

Package ‘GSQR’

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Type Package

Title Group Penalized Smooth Quantile Regression

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Description

This package implements a blockwise-majorization-decent for group quantile regression(BMD-SQR), for efficiently computing the solution paths of the group-lasso penalized quantile regression, the group-Mcp penalized quantile regression, the group-Scad penalized quantile regression and theirs approximations.

License GPL-2

NeedsCompilation yes

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 GSQR-package

Group Penalized Smooth Quantile Regression

Description

This package implements a blockwise-majorization-decent for group quantile regression(BMD-SQR), for efficiently computing the solution paths of the group-lasso penalized quantile regression, the group-Mcp penalized quantile regression, the group-Scad penalized quantile regression and theirs approximations.

Details

The DESCRIPTION file:

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Package:      GSQR
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Title:        Group Penalized Smooth Quantile Regression
Version:      1.2
Date:         2017-11-17
Author:       Mohamed Ouhourane, Yi Yang, Karim Oualkacha
Maintainer:   Mohamed Ouhourane <mohamed.ouhourane@gmail.com>
Description:  This package implements a blockwise-majorization-decent for group quantile regression(BMD-SQR), f
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```

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coef.cv.Gsqr	get coefficients or make coefficient predictions from a "cv.Gsqr" object.
cv.Gsqr	Cross-validation for Gsqr
plot.Gsqr	Plot solution paths from a "Gsqr" object
predict.Gsqr	Outputs predicted responses from an SGL model for new observations
predict.cv.Gsqr	make predictions from a "cv.Gsqr" object.

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Mohamed Ouhourane "Group Penalized Smooth Quantile Regression"

bardet

Simplified gene expression data from Scheetz et al. (2006)

Description

Gene expression data (20 genes for 120 samples) from the microarray experiments of mammalian eye tissue samples of Scheetz et al. (2006).

Usage

```
data(bardet)
```

Details

This data set contains 120 samples with 100 predictors (expanded from 20 genes using 5 basis B-splines, as described in Yang, Y. and Zou, H. (2012)).

Value

A list with the following elements:

- x a [120 x 100] matrix (expanded from a [120 x 20] matrix) giving the expression levels of 20 filtered genes for the 120 samples. Each row corresponds to a subject, each 5 consecutive columns to a grouped gene.
- y a numeric vector of length 120 giving expression level of gene TRIM32, which causes Bardet-Biedl syndrome.

References

Scheetz, T., Kim, K., Swiderski, R., Philp, A., Braun, T., Knudtson, K., Dorrance, A., DiBona, G., Huang, J., Casavant, T. et al. (2006), "Regulation of gene expression in the mammalian eye and its relevance to eye disease", *Proceedings of the National Academy of Sciences* **103**(39), 14429-14434.

Huang, J., S. Ma, and C.-H. Zhang (2008). "Adaptive Lasso for sparse high-dimensional regression models". *Statistica Sinica* 18, 1603-1618.

Yang, Y. and Zou, H. (2012), "A Fast Unified Algorithm for Computing Group-Lasso Penalized Learning Problems," *Statistics and Computing*. Accepted.

Examples

```
# load GSQR library
library(GSQR)

# load data set
data(bardet)

# how many samples and how many predictors ?
dim(bardet$x)

# repsonse y
bardet$y
```

coef.cv.Gsqr	<i>get coefficients or make coefficient predictions from a "cv.Gsqr" object.</i>
--------------	--

Description

This function gets coefficients or makes coefficient predictions from a cross-validated Gsqr model, using the stored "Gsqr" object, and the optimal value chosen for lambda.

Arguments

cv	fitted cv.Gsqr object.
s	value(s) of the penalty parameter lambda at which predictions are required. Default is the value s="lambda.1se" stored on the CV object, it is the largest value of lambda such that error is within 1 standard error of the minimum. Alternatively s="lambda.min" can be used, it is the optimal value of lambda that gives minimum cross validation error cvm.

Details

This function makes it easier to use the results of cross-validation to get coefficients or make coefficient predictions.

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Karim Oulkacha: "Group Penalized Smooth Quantile Regression"

Examples

```
data(bardet)
group <- rep(1:20,each=5)
cv <- cv.Gsqr(x=bardet$x,y=bardet$y,group=group,method="GLasso",check="f1",taux=0.5)
coef.cv.Gsqr(cv,s = "lambda.1se")
```

coef.Gsqr	<i>get coefficients or make coefficient predictions from an "Gsqr" object.</i>
-----------	--

Description

Computes the coefficients at the requested values for lambda from a fitted [Gsqr](#) object.

