell.bootYX,indices=2:8)
plots.confints.bootpls(confints.bootpls(Cornell.bootYX,indices=2:8))
# Graph similar to the one of Bastien et al. in CSDA 2005
boxplot(as.vector(Cornell.bootYX$t[, -1])~factor(rep(1:7,rep(250,7)))),
main="Bootstrap distributions of standardised bj (j = 1, ..., 7).")
points(c(1:7),Cornell.bootYX$t0[-1],col="red",pch=19)

library(boot)
boot.ci(Cornell.bootYX, conf = c(0.90,0.95), type = c("norm","basic","perc","bca"), index=2)
plot(Cornell.bootYX,index=2)
jack.after.boot(Cornell.bootYX, index=2, useJ=TRUE, nt=3)
plot(Cornell.bootYX,index=2,jack=TRUE)

rm(Cornell.bootYX)

# PLS permutation bootstrap

set.seed(500)
Cornell.bootYX <- bootpls(modpls, sim="permutation", R=1000)
boot.array(Cornell.bootYX, indices=TRUE)

# Graph of bootstrap distributions
boxplot(as.vector(Cornell.bootYX$t[, -1])~factor(rep(1:7,rep(1000,7)))),
main="Bootstrap distributions of standardised bj (j = 1, ..., 7).")
points(c(1:7),Cornell.bootYX$t0[-1],col="red",pch=19)
# Using the boxplots.bootpls function
boxplots.bootpls(Cornell.bootYX,indices=2:8)

library(boot)
plot(Cornell.bootYX,index=2)

qqnorm(Cornell.bootYX$t[,2],ylim=c(-1,1))
abline(h=Cornell.bootYX$t0[2],lty=2)
(sum(abs(Cornell.bootYX$t[,2])>=abs(Cornell.bootYX$t0[2]))+1)/(length(Cornell.bootYX$t[,2])+1)

rm(Cornell.bootYX)

```

**Description**

Provides a wrapper for the bootstrap function `boot` from the `boot` R package. Implements non-parametric bootstraps for PLS Generalized Linear Regression models by either (Y,X) or (Y,T) resampling.

**Usage**

```
bootplsglm(object, typeboot="fmodel_np", R=250, statistic=coefs.plsRglmnp,
sim="ordinary", stype="i", stabvalue=1e6, verbose=TRUE,...)
```

**Arguments**

<code>object</code>	An object of class <code>plsRglmmodel</code> to bootstrap
<code>typeboot</code>	The type of bootstrap. Either (Y,X) bootstrap ( <code>typeboot="plsmodel"</code> ) or (Y,T) bootstrap ( <code>typeboot="fmodel_np"</code> ). Defaults to (Y,T) resampling.
<code>R</code>	The number of bootstrap replicates. Usually this will be a single positive integer. For importance resampling, some resamples may use one set of weights and others use a different set of weights. In this case <code>R</code> would be a vector of integers where each component gives the number of resamples from each of the rows of weights.
<code>statistic</code>	A function which when applied to data returns a vector containing the statistic(s) of interest. <code>statistic</code> must take at least two arguments. The first argument passed will always be the original data. The second will be a vector of indices, frequencies or weights which define the bootstrap sample. Further, if predictions are required, then a third argument is required which would be a vector of the random indices used to generate the bootstrap predictions. Any further arguments can be passed to <code>statistic</code> through the <code>...</code> argument.
<code>sim</code>	A character string indicating the type of simulation required. Possible values are "ordinary" (the default), "balanced", "permutation", or "antithetic".
<code>stype</code>	A character string indicating what the second argument of <code>statistic</code> represents. Possible values of <code>stype</code> are "i" (indices - the default), "f" (frequencies), or "w" (weights).
<code>stabvalue</code>	A value to hard threshold bootstrap estimates computed from atypical resamplings. Especially useful for Generalized Linear Models.
<code>verbose</code>	should info messages be displayed ?
<code>...</code>	Other named arguments for <code>statistic</code> which are passed unchanged each time it is called. Any such arguments to <code>statistic</code> should follow the arguments which <code>statistic</code> is required to have for the simulation. Beware of partial matching to arguments of <code>boot</code> listed above.

**Details**

More details on bootstrap techniques are available in the help of the `boot` function.

**Value**

An object of class "boot". See the Value part of the help of the function `boot`.

**Author(s)**

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<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

A. Lazraq, R. Cleroux, and J.-P. Gauchi. (2003). Selecting both latent and explanatory variables in the PLS1 regression model. *Chemometrics and Intelligent Laboratory Systems*, 66(2):117-126.

P. Bastien, V. Esposito-Vinzi, and M. Tenenhaus. (2005). PLS generalised linear regression. *Computational Statistics & Data Analysis*, 48(1):17-46.

A. C. Davison and D. V. Hinkley. (1997). *Bootstrap Methods and Their Applications*. Cambridge University Press, Cambridge.

**See Also**

[boot](#)

**Examples**

```
#Imputed aze dataset
data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y

dataset <- cbind(y=yaze_compl,Xaze_compl)
modplsglm <- plsRglm(y~.,data=dataset,3,modele="pls-glm-logistic")

library(boot)
# Bastien (Y,T) PLS bootstrap
aze_compl.bootYT <- bootplsglm(modplsglm, R=250)
boxplots.bootpls(aze_compl.bootYT)
confints.bootpls(aze_compl.bootYT)
plots.confints.bootpls(confints.bootpls(aze_compl.bootYT))

plot(aze_compl.bootYT,index=2)
jack.after.boot(aze_compl.bootYT, index=2, useJ=TRUE, nt=3)
plot(aze_compl.bootYT, index=2,jack=TRUE)
aze_compl.tilt.boot <- tilt.bootplsglm(modplsglm, statistic=coefs.plsRglm,
R=c(499, 100, 100), alpha=c(0.025, 0.975), sim="ordinary", stype="i", index=1)

# PLS bootstrap balanced
aze_compl.bootYT <- bootplsglm(modplsglm, sim="balanced", R=250)
boxplots.bootpls(aze_compl.bootYT)
confints.bootpls(aze_compl.bootYT)
plots.confints.bootpls(confints.bootpls(aze_compl.bootYT))

plot(aze_compl.bootYT)
jack.after.boot(aze_compl.bootYT, index=1, useJ=TRUE, nt=3)
```

```

plot(aze_compl.bootYT,jack=TRUE)
aze_compl.tilt.boot <- tilt.bootplsglm(modplsglm, statistic=coefs.plsR,
R=c(499, 100, 100), alpha=c(0.025, 0.975), sim="balanced", stype="i", index=1)

# PLS permutation bootstrap

aze_compl.bootYT <- bootplsglm(modplsglm, sim="permutation", R=250)
boxplots.bootpls(aze_compl.bootYT)
plot(aze_compl.bootYT)

#Original aze dataset with missing values
data(aze)
Xaze<-aze[,2:34]
yaze<-aze$y

library(boot)
modplsglm2 <- plsRglm(yaze,Xaze,3,modele="pls-glm-logistic")
aze.bootYT <- bootplsglm(modplsglm2, R=250)
boxplots.bootpls(aze.bootYT)
confints.bootpls(aze.bootYT)
plots.confints.bootpls(confints.bootpls(aze.bootYT))

#Ordinal logistic regression
data(bordeaux)
Xbordeaux<-bordeaux[,1:4]
ybordeaux<-factor(bordeaux$Quality,ordered=TRUE)
dataset <- cbind(y=ybordeaux,Xbordeaux)
options(contrasts = c("contr.treatment", "contr.poly"))
modplsglm3 <- plsRglm(ybordeaux,Xbordeaux,1,modele="pls-glm-polr")
bordeaux.bootYT<- bootplsglm(modplsglm3, sim="permutation", R=250)
boxplots.bootpls(bordeaux.bootYT)
boxplots.bootpls(bordeaux.bootYT,ranget0=TRUE)

bordeaux.bootYT2<- bootplsglm(modplsglm3, sim="permutation", R=250,
strata=unclass(ybordeaux))
boxplots.bootpls(bordeaux.bootYT2,ranget0=TRUE)

if(require(chemometrics)){
data(hyptis)
hyptis
yhyptis <- factor(hyptis$Group,ordered=TRUE)
Xhyptis <- as.data.frame(hyptis[,c(1:6)])
dataset <- cbind(y=yhyptis,Xhyptis)
options(contrasts = c("contr.treatment", "contr.poly"))
modplsglm4 <- plsRglm(yhyptis,Xhyptis,3,modele="pls-glm-polr")
hyptis.bootYT3<- bootplsglm(modplsglm4, sim="permutation", R=250)
rownames(hyptis.bootYT3$t0)<-c("Sabi\nnene", "Pin\nnene",

```

```
"Cine\nole", "Terpi\nnene", "Fenc\nhone", "Terpi\nnolene")
boxplots.bootpls(hyptis.bootYT3)
boxplots.bootpls(hyptis.bootYT3, xaxisticks=FALSE)
boxplots.bootpls(hyptis.bootYT3, ranget0=TRUE)
boxplots.bootpls(hyptis.bootYT3, ranget0=TRUE, xaxisticks=FALSE)
}
```

---

bordeaux

*Quality of wine dataset*

---

## Description

Quality of Bordeaux wines (Quality) and four potentially predictive variables (Temperature, Sunshine, Heat and Rain).

## Usage

```
data(bordeaux)
```

## Format

A data frame with 34 observations on the following 5 variables.

Temperature a numeric vector

Sunshine a numeric vector

Heat a numeric vector

Rain a numeric vector

Quality an ordered factor with levels 1 < 2 < 3

## Source

P. Bastien, V. Esposito-Vinzi, and M. Tenenhaus. (2005). PLS generalised linear regression. *Computational Statistics & Data Analysis*, 48(1):17-46.

## References

M. Tenenhaus. (2005). La regression logistique PLS. In J.-J. Dreesbeke, M. Lejeune, and G. Saporta, editors, *Modeles statistiques pour donnees qualitatives*. Editions Technip, Paris.

## Examples

```
data(bordeaux)
str(bordeaux)
```



---

boxplots.bootpls      *Boxplot bootstrap distributions*

---

## Description

Boxplots for bootstrap distributions.

## Usage

```
boxplots.bootpls(bootobject, indices = NULL, prednames = TRUE,
  articlestyle = TRUE, xaxisticks=TRUE, ranget0= FALSE, las = par("las"),
  mar, mgp, ...)
```

## Arguments

bootobject	a object of class "boot"
indices	vector of indices of the variables to plot. Defaults to NULL: all the predictors will be used.
prednames	do the original names of the predictors shall be plotted ? Defaults to TRUE: the names are plotted.
articlestyle	do the extra blank zones of the margin shall be removed from the plot ? Defaults to TRUE: the margins are removed.
xaxisticks	do ticks for the x axis shall be plotted ? Defaults to TRUE: the ticks are plotted.
ranget0	does the vertical range of the plot shall be computed to include the initial estimates of the coefficients ? Defaults to FALSE: the vertical range is calculated only using the bootstrapped values of the statistics. Especially using for permutation bootstrap.
las	numeric in 0,1,2,3; the style of axis labels. 0: always parallel to the axis [default], 1: always horizontal, 2: always perpendicular to the axis, 3: always vertical.
mar	A numerical vector of the form c(bottom, left, top, right) which gives the number of lines of margin to be specified on the four sides of the plot. The default is c(5, 4, 4, 2) + 0.1.
mgp	The margin line (in mex units) for the axis title, axis labels and axis line. Note that mgp[1] affects title whereas mgp[2:3] affect axis. The default is c(3, 1, 0).
...	further options to pass to the <code>boxplot</code> function.

## Value

NULL

## Author(s)

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**See Also**[bootpls](#)**Examples**

```

data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

# Lazraq-Cleroux PLS ordinary bootstrap
set.seed(250)
modpls <- plsR(yCornell,XCornell,3)
Cornell.bootYX <- bootpls(modpls, R=250)

# Graph similar to the one of Bastien et al. in CSDA 2005
boxplots.bootpls(Cornell.bootYX,indices=2:8)

data(aze_compl)
modplsglm<-plsRglm(y~.,data=aze_compl,3,modele="pls-glm-logistic")
aze_compl.boot3 <- bootplsglm(modplsglm, R=250)
boxplots.bootpls(aze_compl.boot3)
boxplots.bootpls(aze_compl.boot3,las=3,mar=c(5,2,1,1))
boxplots.bootpls(aze_compl.boot3,indices=c(2,4,6),prednames=FALSE)

```

---

coef.plsRglmmodel      *coef method for plsR models*

---

**Description**

This function provides a coef method for the class "plsRglmmodel"

**Usage**

```

## S3 method for class 'plsRglmmodel'
coef(object,type=c("scaled","original"), ...)

```

**Arguments**

object	an object of the class "plsRglmmodel"
type	if scaled, the coefficients of the predictors are given for the scaled predictors, if original the coefficients are to be used with the predictors on their original scale.
...	not used

**Value**

An object of class `coef.plsRglmmodel`.

<code>CoeffC</code>	Coefficients of the components.
<code>Std.Coeffs</code>	Coefficients of the scaled predictors in the regression function.
<code>Coeffs</code>	Coefficients of the untransformed predictors (on their original scale).

**Author(s)**

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**See Also**

[coef](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsRglm(yCornell,XCornell,3,modele="pls-glm-family",family=gaussian())
class(modpls)
coef(modpls)
coef(modpls,type="scaled")
rm(list=c("XCornell","yCornell","modpls"))
```

---

<code>coef.plsRmodel</code>	<i>coef method for plsR models</i>
-----------------------------	------------------------------------

---

**Description**

This function provides a `coef` method for the class `"plsRmodel"`

**Usage**

```
## S3 method for class 'plsRmodel'
coef(object,type=c("scaled","original"), ...)
```

**Arguments**

<code>object</code>	an object of the class <code>"plsRmodel"</code>
<code>type</code>	if <code>scaled</code> , the coefficients of the predictors are given for the scaled predictors, if <code>original</code> the coefficients are to be used with the predictors on their original scale.
<code>...</code>	not used

**Value**

An object of class `coef.plsRmodel`.

<code>CoeffC</code>	Coefficients of the components.
<code>Std.Coeffs</code>	Coefficients of the scaled predictors.
<code>Coeffs</code>	Coefficients of the untransformed predictors (on their original scale).

**Author(s)**

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**See Also**

[coef](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsRglm(yCornell,XCornell,3,modele="pls")
class(modpls)
coef(modpls)
coef(modpls,type="scaled")
rm(list=c("XCornell","yCornell","modpls"))
```

---

coefs.plsR

*Coefficients for bootstrap computations of PLSR models*

---

**Description**

A function passed to `boot` to perform bootstrap.

**Usage**

```
coefs.plsR(dataset,ind,nt,modele, maxcoefvalues,ifbootfail,verbose)
```

**Arguments**

<code>dataset</code>	dataset to resample
<code>ind</code>	indices for resampling
<code>nt</code>	number of components to use
<code>modele</code>	type of modele to use, see <a href="#">plsR</a>

maxcoefvalues maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples

ifbootfail value to return if the estimation fails on a bootstrap sample

verbose should info messages be displayed ?

**Value**

estimates on a bootstrap sample or ifbootfail value if the bootstrap computation fails.

**Author(s)**

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<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

See also [bootpls](#).

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

# Lazraq-Cleroux PLS (Y,X) bootstrap
# statistic=coefs.plsR is the default for (Y,X) resampling of PLSR models.
set.seed(250)
modpls <- plsR(yCornell,XCornell,1)
Cornell.bootYX <- bootpls(modpls, R=250, statistic=coefs.plsR)
```

---

coefs.plsRglm

*Coefficients for bootstrap computations of PLSGLR models*

---

**Description**

A function passed to boot to perform bootstrap.

**Usage**

```
coefs.plsRglm(dataset, ind, nt, modele, family=NULL, maxcoefvalues,ifbootfail,verbose)
```

**Arguments**

dataset	dataset to resample
ind	indices for resampling
nt	number of components to use
modele	type of modele to use, see <a href="#">plsRglm</a>
family	glm family to use, see <a href="#">plsRglm</a>
maxcoefvalues	maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples
ifbootfail	value to return if the estimation fails on a bootstrap sample
verbose	should info messages be displayed ?

**Value**

estimates on a bootstrap sample or ifbootfail value if the bootstrap computation fails.

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

See also [bootplsglm](#).

**Examples**

```
data(Cornell)

# (Y,X) bootstrap of a PLSGLR model
# statistic=coefs.plsRglm is the default for (Y,X) bootstrap of a PLSGLR models.
set.seed(250)
modplsglm <- plsRglm(Y~, data=Cornell, 1, modele="pls-glm-family", family=gaussian)
Cornell.bootYX <- bootplsglm(modplsglm, R=250, typeboot="plsmodel", statistic=coefs.plsRglm)
```

---

 coefs.plsRglmnp

---

*Coefficients for bootstrap computations of PLSGLR models*


---

**Description**

A function passed to boot to perform bootstrap.

**Usage**

```
coefs.plsRglmnp(dataRepYtt, ind, nt, modele, family=NULL,
maxcoefvalues, wwetoile, ifbootfail)
```

**Arguments**

dataRepYtt	components' coordinates to bootstrap
ind	indices for resampling
nt	number of components to use
modele	type of modele to use, see <a href="#">plsRglm</a>
family	glm family to use, see <a href="#">plsRglm</a>
maxcoefvalues	maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples
wwetoile	values of the Wstar matrix in the original fit
ifbootfail	value to return if the estimation fails on a bootstrap sample

**Value**

estimates on a bootstrap sample or ifbootfail value if the bootstrap computation fails.

**Note**

~~some notes~~

**Author(s)**

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**See Also**

See also [bootplsglm](#)

**Examples**

```
data(Cornell)

# (Y,X) bootstrap of a PLSGLR model
# statistic=coefs.plsRglm is the default for (Y,X) bootstrap of a PLSGLR models.
set.seed(250)
modplsglm <- plsRglm(Y~.,data=Cornell,1,modele="pls-glm-family",family=gaussian)
Cornell.bootYT <- bootplsglm(modplsglm, R=250, statistic=coefs.plsRglmnp)
```

---

coefs.plsRnp                      *Coefficients for bootstrap computations of PLSR models*

---

### Description

A function passed to boot to perform bootstrap.

### Usage

```
coefs.plsRnp(dataRepYtt, ind, nt, modele, maxcoefvalues, wwetoile, ifbootfail)
```

### Arguments

dataRepYtt	components' coordinates to bootstrap
ind	indices for resampling
nt	number of components to use
modele	type of modele to use, see <a href="#">plsRglm</a>
maxcoefvalues	maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples
wwetoile	values of the Wstar matrix in the original fit
ifbootfail	value to return if the estimation fails on a bootstrap sample

### Value

estimates on a bootstrap sample or ifbootfail value if the bootstrap computation fails.

