Package 'RLassoCox'

December 24, 2024

Type Package

Title A reweighted Lasso-Cox by integrating gene interaction information

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Depends R (>= 4.1), glmnet

Imports Matrix, igraph, survival, stats

Description RLassoCox is a package that implements the RLasso-Cox model proposed by Wei Liu. The RLasso-Cox model integrates gene interaction information into the Lasso-Cox model for accurate survival prediction and survival biomarker discovery. It is based on the hypothesis that topologically important genes in the gene interaction network tend to have stable expression changes. The RLasso-Cox model uses random walk to evaluate the topological weight of genes, and then highlights topologically important genes to improve the generalization ability of the Lasso-Cox model. The RLasso-Cox model has the advantage of identifying small gene sets with high prognostic performance on independent datasets, which may play an important role in identifying robust survival biomarkers for various cancer types.

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biocViews Survival, Regression, GeneExpression, GenePrediction, Network

BugReports https://github.com/weiliu123/RLassoCox/issues

BiocType Software

Suggests knitr

VignetteBuilder knitr

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Contents

`RLassoCox-package` *A reweighted Lasso-Cox by integrating gene interaction information*

Description

RLassoCox is a package that implements the RLasso-Cox model proposed by Wei Liu. The RLasso-Cox model integrates gene interaction information into the Lasso-Cox model for accurate survival prediction and survival biomarker discovery. It is based on the hypothesis that topologically important genes in the gene interaction network tend to have stable expression changes. The RLasso-Cox model uses random walk to evaluate the topological weight of genes, and then highlights topologically important genes to improve the generalization ability of the Lasso-Cox model. The RLasso-Cox model has the advantage of identifying small gene sets with high prognostic performance on independent datasets, which may play an important role in identifying robust survival biomarkers for various cancer types.

Details

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Index: This package was not yet installed at build time.
Very simple to use. Accepts x,y data for the RLasso-Cox model, and makes predictions for new samples.

`RLassoCox` A rewighted Lasso-Cox model for survival prediction and biomarker discovery. `predict.RLassoCox` This function predicts the risk of new samples from a fitted `RLasso-Cox` model. `cvRLassoCox` Does k-fold cross-validation for the RLasso-Cox model, produces a plot, and returns a value for lambda `predict.cvRLassoCox` This function makes predictions from a cross-validated RLasso-Cox model, using the optimal value chosen for lambda.

Author(s)

Wei Liu [cre, aut] (<https://orcid.org/0000-0002-5496-3641>)

Maintainer: Wei Liu <freelw@qq.com>

References

Integration of gene interaction information into a reweighted Lasso-Cox model for accurate survival prediction. To be published.

Examples

```
library("survival")
library("igraph")
library("glmnet")
library("Matrix")

data(dGMMirGraph)
data(mRNA_matrix)
data(survData)

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(2/3*dim(mRNA_matrix)[1]))
testSmpl.Idx <- setdiff(1:dim(mRNA_matrix)[1], trainSmpl.Idx)
trainSmpl <- mRNA_matrix[trainSmpl.Idx ,]
testSmpl <- mRNA_matrix[testSmpl.Idx ,]

res <- RLassoCox(x=trainSmpl, y=survData[trainSmpl.Idx ,],
                 globalGraph=dGMMirGraph)
lp <- predict(object = res, newx = testSmpl)

cv.res <- cvRLassoCox(x=trainSmpl, y=survData[trainSmpl.Idx ,],
                        globalGraph=dGMMirGraph, nfolds = 5)
cv.lp <- predict(object = cv.res, newx = testSmpl,
                            s = "lambda.min")
```

`cvRLassoCox` *Cross-validation for the RLasso-Cox model*

Description

Does k-fold cross-validation for the RLasso-Cox model, produces a plot, and returns a value for lambda

Usage

```
cvRLassoCox(x, y, globalGraph = NULL, nfolds = 10, Gamma = 0.3,
            DEBUG = TRUE, standardize = TRUE, ...)
```

