Package: RobustMediate (via r-universe)

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Title Causal Mediation Analysis with Diagnostics and Sensitivity Analysis

Version 0.1.1

Description Provides tools for causal mediation analysis with continuous treatments using inverse probability weighting (IPW). Estimates natural direct and indirect effects over a user-defined treatment grid and supports flexible dose-response mediation analysis. Includes diagnostic procedures for assessing covariate balance in both treatment and mediator models using standardized mean differences. Implements pathway-specific extensions of the impact threshold for a confounding variable (ITCV; Frank, 2000 <doi:10.1177/0049124100029002001>) adapted to mediation settings. Provides joint sensitivity analysis combining E-values (VanderWeele and Ding, 2017 <doi:10.7326/M16-2607>) and violations of sequential ignorability (Imai, Keele, and Yamamoto, 2010 <doi:10.1214/10-STS321>). Additional utilities include visualization of dose-response mediation functions, robustness profiles, fragility summaries, and formatted outputs for applied research. Supports clustered data structures and multiple outcome families.

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URL `https://github.com/causalfragility-lab/RobustMediate`

BugReports `https://github.com/causalfragility-lab/RobustMediate/issues`

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Contents

`RobustMediate-package` *RobustMediate: Causal Mediation Analysis with Diagnostics and Sensitivity Analysis*

Description

RobustMediate provides a workflow for causal mediation analysis with continuous treatments using inverse probability weighting (IPW), diagnostic tools, and sensitivity analysis.

Main functions include:

- `robustmediate()` - Fits treatment, mediator, and outcome models and stores precomputed results for downstream plotting and reporting.
- `plot_balance()` - Displays covariate balance before and after weighting for both the treatment and mediator pathways using standardized mean differences.
- `plot_mediation()` - Plots estimated natural direct effects (NDE) and natural indirect effects (NIE) over the treatment range, with pointwise uncertainty bands.
- `plot_sensitivity()` - Displays a bivariate sensitivity surface based on E-values and sequential ignorability violations parameterized by `rho`.
- `sensitivity_meditcv()` - Computes pathway-specific mediation ITCV (`medITCV`) diagnostics based on Frank's impact threshold for a confounding variable framework.
- `plot_meditcv()` - Displays pathway-specific medITCV robustness corridors for the a-path and b-path.
- `diagnose()` - Produces a formatted diagnostic summary of balance, mediation effects, and sensitivity results.

Getting started

```
library(RobustMediate)

data(sim_mediation)

fit <- robustmediate(
  X ~ Z1 + Z2 + Z3,
  M ~ X + Z1 + Z2 + Z3,
  Y ~ X + M + Z1 + Z2 + Z3,
  data = sim_mediation,
  R = 500
)

plot(fit)
plot(fit, type = "balance")
plot(fit, type = "sensitivity")
plot(fit, type = "meditcv")
diagnose(fit)
```

Sensitivity interpretation

The E-value x `rho` surface is a bivariate robustness display rather than a single unified causal model. It is intended to help users examine how large different classes of unmeasured confounding would need to be to attenuate or nullify the estimated indirect effect.

The mediation ITCV (`medITCV`) is reported separately for the a-path and b-path. The indirect-effect summary is interpreted as a minimum-path robustness bound governed by the weaker pathway.

Author(s)

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References

Frank, K. A. (2000). Impact of a confounding variable on a regression coefficient. *Sociological Methods & Research*, 29(2), 147–194.

Imai, K., Keele, L., & Yamamoto, T. (2010). Identification, inference, and sensitivity analysis for causal mediation effects. *Psychological Methods*, 15(4), 309–334.

VanderWeele, T. J., & Ding, P. (2017). Sensitivity analysis in observational research: Introducing the E-value. *Annals of Internal Medicine*, 167(4), 268–274.

See Also

Useful links:

- `https://github.com/causalfragility-lab/RobustMediate`
- Report bugs at `https://github.com/causalfragility-lab/RobustMediate/issues`

`as.data.frame.robmedfit`

Coerce effects curve to a data frame

Description

Convenience accessor returning the NDE/NIE/TE curve data frame.

