Package ‘multe’

July 12, 2024

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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