

Package ‘MAIVE’

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Title Meta Analysis Instrumental Variable Estimator

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BugReports <https://github.com/PetrCala/MAIVE/issues>

Description Meta-analysis traditionally assigns more weight to studies with lower standard errors, assuming higher precision. However, in observational research, precision must be estimated and is vulnerable to manipulation, such as p-hacking, to achieve statistical significance. This can lead to spurious precision, invalidating inverse-variance weighting and bias-correction methods like funnel plots. Common methods for addressing publication bias, including selection models, often fail or exacerbate the problem. This package introduces an instrumental variable approach to limit bias caused by spurious precision in meta-analysis. Methods are described in 'Irsova et al.' (2025) [doi:10.1038/s41467-025-63261-0](https://doi.org/10.1038/s41467-025-63261-0).

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Imports stats, cli, clubSandwich

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Author Zuzana Irsova [aut] (affiliation: Charles University, Prague),
Pedro R. D. Bom [aut] (affiliation: University of Deusto, Bilbao),
Tomas Havranek [aut] (affiliation: Charles University, Prague; CEPR,
London; METRICS, Stanford),
Heiko Rachinger [aut] (affiliation: University of the Balearic Islands,
Palma),
Petr Calá [aut, cre] (affiliation: Charles University, Prague)

Maintainer Petr Calá <cala.p@seznam.cz>

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get_funnel_plot	<i>Draw a funnel plot (base graphics)</i>
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Description

High-level wrapper that accepts the original input data and the result returned by ‘maive()’ / ‘waive()’, prepares the necessary vectors/metadata, and draws the funnel plot on the currently active graphics device.

Usage

```
get_funnel_plot(dat, result, instrument = NULL, model_type = "MAIVE")
```

Arguments

dat	Data frame containing at least numeric columns ‘bs’ (effect sizes) and ‘sebs’ (standard errors).
result	Result list returned by ‘maive()’ or ‘waive()’.
instrument	Optional indicator (0/1). If ‘NULL’, inferred from ‘result’.
model_type	Label used for plot text/legend (e.g., “MAIVE” or “WAIVE”).

Details

Device management (PNG/SVG/PDF, resolution, base64 encoding) is intentionally left to the caller.

Value

Invisibly returns ‘NULL’.

maive

R code for MAIVE

Description

R package for MAIVE: "Spurious Precision in Meta-Analysis of Observational Research" by Zuzana Irsova, Pedro Bom, Tomas Havranek, Petr Cala, and Heiko Rachinger.

Usage

```
maive(
  dat,
  method,
  weight,
  instrument,
  studylevel,
  SE,
  AR,
  first_stage = 0L,
  estimate = NULL,
  se = NULL,
  n = NULL,
  study_id = NULL,
  seed = 123
)
```

Arguments

<code>dat</code>	Data frame with columns <code>bs</code> , <code>sebs</code> , <code>Ns</code> , <code>study_id</code> (optional). Column names can be remapped with <code>estimate</code> , <code>se</code> , <code>n</code> , and <code>study_id</code> .
<code>method</code>	1 FAT-PET, 2 PEESE, 3 PET-PEESE, 4 EK.
<code>weight</code>	0 no weights, 1 standard weights, 2 MAIVE adjusted weights, 3 study weights.
<code>instrument</code>	1 yes, 0 no.
<code>studylevel</code>	Correlation at study level: 0 none, 1 fixed effects, 2 cluster.
<code>SE</code>	SE estimator: 0 CR0 (Huber-White), 1 CR1 (Standard empirical correction), 2 CR2 (Bias-reduced estimator), 3 wild bootstrap.
<code>AR</code>	Anderson Rubin corrected CI for weak instruments (available for unweighted and MAIVE-adjusted weight versions of PET, PEESE, PET-PEESE, not available for fixed effects): 0 no, 1 yes.
<code>first_stage</code>	First-stage specification for the variance model: 0 levels, 1 log.
<code>estimate</code>	Optional column name to use instead of <code>'bs'</code>
<code>se</code>	Optional column name to use instead of <code>'sebs'</code>
<code>n</code>	Optional column name to use instead of <code>'Ns'</code>

study_id	Optional column name for study identifiers. When not supplied, a column named study_id is used if present; otherwise, if dat has four or more columns, the fourth column is used as the study identifier and a warning names the column. Any fourth column (a moderator, a year) would otherwise drive the study dummies and clustering at every studylevel other than 0, so name the column explicitly or drop it.
seed	Seed for the wild bootstrap when SE = 3. Use NULL to avoid setting a seed (results depend on the current RNG state). Default is 123 for historical reproducibility.