Usage

```
## S3 method for class 'robmedfit'
as.data.frame(x, ...)
```

Arguments

`x`	A `robmedfit` object.
`...`	Ignored.

Value

A data frame with columns `dose`, `estimand`, `estimate`, `lower`, `upper`.

`augment.robmedfit` *Augment data with fitted values from a robmedfit object (broom-compatible)*

Description

Returns the original data augmented with IPW weights, fitted mediator values, and fitted outcome values from the pathway models.

Usage

```
## S3 method for class 'robmedfit'
augment(x, data = NULL, ...)
```

Arguments

`x`	A `robmedfit` object.
`data`	Optional data frame to augment. Defaults to the data stored in the outcome model's `$data` slot.
`...`	Ignored.

Value

The original data frame with additional columns:

`.ipw_weight` Stabilised inverse probability weights.

`.fitted_mediator` Predicted mediator values.

`.fitted_outcome` Predicted outcome values.

`.resid_mediator` Residuals from the mediator model.

`.resid_outcome` Residuals from the outcome model.

Examples

```
fit <- robustmediate(
  treatment_formula = X ~ Z1 + Z2 + Z3,
  mediator_formula  = M ~ X + Z1 + Z2 + Z3,
  outcome_formula   = Y ~ X + M + Z1 + Z2 + Z3,
  data = sim_mediation, R = 50
)
aug <- augment(fit)
hist(aug$.ipw_weight)
```

`compare_fits` *Compare Two robmedfit Objects Side by Side*

Description

Overlays the NDE/NIE/TE curves from two `robmedfit` objects on the same panel. Useful for sensitivity comparisons (e.g. different spline degrees, trimming thresholds, or model specifications).

Usage

```
compare_fits(
  fit1,
  fit2,
  label1 = "Model 1",
  label2 = "Model 2",
  estimands = c("NDE", "NIE")
)
```

Arguments

`fit1`	First `robmedfit` object.
`fit2`	Second `robmedfit` object.
`label1`	Label for `fit1`. Default `"Model 1"`.
`label2`	Label for `fit2`. Default `"Model 2"`.
`estimands`	Estimands to display. Default `c("NDE","NIE")`.

Value

A `ggplot2` object.

Examples

```
## Not run:
fit_a <- robustmediate(X~Z, M~X+Z, Y~X+M+Z, data=dat, spline_df=3, R=200)
fit_b <- robustmediate(X~Z, M~X+Z, Y~X+M+Z, data=dat, spline_df=6, R=200)
compare_fits(fit_a, fit_b, label1="df=3", label2="df=6")

## End(Not run)
```

`diagnose` *Diagnose a robmedfit Object*

Description

Prints a formatted diagnostics report covering balance, mediation effects, and sensitivity robustness. The output is structured so that it can be used directly (or with minimal editing) in the Results section of an applied paper. Returns the underlying results invisibly.

Usage

```
diagnose(x, ...)
```

Arguments

`x`	A `robmedfit` object.
`...`	Ignored.

Value

Invisibly returns a list with elements `balance`, `effects`, `sensitivity`, `meditcv`, and `meditcv_profile`.

`fragility_table` *Pathway Fragility Decomposition Table*

Description

Returns a publication-ready table decomposing indirect-effect robustness into pathway-specific components. Columns follow the medITCV reporting convention: pathway, coefficient, SE, t, df, observed partial r, critical r, medITCV, medITCV%, fragility classification, and tipping-point confounder r.

Usage

```
fragility_table(x, alpha = 0.05)
```

Arguments

`x`	A `robmedfit` object.
`alpha`	Significance level. Default `0.05`.

Value

A data frame with three rows (a-path, b-path, indirect effect) and columns `pathway`, `coefficient`, `SE`, `t_stat`, `df`, `r_obs`, `r_crit`, `medITCV`, `medITCV_pct`, `fragility`, `tipping_r_confounder`, and `bottleneck`.

