Package 'MRStdLCRT'

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Type Package

Title Model-Robust Standardization for Longitudinal Cluster-Randomized Trials

Version 0.1.1

Description Provides estimation and leave-one-cluster-out jackknife standard errors for four longitudinal cluster-randomized trial estimands: horizontal individual average treatment effect (h-iATE), horizontal cluster average treatment effect (h-cATE), vertical individual average treatment effect (v-iATE), and vertical cluster-period average treatment effect (v-cATE), using unadjusted and augmented (model-robust standardization) estimators. The working model may be fit using linear mixed models for continuous outcomes or generalized estimating equations and generalized linear mixed models for binary outcomes. Period inclusion for aggregation is determined automatically: only periods with both treated and control clusters are included in the construction of the marginal means and treatment effect contrasts. See Fang et al. (2025) <doi:10.48550/arXiv.2507.17190>.

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Author Xi Fang [aut, cre], Fan Li [aut]

Maintainer Xi Fang <x.fang@yale.edu>

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Contents

`mrstdlcrt_fit` *Model-robust standardization for longitudinal cluster-randomized trials*

Description

Fits *unadjusted* and *augmented* (model-robust standardization) estimators for four longitudinal cluster-randomized trial (L-CRT) estimands, with inference based on leave-one-cluster-out (delete-1) jackknife standard errors.

Usage

```
mrstdlcrt_fit(
  data,
  formula,
  cluster_id = "cluster",
  period = "period",
  trt = "trt",
  method = c("gee", "lmer", "glmer"),
  family = c("gaussian", "binomial"),
  corstr = "independence",
  scale = c("RD", "RR", "OR")
)
```

Arguments

`data`	A `data.frame` containing the outcome, `trt`, `period`, `cluster_id`, and any covariates appearing in `formula`.
`formula`	A model formula for the working model. May include interactions and (for `"lmer"`/`"glmer"`) random effects terms. For `"gee"`, random effects terms are removed prior to fitting.
`cluster_id`	Character string giving the cluster identifier column name.
`period`	Character string giving the period identifier column name. May be numeric, integer, or a factor; ordering is taken from the natural order of the column.

`trt`	Character string giving the binary treatment column name (0/1).
`method`	Working model fitting method: `"gee"`, `"lmer"`, or `"glmer"`.
`family`	Outcome family: `"gaussian"` for continuous outcomes or `"binomial"` for binary outcomes.
`corstr`	Correlation structure passed to `gee` when `method = "gee"` (e.g., `"independence"`, `"exchangeable"`, `"ar1"`).
`scale`	For `family = "binomial"` only: `"RD"` (risk difference), `"RR"` (log risk ratio), or `"OR"` (log odds ratio).

Details

The four supported estimands are:

h-iATE Horizontal individual average treatment effect (individual-weighted within each period).

h-cATE Horizontal cluster average treatment effect (cluster-weighted within each period).

v-iATE Vertical individual average treatment effect (period-weighted; individuals weighted within period).

v-cATE Vertical cluster-period average treatment effect (period-weighted; cluster-period cells equally weighted within period).

For each estimand, the function returns point estimates under:

1. an unadjusted estimator based on cluster-period means, and
2. an augmented estimator that combines model-based counterfactual predictions with a design-based correction term (model-robust standardization).

Data structure. The input `data` must contain: (i) a cluster identifier `cluster_id`, (ii) a period identifier `period`, (iii) a binary treatment indicator `trt` coded as 0/1 (or coercible to 0/1), and (iv) the outcome appearing on the left-hand side of `formula`.

Treatment must be constant within cluster-period. Within each `(cluster, period)` cell, `trt` is required to be constant; otherwise the function errors and prints example problematic cells.

Automatic period inclusion (mixture rule). Marginal means and treatment contrasts are aggregated using only "mixed" periods—periods in which both treated and control clusters are observed. Periods with all clusters in the same arm contribute no information to between-arm contrasts and are excluded automatically.

