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:

  gliomaSet ......................................................... 1
  rbsurv .............................................................. 2
  rbsurv.default .................................................. 3

Index

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

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
Robust likelihood-based survival modeling

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

*Topic datasets
  gliomaSet, 1

*Topic models
  rbsurv, 2
  rbsurv.default, 3
  gliomaSet, 1
  rbsurv, 2, 4
  rbsurv.default, 2, 3