Arguments

`x`	a n x p matrix of gene expression measurements with n samples and p genes.
`y`	a n x 2 matrix of survival data. The two columns represent disease status 'status' and survival time 'time' respectively.
`globalGraph`	An `igraph` R object containing the interaction network.
`nfolds`	number of folds - default is 10.
`Gamma`	A numeric value. The restart probability in directed random walk. Default is `Gamma = 0.3`.
`DEBUG`	Logical. Should debugging information be shown.
`standardize`	Logical flag for `x` standardization, prior to fitting the model. Default is `TRUE`.
`...`	Arguments to be passed to `cv.glmnet` in R package `glmnet`.

Value

glmnetRes	An object of class "cv.glmnet"
PT	The topological weights of genes

Author(s)

Wei Liu

References

Integration of gene interaction information into a reweighted Lasso-Cox model for accurate survival prediction. To be published.

Examples

```
library("survival")
library("igraph")
library("glmnet")
library("Matrix")

data(dGMMirGraph)
data(mRNA_matrix)
data(survData)

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(2/3*dim(mRNA_matrix)[1]))
testSmpl.Idx <- setdiff(1:dim(mRNA_matrix)[1], trainSmpl.Idx)
trainSmpl <- mRNA_matrix[trainSmpl.Idx ,]
testSmpl <- mRNA_matrix[testSmpl.Idx ,]

cv.res <- cvRLassoCox(x=trainSmpl, y=survData[trainSmpl.Idx ,],
                        globalGraph=dGMMirGraph, nfolds = 5)
```

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dGMMirGraph *The KEGG network*

Description

The KEGG network constructed by the R package iSubpathwayMiner.

Usage

```
data("dGMMirGraph")
```

Format

An igraph R object.

Details

There are 7159 nodes and 39930 edges in dGMMirGraph. Each node in the graph represents a gene/miRNA/metabolite. The KEGG network is used to evaluate the topological importance of genes by the random walk method.

Examples

```
data(dGMMirGraph)
```

`mRNA_matrix` *The expression data*

Description

An example of GBM expression data. We acknowledge the TCGA Research Network for generating the GBM datasets.

Usage

```
data("mRNA_matrix")
```

Format

The format is: num [1:314, 1:4853] 0.562167 0.022435 -0.000102 -0.719444 0.620269 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:314] "TCGA-02-0001" "TCGA-02-0003" "TCGA-02-0006" ..$: chr [1:4853] "90993" "4313" "26248" "57680" ...

Examples

```
data(mRNA_matrix)
```

`predict.cvRLassoCox` *Make predictions from a cross-validated RLasso-Cox model*

Description

This function makes predictions from a cross-validated RLasso-Cox model, using the optimal value chosen for lambda.

Usage

```
## S3 method for class 'cvRLassoCox'
predict(object, newx, ...)
```

Arguments

`object`	cross-validated RLasso-Cox model
`newx`	A matrix with new samples to predict.
`...`	Arguments to be passed to `predict.cv.glmnet` in R package `glmnet`.

Value

Predicted results of new patients in `newx`.

Examples

```
library("survival")
library("igraph")
library("glmnet")
library("Matrix")

data(dGMMirGraph)
data(mRNA_matrix)
data(survData)

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(2/3*dim(mRNA_matrix)[1]))
testSmpl.Idx <- setdiff(1:dim(mRNA_matrix)[1], trainSmpl.Idx)
trainSmpl <- mRNA_matrix[trainSmpl.Idx ,]
testSmpl <- mRNA_matrix[testSmpl.Idx ,]

cv.res <- cvRLassoCox(x=trainSmpl, y=survData[trainSmpl.Idx ,],
                        globalGraph=dGMMirGraph, nfolds = 5)
lp <- predict(object = cv.res, newx = testSmpl,
                            s = "lambda.min")
```

`predict.RLassoCox` *Make predictions from a RLasso-Cox model*

Description

This function predicts the risk of new samples from a fitted `RLasso-Cox` model.

