Package ‘psbcGroup’

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Type Package

Title Penalized Parametric and Semiparametric Bayesian Survival Models with Shrinkage and Grouping Priors

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Description Algorithms to implement various Bayesian penalized survival regression models including: semiparametric proportional hazards models with lasso priors (Lee et al., Int J Biostat, 2011 <doi:10.2202/1557-4679.1301>) and three other shrinkage and group priors (Lee et al., Stat Anal Data Min, 2015 <doi:10.1002/sam.11266>); parametric accelerated failure time models with group/ordinary lasso prior (Lee et al. Comput Stat Data Anal, 2017 <doi:10.1016/j.csda.2017.02.014>).

License GPL (>= 2)

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LazyLoad yes

NeedsCompilation yes

Repository CRAN

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R topics documented:

`aftGL` *Function to Fit the Penalized Parametric Bayesian Accelerated Failure Time Model with Group Lasso Prior*

Description

Penalized parametric Bayesian accelerated failure time model with group lasso prior is implemented to analyze survival data with high-dimensional covariates.

Usage

```
aftGL(Y, data, grpInx, hyperParams, startValues, mcmc)
```

Arguments

Y	a data.frame containing univariate time-to-event outcomes from n subjects. It is of dimension $n \times 2$: the columns correspond to y, δ.
data	a data.frame containing p covariate vectors from n subjects. It is of dimension $n \times p$.
grpInx	a vector of p group indicator for each variable
hyperParams	a list containing hyperparameter values in hierarchical models: (nu0, sigSq0): hyperparameters for the prior of σ^2; (alpha0, h0): hyperparameters for the prior of α; (rLam, deltaLam): hyperparameters for the prior of λ^2.
startValues	a list containing starting values for model parameters. See Examples below.
mcmc	a list containing variables required for MCMC sampling. Components include, numReps, total number of scans; thin, extent of thinning; burninPerc, the proportion of burn-in. See Examples below.

Value

aftGL returns an object of class aftGL.

Author(s)

Kyu Ha Lee, Sounak Chakraborty, (Tony) Jianguo Sun

References

Lee, K. H., Chakraborty, S., and Sun, J. (2017). Variable Selection for High-Dimensional Genomic Data with Censored Outcomes Using Group Lasso Prior. *Computational Statistics and Data Analysis*, Volume 112, pages 1-13.

See Also

VS

Examples

```
# generate some survival data
set.seed(204542)

p = 20
n = 200
logHR.true <- c(rep(4, 10), rep(0, (p-10)))

CovX<-matrix(0,p,p)

for(i in 1:10){
for(j in 1:10){
CovX[i,j] <- 0.3^abs(i-j)
}
}

diag(CovX) <- 1

data <- apply(rmvnorm(n, sigma=CovX, method="chol"), 2, scale)
pred <- as.vector(exp(rowSums(scale(data, center = FALSE, scale = 1/logHR.true))))

t  <- rexp(n, rate = pred)
cen <- runif(n, 0, 8)
tcen  <- pmin(t, cen)
di  <- as.numeric(t <= cen)

n <- dim(data)[1]
p <- dim(data)[2]

Y <- data.frame(cbind(tcen, di))
colnames(Y) <- c("time", "event")

grpInx <- 1:p
K <- length(unique(grpInx))

############################
hyperParams <- list(nu0=3, sigSq0=1, alpha0=0, h0=10^6, rLam=0.5, deltaLam=2)

############################
startValues <- list(alpha=0.1, beta=rep(1,p), sigSq=1, tauSq=rep(0.4,p), lambdaSq=5,
  w=log(tcen))

############################
mcmc <- list(numReps=100, thin=1, burninPerc=0.5)

############################
fit <- aftGL(Y, data, grpInx, hyperParams, startValues, mcmc)
## Not run:
vs <- VS(fit, X=data)

## End(Not run)
```

aftGL_LT *Function to Fit the Penalized Parametric Bayesian Accelerated Failure Time Model with Group Lasso Prior for Left-Truncated and Interval-Censored Data*

Description

Penalized parametric Bayesian accelerated failure time model with group lasso prior is implemented to analyze left-truncated and interval-censored survival data with high-dimensional covariates.

