Package: SMNlmec (via r-universe)

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Type Package

Title Scale Mixture of Normal Distribution in Linear Mixed-Effects Model

Version 0.1.0

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Description Bayesian analysis of censored linear mixed-effects models that replace Gaussian assumptions with a flexible class of distributions, such as the scale mixture of normal family distributions, considering a damped exponential correlation structure which was employed to account for within-subject autocorrelation among irregularly observed measures. For more details, see Zhong et al. (2025, forthcoming in Statistics in Medicine).

Depends R (>= 4.2)

Imports rstan (>= 2.26.23), StanHeaders (>= 2.26.28), MASS (>= 7.3-60), tmvtnorm (>= 1.5), mvtnorm (>= 1.2-3), mnormt (>= 2.1.1), methods, stats, LaplacesDemon (>= 16.1.6), TruncatedNormal (>= 2.2.2), numDeriv (>= 2016.8-1.1)

URL `https://github.com/KelinZhong/SMNlmec`

BugReports `https://github.com/KelinZhong/SMNlmec/issues`

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Config/pak/sysreqs make

Repository https://kelinzhong.r-universe.dev

RemoteUrl https://github.com/kelinzhong/smnlmec

RemoteRef HEAD

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Contents

`SMNlmec.est` *Bayesian Censored Mixed-Effects Models with Damped Exponential Correlation Structures for Scale Mixture of Normal distributions error*

Description

This function fits left, right censored mixed-effects linear model, with scale mixture of normal distribution errors, using the Stan. It returns estimates, standard errors and LPML, AIC, BIC and DIC.

Usage

```
SMNlmec.est(
  ID,
  x_set,
  z_set,
  tt,
  y_complete,
  censor_vector,
  dist = "Normal",
  struc = "UNC",
  direction = "left",
  thin_num = 1,
  chains_num = 1,
  iter_num = 3000,
  burn_percen = 0.1,
  seed_set = NULL,
  adapt_delta_set = 0.8
)
```

Arguments

`ID`	Vector `N x 1` of the ID of the data set, specifying the ID for each measurement.
`x_set`	Design matrix of the fixed effects of order `N x p`.
`z_set`	Design matrix of the random effects of order `N x d`.

`tt`	Vector `N x 1` with the time the measurements were made, where `N` is the total number of measurements for all individuals. Default it's considered regular times.
`y_complete`	Vector `N x 1` of the complete responses.
`censor_vector`	Vector `N x 1` of the indicator vector of censored responses.
`dist`	Distribution of the random effects and random error. Available options are `Normal`, `Student` and `Slash`.
`struc`	Structure of the correlation structure. Available options are `UNC`, `DEC`, `CAR`.
`direction`	Direction of censoring type. Available options are `left` and `right`.
`thin_num`	A positive integer specifying the period for saving samples. The default is 5. See more details in rstan::stan().
`chains_num`	A positive integer specifying the number of chains generating by rstan::stan(). The default is 3.
`iter_num`	A positive integer specifying the number of iterations for each chain (including warmup). The default is 5000.
`burn_percen`	A percentage of the warm-up iterations in each chain the Stan. The default is 0.2.
`seed_set`	A random seed. The default is NULL.
`adapt_delta_set`	A parameter to control the sampler's behavior. The default is 0.8. See rstan::stan() for more details.

Value

Return a S4 class SMNlmecfit object. Using function `SMNlmec.summary()` to obtain the estimation of parameters and model selection criteria. The SMNlmecfit include:

`stan_object`	A stanfit object from rstan::stan().
`model_criteria`	A list includes LPML, DIC, EAIC, EBIC, K-L divergence.
`dist_set`	The setting of distribution of the stan model.
`struc_set`	The setting of correlation structure of the stan model.

