Package ‘multibiasmeta’

August 23, 2023

Type Package

Title Sensitivity Analysis for Multiple Biases in Meta-Analyses

Description Meta-analyses can be compromised by studies' internal biases (e.g., confounding in nonrandomized studies) as well as by publication bias. This package conducts sensitivity analyses for the joint effects of these biases (per Mathur (2022) <doi:10.31219/osf.io/u7vcb>). These sensitivity analyses address two questions: (1) For a given severity of internal bias across studies and of publication bias, how much could the results change?; and (2) For a given severity of publication bias, how severe would internal bias have to be, hypothetically, to attenuate the results to the null or by a given amount?

Version 0.2.2

License MIT + file LICENSE

URL `https://github.com/mathurlabstanford/multibiasmeta`, `https://mathurlabstanford.github.io/multibiasmeta/`

BugReports `https://github.com/mathurlabstanford/multibiasmeta/issues`

Encoding UTF-8

LazyData true

Depends R (>= 4.1.0)

Imports dplyr, EValue, metabias, metafor, purrr, Rdpack, rlang, robumeta

RoxygenNote 7.2.3

RdMacros Rdpack

Suggests glue, knitr, phacking, PublicationBias (>= 2.3.0), rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

Author Maya Mathur [aut],
Mika Braginsky [aut],
Peter Solymos [cre, ctb] (<`https://orcid.org/0000-0001-7337-1740`>)

Maintainer Peter Solymos <`peter@analythium.io`>

Repository CRAN

Date/Publication 2023-08-23 13:50:02 UTC

R topics documented:

`meta_meat` *Meta-analysis about meat consumption*

Description

Meta-analysis of the effectiveness of educational behavior interventions that attempt to reduce meat consumption by appealing to animal welfare.

Usage

```
meta_meat
```

Format

A data frame with 100 rows and 4 columns:

yi Point estimate on log-risk ratio scale

vi Variance of point estimate

cluster Paper that contributed the point estimate

randomized Logical indicating whether study was randomized

References

Mathur MB, Peacock J, Reichling DB, Nadler J, Bain PA, Gardner CD, Robinson TN (2021). "Interventions to reduce meat consumption by appealing to animal welfare: Meta-analysis and evidence-based recommendations." *Appetite*, **164**, 105277.

`multibias_evalue` *E-value for meta-analysis with multiple biases*

Description

E-value for meta-analysis with multiple biases

Usage

```
multibias_evalue(
  yi,
  vi,
  sei,
  cluster = 1:length(yi),
  biased = TRUE,
  selection_ratio,
  q = 0,
  favor_positive = TRUE,
  alpha_select = 0.05,
  ci_level = 0.95,
  small = TRUE,
  bias_max = 20,
  assumed_bias_type = NULL
)
```

Arguments

`yi`	A vector of point estimates to be meta-analyzed.
`vi`	A vector of estimated variances (i.e., squared standard errors) for the point estimates.
`sei`	A vector of estimated standard errors for the point estimates. (Only one of `vi` or `sei` needs to be specified).
`cluster`	Vector of the same length as the number of rows in the data, indicating which cluster each study should be considered part of (defaults to treating studies as independent; i.e., each study is in its own cluster).
`biased`	Boolean indicating whether each study is considered internally biased; either single value used for all studies or a vector the same length as the number of rows in the data (defaults to all studies).
`selection_ratio`	Ratio by which publication bias favors affirmative studies (i.e., studies with p-values less than `alpha_select` and estimates in the direction indicated by `favor_positive`).
`q`	The attenuated value to which to shift the point estimate or CI. Should be specified on the same scale as `yi` (e.g., if `yi` is on the log-RR scale, then `q` should be as well).