Usage

```
aftGL_LT(Y, X, XC, grpInx, hyperParams, startValues, mcmcParams)
```

Arguments

Y	Outcome matrix with three column vectors corresponding to lower and upper bounds of interval-censored data and left-truncation time
X	Covariate matrix p covariate vectors from n subjects. It is of dimension $n \times p$.
XC	Matrix for confound variables: q variable vectors from n subjects. It is of dimension $n \times q$.
grpInx	a vector of p group indicator for each variable
hyperParams	a list containing hyperparameter values in hierarchical models: (a.sigSq, a.sigSq): hyperparameters for the prior of σ^2; (mu0, h0): hyperparameters for the prior of μ; (v): hyperparameter for the prior of β_C.
startValues	a list containing starting values for model parameters. See Examples below.
mcmcParams	a list containing variables required for MCMC sampling. Components include, numReps, total number of scans; thin, extent of thinning; burninPerc, the proportion of burn-in. See Examples below.

Value

aftGL_LT returns an object of class aftGL_LT.

Author(s)

Kyu Ha Lee, Harrison Reeder

References

Reeder, H., Haneuse, S., Lee, K. H. (2024+). Group Lasso Priors for Bayesian Accelerated Failure Time Models with Left-Truncated and Interval-Censored Data. *under review*

See Also

VS

Examples

```
## Not run:

data(survData)
X <- survData[,c(4:5)]
XC <- NULL

n <- dim(survData)[1]
p <- dim(X)[2]
q <- 0

c0 <- rep(0, n)
yL <- yU <- survData[,1]
yU[which(survData[,2] == 0)] <- Inf
Y <- cbind(yL, yU, c0)

grpInx <- 1:p
K <- length(unique(grpInx))

#####################
## Hyperparameters

a.sigSq= 0.7
b.sigSq= 0.7

mu0 <- 0
h0 <- 10^6

v = 10^6

hyperParams <- list(a.sigSq=a.sigSq, b.sigSq=b.sigSq, mu0=mu0, h0=h0, v=v)

###################
## MCMC SETTINGS

## Setting for the overall run
##
numReps    <- 100
thin    <- 1
burninPerc <- 0.5

## Tuning parameters for specific updates
##

L.beC <- 50
M.beC <- 1
eps.beC <- 0.001
```

```
L.be <- 100
M.be <- 1
eps.be <- 0.001

mu.prop.var    <- 0.5
sigSq.prop.var    <- 0.01

##

mcmcParams <- list(run=list(numReps=numReps, thin=thin, burninPerc=burninPerc),
tuning=list(mu.prop.var=mu.prop.var, sigSq.prop.var=sigSq.prop.var,
L.beC=L.beC, M.beC=M.beC, eps.beC=eps.beC,
L.be=L.be, M.be=M.be, eps.be=eps.be))

#####################
## Starting Values

w        <- log(Y[,1])
mu     <- 0.1
beta     <- rep(2, p)
sigSq    <- 0.5
tauSq <- rep(0.4, p)
lambdaSq <- 100
betaC     <- rep(0.11, q)

startValues <- list(w=w, beta=beta, tauSq=tauSq, mu=mu, sigSq=sigSq,
lambdaSq=lambdaSq, betaC=betaC)

fit <- aftGL_LT(Y, X, XC, grpInx, hyperParams, startValues, mcmcParams)


## End(Not run)
```

---

psbcEN *Function to Fit the Penalized Semiparametric Bayesian Cox Model with Elastic Net Prior*

Description

Penalized semiparametric Bayesian Cox (PSBC) model with elastic net prior is implemented to analyze survival data with high-dimensional covariates.

