Package 'qlmm'

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Type Package

Title Estimation of Absolute Effect Measures in Analyzing Clustered Categorical Outcome Data by Linear Mixed-Effects Model

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Maintainer Hisashi Noma <noma@ism.ac.jp>

Description The generalized linear mixed-effects model (GLMM) has been a standard statistical tool for analyzing clustered data in clinical and epidemiological studies, e.g., longitudinal studies, clustered randomized trials, and multi-center/regional studies. GLMM requires numerical integrations to implement maximum likelihood estimation, and computationally tractable statistical models that adopt canonical link functions have been widely used, e.g., logistic mixed-effects model for binary outcome (effect measure: odds ratio), Poisson mixed-effects model for count outcome (effect measure: rate ratio). However, absolute effect measures are relevant in assessing treatment or exposure effects for quantifying the impacts of the factors in public health or providing more precise information for the effect size of the treatment or exposure. Noma and Tsubaki (2025+) provides a generic method to estimate absolute effect measures via simple calculations using linear mixed-effects model. This package provides a computational tool to calculate the confidence intervals and P-values of the corresponding measures.

Depends R (>= 3.5.0)

Imports stats, lme4, clubSandwich

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LazyData true

R topics documented:

qlmm-package *The 'qlmm' package*

Description

The generalized linear mixed-effects model (GLMM) has been a standard statistical tool for analyzing clustered data in clinical and epidemiological studies, e.g., longitudinal studies, clustered randomized trials, and multi-center/regional studies. GLMM requires numerical integrations to implement maximum likelihood estimation, and computationally tractable statistical models that adopt canonical link functions have been widely used, e.g., logistic mixed-effects model for binary outcome (effect measure: odds ratio), Poisson mixed-effects model for count outcome (effect measure: rate ratio). However, absolute effect measures are relevant in assessing treatment or exposure effects for quantifying the impacts of the factors in public health or providing more precise information for the effect size of the treatment or exposure. Noma and Tsubaki (2025) provides a generic method to estimate absolute effect measures via simple calculations using linear mixed-effects model. This package provides a computational tool to calculate the confidence intervals and P-values of the corresponding measures.

References

Noma, H. and Tsubaki, H. (2025). Estimation of absolute effect measures in analyzing clustered categorical outcome data by linear mixed-effects model. Forthcoming.

coeff *Computation of the confidence intervals and P-values for the linear mixed-effects model using the robust variance estimators*

Description

Confidence intervals and P-values for the linear mixed-effects model can be calculated using the robust variance estimators. Through simply entering the output objects of `lmer`, the inference results are fastly computed. The Wald-type confidence intervals and P-values based on the asymptotic normal approximation are computed. The robust standard estimates are calculated by `vcovCR` function in `clubSandwich` package.

Usage

```
coeff(gm, type="CR0", cl=0.95, digit=3)
```

Arguments

`gm`	An output object of `lmer`.
`type`	Type of the variance estimator.

- `CR0`: The original form of the sandwich estimator (White, 1982), which does not make any small-sample correction.
- `CR1`: Multiplies `CR0` by m / (m - 1), where m is the number of clusters.

- CR2: The "bias-reduced linearization" adjustment proposed by Bell and McCaffrey (2002) and further developed in Pustejovsky and Tipton (2017). The adjustment is chosen so that the variance-covariance estimator is exactly unbiased under a user-specified working model.
- CR3: Approximation via the leave-one-cluster-out jackknife variance estimator (Bell and McCaffrey, 2002).
- CM0: The ordinary model variance estimator (as a supplement).

cl	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 robust variance estimators.

- coef: Coefficient estimates.
- 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.

References

Bell, R. M., and McCaffrey, D. F. (2002). Bias reduction in standard errors for linear regression with multi-stage samples. *Survey Methodology* **28**, 169-181.

Noma, H. and Tsubaki, H. (2025). Estimation of absolute effect measures in analyzing clustered categorical outcome data by linear mixed-effects model. Forthcoming.

Pustejovsky, J. E. (2024). clubSandwich: Cluster-Robust (Sandwich) Variance Estimators with Small-Sample Corrections. R package ver. 0.5.11. https://doi.org/10.32614/CRAN.package.clubSandwich.

Pustejovsky, J. E. and Tipton, E. (2018). Small sample methods for cluster-robust variance estimation and hypothesis testing in fixed effects models. *Journal of Business and Economic Statistics* **36**, 672-683.

White, H. (1982). Maximum likelihood estimation of misspecified models. *Econometrica* **50**, 1-25.

Examples

```
library(qlmm)
library(lme4)

data(epil)

lmm1 <- lmer(y ~ trt + lbase + lage + (1|subject), data=epil)
summary(lmm1)

coeff(lmm1, type="CR0")
coeff(lmm1, type="CR1")
coeff(lmm1, type="CR2")
coeff(lmm1, type="CR3")
coeff(lmm1, type="CM0")
```

epil *A epilepsy seizures data*

Description

A longitudinal clinical trial dataset for 59 epilepsy patients. Progabide or placebo was randomly assigned to individual patients and the number of epileptic seizures are recorded on each 2 weeks.

- `subject`: ID variable of participants.
- `trt`: Treatment (progabide or placebo).
- `period`: Follow-up periods (=1,2,3,4).
- `y`: The seizure counts during 2-week periods.
- `base`: Number of seizures at baseline.
- `age`: Age in years at baseline.
- `lbase`: Log-transformed `base`.
- `lage`: Log-transformed `age`.

Usage

```
data(epil)
```

Format

A data frame with 236 observations.

References

Thall, P. F. and Vail, S. C. (1990). Some covariance models for longitudinal count data with overdispersion. *Biometrics* **46**, 657-671.

mch *A cluster-randomised trial dataset for the maternal and child health handbook*

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=windowed/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 >= 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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