### Author(s)

Frederic Bertrand  
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### See Also

See also [bootpls](#)

### Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

# Lazraq-Cleroux PLS (Y,X) bootstrap
# statistic=coefs.plsR is the default for (Y,X) resampling of PLSR models.
set.seed(250)
modpls <- plsR(yCornell,XCornell,1)
Cornell.bootYT <- bootpls(modpls, R=250, typeboot="fmodel_np", statistic=coefs.plsRnp)
```



---

confints.bootpls	<i>Bootstrap confidence intervals</i>
------------------	---------------------------------------

---

### Description

This function is a wrapper for `boot.ci` to derive bootstrap-based confidence intervals from a "boot" object.

### Usage

```
confints.bootpls(bootobject, indices = NULL, typeBCa=TRUE)
```

### Arguments

<code>bootobject</code>	an object of class "boot"
<code>indices</code>	the indices of the predictor for which CIs should be calculated. Defaults to NULL: all the predictors will be used.
<code>typeBCa</code>	shall BCa bootstrap based CI derived ? Defaults to TRUE. This is a safety option since sometimes computing BCa bootstrap based CI fails whereas the other types of CI can still be derived.

### Value

Matrix with the limits of bootstrap based CI for all (defaults) or only the selected predictors (`indices` option). The limits are given in that order: Normal Lower then Upper Limit, Basic Lower then Upper Limit, Percentile Lower then Upper Limit, BCa Lower then Upper Limit.

### Author(s)

Frederic Bertrand  
<[frederic.bertrand@math.unistra.fr](mailto:frederic.bertrand@math.unistra.fr)>  
<http://www-irma.u-strasbg.fr/~fbertran/>

### See Also

See also `bootpls` and `bootplsglm`.

### Examples

```
data(Cornell)

#Lazraq-Cleroux PLS (Y,X) bootstrap
set.seed(250)
modpls <- plsR(Y~., data=Cornell, 3)
Cornell.bootYX <- bootpls(modpls, R=250)
confints.bootpls(Cornell.bootYX, 2:8)
confints.bootpls(Cornell.bootYX, 2:8, typeBCa=FALSE)
```

---

CorMat

*Correlation matrix for simulating plsR datasets*

---

**Description**

A correlation matrix to simulate datasets

**Usage**

```
data(CorMat)
```

**Format**

A data frame with 17 observations on the following 17 variables.

y a numeric vector

x11 a numeric vector

x12 a numeric vector

x13 a numeric vector

x21 a numeric vector

x22 a numeric vector

x31 a numeric vector

x32 a numeric vector

x33 a numeric vector

x34 a numeric vector

x41 a numeric vector

x42 a numeric vector

x51 a numeric vector

x61 a numeric vector

x62 a numeric vector

x63 a numeric vector

x64 a numeric vector

**Source**

Handmade.

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**Examples**

```
data(CorMat)
str(CorMat)
```

---

Cornell

*Cornell dataset*

---

**Description**

The famous Cornell dataset. A mixture experiment on X1, X2, X3, X4, X5, X6 and X7 to analyse octane degree (Y) in gasoline.

**Usage**

```
data(Cornell)
```

**Format**

A data frame with 12 observations on the following 8 variables.

X1 a numeric vector

X2 a numeric vector

X3 a numeric vector

X4 a numeric vector

X5 a numeric vector

X6 a numeric vector

X7 a numeric vector

Y response value: a numeric vector

**Source**

M. Tenenhaus. (1998). *La regression PLS, Theorie et pratique*. Editions Technip, Paris.

**References**

N. Kettaneh-Wold. Analysis of mixture data with partial least squares. (1992). *Chemometrics and Intelligent Laboratory Systems*, 14(1):57-69.

**Examples**

```
data(Cornell)
str(Cornell)
```

## Description

This function implements k-fold cross-validation on complete or incomplete datasets for partial least squares regression models

## Usage

```
cv.plsR(x, ...)
## Default S3 method:
cv.plsRmodel(dataY,dataX,nt=2,limQ2set=.0975,modele="pls",
K=5, NK=1, grouplist=NULL, random=TRUE, scaleX=TRUE,
scaleY=NULL, keepcoeffs=FALSE, keepfolds=FALSE, keepdataY=TRUE,
keepMclassified=FALSE, tol_Xi=10^(-12), weights, verbose=TRUE)
## S3 method for class 'formula'
cv.plsRmodel(formula,data=NULL,nt=2,limQ2set=.0975,modele="pls",
K=5, NK=1, grouplist=NULL, random=TRUE, scaleX=TRUE,
scaleY=NULL, keepcoeffs=FALSE, keepfolds=FALSE, keepdataY=TRUE,
keepMclassified=FALSE, tol_Xi=10^(-12), weights,subset,contrasts=NULL, verbose=TRUE)
PLS_lm_kfoldcv(dataY, dataX, nt = 2, limQ2set = 0.0975, modele = "pls",
K = 5, NK = 1, grouplist = NULL, random = TRUE, scaleX = TRUE,
scaleY = NULL, keepcoeffs = FALSE, keepfolds = FALSE, keepdataY = TRUE,
keepMclassified=FALSE, tol_Xi = 10^(-12), weights, verbose=TRUE)
PLS_lm_kfoldcv_formula(formula,data=NULL,nt=2,limQ2set=.0975,modele="pls",
K=5, NK=1, grouplist=NULL, random=TRUE, scaleX=TRUE,
scaleY=NULL, keepcoeffs=FALSE, keepfolds=FALSE, keepdataY=TRUE,
keepMclassified=FALSE, tol_Xi=10^(-12), weights,subset,contrasts=NULL,verbose=TRUE)
```

## Arguments

x	a formula or a response (training) dataset
dataY	response (training) dataset
dataX	predictor(s) (training) dataset
formula	an object of class " <b>formula</b> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
data	an optional data frame, list or environment (or object coercible by <a href="#">as.data.frame</a> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>plsRglm</code> is called.
nt	number of components to be extracted
limQ2set	limit value for the Q2
modele	name of the PLS model to be fitted, only ("pls" available for this fonction.

K	number of groups. Defaults to 5.
NK	number of times the group division is made
grouplist	to specify the members of the K groups
random	should the K groups be made randomly. Defaults to TRUE
scaleX	scale the predictor(s) : must be set to TRUE for <code>modele="pls"</code> and should be for <code>glms pls</code> .
scaleY	scale the response : Yes/No. Ignored since non always possible for <code>glm</code> responses.
keepcoeffs	shall the coefficients for each model be returned
keepfolds	shall the groups' composition be returned
keepdataY	shall the observed value of the response for each one of the predicted value be returned
keepMclassed	shall the number of miss classed be returned
tol_Xi	minimal value for $\text{Norm2}(X_i)$ and $\det(pp' \times pp)$ if there is any missing value in the <code>dataX</code> . It defaults to $10^{-12}$
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
verbose	should info messages be displayed ?
...	arguments to pass to <code>cv.plsRmodel.default</code> or to <code>cv.plsRmodel.formula</code>

## Details

Predicts 1 group with the K-1 other groups. Leave one out cross validation is thus obtained for  $K == \text{nrow}(\text{dataX})$ .

A typical predictor has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for response. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed.

A specification of the form `first:second` indicates the the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the cross of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in `weights` being inversely proportional to the dispersions); or equivalently, when the elements of `weights` are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations.

**Value**

An object of class "cv.plsRmodel".

`results_kfolds` list of NK. Each element of the list sums up the results for a group division:  
 list of K matrices of size about  $nrow(dataX)/K * nt$  with the predicted values for a growing number of components  
 ... ..  
 list of K matrices of size about  $nrow(dataX)/K * nt$  with the predicted values for a growing number of components

`folds` list of NK. Each element of the list sums up the results for a group division:  
 list of K vectors of length about  $nrow(dataX)$  with the numbers of the rows of `dataX` that were used as a training set  
 ... ..  
 list of K vectors of length about  $nrow(dataX)$  with the numbers of the rows of `dataX` that were used as a training set

`dataY_kfolds` list of NK. Each element of the list sums up the results for a group division:  
 list of K matrices of size about  $nrow(dataX)/K * 1$  with the observed values of the response  
 ... ..  
 list of K matrices of size about  $nrow(dataX)/K * 1$  with the observed values of the response

`call` the call of the function

**Note**

Work for complete and incomplete datasets.

**Author(s)**

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**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

Summary method `summary.cv.plsRmodel`. [kfolds2coeff](#), [kfolds2Pressind](#), [kfolds2Press](#), [kfolds2Mclassifiedind](#), [kfolds2Mclassified](#) and [kfolds2CVinfos\\_lm](#) to extract and transform results from k-fold cross-validation.

**Examples**

```

data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

#Leave one out CV (K=nrow(Cornell)) one time (NK=1)
bbb <- cv.plsR(dataY=yCornell,dataX=XCornell,nt=6,K=nrow(Cornell),NK=1)
bbb2 <- cv.plsR(Y~.,data=Cornell,nt=6,K=12,NK=1)
(sum1<-summary(bbb))

#6-fold CV (K=6) two times (NK=2)
#use random=TRUE to randomly create folds for repeated CV
bbb3 <- cv.plsR(dataY=yCornell,dataX=XCornell,nt=6,K=6,NK=2)
bbb4 <- cv.plsR(Y~.,data=Cornell,nt=6,K=6,NK=2)
(sum3<-summary(bbb3))

cvtable(sum1)
cvtable(sum3)
rm(list=c("XCornell","yCornell","bbb","bbb2","bbb3","bbb4"))

```

cv.plsRglm

---

*Partial least squares regression glm models with k-fold cross validation*


---

**Description**

This function implements k-fold cross-validation on complete or incomplete datasets for partial least squares regression generalized linear models

**Usage**

```

cv.plsRglm(x, ...)
## Default S3 method:
cv.plsRglmmodel(dataY,dataX,nt=2,limQ2set=.0975,
modele="pls", family=NULL, K=5, NK=1, grouplist=NULL, random=TRUE,
scaleX=TRUE, scaleY=NULL, keepcoeffs=FALSE, keepfolds=FALSE,
keepdataY=TRUE, keepMclassed=FALSE, tol_Xi=10^(-12), weights, method,
verbose=TRUE)
## S3 method for class 'formula'
cv.plsRglmmodel(formula,data=NULL,nt=2,limQ2set=.0975,
modele="pls", family=NULL, K=5, NK=1, grouplist=NULL, random=TRUE,
scaleX=TRUE, scaleY=NULL, keepcoeffs=FALSE, keepfolds=FALSE,
keepdataY=TRUE, keepMclassed=FALSE, tol_Xi=10^(-12),weights,subset,
start=NULL,etastart,mustart,offset,method,control= list(),contrasts=NULL,
verbose=TRUE)
PLS_glm_kfoldcv(dataY, dataX, nt = 2, limQ2set = 0.0975, modele = "pls",
family = NULL, K = 5, NK = 1, grouplist = NULL, random = TRUE,
scaleX = TRUE, scaleY = NULL, keepcoeffs = FALSE, keepfolds = FALSE,

```

```

keepdataY = TRUE, keepMclassified=FALSE, tol_Xi = 10^(-12), weights, method,
verbose=TRUE)
PLS_glm_kfoldcv_formula(formula,data=NULL,nt=2,limQ2set=.0975,modele="pls",
family=NULL, K=5, NK=1, grouplist=NULL, random=TRUE,
scaleX=TRUE, scaleY=NULL, keepcoeffs=FALSE, keepfolds=FALSE, keepdataY=TRUE,
keepMclassified=FALSE, tol_Xi=10^(-12),weights,subset,start=NULL,etastart,
mustart,offset,method,control= list(),contrasts=NULL, verbose=TRUE)

```

## Arguments

x	a formula or a response (training) dataset
dataY	response (training) dataset
dataX	predictor(s) (training) dataset
formula	an object of class " <b>formula</b> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
data	an optional data frame, list or environment (or object coercible by <a href="#">as.data.frame</a> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>plsRglm</code> is called.
nt	number of components to be extracted
limQ2set	limit value for the Q2
modele	name of the PLS glm model to be fitted ("pls", "pls-glm-Gamma", "pls-glm-gaussian", "pls-glm-inverse.gaussian", "pls-glm-logistic", "pls-glm-poisson", "pls-glm-polr"). Use "modele=pls-glm-family" to enable the family option.
family	a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. (See <a href="#">family</a> for details of family functions.) To use the family option, please set <code>modele="pls-glm-family"</code> . User defined families can also be defined. See details.
K	number of groups. Defaults to 5.
NK	number of times the group division is made
grouplist	to specify the members of the K groups
random	should the K groups be made randomly. Defaults to TRUE
scaleX	scale the predictor(s) : must be set to TRUE for <code>modele="pls"</code> and should be for glms pls.
scaleY	scale the response : Yes/No. Ignored since non always possible for glm responses.
keepcoeffs	shall the coefficients for each model be returned
keepfolds	shall the groups' composition be returned
keepdataY	shall the observed value of the response for each one of the predicted value be returned



keepMclassed	shall the number of miss classed be returned (unavailable)
tol_Xi	minimal value for $\text{Norm2}(X_i)$ and $\det(pp' \times pp)$ if there is any missing value in the dataX. It defaults to $10^{-12}$
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
start	starting values for the parameters in the linear predictor.
etastart	starting values for the linear predictor.
mustart	starting values for the vector of means.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <code>model.offset</code> .
method	<b>for fitting glms with glm</b> ("pls-glm-Gamma", "pls-glm-gaussian", "pls-glm-inverse.gaussian", the method to be used in fitting the model. The default method "glm.fit" uses iteratively reweighted least squares (IWLS). User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as <code>glm.fit</code> . If "model.frame", the model frame is returned. pls-glm-polr logistic, probit, complementary log-log or cauchit (corresponding to a Cauchy latent variable).
control	a list of parameters for controlling the fitting process. For <code>glm.fit</code> this is passed to <code>glm.control</code> .
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
verbose	should info messages be displayed ?
...	arguments to pass to <code>cv.plsRglmmodel.default</code> or to <code>cv.plsRglmmodel.formula</code>

## Details

Predicts 1 group with the K-1 other groups. Leave one out cross validation is thus obtained for  $K = \text{nrow}(\text{dataX})$ .

There are seven different predefined models with predefined link functions available :

"pls" ordinary pls models

"pls-glm-Gamma" glm gaussian with inverse link pls models

"pls-glm-gaussian" glm gaussian with identity link pls models

"pls-glm-inverse-gamma" glm binomial with square inverse link pls models

"pls-glm-logistic" glm binomial with logit link pls models

"pls-glm-poisson" glm poisson with log link pls models

"pls-glm-polr" glm polr with logit link pls models

Using the "family=" option and setting "modele=pls-glm-family" allows changing the family and link function the same way as for the `glm` function. As a consequence user-specified families can also be used.

**The gaussian family** accepts the links (as names) identity, log and inverse.

**The binomial family** accepts the links logit, probit, cauchit, (corresponding to logistic, normal and Cauchy CDFs respectively) log and cloglog (complementary log-log).

**The Gamma family** accepts the links inverse, identity and log.

**The poisson family** accepts the links log, identity, and sqrt.

**The inverse.gaussian family** accepts the links  $1/\mu^2$ , inverse, identity and log.

**The quasi family** accepts the links logit, probit, cloglog, identity, inverse, log,  $1/\mu^2$  and sqrt.

**The function power** can be used to create a power link function.

... arguments to pass to `cv.plsRglmmodel.default` or to `cv.plsRglmmodel.formula`

A typical predictor has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for response. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed.

A specification of the form `first:second` indicates the the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the cross of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in `weights` being inversely proportional to the dispersions); or equivalently, when the elements of `weights` are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations.

## Value

An object of class "cv.plsRglmmodel".

`results_kfolds` list of NK. Each element of the list sums up the results for a group division:  
 list of K matrices of size about  $nrow(dataX)/K * nt$  with the predicted values for a growing number of components  
 ... ..  
 list of K matrices of size about  $nrow(dataX)/K * nt$  with the predicted values for a growing number of components

`folds` list of NK. Each element of the list sums up the informations for a group division:  
 list of K vectors of length about  $nrow(dataX)$  with the numbers of the rows of `dataX` that were used as a training set  
 ... ..

	list of K vectors of length about $nrow(dataX)$ with the numbers of the rows of $dataX$ that were used as a training set
dataY_kfolds	list of NK. Each element of the list sums up the results for a group division: list of K matrices of size about $nrow(dataX)/K * 1$ with the observed values of the response ... .. list of K matrices of size about $nrow(dataX)/K * 1$ with the observed values of the response
call	the call of the function

**Note**

Work for complete and incomplete datasets.

**Author(s)**

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<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18.

**See Also**

Summary method `summary.cv.plsRglmmodel`. `kfolds2coeff`, `kfolds2Pressind`, `kfolds2Press`, `kfolds2Mclassifiedind`, `kfolds2Mclassified` and `summary` to extract and transform results from k-fold cross validation.

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=10)
(sum1<-summary(bbb))
cvtable(sum1)

bbb2 <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,
modele="pls-glm-family",family=gaussian(),K=12)
(sum2<-summary(bbb2))
cvtable(sum2)

#random=TRUE is the default to randomly create folds for repeated CV
bbb3 <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,
modele="pls-glm-family",family=gaussian(),K=6,NK=10)
(sum3<-summary(bbb3))
```

```

plot(cvtable(sum3))

data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
bbb <- cv.plsRglm(yaze_compl,Xaze_compl,nt=10,K=10,modele="pls",keepcoeffs=TRUE)

#For Jackknife computations
kfolds2coeff(bbb)
bbb2 <- cv.plsRglm(yaze_compl,Xaze_compl,nt=10,K=10,modele="pls-glm-family",
family=binomial(probit),keepcoeffs=TRUE)
bbb2 <- cv.plsRglm(yaze_compl,Xaze_compl,nt=10,K=10,
modele="pls-glm-logistic",keepcoeffs=TRUE)
summary(bbb,MClassed=TRUE)
summary(bbb2,MClassed=TRUE)
kfolds2coeff(bbb2)

kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)
summary(bbb2)
rm(list=c("Xaze_compl","yaze_compl","bbb","bbb2"))

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
bbb <- cv.plsRglm(dataY=round(ypine),dataX=Xpine,nt=10,modele="pls-glm-family",
family=poisson(log),K=10,keepcoeffs=TRUE,keepfolds=FALSE)
bbb2 <- cv.plsRglm(dataY=round(ypine),dataX=Xpine,nt=10,
modele="pls-glm-poisson",K=10,keepcoeffs=TRUE,keepfolds=FALSE)

#For Jackknife computations
kfolds2coeff(bbb)
boxplot(kfolds2coeff(bbb)[,1])

kfolds2Chisqind(bbb)
kfolds2Chisq(bbb)
summary(bbb)
PLS_lm(ypine,Xpine,10,typeVC="standard")$InfCrit

XpineNAX21 <- Xpine
XpineNAX21[1,2] <- NA
bbb2 <- cv.plsRglm(dataY=round(ypine),dataX=XpineNAX21,nt=10,
modele="pls-glm-family",family=poisson(log),K=10,keepcoeffs=TRUE,keepfolds=FALSE)
bbb2 <- cv.plsRglm(dataY=round(ypine),dataX=XpineNAX21,nt=10,
modele="pls-glm-poisson",K=10,keepcoeffs=TRUE,keepfolds=FALSE)

#For Jackknife computations
kfolds2coeff(bbb2)
boxplot(kfolds2coeff(bbb2)[,1])

```

```

kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)
summary(bbb2)
PLS_lm(ypine,XpineNAX21,10,typeVC="standard")$InfCrit
rm(list=c("Xpine","XpineNAX21","ypine","bbb","bbb2"))

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
bbb <- cv.plsRglm(dataY=ypine,dataX=Xpine,nt=10,modele="pls-glm-family",
family=Gamma,K=10,keepcoeffs=TRUE,keepfolds=FALSE)
bbb <- cv.plsRglm(dataY=ypine,dataX=Xpine,nt=10,modele="pls-glm-Gamma",
K=10,keepcoeffs=TRUE,keepfolds=FALSE)

#For Jackknife computations
kfolds2coeff(bbb)
boxplot(kfolds2coeff(bbb)[,1])

kfolds2Chisqind(bbb)
kfolds2Chisq(bbb)
summary(bbb)
PLS_lm(ypine,Xpine,10,typeVC="standard")$InfCrit

XpineNAX21 <- Xpine
XpineNAX21[1,2] <- NA
bbb <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=10,
modele="pls-glm-family",family=Gamma(),K=10,keepcoeffs=TRUE,keepfolds=FALSE)
bbb2 <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=10,
modele="pls-glm-Gamma",K=10,keepcoeffs=TRUE,keepfolds=FALSE)

#For Jackknife computations
kfolds2coeff(bbb2)
boxplot(kfolds2coeff(bbb2)[,1])

kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)
summary(bbb2)
PLS_lm(ypine,XpineNAX21,10,typeVC="standard")$InfCrit
rm(list=c("Xpine","XpineNAX21","ypine","bbb","bbb2"))

data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=10,NK=1,modele="pls")
summary(bbb)

cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-inverse.gaussian",K=12)
cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-family",
family=inverse.gaussian,K=12)

```

```

cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-inverse.gaussian",K=6,
NK=2)$results_kfolds
cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-family",family=inverse.gaussian(),
K=6,NK=2)$results_kfolds
cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-inverse.gaussian",K=6,
NK=2)$results_kfolds
cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-family",
family=inverse.gaussian(link = "1/mu^2"),K=6,NK=2)$results_kfolds

bbb2 <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=10,
modele="pls-glm-inverse.gaussian",keepcoeffs=TRUE)

#For Jackknife computations
kfold2coeff(bbb2)
boxplot(kfold2coeff(bbb2)[,1])

kfold2Chisqind(bbb2)
kfold2Chisq(bbb2)
summary(bbb2)
PLS_lm(yCornell,XCornell,10,typeVC="standard")$InfCrit
rm(list=c("XCornell","yCornell","bbb","bbb2"))

data(Cornell)
bbb <- cv.plsRglm(Y~.,data=Cornell,nt=10,NK=1,modele="pls")
summary(bbb)

cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",family=gaussian(),K=12)
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",family=gaussian(),K=6,
NK=2,random=TRUE,keepfolds=TRUE)$results_kfolds

#Different ways of model specifications
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",family=gaussian(),K=6,
NK=2)$results_kfolds
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",family=gaussian,
K=6,NK=2)$results_kfolds
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",family=gaussian(),
K=6,NK=2)$results_kfolds
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",family=gaussian(link=log),
K=6,NK=2)$results_kfolds

bbb2 <- cv.plsRglm(Y~.,data=Cornell,nt=10,
modele="pls-glm-gaussian",keepcoeffs=TRUE)
bbb2 <- cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",
family=gaussian(link=log),K=6,keepcoeffs=TRUE)

#For Jackknife computations
kfold2coeff(bbb2)
boxplot(kfold2coeff(bbb2)[,1])

kfold2Chisqind(bbb2)
kfold2Chisq(bbb2)
summary(bbb2)

