

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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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 censor 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$Fup==9)+0, (
z = matrix(rep(1, length(y)), ncol=1)
cluster = as.numeric(UTIdata$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 tlmecc with Normal mixed-effects
out.N <- tlmecc(cens,y,x,z,nj,family="Normal",criteria=TRUE)

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

## End(Not run)
```

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