

# Package ‘RLassoCox’

October 31, 2024

**Type** Package

**Title** A reweighted Lasso-Cox by integrating gene interaction information

**Version** 1.14.0

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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.

**License** Artistic-2.0

**biocViews** Survival, Regression, GeneExpression, GenePrediction, Network

**BugReports** <https://github.com/weiliu123/RLassoCox/issues>

**BiocType** Software

**Suggests** knitr

**VignetteBuilder** knitr

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RLassoCox-package	<i>A reweighted Lasso-Cox by integrating gene interaction information</i>
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## 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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Very simple to use. Accepts x,y data for the RLasso-Cox model, and makes predictions for new samples.

RLassoCox A reweighted 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](mailto: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*

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**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)
```

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mRNA_matrix	<i>The expression data</i>
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**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)
```

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predict.cvRlassoCox	<i>Make predictions from a cross-validated RLasso-Cox model</i>
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**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*

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**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

*Rewighted 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 survival 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*

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**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.

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survData

*Survival data*

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**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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