```

```

PLS_lm_formula(Y~.,data=Cornell,10,typeVC="standard")$InfCrit
rm(list=c("bbb","bbb2"))

data(pine)
bbb <- cv.plsRglm(x11~.,data=pine,nt=10,modele="pls-glm-family",
family=gaussian(log),K=10,keepcoeffs=TRUE,keepfolds=FALSE)
bbb <- cv.plsRglm(x11~.,data=pine,nt=10,modele="pls-glm-family",family=gaussian(),
K=10,keepcoeffs=TRUE,keepfolds=FALSE)

#For Jackknife computations
kfolds2coeff(bbb)
boxplot(kfolds2coeff(bbb)[,1])

kfolds2Chisqind(bbb)
kfolds2Chisq(bbb)
summary(bbb)
PLS_lm_formula(x11~.,data=pine,nt=10,typeVC="standard")$InfCrit

pineNAX21 <- pine
pineNAX21[1,2] <- NA
bbb2 <- cv.plsRglm(x11~.,data=pineNAX21,nt=10,
modele="pls-glm-family",family=gaussian(log),K=10,keepcoeffs=TRUE,keepfolds=FALSE)
bbb2 <- cv.plsRglm(x11~.,data=pineNAX21,nt=10,
modele="pls-glm-gaussian",K=10,keepcoeffs=TRUE,keepfolds=FALSE)

#For Jackknife computations
kfolds2coeff(bbb2)
boxplot(kfolds2coeff(bbb2)[,1])

kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)
summary(bbb2)
PLS_lm_formula(x11~.,data=pineNAX21,nt=10,typeVC="standard")$InfCrit
rm(list=c("pineNAX21","bbb","bbb2"))

data(aze_compl)
bbb <- cv.plsRglm(y~.,data=aze_compl,nt=10,K=10,modele="pls",
keepcoeffs=TRUE)

#For Jackknife computations
kfolds2coeff(bbb)
bbb2 <- cv.plsRglm(y~.,data=aze_compl,nt=3,K=10,
modele="pls-glm-family",family=binomial(probit),keepcoeffs=TRUE)
bbb2 <- cv.plsRglm(y~.,data=aze_compl,nt=3,K=10,
modele="pls-glm-logistic",keepcoeffs=TRUE)
summary(bbb,MClassed=TRUE)
summary(bbb2,MClassed=TRUE)
kfolds2coeff(bbb2)

kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)

```

```
summary(bbb2)
rm(list=c("bbb", "bbb2"))
```

```
data(pine)
bbb <- cv.plsRglm(round(x11)~., data=pine, nt=10,
  modele="pls-glm-family", family=poisson(log), K=10, keepcoeffs=TRUE, keepfolds=FALSE)
bbb <- cv.plsRglm(round(x11)~., data=pine, nt=10,
  modele="pls-glm-poisson", K=10, keepcoeffs=TRUE, keepfolds=FALSE)
```

```
#For Jackknife computations
kfolds2coeff(bbb)
boxplot(kfolds2coeff(bbb)[,1])
```

```
kfolds2Chisqind(bbb)
kfolds2Chisq(bbb)
summary(bbb)
PLS_lm_formula(x11~., data=pine, 10, typeVC="standard")$InfCrit
```

```
pineNAX21 <- pine
pineNAX21[1,2] <- NA
bbb2 <- cv.plsRglm(round(x11)~., data=pineNAX21, nt=10,
  modele="pls-glm-family", family=poisson(log), K=10, keepcoeffs=TRUE, keepfolds=FALSE)
bbb2 <- cv.plsRglm(round(x11)~., data=pineNAX21, nt=10,
  modele="pls-glm-poisson", K=10, keepcoeffs=TRUE, keepfolds=FALSE)
```

```
#For Jackknife computations
kfolds2coeff(bbb2)
boxplot(kfolds2coeff(bbb2)[,1])
```

```
kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)
summary(bbb2)
PLS_lm_formula(x11~., data=pineNAX21, 10, typeVC="standard")$InfCrit
rm(list=c("pineNAX21", "bbb", "bbb2"))
```

```
data(pine)
bbb <- cv.plsRglm(x11~., data=pine, nt=10, modele="pls-glm-family",
  family=Gamma, K=10, keepcoeffs=TRUE, keepfolds=FALSE)
bbb <- cv.plsRglm(x11~., data=pine, nt=10, modele="pls-glm-Gamma",
  K=10, keepcoeffs=TRUE, keepfolds=FALSE)
```

```
#For Jackknife computations
kfolds2coeff(bbb)
boxplot(kfolds2coeff(bbb)[,1])
```

```
kfolds2Chisqind(bbb)
kfolds2Chisq(bbb)
summary(bbb)
PLS_lm_formula(x11~., data=pine, 10, typeVC="standard")$InfCrit
```



```

pineNAX21 <- pine
pineNAX21[1,2] <- NA
bbb2 <- cv.plsRglm(x11~.,data=pineNAX21,nt=10,
modele="pls-glm-family",family=Gamma(),K=10,keepcoeffs=TRUE,keepfolds=FALSE)
bbb2 <- cv.plsRglm(x11~.,data=pineNAX21,nt=10,
modele="pls-glm-Gamma",K=10,keepcoeffs=TRUE,keepfolds=FALSE)

#For Jackknife computations
kfolds2coeff(bbb2)
boxplot(kfolds2coeff(bbb2)[,1])

kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)
summary(bbb2)
PLS_lm_formula(x11~.,data=pineNAX21,10,typeVC="standard")$InfCrit
rm(list=c("pineNAX21","bbb","bbb2"))

data(Cornell)
bbb <- cv.plsRglm(Y~.,data=Cornell,nt=10,NK=1,modele="pls")
summary(bbb)

cv.plsRglm(Y~.,data=Cornell,nt=3,
modele="pls-glm-inverse.gaussian",K=12)
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",family=inverse.gaussian,K=12)
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-inverse.gaussian",K=6,
NK=2)$results_kfolds
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",
family=inverse.gaussian(),K=6,NK=2)$results_kfolds
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-inverse.gaussian",K=6,NK=2)$results_kfolds
cv.plsRglm(Y~.,data=Cornell,nt=3,modele="pls-glm-family",
family=inverse.gaussian(link = "1/mu^2"),K=6,NK=2)$results_kfolds

bbb2 <- cv.plsRglm(Y~.,data=Cornell,nt=10,
modele="pls-glm-inverse.gaussian",keepcoeffs=TRUE)

#For Jackknife computations
kfolds2coeff(bbb2)
boxplot(kfolds2coeff(bbb2)[,1])

kfolds2Chisqind(bbb2)
kfolds2Chisq(bbb2)
summary(bbb2)
PLS_lm_formula(Y~.,data=Cornell,10,typeVC="standard")$InfCrit
rm(list=c("bbb","bbb2"))

data(bordeaux)
bbb <- cv.plsRglm(Quality~.,data=bordeaux,10,
modele="pls-glm-polr",K=7)
summary(bbb)

```

```

bordeauxNA<-bordeaux
bordeauxNA[1,1] <- NA
bbbNA <- cv.plsRglm(Quality~Temperature+Sunshine+Heat+Rain,
data=bordeauxNA,10,modele="pls-glm-polr",K=10)
summary(bbbNA)
rm(list=c("bbb", "bbbNA"))

bbb2 <- cv.plsRglm(Quality~.,data=bordeaux,nt=2,K=7,
modele="pls-glm-polr",method="logistic")
bbb3 <- cv.plsRglm(Quality~.,data=bordeaux,nt=2,K=7,
modele="pls-glm-polr",method="probit")
bbb4 <- cv.plsRglm(Quality~.,data=bordeaux,nt=2,K=7,
modele="pls-glm-polr",method="cloglog")
bbb5 <- cv.plsRglm(Quality~.,data=bordeaux,nt=2,K=7,
modele="pls-glm-polr",method="cauchit")

summary(bbb2)
summary(bbb3)
summary(bbb4)
summary(bbb5)
rm(list=c("bbb", "bbbNA", "bbb2", "bbb3", "bbb4", "bbb5"))

```

---

cvtable	<i>Table method for summary of cross validated PLSR and PLSGLR models</i>
---------	---

---

## Description

The function `cvtable` is wrapper of `cvtable.plsR` and `cvtable.plsRglm` that provides a table summary for the classes `"summary.cv.plsRmodel"` and `"summary.cv.plsRglmmodel"`

## Usage

```

cvtable.plsR(x,verbose=TRUE, ...)
cvtable.plsRglm(x,verbose=TRUE, ...)

```

## Arguments

<code>x</code>	an object of the class <code>"summary.cv.plsRmodel"</code>
<code>verbose</code>	should results be displayed ?
<code>...</code>	further arguments to be passed to or from methods.

## Value

`list`List of Information Criteria computed for each fold.

**Author(s)**

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[summary](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
cv.modpls <- cv.plsR(dataY=yCornell,dataX=XCornell,nt=6,K=6,NK=100)
res.cv.modpls <- cvtable(summary(cv.modpls))
plot(res.cv.modpls) #defaults to type="CVQ2"
rm(list=c("XCornell","yCornell","cv.modpls","res.cv.modpls"))
```

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
cv.modplsglm <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=6,K=6,
modele="pls-glm-gaussian",NK=100)
res.cv.modplsglm <- cvtable(summary(cv.modplsglm))
plot(res.cv.modplsglm) #defaults to type="CVQ2Chi2"
rm(list=c("XCornell","yCornell","res.cv.modplsglm"))
```

---

dicho

*Dichotomization*

---

**Description**

This function takes a real value and converts it to 1 if it is positive and else to 0.

**Usage**

```
dicho(val)
```

**Arguments**

val                    A real value

**Value**

0 or 1.

**Author(s)**

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<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

[ifelse](#)

**Examples**

```
dimX <- 6
Astar <- 4
(dataAstar4 <- t(replicate(10,simul_data_YX(dimX,Astar))))

dicho(dataAstar4)

rm(list=c("dimX","Astar"))
```

---

fowlkes

*Fowlkes dataset*

---

**Description**

A classic dataset from Fowlkes.

**Usage**

```
data(fowlkes)
```

**Format**

A data frame with 9949 observations on the following 13 variables.

Y    binary response

MA   a numeric vector

MW   a numeric vector

NE   a numeric vector

NW   a numeric vector

PA a numeric vector  
SO a numeric vector  
SW a numeric vector  
color a numeric vector  
age1 a numeric vector  
age2 a numeric vector  
age3 a numeric vector  
sexe a numeric vector

### Examples

```
data(fowlkes)  
str(fowlkes)
```

---

infcrit.dof	<i>Information criteria</i>
-------------	-----------------------------

---

### Description

This function computes information criteria for existing plsR model using Degrees of Freedom estimation.

### Usage

```
infcrit.dof(modplsR, naive = FALSE)
```

### Arguments

modplsR	A plsR model i.e. an object returned by one of the functions <code>plsR</code> , <code>plsRmodel.default</code> , <code>plsRmodel.formula</code> , <code>PLS_lm</code> or <code>PLS_lm.formula</code> .
naive	A boolean.

### Details

If `naive=FALSE` returns AIC, BIC and `gmdl` values for estimated and naive degrees of freedom. If `naive=TRUE` returns NULL.

### Value

matrix	AIC, BIC and <code>gmdl</code> values or NULL.
--------	--

### Author(s)

Frederic Bertrand  
<[frederic.bertrand@math.unistra.fr](mailto:frederic.bertrand@math.unistra.fr)>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

- M. Hansen, B. Yu. (2001). Model Selection and Minimum Description Length Principle, *Journal of the American Statistical Association*, 96, 746-774.
- N. Kraemer, M. Sugiyama. (2011). The Degrees of Freedom of Partial Least Squares Regression. *Journal of the American Statistical Association*, 106(494), 697-705.
- N. Kraemer, M. Sugiyama, M.L. Braun. (2009). Lanczos Approximations for the Speedup of Kernel Partial Least Squares Regression, *Proceedings of the Twelfth International Conference on Artificial Intelligence and Statistics (AISTATS)*, 272-279.

## See Also

[plsR.dof](#) for degrees of freedom computation and [infcrit.dof](#) for computing information criteria directly from a previously fitted plsR model.

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsR(yCornell,XCornell,4)
infcrit.dof(modpls)
```

---

kfolds2Chisq	<i>Computes Predicted Chisquare for k-fold cross-validated partial least squares regression models.</i>
--------------	---

---

## Description

This function computes Predicted Chisquare for k-fold cross validated partial least squares regression models.

## Usage

```
kfolds2Chisq(pls_kfolds)
```

## Arguments

`pls_kfolds` a k-fold cross validated partial least squares regression glm model

## Value

<code>list</code>	Total Predicted Chisquare vs number of components for the first group partition
<code>...</code>	<code>...</code>
<code>list</code>	Total Predicted Chisquare vs number of components for the last group partition

## Note

Use [cv.plsRglm](#) to create k-fold cross validated partial least squares regression glm models.

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[kfolds2coeff](#), [kfolds2Press](#), [kfolds2Pressind](#), [kfolds2Chisqind](#), [kfolds2Mclassifiedind](#) and [kfolds2Mclassified](#) to extract and transforms results from k-fold cross validation.

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-gaussian",K=16)
bbb2 <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-gaussian",K=5)
kfolds2Chisq(bbb)
kfolds2Chisq(bbb2)
rm(list=c("XCornell","yCornell","bbb","bbb2"))

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
bbb <- cv.plsRglm(dataY=ypine,dataX=Xpine,nt=4,modele="pls-glm-gaussian")
bbb2 <- cv.plsRglm(dataY=ypine,dataX=Xpine,nt=10,modele="pls-glm-gaussian",K=10)
kfolds2Chisq(bbb)
kfolds2Chisq(bbb2)

XpineNAX21 <- Xpine
XpineNAX21[1,2] <- NA
bbbNA <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=10,modele="pls",K=10)
kfolds2Press(bbbNA)
kfolds2Chisq(bbbNA)
bbbNA2 <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=4,modele="pls-glm-gaussian")
bbbNA3 <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=10,modele="pls-glm-gaussian",K=10)
kfolds2Chisq(bbbNA2)
kfolds2Chisq(bbbNA3)
rm(list=c("Xpine","XpineNAX21","ypine","bbb","bbb2","bbbNA","bbbNA2","bbbNA3"))

data(aze_comp1)
```

```

Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
bbb <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=4,modele="pls-glm-family",
family="binomial")
bbb <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=4,modele="pls-glm-logistic")
bbb2 <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=10,modele="pls-glm-family",
family=binomial(),K=10)
bbb2 <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=10,modele="pls-glm-logistic",K=10)
kfold2Chisq(bbb)
kfold2Chisq(bbb2)
rm(list=c("Xaze_compl","yaze_compl","bbb","bbb2"))

```

---

kfold2Chisqind	<i>Computes individual Predicted Chisquare for k-fold cross validated partial least squares regression models.</i>
----------------	--

---

### Description

This function computes individual Predicted Chisquare for k-fold cross validated partial least squares regression models.

### Usage

```
kfold2Chisqind(pls_kfolds)
```

### Arguments

pls\_kfolds      a k-fold cross validated partial least squares regression glm model

### Value

list	Individual PChisq vs number of components for the first group partition
...	...
list	Individual PChisq vs number of components for the last group partition

### Note

Use [cv.plsRglm](#) to create k-fold cross validated partial least squares regression glm models.

### Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>



## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[kfold2coeff](#), [kfold2Press](#), [kfold2Pressind](#), [kfold2Chisq](#), [kfold2Mclassified](#) and [kfold2Mclassified](#) to extract and transforms results from k-fold cross-validation.

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-gaussian",K=16)
bbb2 <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-gaussian",K=5)
kfold2Chisqind(bbb)
kfold2Chisqind(bbb2)
rm(list=c("XCornell","yCornell","bbb","bbb2"))

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
bbb <- cv.plsRglm(dataY=ypine,dataX=Xpine,nt=4,modele="pls-glm-gaussian")
bbb2 <- cv.plsRglm(dataY=ypine,dataX=Xpine,nt=10,modele="pls-glm-gaussian",K=10)
kfold2Chisqind(bbb)
kfold2Chisqind(bbb2)

XpineNAX21 <- Xpine
XpineNAX21[1,2] <- NA
bbbNA <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=10,modele="pls",K=10)
kfold2Pressind(bbbNA)
kfold2Chisqind(bbbNA)
bbbNA2 <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=4,modele="pls-glm-gaussian")
bbbNA3 <- cv.plsRglm(dataY=ypine,dataX=XpineNAX21,nt=10,modele="pls-glm-gaussian",K=10)
kfold2Chisqind(bbbNA2)
kfold2Chisqind(bbbNA3)
rm(list=c("Xpine","XpineNAX21","ypine","bbb","bbb2","bbbNA","bbbNA2","bbbNA3"))

data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
bbb <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=4,modele="pls-glm-family",
family=binomial())
bbb <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=4,modele="pls-glm-logistic")
bbb2 <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=10,modele="pls-glm-family",
family=binomial(),K=10)
```

```
bbb2 <- cv.plsRglm(dataY=yaze_compl,dataX=Xaze_compl,nt=10,modele="pls-glm-logistic",K=10)
kfold2Chisqind(bbb)
kfold2Chisqind(bbb2)
rm(list=c("Xaze_compl","yaze_compl","bbb","bbb2"))
```

---

kfold2coeff	<i>Extracts coefficients from k-fold cross validated partial least squares regression models</i>
-------------	--

---

### Description

This fonction extracts coefficients from k-fold cross validated partial least squares regression models

### Usage

```
kfold2coeff(pls_kfolds)
```

### Arguments

pls_kfolds	an object that is a k-fold cross validated partial least squares regression models either lm or glm
------------	---

### Details

This fonctions works for plsR and plsRglm models.

### Value

coef.all	matrix with the values of the coefficients for each leave one out step or NULL if another type of cross validation was used.
----------	--

### Note

Only for NK=1 and leave one out CV

### Author(s)

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

### References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[kfolds2Pressind](#), [kfolds2Press](#), [kfolds2Mclassifiedind](#), [kfolds2Mclassified](#) and [summary](#) to extract and transform results from k-fold cross validation.

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- PLS_lm_kfoldcv(dataY=yCornell,dataX=XCornell,nt=3,K=nrow(XCornell),keepcoeffs=TRUE)
kfolds2coeff(bbb)
boxplot(kfolds2coeff(bbb)[,2])
rm(list=c("XCornell","yCornell","Xpine","ypine","bbb"))

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
bbb2 <- cv.plsR(dataY=ypine,dataX=Xpine,nt=4,K=nrow(Xpine),keepcoeffs=TRUE)
kfolds2coeff(bbb2)
boxplot(kfolds2coeff(bbb2)[,1])
rm(list=c("Xpine","ypine","Xpine","ypine","bbb2"))
```

---

kfolds2CVinfos_glm	<i>Extracts and computes information criteria and fits statistics for k-fold cross validated partial least squares glm models</i>
--------------------	---

---

**Description**

This function extracts and computes information criteria and fits statistics for k-fold cross validated partial least squares glm models for both formula or classic specifications of the model.

**Usage**

```
kfolds2CVinfos_glm(pls_kfolds, MClassed = FALSE, verbose=TRUE)
```

**Arguments**

pls_kfolds	an object computed using <a href="#">cv.plsRglm</a>
MClassed	should number of miss classed be computed ?
verbose	should infos be displayed ?

**Details**

The MClassed option should only set to TRUE if the response is binary.

**Value**

list	table of fit statistics for first group partition
...	...
list	table of fit statistics for last group partition

**Note**

Use [summary](#) and [cv.plsRglm](#) instead.

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[kfolds2coeff](#), [kfolds2Pressind](#), [kfolds2Press](#), [kfolds2Mclassifiedind](#) and [kfolds2Mclassified](#) to extract and transforms results from k-fold cross-validation.