Usage

```
psbcEN(survObj, priorPara, initial, rw=FALSE, mcmcPara, num.reps,
thin, chain = 1, save = 1000)
```

Arguments

survObj	The list containing observed data from n subjects; t, di, x
priorPara	The list containing prior parameter values; eta0, kappa0, c0, r1, r2, delta1, delta2, s
initial	The list containing the starting values of the parameters; beta.ini, lambda1Sq, lambda2, sigmaSq, tauSq, h
rw	When setting to "TRUE", the conventional random walk Metropolis Hastings algorithm is used. Otherwise, the mean and the variance of the proposal density is updated using the jumping rule described in Lee et al. (2011).
mcmcPara	The list containing the values of options for Metropolis-Hastings step for β; numBeta, beta.prop.var
num.reps	the number of iterations of the chain
thin	thinning
chain	the numeric name of chain in the case when running multiple chains.
save	frequency of storing the results in .Rdata file. For example, by setting "save = 1000", the algorithm saves the results every 1000 iterations.

Details

t	a vector of n times to the event
di	a vector of n censoring indicators for the event time (1=event occurred, 0=censored)
x	covariate matrix, n observations by p variables
eta0	scale parameter of gamma process prior for the cumulative baseline hazard, $eta0 > 0$
kappa0	shape parameter of gamma process prior for the cumulative baseline hazard, $kappa0 > 0$
c0	the confidence parameter of gamma process prior for the cumulative baseline hazard, $c0 > 0$
r1	the shape parameter of the gamma prior for λ_1^2
r2	the shape parameter of the gamma prior for λ_2
delta1	the rate parameter of the gamma prior for λ_1^2
delta2	the rate parameter of the gamma prior for λ_2
s	the set of time partitions for specification of the cumulative baseline hazard function
beta.ini	the starting values for β
lambda1Sq	the starting value for λ_1^2
lambda2	the starting value for λ_2
sigmaSq	the starting value for σ^2
tauSq	the starting values for τ^2
h	the starting values for h
numBeta	the number of components in β to be updated at one iteration
beta.prop.var	the variance of the proposal density for β when rw is set to "TRUE"

Value

psbcEN returns an object of class psbcEN

beta.p	posterior samples for β
h.p	posterior samples for h
tauSq.p	posterior samples for τ^2
mcmcOutcome	The list containing posterior samples for the remaining model parameters

Note

If the prespecified value of `save` is less than that of `num.reps`, the results are saved as `.Rdata` file under the directory `working directory/mcmcOutcome`.

Author(s)

Kyu Ha Lee, Sounak Chakraborty, (Tony) Jianguo Sun

References

Lee, K. H., Chakraborty, S., and Sun, J. (2011). Bayesian Variable Selection in Semiparametric Proportional Hazards Model for High Dimensional Survival Data. *The International Journal of Biostatistics*, Volume 7, Issue 1, Pages 1-32.

Lee, K. H., Chakraborty, S., and Sun, J. (2015). Survival Prediction and Variable Selection with Simultaneous Shrinkage and Grouping Priors. *Statistical Analysis and Data Mining*, Volume 8, Issue 2, pages 114-127.

