

Package ‘multe’

January 15, 2024

Title Multiple Treatment Effects Regression

Version 0.0.0.9000

Description This R package implements contamination bias diagnostics and alternative estimators for regressions with multiple treatments. The implementation is based on Goldsmith-Pinkham, Hull, and Kolesár (2022) [arXiv:2106.05024](https://arxiv.org/abs/2106.05024).

Depends R (>= 4.3.0)

Language en-US

URL <https://github.com/kolesarm/multe>

BugReports <https://github.com/kolesarm/multe/issues>

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Imports stats,
nnet,
tidyr

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

Config/testthat/edition 3

LazyData true

VignetteBuilder knitr

R topics documented:

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f1	<i>ECLS data from Fryer and Levitt (2013)</i>
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Description

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

Usage

f1

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](https://doi.org/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](https://doi.org/10.1093/qje/qjy006)

multe

Contamination Bias Diagnostics for Multiple Treatments

Description

Contamination Bias Diagnostics for Multiple Treatments

Usage

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

Arguments

<code>r</code>	Fitted model, output of the <code>lm</code> function.
<code>treatment_name</code>	name of treatment variable
<code>cluster</code>	Factor variable that defines clusters. If <code>NULL</code> (or not supplied), the command computes heteroscedasticity-robust standard errors, rather than cluster-robust standard errors.
<code>tol</code>	Numerical tolerance for computing LM test statistic for testing variability of the propensity score.
<code>cw_uniform</code>	For the CW estimator, use target efficiency when all comparisons have equal probability (if <code>FALSE</code>), or draw from the marginal distribution of treatments (if <code>TRUE</code>)?

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_o** 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.

References

Paul Goldsmith-Pinkham, Peter Hull, and Michal Kolesár. Contamination bias in linear regressions. ArXiv:2106.05024, August 2022.

Examples

```
wbh <- fl[f1$race=="White" | f1$race=="Black" | f1$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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