

# Package ‘rbsurv’

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**Title** Robust likelihood-based survival modeling with microarray data

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**Depends** R (>= 2.5.0), Biobase (>= 2.5.5), survival

**Description** This package selects genes associated with survival.

**License** GPL (>= 2)

**URL** <http://www.korea.ac.kr/~stat2242/>

**biocViews** Microarray

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gliomaSet	<i>Gene expression and survival data of the patients with gliomas</i>
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## Description

These data sets consist of gene expression and survival of the patients with gliomas. Note that it contains a subset of the data published in Freije et al. (2004).

## Source

Freije et al. (2004). Gene Expression Profiling of Gliomas Strongly Predicts Survival, *Cancer Research*, 64: 6503-6510.

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rbsurv

*Robust likelihood-based survival modeling*

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## Description

This selects survival-associated genes with microarray data.

## Usage

```
rbsurv(time, ...)
```

## Arguments

time	an object for which the extraction of model rbsurv is meaningful.
...	other arguments

## Author(s)

HyungJun Cho, Sukwoo Kim, Soo-heang Eo, and Jaewoo Kang

## References

Cho,H., Yu,A., Kim,S., Kang,J., and Hong S-M. (2009). Robust likelihood-based survival modeling for microarray gene expression Data, *Journal of Statistical Software*, 29(1):1-16. URL <http://www.jstatsoft.org/v29/i01/>.

## See Also

[rbsurv.default](#)

## Examples

```
library(rbsurv)
data(gliomaSet)
x <- exprs(gliomaSet)
x <- log2(x)
time <- gliomaSet$Time
status <- gliomaSet$Status
z <- cbind(gliomaSet$Age, gliomaSet$Gender)

fit <- rbsurv(time=time, status=status, x=x, method="efron", max.n.genes=20, n.iter=10, n.fold=3, n.seq=1)
fit$model
```

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rbsurv.default	<i>Robust likelihood-based survival modeling</i>
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**Description**

This selects survival-associated genes with microarray data.

**Usage**

```
## Default S3 method:
rbsurv(time, status, x, z=NULL, alpha=1, gene.ID=NULL, method="efron",
        n.iter=10, n.fold=3, n.seq=1, seed=1234, max.n.genes=nrow(x),...)
```

**Arguments**

time	a vector for survival times
status	a vector for survival status, 0=censored, 1=event
x	a matrix for expression values (genes in rows, samples in columns)
z	a matrix for risk factors
alpha	significance level for evaluating risk factors; significant risk factors included with the alpha level if $\alpha < 1$
gene.ID	a vector for gene IDs; if NULL, row numbers are assigned.
method	a character string specifying the method for tie handling. Choose one of "efron", "breslow", "exact". The default is "efron". If there are no tied death times all the methods are equivalent.
n.iter	the number of iterations for gene selection
n.fold	the number of partitions of samples
n.seq	the number of sequential runs or multiple models
seed	a seed for sample partitioning
max.n.genes	the maximum number of genes considered. If the number of the input genes is greater than the given number, it is reduced by fitting individual Cox models.
...	other arguments

**Value**

model	survival-associated gene model
n.genes	number of genes
n.samples	number of samples
method	method for tie handling
covariates	covariates
n.iter	number of iterations for gene selection
n.fold	number of partitions of samples
n.seq	number of sequential runs or multiple models
gene.list	a list of genes included in the models

**Author(s)**

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**References**

Cho,H., Yu,A., Kim,S., Kang,J., and Hong S-M. (2009). Robust likelihood-based survival modeling for microarray gene expression Data, *Journal of Statistical Software*, 29(1):1-16. URL <http://www.jstatsoft.org/v29/i01/>.

**See Also**

[rbsurv](#)

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