

# Package ‘SMNlmeC’

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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

**NeedsCompilation** no

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|            |  |
|------------|--|
| SMNlmecest | <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

```
SMNlmecest(
  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 $N \times 1$ of the ID of the data set, specifying the ID for each measurement. |
| x_set | Design matrix of the fixed effects of order $N \times p$ .                             |
| z_set | Design matrix of the random effects of order $N \times d$ .                            |

|                              |   |
|------------------------------|---|
| <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>sensor_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 0.2.  |
| <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_perccn = 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, $c(\text{phi}_1, \text{phi}_2)$ for DEC and $c(\text{phi}_1, 1)$ 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 <- SMNlmecc.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 <- SMNlmecc.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)

SMNlmecc.summary(Slash_DEC_est)

```

---

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

---

**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.

---

|                               |                         |
|-------------------------------|-------------------------|
| <code>SMNlmecfit-class</code> | <i>SMNlmecfit Class</i> |
|-------------------------------|-------------------------|

---

**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.

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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.

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.

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