Package ‘rbsurv’

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R topics documented:

  gliomaSet ......................................................... 2
  rbsurv .......................................................... 2
  rbsurv.default .................................................. 3

Index 5
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**


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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)**

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**References**


**See Also**

`rbsurv.default`
Examples

```r
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**

*Robust likelihood-based survival modeling*

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### Description

This selects survival-associated genes with microarray data.

### Usage

```r
# 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


See Also

*rbsurv*
Index

* datasets
  gliomaSet, 2

* models
  rbsurv, 2
  rbsurv.default, 3

gliomaSet, 2

rbsurv, 2, 4
rbsurv.default, 2, 3