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.

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R topics documented:

  tlmec ................................................................. 2
  UTIdata .......................................................... 3

Index 5
**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**

```r
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`
**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**

```r
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**


**Examples**

```r
## 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
```
\begin{verbatim}
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, (UTIdata$Fup==18)*0, (UTIdata$Fup==24)*0, (UTIdata$Fup==30)*0)
z = matrix(rep(1, length(y)), ncol=1)
cluster = as.numeric(UTIdata$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)
\end{verbatim}
Index

*Topic Mixed-effects with censored response
  tlmec, 2
*Topic datasets
  UTIData, 3
*Topic linear
  tlmec, 2

tlmec, 2

UTIData, 2, 3