Package 'rqlm'

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Title Modified Poisson Regression for Binary Outcome and Related Methods

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Description Modified Poisson, logistic and least-squares regression analyses for binary outcomes of Zou (2004) <doi:10.1093/aje/kwh090>, Noma (2026)<doi:10.1016/j.spl.2026.110698>, and Cheung (2007) <doi:10.1093/aje/kwm223> have been standard multivariate analysis methods to estimate risk ratio and risk difference in clinical and epidemiological studies. This R package involves an easy-to-handle function to implement these analyses by simple commands. Missing data analysis tools (multiple imputation) are also involved. In addition, recent studies have shown the ordinary robust variance estimator possibly has serious bias under small or moderate sample size situations for these methods. This package also provides computational tools to calculate alternative accurate confidence intervals.

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`rqlm-package` *The 'rqlm' package.*

Description

Modified Poisson, logistic and least-squares regression analyses for binary outcomes have been standard multivariate analysis methods to estimate risk ratio and risk difference in clinical and epidemiological studies. This R package involves an easy-to-handle function to implement these analyses by simple commands. Missing data analysis tools (multiple imputation) are also involved. In addition, recent studies have shown the ordinary robust variance estimator possibly has serious bias under small or moderate sample size situations for these methods. This package also provides computational tools to calculate accurate confidence intervals. Also, standard computational tools for target trial emulation are included.

References

Cheung, Y. B. (2007). A modified least-squares regression approach to the estimation of risk difference. *American Journal of Epidemiology* **166**, 1337-1344.

Hernan, M. A., Wang, W., and Leaf, D. E. (2022). Target Trial Emulation: A Framework for Causal Inference From Observational Data. *JAMA* **328**, 2446-2447.

Kitano, T. and Noma, H. (2026). Exact unbiased covariance estimation for modified least-squares regression with binary outcomes. In Preparation.

Noma, H. (2026). Robust variance estimators for risk ratio estimators from logistic regression in cohort and case-cohort studies. *Statistics and Probability Letters* **234**, 110698.

Noma, H. and Gosho, M. (2025). Finite-sample improved confidence intervals based on the estimating equation theory for the modified Poisson and least-squares regressions. *Epidemiologic Methods* **14**, 20240030.

Noma, H. and Gosho, M. (2025). Logistic mixed-effects model analysis with pseudo-observations for estimating risk ratios in clustered binary data analysis. *Statistics in Medicine* **44**, e70280.

Noma, H., Sunada, H., and Gosho, M. (2025). Quasi-likelihood ratio tests and the Bartlett-type correction for improved inferences of the modified Poisson and least-squares regressions for binary outcomes. *Statistica Neerlandica* **79**, e70012.

Shiiba, H. and Noma, H. (2025). Confidence intervals of risk ratios for the augmented logistic regression with pseudo-observations. *Stats* **8**, 83.

Zou, G. (2004). A modified poisson regression approach to prospective studies with binary data. *American Journal of Epidemiology* **159**, 702-706.

`bsci.ls` *Calculating bootstrap confidence interval for modified least-squares regression based on the quasi-score statistic*

Description

Recent studies revealed the robust standard error estimates of the modified least-squares regression analysis are generally biased under small or moderate sample settings. To adjust the bias and to provide more accurate confidence intervals, confidence interval and P-value of the test for risk difference by modified least-squares regression are calculated based on the bootstrap approach of Noma and Gosho (2024).

Usage

```
bsci.ls(formula, data, x.name=NULL, B=1000, cl=0.95, C0=10^-5,
 digits=4, seed=527916)
```

Arguments

`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`data`	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
`x.name`	The variable name that the confidence interval is calculated for the regression coefficient; should be involved in `formula` as an explanatory variable. Specify as a character object.
`B`	The number of bootstrap resampling (default: 1000)
`cl`	Confidence level for calculating confidence intervals (default: 0.95)
`C0`	A tuning parameter to control the precisions of numerical computations of confidence limits (default: 10^-5).
`digits`	Number of decimal places in the output (default: 4).
`seed`	Seed to generate random numbers (default: 527916).

Value

Results of the modified least-squares analyses are presented. Three objects are provided: Results of the modified least-squares regression with the Wald-type approximation by `rqlm`, the bootstrap-based confidence interval for the corresponding covariate, and P-value for the bootstrap test of `RD=0`.

References

Noma, H. and Gosho, M. (2025). Finite-sample improved confidence intervals based on the estimating equation theory for the modified Poisson and least-squares regressions. *Epidemiologic Methods* **14**, 20240030.

Examples

```
data(exdata01)

bsci.ls(y ~ x1 + x2 + x3 + x4, data=exdata01, "x3", B=10)
# For illustration. B should be >= 1000 (the number of bootstrap resampling).
```

---

bsci.pois *Calculating bootstrap confidence interval for modified Poisson regression based on the quasi-score statistic*

Description

Recent studies revealed the risk ratio estimates and robust standard error estimates of the modified Poisson regression analysis are generally biased under small or moderate sample settings. To adjust the bias and to provide more accurate confidence intervals, confidence interval and P-value of the test for risk ratio by modified Poisson regression are calculated based on the bootstrap approach of Noma and Gosho (2024).

Usage

```
bsci.pois(formula, data, x.name=NULL, B=1000, eform=FALSE, cl=0.95, C0=10^-5,
 digits=4, seed=527916)
```

Arguments

`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`data`	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
`x.name`	The variable name that the confidence interval is calculated for the regression coefficient; should be involved in `formula` as an explanatory variable. Specify as a character object.
`B`	The number of bootstrap resampling (default: 1000)

eform	A logical value that specify whether the outcome should be transformed by exponential function (default: FALSE)
cl	Confidence level for calculating confidence intervals (default: 0.95)
C0	A tuning parameter to control the precisions of numerical computations of confidence limits (default: 10^-5).
digits	Number of decimal places in the output (default: 4).
seed	Seed to generate random numbers (default: 527916).

