Package ‘multe’

July 23, 2025

Title Multiple Treatment Effects Regression

Version 1.1.0

Description Implements contamination bias diagnostics and alternative estimators for regressions with multiple treatments. The implementation is based on Goldsmith-Pinkham, Hull, and Kolesár (2024) <doi:10.48550/arXiv.2106.05024>.

Depends R (>= 4.3.0)

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Encoding UTF-8

LazyData true

Imports stats, nnet

Suggests spelling, knitr, formatR, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

Language en-US

URL `https://github.com/kolesarm/multe`

BugReports `https://github.com/kolesarm/multe/issues`

RoxygenNote 7.3.2

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Contents

`fl` *ECLS data from Fryer and Levitt (2013)*

Description

This dataset contains a subset of the publicly available Early Childhood Longitudinal Study Birth Cohort data from Fryer and Levitt (2013).

Usage

`fl`

Format

A data frame with 8806 rows corresponding to children and 21 columns corresponding to the variables:

W1C0	Sampling weights (first interview)
W2C0	Sampling weights (second interview)
multiple_birth	Multiple birth status
parent_score	Interviewer rating of the effectiveness of the 'parent as a teacher', Nursing Child Assessment Teaching Scale (total score).
SES_quintile	Quintile of socioeconomic status
region	US region
interviewer_ID_9	Interviewer ID (first interview)
interviewer_ID_24	Interviewer ID (second interview)
mom_age	Age of mother
days_premature	Days premature
siblings	Number of siblings
family_structure	Family structure
birthweight	Birthweight category
female	Female
mom_age_NA	Age of mother missing
age_9	Age at first interview
age_24	Age at second interview
std_iq_9	Standardized IQ at first interview
std_iq_24	Standardized IQ at second interview
parent_score_NA	`parent_score` missing
race	Race

Source

doi:10.3886/E112609V1

References

Roland G Fryer and Steven D Levitt. Testing for racial differences in the mental ability of young children. American Economic Review, 103(2):981–1005, April 2013. doi:10.1093/qje/qjy006

`multe` *Multiple Treatment Effects Regression*

Description

Compute contamination bias diagnostics for the partially linear (PL) regression estimator with multiple treatments. Also report four alternative estimators:

OWN The own treatment effect component of the PL estimator.

ATE The unweighted average treatment effect, implemented using interacted regression.

EW Weighted ATE estimator based on easiest-to-estimate weighting (EW) scheme, implemented by running one-treatment-at-a-time regressions.

CW Weighted ATE estimator using easiest-to-estimate common weighting (CW) scheme, implemented using weighted regression.

Usage

```
multe(r, treatment_name, cluster = NULL, tol = 1e-07, cw_uniform = FALSE)
```

Arguments

`r`	Fitted model, output of the `lm` function.
`treatment_name`	name of treatment variable
`cluster`	Factor variable that defines clusters. If `NULL` (or not supplied), the command computes heteroscedasticity-robust standard errors, rather than cluster-robust standard errors.
`tol`	Numerical tolerance for computing LM test statistic for testing variability of the propensity score.
`cw_uniform`	For the CW estimator, should the target weighting scheme give all comparisons equal weight (if `FALSE`), or should it draw from the marginal empirical treatment distribution (if `TRUE`)?

Value

Returns a list with the following components:

est_f Data frame with alternative estimators and standard errors for the full sample

est_o Data frame with alternative estimators and standard errors for the overlap sample

cb_f, cb_0 Data frame with differences between PL and alternative estimators, along with standard errors for the full, and for the overlap sample.

n_f, n_o Sample sizes for the full, and for the overlap sample.

k_f, k_o Number of controls for the full, and for the overlap sample.

t_f, t_o LM and Wald statistic, degrees of freedom, and p-values for the full and for the overlap sample, for testing the hypothesis of no variation in the propensity scores.

pscore_sd_f, pscore_sd_o Standard deviation of the estimated propensity score in the full and overlap samples.

Y, X, wgt Vector of outcomes, treatments and weights in the overlap sample

Zm Matrix of controls in the overlap sample

References

Paul Goldsmith-Pinkham, Peter Hull, and Michal Kolesár. Contamination bias in linear regressions. ArXiv:2106.05024, February 2024.

Examples

```
wbh <- fl[fl$race=="White" | fl$race=="Black" | fl$race=="Hispanic", ]
wbh <- droplevels(wbh)
r1 <- stats::lm(std_iq_24~race+factor(age_24)+female, weight=W2C0, data=wbh)
m1 <- multe(r1, treatment="race")
```

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