Examples

```
## Not run:

# generate some survival data

set.seed(204542)

p = 20
n = 100
beta.true <- c(rep(4, 10), rep(0, (p-10)))

CovX<- diag(0.1, p)

survObj  <- list()
survObj$x <- apply(rmvnorm(n, sigma=CovX, method="chol"), 2, scale)

pred <- as.vector(exp(rowSums(scale(survObj$x, center = FALSE, scale = 1/beta.true))))

t  <- rexp(n, rate = pred)
cen <- runif(n, 0, 8)
survObj$t  <- pmin(t, cen)
survObj$di  <- as.numeric(t <= cen)
```

```
priorPara  <- list()
priorPara$eta0  <- 1
priorPara$kappa0  <- 1
priorPara$c0  <- 2
priorPara$r1 <- 0.1
priorPara$r2 <- 1
priorPara$delta1 <- 0.1
priorPara$delta2 <- 1
priorPara$s <- sort(survObj$t[survObj$di == 1])
priorPara$s <- c(priorPara$s, 2*max(survObj$t)
- max(survObj$t[-which(survObj$t==max(survObj$t))]))
priorPara$J <- length(priorPara$s)

mcmcPara <- list()
mcmcPara$numBeta <- p
mcmcPara$beta.prop.var <- 1

initial <- list()
initial$beta.ini <- rep(0.5, p)
initial$lambda1Sq <- 1
initial$lambda2 <- 1
initial$sigmaSq <- runif(1, 0.1, 10)
initial$tauSq <- rexp(p, rate = initial$lambda1Sq/2)
initial$h <- rgamma(priorPara$J, 1, 1)

rw = FALSE
num.reps = 20000
chain = 1
thin = 5
save = 5

fitEN <- psbcEN(survObj, priorPara, initial, rw=FALSE, mcmcPara,
num.reps, thin, chain, save)

vs <- VS(fitEN, X=survObj$x)


## End(Not run)
```

---

psbcFL — *Function to Fit the Penalized Semiparametric Bayesian Cox Model with Fused Lasso Prior*

Description

Penalized semiparametric Bayesian Cox (PSBC) model with fused lasso prior is implemented to analyze survival data with high-dimensional covariates.

Usage

```
psbcFL(survObj, priorPara, initial, rw=FALSE, mcmcPara, num.reps,
thin, chain = 1, save = 1000)
```

Arguments

`survObj`	The list containing observed data from `n` subjects; `t`, `di`, `x`
`priorPara`	The list containing prior parameter values; `eta0`, `kappa0`, `c0`, `r1`, `r2`, `delta1`, `delta2`, `s`
`initial`	The list containing the starting values of the parameters; `beta.ini`, `lambda1Sq`, `lambda2Sq`, `sigmaSq`, `tauSq`, `h`, `wSq`
`rw`	When setting to "TRUE", the conventional random walk Metropolis Hastings algorithm is used. Otherwise, the mean and the variance of the proposal density is updated using the jumping rule described in Lee et al. (2011).
`mcmcPara`	The list containing the values of options for Metropolis-Hastings step for β; `numBeta`, `beta.prop.var`
`num.reps`	the number of iterations of the chain
`thin`	thinning
`chain`	the numeric name of chain in the case when running multiple chains.
`save`	frequency of storing the results in .Rdata file. For example, by setting "save = 1000", the algorithm saves the results every 1000 iterations.

Details

`t`	a vector of `n` times to the event
`di`	a vector of `n` censoring indicators for the event time (1=event occurred, 0=censored)
`x`	covariate matrix, `n` observations by `p` variables
`eta0`	scale parameter of gamma process prior for the cumulative baseline hazard, $eta0 > 0$
`kappa0`	shape parameter of gamma process prior for the cumulative baseline hazard, $kappa0 > 0$
`c0`	the confidence parameter of gamma process prior for the cumulative baseline hazard, $c0 > 0$
`r1`	the shape parameter of the gamma prior for λ_1^2
`r2`	the shape parameter of the gamma prior for λ_2^2
`delta1`	the rate parameter of the gamma prior for λ_1^2
`delta2`	the rate parameter of the gamma prior for λ_2^2
`s`	the set of time partitions for specification of the cumulative baseline hazard function
`beta.ini`	the starting values for β
`lambda1Sq`	the starting value for λ_1^2
`lambda2Sq`	the starting value for λ_2^2
`sigmaSq`	the starting value for σ^2
`tauSq`	the starting values for τ^2
`h`	the starting values for h
`wSq`	the starting values for w^2
`numBeta`	the number of components in β to be updated at one iteration
`beta.prop.var`	the variance of the proposal density for β when `rw` is set to "TRUE"

Value

psbcFL returns an object of class psbcFL

beta.p	posterior samples for β
h.p	posterior samples for h
tauSq.p	posterior samples for τ^2
mcmcOutcome	The list containing posterior samples for the remaining model parameters

Note

If the prespecified value of save is less than that of num.reps, the results are saved as .Rdata file under the directory working directory/mcmcOutcome.

