

# Package ‘rbsurv’

June 20, 2021

**Version** 2.50.0

**Date** 2009-07-22

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

**Author** HyungJun Cho <hj4cho@korea.ac.kr>, Sukwoo Kim  
<s4kim@korea.ac.kr>, Soo-heang Eo <hanansh@korea.ac.kr>, Jaewoo  
Kang <kangj@korea.ac.kr>

**Maintainer** Soo-heang Eo <hanansh@korea.ac.kr>

**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

**git\_url** <https://git.bioconductor.org/packages/rbsurv>

**git\_branch** RELEASE\_3\_13

**git\_last\_commit** bd8165b

**git\_last\_commit\_date** 2021-05-19

**Date/Publication** 2021-06-20

## R topics documented:

|                          |   |
|--------------------------|---|
| gliomaSet . . . . .      | 2 |
| rbsurv . . . . .         | 2 |
| rbsurv.default . . . . . | 3 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>5</b> |
|--------------|----------|

---

gliomaSet

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

---

### 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.

---

rbsurv

*Robust likelihood-based survival modeling*

---

### 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

```

---

rbsurv.default                      *Robust likelihood-based survival modeling*

---

**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)**

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](#)

# Index

\* **datasets**

gliomaSet, 2

\* **models**

rbsurv, 2

rbsurv.default, 3

gliomaSet, 2

rbsurv, 2, 4

rbsurv.default, 2, 3