

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

```

| | |
|----------------|--|
| rbsurv.default | <i>Robust likelihood-based survival modeling</i> |
|----------------|--|

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

| | |
|-------------------------|--|
| <code>model</code> | survival-associated gene model |
| <code>n.genes</code> | number of genes |
| <code>n.samples</code> | number of samples |
| <code>method</code> | method for tie handling |
| <code>covariates</code> | covariates |
| <code>n.iter</code> | number of iterations for gene selection |
| <code>n.fold</code> | number of partitions of samples |
| <code>n.seq</code> | number of sequential runs or multiple models |
| <code>gene.list</code> | a list of genes included in the models |

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