Value

Results of the modified Poisson analyses are presented. Three objects are provided: Results of the modified Poisson regression with the Wald-type approximation by rqlm, the bootstrap confidence interval for the corresponding covariate, and P-value for the bootstrap test of RR=1.

References

Noma, H. and Gosho, M. (2025). Finite-sample improved confidence intervals based on the estimating equation theory for the modified Poisson and least-squares regressions. *Epidemiologic Methods* **14**, 20240030.

Examples

```
data(exdata01)

bsci.pois(y ~ x1 + x2 + x3 + x4, data=exdata01, "x3", B=10, eform=TRUE)
# For illustration. B should be >= 1000 (the number of bootstrap resampling).
```

---

coeff *Computation of the ordinary confidence intervals and P-values using the model variance estimator*

Description

Confidence intervals and P-values for the generalized linear model and generalized linear-mixed-effects model can be calculated using the ordinary model variance estimators. Through simply entering the output objects of lm, glm, lmer, or glmer, the inference results are fastly computed. For the linear regression model, the exact confidence intervals and P-values based on the t-distribution are calculated. Also, for the generalized linear model, 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

```
coeff(gm, eform=FALSE, cl=0.95, digits=4)
```

Arguments

gm	An output object of lm, glm, lmer, or glmer.
eform	A logical value that specify whether the outcome should be transformed by exponential function (default: FALSE)
cl	Confidence level for calculating confidence intervals (default: 0.95)
digits	Number of decimal places in the output (default: 4).

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: Robust 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

```
data(exdata02)

gm1 <- glm(y ~ x1 + x2 + x3 + x4, data=exdata02, family=binomial)
coeff(gm1,eform=TRUE)
# Logistic regression analysis
# Coefficient estimates are translated to odds ratio scales

lm1 <- lm(x1 ~ x2 + x3 + x4, data=exdata02)
coeff(lm1)
# Linear regression analysis

data(mch)

if(requireNamespace("lme4", quietly = TRUE)) {
    lmr1 <- lme4::lmer(Y ~ x + (1|SOUM), data=mch)
    coeff(lmr1)
}
# Linear mixed-effects model analysis

if(requireNamespace("lme4", quietly = TRUE)) {
 gmr1 <- lme4::glmer(y ~ x + (1|SOUM), nAGQ=25, family=binomial, data=mch)
 coeff(gmr1, eform=TRUE)
}
# Logistic mixed-effects model analysis
# Coefficient estimates are translated to odds ratio scales
```

exdata01 *A simulated example dataset*

Description

A simulated cohort data with binomial outcome.

- y: Dichotomous outcome variable.
- x1: Continuous covariate.
- x2: Binary covariate.
- x3: Binary covariate.
- x4: Binary covariate.

Usage

```
data(exdata01)
```

Format

A simulated cohort data with binomial outcome (n=40).

exdata02 *A simulated example dataset*

Description

A simulated cohort data with binomial outcome.

- y: Dichotomous outcome variable.
- x1: Continuous covariate.
- x2: Binary covariate.
- x3: Binary covariate.
- x4: Binary covariate.

Usage

```
data(exdata02)
```

Format

A simulated cohort data with binomial outcome (n=1200).

exdata03 *A simulated example dataset with missing covariates*

Description

A simulated cohort data with binomial outcome. Some covariates involve missing data.

- `y`: Dichotomous outcome variable.
- `x1`: Continuous covariate.
- `x2`: Binary covariate.
- `x3`: Binary covariate.
- `x4`: Binary covariate.

Usage

```
data(exdata03)
```

Format

A simulated cohort data with binomial outcome (n=1200). Some covariates involve missing data.

exdata04 *A simulated example dataset for target trial emulation*

Description

A simulated data for sequentially nested emulated trials.

- `ID`: The id variable for individual participants.
- `trial`: The trial id variable.
- `time`: The discrete time index within each emulated trial, representing the interval since trial baseline.
- `A`: Treatment variable.
- `L1`: Baseline confounding variable.
- `Y`: Dichotomous outcome variable.
- `w_pp`: The weight variable.

Usage

```
data(exdata04)
```

Format

A simulated data for sequentially nested emulated trials (n=600).

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.

mi_glm *Multiple imputation analysis for the generalized linear model*

Description

Multiple imputation analysis for the generalized linear model is performed for the imputed datasets generated by `mice` function in `mice` package. For computing covariance matrix estimate, the ordinary Rubin's rule is adapted to the model variance estimates.

Usage

```
mi_glm(ice, formula, family=gaussian, offset=NULL, eform=FALSE, cl=0.95, digits=4)
```

Arguments

`ice`	An output object of `mice` function in `mice` package.
`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`family`	A description of the error distribution and link function to be used in the model.
`offset`	A vector of offset. This can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
`eform`	A logical value that specify whether the outcome should be transformed by exponential function (default: `FALSE`)
`cl`	Confidence level for calculating confidence intervals (default: 0.95)
`digits`	Number of decimal places in the output (default: 4).

Value

Results of the multiple imputation analysis for the generalized linear model. For computing covariance matrix estimate, the ordinary Rubin's rule is adapted to the model variance estimates.

- `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.
- `df`: Degree of freedom for the t-approximation.
- `P-value`: P-values for the coefficient tests.

References

Little, R. J., and Rubin, D. B. (2019). *Statistical Analysis with Missing Data*, 3rd edition. New York: Wiley.

