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**

\[
\text{rbsurv}(\text{time}, \text{status}, \text{x}, \text{z=NULL}, \text{alpha}=1, \text{gene.ID=NULL}, \text{method}="\text{efron}", \\
\quad \text{n.iter}=10, \text{n.fold}=3, \text{ n.seq}=1, \text{ seed}=1234, \text{ max.n.genes}=\text{nrow(x)}
\]

**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.

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


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
Index

∗Topic datasets
gliomaSet, 1
∗Topic models
rbsurv, 1
gliomaSet, 1
rbsurv, 1