rbsurv

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`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,
fit$model
```

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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 seletion
`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

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See Also

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