

Package ‘palasso’

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Version 0.0.8

Title Paired Lasso Regression

Description Implements sparse regression with paired covariates (Rauschenberger et al. 2020 <[doi:10.1007/s11634-019-00375-6](https://doi.org/10.1007/s11634-019-00375-6)>). For the optional shrinkage, install `ashr` (<<https://github.com/stephens999/ashr>>) and `CorShrink` (<<https://github.com/kkdey/CorShrink>>) from GitHub (see README).

Depends R (>= 3.0.0)

Imports glmnet, Matrix, survival

Suggests knitr, testthat, rmarkdown

Enhances `ashr`, `CorShrink`, `pROC`, `edgeR`

VignetteBuilder knitr

License GPL-3

Encoding UTF-8

Language en-GB

RoxygenNote 7.1.1

URL <https://github.com/rauschenberger/palasso>

BugReports <https://github.com/rauschenberger/palasso/issues>

NeedsCompilation no

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<code>.args</code>	<i>Arguments</i>
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Description

Checks the validity of the provided arguments.

Usage

```
.args(...)
```

Arguments

... Arguments supplied to `palasso`, other than `y`, `X` and `max`.

Value

Returns the arguments as a list, including default values for missing arguments.

Examples

```
NA
```

<code>.combine</code>	<i>Combining p-values</i>
-----------------------	---------------------------

Description

This function combines local p -values to a global p -value.

Usage

```
.combine(x, method = "simes")
```

Arguments

x local *p*-values: numeric vector of length *k*
 method character "fisher", "tippet", "sidak", or "simes"

Value

These functions return a numeric vector of length *p* (main effects), or a numeric matrix with *p* rows and *p* columns (interaction effects).

References

Westfall, P. H. (2005). "Combining p-values". Encyclopedia of Biostatistics doi: [10.1002/0470011815.b2a15181](https://doi.org/10.1002/0470011815.b2a15181)

Examples

```
# independence
p <- runif(10)
palasso:::.combine(p)

## dependence
#runif <- function(n,cor=0){
#   Sigma <- matrix(cor,nrow=n,ncol=n)
#   diag(Sigma) <- 1
#   mu <- rep(0,times=n)
#   q <- MASS::mvrnorm(n=1,mu=mu,Sigma=Sigma)
#   stats::pnorm(q=q)
#}
#p <- runif(n=10,cor=0.8)
#combine(p)
```

.cor	<i>Correlation</i>
------	--------------------

Description

Calculates the correlation between the response and the covariates. Shrinks the correlation coefficients for each covariate set separately.

Usage

```
.cor(y, x, args)
```

Arguments

y vector of length *n*
 x matrix with *n* rows and *p* columns
 args options for paired lasso: list of arguments (output from [.dims](#) and [.args](#))

Value

list of vectors

Examples

NA

.cv

Cross-validation

Description

Repeatedly leaves out samples, and predicts their response.

Usage

```
.cv(y, x, foldid, lambda, args)
```

Arguments

y	response: vector of length n
x	covariates: matrix with n rows (samples) and $k * p$ columns (variables)
foldid	fold identifiers: vector of length n , with entries from 1 to n folds
lambda	lambda sequence: vector of decreasing positive values
args	options for paired lasso: list of arguments (output from .dims and .args)

Value

Returns matrix of predicted values (except "cox")

Examples

NA

.dims *Dimensionality*

Description

This function extracts the dimensions.

Usage

```
.dims(y, X, args = NULL)
```

Arguments

- y response: vector of length n
- X covariates: list of matrices, each with n rows (samples) and p columns (variables)
- args options for paired lasso: list of arguments (output from [.dims](#) and [.args](#))

Value

The function `.dims` extracts the dimensionality. It returns the numbers of samples, covariate pairs and covariate sets. It also returns the number of weighting schemes, and the names of these weighting schemes.

Examples

NA

.extract *Extraction*

Description

Extracts cv.glmnet-like object.

Usage

```
.extract(fit, lambda, cvm, type.measure)
```

Arguments

- fit matrix with one row for each sample ("gaussian", "binomial" and "poisson"), or one row for each fold (only "cox"), and one column for each lambda (output from [.fit](#))
- lambda lambda sequence: vector of decreasing positive values
- cvm mean cross-validated loss: vector of same length as lambda (output from [.loss](#))
- type.measure ... loss function: character "deviance", "mse", "mae", "class", or "auc"

Examples

NA

`.fit`*Model bag*

Description

Fits all models from the chosen bag.

Usage`.fit(y, x, args)`**Arguments**

<code>y</code>	response: vector of length n
<code>x</code>	covariates: matrix with n rows (samples) and $k * p$ columns (variables)
<code>args</code>	options for paired lasso: list of arguments (output from <code>.dims</code> and <code>.args</code>)

Value

list of glmnet-like objects

Examples

NA

`.folds`*Cross-validation folds*

Description

Assigns samples to cross-validation folds, balancing the folds in the case of a binary or survival response.

Usage`.folds(y, n folds, foldid = NULL)`**Arguments**

<code>y</code>	response: vector of length n
<code>n folds</code>	number of folds: positive integer (≥ 10 recommended)
<code>foldid</code>	fold identifiers: vector of length n , with entries from 1 to <code>n folds</code>

Value

Returns the fold identifiers.

Examples

NA

.loss *Cross-validation loss*

Description

Calculates mean cross-validated loss

Usage

```
.loss(y, fit, family, type.measure, foldid = NULL)
```

Arguments

y	response: vector of length n
fit	matrix with one row for each sample ("gaussian", "binomial" and "poisson"), or one row for each fold (only "cox"), and one column for each lambda (output from .fit)
family	model family: character "gaussian", "binomial", "poisson", or "cox"
type.measure	... loss function: character "deviance", "mse", "mae", "class", or "auc"
foldid	fold identifiers: vector of length n , with entries from 1 to nolds

Value

Returns list of vectors, one for each model.

