Package 'tlmec'

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Type Package

Title Linear Student-t Mixed-Effects Models with Censored Data

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Depends R (>= 1.9.0), mvtnorm (>= 0.9-9991)

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Description Fit a linear mixed effects model for censored data with
Student-t or normal distributions. The errors are assumed
independent and identically distributed.

License GPL (>= 3.0)

LazyLoad yes

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R topics documented:

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tlmec   *Linear Student-t Mixed-Effects Models with Censored Data*

Description

Fit a linear mixed effects model for censored data with Student-t or normal distributions. The errors are assumed independent and identically distributed.

Usage

```
tlmec(cens = NULL, y = NULL, x = NULL, z = NULL, nj = NULL,
      nu = 4, family = "t", criteria = TRUE, diagnostic = FALSE,
      initial, iter.max = 200, error = 0.001)
```

Arguments

cens	Vector of censures.
y	Vector or matrix of response. If y is a matrix the number of columns must be max(nj) with the missing values set as NA for non balanced design.
x	Design matrix of the fixed effects.
z	Design matrix of the random effects.
nj	A vector with the number of observations for each subject.
nu	Degree of freedom for Student-t distribution.
family	Distribution family to be used in fitting ("t" and "Normal")
criteria	If TRUE AIC, corrected AIC(AICcorr) and BIC are computed.
diagnostic	If TRUE all EM output are returned.
initial	Initial values
iter.max	The maximum number of iteration of the EM algorithm.
error	The convergence maximum error.

Value

Estimated values of beta, sigma2, the covariance matrix of the random effects and the random effects.

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See Also

UTIdata

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 146 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

```
## Not run:
## load data
data(UTIdata)

## Sort the data by Patient and  visit
o <- order(UTIdata$Patid, UTIdata$Fup)
UTIdata <- UTIdata[o,]

## Create censure vector
cens = (UTIdata$RNAcens==1)+0

## Generate response vector
y = log10(UTIdata$RNA)
aa=y[cens==0]

## Create the design matrices
```

```
x = cbind((UTIdata$Fup==0)+0, (UTIdata$Fup==1)+0, (UTIdata$Fup==3)+0, (UTIdata$Fup==6)+0, (UTIdata$Fup==9)+0, (U
z = matrix(rep(1, length(y)), ncol=1)
cluster = as.numeric(UTIdata$Patid)

## Create the nj vector
nj<-matrix(0,72,1)
for (j in 1:72) {
nj[j]=sum(cluster==j)
}

## Number of individuals
m<-dim(nj)[1]

## Call the tlmec with Normal mixed-effects
out.N <- tlmec(cens,y,x,z,nj,family="Normal",criteria=TRUE)

## Call the tlmec with Student-t mixed-effects
out.T <- tlmec(cens,y,x,z,nj,nu=9,family="t",criteria=TRUE)

## End(Not run)
```

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