

# Package ‘lme4’

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**Type** Package

**Title** Linear Mixed-Effects Models with Censored Responses

**Version** 1.0

**Date** 2009-01-28

**Author** Florin Vaida and Lin Liu

**Maintainer** Lin Liu <linliu@ucsd.edu>

**Description** This package includes a function to fit a linear mixed-effects model in the formulation described in Laird and Ware (1982) but allowing for censored normal responses. In this version, the with-in group errors are assumed independent and identically distributed.

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**Depends** mvtnorm

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Imec-package

*Linear Mixed-Effects Models with Censored Responses*

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## Description

This package includes a function to fit a linear mixed-effects model in the formulation described in Laird and Ware (1982) but allowing for censored normal responses. In this version, the within group errors are assumed independent and identically distributed.

## Details

Package: Imec  
Type: Package  
Version: 1.0  
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## Author(s)

Florin Vaida and Lin Liu

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## References

Vaida, Florin and Liu, Lin, Fast Implementation For Normal Mixed Effects Models with Censored Response (submitted).

Vaida, Florin and Fitzgerald, Anthony and DeGruttola, Victor (2007), Efficient Hybrid EM for non-linear mixed effects models with censored response, Computational Statistics and Data Analysis, 51, 5718-5730.

## Examples

```
data(UTIdata)
UTIdata <- subset(UTIdata, !is.na(RNA))
o <- order(UTIdata$Patid, UTIdata$Fup)
UTIdata <- UTIdata[o,]
cens <- (UTIdata$RNAcens==1)+0
yL<- log10(UTIdata$RNA)
X<- cbind((UTIdata$Fup==0)+0, (UTIdata$Fup==1)+0, (UTIdata$Fup==3)+0, (UTIdata$Fup==6)+0, (UTIdata$Fup==9)+0, (U
Z <- matrix(rep(1, length(yL)), ncol=1)
cluster<- as.numeric(UTIdata$Patid)
fit <- Imec(yL,cens, X, Z, cluster, method='ML', maxstep=40)
```

**Description**

This generic function fits a linear mixed-effects model in the formulation described in Laird and Ware (1982) but allowing for censored normal responses. In this version, the with-in group errors are assumed independent and identically distributed.

**Usage**

```
lme4(yL, cens, X, Z, cluster, maxstep = 200, varstruct = "unstructured", init, method = "ML", epsstop = 0
```

**Arguments**

|           |                                                                                                                         |
|-----------|-------------------------------------------------------------------------------------------------------------------------|
| yL        | Observed left-censored response vector                                                                                  |
| cens      | Censoring indicator: if $y_L > y_{true}$ , then $cens=1$                                                                |
| X         | Design matrix for the fixed-effects model, it needs to include a column of 1's if the intercept is present              |
| Z         | If the design matrix for the random-effects is $\text{diag}(Z_1, Z_2, \dots, Z_m)$ , then $Z=(Z_1', Z_2', \dots, Z_m')$ |
| cluster   | Cluster indicator taking values between 1 and m                                                                         |
| maxstep   | The maximum number of EM iterations                                                                                     |
| varstruct | Variance structure for random effects, current options are unstructured and diagonal.                                   |
| init      | Initial estimated parameters (it is optional), it is a list with components beta, bi, sigma and Delta.                  |
| method    | Options are ML, REML and MLmcmc                                                                                         |
| epsstop   | The threshold for the difference between two consecutive likelihood values in EM sequence                               |
| abspmv    | Absolute error tolerance for pmvnorm() function                                                                         |
| mcmc0     | The burn-in MCMC sample size for E-step of EM                                                                           |
| sd1       | The target standard deviation for the log-likelihood                                                                    |
| iter2     | Number of steps in stage 2 for evaluating standard deviation of log-likelihood                                          |
| trs       | Number of increase in sample size during transition face                                                                |
| p1s       | Number of steps in plateau face of MCEM                                                                                 |
| mcmcmax   | Maximum MCEM sample size                                                                                                |

**Value**

|           |                                                                                      |
|-----------|--------------------------------------------------------------------------------------|
| beta      | Estimated fixed effects                                                              |
| bi        | Estimated random effects                                                             |
| sigma     | Residual standard deviation                                                          |
| Psi       | Variance matrix of random effects                                                    |
| Delta     | Matrix such that $\Delta' * \Delta = \sigma^2 * \text{solve}(\Psi)$                  |
| loglik    | Maximum log-likelihood value (or surrogate objective function)                       |
| varFix    | Variance matrix for fixed effects                                                    |
| method    | Options are ML, REML and MLmcmc                                                      |
| varstruct | Variance structure for random effects, current options are unstructured and diagonal |
| step      | Number of EM iterations                                                              |
| likseq    | Log-likelihood EM sequence                                                           |

**Author(s)**

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**References**

Vaida, Florin and Liu, Lin, Fast Implementation For Normal Mixed Effects Models with Censored Response (submitted).

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**Examples**

```
data(UTIdata)
UTIdata <- subset(UTIdata, !is.na(RNA))
o <- order(UTIdata$Patid, UTIdata$Fup)
UTIdata <- UTIdata[o,]
cens = (UTIdata$RNAcens==1)+0
y = log10(UTIdata$RNA)
X = cbind((UTIdata$Fup==0)+0, (UTIdata$Fup==1)+0, (UTIdata$Fup==3)+0, (UTIdata$Fup==6)+0, (UTIdata$Fup==9)+0, (UTIdata$Fup==12)+0)
Z = matrix(rep(1, length(y)), ncol=1)
cluster = as.numeric(UTIdata$Patid)
fit = lmec(yL=y, cens=cens, X=X, Z=Z, cluster=cluster, method='ML', maxstep=40)
```

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UTIdata

*Data set for Unstructured Treatment Interruption Study*

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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.

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.

**Examples**

```
data(UTIdata)
## maybe str(UTIdata) ; plot(UTIdata) ...
```

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