Package ‘lol’

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Description

Various optimization methods for Lasso inference with matrix wrapper.

Details

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Author(s)

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References


See Also

lasso, matrixLasso

Examples

```r
data(chin07)
data <- list(y=t(chin07$ge), x=t(chin07$cn))
res <- matrixLasso(data, method='cv', nFold=5)
res
```

Description

A subset of breast cancer data as used in Yuan et al. (to be submitted).
getLambdaNcoef

Usage

data(chin07)

Format

A list object of two named data matrices, cn: DNA copy number, ge: RNA expression. The matrices columns are samples and rows are probes/variables.

Details

Genome-wide copy number data was merged using CGHregions resulting in 339 regions across 106 samples. Expression data are 7 probes mapped to important breast cancer genes such as CCNE2, MYC, etc, also of 106 samples.

References


Examples

data(chin07)
gain <- rowSums(chin07$cn >= .2)
loss <- -rowSums(chin07$cn <= -.2)
plotGW(data=cbind(gain, loss), pos=attr(chin07$cn, 'chrome'), legend=c('gain', 'loss'))

getLambdaNcoef

get the lambda value that yield certain number of non-zero coefficients

Description

get the lambda value that yield certain number of non-zero coefficients

Usage

getLambdaNcoef(y, x, lambda1, nCoef, track=FALSE, model='linear', standardize=FALSE)

Arguments

y A vector of expressions
x a matrix of CN variables
lambda1 minimum lambda to use
nCoef the number of coefficients to get
track logical value for tracking the progress
model which model to use, default to 'linear'
standardize standardize the data or not
lasso

Value

lambda  The lambda value that gives approximate same number of non-zero coefficients as required

Author(s)

Yinyin Yuan

See Also

lasso

Examples

data(chin07)
data <- list(y=chin07$ge[1,], x=t(chin07$cn))getLambdaNcoef(data$y, data$x, lambda1=.1, nCoef=10, track=TRUE)

Description

Lasso penalized linear regression with different optimizers

Usage

lasso(y, ...)

Arguments

y  A list object of one of the four classes: 'cv', 'stability', 'multiSplit', and 'simultaneous'. If x is NULL then y should a list of two components y and x, y is a vector of expression and x is a matrix containing copy number variables

...  other parameters

Details

The function contains various optimization methods for Lasso inference, such as cross-validation, randomised lasso, simultaneous lasso etc. It is specifically designed for multicollinear predictor variables.

Value

Varied depending on the optimizer used. Generally it contains

beta  coefficients
residuals  residuals of regression model
fit  the corresponding fit of regression
lasso.cv

Author(s)
Yinyin Yuan

References

See Also
matrixLasso

Examples
data(chin07)
data <- list(y=chin07$ge[1,], x=t(chin07$cn))
class(data) <- 'cv'
res <- lasso(data)

---

lasso.cv

Cross validation optimizer for lasso

Description
Cross validation lasso. This function optimizes the lasso solution for correlated regulators by an algorithm. This algorithm chooses the minimum lambda since the penalized package by default use 0 for the minimum, which sometimes take a long time to compute

Usage
lasso.cv(y, x=NULL, lambda1=NULL, model='linear', steps=15, minsteps=5, log=TRUE, track=FALSE, standardize=FALSE)

Arguments
y A vector of gene expression of a probe, or a list object if x is NULL. In the latter case y should a list of two components y and x. y is a vector of expression and x is a matrix containing copy number variables
x Either a matrix containing CN variables or NULL
lambda1 minimum lambda to use
model which model to use, one of "cox", "logistic", "linear", or "poisson". Default to 'linear'
steps parameter to be passed to penalized
minsteps parameter to be passed to penalized
log parameter to be passed to penalized
track parameter to be passed to penalized
standardize parameter to be passed to penalized
lasso.multiSplit

Description

Multi-split lasso as described in Meinshausen 2009

Usage

lasso.multiSplit(y, x=NULL, lambda1=NULL, nSubsampling=200, model='linear', alpha=0.05, gamma.min=0.05, gamma.max=0.95, track=FALSE, ...)

unpenalized

nFold

nMaxiter

... other parameter to be passed to penalized

Value

A list object of class 'lol', consisting of:

fit

The final sparse regression fit

beta

the coefficients, non-zero ones are significant

lambda

the penalty parameter lambda used

residuals

regression residuals

conv

logical value indicating whether the optimization has converged

Author(s)

Yinyin Yuan

References

Goeman, J. J. (2009), L1 penalized estimation in the cox proportional hazards model, Biometrical Journal.