Examples

```
data(sim_mediation)
  fit <- robustmediate(
    X ~ Z1 + Z2, M ~ X + Z1 + Z2, Y ~ X + M + Z1 + Z2,
    data = sim_mediation, R = 20, verbose = FALSE
  )
fragility_table(fit)
```

`glance.robmedfit` *Glance at a robmedfit object (broom-compatible)*

Description

Returns a one-row summary of the fit: sample size, bootstrap reps, reference dose, percentage mediated, and the two tipping-point sensitivity values.

Usage

```
## S3 method for class 'robmedfit'
glance(x, ...)
```

Arguments

`x`	A `robmedfit` object.
`...`	Ignored.

Value

A one-row data frame.

Examples

```
fit <- robustmediate(
  treatment_formula = X ~ Z1 + Z2 + Z3,
  mediator_formula  = M ~ X + Z1 + Z2 + Z3,
  outcome_formula   = Y ~ X + M + Z1 + Z2 + Z3,
  data = sim_mediation, R = 50
)
glance(fit)
```

`plot.robmedfit` *Plot a robmedfit object*

Description

Dispatches to the appropriate plot function based on `type`.

Usage

```
## S3 method for class 'robmedfit'
plot(
  x,
  type = c("mediation", "balance", "sensitivity", "meditcv", "meditcv_profile",
    "curvature"),
  ...
)
```

Arguments

`x`	A `robmedfit` object.
`type`	Which plot to produce. One of: `"mediation"` Dose-response curve of NDE/NIE/TE (default). `"balance"` Dual love plot of covariate balance. `"sensitivity"` E-value x rho sensitivity contour. `"meditcv"` Pathway-specific medITCV robustness corridor. `"meditcv_profile"` medITCV robustness profile (fragility decomposition). `"curvature"` Dose-varying fragility (curvature-based sensitivity).
`...`	Passed to the underlying plot function.

Value

A `ggplot2` object.

`plot_balance` *Love Plot: Balance Diagnostics for Both Pathways*

Description

Produces a publication-ready love plot showing standardised mean differences (SMDs) before and after IPW weighting for **both** the treatment and mediator pathways — stacked vertically in a single panel. This dual-pathway display is unique to **RobustMediate**; no other mediation package provides it.

Usage

```
plot_balance(x, threshold = 0.1, pathways = c("treatment", "mediator"), ...)
```

Arguments

`x`	A `robmedfit` object.
`threshold`	Absolute SMD threshold displayed as dashed reference lines. Reviewers conventionally accept $\|SMD\| < 0.10$. Default `0.1`.
`pathways`	Character vector indicating which pathways to show. Options: `"treatment"`, `"mediator"`, or both (default).
`...`	Ignored (for S3 consistency).

Value

A `ggplot2` object. Add layers or themes as usual.

Examples

```
## Not run:
fit <- robustmediate(X ~ Z, M ~ X + Z, Y ~ X + M + Z, data = mydata)
plot_balance(fit)
plot_balance(fit, threshold = 0.05, pathways = "treatment")

## End(Not run)
```

`plot_curvature` *Plot Dose-Varying Fragility (Curvature-Based Sensitivity)*

Description

Three-panel visualisation of dose-varying fragility: (1) effect curve with CI bands and fragility zones, (2) local fragility index, (3) normalised curvature.

Usage

```
plot_curvature(x, estimand = "NIE", ref_dose = NULL, ...)
```

Arguments

`x`	Data frame from `sensitivity_curvature()`.
`estimand`	Label for the estimand. Default `"NIE"`.
`ref_dose`	Optional reference dose vertical line.
`...`	Ignored.

Value

A `ggplot2` object.

Examples

```
data(sim_mediation)
  fit <- robustmediate(
    X ~ Z1 + Z2, M ~ X + Z1 + Z2, Y ~ X + M + Z1 + Z2,
    data = sim_mediation, R = 20, verbose = FALSE
  )
curv <- sensitivity_curvature(fit)
plot_curvature(curv, ref_dose = fit$meta$ref_dose)
```

`plot_mediation` *Dose-Response Curve: Natural Direct and Indirect Effects*

Description

Plots NDE, NIE, and (optionally) total effect as smooth spline curves over the full range of treatment values, with pointwise bootstrap confidence bands. This is the signature visualisation of **RobustMediate** and is publication-ready out of the box.