Usage

```
## S3 method for class 'RLassoCox'
predict(object, newx, ...)
```

Arguments

`object`	Fitted `"RLassoCox"` model object.
`newx`	A matrix with new samples to predict.
`...`	Arguments to be passed to `predict.glmnet` in R package `glmnet`.

Value

Predicted results of new patients in `newx`.

Author(s)

Wei Liu

Examples

```
library("survival")
library("igraph")
library("glmnet")
library("Matrix")

data(dGMMirGraph)
data(mRNA_matrix)
data(survData)

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(2/3*dim(mRNA_matrix)[1]))
testSmpl.Idx <- setdiff(1:dim(mRNA_matrix)[1], trainSmpl.Idx)
trainSmpl <- mRNA_matrix[trainSmpl.Idx ,]
testSmpl <- mRNA_matrix[testSmpl.Idx ,]

res <- RLassoCox(x=trainSmpl, y=survData[trainSmpl.Idx ,],
                 globalGraph=dGMMirGraph)
lp <- predict(object = res, newx = testSmpl)
```

RLassoCox *Reweighted Lasso-Cox model*

Description

A rewighted Lasso-Cox model for survival prediction and biomarker discovery.

Usage

```
RLassoCox(x, y, globalGraph = NULL, Gamma = 0.3, DEBUG = TRUE,
            standardize = TRUE, ...)
```

Arguments

x	a n x p matrix of gene expression measurements with n samples and p genes.
y	a n x 2 matrix of survival data. The two columns represent disease status 'status' and survival time 'time' respectively.
globalGraph	An igraph R object containing the interaction network.
Gamma	A numeric value. The restart probability in directed random walk. Default is Gamma = 0.3.
DEBUG	Logical. Should debugging information be shown.
standardize	Logical flag for x standardization, prior to fitting the model. Default is TRUE.
...	Arguments to be passed to glmnet in R package glmnet.

Details

RLassoCox integrates gene interaction information into the Lasso-Cox model for accurate survial prediction and biomarker discovery.

Value

glmnetRes	An object of class "glmnet"
PT	The topological weights of genes

Author(s)

Wei Liu

References

Integration of gene interaction information into a reweighted Lasso-Cox model for accurate survival prediction. To be published.

See Also

predict

Examples

```
library("survival")
library("igraph")
library("glmnet")
library("Matrix")

data(dGMMirGraph)
data(mRNA_matrix)
data(survData)

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(2/3*dim(mRNA_matrix)[1]))
testSmpl.Idx <- setdiff(1:dim(mRNA_matrix)[1], trainSmpl.Idx)
trainSmpl <- mRNA_matrix[trainSmpl.Idx ,]
testSmpl <- mRNA_matrix[testSmpl.Idx ,]

res <- RLassoCox(x=trainSmpl, y=survData[trainSmpl.Idx ,],
                 globalGraph=dGMMirGraph)
```

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rw *Directed Random Walk*

Description

The directed random walk algorithm proposed by Liu et al (2013).

Usage

```
rw(W, p0, gamma)
```

Arguments

W	The adjacency matrix of the gene interaction network.
p0	A vector containing the initial weights of genes in the gene interaction network.
gamma	A numeric value. The restart probability in directed random walk.

Details

This function implements the directed random walk algorithm proposed by Liu et al (2013). It evaluates the topological weight of each gene according to its topological importance in the gene interaction network. The genes that close to many other genes that have large weights will receive larger weights. The final weights reflect the topological importances of genes in the gene interaction network.

Value

A matrix containing the topological weights of nodes in `igraphM`.

Author(s)

Wei Liu <freelw@qq.com>

References

Liu, W., et al., Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. Bioinformatics, 2013. 29(17): p. 2169-77.

`survData` *Survival data*

Description

The survival data of patients in `mRNA_matrix`.

Usage

```
data("survData")
```

Format

A data frame with 314 observations on the following 2 variables.

`status` a logical vector

`time` a numeric vector

Examples

```
data(survData)
```

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