Examples

```
library("mice")

data(exdata03)

exdata03$x2 <- factor(exdata03$x2)
exdata03$x3 <- factor(exdata03$x3)
exdata03$x4 <- factor(exdata03$x4)

ice5 <- mice(exdata03,m=5)
# For illustration. m should be >=100.

mi_glm(ice5, y ~ x1 + x2 + x3 + x4, family=binomial, eform=TRUE)
# Logistic regression analysis
# Coefficient estimates are translated to odds ratio scales

mi_glm(ice5, x1 ~ x2 + x3 + x4, family=gaussian)
# Ordinary least-squares regression analysis with the model variance estimator
```

`mi_rqlm` *Multiple imputation analysis for modified Poisson and least-squares regressions*

Description

Multiple imputation analysis for modified Poisson and least-squares regressions is performed for the imputed datasets generated by `mice` function in `mice` package. For computing covariance matrix estimate, the ordinary Rubin's rule is adapted to the sandwich variance estimates. Its validity is checked by several simulation studies for general GEE applications by Beunckens et al. (2008), Birhanu et al. (2011) and Yoo (2010).

Usage

```
mi_rqlm(ice, formula, family=poisson, eform=FALSE, cl=0.95, digits=4)
```

Arguments

`ice`	An output object of `mice` function in `mice` package.
`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`family`	A description of the error distribution and link function to be used in the model. `gaussian`: Modified least-squares regression. `poisson`: Modified Poisson regression.
`eform`	A logical value that specify whether the outcome should be transformed by exponential function (default: `FALSE`)
`cl`	Confidence level for calculating confidence intervals (default: 0.95)
`digits`	Number of decimal places in the output (default: 4).

Value

Results of the multiple imputation analysis for modified Poisson and least-squares regressions. For computing covariance matrix estimate, the ordinary Rubin's rule is adapted to the sandwich variance estimates.

- `coef`: Coefficient estimates; transformed to the exponential scale if `eform=TRUE`.
- `SE`: Robust standard error estimates for `coef`.
- `CL`: Lower limits of confidence intervals.
- `CU`: Upper limits of confidence intervals.
- `df`: Degree of freedom for the t-approximation.
- `P-value`: P-values for the coefficient tests.

References

Aloisio, K. M., Swanson, S. A., Micali, N., Field, A., and Horton, N. J. (2014). Analysis of partially observed clustered data using generalized estimating equations and multiple imputation. *Stata Journal*, **14**, 863-883.

Beunckens, C., Sotto, C., and Molenberghs., G. (2008). A simulation study comparing weighted estimating equations with multiple imputation based estimating equations for longitudinal binary data. *Computational Statistics and Data Analysis*, **52**, 1533-1548.

Birhanu, T., Molenberghs, G., Sotto, C., and Kenward, M. G. (2011). Doubly robust and multiple-imputation-based generalized estimating equations. *Journal of Biopharmaceutical Statistics*, **21**, 202-225.

Little, R. J., and Rubin, D. B. (2019). *Statistical Analysis with Missing Data*, 3rd edition. New York: Wiley.

Yoo, B. (2010). The impact of dichotomization in longitudinal data analysis: a simulation study. *Pharmaceutical Statistics*, **9**, 298-312.

Examples

```
library("mice")

data(exdata03)

exdata03$x2 <- factor(exdata03$x2)
exdata03$x3 <- factor(exdata03$x3)
exdata03$x4 <- factor(exdata03$x4)

ice5 <- mice(exdata03,m=5)
# For illustration. m should be >=100.

mi_rqlm(ice5, y ~ x1 + x2 + x3 + x4, family=poisson, eform=TRUE)
# Modifed Poisson regression analysis
# Coefficient estimates are translated to risk ratio scales

mi_rqlm(ice5, y ~ x1 + x2 + x3 + x4, family=gaussian)
# Modifed least-squares regression analysis
```

`qesci.ls` *Calculating confidence interval for modified least-squares regression based on the quasi-score test*

Description

Recent studies revealed the robust standard error estimates of the modified least-squares regression analysis are generally biased under small or moderate sample settings. To adjust the bias and to provide more accurate confidence intervals, confidence interval and P-value of the test for risk difference by modified least-squares regression are calculated based on the quasi-score test of Noma and Gosho (2024).

Usage

```
qesci.ls(formula, data, x.name=NULL, cl=0.95, C0=10^-5, digits=4)
```

Arguments

`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`data`	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
`x.name`	The variable name that the confidence interval is calculated for the regression coefficient; should be involved in `formula` as an explanatory variable. Specify as a character object.
`cl`	Confidence level for calculating confidence intervals (default: 0.95)
`C0`	A tuning parameter to control the precisions of numerical computations of confidence limits (default: 10^-5).
`digits`	Number of decimal places in the output (default: 4).

Value

Results of the modified least-squares analyses are presented. Three objects are provided: Results of the modified least-squares regression with the Wald-type approximation by `rqlm`, quasi-score confidence interval for the corresponding covariate, and P-value for the quasi-score test of `RD=0`.

References

Noma, H. and Gosho, M. (2025). Finite-sample improved confidence intervals based on the estimating equation theory for the modified Poisson and least-squares regressions. *Epidemiologic Methods* **14**, 20240030.

Examples

```
data(exdata01)

qesci.ls(y ~ x1 + x2 + x3 + x4, data=exdata01, "x3")
```

`qesci.pois` *Calculating confidence interval for modified Poisson regression based on the quasi-score test*

Description

Recent studies revealed the risk ratio estimates and robust standard error estimates of the modified Poisson regression analysis are generally biased under small or moderate sample settings. To adjust the bias and to provide more accurate confidence intervals, confidence interval and P-value of the test for risk ratio by modified Poisson regression are calculated based on the quasi-score test of Noma and Gosho (2024).