Author(s)

Kyu Ha Lee, Sounak Chakraborty, (Tony) Jianguo Sun

References

Lee, K. H., Chakraborty, S., and Sun, J. (2011). Bayesian Variable Selection in Semiparametric Proportional Hazards Model for High Dimensional Survival Data. *The International Journal of Biostatistics*, Volume 7, Issue 1, Pages 1-32.

Lee, K. H., Chakraborty, S., and Sun, J. (2015). Survival Prediction and Variable Selection with Simultaneous Shrinkage and Grouping Priors. *Statistical Analysis and Data Mining*, Volume 8, Issue 2, pages 114-127.

Examples

```
## Not run:

# generate some survival data

set.seed(204542)

p = 20
n = 100
beta.true <- c(rep(4, 10), rep(0, (p-10)))

CovX<- diag(0.1, p)

survObj  <- list()
survObj$x <- apply(rmvnorm(n, sigma=CovX, method="chol"), 2, scale)

pred <- as.vector(exp(rowSums(scale(survObj$x, center = FALSE, scale = 1/beta.true))))
```

```
t  <- rexp(n, rate = pred)
cen <- runif(n, 0, 8)
survObj$t  <- pmin(t, cen)
survObj$di  <- as.numeric(t <= cen)

priorPara  <- list()
priorPara$eta0  <- 2
priorPara$kappa0  <- 2
priorPara$c0  <- 2
priorPara$r1 <- 0.5
priorPara$r2 <- 0.5
priorPara$delta1 <- 0.0001
priorPara$delta2 <- 0.0001
priorPara$s <- sort(survObj$t[survObj$di == 1])
priorPara$s <- c(priorPara$s, 2*max(survObj$t)
-max(survObj$t[-which(survObj$t==max(survObj$t))]))
priorPara$J <- length(priorPara$s)

mcmcPara <- list()
mcmcPara$numBeta <- p
mcmcPara$beta.prop.var <- 1

initial <- list()
initial$beta.ini <- rep(0.5, p)
initial$lambda1Sq <- 1
initial$lambda2Sq <- 1
initial$sigmaSq <- runif(1, 0.1, 10)
initial$tauSq <- rexp(p, rate = initial$lambda1Sq/2)
initial$h <- rgamma(priorPara$J, 1, 1)
initial$wSq   <- rexp((p-1), rate = initial$lambda2Sq/2)

rw = FALSE
num.reps = 20000
chain = 1
thin = 5
save = 5

fitFL <- psbcFL(survObj, priorPara, initial, rw=FALSE, mcmcPara,
num.reps, thin, chain, save)
vs <- VS(fitFL, X=survObj$x)


## End(Not run)
```

---

psbcGL — *Function to Fit the Penalized Semiparametric Bayesian Cox Model with Group Lasso Prior*

Description

Penalized semiparametric Bayesian Cox (PSBC) model with group lasso prior is implemented to analyze survival data with high-dimensional covariates.

Usage

```
psbcGL(survObj, priorPara, initial, rw=FALSE, mcmcPara, num.reps,
thin, chain = 1, save = 1000)
```

Arguments

`survObj`	The list containing observed data from `n` subjects; `t`, `di`, `x`
`priorPara`	The list containing prior parameter values; `eta0`, `kappa0`, `c0`, `r`, `delta`, `s`, `groupInd`
`initial`	The list containing the starting values of the parameters; `beta.ini`, `lambdaSq`, `sigmaSq`, `tauSq`, `h`
`rw`	When setting to "TRUE", the conventional random walk Metropolis Hastings algorithm is used. Otherwise, the mean and the variance of the proposal density is updated using the jumping rule described in Lee et al. (2011).
`mcmcPara`	The list containing the values of options for Metropolis-Hastings step for β; `numBeta`, `beta.prop.var`
`num.reps`	the number of iterations of the chain
`thin`	thinning
`chain`	the numeric name of chain in the case when running multiple chains.
`save`	frequency of storing the results in .Rdata file. For example, by setting "save = 1000", the algorithm saves the results every 1000 iterations.

