

# Package ‘glmmrr’

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**Type** Package

**Title** Logistic Mixed-Effects Model with Pseudo-  
Observations for Estimating Risk Ratios in Clustered Binary Data Analysis

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**Description** Logistic mixed-effects model has been widely used as a multilevel statistical model for analyzing clustered binary outcome data (e.g., longitudinal studies, cluster-randomised trials, and multi-center clinical trials). However, the resultant odds ratio estimator can only be interpreted as an approximation of the risk ratio estimator for low-frequency events; it cannot be directly interpreted as an effect measure. To overcome this issue, the modified Poisson regression analysis and its extension to GEE methodology has been widely applied in recent clinical and epidemiological studies, but these estimating equation-based semiparametric methods cannot be straightforwardly extended to mixed-effects models. Noma and Goshio (2025) proposed a new method to provide consistent risk ratio estimator on a multilevel statistical model framework using logistic mixed-effects model incorporating pseudo-observations. The advantage of the new method is it is implementable using a standard statistical software of GLMM only through modifying dataset. This package involves computational functions for implementing the risk ratio estimation method through multilevel modelling framework.

**Depends** R (>= 3.5.0)

**Imports** stats, glmmML, doSNOW, doParallel

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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 glmmrr-package

*The 'glmmrr' package*


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## Description

Logistic mixed-effects model has been widely used as a multilevel statistical model for analyzing clustered binary outcome data (e.g., longitudinal studies, cluster-randomised trials, and multi-center clinical trials). However, the resultant odds ratio estimator can only be interpreted as an approximation of the risk ratio estimator for low-frequency events; it cannot be directly interpreted as an effect measure. To overcome this issue, the modified Poisson regression analysis and its extension to GEE methodology has been widely applied in recent clinical and epidemiological studies, but these estimating equation-based semiparametric methods cannot be straightforwardly extended to mixed-effects models. Noma and Gosho (2025) proposed a new method to provide consistent risk ratio estimator on a multilevel statistical model framework using logistic mixed-effects model incorporating pseudo-observations. The advantage of the new method is it is implementable using a standard statistical software of GLMM only through modifying dataset. This package involves computational functions for implementing the risk ratio estimation method through multilevel modelling framework.

## References

Noma, H. and Gosho, M. (2025). Logistic mixed-effects model analysis with pseudo-observations for estimating risk ratios in clustered binary data analysis. Forthcoming.

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 adpdt

*Creating a dataset for fitting the logistic mixed-effects model for estimating risk ratios via adding pseudo-observations*


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## Description

Creating a dataset for fitting the logistic mixed-effects model for estimating risk ratios. Pseudo-observations are added to the original dataset object.

## Usage

```
adpdt(y, data=NULL)
```

## Arguments

y	The outcome variable (should be coded as 0, 1 contained in the dataset object).
data	The dataset object.

## Value

A data frame object added the pseudo-observations for fitting the logistic mixed-effects model for estimating risk ratios.

## References

Noma, H. and Gosho, M. (2025). Logistic mixed-effects model analysis with pseudo-observations for estimating risk ratios in clustered binary data analysis. Forthcoming.

## Examples

```
library(glmML)

data(resp)

resp.t <- adpdt(y, resp) # Adding pseudo-observations to the original dataset

gmm2 <- glmML(y ~ treat + baseline + center + sex + age, data=resp.t, family =binomial,
  cluster=id, method="ghq") # Logistic mixed model with pseudo-observations

scoef(gmm2, eform=TRUE)
# 95% CIs and P-values are incorrect (based on the naive model variances)
```

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cboot	<i>Perform the cluster-level bootstrap resampling</i>
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## Description

Cluster-level bootstrap resampling is performed from the corresponding dataset.

## Usage

```
cboot(cluster, data=NULL)
```

## Arguments

cluster	The variable specifying clusters contained in the dataset object.
data	The dataset object.

## Value

A data frame object obtained by cluster-level resampling. The cluster variable after resampling was named as `cluster.b`.

## Examples

```
data(resp)
cboot(id, resp)
```

---

mch	<i>A cluster-randomised trial dataset for the maternal and child health handbook</i>
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## Description

A cluster-randomised trial dataset with binomial outcome.