Usage

```
qesci.pois(formula, data, x.name=NULL, eform=FALSE, cl=0.95, C0=10^-5, digits=4)
```

Arguments

`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`data`	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
`x.name`	The variable name that the confidence interval is calculated for the regression coefficient; should be involved in `formula` as an explanatory variable. Specify as a character object.
`eform`	A logical value that specify whether the outcome should be transformed by exponential function (default: `FALSE`)
`cl`	Confidence level for calculating confidence intervals (default: 0.95)
`C0`	A tuning parameter to control the precisions of numerical computations of confidence limits (default: 10^-5).
`digits`	Number of decimal places in the output (default: 4).

Value

Results of the modified Poisson analyses are presented. Three objects are provided: Results of the modified Poisson regression with the Wald-type approximation by `rqlm`, quasi-score confidence interval for the corresponding covariate, and P-value for the quasi-score test of `RR=1`.

References

Noma, H. and Gosho, M. (2025). Finite-sample improved confidence intervals based on the estimating equation theory for the modified Poisson and least-squares regressions. *Epidemiologic Methods* **14**, 20240030.

Examples

```
data(exdata01)

qesci.pois(y ~ x1 + x2 + x3 + x4, data=exdata01, "x3", eform=TRUE)
```

`qlogist` *Augmented (modified) logistic regression analyses for estimating risk ratio*

Description

Logistic regression with augmented pseudo-observations for estimating risk ratios is performed. This function is handled by a similar way with `lm` or `glm`. Also, the resultant coefficients and confidence limits can be transformed to exponential scales by specifying `eform`. The Morel-Bokossa-Neerchaal-type small-sample corrected estimator is adopted for standard error estimation as the default method.

Usage

```
qlogist(formula, data, eform=TRUE, cl=0.95, digits=4, var.method="MBN", id=NULL)
```

Arguments

`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`data`	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
`eform`	A logical value that specify whether the outcome should be transformed by exponential function (default: `TRUE`)
`cl`	Confidence level for calculating confidence intervals (default: 0.95)
`digits`	Number of decimal places in the output (default: 4).
`var.method`	Method for estimating standard errors. Standard robust variance estimator (`standard`), Morel-Bokossa-Neerchaal-type corrected estimator (`MBN`), Gosho-Sato-Takeuchi-type corrected estimator (`GST`), and Wang-Long-type corrected estimator (`WL`) are available (default: `MBN`).
`id`	Optional column name in `data`, supplied without quotes or as one character string, identifying independent clusters. With `NULL`, each original observation and its pseudo-observation form one cluster. With an external ID, all original and pseudo-observations with that ID are grouped together. Only `standard` and `MBN` support an external ID. Missing IDs in the analysis sample are not allowed.

Details

The model frame and design matrix are constructed from the original observations before augmentation. This keeps transformations and matrix predictors aligned with their original observations and avoids overwriting user columns named `id` or `d`. Missing model values are handled by `model.frame` using the current `na.action` option; IDs are then aligned with the retained rows. Adaptive transformations such as `poly` or splines are therefore defined before, rather than after, augmentation.

At least two independent clusters are needed for `standard`. For `MBN`, their number must exceed the number of model parameters. The existing MBN formula, including the cluster-count adjustment in `sandwich::vcovCL` before the additional MBN factors, is retained. The `GST` and `WL` calculations are restricted to `id = NULL`.

The methods `coef`, `vcov`, and `family` are available; see `rqlm-methods`. The family returned by `family` is the binomial-logit family of the augmented-data working model, not a logit model for the original outcome. The coefficients represent log risks in the original cohort. When using `dlnm::crosspred`, specify `model.link = "log"` explicitly and use the outer object to retain the robust covariance. The response predictions from `model` refer to the augmented outcome; they are not the original risks.

Value

An object of class `"rqlm"` containing the following components.

- `call`: The matched function call.
- `formula`: The original model formula.
- `coefficients`: Coefficient estimates on the log-risk scale, irrespective of `eform`.
- `se`: Robust standard errors on the coefficient scale.
- `cl`, `cu`: Lower and upper confidence limits on the coefficient scale.
- `z`, `p`: Wald statistics and two-sided P-values.
- `eform`, `cl.level`, `digits`, `var.method`: The corresponding analysis and display settings.
- `vcov`: The full estimated covariance matrix, with coefficient names.
- `model`: The fitted augmented-data `glm` object.
- `n`: The number of original observations in the analysis sample.
- `n.clusters`: The number of independent clusters.

References

Diaz-Quijano, F. A. (2012). A simple method for estimating relative risk using logistic regression. *BMC Medical Research Methodology* **12**, 14.

Gosho, M., Sato, Y., and Takeuchi, H. (2014). Robust covariance estimator for small-sample adjustment in the generalized estimating equations: a simulation study. *Science Journal of Applied Mathematics and Statistics* **2**, 20-25.

Morel, J. G., Bokossa, M., and Neerchal, N. (2003). Small sample correction for the variance of GEE estimators. *Biometrical Journal* **45**, 395-409.

Noma, H. (2026). Robust variance estimators for risk ratio estimators from logistic regression in cohort and case-cohort studies. *Statistics and Probability Letters* **234**, 110698.

Noma, H., and Gosho, M. (2025). Logistic mixed-effects model analysis with pseudo-observations for estimating risk ratios in clustered binary data analysis. *Statistics in Medicine* **44**, e70280.

Schouten, E. G., Dekker, J. M., Kok, F. J., et al. (1993). Risk ratio and rate ratio estimation in case-cohort designs: hypertension and cardiovascular mortality. *Statistics in Medicine* **12**, 1733-1745.

Shiiba, H., and Noma, H. (2025). Confidence intervals of risk ratios for the augmented logistic regression with pseudo-observations. *Stats* **8**, 83.

Wang, M., and Long, Q. (2011). Modified robust variance estimator for generalized estimating equations with improved small-sample performance. *Statistics in Medicine* **30**, 1278-1291.

