

Package ‘`intsurvbin`’

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Title Survival and Binary Data Integration

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Description Function to implement the horseshoe shrinkage prior in integrated survival and binary regression as developed in Maity et. al. (2019) <doi:10.1111/rssc.12377>.

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Suggests smoothmest

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Author Arnab Maity [aut, cre],
Antik Chakraborty [aut],
Anirban Bhattacharya [aut],
Raymond Carroll [aut],
Bani K. Mallick [aut]

Maintainer Arnab Maity <arnab.maity@pfizer.com>

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R topics documented:

afths	2
aftprobiths	4
Index	8

Description

This function employs the algorithm provided by van der Pas et. al. (2016) for log normal Accelerated Failure Rate (AFT) model to fit survival regression. The censored observations are updated according to the data augmentation of approach of Tanner and Wong (1984).

Usage

```
afths(ct, X, method.tau = c("fixed", "truncatedCauchy", "halfCauchy"),
      tau = 1, method.sigma = c("fixed", "Jeffreys"), Sigma2 = 1,
      burn = 1000, nmc = 5000, thin = 1, alpha = 0.05, Xtest = NULL,
      cttest = NULL)
```

Arguments

ct	survival response, a $n \times 2$ matrix with first column as response and second column as right censored indicator, 1 is event time and 0 is right censored.
X	Matrix of covariates, dimension $n \times p$.
method.tau	Method for handling τ . Select "truncatedCauchy" for full Bayes with the Cauchy prior truncated to $[1/p, 1]$, "halfCauchy" for full Bayes with the half-Cauchy prior, or "fixed" to use a fixed value (an empirical Bayes estimate, for example).
tau	Use this argument to pass the (estimated) value of τ in case "fixed" is selected for method.tau. Not necessary when method.tau is equal to "halfCauchy" or "truncatedCauchy". The default (tau = 1) is not suitable for most purposes and should be replaced.
method.sigma	Select "Jeffreys" for full Bayes with Jeffrey's prior on the error variance σ^2 , or "fixed" to use a fixed value (an empirical Bayes estimate, for example).
Sigma2	A fixed value for the error variance σ^2 . Not necessary when method.sigma is equal to "Jeffreys". Use this argument to pass the (estimated) value of Sigma2 in case "fixed" is selected for method.sigma. The default (Sigma2 = 1) is not suitable for most purposes and should be replaced.
burn	Number of burn-in MCMC samples. Default is 1000.
nmc	Number of posterior draws to be saved. Default is 5000.
thin	Thinning parameter of the chain. Default is 1 (no thinning).
alpha	Level for the credible intervals. For example, alpha = 0.05 results in 95% credible intervals.
Xtest	test design matrix.
cttest	test survival response.

Details

The model is: t_i is response, c_i is censored time, $t_i^* = \min(t_i, c_i)$ is observed time, w_i is censored data, so $w_i = \log t_i^*$ if t_i is event time and $w_i = \log t_i^*$ if t_i is right censored $\log t_i = X\beta + \epsilon$, $\epsilon \sim N(0, \sigma^2)$.

Value

SurvivalHat	Predictive survival probability
LogTimeHat	Predictive log time
Beta.sHat	Posterior mean of Beta, a p by 1 vector
LeftCI.s	The left bounds of the credible intervals
RightCI.s	The right bounds of the credible intervals
Beta.sMedian	Posterior median of Beta, a p by 1 vector
LambdaHat	Posterior samples of λ , a $p * 1$ vector
Sigma2Hat	Posterior mean of error variance σ^2 . If <code>method.sigma = "fixed"</code> is used, this value will be equal to the user-selected value of <code>Sigma2</code> passed to the function
TauHat	Posterior mean of global scale parameter tau, a positive scalar
Beta.sSamples	Posterior samples of β
TauSamples	Posterior samples of τ
Sigma2Samples	Posterior samples of <code>Sigma2</code>

References

Maity, A. K., Carroll, R. J., and Mallick, B. K. (2019) "Integration of Survival and Binary Data for Variable Selection and Prediction: A Bayesian Approach", *Journal of the Royal Statistical Society: Series C (Applied Statistics)*.

Examples

```
burnin <- 500
nmc <- 500
thin <- 1
y.sd <- 1 # standard deviation of the response

p <- 100 # number of predictors
ntrain <- 100 # training size
ntest <- 50 # test size
n <- ntest + ntrain # sample size
q <- 10 # number of true predictors

beta.t <- c(sample(x = c(1, -1), size = q, replace = TRUE), rep(0, p - q)) # randomly assign sign

Sigma <- matrix(0.9, nrow = p, ncol = p)
for(j in 1:p)
{
  Sigma[j, j] <- 1
}
```

```

x <- mvtnorm::rmvnorm(n, mean = rep(0, p), sigma = Sigma) # correlated design matrix

tmean <- x %*% beta.t
yCorr <- 0.5
yCov <- matrix(c(1, yCorr, yCorr, 1), nrow = 2)

y <- mvtnorm::rmvnorm(n, sigma = yCov)
t <- y[, 1] + tmean
X <- scale(as.matrix(x)) # standarization

t <- as.numeric(as.matrix(c(t)))
T <- exp(t) # AFT model
C <- rgamma(n, shape = 1.75, scale = 3) # 42% censoring time
time <- pmin(T, C) # observed time is min of censored and true
status = time == T # set to 1 if event is observed
ct <- as.matrix(cbind(time = time, status = status)) # censored time

# Training set
cttrain <- ct[1:ntrain, ]
Xtrain <- X[1:ntrain, ]

# Test set
cttest <- ct[(ntrain + 1):n, ]
Xtest <- X[(ntrain + 1):n, ]

posterior.fit.aft <- aftbs(ct = cttrain, X = Xtrain, method.tau = "halfCauchy",
                          method.sigma = "Jeffreys", burn = burnin, nmc = nmc, thin = 1,
                          Xtest = Xtest, cttest = cttest)

posterior.fit.aft$Beta.sHat

