

# Package ‘RobustMediate’

May 7, 2026

**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](https://doi.org/10.1177/0049124100029002001)>) adapted to mediation settings. Provides joint sensitivity analysis combining E-values (VanderWeele and Ding, 2017 <[doi:10.7326/M16-2607](https://doi.org/10.7326/M16-2607)>) and violations of sequential ignorability (Imai, Keele, and Yamamoto, 2010 <[doi:10.1214/10-STS321](https://doi.org/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>

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.3.3

**Depends** R (>= 4.1.0)

**Imports** cli, ggplot2 (>= 3.4.0), rlang, scales, stats, broom

**Suggests** covr, dplyr, knitr, lme4, pkgdown, rmarkdown, splines, testthat (>= 3.0.0), tidyr

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**NeedsCompilation** no

**Author** Subir Hait [aut, cre] (ORCID: <<https://orcid.org/0009-0004-9871-9677>>)

**Maintainer** Subir Hait <haitsubi@msu.edu>

**Repository** CRAN

**Date/Publication** 2026-04-16 09:12:11 UTC

## Contents

RobustMediate-package . . . . .	2
as.data.frame.robmedfit . . . . .	4
augment.robmedfit . . . . .	5
compare_fits . . . . .	6
diagnose . . . . .	7
fragility_table . . . . .	7
glance.robmedfit . . . . .	8
plot.robmedfit . . . . .	9
plot_balance . . . . .	9
plot_curvature . . . . .	10
plot_mediation . . . . .	11
plot_meditcv . . . . .	12
plot_meditcv_profile . . . . .	13
plot_sensitivity . . . . .	13
print.meditcv . . . . .	14
print.meditcv_profile . . . . .	15
print.robmedfit . . . . .	15
robustmediate . . . . .	16
sensitivity_curvature . . . . .	18
sensitivity_meditcv . . . . .	19
sensitivity_meditcv_profile . . . . .	20
sim_mediation . . . . .	21
summary.robmedfit . . . . .	22
tidy.robmedfit . . . . .	23
tipping_table . . . . .	24
<b>Index</b>	<b>25</b>

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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  $\times$   $\rho$  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)

**Maintainer:** Subir Hait <haitsubi@msu.edu> ([ORCID](#))

## 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	<i>Augment data with fitted values from a robmedfit object (broom-compatible)</i>
-------------------	---

---

### 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)
```

**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**

```
fit_a <- 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, spline_df = 3, R = 50
)
fit_b <- 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, spline_df = 6, R = 50
)
compare_fits(fit_a, fit_b, label1 = "df=3", label2 = "df=6")
```

---

diagnose	<i>Diagnose a robmedfit Object</i>
----------	------------------------------------

---

**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	<i>Pathway Fragility Decomposition Table</i>
-----------------	--

---

**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	<i>Plot a robmedfit object</i>
----------------	--------------------------------

---

### 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	<i>Love Plot: Balance Diagnostics for Both Pathways</i>
--------------	---

---

### 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  SMDI  < 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**

```
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
)
plot_balance(fit)
plot_balance(fit, threshold = 0.05, pathways = "treatment")
```

---

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 <a href="#">sensitivity_curvature()</a> .
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	<i>Dose-Response Curve: Natural Direct and Indirect Effects</i>
----------------	---

---

**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 **Robust-Mediate** 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**

```
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
)
plot_mediation(fit)
plot_mediation(fit, estimands = c("NDE", "NIE", "TE"), facet = TRUE)
```

---

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**

```
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
)
plot_sensitivity(fit)
plot_sensitivity(fit, annotate_zero = FALSE, palette = "PuOr")
```

---

```
print.meditcv
```

```
Print a meditecv object
```

---

**Description**

Print a meditecv object

**Usage**

```
## S3 method for class 'meditecv'
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,  $X \sim Z1 + Z2$ ).

`mediator_formula`  
 Formula for the mediator model (for example,  $M \sim X + Z1 + Z2$ ).

outcome_formula	Formula for the outcome model (for example, $Y \sim X + M + Z1 + Z2$ ).
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 <code>stats::gaussian()</code> .
family_mediator	GLM family for the mediator model. Default is <code>stats::gaussian()</code> .
family_outcome	GLM family for the outcome model. Default is <code>stats::gaussian()</code> .
spline_df	Degrees of freedom for spline-based effect summaries. Default is 4.
evaluate_seq	Sequence of E-values used to build the sensitivity surface. Default is <code>seq(1, 10, by = 0.25)</code> .
rho_seq	Sequence of rho values used to build the sensitivity surface. Default is <code>seq(-1, 1, by = 0.05)</code> .
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_mediatecv_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\_mediatecv(), plot\_mediatecv\_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_mediatecv_profile(fit)
print(mp)
plot_mediatecv_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,  $\geq 0$ ).

**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** ( $X \rightarrow Y$  direct path)  $\approx$  **0.25**
- **NIE** ( $X \rightarrow M \rightarrow Y$  path)  $\approx$  **0.35**
- **TE**  $\approx$  **0.60**
- **% mediated**  $\approx$  **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")])

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)
```

---

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	<i>Tidy a robmedfit object (broom-compatible)</i>
----------------	---

---

**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**

<code>x</code>	A robmedfit object.
<code>conf.int</code>	Logical. Include confidence interval columns? Default TRUE.
<code>...</code>	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	<i>Extract Tipping-Point Table</i>
---------------	------------------------------------

---

**Description**

Returns a formatted data frame of sensitivity tipping points: the minimum E-value and minimum lrhol 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.

# Index

## \* datasets

- sim\_mediation, [21](#)
  
- as.data.frame.robmedfit, [4](#)
- augment.robmedfit, [5](#)
  
- compare\_fits, [6](#)
  
- diagnose, [7](#)
  
- fragility\_table, [7](#)
  
- glance.robmedfit, [8](#)
  
- plot.robmedfit, [9](#)
- plot\_balance, [9](#)
- plot\_curvature, [10](#)
- plot\_mediation, [11](#)
- plot\_meditcv, [12](#)
- plot\_meditcv\_profile, [13](#)
- plot\_sensitivity, [13](#)
- print.meditcv, [14](#)
- print.meditcv\_profile, [15](#)
- print.robmedfit, [15](#)
  
- RobustMediate (RobustMediate-package), [2](#)
- robustmediate, [16](#)
- robustmediate(), [16](#), [19](#)
- RobustMediate-package, [2](#)
  
- sensitivity\_curvature, [18](#)
- sensitivity\_curvature(), [10](#)
- sensitivity\_meditcv, [19](#)
- sensitivity\_meditcv\_profile, [20](#)
- sim\_mediation, [21](#)
- summary.robmedfit, [22](#)
  
- tidy.robmedfit, [23](#)
- tipping\_table, [24](#)