Examples

NA

<code>.weight</code>	<i>Weighting schemes</i>
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Description

Calculates the weighting schemes.

Usage

```
.weight(cor, args)
```

Arguments

<code>cor</code>	correlation coefficients: list of k vectors of length p (one vector for each covariate set with one entry for each covariate)
<code>args</code>	options for paired lasso: list of arguments (output from <code>.dims</code> and <code>.args</code>)

Value

list of named vectors (one for each weighting scheme)

Examples

```
NA
```

arguments	<i>Arguments for "palasso"</i>
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Description

This page lists the arguments for the (internal) "palasso" function(s).

Arguments

<code>y</code>	response: vector of length n
<code>X</code>	covariates: list of matrices, each with n rows (samples) and p columns (variables)
<code>max</code>	maximum number of non-zero coefficients: positive numeric, or NULL (no sparsity constraint)
<code>...</code>	further arguments for <code>cv.glmnet</code> or <code>glmnet</code>
<code>x</code>	covariates: matrix with n rows (samples) and $k * p$ columns (variables)
<code>args</code>	options for paired lasso: list of arguments (output from <code>.dims</code> and <code>.args</code>)
<code>nfolds</code>	number of folds: positive integer (≥ 10 recommended)

<code>foldid</code>	fold identifiers: vector of length n , with entries from 1 to <code>nfolds</code>
<code>cor</code>	correlation coefficients: list of k vectors of length p (one vector for each covariate set with one entry for each covariate)
<code>lambda</code>	lambda sequence: vector of decreasing positive values
<code>family</code>	model family: character "gaussian", "binomial", "poisson", or "cox"
<code>type.measure</code>	... loss function: character "deviance", "mse", "mae", "class", or "auc"
<code>fit</code>	matrix with one row for each sample ("gaussian", "binomial" and "poisson"), or one row for each fold (only "cox"), and one column for each lambda (output from <code>.fit</code>)
<code>cvm</code>	mean cross-validated loss: vector of same length as lambda (output from <code>.loss</code>)

 methods

Methods for class "palasso"

Description

This page lists the main methods for class "palasso".

Usage

```
## S3 method for class 'palasso'
predict(object, newdata, model = "paired", s = "lambda.min", max = NULL, ...)

## S3 method for class 'palasso'
coef(object, model = "paired", s = "lambda.min", max = NULL, ...)

## S3 method for class 'palasso'
weights(object, model = "paired", max = NULL, ...)

## S3 method for class 'palasso'
fitted(object, model = "paired", s = "lambda.min", max = NULL, ...)

## S3 method for class 'palasso'
residuals(object, model = "paired", s = "lambda.min", max = NULL, ...)

## S3 method for class 'palasso'
deviance(object, model = "paired", max = NULL, ...)

## S3 method for class 'palasso'
logLik(object, model = "paired", max = NULL, ...)

## S3 method for class 'palasso'
summary(object, model = "paired", ...)
```

Arguments

object	palasso object
newdata	covariates: list of matrices, each with n rows (samples) and p columns (variables)
model	character "paired", or an entry of names(object)
s	penalty parameter: character "lambda.min" or "lambda.1se", positive numeric, or NULL (entire sequence)
max	maximum number of non-zero coefficients, positive integer, or NULL
...	further arguments for predict.cv.glmnet , coef.cv.glmnet , or deviance.glmnet

Details

By default, the function `predict` returns the linear predictor (`type="link"`). Consider predicting the response (`type="response"`).

See Also

Use [palasso](#) to fit the paired lasso.

palasso	<i>Paired lasso</i>
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Description

The function `palasso` fits the paired lasso. Use this function if you have *paired covariates* and want a *sparse model*.

Usage

```
palasso(y = y, X = X, max = 10, ...)
```

Arguments

y	response: vector of length n
X	covariates: list of matrices, each with n rows (samples) and p columns (variables)
max	maximum number of non-zero coefficients: positive numeric, or NULL (no sparsity constraint)
...	further arguments for cv.glmnet or glmnet

Details

Let x denote one entry of the list X . See [glmnet](#) for alternative specifications of y and x . Among the further arguments, family must equal "gaussian", "binomial", "poisson", or "cox", and `penalty.factor` must not be used.

Hidden arguments: Deactivate adaptive lasso by setting `adaptive` to FALSE, activate standard lasso by setting `standard` to TRUE, and activate shrinkage by setting `shrink` to TRUE.

Value

This function returns an object of class `palasso`. Available methods include `predict`, `coef`, `weights`, `fitted`, `residuals`, `deviance`, `logLik`, and `summary`.

References

A Rauschenberger, I Ciocanea-Teodorescu, RX Menezes, MA Jonker, and MA van de Wiel (2020). "Sparse classification with paired covariates." *Advances in Data Analysis and Classification*. 14:571-588. doi: [10.1007/s11634019003756](https://doi.org/10.1007/s11634019003756), [pdf](#), <armin.rauschenberger@uni.lu>

Examples

```
set.seed(1)
n <- 50; p <- 20
y <- rbinom(n=n,size=1,prob=0.5)
X <- lapply(1:2,function(x) matrix(rnorm(n*p),nrow=n,ncol=p))
object <- palasso(y=y,X=X,family="binomial") # adaptive=TRUE,standard=FALSE
names(object)
```

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