

Package ‘lme4’

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Type Package

Title 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 with-in group errors are assumed independent and identically distributed.

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 Imec-package

Linear Mixed-Effects Models with Censored Responses

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)

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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 <- lme(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
pls	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).

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$RNAcens==1)+0
y = log10(UTIdata$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)
```

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.

Examples

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

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