References

Kelin Zhong, Fernanda L. Schumacher, Luis M. Castro and Victor H. Lachos. Bayesian analysis of censored linear mixed-effects models for heavy-tailed irregularly observed repeated measures. Statistics in Medicine, 2025. doi:10.1002/sim.10295

Examples

```
require(rstan)
require(StanHeaders)
require(MASS)
require(tmvtnorm)
require(mvtnorm)
require(mnormt)
```

```
data("UTIdata_sub")
data1 <- UTIdata_sub
y1 <- c(log10(data1$RNA))
cc <- (data1$RNAcens==1)+0
y_com<-as.numeric(y1)
rho_com<-as.numeric(cc)
x <- cbind(
 (data1$Fup==0)+0,
 (data1$Fup==1)+0,
 (data1$Fup==3)+0,
 (data1$Fup==6)+0,
 (data1$Fup==9)+0,
 (data1$Fup==12)+0,
 (data1$Fup==18)+0,
 (data1$Fup==24)+0
 )
z <- matrix(rep(1, length(y1)), ncol=1)

UTI_T_DEC <- SMNlmec.est(ID = data1$Patid, x_set = x, z_set = z,
                         tt = data1$Fup, y_complete = y_com,
                         censor_vector = rho_com, dist = "Student",
                         struc = "DEC", direction = "left",
                         thin_num = 1, chains_num = 1, iter_num = 3000,
                         burn_percen = 0.1, seed_set = 9955,
                         adapt_delta_set = 0.8)

SMNlmec.summary(UTI_T_DEC)
```

`SMNlmec.sim` *Generating Censored UNC, DEC, CAR errors with Mixed Effects, for normal, student's-t and slash distribution.*

Description

Generating Censored UNC, DEC, CAR errors with Mixed Effects, for normal, student's-t and slash distribution.

Usage

```
SMNlmec.sim(
  m,
  x,
  z,
  tt,
  nj,
  beta,
```

```
  sigma2,
  D,
  phi,
  struc = "UNC",
  typeModel = "Normal",
  p.cens = 0.1,
  n.cens = NULL,
  cens_type = "right",
  nu_set = NULL
)
```

Arguments

`m`	Number of individuals.
`x`	Design matrix of the fixed effects of order `N x p`, corresponding to vector of fixed effects.
`z`	Design matrix of the random effects of order`N x d`, corresponding to vector of random effects.
`tt`	Vector `N x 1` with the time the measurements were made, where `N` is the total number of measurements for all individuals.
`nj`	Vector `m x 1` with the number of measurements of each individual, where `m` is the total number of individuals.
`beta`	Vector of values fixed effects.
`sigma2`	Values of the scalar of the variance matrix.
`D`	Variance matrix of the random effects of order `d x d`.
`phi`	Vector of parameter in the `DEC` and `CAR` structure. NULL for `UNC`, c(phi_1,phi_2) for `DEC` and c(phi_1,1) for `CAR`.
`struc`	Structure for the simulated data. Available options are `UNC`, `DEC` and `CAR`.
`typeModel`	Distribution of the simulated data. Available options are `Normal`, `Student` and `Slash`.
`p.cens`	Percentage of censored measurements in the responses. The default value is 0.1.
`n.cens`	Number of censored measurements in the responses. The default value is NULL.
`cens_type`	The direction of cesoring. Available options are `left` and `right`.
`nu_set`	degrees of freedom for student's-t or slash simulated data. The default value is NULL.

Value

return list:

`cc`	Vector of censoring indicators.
`y_cc`	Vector of responses censoring.

Examples

```
p.cens <- 0.1
m <- 50
D <- matrix(c(0.049,0.001,0.001,0.002),2,2)
sigma2_set <- 0.15
beta <- c(-2.83,-0.18)
nu <- 2
phi <- c(0.6,2)
nj <- rep(6,m)
tt <- rep(1:6,length(nj))
X1 <- rep(1,sum(nj))
X2 <- tt
x <- as.matrix(cbind(X1,X2))
Z1 <- rep(1,sum(nj))
Z2 <- tt
z <- as.matrix(cbind(Z1,Z2))

ID_sim <- rep(0,length(tt))
ID_log <- 0
for(i in 1:m) {
  for(j in 1:nj[i]) {
    ID_sim[ID_log + j] <- i
  }
  ID_log <- ID_log + nj[i]
}

Slash_DEC_sim <- SMNlmec.sim(m = m,x = x,z = z,tt = tt,nj = nj,beta = beta,
                      sigma2 = sigma2_set,D = D,phi= phi,struc ="DEC",
                      typeModel="Slash",p.cens = p.cens,n.cens = NULL,
                      cens_type="right",nu_set=nu)

head(Slash_DEC_sim$cc)
sum(Slash_DEC_sim$cc)/length(Slash_DEC_sim$cc)

head(Slash_DEC_sim$y_cc)


y_com <- as.numeric(Slash_DEC_sim$y_cc)
rho_com <- as.numeric(Slash_DEC_sim$cc)
tem <- tt

Slash_DEC_est <- SMNlmec.est(ID = ID_sim, x_set = x, z_set = z,
                         tt = tem, y_complete = y_com,
                         censor_vector = rho_com, dist = "Slash",
                         struc = "DEC", direction = "right",
                         thin_num = 1, chains_num = 1, iter_num = 3000,
                         burn_percen = 0.1, seed_set = 9955,
                         adapt_delta_set = 0.8)

SMNlmec.summary(Slash_DEC_est)
```