- ID: ID variable of participants.
- SOUM: ID variable of soums (involving 18 soums).
- x: Binary variable specifying intervention groups (1=Intervention, 0=Control).
- mage: Mother's age.
- medu: Mother's education (1=uneducated, 2=elementary, 3=incomplete secondary, 4=complete secondary, 5=incomplete high, 6=high (completed collage or university)).
- mmarry: Mother's marital status (1=single, 2=married/cohabitating, 3=separated/divorce, 4=widowed/other).
- mprig1: First pregnancy (1=Yes, 2=No).
- height: Mother's height.
- weight: Mother's weight.
- time: Travel time from mother's home to antenatal care clinic.
- Y: Outcome variable: Number of antenatal visits.
- y: Outcome variable: Whether the number of antenatal visits is  $\geq 6$  (0 or 1).
- ses: Quintile groups by the social-economic index (= 1, 2, 3, 4, 5).

## Usage

```
data(mch)
```

## Format

A data frame with 500 participants with 18 soums.

## References

Mori, R., Yonemoto, N., Noma, H., et al. (2015). The Maternal and Child Health (MCH) handbook in Mongolia: a cluster-randomized, controlled trial. *PloS One* **10**: e0119772.

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 resp

*A longitudinal clinical trial dataset for a respiratory disease*


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### Description

A longitudinal clinical trial dataset with binomial outcome.

- id: ID variable of participants.
- center: Numerical variable specifying center (involving two centers).
- treat: Binary variable specifying treatment groups (1=Active, 0=Placebo).
- age: Age.
- sex: Gender (1=Male, 0=Female).
- baseline: Respiratory status at baseline (0 or 1).
- visit: Visit times (=1,2,3,4).
- y: Outcome variable for respiratory status (0 or 1).

### Usage

```
data(resp)
```

### Format

A data frame with 111 patients.

### References

Berry, D. A. (1989). *Statistical Methodology in the Pharmaceutical Sciences*. New York: CRC Press.

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 sboot

*Computation of the bootstrap confidence intervals and P-values*


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### Description

Bootstrap confidence intervals and P-values are calculated by coefficient estimates obtained by bootstrap.

### Usage

```
sboot(x, eform=FALSE, conf.level=0.95, digit=3)
```

### Arguments

- |            |   |
|------------|---|
| x          | An array-type object involving coefficient estimates obtained by bootstrap.                                     |
| eform      | A logical value that specify whether the outcome should be transformed by exponential function (default: FALSE) |
| conf.level | Confidence level for calculating confidence intervals (default: 0.95)   |
| digit      | Number of decimal places in the output (default: 3).  |

**Value**

Results of bootstrap inferences of the regression coefficients.

- CL: Lower limits of confidence intervals.
- CU: Upper limits of confidence intervals.
- P-value: P-values for the coefficient tests.

**Examples**

```
R1 <- data.frame(rnorm(100), rnorm(100, sd=3), runif(100))

sboot(R1)
sboot(R1, eform=TRUE)
```

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scoef

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*Computation of the ordinary confidence intervals and P-values for the logistic mixed-effects model using the model variance estimator*


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**Description**

Confidence intervals and P-values for the logistic mixed-effects model can be calculated using the ordinary model variance estimators. Through simply entering the output objects of glmmML, the inference results are fastly computed. The Wald-type confidence intervals and P-values based on the asymptotic normal approximation are computed. The resultant coefficients and confidence limits can be transformed to exponential scales by specifying eform.

**Usage**

```
scoef(x, eform=FALSE, conf.level=0.95, digit=3)
```

**Arguments**

x	An output object of glmmML.
eform	A logical value that specify whether the outcome should be transformed by exponential function (default: FALSE)
conf.level	Confidence level for calculating confidence intervals (default: 0.95)
digit	Number of decimal places in the output (default: 3).

**Value**

Results of inferences of the regression coefficients using the ordinary model variance estimators.

- coef: Coefficient estimates; transformed to the exponential scale if eform=TRUE.
- SE: Standard error estimates for coef.
- CL: Lower limits of confidence intervals.
- CU: Upper limits of confidence intervals.
- P-value: P-values for the coefficient tests.

**Examples**

```
library(glmML)

data(resp)

gmm1 <- glmML(y ~ treat + baseline + center + sex + age, data=resp, family =binomial,
cluster=id, method="ghq") # Logistic mixed model

resp.t <- adpdt(y, resp) # Adding pseudo-observations to the original dataset

gmm2 <- glmML(y ~ treat + baseline + center + sex + age, data=resp.t, family =binomial,
cluster=id, method="ghq") # Logistic mixed model with pseudo-observations

scoef(gmm1, eform=TRUE)
scoef(gmm2, eform=TRUE)
# 95%CI's and P-values are incorrect (based on the naive model variances)
```

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