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=data.frame(scale(as.matrix(XCornell))[,,]),
nt=6,K=12,NK=1,keepfolds=FALSE,keepdataY=TRUE,modele="pls")
summary(bbb,MClassed=TRUE)
rm(list=c("XCornell","yCornell","bbb"))
```

```
data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
bbb <- cv.plsR(yaze_compl,Xaze_compl,nt=10,K=8,modele="pls")
summary(bbb,MClassed=TRUE)
bbbbis <- cv.plsRglm(yaze_compl,Xaze_compl,nt=10,K=8,modele="pls")
summary(bbbbis,MClassed=TRUE)
bbba <- cv.plsRglm(yaze_compl,Xaze_compl,nt=10,K=8,
modele="pls-glm-family",family=gaussian())
summary(bbba,MClassed=TRUE)
bbb2 <- cv.plsRglm(yaze_compl,Xaze_compl,nt=10,K=8,
```

```

modele="pls-glm-logistic")
summary(bbb2,MClassed=TRUE)
bbb2a <- cv.plsRglm(yaze_compl,Xaze_compl,nt=10,K=8,
modele="pls-glm-family",family=binomial())
summary(bbb2a,MClassed=TRUE)
rm(list=c("Xaze_compl","yaze_compl","bbb","bbbis","bbb2","bbba","bbb2a"))

if(require(chemometrics)){
data(hyptis)
hyptis
hyptis <- factor(hyptis$Group,ordered=TRUE)
Xhyptis <- as.data.frame(hyptis[,c(1:6)])
options(contrasts = c("contr.treatment", "contr.poly"))
modpls2 <- plsRglm(yhyptis,Xhyptis,6,modele="pls-glm-polr")
modpls2$Coeffsmodel_vals
modpls2$InfCrit
modpls2$Coeffs
modpls2$std.coeffs

table(yhyptis,predict(modpls2$FinalModel,type="class"))

modpls3 <- PLS_glm(yhyptis[-c(1,2,3)],Xhyptis[-c(1,2,3)],3,modele="pls-glm-polr",
dataPredictY=Xhyptis[c(1,2,3),])
bbb <- cv.plsRglm(yhyptis,Xhyptis,nt=4,K=10,random=TRUE,modele="pls-glm-polr",
keepcoeffs=TRUE)
summary(bbb,MClassed=TRUE)
}

```

---

kfold2Mclassified	<i>Number of missclassified individuals for k-fold cross validated partial least squares regression models.</i>
-------------------	---

---

## Description

This function indicates the total number of missclassified individuals for k-fold cross validated partial least squares regression models.

## Usage

```
kfold2Mclassified(pls_kfolds)
```

## Arguments

pls_kfolds	a k-fold cross validated partial least squares regression model used on binary data
------------	---

**Value**

list	Total number of missclassified individuals vs number of components for the first group partition
...	...
list	Total number of missclassified individuals vs number of components for the last group partition

**Note**

Use `cv.plsR` to create k-fold cross validated partial least squares regression models.

**Author(s)**

Frederic Bertrand  
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<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

`kfold2coeff`, `kfold2Press`, `kfold2Pressind` and `kfold2Mclassifiedind` to extract and transform results from k-fold cross validation.

**Examples**

```
data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
bbb <- cv.plsR(dataY=yaze_compl,dataX=Xaze_compl,nt=10,K=8,NK=1)
bbb2 <- cv.plsR(dataY=yaze_compl,dataX=Xaze_compl,nt=10,K=8,NK=2)
kfold2Mclassified(bbb)
kfold2Mclassified(bbb2)
rm(list=c("Xaze_compl","yaze_compl","bbb","bbb2"))
```

---

kfolds2Mclassifiedind	<i>Number of missclassified individuals per group for k-fold cross validated partial least squares regression models.</i>
-----------------------	---

---

### Description

This function indicates the number of missclassified individuals per group for k-fold cross validated partial least squares regression models.

### Usage

```
kfolds2Mclassifiedind(pls_kfolds)
```

### Arguments

pls_kfolds	a k-fold cross validated partial least squares regression model used on binary data
------------	---

### Value

list	Number of missclassified individuals per group vs number of components for the first group partition
...	...
list	Number of missclassified individuals per group vs number of components for the last group partition

### Note

Use [cv.plsR](#) or [cv.plsRglm](#) to create k-fold cross validated partial least squares regression models or generalized linear ones.

### Author(s)

Frederic Bertrand  
<[frederic.bertrand@math.unistra.fr](mailto:frederic.bertrand@math.unistra.fr)>  
<http://www-irma.u-strasbg.fr/~fbertran/>

### References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

### See Also

[kfolds2coeff](#), [kfolds2Press](#), [kfolds2Pressind](#) and [kfolds2Mclassified](#) to extract and transform results from k-fold cross-validation.

**Examples**

```

data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
bbb <- cv.plsR(dataY=yaze_compl,dataX=Xaze_compl,nt=10,K=8,NK=1)
bbb2 <- cv.plsR(dataY=yaze_compl,dataX=Xaze_compl,nt=10,K=8,NK=2)
kfolds2Mclassifiedind(bbb)
kfolds2Mclassifiedind(bbb2)
rm(list=c("Xaze_compl","yaze_compl","bbb","bbb2"))

```

---

kfolds2Press	<i>Computes PRESS for k-fold cross validated partial least squares regression models.</i>
--------------	---

---

**Description**

This function computes PRESS for k-fold cross validated partial least squares regression models.

**Usage**

```
kfolds2Press(pls_kfolds)
```

**Arguments**

`pls_kfolds` a k-fold cross validated partial least squares regression model

**Value**

`list` Press vs number of components for the first group partition

...

`list` Press vs number of components for the last group partition

**Note**

Use [cv.plsR](#) to create k-fold cross validated partial least squares regression models.

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>



## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[kfold2coeff](#), [kfold2Pressind](#), [kfold2Mclassifiedind](#) and [kfold2Mclassified](#) to extract and transforms results from k-fold cross validation.

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsR(dataY=yCornell,dataX=data.frame(scale(as.matrix(XCornell))[, ]),nt=6,K=12,NK=1)
bbb2 <- cv.plsR(dataY=yCornell,dataX=data.frame(scale(as.matrix(XCornell))[, ]),nt=6,K=6,NK=1)
kfold2Press(bbb)
kfold2Press(bbb2)
rm(list=c("XCornell","yCornell","bbb","bbb2"))
```

```
data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
bbb <- cv.plsR(dataY=ypine,dataX=Xpine,nt=10,NK=1)
bbb2 <- cv.plsR(dataY=ypine,dataX=Xpine,nt=10,NK=2)
kfold2Press(bbb)
kfold2Press(bbb2)
```

```
XpineNAX21 <- Xpine
XpineNAX21[1,2] <- NA
bbbNA <- cv.plsR(dataY=ypine,dataX=XpineNAX21,nt=10,NK=1)
bbbNA2 <- cv.plsR(dataY=ypine,dataX=XpineNAX21,nt=10,NK=2)
kfold2Press(bbbNA)
kfold2Press(bbbNA2)
rm(list=c("Xpine","XpineNAX21","ypine","bbb","bbb2","bbbNA","bbbNA2"))
```

---

kfold2Pressind

*Computes individual PRESS for k-fold cross validated partial least squares regression models.*

---

## Description

This function computes individual PRESS for k-fold cross validated partial least squares regression models.

**Usage**

```
kfolds2Pressind(pls_kfolds)
```

**Arguments**

pls\_kfolds      a k-fold cross validated partial least squares regression model

**Value**

list            Individual Press vs number of components for the first group partition  
 ...            ...  
 list            Individual Press vs number of components for the last group partition

**Note**

Use [cv.plsR](#) to create k-fold cross validated partial least squares regression models.

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[kfolds2coeff](#), [kfolds2Press](#), [kfolds2Mclassifiedind](#) and [kfolds2Mclassified](#) to extract and transform results from k-fold cross validation.

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsR(dataY=yCornell,dataX=data.frame(scale(as.matrix(XCornell))[,])),nt=6,K=12,NK=1)
bbb2 <- cv.plsR(dataY=yCornell,dataX=data.frame(scale(as.matrix(XCornell))[,])),nt=6,K=6,NK=1)
kfolds2Pressind(bbb)
kfolds2Pressind(bbb2)
rm(list=c("XCornell","yCornell","bbb","bbb2"))

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
```

```
bbb <- cv.plsR(dataY=ypine,dataX=Xpine,nt=10,NK=1)
bbb2 <- cv.plsR(dataY=ypine,dataX=Xpine,nt=10,NK=2)
kfolds2Pressind(bbb)
kfolds2Pressind(bbb2)

XpineNAX21 <- Xpine
XpineNAX21[1,2] <- NA
bbbNA <- cv.plsR(dataY=ypine,dataX=XpineNAX21,nt=10,NK=1)
bbbNA2 <- cv.plsR(dataY=ypine,dataX=XpineNAX21,nt=10,NK=2)
kfolds2Pressind(bbbNA)
kfolds2Pressind(bbbNA2)
rm(list=c("Xpine","XpineNAX21","ypine","bbb","bbb2","bbbNA","bbbNA2"))
```

---

loglikpls

*loglikelihood function for plsR models*

---

### Description

This function provides loglikelihood computation for an univariate plsR model.

### Usage

```
loglikpls(residpls, weights=rep.int(1,length(residpls)))
```

### Arguments

residpls	Residuals of a fitted univariate plsR model
weights	Weights of observations

### Details

Loglikelihood functions for plsR models with univariate response.

### Value

real	Loglikelihood value
------	---------------------

### Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

### References

Baibing Li, Julian Morris, Elaine B. Martin, Model selection for partial least squares regression, *Chemometrics and Intelligent Laboratory Systems* 64 (2002) 79-89. [http://dx.doi.org/10.1016/S0169-7439\(02\)00051-5](http://dx.doi.org/10.1016/S0169-7439(02)00051-5)

**See Also**

[AICpls](#) for AIC computation and [logLik](#) for loglikelihood computations for linear models

**Examples**

```
data(pine)
ypine <- pine[,11]
Xpine <- pine[,1:10]
(Pinscaled <- as.data.frame(cbind(scale(ypine),scale(as.matrix(Xpine))))))
colnames(Pinscaled)[1] <- "y"

lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)

modpls <- plsR(ypine,Xpine,10)
modpls$Std.Coeffs
lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)

AIC(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled))
print(logLik(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)))

sum(dnorm(modpls$RepY, modpls$Std.ValsPredictY, sqrt(mean(modpls$residY^2)), log=TRUE))
sum(dnorm(Pinscaled$yy,fitted(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)),
sqrt(mean(residuals(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled))^2)), log=TRUE))
loglikpls(modpls$residY)
loglikpls(residuals(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)))
AICpls(10,residuals(lm(yy~x1+x2+x3+x4+x5+x6+x7+x8+x9+x10,data=Pinscaled)))
AICpls(10,modpls$residY)
```

---

permcoefs.plsR

*Coefficients for permutation bootstrap computations of PLSR models*


---

**Description**

A function passed to boot to perform bootstrap.

**Usage**

```
permcoefs.plsR(dataset,ind,nt,modele, maxcoefvalues,ifbootfail,verbose)
```

**Arguments**

dataset	dataset to resample
ind	indices for resampling
nt	number of components to use
modele	type of modele to use, see <a href="#">plsR</a>
maxcoefvalues	maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples
ifbootfail	value to return if the estimation fails on a bootstrap sample
verbose	should info messages be displayed ?

**Value**

estimates on a bootstrap sample or ifbootfail value if the bootstrap computation fails.

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

See also [bootpls](#).

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

# Lazraq-Cleroux PLS (Y,X) bootstrap
# statistic=permcoefs.plsR is the default for (Y,X) permutation resampling of PLSR models.
set.seed(250)
modpls <- plsR(yCornell,XCornell,1)
Cornell.bootYX <- bootpls(modpls, sim="permutation", R=250, statistic=permcoefs.plsR)
```

---

permcoefs.plsRglm	<i>Coefficients for permutation bootstrap computations of PLSGLR models</i>
-------------------	---

---

**Description**

A function passed to boot to perform bootstrap.

**Usage**

```
permcoefs.plsRglm(dataset, ind, nt, modele, family=NULL, maxcoefvalues,ifbootfail,verbose)
```

**Arguments**

dataset	dataset to resample
ind	indices for resampling
nt	number of components to use
modele	type of modele to use, see <a href="#">plsRglm</a>
family	glm family to use, see <a href="#">plsRglm</a>
maxcoefvalues	maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples
ifbootfail	value to return if the estimation fails on a bootstrap sample
verbose	should info messages be displayed ?

**Value**

estimates on a bootstrap sample or ifbootfail value if the bootstrap computation fails.

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

See also [bootplsglm](#).

**Examples**

```
data(Cornell)

# (Y,X) bootstrap of a PLSGLR model
# statistic=coefs.plsRglm is the default for (Y,X) bootstrap of a PLSGLR models.
set.seed(250)
modplsglm <- plsRglm(Y~.,data=Cornell,1,modele="pls-glm-family",family=gaussian)
Cornell.bootYX <- bootplsglm(modplsglm, R=250, typeboot="plsmodel",
sim="permutation", statistic=permcoefs.plsRglm)
```

---

permcoefs.plsRglmnp     *Coefficients for permutation bootstrap computations of PLSGLR models*

---

**Description**

A function passed to boot to perform bootstrap.

**Usage**

```
permcoefs.plsRglmnp(dataRepYtt, ind, nt, modele, family=NULL,
maxcoefvalues, wwetoile,ifbootfail)
```

**Arguments**

dataRepYtt	components' coordinates to bootstrap
ind	indices for resampling
nt	number of components to use
modele	type of modele to use, see <a href="#">plsRglm</a>
family	glm family to use, see <a href="#">plsRglm</a>
maxcoefvalues	maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples
wwetoile	values of the Wstar matrix in the original fit
ifbootfail	value to return if the estimation fails on a bootstrap sample

**Value**

estimates on a bootstrap sample or ifbootfail value if the bootstrap computation fails.

**Note**

~~some notes~~

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

See also [bootplsglm](#)

**Examples**

```
data(Cornell)

# (Y,X) bootstrap of a PLSGLR model
# statistic=coef.plsRglm is the default for (Y,X) bootstrap of a PLSGLR models.
set.seed(250)
modplsglm <- plsRglm(Y~.,data=Cornell,1,modele="pls-glm-family",family=gaussian)
Cornell.bootYT <- bootplsglm(modplsglm, R=250, statistic=permcoef.plsRglmnp)
```

---

permcoef.plsRnp      *Coefficients computation for permutation bootstrap*

---

**Description**

A function passed to boot to perform bootstrap.

**Usage**

```
permcoef.plsRnp(dataRepYtt,ind,nt,modele, maxcoefvalues,wwetoile,ifbootfail)
```

**Arguments**

dataRepYtt	components' coordinates to bootstrap
ind	indices for resampling
nt	number of components to use
modele	type of modele to use, see <a href="#">plsRglm</a>
maxcoefvalues	maximum values allowed for the estimates of the coefficients to discard those coming from singular bootstrap samples
wwetoile	values of the Wstar matrix in the original fit
ifbootfail	value to return if the estimation fails on a bootstrap sample

**Value**

estimates on a bootstrap sample or `ifbootfail` value if the bootstrap computation fails.

**Author(s)**

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

See also [bootpls](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

# Lazraq-Cleroux PLS (Y,X) bootstrap
# statistic=coefs.plsR is the default for (Y,X) resampling of PLSR models.
set.seed(250)
modpls <- plsR(yCornell,XCornell,1)
Cornell.bootYT <- bootpls(modpls, R=250, typeboot="fmodel_np", sim="permutation",
statistic=permcoefs.plsRnp)
```

---

pine

*Pine dataset*

---

**Description**

The caterpillar dataset was extracted from a 1973 study on pine processionary caterpillars. It assesses the influence of some forest settlement characteristics on the development of caterpillar colonies. The response variable is the logarithmic transform of the average number of nests of caterpillars per tree in an area of 500 square meters (x11). There are k=10 potentially explanatory variables defined on n=33 areas.

**Usage**

```
data(pine)
```

**Format**

A data frame with 33 observations on the following 11 variables.

x1 altitude (in meters)

x2 slope (en degrees)

x3 number of pines in the area



- x4 height (in meters) of the tree sampled at the center of the area
- x5 diameter (in meters) of the tree sampled at the center of the area
- x6 index of the settlement density
- x7 orientation of the area (from 1 if southbound to 2 otherwise)
- x8 height (in meters) of the dominant tree
- x9 number of vegetation strata
- x10 mix settlement index (from 1 if not mixed to 2 if mixed)
- x11 logarithmic transform of the average number of nests of caterpillars per tree

### Details

These caterpillars got their names from their habit of moving over the ground in incredibly long head-to-tail processions when leaving their nest to create a new colony.

The pine\_sup dataset can be used as a test set to assess model prediction error of a model trained on the pine dataset.

### Source

Tomassone R., Audrain S., Lesquoy-de Turckheim E., Millier C. (1992), “La regression, nouveaux regards sur une ancienne methode statistique”, INRA, *Actualites Scientifiques et Agronomiques*, Masson, Paris.

### References

J.-M. Marin, C. Robert. (2007). *Bayesian Core: A Practical Approach to Computational Bayesian Statistics*. Springer, New-York, pages 48-49.

### Examples

```
data(pine)
str(pine)
```

---

pine\_full

*Complete Pine dataset*

---

### Description

This is the complete caterpillar dataset from a 1973 study on pine\_full processionary caterpillars. It assesses the influence of some forest settlement characteristics on the development of caterpillar colonies. The response variable is the logarithmic transform of the average number of nests of caterpillars per tree in an area of 500 square meters (x11). There are k=10 potentially explanatory variables defined on n=55 areas.

**Usage**

```
data(pine_full)
```

**Format**

A data frame with 55 observations on the following 11 variables.

x1 altitude (in meters)

x2 slope (en degrees)

x3 number of pine\_fulls in the area

x4 height (in meters) of the tree sampled at the center of the area

x5 diameter (in meters) of the tree sampled at the center of the area

x6 index of the settlement density

x7 orientation of the area (from 1 if southbound to 2 otherwise)

x8 height (in meters) of the dominant tree

x9 number of vegetation strata

x10 mix settlement index (from 1 if not mixed to 2 if mixed)

x11 logarithmic transform of the average number of nests of caterpillars per tree

**Details**

These caterpillars got their names from their habit of moving over the ground in incredibly long head-to-tail processions when leaving their nest to create a new colony.

**Source**

Tomassone R., Audrain S., Lesquoy-de Turckheim E., Millier C. (1992), “La regression, nouveaux regards sur une ancienne methode statistique”, INRA, *Actualites Scientifiques et Agronomiques*, Masson, Paris.

**References**

J.-M. Marin, C. Robert. (2007). *Bayesian Core: A Practical Approach to Computational Bayesian Statistics*. Springer, New-York, pages 48-49.

**Examples**

```
data(pine_full)
str(pine_full)
```

---

pine\_sup

*Complete Pine dataset*

---

### Description

This is a supplementary dataset (used as a test set for the pine dataset) that was extracted from a 1973 study on pine\_sup processionary caterpillars. It assesses the influence of some forest settlement characteristics on the development of caterpillar colonies. The response variable is the logarithmic transform of the average number of nests of caterpillars per tree in an area of 500 square meters (x11). There are k=10 potentially explanatory variables defined on n=22 areas.

### Usage

```
data(pine_sup)
```

### Format

A data frame with 22 observations on the following 11 variables.

x1 altitude (in meters)

x2 slope (en degrees)

x3 number of pine\_sups in the area

x4 height (in meters) of the tree sampled at the center of the area

x5 diameter (in meters) of the tree sampled at the center of the area

x6 index of the settlement density

x7 orientation of the area (from 1 if southbound to 2 otherwise)

x8 height (in meters) of the dominant tree

x9 number of vegetation strata

x10 mix settlement index (from 1 if not mixed to 2 if mixed)

x11 logarithmic transform of the average number of nests of caterpillars per tree

### Details

These caterpillars got their names from their habit of moving over the ground in incredibly long head-to-tail processions when leaving their nest to create a new colony.

The pine\_sup dataset can be used as a test set to assess model prediction error of a model trained on the pine dataset.

### Source

Tomassone R., Audrain S., Lesquoy-de Turckheim E., Millier C. (1992), “La regression, nouveaux regards sur une ancienne methode statistique”, INRA, *Actualites Scientifiques et Agronomiques*, Masson, Paris.

## References

J.-M. Marin, C. Robert. (2007). *Bayesian Core: A Practical Approach to Computational Bayesian Statistics*. Springer, New-York, pages 48-49.

## Examples

```
data(pine_sup)
str(pine_sup)
```

---

```
plot.table.summary.cv.plsRglmmodel
```

*Plot method for table of summary of cross validated plsRglm models*

---

## Description

This function provides a table method for the class "summary.cv.plsRglmmodel"

## Usage

```
## S3 method for class 'table.summary.cv.plsRglmmodel'
plot(x, type=c("CVMC", "CVQ2Chi2", "CVPreChi2"), ...)
```

## Arguments

x	an object of the class "table.summary.cv.plsRglmmodel"
type	the type of cross validation criterion to plot.
...	further arguments to be passed to or from methods.

## Value

NULL

## Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[summary](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=10,NK=1,
modele="pls-glm-family",family=gaussian())
plot(cvtable(summary(bbb)),type="CVQ2Chi2")
rm(list=c("XCornell","yCornell","bbb"))
```

---

plot.table.summary.cv.plsRmodel

*Plot method for table of summary of cross validated plsR models*

---

## Description

This function provides a table method for the class "summary.cv.plsRmodel"

## Usage

```
## S3 method for class 'table.summary.cv.plsRmodel'
plot(x, type=c("CVMC","CVQ2","CVPress"), ...)
```

## Arguments

x	an object of the class "table.summary.cv.plsRmodel"
type	the type of cross validation criterion to plot.
...	further arguments to be passed to or from methods.

