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)

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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)

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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, 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 seletion
`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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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`

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