Details

`t`	a vector of `n` times to the event
`di`	a vector of `n` censoring indicators for the event time (1=event occurred, 0=censored)
`x`	covariate matrix, `n` observations by `p` variables
`eta0`	scale parameter of gamma process prior for the cumulative baseline hazard, $eta0 > 0$
`kappa0`	shape parameter of gamma process prior for the cumulative baseline hazard, $kappa0 > 0$
`c0`	the confidence parameter of gamma process prior for the cumulative baseline hazard, $c0 > 0$
`r`	the shape parameter of the gamma prior for λ^2
`delta`	the rate parameter of the gamma prior for λ^2
`s`	the set of time partitions for specification of the cumulative baseline hazard function
`groupInd`	a vector of `p` group indicator for each variable
`beta.ini`	the starting values for β
`lambdaSq`	the starting value for λ^2
`sigmaSq`	the starting value for σ^2
`tauSq`	the starting values for τ^2
`h`	the starting values for h
`numBeta`	the number of components in β to be updated at one iteration
`beta.prop.var`	the variance of the proposal density for β when `rw` is set to "TRUE"

Value

psbcGL returns an object of class psbcGL

beta.p	posterior samples for β
h.p	posterior samples for h
tauSq.p	posterior samples for τ^2
mcmcOutcome	The list containing posterior samples for the remaining model parameters

Note

To fit the PSBC model with the ordinary Bayesian lasso prior (Lee et al., 2011), groupInd needs to be set to 1:p. If the prespecified value of save is less than that of num.reps, the results are saved as .Rdata file under the directory working directory/mcmcOutcome.

Author(s)

Kyu Ha Lee, Sounak Chakraborty, (Tony) Jianguo Sun

References

Lee, K. H., Chakraborty, S., and Sun, J. (2011). Bayesian Variable Selection in Semiparametric Proportional Hazards Model for High Dimensional Survival Data. *The International Journal of Biostatistics*, Volume 7, Issue 1, Pages 1-32.

Lee, K. H., Chakraborty, S., and Sun, J. (2015). Survival Prediction and Variable Selection with Simultaneous Shrinkage and Grouping Priors. *Statistical Analysis and Data Mining*, Volume 8, Issue 2, pages 114-127.

Examples

```
## Not run:

# generate some survival data

set.seed(204542)

p = 20
n = 100
beta.true <- c(rep(4, 10), rep(0, (p-10)))

CovX<-matrix(0,p,p)

for(i in 1:10){
for(j in 1:10){
CovX[i,j] <- 0.5^abs(i-j)
```

```
}
}

diag(CovX) <- 1

survObj  <- list()
survObj$x <- apply(rmvnorm(n, sigma=CovX, method="chol"), 2, scale)

pred <- as.vector(exp(rowSums(scale(survObj$x, center = FALSE, scale = 1/beta.true))))

t  <- rexp(n, rate = pred)
cen <- runif(n, 0, 8)
survObj$t  <- pmin(t, cen)
survObj$di  <- as.numeric(t <= cen)

priorPara  <- list()
priorPara$eta0  <- 1
priorPara$kappa0  <- 1
priorPara$c0  <- 2
priorPara$r <- 0.5
priorPara$delta <- 0.0001
priorPara$s <- sort(survObj$t[survObj$di == 1])
priorPara$s <- c(priorPara$s, 2*max(survObj$t)
-max(survObj$t[-which(survObj$t==max(survObj$t))]))
priorPara$J <- length(priorPara$s)
priorPara$groupInd <- c(rep(1,10),2:11)

mcmcPara <- list()
mcmcPara$numBeta <- p
mcmcPara$beta.prop.var <- 1

initial <- list()
initial$beta.ini <- rep(0.5, p)
initial$lambdaSq <- 1
initial$sigmaSq <- runif(1, 0.1, 10)
initial$tauSq <- rexp(length(unique(priorPara$groupInd)),
rate = initial$lambdaSq/2)
initial$h <- rgamma(priorPara$J, 1, 1)

rw = FALSE
num.reps = 20000
chain = 1
thin = 5
save = 5

fitGL <- psbcGL(survObj, priorPara, initial, rw=FALSE, mcmcPara,
num.reps, thin, chain, save)
vs <- VS(fitGL, X=survObj$x)


## End(Not run)
```