Details

Guided, interactive workflow available at <https://www.easymeta.org>.

Data dat can be imported from an Excel file via: `dat <- read_excel("inputdata.xlsx")` or from a csv file via: `dat <- read.csv("inputdata.csv")` It should contain:

- Estimates: bs
- Standard errors: sebs
- Number of observations: Ns
- Optional: study_id

Default option for MAIVE: MAIVE-PET-PEESE, unweighted, instrumented, cluster SE, wild bootstrap, AR.

Value

- beta: MAIVE meta-estimate
- SE: MAIVE standard error
- F-test: heteroskedastic robust F-test of the first step instrumented SEs
- beta_standard: point estimate from the conventional (non-instrumented, inverse-variance weighted) fit of the method chosen
- SE_standard: standard error from the same conventional fit as beta_standard
- Hausman: Hausman type test: comparison between MAIVE and standard version
- Chi2: 5
- SE_instrumented: instrumented standard errors
- AR_CI: Anderson-Rubin confidence interval for weak instruments
- pub bias p-value: p-value of test for publication bias / p-hacking based on instrumented FAT
- egger_coef: Egger Coefficient (PET estimate)
- egger_se: Egger Standard Error (PET standard error)
- egger_boot_ci: Confidence interval for the Egger coefficient using the selected resampling scheme
- egger_ar_ci: Anderson-Rubin confidence interval for the Egger coefficient (when available)
- is_quadratic_fit: Details on quadratic selection and slope behaviour

- `ek_structure`: Structure of the fitted EK model when `method=4`: "kink", "linear", or "intercept" (intercept-only degenerate fit); NA for other methods
- `boot_result`: Boot result
- `slope_coef`: Slope coefficient
- `petpeese_selected`: Which model (PET or PEESE) was selected when `method=3` (NA otherwise)
- `peese_se2_coef`: Coefficient on SE^2 when PEESE is the final model (NA otherwise)
- `peese_se2_se`: Standard error of the PEESE SE^2 coefficient (NA otherwise)

Examples

```
dat <- data.frame(
  bs = c(0.5, 0.45, 0.55, 0.6),
  sebs = c(0.25, 0.2, 0.22, 0.27),
  Ns = c(50, 80, 65, 90)
)

result <- maive(dat,
  method = 3, weight = 0, instrument = 1,
  studylevel = 0, SE = 0, AR = 0, first_stage = 0
)
```

<code>maive_from_metafor</code>	<i>Convert metafor objects into MAIVE input data</i>
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Description

Builds the data frame that `maive()` and `waive()` expect (columns `bs`, `sebs`, `Ns`, and optionally `study_id`) from a **metafor** `escalc` data frame or an `rma.uni` model fit.

Usage

```
maive_from_metafor(x, ni = NULL, study_id = NULL)
```

Arguments

- | | |
|-----------------------|---|
| <code>x</code> | An <code>escalc</code> data frame (or any data frame with <code>yi</code> and <code>vi</code> columns) or an <code>rma.uni</code> fit. |
| <code>ni</code> | Optional sample sizes: a numeric vector, or the name of a column in <code>x</code> (or in the data stored with the fit). Overrides any sample sizes carried by <code>x</code> . |
| <code>study_id</code> | Optional study identifiers: a vector, or the name of a column in <code>x</code> (or in the data stored with the fit). Vectors may have either the length of the original data or the number of rows the fit kept. |

Details

The conversion takes the standard error as $\sqrt{vi}$, so metafor's sampling variance cannot end up in the sebs slot by mistake. Sample sizes are never inferred from the variances; doing so would reintroduce the spurious precision that MAIVE corrects for. They are resolved, in order, from the `ni` argument, an `ni` column (or the fit's `ni`), the `ni` attribute that `escalc()` stamps on the effect size column, and finally the exact two-group total $n1i + n2i$. When none of these is available the function stops and names what it needs.

For `rma.uni` fits the effect sizes, variances, sample sizes, and any vector supplied through `ni` or `study_id` are taken through the same subset and missing-value masks the fit applied, so the rows stay aligned. Multivariate (`rma.mv`), GLMM (`rma.glmm`), and other `rma` subclasses are refused rather than silently flattened.

Value

A data frame with columns `bs`, `sebs`, `Ns`, and, when identifiers were supplied, `study_id`, ready for `maive()` or `waive()`.