Examples

```
data(exdata02)

qlogist(y ~ x1 + x2 + x3 + x4, data=exdata02)
# Augmented logistic regression analysis
# Coefficient estimates are translated to risk ratio scales
# MBN robust variance estimator is adopted.

qlogist(y ~ x1 + x2 + x3 + x4, data=exdata02, var.method="GST")
# GST robust variance estimator is adopted.

qlogist(y ~ x1 + x2 + x3 + x4, data=exdata02, var.method="WL")
# WL robust variance estimator is adopted.
```

---

rqlm *Modified Poisson and Least-Squares Regression Analyses for Binary Outcomes*

Description

Performs modified Poisson or modified least-squares regression for a binary outcome. The function is used in a manner similar to `lm` or `glm`. The regression family determines the fitted mean model, and setting `eform = TRUE` exponentiates the coefficient estimates and confidence limits. The Morel–Bokossa–Neerchal-type small-sample corrected estimator is used by default.

Usage

```
rqlm(formula, data, family = poisson, eform = FALSE, cl = 0.95,
     digits = 4, var.method = "MBN", id = NULL)
```

Arguments

`formula`	An object of class `"formula"` (or one that can be coerced to that class): a symbolic description of the model to be fitted.
`data`	A data frame, list, or environment (or an object coercible by `as.data.frame`) containing the variables in the model.

`family` A description of the error distribution and link function to be used in the model. Specify `gaussian` for modified least-squares regression or `poisson` for modified Poisson regression.

`eform` A logical value indicating whether the coefficient estimates and confidence limits should be exponentiated (default: `FALSE`).

`cl` Confidence level used to calculate confidence intervals (default: `0.95`).

`digits` Number of decimal places displayed in the printed output (default: `4`).

`var.method` Method used to estimate the covariance matrix and standard errors. Available options are:

- `"standard"`: the standard heteroskedasticity-robust sandwich covariance estimator;
- `"MBN"`: the Morel–Bokossa–Neerchal-type corrected estimator;
- `"GST"`: the Gosho–Sato–Takeuchi-type corrected estimator;
- `"WL"`: the Wang–Long-type corrected estimator;
- `"HAD"`: the Hadamard finite-sample unbiased covariance estimator;
- `"HAD0"`: the Hadamard estimator with negative observation-level variance estimates truncated at zero;
- `"HAD025"`: the Hadamard estimator with observation-level variance estimates truncated to the interval $[0, 1/4]$.

The `"HAD"`, `"HAD0"`, and `"HAD025"` options are available only with a Gaussian family and identity link. The default is `"MBN"`.

`id` Optional column name in `data`, supplied without quotes or as one character string, identifying independent clusters. The default `NULL` retains the independent-observation analysis. With `id` supplied, only `"standard"` and `"MBN"` are available. Missing IDs in the analysis sample are not allowed.

Details

With `id` supplied, scores are aggregated within the specified clusters. At least two clusters are needed for `"standard"`; `"MBN"` requires more clusters than model parameters. The cluster covariance convention follows `ttemsm`; the existing MBN correction formula is retained. In particular, the cluster-count adjustment in `sandwich::vcovCL` is retained before the additional MBN factors. With `id = NULL`, the existing covariance calculations are unchanged. The `"GST"`, `"WL"`, and Hadamard options are not extended to general clusters.

The methods `coef`, `vcov`, and `family` are available; see `rqlm-methods`. Coefficients and their covariance matrix are returned on the model scale, irrespective of `eform`.

The Hadamard methods are implemented for modified least-squares regression fitted using a Gaussian family with an identity link.

Let X denote the model matrix, $H = X(X^\top X)^{-1}X^\top$ the hat matrix, and $M = I - H$ the residual-maker matrix. If r is the vector of least-squares residuals, the `"HAD"` option estimates the observation-specific error variances by

$$\widehat{\boldsymbol{\sigma}}^2 = (M \circ M)^{-1}(r \circ r),$$

where $\circ$ denotes the elementwise Hadamard product. The covariance matrix is then estimated as

$$(X^\top X)^{-1}X^\top \mathrm{diag}(\widehat{\boldsymbol{\sigma}}^2)X(X^\top X)^{-1}.$$

Under independent observations, a correctly specified linear conditional-mean model, and invertibility of $M \circ M$, this covariance estimator is conditionally finite-sample unbiased.

Unbiased observation-level variance estimates can be negative in a particular sample. The `"HAD0"` option replaces negative values by zero. For a Bernoulli outcome, whose conditional variance cannot exceed $1/4$, `"HAD025"` truncates the estimates to $[0, 1/4]$. These truncations can improve numerical stability but do not preserve exact finite-sample unbiasedness.

The matrix $M \circ M$ is an $n \times n$ matrix. Consequently, the Hadamard methods can require substantial memory and computation for large datasets. An error is returned if this matrix is singular or numerically non-invertible, and a warning is returned when it is severely ill-conditioned.

Value

An object of class `"rqlm"`, containing the following components:

`call`	The matched function call.
`formula`	The model formula.
`coefficients`	Coefficient estimates on the model scale.
`se`	Estimated robust standard errors.
`cl`	Lower confidence limits on the model scale.
`cu`	Upper confidence limits on the model scale.
`z`	Wald z statistics.
`p`	Two-sided Wald P-values.
`eform`	The value supplied to `eform`.
`cl.level`	The confidence level.
`digits`	The number of displayed decimal places.
`var.method`	The selected covariance estimator.
`vcov`	The estimated covariance matrix.
`model`	The fitted `glm` object.
`n`	The number of observations in the analysis sample after missing-value handling.
`n.clusters`	The number of independent clusters; equal to `n` when `id = NULL`.
`vhat.had`	For a Hadamard method, the observation-level variance estimates after any requested truncation; otherwise `NULL`.
`vhat.had.raw`	For a Hadamard method, the untruncated observation-level variance estimates; otherwise `NULL`.
`kappa.had`	For a Hadamard method, the estimated condition number of the Hadamard-squared residual-maker matrix; otherwise `NULL`.
`n.neg.had`	For a Hadamard method, the number of negative untruncated observation-level variance estimates.
`n.above025.had`	For a Hadamard method, the number of untruncated observation-level variance estimates exceeding $1/4$.
`min.vhat.had`, `max.vhat.had`	The minimum and maximum of the untruncated observation-level variance estimates.

