

# 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

*Gene expression and survival data of the patients with gliomas*


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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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