

rbsurv

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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.

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

<code>time</code>	a vector for survival times
<code>status</code>	a vector for survival status, 0=censored, 1=event
<code>x</code>	a matrix for expression values (genes in rows, samples in columns)
<code>z</code>	a matrix for risk factors
<code>alpha</code>	significance level for evaluating risk factors; significant risk factors included with the alpha level if $\alpha < 1$
<code>gene.ID</code>	a vector for gene IDs; if NULL, row numbers are assigned.
<code>method</code>	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.
<code>n.iter</code>	the number of iterations for gene selection
<code>n.fold</code>	the number of partitions of samples
<code>n.seq</code>	the number of sequential runs or multiple models
<code>seed</code>	a seed for sample partitioning
<code>max.n.genes</code>	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.
<code>...</code>	other arguments

Value

<code>model</code>	survival-associated gene model
<code>n.genes</code>	number of genes
<code>n.samples</code>	number of samples
<code>method</code>	method for tie handling
<code>covariates</code>	covariates
<code>n.iter</code>	number of iterations for gene selection
<code>n.fold</code>	number of partitions of samples
<code>n.seq</code>	number of sequential runs or multiple models
<code>gene.list</code>	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](#)

`rbsurv`*Robust likelihood-based survival modeling*

Description

This selects survival-associated genes with microarray data.

Usage

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

Arguments

<code>time</code>	an object for which the extraction of model <code>rbsurv</code> is meaningful.
<code>...</code>	other arguments

Author(s)

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

References

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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,
fit$model
```

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