## Value

NULL

## Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[summary](#)

**Examples**

```

data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsR(dataY=yCornell,dataX=XCornell,nt=6,K=6,NK=100)
plot(cvtable(summary(bbb)),type="CVQ2")
rm(list=c("XCornell","yCornell","bbb"))

```

---

plots.confints.bootpls

*Plot bootstrap confidence intervals*


---

**Description**

This function plots the confidence intervals derived using the function `confints.bootpls` from from a `bootpls` based object.

**Usage**

```

plots.confints.bootpls(ic_bootobject, indices = NULL, legendpos = "topleft",
prednames = TRUE, articlestyle = TRUE, xaxisticks=TRUE, ltyIC=c(2, 4, 5, 1),
colIC=c("darkgreen", "blue", "red", "black"), typeIC, las = par("las"),
mar, mgp, ...)

```

**Arguments**

<code>ic_bootobject</code>	an object created with the <code>confints.bootpls</code> function.
<code>indices</code>	vector of indices of the variables to plot. Defaults to <code>NULL</code> : all the predictors will be used.
<code>legendpos</code>	position of the legend as in <a href="#">legend</a> , defaults to "topleft".
<code>prednames</code>	do the original names of the predictors shall be plotted ? Defaults to <code>TRUE</code> : the names are plotted.
<code>articlestyle</code>	do the extra blank zones of the margin shall be removed from the plot ? Defaults to <code>TRUE</code> : the margins are removed.
<code>xaxisticks</code>	do ticks for the x axis shall be plotted ? Defaults to <code>TRUE</code> : the ticks are plotted.
<code>ltyIC</code>	lty as in <a href="#">plot</a>
<code>colIC</code>	col as in <a href="#">plot</a>
<code>typeIC</code>	type of CI to plot. Defaults to <code>typeIC=c("Normal", "Basic", "Percentile", "BCa")</code> if <code>BCa</code> intervals limits were computed and to <code>typeIC=c("Normal", "Basic", "Percentile")</code> otherwise.
<code>las</code>	numeric in 0,1,2,3; the style of axis labels. 0: always parallel to the axis [default], 1: always horizontal, 2: always perpendicular to the axis, 3: always vertical.

mar	A numerical vector of the form <code>c(bottom, left, top, right)</code> which gives the number of lines of margin to be specified on the four sides of the plot. The default is <code>c(5, 4, 4, 2) + 0.1</code> .
mgp	The margin line (in mex units) for the axis title, axis labels and axis line. Note that <code>mgp[1]</code> affects title whereas <code>mgp[2:3]</code> affect axis. The default is <code>c(3, 1, 0)</code> .
...	further options to pass to the <code>plot</code> function.

**Value**

NULL

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**[confints.bootpls](#)**Examples**

```
data(Cornell)
modpls <- plsR(Y~.,data=Cornell,3)

# Lazraq-Cleroux PLS (Y,X) bootstrap
set.seed(250)
Cornell.bootYX <- bootpls(modpls, R=250)
temp.ci <- confints.bootpls(Cornell.bootYX,2:8)

plots.confints.bootpls(temp.ci)
plots.confints.bootpls(temp.ci,prednames=FALSE)
plots.confints.bootpls(temp.ci,prednames=FALSE,articlestyle=FALSE,
main="Bootstrap confidence intervals for the bj")
plots.confints.bootpls(temp.ci,indices=1:3,prednames=FALSE)
plots.confints.bootpls(temp.ci,c(2,4,6),"bottomright")
plots.confints.bootpls(temp.ci,c(2,4,6),articlestyle=FALSE,
main="Bootstrap confidence intervals for some of the bj")

temp.ci <- confints.bootpls(Cornell.bootYX,typeBCa=FALSE)
plots.confints.bootpls(temp.ci)
plots.confints.bootpls(temp.ci,2:8)
plots.confints.bootpls(temp.ci,prednames=FALSE)

# Bastien CSDA 2005 (Y,T) bootstrap
Cornell.boot <- bootpls(modpls, typeboot="fmodel_np", R=250)
temp.ci <- confints.bootpls(Cornell.boot,2:8)

plots.confints.bootpls(temp.ci)
```

```

plots.confints.bootpls(temp.ci,prednames=FALSE)
plots.confints.bootpls(temp.ci,prednames=FALSE,articlestyle=FALSE,
main="Bootstrap confidence intervals for the bj")
plots.confints.bootpls(temp.ci,indices=1:3,prednames=FALSE)
plots.confints.bootpls(temp.ci,c(2,4,6),"bottomright")
plots.confints.bootpls(temp.ci,c(2,4,6),articlestyle=FALSE,
main="Bootstrap confidence intervals for some of the bj")

temp.ci <- confints.bootpls(Cornell.boot,typeBCa=FALSE)
plots.confints.bootpls(temp.ci)
plots.confints.bootpls(temp.ci,2:8)
plots.confints.bootpls(temp.ci,prednames=FALSE)

data(aze_compl)
modplsglm <- plsRglm(y~.,data=aze_compl,3,modele="pls-glm-logistic")

# Lazraq-Cleroux PLS (Y,X) bootstrap
# should be run with R=1000 but takes much longer time
aze_compl.bootYX3 <- bootplsglm(modplsglm, typeboot="plsmode1", R=250)
temp.ci <- confints.bootpls(aze_compl.bootYX3)

plots.confints.bootpls(temp.ci)
plots.confints.bootpls(temp.ci,prednames=FALSE)
plots.confints.bootpls(temp.ci,prednames=FALSE,articlestyle=FALSE,
main="Bootstrap confidence intervals for the bj")
plots.confints.bootpls(temp.ci,indices=1:33,prednames=FALSE)
plots.confints.bootpls(temp.ci,c(2,4,6),"bottomleft")
plots.confints.bootpls(temp.ci,c(2,4,6),articlestyle=FALSE,
main="Bootstrap confidence intervals for some of the bj")
plots.confints.bootpls(temp.ci,indices=1:34,prednames=FALSE)
plots.confints.bootpls(temp.ci,indices=1:33,prednames=FALSE,ltyIC=1,colIC=c(1,2))

temp.ci <- confints.bootpls(aze_compl.bootYX3,1:34,typeBCa=FALSE)
plots.confints.bootpls(temp.ci,indices=1:33,prednames=FALSE)

# Bastien CSDA 2005 (Y,T) Bootstrap
# much faster
aze_compl.bootYT3 <- bootplsglm(modplsglm, R=1000)
temp.ci <- confints.bootpls(aze_compl.bootYT3)

plots.confints.bootpls(temp.ci)
plots.confints.bootpls(temp.ci,typeIC="Normal")
plots.confints.bootpls(temp.ci,typeIC=c("Normal","Basic"))
plots.confints.bootpls(temp.ci,typeIC="BCa",legendpos="bottomleft")
plots.confints.bootpls(temp.ci,prednames=FALSE)
plots.confints.bootpls(temp.ci,prednames=FALSE,articlestyle=FALSE,
main="Bootstrap confidence intervals for the bj")
plots.confints.bootpls(temp.ci,indices=1:33,prednames=FALSE)
plots.confints.bootpls(temp.ci,c(2,4,6),"bottomleft")
plots.confints.bootpls(temp.ci,c(2,4,6),articlestyle=FALSE,

```



```

main="Bootstrap confidence intervals for some of the bj")
plots.confints.bootpls(temp.ci,prednames=FALSE,ltyIC=c(2,1),colIC=c(1,2))

temp.ci <- confints.bootpls(aze_compl.bootYT3,1:33,typeBCa=FALSE)
plots.confints.bootpls(temp.ci,prednames=FALSE)

```

plsR

*Partial least squares Regression models with leave one out cross validation*

## Description

This function implements Partial least squares Regression models with leave one out cross validation for complete or incomplete datasets.

## Usage

```

plsR(x, ...)
## Default S3 method:
plsRmodel(dataY, dataX, nt = 2, limQ2set = 0.0975,
dataPredictY = dataX, modele = "pls", family = NULL, typeVC = "none",
EstimXNA = FALSE, scaleX = TRUE, scaleY = NULL, pvals.expli = FALSE,
alpha.pvals.expli = 0.05, MClassed = FALSE, tol_Xi = 10^(-12), weights,
sparse = FALSE, sparseStop = TRUE, naive = FALSE, verbose=TRUE)
## S3 method for class 'formula'
plsRmodel(formula, data, nt = 2, limQ2set = 0.0975,
dataPredictY, modele = "pls", family = NULL, typeVC = "none",
EstimXNA = FALSE, scaleX = TRUE, scaleY = NULL, pvals.expli = FALSE,
alpha.pvals.expli = 0.05, MClassed = FALSE, tol_Xi = 10^(-12), weights,
subset, contrasts = NULL, sparse = FALSE, sparseStop = TRUE, naive = FALSE,
verbose=TRUE)
PLS_lm(dataY, dataX, nt = 2, limQ2set = 0.0975, dataPredictY = dataX,
modele = "pls", family = NULL, typeVC = "none", EstimXNA = FALSE,
scaleX = TRUE, scaleY = NULL, pvals.expli = FALSE,
alpha.pvals.expli = 0.05, MClassed = FALSE, tol_Xi = 10^(-12),
weights,sparse=FALSE,sparseStop=FALSE,naive=FALSE,verbose=TRUE)
PLS_lm_formula(formula,data=NULL,nt=2,limQ2set=.0975,dataPredictY=dataX,
modele="pls",family=NULL,typeVC="none",EstimXNA=FALSE,scaleX=TRUE,
scaleY=NULL,pvals.expli=FALSE,alpha.pvals.expli=.05,MClassed=FALSE,
tol_Xi=10^(-12),weights,subset,contrasts=NULL,sparse=FALSE,
sparseStop=FALSE,naive=FALSE,verbose=TRUE)

```

## Arguments

x	a formula or a response (training) dataset
dataY	response (training) dataset

<code>dataX</code>	predictor(s) (training) dataset
<code>formula</code>	an object of class " <code>formula</code> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
<code>data</code>	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>plsR</code> is called.
<code>nt</code>	number of components to be extracted
<code>limQ2set</code>	limit value for the Q2
<code>dataPredictY</code>	predictor(s) (testing) dataset
<code>modele</code>	name of the PLS model to be fitted, only (" <code>pls</code> " available for this fonction.
<code>family</code>	for the present moment the family argument is ignored and set thanks to the value of <code>modele</code> .
<code>typeVC</code>	<p>type of leave one out cross validation. Several procedures are available. If cross validation is required, one needs to select the way of predicting the response for left out observations. For complete rows, without any missing value, there are two different ways of computing these predictions. As a consequence, for mixed datasets, with complete and incomplete rows, there are two ways of computing prediction : either predicts any row as if there were missing values in it (<code>missingdata</code>) or selects the prediction method accordingly to the completeness of the row (<code>adaptative</code>).</p> <p><code>none</code> no cross validation</p> <p><code>standard</code> as in SIMCA for datasets without any missing value. For datasets with any missing value, it is the as using <code>missingdata</code></p> <p><code>missingdata</code> all values predicted as those with missing values for datasets with any missing values</p> <p><code>adaptative</code> predict a response value for an x with any missing value as those with missing values and for an x without any missing value as those without missing values.</p>
<code>EstimXNA</code>	only for <code>modele="pls"</code> . Set whether the missing X values have to be estimated.
<code>scaleX</code>	scale the predictor(s) : must be set to <code>TRUE</code> for <code>modele="pls"</code> and should be for <code>glms pls</code> .
<code>scaleY</code>	scale the response : Yes/No. Ignored since non always possible for <code>glm</code> responses.
<code>pvals.expli</code>	should individual p-values be reported to tune model selection ?
<code>alpha.pvals.expli</code>	level of significance for predictors when <code>pvals.expli=TRUE</code>
<code>MClassed</code>	number of missclassified cases, should only be used for binary responses
<code>tol_Xi</code>	minimal value for $\text{Norm2}(X_i)$ and $\det(pp' \times pp)$ if there is any missing value in the <code>dataX</code> . It defaults to $10^{-12}$
<code>weights</code>	an optional vector of 'prior weights' to be used in the fitting process. Should be <code>NULL</code> or a numeric vector.

subset	an optional vector specifying a subset of observations to be used in the fitting process.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
sparse	should the coefficients of non-significant predictors ( <code>&lt;alpha.pvals.expli</code> ) be set to 0
sparseStop	should component extraction stop when no significant predictors ( <code>&lt;alpha.pvals.expli</code> ) are found
naive	Use the naive estimates for the Degrees of Freedom in plsR? Default is FALSE.
verbose	should info messages be displayed ?
...	arguments to pass to <code>plsRmodel.default</code> or to <code>plsRmodel.formula</code>

## Details

There are several ways to deal with missing values that leads to different computations of leave one out cross validation criteria.

A typical predictor has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for response. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed.

A specification of the form `first:second` indicates the the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the cross of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in `weights` being inversely proportional to the dispersions); or equivalently, when the elements of `weights` are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations.

The default estimator for Degrees of Freedom is the Kramer and Sugiyama's one. Information criteria are computed accordingly to these estimations. Naive Degrees of Freedom and Information Criteria are also provided for comparison purposes. For more details, see N. Kraemer and M. Sugiyama. (2011). The Degrees of Freedom of Partial Least Squares Regression. *Journal of the American Statistical Association*, 106(494), 697-705, 2011.

## Value

nr	Number of observations
nc	Number of predictors
nt	Number of requested components
ww	raw weights (before L2-normalization)
wwnorm	L2 normed weights (to be used with deflated matrices of predictor variables)
wwetoile	modified weights (to be used with original matrix of predictor variables)
tt	PLS components

pp	loadings of the predictor variables
Coeffc	coefficients of the PLS components
uscores	scores of the response variable
YChapeau	predicted response values for the dataX set
residYChapeau	residuals of the deflated response on the standardized scale
RepY	scaled response vector
na.miss.Y	is there any NA value in the response vector
YNA	indicator vector of missing values in RepY
residY	deflated scaled response vector
ExpliX	scaled matrix of predictors
na.miss.X	is there any NA value in the predictor matrix
XXNA	indicator of non-NA values in the predictor matrix
residXX	deflated predictor matrix
PredictY	response values with NA replaced with 0
press.ind	individual PRESS value for each observation (scaled scale)
press.tot	total PRESS value for all observations (scaled scale)
family	glm family used to fit PLSGLR model
ttPredictY	PLS components for the dataset on which prediction was requested
typeVC	type of leave one out cross-validation used
dataX	predictor values
dataY	response values
computed_nt	number of components that were computed
CoeffcFull	matrix of the coefficients of the predictors
CoeffConstante	value of the intercept (scaled scale)
Std.Coeffs	Vector of standardized regression coefficients
press.ind2	individual PRESS value for each observation (original scale)
RSSresidY	residual sum of squares (scaled scale)
Coeffs	Vector of regression coefficients (used with the original data scale)
Yresidus	residuals of the PLS model
RSS	residual sum of squares (original scale)
residusY	residuals of the deflated response on the standardized scale
AIC.std	AIC.std vs number of components (AIC computed for the standardized model)
AIC	AIC vs number of components
optional	If the response is assumed to be binary: i.e. MClassed=TRUE. MissClassed Number of miss classed results Probs "Probability" predicted by the model. These are not true probabilities since they may lay outside of [0,1]

	Probs.trc	Probability predicted by the model and constrained to belong to [0,1]
ttPredictFittedMissingY		Description of 'comp2'
optional		If cross validation was requested: i.e. typeVC="standard", typeVC="missingdata" or typeVC="adaptative".
	R2residY	R2 coefficient value on the standardized scale
	R2	R2 coefficient value on the original scale
	press.tot2	total PRESS value for all observations (original scale)
	Q2	Q2 value (standardized scale)
	limQ2	limit of the Q2 value
	Q2_2	Q2 value (original scale)
	Q2cum	cumulated Q2 (standardized scale)
	Q2cum_2	cumulated Q2 (original scale)
InfCrit		table of Information Criteria
Std.ValsPredictY		predicted response values for supplementary dataset (standardized scale)
ValsPredictY		predicted response values for supplementary dataset (original scale)
Std.XChapeau		estimated values for missing values in the predictor matrix (standardized scale)
XXwotNA		predictor matrix with missing values replaced with 0

### Note

Use `cv.plsR` to cross-validate the `plsRglm` models and `bootpls` to bootstrap them.

### Author(s)

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

### References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

### See Also

See also `plsRglm` to fit PLSGLR models.

**Examples**

```

data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

#maximum 6 components could be extracted from this dataset
#trying 10 to trigger automatic stopping criterion
modpls10<-plsR(yCornell,XCornell,10)
modpls10

#With iterative leave one out CV PRESS
modpls6cv<-plsR(yCornell,XCornell,6,typeVC="standard")
modpls6cv
cv.modpls<-cv.plsR(yCornell,XCornell,6,NK=100)
res.cv.modpls<-cvtable(summary(cv.modpls))
plot(res.cv.modpls)

rm(list=c("XCornell","yCornell","modpls10","modpls6cv"))

#A binary response example
data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
modpls.aze <- plsR(yaze_compl,Xaze_compl,10,MClassed=TRUE,typeVC="standard")
modpls.aze

#Direct access to not cross validated values
modpls.aze$AIC
modpls.aze$AIC.std
modpls.aze$MissClassed

#Raw predicted values (not really probably since not constrained in [0,1])
modpls.aze$Probs
#Truncated to [0;1] predicted values (true probabilities)
modpls.aze$Probs.trc
modpls.aze$Probs-modpls.aze$Probs.trc

#Repeated cross validation of the model (NK=100 times)
cv.modpls.aze<-cv.plsR(yaze_compl,Xaze_compl,10,NK=100)
res.cv.modpls.aze<-cvtable(summary(cv.modpls.aze,MClassed=TRUE))
#High discrepancy in the number of component choice using repeated cross validation
#and missclassified criterion
plot(res.cv.modpls.aze)

rm(list=c("Xaze_compl","yaze_compl","modpls.aze","cv.modpls.aze","res.cv.modpls.aze"))

#24 predictors
dimX <- 24
#2 components
Astar <- 2
simul_data_UniYX(dimX,Astar)

```

```

dataAstar2 <- t(replicate(250,simul_data_UniYX(dimX,Astar)))
ydataAstar2 <- dataAstar2[,1]
XdataAstar2 <- dataAstar2[,2:(dimX+1)]
modpls.A2<- plsR(ydataAstar2,XdataAstar2,10,typeVC="standard")
modpls.A2
cv.modpls.A2<-cv.plsR(ydataAstar2,XdataAstar2,10,NK=100)
res.cv.modpls.A2<-cvtable(summary(cv.modpls.A2))
#Perfect choice for the Q2 criterion in PLSR
plot(res.cv.modpls.A2)

#Binarized response
ysimbin1 <- dicho(ydataAstar2)
#Binarized predictors
Xsimbin1 <- dicho(XdataAstar2)
modpls.B2 <- plsR(ysimbin1,Xsimbin1,10,typeVC="standard",MClassed=TRUE)
modpls.B2
modpls.B2$Probs
modpls.B2$Probs.trc
modpls.B2$MissClassed
plsR(ysimbin1,XdataAstar2,10,typeVC="standard",MClassed=TRUE)$InfCrit
cv.modpls.B2<-cv.plsR(ysimbin1,Xsimbin1,2,NK=100)
res.cv.modpls.B2<-cvtable(summary(cv.modpls.B2,MClassed=TRUE))
#Only one component found by repeated CV missclassified criterion
plot(res.cv.modpls.B2)

rm(list=c("dimX", "Astar", "dataAstar2", "XdataAstar2", "ydataAstar2", "modpls.A2", "cv.modpls.A2",
"res.cv.modpls.A2", "Xsimbin1", "ysimbin1", "modpls.B2", "cv.modpls.B2", "res.cv.modpls.B2"))

```

---

plsR.dof

*Computation of the Degrees of Freedom*


---

## Description

This function computes the Degrees of Freedom using the Krylov representation of PLS and other quantities that are used to get information criteria values. For the time present, it only works with complete datasets.

