

# Package ‘RRSF’

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**Type** Package

**Title** A reweighted random survival forest approach by integrating gene interactionn information

**Version** 1.0

**Date** 2018-06-18

**Author** Wei Liu

**Maintainer** Wei Liu <freelw@qq.com>

**Depends** R (>= 2.10), igraph, Matrix, survival, randomForestSRC

**Description** Integration of gene interaction information into a reweighted random survival forest approach for accurate survival prediction and survival biomarker discovery.

**License** GPL(>=2)

**NeedsCompilation** no

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RRSF-package	<i>A reweighted random survival forest approach by integrating gene interactionn information</i>
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## Description

Integration of gene interaction information into a reweighted random survival forest approach for accurate survival prediction and survival biomarker discovery.

## Details

The DESCRIPTION file:

```
Package:      RRSF
Type:         Package
Title:        A reweighted random survival forest approach by integrating gene interactionn information
Version:      1.0
Date:         2018-06-18
Author:       Wei Liu
Maintainer:   Wei Liu <freelw@qq.com>
Depends:      igraph, Matrix, survival, randomForestSRC
Description:  Integration of gene interaction information into a reweighted random survival forest approach for accurate
License:      GPL(>=2)
```

Index of help topics:

CreatLadder	Create a decreasing sequence
DRW	Directed Random Walk
RRSF	Reweighted random survival forest
RRSF-package	A reweighted random survival forest approach by integrating gene interactionn information
dGMMirGraph	The global pathway graph
getW	Calculating the weights of genes
mRNA_matrix	The expression data
predict.RRSF	Make predictions from a "RRSF" object
survData	Survival data

Very simple to use. Accepts x,y data for RRSF models, and makes predictions for new samples. Only 2 functions: RRSF A rewighted random survival forest algorithm for survival prediction and gene selection. predict.RRSF predicts the risk of new patients using the model fitted by RRSF.

## Author(s)

Wei Liu

Maintainer: Wei Liu <freelw@qq.com>

## References

A rewighted random survival forest algorithm for survival prediction and gene selection.

## Examples

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

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(1/2*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 <- RRSF(x=trainSmpl, y=survData[trainSmpl.Idx ,], geneSel = TRUE, DEBUG=TRUE, standardize=TRUE,
```

```
globalGraph = dGMMirGraph, topo.Wt = NULL, Gamma=0.3, ntree=100)
lp <- predict.RRSF(res$RRSFmodel,testSmpl)
```

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CreatLadder	<i>Create a decreasing sequence</i>
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### Description

This function creates a decreasing sequence according to a specific decreasing ratio.

### Usage

```
CreatLadder(Ntotal, pRatio = 0.75, Nmin = 5)
```

### Arguments

Ntotal	Total number
pRatio	Decreasing ratio
Nmin	Minimum number

### Value

A decreasing sequence.

### Examples

```
ladder <- CreatLadder(Ntotal = 300, pRatio = 0.9, Nmin = 2)
```

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dGMMirGraph	<i>The global pathway graph</i>
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### Description

The directed global pathway graph 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 global pathway graph is used to evaluate the topological importance of genes by directed random walk.

### Examples

```
data(dGMMirGraph)
```

DRW

*Directed Random Walk***Description**

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

**Usage**

```
DRW(igraphM, p0, EdgeWeight = FALSE, gamma = 0.3)
```

**Arguments**

<code>igraphM</code>	An igraph object containing the directed global pathway graph.
<code>p0</code>	A unit vector containing the initial weights of genes in the global pathway graph.
<code>EdgeWeight</code>	Logical. Should <code>igraphM</code> be converted to a weighted matrix or an un-weighted matrix (the default)?
<code>gamma</code>	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 global pathway graph. The genes that close to many other genes that have large initial weights will receive larger weights. The final weights reflect the topological importances of genes in the global pathway graph.

**Value**

A numerical vector 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.

**Examples**

```
data(dGMMirGraph)
vertexs <- V(dGMMirGraph)
p0 <- runif(length(vertexs), min = 0, max = 1)
names(p0) <- vertexs$name
p0 <- p0/sum(p0)
vertexWeight <- DRW(igraphM = dGMMirGraph, p0, EdgeWeight=FALSE, gamma = 0.3)
names(vertexWeight) <- names(p0)
```

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getW

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*Calculating the weights of genes*


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### Description

This function gets the weights of nodes in globalGraph.

### Usage

