Package 'MBRM'

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Type Package

Title Mixed Regression Models with Generalized Log-Gamma Random Effects

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Description ``This package 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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LazyData true

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LinkingTo Rcpp

Imports Rcpp,
stats,
Formula,
tibble,
dplyr,
ggplot2

Depends R (>= 3.5)

Contents

Arthritis1   *Arthritis1 Dataset*

Description

This dataset contains binary response data from a longitudinal study on rheumatoid arthritis. The data include 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 = <=55 years 1 = > 55 uears)

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

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 symptoms).

Source

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

References

Fitzmaurice, G. M. and Lipsitz, S. (1995). A model for binary time series data with serial odds ratio patterns. *Journal of the Royal Statistical Society: Series B*, 44, 51–61.

Examples

```
## Not run:
data(Arthritis1)
head(Arthritis1)

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

## End(Not run)
```

---

envelope.MRM   *Compute simulation envelopes for MRM model*

Description

This function computes the envelopes simulation of the randomized quantile residuals for objects of class MRM.

Usage

```
envelope.MRM(object, R = 100, ...)
```

Arguments

object	An object of class MRM, typically returned from `MRMfit`.
R	Integer. Number of replications to simulate the envelopes (default is 100).
...	Additional arguments passed to `MRMfit` when envelope = TRUE.

Value

A QQ-plot with envelope.

Examples

```
data(Arthritis1)
fit <- MRMfit(y ~ Sex + Age + Treatment + Time, data = Arthritis1)
envelope.MRM(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 via `optim`.

Usage

```
MRMfit(formula, data, hessian = TRUE, 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.
hessian	Logical. Should a numerically differentiated Hessian matrix be returned?
method	Optimization method to be used in [optim](). One of "Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN", or "Brent". Default is "BFGS".
...	Additional arguments passed to [optim](), such as control, lower, or upper (when supported by the chosen method).

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 of the parameters.
iter	Number of iterations used by the optimizer.
method	Optimization method used.
data	The original data frame used.

Examples

```
## Not run:
# Simulated data
data1 <- rMRM(n = 50, m = rep(3, 50),
              theta = c(0.8, 1, -1),
              X = data.frame(x1 = rnorm(150), x2 = rnorm(150)))

# Fit using BFGS (default)
fit1 <- MRMfit(y ~ x1 + x2, data = data1)
summary(fit1)

# Fit using L-BFGS-B with bounds
fit2 <- MRMfit(y ~ x1 + x2, data = data1,
               method = "L-BFGS-B",
               lower = c(1e-5, rep(-Inf, 3)),
               upper = rep(Inf, 4),
               control = list(factr = 1e7))
summary(fit2)

## End(Not run)
```

---

residuals.MRM   *Compute the randomized quantile residuals for MRM model*

Description

This function computes the randomized quantile residuals for objects of class MRM.

Usage

```
## S3 method for class 'MRM'
residuals(object, ...)
```

Arguments

object   An object of class MRM, typically returned from `MRMfit`.

...   Additional arguments passed to `MRMfit`.

Value

A numeric vector of randomized quantile residuals.

Examples

```
data(Arthritis1)
fit <- MRMfit(y ~ Sex + Age + Treatment + Time, data = Arthritis1)
summary(residuals(fit))
```

---

rMRM   *Simulate Data from a Mixed Regression Model with GLG 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)
```

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.

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 proportions 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)
head(data1)

## End(Not run)
```

---

toenail	*toenail Dataset*

Description

A data frame with 1908 observations on the following 4 variables.

Usage

```
toenail
```

Format

A data frame with 1908 rows and 4 variables:

Ind Subject identifier (integer from 1 to 38)

y Binary response is the severity of infection, 0 (not severe) and 1(severe).

treatment Treatment group (0 = Treatment A, 1 = Treatment B)

month a numeric vector giving the time of the visit (not exactly monthly intervals hence not round numbers)

visit a numeric vector giving the number of the visit

Details

The Toenail data discussed in Molenberghs and Verbeke (2010) were obtained from a randomized, double-blind, parallel-group, multicenter study for the comparison of two oral treatments (coded as A and B) for Toenail Dermatophyte Onychomycosis (TDO). The present study aimed to compare the efficacy of 12 weeks of continuous therapy with Treatment A or B. In total, 294 patients, distributed over 36 centers, were randomized. Subjects were followed during 12 weeks (3 months) of treatment and followed further up to 48 weeks (12 months). Measurements were taken at baseline every month during treatment and every 3 months afterward, resulting in a maximum of 7 measurements per subject.

References

Molenberghs G, Verbeke G (2010). Models for Discrete Longitudinal data. Springer, New York.

Examples

```
## Not run:
data(toenail)
head(toenail)

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

## End(Not run)
```

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