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
NeedsCompilation no

R topics documented:

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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

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
```
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)

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