```
getW(geneWeight, globalGraph)
```

### Arguments

geneWeight	The weights of genes.
globalGraph	The global pathway graph.

### Value

The weights of nodes in globalGraph.

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mRNA\_matrix

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*The expression data*


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### Description

An example of GBM expression data with 200 samples and 300 genes. We acknowledge the TCGA Research Network for generating the GBM datasets.

### Usage

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

### Format

The format is: num [1:200, 1:300] -0.929 2.12 -1.59 0.112 1.86 ... - attr(\*, "dimnames")=List of 2 ..\$ : chr [1:200] "TCGA-12-1597" "TCGA-02-0033" "TCGA-76-4929" "TCGA-06-0648" ... ..\$ : chr [1:300] "5806" "3588" "3627" "55240" ...

### Examples

```
data(mRNA_matrix)
```

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predict.RRSF	<i>Make predictions from a "RRSF" object</i>
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### Description

This function predicts the risk of new samples from a fitted RRSF object.

### Usage

```
predict.RRSF(object, newx, ...)
```

### Arguments

object	Fitted "rfsrc" model object.
newx	A matrix with new samples to predict.
...	Arguments to be passed to predict.rfsrc in R package randomForestSRC.

### Value

Predicted results of new patients in newx.

### See Also

[RRSF](#)

### Examples

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

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(1/2*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 <- RRSF(x=trainSmpl, y=survData[trainSmpl.Idx ,], geneSel = TRUE, DEBUG=TRUE, standardize=TRUE,
            globalGraph = dGMMirGraph, topo.Wt = NULL, Gamma=0.3, ntree=100)
lp <- predict.RRSF(res$RRSFmodel, testSmpl)
```

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RRSF	<i>Reweighted random survival forest</i>
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### Description

A reweighted random survival forest algorithm for survival prediction and gene selection.

### Usage

```
RRSF(x, y, geneSel = FALSE, DEBUG = FALSE, standardize = TRUE, globalGraph = NULL, topo.Wt = NULL, Gar
```

**Arguments**

<code>x</code>	a $n \times p$ matrix of gene expression measurements with $n$ samples and $p$ genes.
<code>y</code>	a $n \times 2$ matrix of survival data. The two columns represent disease status 'status' and survival time 'time' respectively.
<code>geneSel</code>	Logical. Should gene selection be performed.
<code>DEBUG</code>	Logical. Should debugging information be shown.
<code>standardize</code>	Logical flag for $x$ standardization, prior to fitting the model. Default is TRUE.
<code>globalGraph</code>	An igraph R object containing the global pathway graph.
<code>topo.Wt</code>	The topological weights of genes.
<code>Gamma</code>	A numeric value. The restart probability in directed random walk. Default is $\Gamma = 0.3$ .
<code>...</code>	Arguments to be passed to <code>rfsrc</code> in R package <code>randomForestSRC</code> .

**Details**

RRSF integrates gene interaction information into the random survival forest algorithm for accurate survival prediction and robust gene selection.

**Value**

Fitted "RRSF" model object.

<code>RRSFmodel</code>	An object of class "rfsrc"
<code>topo.Wt</code>	The topological weights of genes
<code>geneSelected</code>	If <code>geneSel = TRUE</code> , A matrix recording the genes selected at each level, else NULL

**Author(s)**

Wei Liu

**References**

Liu, W., et al., Integration of gene interaction information into a reweighted random survival forest approach for accurate survival prediction and survival biomarker discovery. To be published.

**See Also**

[predict.RRSF](#)

**Examples**

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

trainSmpl.Idx <- sample(1:dim(mRNA_matrix)[1], floor(1/2*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 <- RRSF(x=trainSmpl, y=survData[trainSmpl.Idx ,], geneSel = TRUE, DEBUG=TRUE, standardize=TRUE,  
            globalGraph = dGMMirGraph, topo.Wt = NULL, Gamma=0.3, ntree=100)
```

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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 200 observations on the following 2 variables.

status a logical vector

time a numeric vector

### Examples

```
data(survData)
```



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