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)

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

References


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
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

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See Also

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