Details of the functions available in the file Functions-SIC.R

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Related article : Amico, M., Van Keilegom, I. And Legrand, C. (2017). The single-index/Cox mixture cure model.

NZD

(from np package - `https://cran.r-project.org/web/packages/np/index.html`)

NZD stands for 'no zero divide'. This function is used to deal with division by zero when using fixed precision architectures. This accomplishes the fact using a simple algorithm from computer science (in the underlying C code). It avoids NaN (not a number) in computations.

Fed a vector/scalar, it checks for a negative/positive value and, if positive divides by the smallest positive floating-point number 'x' such that $1 + x! = 1$, if negative returns the same with appropriate sign.

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smsurv

(from smcure package - `https://cran.r-project.org/web/packages/smcure/index.html`)

Description :

The estimated baseline survival function of the mixuture cure model based on the Breslow method, which is used in order to update the E-step in the EM algorithm.

Usage :

`smsurv(Time, Status, X, beta, w, model)`

Arguments :

Time	follow up time for 'ph' model. If model is 'aft', then this is residual $\log(t) - \beta x$.
Status	censoring indicator, 1 = event of interest happens, and 0 = censoring.
X	covariates considered in the conditional survival function (latency)
beta	initial beta from coxph
w	conditional probability of the ith individual remains uncured at the mth iteration. We use Status as initial value
model	specifies your model, it can be 'ph' or 'aft'

SIC

Description:

EM algorithm for the estimation of a single-index/Cox mixture cure model.

Usage :

```
SIC(Time, Status, gamma.init, beta.init, X, Z, LCMM, eps, emmax,
dataset, rescale)
```

Arguments :

Time	follow-up time
Status	censoring indicator - 1 = event of interest happens, and 0 = censoring
beta.init	initial value for the single-index model (incidence)
gamma.init	initial value for the Cox PH model (latency)
X	covariates considered in the single-index (incidence)
Z	covariates considered in the Cox PH model (latency)
LCMM	a smcure object
	(see smcure package - `https://cran.r-project.org/web/packages/smcure/index.html` - for more details about the smcure function)
eps	value of the convergence criterion
emmax	maximum number of iteration for the EM algorithm
dataset	a matrix or a data.frame containing the data on which the model has to be estimated
rescale	TRUE/FALSE - if TRUE, parameters of the incidence are rescaled according to an euclidian norm equal to 1

Value :

b	parameter estimates for the single-index (incidence)
h	bandwidth value
beta	parameter estimates for the Cox PH model (latency)
iteration	number of iteration of the EM algorithm
survival	baseline conditional survival function estimate
uncured	conditional probability of the ith individual remains uncured at the final iteration
pred	estimated value of $\boldsymbol{\gamma}^t\mathbf{X}$ and $p(\mathbf{X})$ at the final iteration
h.conv	value given by the value 'convergence' of the optim function for the bandwidth computation
conv	value given by the value 'convergence' of the optim function for the maximum likelihood

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SICMM

Description :

Estimation of a single-index/Cox mixture cure model with computation of the standard errors of the parameters by bootstrap.

Usage :

```
SICMM(Time, Status, X, Z, LCMM, eps, emmax, dataset, rescale,
bootstrap, nboot)
```

Arguments :

Time	follow-up time
Delta	censoring indicator - 1 = event of interest happens, and 0 = censoring
X	covariates considered in the single-index (incidence)
Z	covariates considered in the Cox PH model (latency)
LCMM	a smcure object
	(see smcure package - `https://cran.r-project.org/web/packages/smcure/index.html` - for more details about the secure function)
eps	value of the convergence criterion
emmax	maximum number of iteration for the EM algorithm
dataset	a matrix or a data.frame containing the data on which the model has to be estimated
rescale	TRUE/FALSE - if TRUE, parameters of the incidence are rescaled according to an euclidian norm equal to 1
bootstrap	TRUE/FALSE - if TRUE, computation of the standard errors of the parameters based on a bootstrap approach
nboot	number of bootstrap sampling

Value :

b	parameter estimates for the single-index (incidence)
b.se	standard errors for vector of parameters b
b.pvalue	p-value for the Wald test for the vector of estimated parameters b
h	bandwidth value
beta	parameter estimates for the Cox PH model (latency)
beta.se	standard errors for vector of parameters beta
beta.pvalue	p-value for the Wald test for the vector of estimated parameters beta
survival	baseline conditional survival function estimate
pred	estimated value of the $\boldsymbol{\gamma}^t\mathbf{X}$ and $p(\mathbf{X})$
h.conv	value given by the value 'convergence' of the optim function for the bandwidth computation
conv	value given by the value 'convergence' of the optim function for the maximum likelihood