Package 'lmec'

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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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`lmec-package` *Linear Mixed-Effects Models with Censored Responses*

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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.

Details

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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, (U
Z <- matrix(rep(1, length(yL)), ncol=1)
cluster<-  as.numeric(UTIdata$Patid)
fit <- lmec(yL,cens, X, Z, cluster, method='ML', maxstep=40)
```

`lmec` *Linear Mixed-Effects Models with Censored Responses*

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

```
lmec(yL, cens, X, Z, cluster, maxstep = 200, varstruct = "unstructured", init, meth
```

Arguments

`yL`	Observed left-censored response vector
`cens`	Censoring indicator: if yL>ytrue, 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 diag(Z1, Z2, ..., Zm), then Z=(Z1',Z2', ..., Zm')'
`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`	Intial 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
`sdl`	The target standard deviation for the log-likelihood
`iter2`	Number of steps in stage 2 for evaluating standard deviation of log-likelihhood
`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=sigma2*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, (U
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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