`psbcGroup` *Penalized Parametric and Semiparametric Bayesian Survival Models with Shrinkage and Grouping Priors*

Description

The package provides algorithms for fitting penalized parametric and semiparametric Bayesian survival models with elastic net, fused lasso, and group lasso priors.

Details

The package includes following functions:

`psbcEN`	The function to fit the PSBC model with elastic net prior
`psbcFL`	The function to fit the PSBC model with fused lasso prior
`psbcGL`	The function to fit the PSBC model with group lasso or Bayesian lasso prior
`aftGL`	The function to fit the parametric accelerated failure time model with group lasso
`aftGL_LT`	The function to fit the parametric accelerated failure time model with group lasso for left-truncated and interval-c

Package:	psbcGroup
Type:	Package
Version:	1.7
Date:	2024-1-9
License:	GPL (>= 2)
LazyLoad:	yes

Author(s)

Kyu Ha Lee, Sounak Chakraborty, Harrison Reeder, (Tony) Jianguo Sun
Maintainer: Kyu Ha Lee <klee@hsph.harvard.edu>

References

Lee, K. H., Chakraborty, S., and Sun, J. (2011). Bayesian Variable Selection in Semiparametric Proportional Hazards Model for High Dimensional Survival Data. *The International Journal of Biostatistics*, Volume 7, Issue 1, Pages 1-32.

Lee, K. H., Chakraborty, S., and Sun, J. (2015). Survival Prediction and Variable Selection with Simultaneous Shrinkage and Grouping Priors. *Statistical Analysis and Data Mining*, Volume 8, Issue 2, pages 114-127.

Lee, K. H., Chakraborty, S., and Sun, J. (2017). Variable Selection for High-Dimensional Genomic Data with Censored Outcomes Using Group Lasso Prior. *Computational Statistics and Data Anal-*

ysis, Volume 112, pages 1-13.

Reeder, H., Haneuse, S., Lee, K. H. (2023+). Group Lasso Priors for Bayesian Accelerated Failure Time Models with Left-Truncated and Interval-Censored Time-to-Event Data. *under review*

`survData` *A simulated survival dataset.*

Description

Univariate survival data.

Usage

```
data(survData)
```

Format

a data frame with 2000 observations on the following 4 variables.

`time` the time to event

`event` the censoring indicators for the event time; 1=event observed, 0=censored

`cluster` cluster numbers

`cov1` the first column of covariate matrix x

`cov2` the second column of covariate matrix x

Examples

```
data(survData)
```

`VS` *Function to perform variable selection using SNC-BIC thresholding method*

Description

The `VS` is a function to perform variable selection using SNC-BIC thresholding method

Usage

```
VS(fit, X, psiVec=seq(0.001, 1, 0.001))
```

Arguments

`fit` an object of class `aftGL`, `psbcEN`, `psbcFL`, or `psbcGL`.

`X` a covariate matrix, `n` observations by `p` variables

`psiVec` a vector of candidate threshold values for the SNC step

Author(s)

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References

Lee, K. H., Chakraborty, S., and Sun, J. (2017). Variable Selection for High-Dimensional Genomic Data with Censored Outcomes Using Group Lasso Prior. *Computational Statistics and Data Analysis*, Volume 112, pages 1-13.

See Also

`psbcEN`, `psbcFL`, `psbcGL`, `aftGL`

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