Package ‘lmec’

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Type Package

Title Linear Mixed-Effects Models with Censored Responses

Version 1.0

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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.

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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: lmec
Type: Package
Version: 1.0
Date: 2009-01-28

Author(s)
Florin Vaida and Lin Liu
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References

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$Fup==9)+0, (UTIdata$Fup==15)+0, (UTIdata$Fup==20)+0, (UTIdata$Fup==27)+0)
Z <- matrix(rep(1, length(yL)), ncol=1)
ccluster <- 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 within-group errors are assumed independent and identically distributed.

Usage
```
lmec(yL, censL, xL, ZL, clusterL, maxstepL = 200, varstructL = "unstructured", initL, methodL = "ML", epsstopL = 1E-08, abspmvL = 0.0001, mcmcP = 0, sdlL = 2, iterR = 10, trsL = 8, mcmcmaxL = 2)
```

Arguments
- `yL`: Observed left-censored response vector
- `censL`: Censoring indicator: if `yL` > `ytrue`, then `censL` = 1
- `xL`: Design matrix for the fixed-effects model, it needs to include a column of 1's if the intercept is present
- `ZL`: If the design matrix for the random-effects is diag(Z1, Z2, ..., Zm), then Z=(Z1', Z2', ..., Zm')
- `clusterL`: Cluster indicator taking values between 1 and m
- `maxstepL`: The maximum number of EM iterations
- `varstructL`: Variance structure for random effects, current options are unstructured and diagonal.
- `initL`: Initial estimated parameters (it is optional), it is a list with components beta, bi, sigma and Delta.
- `methodL`: Options are ML, REML and MLmcmc
- `epsstopL`: The threshold for the difference between two consecutive likelihood values in EM sequence
- `abspmvL`: Absolute error tolerance for pmvnorm() function
- `mcmcP`: The burn-in MCMC sample size for E-step of EM
- `sdlL`: The target standard deviation for the log-likelihood
- `iterR`: Number of steps in stage 2 for evaluating standard deviation of log-likelihood
- `trsL`: Number of increase in sample size during transition face
- `plsL`: Number of steps in plateau face of MCEM
- `mcmcmaxL`: 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


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(y=y, cens=cens, X=X, Z=Z, cluster=cluster, method='ML', maxstep=40)
**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**


**Examples**

data(UTIdata)

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