Working model options.

`method = "lmer"` Linear mixed model via **lme4** for continuous outcomes.

`method = "glmer"` Logistic mixed model via **lme4** for binary outcomes.

`method = "gee"` Generalized estimating equations via **gee**. Random-effects terms in `formula` (e.g., `(1|cluster)`) are ignored automatically.

For `family = "binomial"`, treatment effects can be reported on the risk-difference scale (`scale = "RD"`), log risk-ratio scale (`scale = "RR"`), or log odds-ratio scale (`scale = "OR"`). For `family = "gaussian"`, effects are mean differences (and `scale` is ignored).

Inference. Standard errors are computed using a delete-1 cluster jackknife: refit the procedure leaving out one cluster at a time, compute the jackknife covariance, and report per-estimand jackknife SEs. Downstream methods `summary` and `plot` use `t`-critical values with `df = I - 1`, where `I` is the number of clusters.

Value

An object of class "mrs" with components:

`estimates` A tibble of unadjusted and adjusted point estimates for the four estimands.

`jk_se` A tibble of corresponding delete-1 cluster jackknife standard errors.

`jk_cov_unadj`, `jk_cov_aug` Jackknife covariance matrices for unadjusted and adjusted estimators.

`reps` Internal components used for fitting and aggregation (including kept periods and mixture table).

`meta` Metadata: call, method/family/scale, kept periods, cluster/period counts, etc.

The class has `print`, `summary`, and `plot` methods.

References

Fang, X. and Li, F. (2025). Model-Robust Standardization for Longitudinal Cluster-Randomized Trials. arXiv:2507.17190.

Examples

```
data(sw_c)

# Keep the example fast for R CMD check: use a small subset of clusters
cl_keep <- sort(unique(sw_c$cluster))[1:6]
dat <- sw_c[sw_c$cluster %in% cl_keep, ]

fit <- mrstdlcrt_fit(
  data = dat,
  formula = y ~ trt + factor(period) + x1 + x2 + (1 | cluster),
  cluster_id = "cluster",
  period = "period",
  trt = "trt",
  method = "lmer",
  family = "gaussian"
)

fit
summary(fit, show_counts = FALSE, ics = "none")
plot(fit)
```

---

plot.mrs *Plot estimates from an mrs fit*

Description

Plots unadjusted vs adjusted estimates with t-based confidence intervals computed from delete-1 cluster jackknife SEs (df = I - 1). Facets by estimand.

Usage

```
## S3 method for class 'mrs'
plot(x, level = 0.95, estimand = NULL, point_size = 2.8, ...)
```

Arguments

x	An object of class "mrs".
level	Confidence level.
estimand	Optional subset of estimands to plot.
point_size	Point size.
...	Unused.

Value

Invisibly returns a ggplot2 object.

Examples

```
data(sw_c)
dat <- sw_c[sw_c$cluster %in% sort(unique(sw_c$cluster))[1:6], ]

fit <- mrstdlcrt_fit(
  data = dat,
  formula = y ~ trt + factor(period) + x1 + x2 + (1 | cluster),
  cluster_id = "cluster", period = "period", trt = "trt",
  method = "lmer", family = "gaussian"
)

plot(fit)
```

---

print.mrs *Print method for mrs objects*

Description

Print method for mrs objects

Usage

```
## S3 method for class 'mrs'
print(x, ...)
```

Arguments

x	An object of class "mrs".
...	Unused.

Value

x invisibly.

`summary.mrs` *Summarize an mrs fit*

Description

Prints key diagnostics (kept periods / mixture table), and per-estimand point estimates with delete-1 cluster jackknife SEs and t-based confidence intervals (df = I - 1). Optionally prints an ICS linear-contrast F-test.