References

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Wang, M. and Long, Q. (2011). Modified robust variance estimator for generalized estimating equations with improved small-sample performance. *Statistics in Medicine* **30**, 1278–1291.

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

Zou, G. (2004). A modified Poisson regression approach to prospective studies with binary data. *American Journal of Epidemiology* **159**, 702–706.

Examples

```
data(exdata02)

rqlm(
  y ~ x1 + x2 + x3 + x4,
  data = exdata02,
  family = poisson,
  eform = TRUE
)
# Modified Poisson regression analysis.
# Coefficients and confidence limits are displayed as risk ratios.
# The MBN robust covariance estimator is used by default.

rqlm(
  y ~ x1 + x2 + x3 + x4,
  data = exdata02,
  family = gaussian
)
# Modified least-squares regression analysis.
# Coefficients are risk differences.
```

```
rqlm(
  y ~ x1 + x2 + x3 + x4,
  data = exdata02,
  family = gaussian,
  var.method = "HAD"
)
# Modified least-squares regression with the finite-sample unbiased
# Hadamard covariance estimator.

rqlm(
  y ~ x1 + x2 + x3 + x4,
  data = exdata02,
  family = gaussian,
  var.method = "HAD0"
)
# Negative observation-level variance estimates are truncated at zero.

rqlm(
  y ~ x1 + x2 + x3 + x4,
  data = exdata02,
  family = gaussian,
  var.method = "HAD025"
)
# Observation-level variance estimates are truncated to [0, 1/4].

rqlm(
  y ~ x1 + x2 + x3 + x4,
  data = exdata02,
  family = poisson,
  eform = TRUE,
  var.method = "GST"
)

rqlm(
  y ~ x1 + x2 + x3 + x4,
  data = exdata02,
  family = poisson,
  eform = TRUE,
  var.method = "WL"
)
```

SGLT2i01 *Simulated example data based on a target trial emulation for SGLT2i: risk ratio estimation*

Description

Simulated example data representing an active-comparator new-user comparison of SGLT2i and DPP-4i initiation in older adults with type 2 diabetes. The outcome is binary at a fixed 36-month horizon. These are not patient records and provide no clinical evidence about either drug.

- `id`: Unique synthetic individual identifier; one row per individual.
- `A`: Treatment indicator: 0 for DPP-4i and 1 for SGLT2i.
- `treatment`: Treatment factor with levels DPP-4i and SGLT2i.
- `death36`: Simulated all-cause death by 36 months, coded 0/1.
- `age`: Baseline age in years.
- `female`: Female indicator, coded 0/1.
- `bmi`: Body mass index in kg/m^2.
- `hba1c`: Glycated haemoglobin in percent.
- `egfr`: Estimated glomerular filtration rate in mL/min/1.73 m^2.
- `proteinuria`: Proteinuria indicator, coded 0/1.
- `prior_heart_failure`: History of heart failure, coded 0/1.
- `prior_stroke`: History of stroke, coded 0/1.
- `recent_hospitalization`: Recent hospitalization indicator, coded 0/1.
- `trial_period`: Factor identifying the synthetic treatment-initiation period.
- `risk_score`: Fixed baseline-covariate score used in the simulation; not a validated clinical score.
- `followup_months`: Common ascertainment horizon, equal to 36 for every individual; not an event time.

Usage

```
data(SGLT2i01)
```

Format

A data frame with 700 observations and 16 variables.

Details

The datasets were independently simulated and include no participant records from the motivating study. They are intended solely for education, software testing, and reproducible examples; numerical results obtained from them have no clinical interpretation.

References

Noma, H., Goto, A., Sugimoto, T., Sunada, H., Oda, F., Maeda, M., and Fukuda, H. (2026). Real-world effectiveness of SGLT2 inhibitors in adults aged 75 years or older: a target trial emulation. *Age and Ageing* **55**, afag246.

See Also

`rqlm`, `qlogist`, `SGLT2i02`

Examples

```
data(SGLT2i01)
rqlm(death36 ~ A + age + hba1c + egfr + proteinuria +
      prior_heart_failure + prior_stroke + recent_hospitalization,
      data=SGLT2i01, family=poisson, eform=TRUE)

qlogist(death36 ~ A + risk_score, data=SGLT2i01)
```

SGLT2i02 *Simulated example data based on a target trial emulation for SGLT2i: risk difference estimation*

Description

Simulated example data representing an active-comparator new-user comparison of SGLT2i and DPP-4i initiation in older adults with type 2 diabetes. The outcome is binary at a fixed 36-month horizon. These are not patient records and provide no clinical evidence about either drug.

- `id`: Unique synthetic individual identifier; one row per individual.
- `A`: Treatment indicator: 0 for DPP-4i and 1 for SGLT2i.
- `treatment`: Treatment factor with levels DPP-4i and SGLT2i.
- `death36`: Simulated all-cause death by 36 months, coded 0/1.
- `age`: Baseline age in years.
- `female`: Female indicator, coded 0/1.
- `bmi`: Body mass index in kg/m^2.
- `hba1c`: Glycated haemoglobin in percent.
- `egfr`: Estimated glomerular filtration rate in mL/min/1.73 m^2.
- `proteinuria`: Proteinuria indicator, coded 0/1.
- `prior_heart_failure`: History of heart failure, coded 0/1.
- `prior_stroke`: History of stroke, coded 0/1.
- `recent_hospitalization`: Recent hospitalization indicator, coded 0/1.
- `trial_period`: Factor identifying the synthetic treatment-initiation period.
- `risk_score`: Fixed baseline-covariate score used in the simulation; not a validated clinical score.
- `followup_months`: Common ascertainment horizon, equal to 36 for every individual; not an event time.