See Also

lasso

data(chin07)
data <- list(y=chin07$ge[1,], x=t(chin07$cn), nFold=5)
res <- lasso.cv(data)
res
lasso.multiSplit

Arguments

y  A vector of gene expression of a probe, or a list object if x is NULL. In the latter
case y should a list of two components y and x, y is a vector of expression and x
is a matrix containing copy number variables

x  Either a matrix containing CN variables or NULL

nSubsampling  number of splits, default to 200

model  which model to use, one of "cox", "logistic", "linear", or "poisson". Default to
"linear"

alpha  specify significant level to determine the non-zero coefficients in the range of 0
and 1, default to 0.05

gamma.min  the lower bound of gamma

gamma.max  the higher bound of gamma

lambda1  minimum lambda to be used, if known

track  track progress

...  other parameters to be passed to lass.cv

Details

This function performs the multi-split lasso as proposed by Meinshausen et al. 2009. The samples
are first randomly split into two disjoint sets, one of which is used to find non-zero coefficients
with a regular lasso regression, then these non-zero coefficients are fitted to another sample set with
OLS. The resulting p-values after multiple runs can then be aggregated using quantiles.

Value

A list object of class 'lol', consisting of:

beta  coefficients

mat  the Q_gamma matrix as described in the paper

residuals  residuals, here is only the input y

pmat  the adjusted p matrix as described in the paper

Author(s)

Yinyin Yuan

References

Nicolai Meinshausen, Lukas Meier and Peter Buehlmann (2009), P-values for high-dimensional

See Also

lasso

Examples

data(chin07)
data <- list(y=chin07$ge[,1], x=t(chin07$cn))
res <- lasso.multiSplit(data, nSubsampling=50)
res
lasso.simultaneous

Simultaneous lasso

Description
The function performs lasso with multiple random sample splits, selecting coefficients that are simultaneously non-zero in both subsets of samples.

Usage
lasso.simultaneous(y, x=NULL, model='linear', nSubsampling=200, alpha=.5, lambda1=NULL, track=FALSE, ...)

Arguments
- y: A vector of gene expression of a probe, or a list object if x is NULL. In the latter case y should a list of two components y and x, y is a vector of expression and x is a matrix containing copy number variables.
- x: Either a matrix containing CN variables or NULL.
- model: which model to use, one of "cox", "logistic", "linear", or "poisson". Default to 'linear'.
- nSubsampling: The number of random permutations, both on sample splitting and on variable scaling, default to 200.
- alpha: weakness parameter: control the shrinkage of regulators. The lower alpha is, the bigger the vanishing effect on small coefficients.
- lambda1: minimum lambda, default to NULL.
- track: logical value, whether to track the progress.
- ...: Other parameters to be passed to the penalized function.

Details
In each run the function splits samples randomly to two equal sets, run lasso on both sets, then select those coefficients that are simultaneously non-zero across two sets. Finally the results across many runs are summarized as the frequency of selected predictors - the higher the frequency the more confidence that the corresponding predictors are significant.

Value
A list object of class 'lol', consisting of:
- beta: Coefficient vector.
- n: Number of actual subsampling, should be equal or smaller than nSubsampling in case of failing.
- mat: result matrix of the subsampling.

Author(s)
Yinyin Yuan
lasso.stability

References


See Also

lasso

Examples

data(chin07)
data <- list(y=chin07$ge[1,], x=t(chin07$cn))
res <- lasso.simultaneous(data, nSubsampling=50)
res

lasso.stability

Stability and randomised lasso

Description

point-wise controled lasso stability selection

Usage

lasso.stability(y, x=NULL, alpha=.5, subsampling=.5, nSubsampling=200, model="linear", pi_th=.6, alpha.fwer=1, lambda1=NULL, steps=10, track=FALSE, standardize=FALSE, ...)

