

# Package ‘multe’

February 12, 2024

**Title** Multiple Treatment Effects Regression

**Version** 1.0.0

**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)

**License** MIT + file LICENSE

**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>

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**VignetteBuilder** knitr

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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)

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multe	<i>Multiple Treatment Effects Regression</i>
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**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**

<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, should the target weighting scheme give all comparisons equal weight (if <code>FALSE</code> ), or should it draw from the marginal empirical treatment distribution (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.

**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, 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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