Usage

```
coef.Gsqr(object, s = NULL, ...)
```

Arguments

object	fitted Gsqr model object.
s	value(s) of the penalty parameter lambda at which predictions are required. Default is the entire sequence used to create the model.
...	not used. Other arguments to predict.

Details

s is the new vector at which predictions are requested. If s is not in the lambda sequence used for fitting the model, the coef function will use linear interpolation to make predictions. The new values are interpolated using a fraction of coefficients from both left and right lambda indices.

Value

The coefficients at the requested values for lambda.

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Karim Oulkacha: "Group Penalized Smooth Quantile Regression"

Examples

```
data(bardet)
group <- rep(1:20,each=5)
fit <- Gsqr(x=bardet$x,y=bardet$y,group=group,method="GLasso",check="f1",taux=0.5)
coef(fit)
```

cv.Gsqr

*Cross-validation for Gsqr***Description**

Does k-fold cross-validation for Gsqr.

Usage

```
cv.Gsqr(x, y, group, Kfold = 5, delta, tau = 0.5, check = c("f1", "f2"), gamm = ifelse(method == "GMcp",
```

Arguments

x	matrix of predictors, of dimension $N \times p$; each row is an observation vector.
y	response variable: vector of N observations.
group	a vector of consecutive integers describing the grouping of the coefficients (see example below).
Kfold	number of folds - default is 5. Although nfolds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is nfolds=3.
delta	the parameter δ in the approximation check function . Default is 2.
tau	quantile to be targeted. Must be in (0,1).
check	a character string specifying the ccheck function approximation to use, valid options are: <ul style="list-style-type: none"> • "f1": the check function 1, • "f2": the check function 2. Default is "f1".
gamm	regularization parameter for the Group Scad or Group Mcp penalty of the coefficients
method	a character string specifying the function penalty to use, valid options are: <ul style="list-style-type: none"> • "GLasso": the group Lasso penalty, • "GScad": the group SCAD penalty, • "GMcp": the group MCP penalty, • "AGScad": the approximate group SCAD penalty, • "AGMcp": the approximate group MCP penalty, Default is GLasso.
plot.it	plot cross-validation the error
...	other arguments that can be passed to gglasso.

Details

The function runs Gsqr Kfold+1 times; the first to get the lambda sequence, and then the remainder to compute the fit with each of the folds omitted. The average error and standard deviation over the folds are computed.

Value

an object of class `cv.Gsqr` is returned, which is a list with the ingredients of the cross-validation fit.

<code>cv</code>	the mean cross-validated error - a vector of length
<code>cv.error</code>	estimate of standard error of <code>cv</code> .
<code>finalfit</code>	An object with S3 class <code>Gsqr</code> .
<code>all.folds</code>	The folds used in cross-validation.
<code>lambda</code>	the values of <code>lambda</code> used in the fits.

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Karim Oulkacha: "Group Penalized Smooth Quantile Regression"

Examples

```
data(bardet)
group <- rep(1:20, each=5)
fit <- cv.Gsqr(x=bardet$x, y=bardet$y, group=group, method="GLasso", check="f1", taux=0.5)
```

Gsqr

Fits the regularization paths for group penalized quantile regression

Description

Fits a regularization path for the group penalized quantile regression at a sequence of regularization parameters `lambda`.

Usage

```
Gsqr(x, y, group = NULL, method = c("GLasso", "SGLasso", "GMcp", "GScad", "AGMcp", "AGScad"), check =
```

Arguments

<code>x</code>	matrix of predictors, of dimension $N \times p$; each row is an observation vector.
<code>y</code>	response variable: vector of N observations.
<code>group</code>	a vector of consecutive integers describing the grouping of the coefficients (see example below).
<code>method</code>	a character string specifying the function penalty to use, valid options are: <ul style="list-style-type: none"> "GLasso": the group Lasso penalty, "GScad": the group SCAD penalty,