Usage

```
plot_mediation(
  x,
  estimands = c("NDE", "NIE"),
  show_total = FALSE,
  facet = FALSE,
  ...
)
```

Arguments

`x`	A `robmedfit` object.
`estimands`	Character vector of estimands to display. Any subset of `c("NDE", "NIE", "TE")`. Default `c("NDE","NIE")`.
`show_total`	Shorthand for adding `"TE"` to `estimands`. Default `FALSE`.
`facet`	Logical. Split estimands into separate facets? Default `FALSE`.
`...`	Ignored.

Value

A `ggplot2` object.

Examples

```
## Not run:
fit <- robustmediate(X ~ Z, M ~ X + Z, Y ~ X + M + Z, data = mydata)
plot_mediation(fit)
plot_mediation(fit, estimands = c("NDE","NIE","TE"), facet = TRUE)

## End(Not run)
```

`plot_meditcv` *Plot medITCV robustness corridors for both mediation pathways*

Description

Produces a two-panel pathway-specific robustness corridor plot showing the observed partial correlation, critical partial correlation threshold, medITCV corridor, and benchmark confounder impacts for each pathway.

Usage

```
plot_meditcv(x, ...)
```

Arguments

`x`	A `meditcv` object from `sensitivity_meditcv()`.
`...`	Ignored.

Value

A `ggplot2` object.

Examples

```
data(sim_mediation)
  fit <- robustmediate(
    X ~ Z1 + Z2, M ~ X + Z1 + Z2, Y ~ X + M + Z1 + Z2,
    data = sim_mediation, R = 20, verbose = FALSE
  )
med <- sensitivity_meditcv(fit)
plot_meditcv(med)
```

`plot_meditcv_profile` *Plot the medITCV Robustness Profile*

Description

Visualises how each pathway's partial correlation is attenuated as confounding impact delta increases, with tipping points and a fragility zone marked.

Usage

```
plot_meditcv_profile(x, ...)
```

Arguments

`x`	A `meditcv_profile` object from `sensitivity_meditcv_profile()`.
`...`	Ignored.

Value

A `ggplot2` object.

Examples

```
data(sim_mediation)
  fit <- robustmediate(
    X ~ Z1 + Z2, M ~ X + Z1 + Z2, Y ~ X + M + Z1 + Z2,
    data = sim_mediation, R = 20, verbose = FALSE
  )
mp  <- sensitivity_meditcv_profile(fit)
plot_meditcv_profile(mp)
```

`plot_sensitivity` *Sensitivity Contour Plot: Joint E-value x Rho Display*

Description

Renders the novel bivariate robustness map unique to **RobustMediate**: a 2-D heatmap where the x-axis is the E-value (VanderWeele-style unmeasured treatment–outcome confounding) and the y-axis is Imai's sequential-ignorability violation parameter rho. Contour lines show where the mediation effect crosses zero, so readers can judge robustness to **two different** sensitivity dimensions simultaneously.

This visualisation does not exist elsewhere in the R ecosystem. The correct interpretation is as a *bivariate robustness display*, not a joint causal model — see the package paper for theoretical justification.

Usage

```
plot_sensitivity(
  x,
  annotate_zero = TRUE,
  n_breaks = 12,
  palette = "RdYlGn",
  ...
)
```

Arguments

`x`	A `robmedfit` object.
`annotate_zero`	Logical. Draw a bold dashed zero-crossing contour? Default `TRUE`. Highly recommended for applied papers.
`n_breaks`	Number of fill colour breaks in the heatmap. Default `12`.
`palette`	RColorBrewer palette name. Default `"RdYlGn"`.
`...`	Ignored.

Value

A `ggplot2` object.

Examples

```
## Not run:
fit <- robustmediate(X ~ Z, M ~ X + Z, Y ~ X + M + Z, data = mydata)
plot_sensitivity(fit)
plot_sensitivity(fit, annotate_zero = FALSE, palette = "PuOr")

## End(Not run)
```

`print.meditcv` *Print a meditcv object*

Description

Print a meditcv object

Usage

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

Arguments

`x`	A `meditcv` object from `sensitivity_meditcv()`.
`...`	Ignored.