Usage

```
## S3 method for class 'mrs'
summary(
  object,
  level = 0.95,
  estimand = NULL,
  digits = 6,
  show_counts = TRUE,
  ics = "global",
  ics_method = c("both", "unadjusted", "adjusted"),
  ics_tol = 1e-10,
  ...
)
```

Arguments

`object`	An object of class `"mrs"`.
`level`	Confidence level for Wald-type confidence intervals.
`estimand`	Optional subset of estimands to print.
`digits`	Digits to print.
`show_counts`	If `TRUE`, print aggregation counts tables.
`ics`	ICS test specification. Use `"global"` (default) or `"none"` to disable. You may also pass a character vector, list spec, or numeric contrast matrix.
`ics_method`	Which covariance to use for ICS test: `"both"`, `"unadjusted"`, `"adjusted"`.
`ics_tol`	Numerical tolerance for rank / generalized inverse.
`...`	Unused (accepts `method_type=` as alias for `ics_method=`).

Value

Invisibly returns a list containing printed tables/metadata and (if requested) ICS results.

Examples

```
data(sw_c)
dat <- sw_c[sw_c$cluster %in% sort(unique(sw_c$cluster))[1:6], ]

fit <- mrstdlcrt_fit(
  data = dat,
  formula = y ~ trt + factor(period) + x1 + x2 + (1 | cluster),
  cluster_id = "cluster", period = "period", trt = "trt",
  method = "lmer", family = "gaussian"
)

summary(fit, show_counts = FALSE, ics = "none")
```

---

sw_b *Example stepped wedge CRT dataset with binary outcome*

Description

A toy dataset with cluster, period, and individual records for illustrating estimands in stepped wedge CRT with a binary outcome.

Usage

```
data(sw_b)
```

Format

A data frame with columns:

cluster Cluster identifier (integer).

period Period index (integer).

id Individual identifier within cluster-period (integer).

trt Treatment indicator (0/1).

x1 Auxiliary covariate (0/1).

x2 Auxiliary covariate (numeric).

y Outcome (0/1, binary).

Examples

```
data(sw_b)
head(sw_b)
```

sw_c — *Example of stepped wedge CRT dataset for continuous outcome*

Description

A toy dataset with cluster, period, and individual records for illustrating estimands in stepped wedge CRT with a continuous outcome.

Usage

```
data(sw_c)
```

Format

A data frame with columns:

cluster Cluster identifier (integer).

period Period index (integer).

id Individual identifier within cluster-period (integer).

trt Treatment indicator (0/1).

x1 Auxiliary covariate (0/1).

x2 Auxiliary covariate (numeric).

y Outcome (numeric, continuous).

Examples

```
data(sw_c)
head(sw_c)
```

xo_b — *Example crossover cluster-randomized trial dataset with binary outcome*

Description

A small simulated 2×2 crossover trial dataset with a binary outcome.

Usage

```
xo_b
```

Format

A tibble/data.frame with one row per subject and the following columns:

h Integer cluster ID (hospital)

p Integer period (1 or 2)

k Integer subject index within cluster-period

trt Treatment indicator (0 = control, 1 = treatment)

x_c01, x_c02 Continuous covariates

x_b01 Binary covariate (0/1)

x_cat1_2, x_cat1_3 Dummy variables for a 3-level categorical covariate (level 1 is reference)

y_bin Observed binary outcome (0/1)

Examples

```
data(xo_b)
str(xo_b)
head(xo_b)
```

---

xo_c — *Example crossover cluster-randomized trial dataset with continuous outcome*

Description

A small simulated 2×2 crossover trial dataset with a continuous outcome.

Usage

```
xo_c
```

Format

A tibble/data.frame with one row per subject and the following columns:

h Integer cluster ID (hospital)

p Integer period (1 or 2)

k Integer subject index within cluster-period

trt Treatment indicator (0 = control, 1 = treatment)

x_c01, x_c02 Continuous covariates

x_b01 Binary covariate (0/1)

x_cat1_2, x_cat1_3 Dummy variables for a 3-level categorical covariate (level 1 is reference)

y_cont Observed continuous outcome

Examples

```
data(xo_c)
str(xo_c)
head(xo_c)
```

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