Package 'MBRM'

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Type Package

Title Mixed Regression Models with Generalized Log-Gamma Random Effects

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Description ``Fits binary mixed regression models with random effects
based on the generalized log-gamma distribution. Estimation is
performed by maximizing the log-likelihood using numerical
optimization."

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

LinkingTo Rcpp

Imports Rcpp,
stats,
Formula,
tibble,
dplyr

Depends R (>= 3.5)

R topics documented:

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Arthritis1   *Arthritis1 Dataset*

Description

This dataset contains binary response data from a longitudinal study on rheumatoid arthritis. The data includes repeated measurements on 38 individuals, each with 5 time points.

Usage

```
Arthritis1
```

Format

A data frame with 190 rows and 6 variables:

Ind Subject identifier (integer from 1 to 38)

y Binary response variable (0 or 1)

Sex Sex indicator (0 = Female, 1 = Male)

Age Age indicator (0 = below median, 1 = above median)

Treatment Treatment group (0 = Placebo, 1 = Treated)

Time Time indicator (0 = baseline, 1 = follow-up)

Details

The original data was collected to evaluate the effect of a treatment over time on arthritis severity. Covariates include demographic and clinical variables, and the response is binary (presence/absence of symptom).

Source

Derived from the original dataset included in:
Arthritis.txt — internal clinical dataset used in Bernoulli-GLG modeling study.

Examples

```
data(Arthritis1)
head(Arthritis1)

# Fit the Bernoulli-LGG model
fit <- MRMfit(y ~ Sex + Age + Treatment + Time, data = Arthritis1)
summary(fit)
```

MRMfit   *Fit Mixed Regression Model with Log-Gamma Random Effects*

Description

This function fits a mixed regression model for binary outcomes with random effects following a generalized log-gamma distribution. The estimation is performed by maximizing a custom log-likelihood using numerical optimization.

Usage

```
MRMfit(formula, data, family = "bernoulli", method = "BFGS")
```

Arguments

formula	A symbolic description of the model to be fitted, e.g., y ~ x1 + x2. The response variable must be binary (0/1).
data	A data frame containing the variables in the model. The data must include an Ind column indicating cluster or subject IDs for the random effects.
family	A character string specifying the response distribution. Currently only "bernoulli" is supported (default).
method	Optimization method to be used in optim. Default is "BFGS".

Value

An object of class "MRM" containing:

call	The matched function call.
formula	The model formula.
coefficients	Estimated fixed effects coefficients.
scale	Estimated scale parameter for the random effects distribution.
loglik	Maximized log-likelihood value.
n	Number of clusters or subjects.
m	Vector with the number of observations per cluster.
ep	Estimated standard errors for parameters.
iter	Number of iterations used by the optimizer.
family	Family string used.
data	The original data frame used.

Examples

```
## Not run:
data1 <- rMRM(n = 50, m = rep(3, 50),
theta = c(0.8, 1, -1), X = data.frame(x1 = rnorm(50),
x2 = rnorm(50)))
fit <- MRMfit(y ~ x1 + x2, data = data1)
print(fit)
summary(fit)

## End(Not run)
```

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rMRM   *Simulate Data from a Mixed Regression Model with Random Effects*

Description

This function simulates clustered binary response data from a mixed regression model with random effects. The model allows for different link functions and random effect distributions.

Usage

```
rMRM(
  n,
  m,
  theta,
  X,
  family = "bernoulli",
  link = "cloglog",
  random = "gengamma"
)
```

Arguments

n	Integer. Number of clusters or subjects.
m	Integer vector of length n. Each element indicates the number of observations per cluster.
theta	Numeric vector. The first element is the scale or dispersion parameter for the random effects, and the remaining values are the fixed effects coefficients, including the intercept.
X	A data frame or matrix of covariates with n rows (one per cluster). Should not include the intercept.
family	Character. The response distribution. Currently only "bernoulli" is supported (default).
link	Character. The link function to use. One of: "cloglog", "logit", or "probit". Default is "cloglog".
random	Character. Distribution for the random effects. One of: "gengamma" or "normal". Default is "gengamma".

Value

A `tibble` containing the simulated dataset with the following columns:

Ind Cluster or subject ID (integer from 1 to n).

y Binary response variable (0 or 1).

x1, x2, ... Covariates as defined in X, repeated according to cluster size.

The output also has an attribute "proportions" indicating the proportion of 0's and 1's in y.

Examples

```
## Not run:
set.seed(123)
n <- 500
m <- rep(3,n)
theta <- c(0.5,1,-2,1)
set.seed(123)
X <- cbind(runif(n),rnorm(n))
set.seed(456)
data1 <- rMRM(n,m,theta,X,family="bernoulli",
link="cloglog",random = "gengamma")
head(data1

## End(Not run)
```

---

toenail   *toenail Dataset*

Description

This dataset contains binary response data from a longitudinal study on rheumatoid arthritis. The data includes repeated measurements on 38 individuals, each with 5 time points.

Usage

```
toenail
```

Format

A data frame with 190 rows and 6 variables:

Ind Subject identifier (integer from 1 to 38)

y Binary response variable (0 or 1)

Treatment Treatment group (0 = Placebo, 1 = Treated)

Time Time indicator (0 = baseline, 1 = follow-up)

Details

The original data was collected to evaluate the effect of a treatment over time on arthritis severity. Covariates include demographic and clinical variables, and the response is binary (presence/absence of symptom).

Source

Derived from the original dataset included in:
toenail.txt — internal clinical dataset used in Bernoulli-GLG modeling study.

Examples

```
data(toenail)
head(toenail)

# Fit the Bernoulli-LGG model
fit <- MRMfit(y ~ Treatment + Time + Treatment:Time, data = toenail)
summary(fit)
```

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