

Package ‘SMNlmec’

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Type Package

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

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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 Kelin Zhong, Fernanda L. Schumacher, Luis M. Castro, Victor H. Lachos (2025) <[doi:10.1002/sim.10295](https://doi.org/10.1002/sim.10295)>.

Depends R (>= 4.2)

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URL <https://github.com/KelinZhong/SMNlmec>

BugReports <https://github.com/KelinZhong/SMNlmec/issues>

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Contents

SMNlmec.est	2
SMNlmec.sim	4
SMNlmec.summary	7
SMNlmecfit-class	7
SMNlmecfit.creator	8
UTIdata	8
UTIdata_sub	9
Index	10

SMNlmec.est	<i>Bayesian Censored Mixed-Effects Models with Damped Exponential Correlation Structures for Scale Mixture of Normal distributions error</i>
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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.

<code>tt</code>	Vector $N \times 1$ with the time the measurements were made, where N is the total number of measurements for all individuals. Default it's considered regular times.
<code>y_complete</code>	Vector $N \times 1$ of the complete responses.
<code>censor_vector</code>	Vector $N \times 1$ of the indicator vector of censored responses.
<code>dist</code>	Distribution of the random effects and random error. Available options are Normal, Student and Slash.
<code>struc</code>	Structure of the correlation structure. Available options are UNC, DEC, CAR.
<code>direction</code>	Direction of censoring type. Available options are left and right.
<code>thin_num</code>	A positive integer specifying the period for saving samples. The default is 5. See more details in <code>rstan::stan()</code> .
<code>chains_num</code>	A positive integer specifying the number of chains generating by <code>rstan::stan()</code> . The default is 3.
<code>iter_num</code>	A positive integer specifying the number of iterations for each chain (including warmup). The default is 5000.
<code>burn_percen</code>	A percentage of the warm-up iterations in each chain the Stan. The default is 0.1.
<code>seed_set</code>	A random seed. The default is NULL.
<code>adapt_delta_set</code>	A parameter to control the sampler's behavior. The default is 0.8. See <code>rstan::stan()</code> 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:

<code>stan_object</code>	A stanfit object from <code>rstan::stan()</code> .
<code>model_criteria</code>	A list includes LPML, DIC, EAIC, EBIC, K-L divergence.
<code>dist_set</code>	The setting of distribution of the stan model.
<code>struc_set</code>	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 $N \times p$, corresponding to vector of fixed effects.
z	Design matrix of the random effects of order $N \times d$, corresponding to vector of random effects.
tt	Vector $N \times 1$ with the time the measurements were made, where N is the total number of measurements for all individuals.
nj	Vector $m \times 1$ 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 $d \times d$.
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 censoring. 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_perccn = 0.1, seed_set = 9955,
  adapt_delta_set = 0.8)

SMNlmec.summary(Slash_DEC_est)

```

SMNlmec.summary	<i>SMNlmecfit Summary</i>
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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.

SMNlmecfit-class	<i>SMNlmecfit Class</i>
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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	<i>Create SMNlmecfit Objects</i>
--------------------	----------------------------------

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	<i>Data set for Unstructured Treatment Interruption Study</i>
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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.

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

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.

Index

SMNlmec.est, [2](#)
SMNlmec.sim, [4](#)
SMNlmec.summary, [7](#)
SMNlmec.summary, SMNlmecfit-method
 (SMNlmec.summary), [7](#)
SMNlmecfit-class, [7](#)
SMNlmecfit.creator, [8](#)

UTIdata, [8](#)
UTIdata_sub, [9](#)