## Usage

```
plsR.dof(modplsR, naive = FALSE)
```

## Arguments

modplsR	A plsR model i.e. an object returned by one of the functions <code>plsR</code> , <code>plsRmodel.default</code> , <code>plsRmodel.formula</code> , <code>PLS_lm</code> or <code>PLS_lm.formula</code> .
naive	A boolean.

## Details

If `naive=FALSE` returns values for estimated degrees of freedom and error dispersion. If `naive=TRUE` returns values for naive degrees of freedom and error dispersion. The original code from Nicole Kraemer and Mikio L. Braun was unable to handle models with only one component.

## Value

DoF	Degrees of Freedom
sigmahat	Estimates of dispersion
Yhat	Predicted values
yhat	Square Euclidean norms of the predicted values
RSS	Residual Sums of Squares

## Author(s)

Nicole Kraemer, Mikio L. Braun with improvements from Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

N. Kraemer, M. Sugiyama. (2011). The Degrees of Freedom of Partial Least Squares Regression. *Journal of the American Statistical Association*, 106(494), 697-705.  
N. Kraemer, M. Sugiyama, M.L. Braun. (2009). Lanczos Approximations for the Speedup of Kernel Partial Least Squares Regression. *Proceedings of the Twelfth International Conference on Artificial Intelligence and Statistics (AISTATS)*, 272-279.

## See Also

[aic.dof](#) and [infcrit.dof](#) for computing information criteria directly from a previously fitted plsR model.

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsR(yCornell,XCornell,4)
plsR.dof(modpls)
plsR.dof(modpls,naive=TRUE)
```



**Description**

This function implements Partial least squares Regression generalized linear models complete or incomplete datasets.

**Usage**

```
plsRglm(x, ...)
## Default S3 method:
plsRglmmodel(dataY,dataX,nt=2,limQ2set=.0975,
dataPredictY=dataX,modele="pls",family=NULL,typeVC="none",
EstimXNA=FALSE,scaleX=TRUE,scaleY=NULL,pvals.expli=FALSE,
alpha.pvals.expli=.05,MClassed=FALSE,tol_Xi=10^(-12),weights,
sparse=FALSE,sparseStop=TRUE,naive=FALSE,verbose=TRUE)
## S3 method for class 'formula'
plsRglmmodel(formula,data=NULL,nt=2,limQ2set=.0975,
dataPredictY,modele="pls",family=NULL,typeVC="none",
EstimXNA=FALSE,scaleX=TRUE,scaleY=NULL,pvals.expli=FALSE,
alpha.pvals.expli=.05,MClassed=FALSE,tol_Xi=10^(-12),weights,subset,
start=NULL,etastart,mustart,offset,method="glm.fit",control= list(),
contrasts=NULL,sparse=FALSE,sparseStop=TRUE,naive=FALSE,verbose=TRUE)
PLS_glm(dataY, dataX, nt = 2, limQ2set = 0.0975, dataPredictY = dataX,
modele = "pls", family = NULL, typeVC = "none", EstimXNA = FALSE,
scaleX = TRUE, scaleY = NULL, pvals.expli = FALSE,
alpha.pvals.expli = 0.05, MClassed = FALSE, tol_Xi = 10^(-12), weights,
method, sparse = FALSE, sparseStop=FALSE, naive=FALSE,verbose=TRUE)
PLS_glm_formula(formula,data=NULL,nt=2,limQ2set=.0975,dataPredictY=dataX,
modele="pls",family=NULL,typeVC="none",EstimXNA=FALSE,scaleX=TRUE,
scaleY=NULL,pvals.expli=FALSE,alpha.pvals.expli=.05,MClassed=FALSE,
tol_Xi=10^(-12),weights,subset,start=NULL,etastart,mustart,offset,method,
control= list(),contrasts=NULL,sparse=FALSE,sparseStop=FALSE,naive=FALSE,verbose=TRUE)
```

**Arguments**

x	a formula or a response (training) dataset
dataY	response (training) dataset
dataX	predictor(s) (training) dataset
formula	an object of class " <b>formula</b> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
data	an optional data frame, list or environment (or object coercible by <a href="#">as.data.frame</a> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>plsRglm</code> is called.

nt	number of components to be extracted
limQ2set	limit value for the Q2
dataPredictY	predictor(s) (testing) dataset
modele	name of the PLS glm model to be fitted ("pls", "pls-glm-Gamma", "pls-glm-gaussian", "pls-glm-inverse.gaussian", "pls-glm-logistic", "pls-glm-poisson", "pls-glm-polr"). Use "modele=pls-glm-family" to enable the family option.
family	a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. (See <a href="#">family</a> for details of family functions.) To use the family option, please set modele="pls-glm-family". User defined families can also be defined. See details.
typeVC	type of leave one out cross validation. For back compatibility purpose. none no cross validation
EstimXNA	only for modele="pls". Set whether the missing X values have to be estimated.
scaleX	scale the predictor(s) : must be set to TRUE for modele="pls" and should be for glms pls.
scaleY	scale the response : Yes/No. Ignored since non always possible for glm responses.
pvals.expli	should individual p-values be reported to tune model selection ?
alpha.pvals.expli	level of significance for predictors when pvals.expli=TRUE
MClassed	number of missclassified cases, should only be used for binary responses
tol_Xi	minimal value for Norm2(Xi) and $\det(pp' \times pp)$ if there is any missing value in the dataX. It defaults to $10^{-12}$
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
start	starting values for the parameters in the linear predictor.
etastart	starting values for the linear predictor.
mustart	starting values for the vector of means.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more <a href="#">offset</a> terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <a href="#">model.offset</a> .
method	For a glm model (modele="pls-glm-family"), the method to be used in fitting the model. The default method "glm.fit" uses iteratively reweighted least squares (IWLS). User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as glm.fit. For a polr model (modele="pls-glm-polr"), logistic or probit or (complementary) log-log (loglog or cloglog) or cauchit (corresponding to a Cauchy latent variable).

control	a list of parameters for controlling the fitting process. For <code>glm.fit</code> this is passed to <code>glm.control</code> .
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
sparse	should the coefficients of non-significant predictors ( <code>&lt;alpha.pvals.expli</code> ) be set to 0
sparseStop	should component extraction stop when no significant predictors ( <code>&lt;alpha.pvals.expli</code> ) are found
naive	Use the naive estimates for the Degrees of Freedom in plsR? Default is FALSE.
verbose	Should details be displayed ?
...	arguments to pass to <code>plsRmodel.default</code> or to <code>plsRmodel.formula</code>

## Details

There are seven different predefined models with predefined link functions available :

"pls" ordinary pls models

"pls-glm-Gamma" glm gaussian with inverse link pls models

"pls-glm-gaussian" glm gaussian with identity link pls models

"pls-glm-inverse-gamma" glm binomial with square inverse link pls models

"pls-glm-logistic" glm binomial with logit link pls models

"pls-glm-poisson" glm poisson with log link pls models

"pls-glm-polr" glm polr with logit link pls models

Using the "family=" option and setting "modele=pls-glm-family" allows changing the family and link function the same way as for the `glm` function. As a consequence user-specified families can also be used.

**The gaussian family** accepts the links (as names) identity, log and inverse.

**The binomial family** accepts the links logit, probit, cauchit, (corresponding to logistic, normal and Cauchy CDFs respectively) log and cloglog (complementary log-log).

**The Gamma family** accepts the links inverse, identity and log.

**The poisson family** accepts the links log, identity, and sqrt.

**The inverse.gaussian family** accepts the links  $1/\mu^2$ , inverse, identity and log.

**The quasi family** accepts the links logit, probit, cloglog, identity, inverse, log,  $1/\mu^2$  and sqrt.

**The function power** can be used to create a power link function.

A typical predictor has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for response. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed.

A specification of the form `first:second` indicates the the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the cross of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in weights being inversely proportional to the dispersions); or equivalently, when the elements of weights are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations.

The default estimator for Degrees of Freedom is the Kramer and Sugiyama's one which only works for classical plsR models. For these models, Information criteria are computed accordingly to these estimations. Naive Degrees of Freedom and Information Criteria are also provided for comparison purposes. For more details, see N. Kraemer and M. Sugiyama. (2011). The Degrees of Freedom of Partial Least Squares Regression. *Journal of the American Statistical Association*, 106(494), 697-705, 2011.

## Value

Depends on the model that was used to fit the model. You can generally at least find these items.

nr	Number of observations
nc	Number of predictors
nt	Number of requested components
ww	raw weights (before L2-normalization)
wwnorm	L2 normed weights (to be used with deflated matrices of predictor variables)
wwetoile	modified weights (to be used with original matrix of predictor variables)
tt	PLS components
pp	loadings of the predictor variables
Coeffc	coefficients of the PLS components
uscores	scores of the response variable
YChapeau	predicted response values for the dataX set
residYChapeau	residuals of the deflated response on the standardized scale
RepY	scaled response vector
na.miss.Y	is there any NA value in the response vector
YNA	indicatrix vector of missing values in RepY
residY	deflated scaled response vector
ExpliX	scaled matrix of predictors
na.miss.X	is there any NA value in the predictor matrix
XXNA	indicator of non-NA values in the predictor matrix
residXX	deflated predictor matrix
PredictY	response values with NA replaced with 0
RSS	residual sum of squares (original scale)
RSSresidY	residual sum of squares (scaled scale)

R2residY	R2 coefficient value on the standardized scale
R2	R2 coefficient value on the original scale
press.ind	individual PRESS value for each observation (scaled scale)
press.tot	total PRESS value for all observations (scaled scale)
Q2cum	cumulated Q2 (standardized scale)
family	glm family used to fit PLSGLR model
ttPredictY	PLS components for the dataset on which prediction was requested
typeVC	type of leave one out cross-validation used
dataX	predictor values
dataY	response values
weights	weights of the observations
computed_nt	number of components that were computed
AIC	AIC vs number of components
BIC	BIC vs number of components
Coeffsmodel_vals	
ChisqPearson	
CoeffCFull	matrix of the coefficients of the predictors
CoeffConstante	value of the intercept (scaled scale)
Std.Coeffs	Vector of standardized regression coefficients
Coeffs	Vector of regression coefficients (used with the original data scale)
Yresidus	residuals of the PLS model
residusY	residuals of the deflated response on the standardized scale
InfCrit	table of Information Criteria:
	AIC AIC vs number of components
	BIC BIC vs number of components
	MissClassed Number of miss classed results
	Chi2_Pearson_Y Q2 value (standardized scale)
	RSS residual sum of squares (original scale)
	R2 R2 coefficient value on the original scale
	R2residY R2 coefficient value on the standardized scale
	RSSresidY residual sum of squares (scaled scale)
Std.ValsPredictY	predicted response values for supplementary dataset (standardized scale)
ValsPredictY	predicted response values for supplementary dataset (original scale)
Std.XChapeau	estimated values for missing values in the predictor matrix (standardized scale)
FinalModel	final GLR model on the PLS components
XXwotNA	predictor matrix with missing values replaced with 0
call	call
AIC.std	AIC.std vs number of components (AIC computed for the standardized model)

**Note**

Use `cv.plsRglm` to cross-validate the `plsRglm` models and `bootpls` to bootstrap them.

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**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparaison de la regression PLS et de la regression logistique PLS : application aux donnees d'allelotypage. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

See also `plsR`.

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

modplsglm <- plsRglm(yCornell,XCornell,10,modele="pls-glm-gaussian")

#To retrieve the final GLR model on the PLS components
finalmod <- plsRglm(yCornell,XCornell,10,modele="pls-glm-gaussian")$FinalModel
#It is a glm object.
plot(finalmod)

#Cross validation
cv.modplsglm<-cv.plsRglm(yCornell,XCornell,6,NK=100,modele="pls-glm-gaussian")
res.cv.modplsglm<-cvtable(summary(cv.modplsglm))
plot(res.cv.modplsglm)

#If no model specified, classic PLSR model
modpls <- plsRglm(yCornell,XCornell,6)
modpls
modpls$tt
modpls$scores
modpls$pp
modpls$Coeffs

#rm(list=c("XCornell","yCornell",modpls,cv.modplsglm,res.cv.modplsglm))

data(aze_compl)
```

```

Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
plsRglm(yaze_compl,Xaze_compl,nt=10,modele="pls",MClassed=TRUE)$InfCrit
modpls <- plsRglm(yaze_compl,Xaze_compl,nt=10,modele="pls-glm-logistic",
MClassed=TRUE,pvals.expli=TRUE)
modpls
colSums(modpls$pvalstep)
modpls$Coeffsmodel_vals

plot(plsRglm(yaze_compl,Xaze_compl,4,modele="pls-glm-logistic")$FinalModel)
plsRglm(yaze_compl[-c(99,72)],Xaze_compl[-c(99,72)],,4,
modele="pls-glm-logistic",pvals.expli=TRUE)$pvalstep
plot(plsRglm(yaze_compl[-c(99,72)],Xaze_compl[-c(99,72)],,4,
modele="pls-glm-logistic",pvals.expli=TRUE)$FinalModel)
rm(list=c("Xaze_compl","yaze_compl","modpls"))

data(bordeaux)
Xbordeaux<-bordeaux[,1:4]
ybordeaux<-factor(bordeaux$Quality,ordered=TRUE)
modpls <- plsRglm(ybordeaux,Xbordeaux,10,modele="pls-glm-polr",pvals.expli=TRUE)
modpls
colSums(modpls$pvalstep)

XbordeauxNA<-Xbordeaux
XbordeauxNA[1,1] <- NA
modplsNA <- plsRglm(ybordeaux,XbordeauxNA,10,modele="pls-glm-polr",pvals.expli=TRUE)
modpls
colSums(modpls$pvalstep)
rm(list=c("Xbordeaux","XbordeauxNA","ybordeaux","modplsNA"))

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
modpls1 <- plsRglm(ypine,Xpine,1)
modpls1$Std.Coeffs
modpls1$Coeffs
modpls4 <- plsRglm(ypine,Xpine,4)
modpls4$Std.Coeffs
modpls4$Coeffs
modpls4$PredictY[1,]
plsRglm(ypine,Xpine,4,dataPredictY=Xpine[1,])$PredictY[1,]

XpineNAX21 <- Xpine
XpineNAX21[1,2] <- NA
modpls4NA <- plsRglm(ypine,XpineNAX21,4)
modpls4NA$Std.Coeffs
modpls4NA$YChapeau[1,]
modpls4$YChapeau[1,]
modpls4NA$CoeffC
plsRglm(ypine,XpineNAX21,4,EstimXNA=TRUE)$XChapeau

```

```

plsRglm(ypine,XpineNAX21,4,EstimXNA=TRUE)$XChapeauNA

# compare pls-glm-gaussian with classic plsR
modpls4 <- plsRglm(ypine,Xpine,4,modele="pls-glm-gaussian")
cbind(modpls4$Std.Coeffs,modpls4$Std.Coeffs)

# without missing data
cbind(ypine,modpls4$ValsPredictY,modpls4$ValsPredictY)

# with missing data
modpls4NA <- plsRglm(ypine,XpineNAX21,4,modele="pls-glm-gaussian")
cbind((ypine),modpls4NA$ValsPredictY,modpls4NA$ValsPredictY)
rm(list=c("Xpine","ypine","modpls4","modpls4NA","modpls4NA","modpls4NA"))

data(fowlkes)
Xfowlkes <- fowlkes[,2:13]
yfowlkes <- fowlkes[,1]
modpls <- plsRglm(yfowlkes,Xfowlkes,4,modele="pls-glm-logistic",pvals.expli=TRUE)
modpls
colSums(modpls$pvalstep)
rm(list=c("Xfowlkes","yfowlkes","modpls"))

if(require(chemometrics)){
data(hyptis)
hyptis <- factor(hyptis$Group,ordered=TRUE)
Xhyptis <- as.data.frame(hyptis[,c(1:6)])
options(contrasts = c("contr.treatment", "contr.poly"))
modpls2 <- plsRglm(hyptis,Xhyptis,6,modele="pls-glm-polr")
modpls2$Coeffsmodel_vals
modpls2$InfCrit
modpls2$Coeffs
modpls2$Std.Coeffs

table(hyptis,predict(modpls2$FinalModel,type="class"))
rm(list=c("hyptis","Xhyptis","modpls2"))
}

dimX <- 24
Astar <- 6
dataAstar6 <- t(replicate(250,simul_data_UniYX(dimX,Astar)))
ysimbin1 <- dicho(dataAstar6)[,1]
Xsimbin1 <- dicho(dataAstar6)[,2:(dimX+1)]
modpls4 <- plsRglm(ysimbin1,Xsimbin1,10,modele="pls-glm-logistic")
modpls4
cv.modpls4 <- cv.plsRglm(ysimbin1,Xsimbin1,nt=10,
modele="pls-glm-logistic",NK=100)
res.cv.modpls4 <- cvtable(summary(cv.modpls4,MClassed=TRUE))
plot(res.cv.modpls4) #defaults to type="CVMC"

rm(list=c("dimX","Astar","dataAstar6","ysimbin1","Xsimbin1","modpls4","cv.modpls4",
"res.cv.modpls4"))

```



PLS\_glm\_wvc

*Light version of PLS\glm for cross validation purposes***Description**

Light version of PLS\_glm for cross validation purposes either on complete or incomplete datasets.

**Usage**

```
PLS_glm_wvc(dataY, dataX, nt = 2, dataPredictY = dataX, modele = "pls",
family = NULL, scaleX = TRUE, scaleY = NULL, keepcoeffs = FALSE,
keepstd.coeffs=FALSE, tol_Xi = 10^(-12), weights, method = "logistic",
verbose = TRUE)
```

**Arguments**

dataY	response (training) dataset
dataX	predictor(s) (training) dataset
nt	number of components to be extracted
dataPredictY	predictor(s) (testing) dataset
modele	name of the PLS glm model to be fitted ("pls", "pls-glm-Gamma", "pls-glm-gaussian", "pls-glm-inverse.gaussian", "pls-glm-logistic", "pls-glm-poisson", "pls-glm-polr"). Use "modele=pls-glm-family" to enable the family option.
family	a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. (See <a href="#">family</a> for details of family functions.) To use the family option, please set modele="pls-glm-family". User defined families can also be defined. See details.
scaleX	scale the predictor(s) : must be set to TRUE for modele="pls" and should be for glms pls.
scaleY	scale the response : Yes/No. Ignored since non always possible for glm responses.
keepcoeffs	whether the coefficients of the linear fit on link scale of unstandardized eXplanatory variables should be returned or not.
keepstd.coeffs	whether the coefficients of the linear fit on link scale of standardized eXplanatory variables should be returned or not.
tol_Xi	minimal value for Norm2(Xi) and $\det(pp' \times pp)$ if there is any missing value in the dataX. It defaults to $10^{-12}$
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
method	logistic, probit, complementary log-log or cauchit (corresponding to a Cauchy latent variable).
verbose	should info messages be displayed ?

## Details

This function is called by `PLS_glm_kfoldcv_formula` in order to perform cross-validation either on complete or incomplete datasets.

There are seven different predefined models with predefined link functions available :

"pls" ordinary pls models

"pls-glm-Gamma" glm gaussian with inverse link pls models

"pls-glm-gaussian" glm gaussian with identity link pls models

"pls-glm-inverse-gamma" glm binomial with square inverse link pls models

"pls-glm-logistic" glm binomial with logit link pls models

"pls-glm-poisson" glm poisson with log link pls models

"pls-glm-polr" glm polr with logit link pls models

Using the "family=" option and setting "modele=pls-glm-family" allows changing the family and link function the same way as for the `glm` function. As a consequence user-specified families can also be used.

**The gaussian family** accepts the links (as names) identity, log and inverse.

**The binomial family** accepts the links logit, probit, cauchit, (corresponding to logistic, normal and Cauchy CDFs respectively) log and cloglog (complementary log-log).

**The Gamma family** accepts the links inverse, identity and log.

**The poisson family** accepts the links log, identity, and sqrt.

**The inverse.gaussian family** accepts the links  $1/\mu^2$ , inverse, identity and log.

**The quasi family** accepts the links logit, probit, cloglog, identity, inverse, log,  $1/\mu^2$  and sqrt.

**The function power** can be used to create a power link function.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in weights being inversely proportional to the dispersions); or equivalently, when the elements of weights are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations.