Examples

```
dat <- metafor::escalc(
  measure = "SMD",
  m1i = c(2.1, 2.5, 1.9, 2.4, 2.2, 2.6),
  sd1i = c(1.0, 1.2, 0.9, 1.1, 1.0, 1.3),
  n1i = c(40, 50, 30, 45, 60, 35),
  m2i = c(1.8, 2.0, 1.7, 2.1, 1.9, 2.2),
  sd2i = c(1.0, 1.1, 1.0, 1.0, 1.1, 1.2),
  n2i = c(42, 55, 33, 48, 58, 37)
)
maive_dat <- maive_from_metafor(dat)
head(maive_dat)

fit <- metafor::rma(yi, vi, data = dat)
identical(maive_from_metafor(fit), maive_dat)

result <- maive(maive_dat,
  method = 3, weight = 0, instrument = 1,
  studylevel = 0, SE = 0, AR = 0
)
```

waive

WAIVE: More Aggressive Correction for P-Hacking and Spurious Precision

Description

WAIVE (Weighted Adjusted Instrumental Variable Estimator) provides a more aggressive correction for p-hacking and spurious precision by extending MAIVE with exponential-decay weights that downweight both spuriously precise estimates and extreme outliers.

Usage

```

waive(
  dat,
  method,
  weight,
  instrument,
  studylevel,
  SE,
  AR,
  first_stage = 0L,
  estimate = NULL,
  se = NULL,
  n = NULL,
  study_id = NULL,
  seed = 123
)

```

Arguments

<code>dat</code>	Data frame with columns <code>bs</code> , <code>sebs</code> , <code>Ns</code> , <code>study_id</code> (optional). Column names can be remapped with <code>estimate</code> , <code>se</code> , <code>n</code> , and <code>study_id</code> .
<code>method</code>	1 FAT-PET, 2 PEESE, 3 PET-PEESE, 4 EK.
<code>weight</code>	0 no weights, 1 standard weights, 2 MAIVE adjusted weights, 3 study weights.
<code>instrument</code>	1 yes, 0 no.
<code>studylevel</code>	Correlation at study level: 0 none, 1 fixed effects, 2 cluster.
<code>SE</code>	SE estimator: 0 CR0 (Huber-White), 1 CR1 (Standard empirical correction), 2 CR2 (Bias-reduced estimator), 3 wild bootstrap.
<code>AR</code>	Anderson Rubin corrected CI for weak instruments (available for unweighted and MAIVE-adjusted weight versions of PET, PEESE, PET-PEESE, not available for fixed effects): 0 no, 1 yes.
<code>first_stage</code>	First-stage specification for the variance model: 0 levels, 1 log.
<code>estimate</code>	Optional column name to use instead of 'bs'
<code>se</code>	Optional column name to use instead of 'sebs'
<code>n</code>	Optional column name to use instead of 'Ns'
<code>study_id</code>	Optional column name for study identifiers. When not supplied, a column named <code>study_id</code> is used if present; otherwise, if <code>dat</code> has four or more columns, the fourth column is used as the study identifier and a warning names the column. Any fourth column (a moderator, a year) would otherwise drive the study dummies and clustering at every <code>studylevel</code> other than 0, so name the column explicitly or drop it.
<code>seed</code>	Seed for the wild bootstrap when <code>SE = 3</code> . Use <code>NULL</code> to avoid setting a seed (results depend on the current RNG state). Default is 123 for historical reproducibility.

Details

Guided, interactive workflow available at <https://www.easymeta.org>.

For technical details on WAIVE methodology, see: https://meta-analysis.cz/waive_ottawa.pdf

WAIVE combines variance instrumentation (as in MAIVE) with robust downweighting based on first-stage residuals. Studies with negative residuals (spurious precision) or extreme residuals (outliers) receive exponentially reduced influence in the meta-analytic estimate. This makes WAIVE more aggressive than standard MAIVE at correcting for p-hacking and handling outliers.

Value

List with the same structure as `maive()`. See `?maive` for details.

Examples

```
dat <- data.frame(
  bs = c(0.5, 0.45, 0.55, 0.6),
  sebs = c(0.25, 0.2, 0.22, 0.27),
  Ns = c(50, 80, 65, 90)
)

result <- waive(dat,
  method = 3, weight = 0, instrument = 1,
  studylevel = 0, SE = 0, AR = 0, first_stage = 0
)
```

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