```

aftprobiths	<i>Horseshoe shrinkage prior in integrated survival and binary regression</i>
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Description

This function provides the implementation of integrated survival and binary high dimensiona regression utilizing Horseshoe prior on the paramters

Usage

```

aftprobiths(ct, z, X, burn = 1000, nmc = 5000, thin = 1,
            alpha = 0.05, Xtest = NULL, cttest = NULL, ztest = NULL)

```

Arguments

ct	survival response, a $n \times 2$ matrix with first column as response and second column as right censored indicator, 1 is event time and 0 is right censored.
z	binary response, a $n \times 1$ vector with numeric values 0 or 1.
X	Matrix of covariates, dimension $n \times p$.
burn	Number of burn-in MCMC samples. Default is 1000.
nmc	Number of posterior draws to be saved. Default is 5000.
thin	Thinning parameter of the chain. Default is 1 (no thinning).
alpha	Level for the credible intervals. For example, alpha = 0.05 results in 95% credible intervals.
Xtest	test design matrix.
cttest	test survival response.
ztest	test binary response.

Value

Beta.sHat	Posterior mean of β for survival model, a p by 1 vector.
Beta.bHat	Posterior mean of β for binary model, a p by 1 vector.
LeftCI.s	The left bounds of the credible intervals for Beta.sHat.
RightCI.s	The right bounds of the credible intervals for Beta.sHat.
LeftCI.b	The left bounds of the credible intervals for Beta.bHat.
RightCI.b	The right bounds of the credible intervals for Beta.bHat.
Beta.sMedian	Posterior median of β for survival model, a p by 1 vector.
Beta.bMedian	Posterior median of β for binary model, a p by 1 vector.
SigmaHat	Posterior mean of variance covariance matrix.
LambdaHat	Posterior mean of λ , a $p \times 1$ vector.
TauHat	Posterior mean of τ , a 2×1 vector.
Beta.sSamples	Posterior samples of β for survival model.
Beta.bSamples	Posterior samples of β for binary model.
LambdaSamples	Posterior samples of λ .
TauSamples	Posterior samples of τ .
SigmaSamples	Posterior samples of variance covariance matrix.
DIC.s	DIC for survival model.
DIC.b	DIC for binary model.
SurvivalHat	Predictive survival probability.
LogTimeHat	Predictive log time.

References

Maity, A. K., Carroll, R. J., and Mallick, B. K. (2019) "Integration of Survival and Binary Data for Variable Selection and Prediction: A Bayesian Approach", Journal of the Royal Statistical Society: Series C (Applied Statistics).

Examples

```

burnin <- 50
nmc    <- 150
thin   <- 1
y.sd   <- 1 # standard deviation of the response

p <- 100 # number of predictors
ntrain <- 100 # training size
ntest  <- 50 # test size
n <- ntest + ntrain # sample size
q <- 10 # number of true predictos

beta.t <- c(sample(x = c(1, -1), size = q, replace = TRUE), rep(0, p - q)) # randomly assign sign

Sigma <- matrix(0.9, nrow = p, ncol = p)
for(j in 1:p)
{
Sigma[j, j] <- 1
}

x <- mvtnorm::rmvnorm(n, mean = rep(0, p), sigma = Sigma) # correlated design matrix

zmean <- x %*% beta.t
tmean <- x %*% beta.t
yCorr <- 0.5
yCov <- matrix(c(1, yCorr, yCorr, 1), nrow = 2)

y <- mvtnorm::rmvnorm(n, sigma = yCov)
t <- y[, 1] + tmean
z <- ifelse((y[, 2] + zmean) > 0, 1, 0)
X <- scale(as.matrix(x)) # standarization

z <- as.numeric(as.matrix(c(z)))
t <- as.numeric(as.matrix(c(t)))
T <- exp(t) # AFT model
C <- rgamma(n, shape = 1.75, scale = 3) # 42% censoring time
time <- pmin(T, C) # observed time is min of censored and true
status = time == T # set to 1 if event is observed
ct <- as.matrix(cbind(time = time, status = status)) # censored time

# Training set
ztrain <- z[1:ntrain]
cttrain <- ct[1:ntrain, ]
Xtrain <- X[1:ntrain, ]

# Test set
ztest <- z[(ntrain + 1):n]
cttest <- ct[(ntrain + 1):n, ]
Xtest <- X[(ntrain + 1):n, ]

```

```
posterior.fit.joint <- aftprobiths(ct = cttrain, z = ztrain, X = Xtrain,  
                                burn = burnin, nmc = nmc, thin = thin,  
                                Xtest = Xtest, cttest = cttest, ztest = ztest)  
  
posterior.fit.joint$Beta.sHat
```

Index

afths, [2](#)
aftprobiths, [4](#)