## Value

<code>valsPredict</code>	<code>nrow(dataPredictY) * nt</code> matrix of the predicted values
<code>coeffs</code>	If the coefficients of the explanatory variables were requested: i.e. <code>keepcoeffs=TRUE</code> . <code>ncol(dataX) * 1</code> matrix of the coefficients of the the explanatory variables

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## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[PLS\\_glm](#) for more detailed results, [PLS\\_glm\\_kfoldcv](#) for cross-validating models and [PLS\\_lm\\_wvc](#) for the same function dedicated to plsR models

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
PLS_glm_wvc(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-gaussian",
dataPredictY=XCornell[1,])
PLS_glm_wvc(dataY=yCornell,dataX=XCornell,nt=3,modele="pls-glm-family",
family=gaussian(),dataPredictY=XCornell[1,])
PLS_glm_wvc(dataY=yCornell[-1],dataX=XCornell[-1,],nt=3,modele="pls-glm-gaussian",
dataPredictY=XCornell[1,])
PLS_glm_wvc(dataY=yCornell[-1],dataX=XCornell[-1,],nt=3,modele="pls-glm-family",
family=gaussian(),dataPredictY=XCornell[1,])
rm("XCornell","yCornell")
```

```
## With an incomplete dataset (X[1,2] is NA)
data(pine)
ypine <- pine[,11]
data(XpineNAX21)
PLS_glm_wvc(dataY=ypine,dataX=XpineNAX21,nt=10,modele="pls-glm-gaussian")
rm("XpineNAX21","ypine")
```

```
data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
PLS_glm_wvc(ypine,Xpine,10,modele="pls")
PLS_glm_wvc(ypine,Xpine,10,modele="pls-glm-Gamma")
PLS_glm_wvc(ypine,Xpine,10,modele="pls-glm-family",family=Gamma())
PLS_glm_wvc(ypine,Xpine,10,modele="pls-glm-gaussian")
PLS_glm_wvc(ypine,Xpine,10,modele="pls-glm-family",family=gaussian(log))
PLS_glm_wvc(round(ypine),Xpine,10,modele="pls-glm-poisson")
PLS_glm_wvc(round(ypine),Xpine,10,modele="pls-glm-family",family=poisson(log))
rm(list=c("pine","ypine","Xpine"))
```

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
PLS_glm_wvc(yCornell,XCornell,10,modele="pls-glm-inverse.gaussian")
PLS_glm_wvc(yCornell,XCornell,10,modele="pls-glm-family",
```

```

family=inverse.gaussian()
rm(list=c("XCornell", "yCornell"))

data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
PLS_glm_wvc(dataY=yCornell, dataX=XCornell, nt=3, modele="pls-glm-gaussian",
dataPredictY=XCornell[,1,])
PLS_glm_wvc(dataY=yCornell[-1,], dataX=XCornell[-1,], nt=3, modele="pls-glm-gaussian",
dataPredictY=XCornell[,1,])
rm("XCornell", "yCornell")

data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y
PLS_glm(yaze_compl, Xaze_compl, 10, modele="pls-glm-logistic", typeVC="none")$InfCrit
PLS_glm_wvc(yaze_compl, Xaze_compl, 10, modele="pls-glm-logistic", keepcoeffs=TRUE)
rm("Xaze_compl", "yaze_compl")

```

---

PLS\_lm\_wvc

*Light version of PLS\_lm for cross validation purposes*


---

## Description

Light version of PLS\_lm for cross validation purposes either on complete or incomplete datasets.

## Usage

```

PLS_lm_wvc(dataY, dataX, nt = 2, dataPredictY = dataX, modele = "pls",
scaleX = TRUE, scaleY = NULL, keepcoeffs = FALSE,
keepstd.coeffs=FALSE, tol_Xi = 10^(-12), weights, verbose=TRUE)

```

## Arguments

dataY	response (training) dataset
dataX	predictor(s) (training) dataset
nt	number of components to be extracted
dataPredictY	predictor(s) (testing) dataset
modele	name of the PLS model to be fitted, only ("pls" available for this fonction.
scaleX	scale the predictor(s) : must be set to TRUE for modele="pls" and should be for glms pls.
scaleY	scale the response : Yes/No. Ignored since non always possible for glm responses.
keepcoeffs	whether the coefficients of unstandardized eXplanatory variables should be returned or not.

keepstd.coeffs	whether the coefficients of standardized eXplanatory variables should be returned or not.
tol_Xi	minimal value for $\text{Norm2}(X_i)$ and $\det(pp' \times pp)$ if there is any missing value in the dataX. It defaults to $10^{-12}$
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
verbose	should info messages be displayed ?

### Details

This function is called by [PLS\\_lm\\_kfoldcv](#) in order to perform cross-validation either on complete or incomplete datasets.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in weights being inversely proportional to the dispersions); or equivalently, when the elements of weights are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations.

### Value

valsPredict	$nrow(\text{dataPredictY}) \times nt$ matrix of the predicted values
coeffs	If the coefficients of the eXplanatory variables were requested: i.e. keepcoeffs=TRUE. $ncol(\text{dataX}) \times 1$ matrix of the coefficients of the the eXplanatory variables

### Note

Use [PLS\\_lm\\_kfoldcv](#) for a wrapper in view of cross-validation.

### Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

### References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

### See Also

[PLS\\_lm](#) for more detailed results, [PLS\\_lm\\_kfoldcv](#) for cross-validating models and [PLS\\_glm\\_wvc](#) for the same function dedicated to plsRglm models

**Examples**

```

data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
PLS_lm_wvc(dataY=yCornell,dataX=XCornell,nt=3,dataPredictY=XCornell[1,])
PLS_lm_wvc(dataY=yCornell[-c(1,2)],dataX=XCornell[-c(1,2),],nt=3,dataPredictY=XCornell[c(1,2),])
PLS_lm_wvc(dataY=yCornell[-c(1,2)],dataX=XCornell[-c(1,2),],nt=3,dataPredictY=XCornell[c(1,2),],
keepcoeffs=TRUE)
rm("XCornell","yCornell")

## With an incomplete dataset (X[1,2] is NA)
data(pine)
ypine <- pine[,11]
data(XpineNAX21)
PLS_lm_wvc(dataY=ypine[-1],dataX=XpineNAX21[-1,],nt=3)
PLS_lm_wvc(dataY=ypine[-1],dataX=XpineNAX21[-1,],nt=3,dataPredictY=XpineNAX21[1,])
PLS_lm_wvc(dataY=ypine[-2],dataX=XpineNAX21[-2,],nt=3,dataPredictY=XpineNAX21[2,])
PLS_lm_wvc(dataY=ypine,dataX=XpineNAX21,nt=3)
rm("XpineNAX21","ypine")

```

---

predict.plsRglmmodel    *Print method for plsRcox models*

---

**Description**

This function provides a predict method for the class "plsRglmmodel"

**Usage**

```

## S3 method for class 'plsRglmmodel'
predict(object,newdata,comps=object$computed_nt,
type=c("link", "response", "terms", "scores", "class", "probs"),
se.fit=FALSE,weights, dispersion = NULL,methodNA="adaptative",verbose=TRUE,...)

```

**Arguments**

object	An object of the class "plsRmodel".
newdata	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
comps	A value with a single value of component to use for prediction.
type	Type of predicted value. Available choices are the glms ones ("link", "response", "terms"), the polr ones ("class", "probs") or the scores ("scores").
se.fit	If TRUE, pointwise standard errors are produced for the predictions using the Cox model.
weights	Vector of case weights. If weights is a vector of integers, then the estimated coefficients are equivalent to estimating the model from data with the individual cases replicated as many times as indicated by weights.

dispersion	the dispersion of the GLM fit to be assumed in computing the standard errors. If omitted, that returned by summary applied to the object is used.
methodNA	Selects the way of predicting the response or the scores of the new data. For complete rows, without any missing value, there are two different ways of computing the prediction. As a consequence, for mixed datasets, with complete and incomplete rows, there are two ways of computing prediction : either predicts any row as if there were missing values in it (missingdata) or selects the prediction method accordingly to the completeness of the row (adaptative).
verbose	should info messages be displayed ?
...	Arguments to be passed on to stats::glm and plsRglm::plsRglm.

### Value

When type is "response", a matrix of predicted response values is returned.  
When type is "scores", a score matrix is returned.

### Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

### References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

### See Also

See Also [predict.glm](#)

### Examples

```
data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
data(pine_sup)
Xpine_sup<-pine_sup[,1:10]
Xpine_supNA<-Xpine_sup
Xpine_supNA[1,1]<-NA

modpls=plsRglm(dataY=ypine,dataX=Xpine,nt=6,modele="pls-glm-family",family="gaussian")
modplsform=plsRglm(x11~.,data=pine,nt=6,modele="pls-glm-family",family="gaussian")
modpls2=plsRglm(dataY=ypine,dataX=Xpine,nt=6,modele="pls-glm-family",
dataPredictY=Xpine_sup,family="gaussian")
modpls2NA=plsRglm(dataY=ypine,dataX=Xpine,nt=6,modele="pls-glm-family",
dataPredictY=Xpine_supNA,family="gaussian")
```

```

#Identical to predict(modpls,type="link") or modpls$Std.ValsPredictY
cbind(modpls$Std.ValsPredictY,modplsform$Std.ValsPredictY,
predict(modpls),predict(modplsform))

#Identical to predict(modpls,type="response") or modpls$ValsPredictY
cbind(modpls$ValsPredictY,modplsform$ValsPredictY,
predict(modpls,type="response"),predict(modplsform,type="response"))

#Identical to modpls$ttPredictY
predict(modpls,type="scores")
predict(modplsform,type="scores")

#Identical to modpls2$ValsPredictY
cbind(predict(modpls,newdata=Xpine_sup,type="response"),
predict(modplsform,newdata=Xpine_sup,type="response"))

#Select the number of components to use to derive the prediction
predict(modpls,newdata=Xpine_sup,type="response",comps=1)
predict(modpls,newdata=Xpine_sup,type="response",comps=3)
predict(modpls,newdata=Xpine_sup,type="response",comps=6)
try(predict(modpls,newdata=Xpine_sup,type="response",comps=8))

#Identical to modpls2$ttValsPredictY
predict(modpls,newdata=Xpine_sup,type="scores")

#Select the number of components in the scores matrix
predict(modpls,newdata=Xpine_sup,type="scores",comps=1)
predict(modpls,newdata=Xpine_sup,type="scores",comps=3)
predict(modpls,newdata=Xpine_sup,type="scores",comps=6)
try(predict(modpls,newdata=Xpine_sup,type="scores",comps=8))

#Identical to modpls2NA$ValsPredictY
predict(modpls,newdata=Xpine_supNA,type="response",methodNA="missingdata")

cbind(predict(modpls,newdata=Xpine_supNA,type="response"),
predict(modplsform,newdata=Xpine_supNA,type="response"))

predict(modpls,newdata=Xpine_supNA,type="response",comps=1)
predict(modpls,newdata=Xpine_supNA,type="response",comps=3)
predict(modpls,newdata=Xpine_supNA,type="response",comps=6)
try(predict(modpls,newdata=Xpine_supNA,type="response",comps=8))

#Identical to modpls2NA$ttPredictY
predict(modpls,newdata=Xpine_supNA,type="scores",methodNA="missingdata")
predict(modplsform,newdata=Xpine_supNA,type="scores",methodNA="missingdata")

predict(modpls,newdata=Xpine_supNA,type="scores")
predict(modplsform,newdata=Xpine_supNA,type="scores")
predict(modpls,newdata=Xpine_supNA,type="scores",comps=1)
predict(modpls,newdata=Xpine_supNA,type="scores",comps=3)
predict(modpls,newdata=Xpine_supNA,type="scores",comps=6)
try(predict(modpls,newdata=Xpine_supNA,type="scores",comps=8))

```



---

predict.plsRmodel      *Print method for plsRcox models*

---

### Description

This function provides a predict method for the class "plsRcoxmodel"

### Usage

```
## S3 method for class 'plsRmodel'  
predict(object,newdata,comps=object$computed_nt,  
type=c("response","scores"),weights,methodNA="adaptative",verbose=TRUE,...)
```

### Arguments

object	An object of the class "plsRmodel".
newdata	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
comps	A value with a single value of component to use for prediction.
type	Type of predicted value. Available choices are the response values ("response") or the scores ("scores").
weights	Vector of case weights. If weights is a vector of integers, then the estimated coefficients are equivalent to estimating the model from data with the individual cases replicated as many times as indicated by weights.
methodNA	Selects the way of predicting the response or the scores of the new data. For complete rows, without any missing value, there are two different ways of computing the prediction. As a consequence, for mixed datasets, with complete and incomplete rows, there are two ways of computing prediction : either predicts any row as if there were missing values in it (missingdata) or selects the prediction method accordingly to the completeness of the row (adaptative).
verbose	should info messages be displayed ?
...	Arguments to be passed on to plsRglm::plsR.

### Value

When type is "response", a matrix of predicted response values is returned.  
When type is "scores", a score matrix is returned.

### Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## Examples

```

data(pine)
Xpine<-pine[,1:10]
ypine<-pine[,11]
data(pine_sup)
Xpine_sup<-pine_sup[,1:10]
Xpine_supNA<-Xpine_sup
Xpine_supNA[1,1]<-NA

modpls=plsR(dataY=ypine,dataX=Xpine,nt=6,modele="pls")
modplsform=plsR(x11~.,data=pine,nt=6,modele="pls")
modpls2=plsR(dataY=ypine,dataX=Xpine,nt=6,modele="pls",dataPredictY=Xpine_sup)
modpls2NA=plsR(dataY=ypine,dataX=Xpine,nt=6,modele="pls",dataPredictY=Xpine_supNA)

#Identical to predict(modpls,type="response") or modpls$ValsPredictY
cbind(predict(modpls),predict(modplsform))

#Identical to modpls$ttPredictY
predict(modpls,type="scores")
predict(modplsform,type="scores")

#Identical to modpls2$ValsPredictY
cbind(predict(modpls,newdata=Xpine_sup,type="response"),
predict(modplsform,newdata=Xpine_sup,type="response"))

#Select the number of components to use to derive the prediction
predict(modpls,newdata=Xpine_sup,type="response",comps=1)
predict(modpls,newdata=Xpine_sup,type="response",comps=3)
predict(modpls,newdata=Xpine_sup,type="response",comps=6)
try(predict(modpls,newdata=Xpine_sup,type="response",comps=8))

#Identical to modpls2$ttValsPredictY
predict(modpls,newdata=Xpine_sup,type="scores")

#Select the number of components in the scores matrix
predict(modpls,newdata=Xpine_sup,type="scores",comps=1)
predict(modpls,newdata=Xpine_sup,type="scores",comps=3)
predict(modpls,newdata=Xpine_sup,type="scores",comps=6)
try(predict(modpls,newdata=Xpine_sup,type="scores",comps=8))

#Identical to modpls2NA$ValsPredictY
predict(modpls,newdata=Xpine_supNA,type="response",methodNA="missingdata")

cbind(predict(modpls,newdata=Xpine_supNA,type="response"),

```

```

predict(modplsform,newdata=Xpine_supNA,type="response")

predict(modpls,newdata=Xpine_supNA,type="response",comps=1)
predict(modpls,newdata=Xpine_supNA,type="response",comps=3)
predict(modpls,newdata=Xpine_supNA,type="response",comps=6)
try(predict(modpls,newdata=Xpine_supNA,type="response",comps=8))

#Identical to modpls2NA$ttPredictY
predict(modpls,newdata=Xpine_supNA,type="scores",methodNA="missingdata")
predict(modplsform,newdata=Xpine_supNA,type="scores",methodNA="missingdata")

predict(modpls,newdata=Xpine_supNA,type="scores")
predict(modplsform,newdata=Xpine_supNA,type="scores")
predict(modpls,newdata=Xpine_supNA,type="scores",comps=1)
predict(modpls,newdata=Xpine_supNA,type="scores",comps=3)
predict(modpls,newdata=Xpine_supNA,type="scores",comps=6)
try(predict(modpls,newdata=Xpine_supNA,type="scores",comps=8))

```

---

```
print.coef.plsRglmmodel
```

*Print method for plsRglm models*

---

## Description

This function provides a print method for the class "coef.plsRglmmodel"

## Usage

```
## S3 method for class 'coef.plsRglmmodel'
print(x, ...)
```

## Arguments

x	an object of the class "coef.plsRglmmodel"
...	not used

## Value

NULL

## Author(s)

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modplsglm <- plsRglm(yCornell,XCornell,3,modele="pls-glm-family",family=gaussian())
class(modplsglm)
print(coef(modplsglm))
rm(list=c("XCornell","yCornell","modplsglm"))
```

---

print.coef.plsRmodel *Print method for plsR models*

---

## Description

This function provides a print method for the class "coef.plsRmodel"

## Usage

```
## S3 method for class 'coef.plsRmodel'
print(x, ...)
```

## Arguments

x	an object of the class "coef.plsRmodel"
...	not used

## Value

NULL

## Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsRglm(yCornell,XCornell,3,modele="pls")
class(modpls)
print(coef(modpls))
rm(list=c("XCornell","yCornell","modpls"))
```

---

print.cv.plsRglmmodel *Print method for plsRglm models*

---

## Description

This function provides a print method for the class "cv.plsRglmmodel"

## Usage

```
## S3 method for class 'cv.plsRglmmodel'
print(x, ...)
```

## Arguments

x	an object of the class "cv.plsRglmmodel"
...	not used

## Value

NULL

## Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frédéric Bertrand (2010). Comparaison de la régression PLS et de la régression logistique PLS : application aux données d'allotypage. *Journal de la Société Française de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=10,NK=1,
modele="pls-glm-family",family=gaussian())
print(bbb)
rm(list=c("XCornell","yCornell","bbb"))
```

---

print.cv.plsRmodel      *Print method for plsR models*

---

## Description

This function provides a print method for the class "cv.plsRmodel"

## Usage

```
## S3 method for class 'cv.plsRmodel'
print(x, ...)
```

## Arguments

x	an object of the class "cv.plsRmodel"
...	not used

## Value

NULL

## Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsR(dataY=yCornell,dataX=XCornell,nt=10,K=6)
print(bbb)
rm(list=c("XCornell","yCornell","bbb"))
```

---

print.plsRglmmodel      *Print method for plsRglm models*

---

## Description

This function provides a print method for the class "plsRglmmodel"

## Usage

```
## S3 method for class 'plsRglmmodel'
print(x, ...)
```

## Arguments

x	an object of the class "plsRglmmodel"
...	not used

## Value

NULL

## Author(s)

Frédéric Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frédéric Bertrand (2010). Comparaison de la régression PLS et de la régression logistique PLS : application aux données d'allélotypage. *Journal de la Société Française de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modplsglm <- plsRglm(yCornell,XCornell,3,modele="pls-glm-gaussian")
class(modplsglm)
print(modplsglm)
rm(list=c("XCornell","yCornell","modplsglm"))
```

---

print.plsRmodel	<i>Print method for plsR models</i>
-----------------	-------------------------------------

---

## Description

This function provides a print method for the class "plsRmodel"

## Usage

```
## S3 method for class 'plsRmodel'
print(x, ...)
```

## Arguments

x	an object of the class "plsRmodel"
...	not used

## Value

NULL

## Author(s)

Frédéric Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>



## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frédéric Bertrand (2010). Comparaison de la régression PLS et de la régression logistique PLS : application aux données d'allélotypage. *Journal de la Société Française de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsRglm(yCornell,XCornell,3,modele="pls")
class(modpls)
print(modpls)
rm(list=c("XCornell","yCornell","modpls"))
```

---

```
print.summary.plsRglmmodel
```

*Print method for summaries of plsRglm models*

---

## Description

This function provides a print method for the class "summary.plsRglmmodel"

## Usage

```
## S3 method for class 'summary.plsRglmmodel'
print(x, ...)
```

## Arguments

x	an object of the class "summary.plsRglmmodel"
...	not used

## Value

language	call of the model
----------	-------------------

## Author(s)

Frédéric Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frédéric Bertrand (2010). Comparaison de la régression PLS et de la régression logistique PLS : application aux données d'allélotypage. *Journal de la Société Française de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#) and [summary](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modplsglm <- plsRglm(yCornell,XCornell,3,modele="pls-glm-gaussian")
class(modplsglm)
print(summary(modplsglm))
rm(list=c("XCornell","yCornell","modplsglm"))
```

---

```
print.summary.plsRmodel
```

*Print method for summaries of plsR models*

---

## Description

This function provides a print method for the class "summary.plsRmodel"

## Usage

```
## S3 method for class 'summary.plsRmodel'
print(x, ...)
```

## Arguments

x	an object of the class "summary.plsRmodel"
...	not used

## Value

language	call of the model
----------	-------------------

## Author(s)

Frédéric Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

Nicolas Meyer, Myriam Maumy-Bertrand et Frédéric Bertrand (2010). Comparaison de la régression PLS et de la régression logistique PLS : application aux données d'allélotypage. *Journal de la Société Française de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

## See Also

[print](#) and [summary](#)

## Examples

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsRglm(yCornell,XCornell,3,modele="pls")
class(modpls)
print(summary(modpls))
rm(list=c("XCornell","yCornell","modpls"))
```

---

signpred

*Graphical assessment of the stability of selected variables*

---

## Description

This functions plots, for each of the model, the

## Usage

```
signpred(matbin, pred.lablength = max(sapply(rownames(matbin), nchar)),
labsize = 1, plotsize = 12)
```

## Arguments

matbin	Matrix with 0 or 1 entries. Each row per predictor and a column for every model. 0 means the predictor is not significant in the model and 1 that, on the contrary, it is significant.
pred.lablength	Maximum length of the predictors labels. Defaults to full label length.
labsize	Size of the predictors labels.
plotsize	Global size of the graph.