Usage

```
data(SGLT2i02)
```

Format

A data frame with 700 observations and 16 variables.

Details

The datasets were independently simulated and include no participant records from the motivating study. They are intended solely for education, software testing, and reproducible examples; numerical results obtained from them have no clinical interpretation.

References

Noma, H., Goto, A., Sugimoto, T., Sunada, H., Oda, F., Maeda, M., and Fukuda, H. (2026). Real-world effectiveness of SGLT2 inhibitors in adults aged 75 years or older: a target trial emulation. *Age and Ageing* **55**, afag246.

See Also

rqlm, qlogist, SGLT2i01

Examples

```
data(SGLT2i02)
rqlm(death36 ~ A + I(exp(2.4 * risk_score)),
      data=SGLT2i02, family=gaussian, var.method="standard")

rqlm(death36 ~ A + I(exp(2.4 * risk_score)),
     data=SGLT2i02, family=gaussian, var.method="HAD")
```

---

stabwt *Calculating stabilized weights for IPW analysis: Single time point*

Description

This function calculates stabilized weights for IPW analysis using logistic regression model. Both of untruncated and utruncated weights are provided.

Usage

```
stabwt(formula, data, trunc=c(0.01,0.99), digits=4)
```

Arguments

formula	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the logistic regression model to be fitted.
data	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
trunc	Quantiles to be truncated the weights (default: 0.01, 0.99).
digits	Number of decimal places in the output (default: 4).

Value

Truncated and untruncated stabilized weights are calculated.

- sw1: Untruncated stabilized weights.
- sw2: Truncated stabilized weights.

References

Cole, S. R., and Hernan, M. A. (2008). Constructing inverse probability weights for marginal structural models. *American Journal of Epidemiology* **168**, 656-664.

Westreich, D., Edwards, J. K., Lesko, C. R., Stuart, E., and Cole, S. R. (2017). Transportability of trial results using inverse odds of sampling weights. *American Journal of Epidemiology* **186**, 1010-1014.

Examples

```
data(exdata02)

stabwt(x2 ~ x1 + x3 + x4, data=exdata02)
```

---

stabwtlong *Calculating stabilized weights for IPW analysis: Longitudinal data*

Description

This function calculates stabilized weights for IPW analysis of longitudinal data using logistic regressions. Both of untruncated and utruncated weights are provided.

Usage

```
stabwtlong(formula_denom, formula_num, data, trunc=c(0.01,0.99), digits=4)
```

Arguments

formula_denom	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the denominator logistic regression model to be fitted.
formula_num	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the numerator logistic regression model to be fitted.
data	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
trunc	Quantiles to be truncated the weights (default: 0.01, 0.99).
digits	Number of decimal places in the output (default: 4).

Value

Truncated and untruncated stabilized weights are calculated.

- sw1: Untruncated stabilized weights.
- sw2: Truncated stabilized weights.

References

Cole, S. R., and Hernan, M. A. (2008). Constructing inverse probability weights for marginal structural models. *American Journal of Epidemiology* **168**, 656-664.

Westreich, D., Edwards, J. K., Lesko, C. R., Stuart, E., and Cole, S. R. (2017). Transportability of trial results using inverse odds of sampling weights. *American Journal of Epidemiology* **186**, 1010-1014.

Examples

```
data(exdata04)

stabwtlong(formula_denom = A ~ L1 + L2 + L3, formula_num = A ~ L1, data = exdata04)
```

---

stabwtmulti *Calculating stabilized weights for IPW analysis: Single time point (for more than 3 groups)*

Description

This function calculates stabilized weights for IPW analysis using logistic regression model. Both of untruncated and utruncated weights are provided.

Usage

```
stabwtmulti(formula, data, trunc=c(0.01,0.99), digits=4)
```

Arguments

formula	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the logistic regression model to be fitted.
data	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
trunc	Quantiles to be truncated the weights (default: 0.01, 0.99).
digits	Number of decimal places in the output (default: 4).

Value

Truncated and untruncated stabilized weights are calculated.

- sw1: Untruncated stabilized weights.
- sw2: Truncated stabilized weights.

References

Cole, S. R., and Hernan, M. A. (2008). Constructing inverse probability weights for marginal structural models. *American Journal of Epidemiology* **168**, 656-664.

Westreich, D., Edwards, J. K., Lesko, C. R., Stuart, E., and Cole, S. R. (2017). Transportability of trial results using inverse odds of sampling weights. *American Journal of Epidemiology* **186**, 1010-1014.

`SumStat` *Creating summary table for IPTW analysis using stabilized weights*

Description

Summary statistics are computed before and after weighting for IPTW analyses. For all covariates included in the weight model, the mean, standard deviation, and standardized mean difference (SMD) are calculated. Weighting can be performed using either stabilized or unstabilized weights, with optional truncation. For binary covariates, summary statistics are computed using unbiased estimators of the binomial mean and variance.

Usage

```
SumStat(formula, data, trunc=c(0.01,0.99), digits=3)
```

Arguments

`formula`	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the logistic regression model to be fitted.
`data`	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
`trunc`	Quantiles to be truncated the weights (default: 0.01, 0.99).
`digits`	Number of decimal places in the output (default: 4).

Value

Summary statistics for unadjusted and IPTW-adjusted populations are provided. For each covariate, the mean and standard deviation, as well as the standardized mean difference (SMD), were calculated. Truncated stabilized weights were used for weighting. Setting the `trunc` argument to c(0, 1) allows weighting with untruncated stabilized weights.