	<ul style="list-style-type: none"> • "GMcp": the group MCP penalty, • "AGScad": the approximate group SCAD penalty, • "AGMcp": the approximate group MCP penalty, <p>Default is "GLasso".</p>
check	<p>a character string specifying the ckeck function approximation to use, valid options are:</p> <ul style="list-style-type: none"> • "f1": the check function 1, • "f2": the check function 2. <p>Default is "f1".</p>
nlambda	the number of lambda values - default is 100.
maxit	maximum number of outer-loop iterations allowed at fixed lambda value. Default is 3e8. If models do not converge, consider increasing maxit.
lambda.factor	The factor for getting the minimal lambda in lambda sequence, where $\min(\lambda) = \lambda.factor * \max(\lambda)$. $\max(\lambda)$ is the smallest value of lambda for which all coefficients are zero. The default depends on the relationship between N (the number of rows in the matrix of predictors) and p (the number of predictors). If $N > p$, the default is 0.0001, close to zero. If $N < p$, the default is 0.01. A very small value of lambda.factor will lead to a saturated fit. It takes no effect if there is user-defined lambda sequence.
lambda	a user supplied lambda sequence. Typically, by leaving this option unspecified users can have the program compute its own lambda sequence based on nlambda and lambda.factor. Supplying a value of lambda overrides this. It is better to supply a decreasing sequence of lambda values than a single (small) value, if not, the program will sort user-defined lambda sequence in decreasing order automatically.
pf	penalty factor, a vector in length of bn (bn is the total number of groups). Separate penalty weights can be applied to each group of β s to allow
dfmax	limit the maximum number of groups in the model. Useful for very large bs (group size), if a partial path is desired. Default is bs+1.
pmax	limit the maximum number of groups ever to be nonzero. For example once a group enters the model, no matter how many times it exits or re-enters model through the path, it will be counted only once. Default is $\min(dfmax*1.2, bs)$.
eps	convergence termination tolerance. Defaults value is 1e-8.
gamm	regularization parameter for the Group Scad or Group Mcp penalty of the coefficients
taux	quantile to be targeted. Must be in (0,1).
delta	the parameter δ in the approximation check function . Default is 2.
intercept	Whether to include intercept in the model. Default is TRUE.

Value

b0	intercept sequence of length $\text{length}(\lambda)$
beta	a $p \times \text{length}(\lambda)$ matrix of coefficients, stored as a sparse matrix class
lambda	the actual sequence of lambda values used

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Karim Oulkacha: "Group Penalized Smooth Quantile Regression"

Examples

```
data(bardet)
group <- rep(1:20,each=5)
fit <- Gsqr(x=bardet$x,y=bardet$y,group=group,method="GLasso",check="f1",taux=0.5)
plot(fit)
```

plot.Gsqr

Plot solution paths from a "Gsqr" object

Description

Produces a coefficient profile plot of the coefficient paths for a fitted [Gsqr](#) object.

Usage

```
## S3 method for class 'Gsqr'
plot(x, group = FALSE, log.l = TRUE, ...)
```

Arguments

x	fitted Gsqr model
group	what is on the Y-axis. Plot the norm of each group if TRUE. Plot each coefficient if FALSE.
log.l	what is on the X-axis. Plot against the log-lambda sequence if TRUE. Plot against the lambda sequence if FALSE.
...	other graphical parameters to plot

Details

A coefficient profile plot is produced.

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Karim Oulkacha: "Group Penalized Smooth Quantile Regression"

Examples

```
data(bardet)
group <- rep(1:20,each=5)
fit <- Gsqr(x=bardet$x,y=bardet$y,group=group,method="GLasso",check="f1",taux=0.5)
plot(fit)
```

predict.cv.Gsqr	<i>make predictions from a "cv.Gsqr" object.</i>
-----------------	--

Description

This function makes predictions from a cross-validated Gsqr model, using the stored "Gsqr" object, and the optimal value chosen for lambda.

Usage

```
predict.cv.Gsqr(cv, newx, s = c("lambda.1se", "lambda.min"), ...)
```

Arguments

cv	fitted cv.Gsqr object.
newx	matrix of new values for x at which predictions are to be made. Must be a matrix. See documentation for predict.Gsqr.
s	value(s) of the penalty parameter lambda at which predictions are required. Default is the value s="lambda.1se" stored on the CV object. Alternatively s="lambda.min" can be used
...	not used. Other arguments to predict.

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Karim Oulkacha: "Group Penalized Smooth Quantile Regression"

Examples

```
data(bardet)
group <- rep(1:20,each=5)
cv <- cv.Gsqr(x=bardet$x,y=bardet$y,group=group,method="GLasso",check="f1",taux=0.5)
predict.cv.Gsqr(cv,bardet$x,s = "lambda.1se")
```

predict.Gsqr	<i>Outputs predicted responses from an SGL model for new observations</i>
--------------	---

Description

Outputs predicted response values for new user input observations at a specified s value

Usage

```
predict.Gsqr(object, newx, s = NULL)
```

Arguments

object	fitted "GSQR" object
newx	covariate matrix for new observations whose responses we wish to predict
s	the index of the lambda value for the model with which we desire to predict

Value

prediction vector of news

Author(s)

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References

Mohamed Ouhourane, Yi Yang, Karim Oulkacha: "Group Penalized Smooth Quantile Regression"

Examples

```
data(bardet)
group <- rep(1:20, each=5)
fit <- Gsqr(x=bardet$x, y=bardet$y, group=group, method="GLasso", check="f1", tau=0.5)
predict(fit, bardet$x)
```

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