## Details

This function is based on the [visweb](#) function from the bipartite package.

## Value

A plot window.

**Author(s)**

Bernd Gruber with minor modifications from Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Vazquez, P.D., Chacoff, N.,P. and Cagnolo, L. (2009) Evaluating multiple determinants of the structure of plant-animal mutualistic networks. *Ecology*, 90:2039-2046.

**See Also**

See Also [visweb](#)

**Examples**

```
signedpred(matrix(rbinom(160,1,.2),ncol=8,dimnames=list(as.character(1:20),as.character(1:8))))
```

---

simul\_data\_complete     *Data generating detailed process for multivariate plsR models*

---

**Description**

This function generates a single multivariate response value  $\mathbf{Y}$  and a vector of explanatory variables  $(X_1, \dots, X_{totdim})$  drawn from a model with a given number of latent components.

**Usage**

```
simul_data_complete(totdim, ncomp)
```

**Arguments**

totdim	Number of columns of the X vector (from ncomp to hardware limits)
ncomp	Number of latent components in the model (from 2 to 6)

**Details**

This function should be combined with the replicate function to give rise to a larger dataset. The algorithm used is a R port of the one described in the article of Li which is a multivariate generalization of the algorithm of Naes and Martens.

**Value**

simX	Vector of explanatory variables
HH	Dimension of the response $Y$
eta	See Li et al.
r	See Li et al.
epsilon	See Li et al.
ksi	See Li et al.
f	See Li et al.
z	See Li et al.
Y	See Li et al.

**Note**

The value of  $r$  depends on the value of ncomp :

ncomp	$r$
2	3
3	3
4	4

**Author(s)**

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

- T. Naes, H. Martens, Comparison of prediction methods for multicollinear data, *Commun. Stat., Simul.* 14 (1985) 545-576.  
<http://dx.doi.org/10.1080/03610918508812458>
- Baibing Li, Julian Morris, Elaine B. Martin, Model selection for partial least squares regression, *Chemometrics and Intelligent Laboratory Systems* 64 (2002) 79-89.  
[http://dx.doi.org/10.1016/S0169-7439\(02\)00051-5](http://dx.doi.org/10.1016/S0169-7439(02)00051-5)

**See Also**

[simul\\_data\\_YX](#) for data simulation purpose

**Examples**

```
simul_data_complete(20,6)

dimX <- 6
Astar <- 2
simul_data_complete(dimX,Astar)
```

```
dimX <- 6
Astar <- 3
simul_data_complete(dimX,Astar)
```

```
dimX <- 6
Astar <- 4
simul_data_complete(dimX,Astar)
```

```
rm(list=c("dimX", "Astar"))
```

---

simul\_data\_UniYX      *Data generating function for univariate plsR models*

---

### Description

This function generates a single univariate response value  $Y$  and a vector of explanatory variables  $(X_1, \dots, X_{totdim})$  drawn from a model with a given number of latent components.

### Usage

```
simul_data_UniYX(totdim, ncomp)
```

### Arguments

totdim	Number of columns of the X vector (from ncomp to hardware limits)
ncomp	Number of latent components in the model (from 2 to 6)

### Details

This function should be combined with the replicate function to give rise to a larger dataset. The algorithm used is a R port of the one described in the article of Li which is a multivariate generalization of the algorithm of Naes and Martens.

### Value

vector       $(Y, X_1, \dots, X_{totdim})$

### Author(s)

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

## References

T. Naes, H. Martens, Comparison of prediction methods for multicollinear data, *Commun. Stat., Simul.* 14 (1985) 545-576.

<http://dx.doi.org/10.1080/03610918508812458>

Baibing Li, Julian Morris, Elaine B. Martin, Model selection for partial least squares regression, *Chemometrics and Intelligent Laboratory Systems* 64 (2002) 79-89.

[http://dx.doi.org/10.1016/S0169-7439\(02\)00051-5](http://dx.doi.org/10.1016/S0169-7439(02)00051-5)

## See Also

[simul\\_data\\_YX](#) and [simul\\_data\\_complete](#) for generating multivariate data

## Examples

```
simul_data_UniYX(20,6)

dimX <- 6
Astar <- 2
simul_data_UniYX(dimX,Astar)
(dataAstar2 <- t(replicate(50,simul_data_UniYX(dimX,Astar))))
cvtable(summary(cv.plsR(dataAstar2[,1],dataAstar2[,2:7],5,NK=100)))

dimX <- 6
Astar <- 3
simul_data_UniYX(dimX,Astar)
(dataAstar3 <- t(replicate(50,simul_data_UniYX(dimX,Astar))))
cvtable(summary(cv.plsR(dataAstar3[,1],dataAstar3[,2:7],5,NK=100)))

dimX <- 6
Astar <- 4
simul_data_UniYX(dimX,Astar)
(dataAstar4 <- t(replicate(50,simul_data_UniYX(dimX,Astar))))
cvtable(summary(cv.plsR(dataAstar4[,1],dataAstar4[,2:7],5,NK=100)))

rm(list=c("dimX","Astar"))
```

---

simul\_data\_UniYX\_binom

*Data generating function for univariate binomial plsR models*

---

## Description

This function generates a single univariate binomial response value  $Y$  and a vector of explanatory variables  $(X_1, \dots, X_{totdim})$  drawn from a model with a given number of latent components.

**Usage**

```
simul_data_UniYX_binom(totdim, ncomp, link="logit", offset = 0)
```

**Arguments**

totdim	Number of columns of the X vector (from ncomp to hardware limits)
ncomp	Number of latent components in the model (from 2 to 6)
link	Character specification of the link function in the mean model ( $\mu$ ). Currently, "logit", "probit", "cloglog", "cauchit", "log", "loglog" are supported. Alternatively, an object of class "link-glm" can be supplied.
offset	Offset on the linear scale

**Details**

This function should be combined with the replicate function to give rise to a larger dataset. The algorithm used is a modification of a R port of the one described in the article of Li which is a multivariate generalization of the algorithm of Naes and Martens.

**Value**

vector  $(Y, X_1, \dots, X_{totdim})$

**Author(s)**

Frédéric Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

T. Naes, H. Martens, Comparison of prediction methods for multicollinear data, Commun. Stat., Simul. 14 (1985) 545-576.  
<http://dx.doi.org/10.1080/03610918508812458>  
 Baibing Li, Julian Morris, Elaine B. Martin, Model selection for partial least squares regression, Chemometrics and Intelligent Laboratory Systems 64 (2002) 79-89.  
[http://dx.doi.org/10.1016/S0169-7439\(02\)00051-5](http://dx.doi.org/10.1016/S0169-7439(02)00051-5)

**See Also**

[simul\\_data\\_UniYX](#)

**Examples**

```
layout(matrix(1:6,nrow=2))
# logit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4)))[,1])
# probit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="probit")))[,1])
```



```

# cloglog link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="cloglog")))[,1])
# cauchit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="cauchit")))[,1])
# loglog link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="loglog")))[,1])
# log link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="log")))[,1])
layout(1)

layout(matrix(1:6,nrow=2))
# logit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,offset=5)))[,1])
# probit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="probit",offset=5)))[,1])
# cloglog link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="cloglog",offset=5)))[,1])
# cauchit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="cauchit",offset=5)))[,1])
# loglog link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="loglog",offset=5)))[,1])
# log link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="log",offset=5)))[,1])
layout(1)

layout(matrix(1:6,nrow=2))
# logit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,offset=-5)))[,1])
# probit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="probit",offset=-5)))[,1])
# cloglog link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="cloglog",offset=-5)))[,1])
# cauchit link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="cauchit",offset=-5)))[,1])
# loglog link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="loglog",offset=-5)))[,1])
# log link
hist(t(replicate(100,simul_data_UniYX_binom(4,4,link="log",offset=-5)))[,1])
layout(1)

```

---

simul\_data\_YX

*Data generating function for multivariate plsR models*


---

### Description

This function generates a single multivariate response value  $Y$  and a vector of explanatory variables  $(X_1, \dots, X_{totdim})$  drawn from a model with a given number of latent components.

**Usage**

```
simul_data_YX(totdim, ncomp)
```

**Arguments**

totdim	Number of column of the X vector (from ncomp to hardware limits)
ncomp	Number of latent components in the model (from 2 to 6)

**Details**

This function should be combined with the replicate function to give rise to a larger dataset. The algorithm used is a R port of the one described in the article of Li which is a multivariate generalization of the algorithm of Naes and Martens.

**Value**

vector  $(Y_1, \dots, Y_r, X_1, \dots, X_{totdim})$

**Note**

The value of  $r$  depends on the value of ncomp :

ncomp	$r$
2	3
3	3
4	4

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

T. Naes, H. Martens, Comparison of prediction methods for multicollinear data, Commun. Stat., Simul. 14 (1985) 545-576.  
<http://dx.doi.org/10.1080/03610918508812458>  
 Baibing Li, Julian Morris, Elaine B. Martin, Model selection for partial least squares regression, Chemometrics and Intelligent Laboratory Systems 64 (2002) 79-89.  
[http://dx.doi.org/10.1016/S0169-7439\(02\)00051-5](http://dx.doi.org/10.1016/S0169-7439(02)00051-5)

**See Also**

[simul\\_data\\_complete](#) for highlighting the simulations parameters

**Examples**

```
simul_data_YX(20, 6)
```

```
if(require(plsdepot)){
  dimX <- 6
  Astar <- 2
  (dataAstar2 <- t(replicate(50,simul_data_YX(dimX,Astar))))
  library(plsdepot)
  resAstar2 <- plsreg2(dataAstar2[,4:9],dataAstar2[,1:3],comps=5)
  resAstar2$Q2
  resAstar2$Q2[,4]>0.0975

  dimX <- 6
  Astar <- 3
  (dataAstar3 <- t(replicate(50,simul_data_YX(dimX,Astar))))
  library(plsdepot)
  resAstar3 <- plsreg2(dataAstar3[,4:9],dataAstar3[,1:3],comps=5)
  resAstar3$Q2
  resAstar3$Q2[,4]>0.0975

  dimX <- 6
  Astar <- 4
  (dataAstar4 <- t(replicate(50,simul_data_YX(dimX,Astar))))
  library(plsdepot)
  resAstar4 <- plsreg2(dataAstar4[,5:10],dataAstar4[,1:4],comps=5)
  resAstar4$Q2
  resAstar4$Q2[,5]>0.0975

  rm(list=c("dimX","Astar"))
}
```

---

summary.cv.plsRglmmodel

*Summary method for plsRglm models*

---

## Description

This function provides a summary method for the class "cv.plsRglmmodel"

## Usage

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

## Arguments

object            an object of the class "cv.plsRglmmodel"  
...                further arguments to be passed to or from methods.

**Value**

An object of class "summary.cv.plsRmodel" if model is missing or model="pls". Otherwise an object of class "summary.cv.plsRglmmodel".

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[summary](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsRglm(dataY=yCornell,dataX=XCornell,nt=10,NK=1,
modele="pls-glm-family",family=gaussian())
summary(bbb)
rm(list=c("XCornell","yCornell","bbb"))
```

---

summary.cv.plsRmodel    *Summary method for plsR models*

---

**Description**

This function provides a summary method for the class "cv.plsRmodel"

**Usage**

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

**Arguments**

object            an object of the class "cv.plsRmodel"  
 ...              further arguments to be passed to or from methods.

**Value**

An object of class "summary.cv.plsRglmmodel".

**Author(s)**

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[summary](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
bbb <- cv.plsR(dataY=yCornell,dataX=XCornell,nt=10,K=6)
summary(bbb)
rm(list=c("XCornell","yCornell","bbb"))
```

---

summary.plsRglmmodel    *Summary method for plsRglm models*

---

**Description**

This function provides a summary method for the class "plsRglmmodel"

**Usage**

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

**Arguments**

object            an object of the class "plsRglmmodel"  
...                further arguments to be passed to or from methods.

**Value**

call                    function call of plsRglmmodel

**Author(s)**

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[summary](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modplsglm <- plsRglm(yCornell,XCornell,3,modele="pls-glm-gaussian")
class(modplsglm)
summary(modplsglm)
rm(list=c("XCornell","yCornell","modplsglm"))
```

---

summary.plsRmodel            *Summary method for plsR models*

---

**Description**

This function provides a summary method for the class "plsRmodel"

**Usage**

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

**Arguments**

object                    an object of the class "plsRmodel"  
...                        further arguments to be passed to or from methods.

**Value**

call                    function call of plsRmodel

**Author(s)**

Frederic Bertrand  
<frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**References**

Nicolas Meyer, Myriam Maumy-Bertrand et Frederic Bertrand (2010). Comparing the linear and the logistic PLS regression with qualitative predictors: application to allelotyping data. *Journal de la Societe Francaise de Statistique*, 151(2), pages 1-18. [http://smf4.emath.fr/Publications/JSFds/151\\_2/pdf/sfds\\_jsfds\\_151\\_2\\_1-18.pdf](http://smf4.emath.fr/Publications/JSFds/151_2/pdf/sfds_jsfds_151_2_1-18.pdf)

**See Also**

[summary](#)

**Examples**

```
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]
modpls <- plsR(yCornell,XCornell,3,modele="pls")
class(modpls)
summary(modpls)
rm(list=c("XCornell","yCornell","modpls"))
```

---

tilt.bootpls

*Tilted bootstrap for PLS models*

---

**Description**

~~ A (1-5 lines) description of what the function does. ~~

**Usage**

```
tilt.bootpls(object, typeboot="plsmodel", statistic=coefs.plsR,  
R=c(499, 250, 250), alpha=c(0.025, 0.975), sim="ordinary",  
stype="i", index=1, stabvalue=1e6,...)
```

**Arguments**

object	~~Explain object here~~
typeboot	~~Explain typeboot here~~
statistic	~~Explain statistic here~~
R	~~Explain R here~~
alpha	~~Explain alpha here~~
sim	~~Explain sim here~~
stype	~~Explain stype here~~
index	~~Explain index here~~
stabvalue	~~Explain stabvalue here~~
...	~~Explain ... here~~

**Details**

~~ More details than the description above ~~

**Value**

~Describe the value returned If it is a LIST, use

comp1	Description of 'comp1'
comp2	Description of 'comp2'
...	

**Author(s)**

Frederic Bertrand  
 <frederic.bertrand@math.unistra.fr>  
<http://www-irma.u-strasbg.fr/~fbertran/>

**See Also**

[tilt.boot](#)

**Examples**

```
## Not run:
data(Cornell)
XCornell<-Cornell[,1:7]
yCornell<-Cornell[,8]

set.seed(1385)
Cornell.tilt.boot <- tilt.bootpls(plsR(yCornell,XCornell,3), statistic=coefs.plsR,
R=c(499, 100, 100), alpha=c(0.025, 0.975), sim="ordinary", stype="i", index=1)
Cornell.tilt.boot
str(Cornell.tilt.boot)
```



```

boxplots.bootpls(Cornell.tilt.boot,indices=2:7)

rm(Cornell.tilt.boot)

## End(Not run)

```

---

tilt.bootplsglm	<i>Tilted bootstrap for PLS models</i>
-----------------	--

---

### Description

~~ A (1-5 lines) description of what the function does. ~~

### Usage

```

tilt.bootplsglm(object, typeboot="fmodel_np", statistic=coefs.plsRglm,
R=c(499, 250, 250), alpha=c(0.025, 0.975), sim="ordinary",
stype="i", index=1, stabvalue=1e6,...)

```

### Arguments

object	~~Explain object here~~
typeboot	~~Explain typeboot here~~
statistic	~~Explain statistic here~~
R	~~Explain R here~~
alpha	~~Explain alpha here~~
sim	~~Explain sim here~~
stype	~~Explain stype here~~
index	~~Explain index here~~
stabvalue	~~Explain stabvalue here~~
...	~~Explain ... here~~

### Details

~~ More details than the description above ~~

### Value

~Describe the value returned If it is a LIST, use

comp1	Description of 'comp1'
comp2	Description of 'comp2'
...	

**Author(s)**

Frederic Bertrand  
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**See Also**

[tilt.boot](#)

**Examples**

```
data(aze_compl)
Xaze_compl<-aze_compl[,2:34]
yaze_compl<-aze_compl$y

dataset <- cbind(y=yaze_compl,Xaze_compl)

# Lazraq-Cleroux PLS bootstrap Classic

aze_compl.tilt.boot <- tilt.bootplsglm(plsRglm(yaze_compl,Xaze_compl,3,
modele="pls-glm-logistic", family=NULL), statistic=coefs.plsRglm, R=c(499, 100, 100),
alpha=c(0.025, 0.975), sim="ordinary", stype="i", index=1)
aze_compl.tilt.boot <- tilt.bootplsglm(plsRglm(yaze_compl,Xaze_compl,3,
modele="pls-glm-logistic"), statistic=coefs.plsRglm, R=c(499, 100, 100),
alpha=c(0.025, 0.975), sim="ordinary", stype="i", index=1)
aze_compl.tilt.boot <- tilt.bootplsglm(plsRglm(yaze_compl,Xaze_compl,3,
modele="pls-glm-family", family=binomial), statistic=coefs.plsRglm, R=c(499, 100, 100),
alpha=c(0.025, 0.975), sim="ordinary", stype="i", index=1)

boxplots.bootpls(aze_compl.tilt.boot,1:2)

# PLS bootstrap balanced

aze_compl.tilt.boot <- tilt.bootplsglm(plsRglm(yaze_compl,Xaze_compl,3,
modele="pls-glm-logistic"), statistic=coefs.plsRglm, R=c(499, 100, 100),
alpha=c(0.025, 0.975), sim="balanced", stype="i", index=1)
```

**Description**

Quality of Bordeaux wines (Quality) and four potentially predictive variables (Temperature, Sunshine, Heat and Rain).  
 The value of Temperature for the first observation was remove from the matrix of predictors on purpose.

**Usage**

```
data(XbordeauxNA)
```

**Format**

A data frame with 34 observations on the following 4 variables.

Temperature a numeric vector

Sunshine a numeric vector

Heat a numeric vector

Rain a numeric vector

**Source**

P. Bastien, V. Esposito-Vinzi, and M. Tenenhaus. (2005). PLS generalised linear regression. *Computational Statistics & Data Analysis*, 48(1):17-46.

**References**

M. Tenenhaus. (2005). La regression logistique PLS. In J.-J. Dreesbeke, M. Lejeune, and G. Saporta, editors, *Modeles statistiques pour donnees qualitatives*. Editions Technip, Paris.

**Examples**

```
data(XbordeauxNA)
str(XbordeauxNA)
```

---

XpineNAX21

*Incomplete dataset from the pine caterpillars example*

---

**Description**

The caterpillar dataset was extracted from a 1973 study on pine processionary caterpillars. It assesses the influence of some forest settlement characteristics on the development of caterpillar colonies. There are k=10 potentially explanatory variables defined on n=33 areas.

The value of x2 for the first observation was remove from the matrix of predictors on purpose.

**Usage**

```
data(XpineNAX21)
```

**Format**

A data frame with 33 observations on the following 10 variables.

x1 altitude (in meters)

x2 slope (en degrees)

x3 number of pines in the area

x4 height (in meters) of the tree sampled at the center of the area

x5 diameter (in meters) of the tree sampled at the center of the area

x6 index of the settlement density

x7 orientation of the area (from 1 if southbound to 2 otherwise)

x8 height (in meters) of the dominant tree

x9 number of vegetation strata

x10 mix settlement index (from 1 if not mixed to 2 if mixed)

**Details**

These caterpillars got their names from their habit of moving over the ground in incredibly long head-to-tail processions when leaving their nest to create a new colony.

The XpineNAX21 is a dataset with a missing value for testing purpose.

**Source**

Tomassone R., Audrain S., Lesquoy-de Turckheim E., Millier C. (1992). “La regression, nouveaux regards sur une ancienne methode statistique”, INRA, *Actualit?s Scientifiques et Agronomiques*, Masson, Paris.

**Examples**

```
data(XpineNAX21)
str(XpineNAX21)
```

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