Value

The input object, invisibly. Called for its side effect of printing a formatted medITCV report to the console.

`print.meditcv_profile` *Print a meditcv_profile object*

Description

Print a meditcv_profile object

Usage

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

Arguments

`x`	A `meditcv_profile` object from `sensitivity_meditcv_profile()`.
`...`	Ignored.

Value

The input object, invisibly. Called for its side effect of printing a formatted medITCV robustness profile to the console.

`print.robmedfit` *Print a robmedfit object*

Description

Print a robmedfit object

Usage

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

Arguments

`x`	A `robmedfit` object returned by `robustmediate()`.
`...`	Ignored.

Value

The input object, invisibly.

`robustmediate` *Robust Causal Mediation Analysis*

Description

Fits treatment, mediator, and outcome models for causal mediation analysis with continuous treatments using inverse probability weighting (IPW), and returns a precomputed `robmedfit` object for plotting and diagnostics.

Usage

```
robustmediate(
  treatment_formula,
  mediator_formula,
  outcome_formula,
  data,
  ref_dose = NULL,
  dose_grid = NULL,
  R = 500,
  alpha = 0.05,
  covariates = NULL,
  cluster_var = NULL,
  family_treatment = stats::gaussian(),
  family_mediator = stats::gaussian(),
  family_outcome = stats::gaussian(),
  spline_df = 4,
  evalue_seq = seq(1, 10, by = 0.25),
  rho_seq = seq(-1, 1, by = 0.05),
  verbose = TRUE
)
```

Arguments

`treatment_formula`	Formula for the treatment model (for example, `X ~ Z1 + Z2`).
`mediator_formula`	Formula for the mediator model (for example, `M ~ X + Z1 + Z2`).
`outcome_formula`	Formula for the outcome model (for example, `Y ~ X + M + Z1 + Z2`).
`data`	A data frame containing all analysis variables.
`ref_dose`	Reference dose value. Defaults to the sample mean of the treatment variable.
`dose_grid`	Numeric vector of dose values over which NDE, NIE, and TE are evaluated. Defaults to 100 evenly spaced points across the observed treatment range.
`R`	Number of bootstrap replicates. Default is `500`.
`alpha`	Significance level. Default is `0.05`.

`covariates`	Covariate names for balance diagnostics. If `NULL`, covariates are inferred from the treatment formula.
`cluster_var`	Optional clustering variable name. `NULL` assumes independent observations.
`family_treatment`	GLM family for the treatment model. Default is `stats::gaussian()`.
`family_mediator`	GLM family for the mediator model. Default is `stats::gaussian()`.
`family_outcome`	GLM family for the outcome model. Default is `stats::gaussian()`.
`spline_df`	Degrees of freedom for spline-based effect summaries. Default is `4`.
`evalue_seq`	Sequence of E-values used to build the sensitivity surface. Default is `seq(1, 10, by = 0.25)`.
`rho_seq`	Sequence of `rho` values used to build the sensitivity surface. Default is `seq(-1, 1, by = 0.05)`.
`verbose`	Logical; if `TRUE`, display progress messages.

Value

An object of class `"robmedfit"` containing:

`models` Fitted treatment, mediator, and outcome models.

`balance` Balance statistics before and after weighting.

`effects` Dose-response summaries for NDE, NIE, and TE, including bootstrap intervals.

`sensitivity` Bivariate E-value and `rho` sensitivity surface.

`meditcv` Pathway-specific medITCV object from `sensitivity_meditcv()`.

`meditcv_profile` medITCV robustness profile from `sensitivity_meditcv_profile()`.

`cluster` Cluster information, or `NULL` if clustering was not used.

`meta` Call, variable names, dose settings, bootstrap settings, and sample information.