Arguments

y 
A vector of gene expression of a probe, or a list object if x is NULL. In the latter case y should a list of two components y and x, y is a vector of expression and x is a matrix containing copy number variables

x
Either a matrix containing CN variables or NULL

alpha
weakness parameter: control the shrinkage of regulators, if alpha = 1 then no randomisation, if NULL then a randomly generated vector is used

subsampling
fraction of samples to use in the sampling process, default to 0.5

nSubsampling
The number of subsampling to do, default to 200

model
which model to use, one of "cox", "logistic", "linear", or "poisson". Default to 'linear'

pi_th
The threshold of the stability probability for selecting a regulator. It is to determine whether a coefficient is non-zero based on the frequency it is subsampled to be non-zero, default to 0.6

alpha.fwer
Parameter to control for the FWER, choosing alpha.fwer and alpha control the E(V), V being the number of noise variables, eg. when alpha=0.9, alpha.fwer = 1 control the E(V)<=1

lambda1
minimum lambda to use

steps
parameter to be passed on to penalized

track
track the progress, 0 none tracking, 1 minimum amount of information and 2 full information

standardize
standardize the data or not?

...
Details

The function first selects lambda that approximately give maximum $\sqrt{.8p}$ predictors, while $p$ is the number of total predictors. Then it runs lasso a number of times keeping lambda fixed. These runs are randomised with scaled predictors and subsamples. At the end, the non-zero coefficients are determined by their frequencies of selections.

Value

A list object of class `lol`, consisting of:

- **beta**: coefficients
- **beta.bin**: binary beta vector as thresholded by $\pi_{th}$
- **mat**: the sampling matrix, each column is the result of one sampling
- **residuals**: residuals of regression model

Author(s)

Yinyin Yuan

References


See Also

lasso

Examples

```r
data(chin07)
data <- list(y=chin07$ge[1,], x=t(chin07$cn))
res <- lasso.stability(data, nSubsampling=50)
res
```

---

**lmMatrixFit**

*Multiple lm fit for penalized regressions*

Description

Refit the regressions given matrices of responses, predictors, and the coefficients/interactions matrix. This is typically used after the lasso, since the coefficients were shrinked.

Usage

```r
lmMatrixFit(y, x = NULL, mat, th = NULL)
```
matrixLasso

Arguments

y  
Input response matrix, typically expression data with genes/variables in columns and samples/measurements in rows. Or when input x is NULL, y should be an object of two lists: y: expression data and x: copy number data.

x  
Input predictor matrix, typically copy number data, genes/predictors in columns and samples/measurements in rows. Can be NULL.

mat  
Coefficient matrix, number of columns is the number of predictors (y) and number of rows is the number of responses (x).

th  
The threshold to use in order to determine which coefficients are non-zero, so the corresponding predictors are used.

Value

coefMat  
A coefficient matrix, rows are responses and columns are predictors.

resMat  
A residual matrix, each row is the residuals of a response.

pvalMat  
Matrix of p-values for each coefficients.

Author(s)

Yinyin Yuan

See Also

lm, matrixLasso

Examples

data(chin07)
data <- list(y=t(chin07$ge), x=t(chin07$cn))
res <- matrixLasso(data, method='cv', nFold=5)
res
res.lm <- lmMatrixFit(y=data, mat=abs(res$coefMat), th=0.01)
res.lm

matrixLasso  
A wrapper function for matrix-to-matrix Lasso regressions

Description

This function wraps up different types of lasso optimizers and perform multiple, independent lasso inference on matrix responses. If the dimensionality of the input is small, the function converts the matrix of input response into a vector and solves the problem with one lasso inference. Otherwise, lasso regression is performed independently for each variables in the response matrix.

Usage

matrixLasso(y, x=NULL, method='cv', nameControl=FALSE, standardize=FALSE, track=0, lambda1=NULL, nFold=10, ...)


**matrixLasso**

**Arguments**

- **y**: Input response matrix, typically expression data with genes/variables in columns and samples/measurements in rows. Or when input x is NULL, y should be an object of two lists: y: expression data and x: copy number data.