`SMNlmec.summary` *SMNlmecfit Summary*

Description

A generic function to provide a summary for objects of class `SMNlmecfit`.

Usage

```
SMNlmec.summary(object)

## S4 method for signature 'SMNlmecfit'
SMNlmec.summary(object)
```

Arguments

`object`	An object of class `SMNlmecfit`.

Value

A summary of model estimations, R-hats, standard errors, and criteria.

A printed summary of the SMNlmecfit object.

`SMNlmec.summary,SMNlmecfit-method` *Get a summary of results from SMNlmec.est.*

Description

Get a summary of results from SMNlmec.est.

Usage

```
## S4 method for signature 'SMNlmecfit'
SMNlmec.summary(object)
```

Arguments

`object`	An object of class `SMNlmecfit`.

Value

The summary of estimations, R hats, standard errors and 95

`SMNlmecfit-class` *SMNlmecfit Class*

Description

SMNlmecfit Class

Slots

`stan_object` stanfit object from rstan.

`model_criteria` list, model selection criteria.

`dist_set` character, the name of distribution.

`struc_set` character, the name of correlation structure.

`SMNlmecfit.creator` *Create SMNlmecfit Objects*

Description

A function to create objects of class `SMNlmecfit`.

Usage

```
SMNlmecfit.creator(stan_object, model_criteria, dist_set, struc_set)
```

Arguments

`stan_object`	stanfit object from rstan.
`model_criteria`	list, model selection criteria.
`dist_set`	character, the name of distribution.
`struc_set`	character, the name of correlation structure.

Value

A SMNlmecfit object containing:

`stan_object`	A stanfit object from rstan::stan().
`model_criteria`	A list includes LPML, DIC, EAIC, EBIC, K-L divergence.
`dist_set`	The setting of distribution of the stan model.
`struc_set`	The setting of correlation structure of the stan model.

`UTIdata` *Data set for Unstructured Treatment Interruption Study*

Description

Data set from a study of Unstructured Treatment Interruption in HIV-infected adolescents in four institutions in the US. The main outcome is the HIV-1 RNA viral load, which is subject to censoring below the lower limit of detection of the assay (50 copies/mL). The censored observations are indicated by the variable RNAcens.

Usage

`data(UTIdata)`

Format

A data frame with 373 observations on the following 5 variables.

Patid patient ID

Days.after.TI days after treatment interruption.

Fup follow-up months

RNA viral load RNA

RNAcens censoring indicator for viral load

References

Saitoh, A., Foca, M, et al. (2008), Clinical outcome in perinatally acquired HIV-infected children and adolescents after unstructured treatment interruption, Pediatrics,121, e513-e521.

`UTIdata_sub` *Sub data set for Unstructured Treatment Interruption Study*

Description

Data set from a study of Unstructured Treatment Interruption in HIV-infected adolescents in four institutions in the US. The main outcome is the HIV-1 RNA viral load, which is subject to censoring below the lower limit of detection of the assay (50 copies/mL). The censored observations are indicated by the variable RNAcens. Excluding subjects whose observations are less than 2 and with missing RNA (excluding subject ID C6 T16).

Usage

`data(UTIdata_sub)`

Format

A data frame with 360 observations on the following 5 variables.

patient ID

Patid **Days.after.TI** days after treatment interruption.

Fup follow-up months

RNA viral load RNA

RNAcens censoring indicator for viral load

References

Saitoh, A., Foca, M, et al. (2008), Clinical outcome in perinatally acquired HIV-infected children and adolescents after unstructured treatment interruption, Pediatrics,121, e513-e521.

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