Examples

```
n <- 400
Z1 <- rnorm(n)
Z2 <- rbinom(n, 1, 0.5)
X  <- 0.5 * Z1 + 0.3 * Z2 + rnorm(n)
M  <- 0.4 * X + 0.2 * Z1 + rnorm(n)
Y  <- 0.3 * X + 0.5 * M + 0.1 * Z1 + rnorm(n)
dat <- data.frame(Y, X, M, Z1, Z2)

fit <- robustmediate(
  treatment_formula = X ~ Z1 + Z2,
  mediator_formula = M ~ X + Z1 + Z2,
  outcome_formula = Y ~ X + M + Z1 + Z2,
  data = dat,
  R = 100
)

print(fit)
```

`sensitivity_curvature` *Dose-Varying Fragility: Curvature-Based Sensitivity*

Description

Computes the fragility curvature of the mediation effect across the full treatment dose grid. Returns local fragility index, numerical curvature of the effect curve, and a fragility zone flag at each dose value.

Usage

```
sensitivity_curvature(x, estimand = c("NIE", "NDE", "TE"))
```

Arguments

`x`	A `robmedfit` object.
`estimand`	Which estimand to analyse: `"NIE"` (default), `"NDE"`, or `"TE"`.

Value

A data frame with columns `dose`, `estimate`, `lower`, `upper`, `se_approx`, `frag_local`, `curvature`, and `in_fragility_zone`.

See Also

`plot_curvature()`, `sensitivity_meditcv_profile()`

Examples

```
data(sim_mediation)
  fit <- robustmediate(
    X ~ Z1 + Z2, M ~ X + Z1 + Z2, Y ~ X + M + Z1 + Z2,
    data = sim_mediation, R = 20, verbose = FALSE
  )
curv <- sensitivity_curvature(fit, estimand = "NIE")
plot_curvature(curv)
```

`sensitivity_meditcv` *Mediation ITCV (medITCV) for pathway-specific robustness*

Description

Computes a mediation-specific extension of Kenneth Frank's (2000) Impact Threshold for a Confounding Variable (ITCV) for both pathways of a mediation model:

- **a-path**: treatment -> mediator
- **b-path**: mediator -> outcome (controlling for treatment)

The mediation ITCV (medITCV) quantifies how strong an unmeasured confounder would need to be, in terms of the product $r_{XC} \cdot r_{YC}$, to invalidate inference for each pathway.

Usage

```
sensitivity_meditcv(x, alpha = 0.05)
```

Arguments

`x`	A `robmedfit` object returned by `robustmediate()`.
`alpha`	Significance level. Default is `0.05`.

Value

An object of class `"meditcv"`: a named list with elements `a_path`, `b_path`, `indirect`, and `alpha`. Each pathway element contains the observed partial correlation, critical partial correlation, medITCV value, and benchmark confounder impacts.

References

Frank, K. A. (2000). Impact of a confounding variable on a regression coefficient. *Sociological Methods & Research*, 29(2), 147–194.

See Also

`plot_meditcv()`, `print.meditcv()`

Examples

```
data(sim_mediation)
  fit <- robustmediate(
    X ~ Z1 + Z2, M ~ X + Z1 + Z2, Y ~ X + M + Z1 + Z2,
    data = sim_mediation, R = 20, verbose = FALSE
  )
med <- sensitivity_meditcv(fit)
print(med)
plot_meditcv(med)
```

`sensitivity_meditcv_profile`

medITCV Robustness Profile: Pathway-Specific Fragility Framework

---

Description

Implements the medITCV robustness profile, a formal extension of Frank's ITCV to causal mediation. Computes pathway-specific fragility thresholds, applies the minimum robustness principle, and identifies the bottleneck pathway that governs indirect-effect fragility.

Usage

```
sensitivity_meditcv_profile(
  x,
  alpha = 0.05,
  delta_grid = seq(0, 0.5, by = 0.01)
)
```

Arguments

`x`	A `robmedfit` object.
`alpha`	Significance level. Default `0.05`.
`delta_grid`	Numeric vector of confounding impact values over which the robustness profile is evaluated. Default `seq(0, 0.5, by = 0.01)`.

Value

An object of class `"meditcv_profile"`: a named list with elements `a_path`, `b_path`, `meditcv_indirect`, `bottleneck`, `robustness_profile`, `fragility_ratio`, `meditcv_detail`, and `alpha`.