- **x**: Input predictor matrix, typically copy number data, genes/predictors in columns and samples/measurements in rows. Can be missing if the data is input to y.

- **method**: Which optimization method to use for lasso inference, such as 'cv', 'stability', 'simultaneous', and 'multiSplit'.

- **nameControl**: If the same item appears in both responses and predictors, the regression should remove the one same as the response from the predictors. This happens when for example a single data type is use for inferring gene network from expression data. Enable nameControl in this case.

- **standardize**: Option to standardize the data, default to TRUE.

- **track**: Option to display progress, default to 0, 1 gives a brief summary of each fit, and 2 gives the full detail.

- **lambda1**: The minimum lambda to use, default to NULL for which the program will select it automatically.

- **nFold**: Number of folds for cross-validation, default to 10

**Value**

- **coefMat**: A coefficient matrix, rows are responses and columns are predictors.

- **fit**: If only a single regression is used for matrix lasso, the fit return.

- **resMat**: A residual matrix, each row is the residuals of a response.

**Author(s)**

Yinyin Yuan

**See Also**

lasso

**Examples**

```r
data(chin07)
data <- list(y=t(chin07$ge), x=t(chin07$cn))
res <- matrixLasso(data, method='cv', nFold=5)
res
```
**plotGW**

*Plot genome-wide data along the genome*

**Description**

Plot different measurements across the genome such as copy number amplifications and deletions.

**Usage**

```
plotGW(data, pos, marks=NULL, fileType='png', file='plotGW', width=1000, height=500, autoscale=FALSE, col=c('lightblue', 'lightgreen', 'darkblue', 'darkgreen'), legend=1:10, ylab='', pch=19, cex.axis=1.2, cex.lab=1.2, cex=0.5, legend.pos='bottomright', mtext=NULL, mtext.side=2, mtext.at=NULL, mtext.line=3, ...)
```

**Arguments**

- **data**: data matrix to plot, each column is plotted individually across the genome
- **pos**: the chromosome locations for the data, can be a matrix or data frame with a column named chromosome_name, or a numeric vector
- **marks**: if there is specific marks to plot on the baseline, eg. to indicate where are the SNPs, should be a vector of numbers indicating where the marks is relative to the input data matrix
- **fileType**: either png or pdf file type
- **file**: file name
- **width**: width of the plot
- **height**: height of the plot
- **autoscale**: should the columns of data be scaled?
- **col**: colors for each of the data columns to be plotted, should be no shorter than the number of columns in 'data'
- **legend**: legend text in the legend box
- **ylab**: parameter for par, default to "
- **pch**: parameter for par, default to 19
- **cex.axis**: parameter for par, default to 1.2
- **cex.lab**: parameter for par, default to 1.2
- **cex**: parameter for par, default to 0.5
- **legend.pos**: parameter for legend, default to 'bottomright'
- **mtext**: parameter for mtext, default to NULL
- **mtext.side**: parameter for mtext, default to 2
- **mtext.at**: parameter for mtext, default to 2
- **mtext.line**: parameter for mtext, default to 3
- **...**: Other parameters to pass to plot() or legend()

**Details**

This function requires as input data a vector or a matrix with different variables in columns, and a position matrix of chromosome name and start position. The number of rows in the position matrix should be the same as the length of the data vector or the number of rows of the data matrix. The function plots the data according to the position across the genome, providing a genome-wide description.
Value

Write an image file to disk, either in png or pdf format.

Author(s)

Yinyin Yuan

See Also

lasso.cv

Examples

data(chin07)
gain <- rowSums(chin07$cn >= .2)
loss <- -rowSums(chin07$cn <= -.2)
plotGW(data=cbind(gain, loss), pos=attr(chin07$cn, 'chrome'), legend=c('gain', 'loss'))

print.lol

Description

print function for class lol

Usage

print.lol(x,...)

Arguments

x an object of class lol

... other parameters for consistency

Author(s)

Yinyin Yuan
Description

print function for class lolMatrix

Usage

print.lolMatrix(x, ...)

Arguments

x an object of class lolMatrix
...
other parameters for consistency

Author(s)

Yinyin Yuan
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