- `mean0`: Mean for group 0.
- `mean1`: Mean for group 1.
- `sd0`: SD for group 0.
- `sd1`: SD for group 1.
- `SMD`: SMD for the original population.
- `wmean0`: IPTW-weighted mean for group 0.

- wmean1: IPTW-weighted mean for group 1.
- wsd0: IPTW-weighted SD for group 0.
- wsd1: IPTW-weighted SD for group 1.
- wSMD: IPTW-weighted SMD for the adjusted pseudo-population.
- type: Type of the variable.

References

Austin, P. C. (2009). Balance diagnostics for comparing the distribution of baseline covariates between treatment groups in propensity-score matched samples. *Statistics in Medicine* **28**, 3083-3107.

Examples

```
data(exdata02)

SumStat(x2 ~ x1 + x3 + x4, data=exdata02)
```

---

ttemsm *Pooled logistic regression for target trial emulation*

Description

This function implements pooled logistic regression for use in target trial emulation. Before running the function, the user must prepare an analysis dataset by stacking the sequential-trial datasets in long format. If inverse probability weights (such as IPCW) are required, the corresponding weight variable should be included in the dataset in advance. The regression model is specified through the formula argument, and the individual identifier must be provided via the id argument, so that cluster-robust standard errors are computed across repeated trials for each individual. When a weight variable is specified through weights, the function performs inverse probability weighting. The output includes point estimates of the hazard ratio, corresponding confidence intervals, and P-values.

Usage

```
ttemsm(formula, data, id, weight=NULL, family=quasibinomial(link="cloglog"),
eform=TRUE, cl=0.95, digits=4, var.method="MBN")
```

Arguments

formula	An object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.
data	A data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
id	Column name in data identifying individual participants, supplied without quotes or as one character string. Missing IDs in the analysis sample are not allowed.

weight	Column name in data containing the analysis weights, supplied without quotes or as one character string. The default NULL uses uniform weights of one.
family	A description of the error distribution and link function to be used in the model. When the goal is to estimate hazard ratios using a discrete-time Cox model, the complementary log–log (cloglog) link should be used. When the objective is to estimate risk differences or cumulative incidence (e.g., via the g-formula or standardization), the logit link should be used.
eform	A logical value that specify whether the outcome should be transformed by exponential function (default: TRUE)
cl	Confidence level for calculating confidence intervals (default: 0.95)
digits	Number of decimal places in the output (default: 4).
var.method	Method for estimating standard errors. Standard cluster-robust variance estimator (standard) and Morel-Bokossa-Neerchaal-type corrected cluster-robust estimator (MBN) are available (default: MBN).

Details

The methods coef, vcov, and family are available; see rqlm-methods. The full covariance matrix can be used for contrasts involving several coefficients. Predictions from model are available through predict, but its default prediction standard errors are model-based, not based on the outer object's robust covariance. Supplied weights are treated as fixed. At least two participants are needed for standard; MBN requires more independent participants than model parameters. The existing MBN formula, including the cluster-count adjustment in sandwich::vcovCL before the additional MBN factors, is retained.

This function is retained for compatibility. Further target trial emulation development is provided in the **TTE** package, including TTE::discsurvreg; its arguments and defaults are not identical.

Value

An object of class "ttemsm" containing the following components.

- call: The matched function call.
- formula: The model formula.
- coefficients: Coefficient estimates on the model scale, irrespective of eform.
- se: Cluster-robust standard errors on the coefficient scale.
- cl, cu: Lower and upper confidence limits on the coefficient scale.
- z, p: Wald statistics and two-sided P-values.
- eform, cl.level, digits, var.method: The corresponding analysis and display settings.
- vcov: The full estimated covariance matrix.
- model: The fitted glm object.
- n: The number of analysis rows after missing-value handling.
- n.clusters: The number of independent participants.

References

Gosho, M., Ishii, R., Noma, H., and Maruo, K. (2023). A comparison of bias-adjusted generalized estimating equations for sparse binary data in small-sample longitudinal studies. *Statistics in Medicine* **42**, 2711-2727.

Hernan, M. A., Alonso, A., Logan, R., et al. (2008). Observational studies analyzed like randomized experiments: an application to postmenopausal hormone therapy and coronary heart disease. *Epidemiology* **19**, 766-779.

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Hernan, M. A., Wang, W., and Leaf, D. E. (2022). Target Trial Emulation: A Framework for Causal Inference From Observational Data. *JAMA* **328**, 2446-2447.

Morel, J. G., Bokossa, M., and Neerchal, N. (2003). Small sample correction for the variance of GEE estimators. *Biometrical Journal* **45**, 395-409.

Examples

```
data(exdata04)

ttemsm( Y ~ A + L1 + L2 + L3 + time + I(time^2) + trial,
  data    = exdata04, id = ID, weight = w_pp,
  family = quasibinomial(link="cloglog"),
  eform   = TRUE, cl = 0.95, var.method="standard")
# Pooled logistic regression for target trial emulation with cloglog link
# For estimating hazard ratios using a discrete-time Cox model

ttemsm( Y ~ A + L1 + L2 + L3 + time + I(time^2) + trial,
  data    = exdata04, id = ID, weight = w_pp,
  family = quasibinomial(link="logit"),
  eform   = TRUE, cl = 0.95, var.method="standard")
# Pooled logistic regression for target trial emulation with logit link
# For estimating RDs or cumulative incidence (e.g., via the g-formula)

ttemsm( Y ~ A + L1 + L2 + L3 + time + I(time^2) + trial,
  data    = exdata04, id = ID, weight = w_pp,
  eform   = TRUE, cl = 0.95, var.method="MBN")
# Pooled logistic regression for target trial emulation with cloglog link
# Morel-Bokossa-Neerchaal-type corrected SE estimator is used.
```

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