References

Frank, K. A. (2000). Impact of a confounding variable on a regression coefficient. *Sociological Methods & Research*, 29(2), 147–194.

See Also

`sensitivity_meditcv()`, `plot_meditcv_profile()`, `sensitivity_curvature()`

Examples

```
data(sim_mediation)
  fit <- robustmediate(
    X ~ Z1 + Z2, M ~ X + Z1 + Z2, Y ~ X + M + Z1 + Z2,
    data = sim_mediation, R = 20, verbose = FALSE
  )
mp  <- sensitivity_meditcv_profile(fit)
print(mp)
```

```
plot_meditcv_profile(mp)
```

`sim_mediation` *Simulated Mediation Study Data*

Description

A synthetic dataset mimicking a clustered education study with a continuous treatment (tutoring hours), a continuous mediator (mid-year test score), and a continuous outcome (end-of-year test score). Designed to illustrate **RobustMediate** with realistic effect sizes and non-trivial confounding.

Usage

```
sim_mediation
```

Format

A data frame with 600 rows (30 schools x 20 students) and 7 columns:

school Factor. School identifier (30 levels). Use as `cluster_var`.

Y Numeric. End-of-year test score (outcome).

X Numeric. Tutoring hours received (continuous treatment, >= 0).

M Numeric. Mid-year test score (mediator).

Z1 Numeric. Prior achievement (continuous covariate).

Z2 Integer (0/1). Free-lunch status (binary covariate).

Z3 Numeric. Parental education index (continuous covariate).

True parameter targets

The data-generating process sets:

- **NDE** (X → Y direct path) ~= **0.25**
- **NIE** (X → M → Y path) ~= **0.35**
- **TE ~= 0.60**
- **% mediated ~= 58%**

Use these as a ground truth to assess estimation accuracy.

Source

Generated via `data-raw/generate_sim_data.R`. See that script for the full data-generating process.

Examples

```
data(sim_mediation)
str(sim_mediation)
summary(sim_mediation[, c("Y","X","M")])

## Not run:
fit <- robustmediate(
  treatment_formula = X ~ Z1 + Z2 + Z3,
  mediator_formula  = M ~ X + Z1 + Z2 + Z3,
  outcome_formula   = Y ~ X + M + Z1 + Z2 + Z3,
  data        = sim_mediation,
  cluster_var = "school",
  R           = 500
)
diagnose(fit)

## End(Not run)
```

`summary.robmedfit` *Summary method for robmedfit objects*

Description

Summary method for robmedfit objects

Usage

```
## S3 method for class 'robmedfit'
summary(object, ...)
```

Arguments

`object`	A `robmedfit` object.
`...`	Ignored.

Value

A list with effect, balance, and sensitivity summaries, invisibly.

`tidy.robmedfit` *Tidy a robmedfit object (broom-compatible)*

Description

Returns a tidy data frame of the mediation effect estimates (NDE, NIE, TE) at the reference dose, with confidence intervals. Compatible with `broom::tidy()` and the broader `tidymodels` ecosystem.

Usage

```
## S3 method for class 'robmedfit'
tidy(x, conf.int = TRUE, ...)
```

Arguments

`x`	A `robmedfit` object.
`conf.int`	Logical. Include confidence interval columns? Default `TRUE`.
`...`	Ignored.

Value

A data frame with columns `term`, `estimate`, `conf.low`, `conf.high`, and `ref_dose`.

Examples

```
fit <- robustmediate(
  treatment_formula = X ~ Z1 + Z2 + Z3,
  mediator_formula  = M ~ X + Z1 + Z2 + Z3,
  outcome_formula   = Y ~ X + M + Z1 + Z2 + Z3,
  data = sim_mediation, R = 50
)
tidy(fit)
```

`tipping_table` *Extract Tipping-Point Table*

Description

Returns a formatted data frame of sensitivity tipping points: the minimum E-value and minimum |rho| required to nullify the NIE. Designed for direct insertion into a table in a manuscript.

Usage

```
tipping_table(x)
```

Arguments

`x`	A `robmedfit` object.

Value

A data frame with columns `parameter`, `tipping_value`, `interpretation`.

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