`favor_positive`	`TRUE` if publication bias are assumed to favor significant positive estimates; `FALSE` if assumed to favor significant negative estimates.
`alpha_select`	Alpha level at which an estimate's probability of being favored by publication bias is assumed to change (i.e., the threshold at which study investigators, journal editors, etc., consider an estimate to be significant).
`ci_level`	Confidence interval level (as proportion) for the corrected point estimate. (The alpha level for inference on the corrected point estimate will be calculated from `ci_level`.)
`small`	Should inference allow for a small meta-analysis? We recommend always using `TRUE`.
`bias_max`	The largest value of `bias`, on the additive scale, that should be included in the grid search. The bias has the same units as `yi`.
`assumed_bias_type`	List of biases to consider for computing evalues (objects of `bias` as returned by `EValue::confounding()`, `EValue::selection()`, `EValue::misclassification()`) (defaults to NULL, i.e. agnostic as to the nature of the internal bias). If not NULL, the `yi` argument must be on the log-RR scale (if `yi` is not already on that scale, use `EValue::convert_measures()` to make it so).

Details

For more on the functions passed as `assumed_bias_type`, see the `EValue` package multiple-bias vignette: `vignette("multiple-bias", package = "EValue")`

Value

An object of class `metabias::metabias()`, a list containing:

data A tibble with one row per study and the columns `yi`, `vi`, `sei`, `cluster`, `biased`.

values A list with the elements `selection_ratio`, `q`, `favor_positive`, `alpha_select`, `ci_level`, `small`, `bias_max`.

stats A tibble with the columns `bias_est`, `bias_ci`, `evalue_est`, `evalue_ci`.

References

Mathur MB (2022). "Sensitivity analysis for the interactive effects of internal bias and publication bias in meta-analyses." doi:10.31219/osf.io/u7vcb.

Ding P, VanderWeele TJ (2016). "Sensitivity analysis without assumptions." *Epidemiology (Cambridge, Mass.)*, **27**(3), 368.

Smith LH, VanderWeele TJ (2019). "Bounding bias due to selection." *Epidemiology (Cambridge, Mass.)*, **30**(4), 509.

VanderWeele TJ, Li Y (2019). "Simple sensitivity analysis for differential measurement error." *American journal of epidemiology*, **188**(10), 1823–1829.

Examples

```
# specify confounding as internal bias
evalues <- multibias_evalue(yi = meta_meat$yi,
                            vi = meta_meat$vi,
                            biased = !meta_meat$randomized,
                            selection_ratio = 4)
evalues$stats

# specify confounding as internal bias
evalues_confounding <- multibias_evalue(yi = meta_meat$yi,
                                        vi = meta_meat$vi,
                                        biased = !meta_meat$randomized,
                                        selection_ratio = 4,
                                      assumed_bias_type = list(EValue::confounding()))
evalues_confounding$stats
```

`multibias_meta` *Correction for meta-analysis with multiple biases*

Description

Correction for meta-analysis with multiple biases

Usage

```
multibias_meta(
  yi,
  vi,
  sei,
  cluster = 1:length(yi),
  biased = TRUE,
  selection_ratio,
  bias_affirmative,
  bias_nonaffirmative,
  favor_positive = TRUE,
  alpha_select = 0.05,
  ci_level = 0.95,
  small = TRUE,
  return_worst_meta = FALSE,
  return_pubbias_meta = FALSE
)
```

Arguments

`yi`	A vector of point estimates to be meta-analyzed.

`vi`	A vector of estimated variances (i.e., squared standard errors) for the point estimates.
`sei`	A vector of estimated standard errors for the point estimates. (Only one of `vi` or `sei` needs to be specified).
`cluster`	Vector of the same length as the number of rows in the data, indicating which cluster each study should be considered part of (defaults to treating studies as independent; i.e., each study is in its own cluster).
`biased`	Boolean indicating whether each study is considered internally biased; either single value used for all studies or a vector the same length as the number of rows in the data (defaults to all studies).
`selection_ratio`	Ratio by which publication bias favors affirmative studies (i.e., studies with p-values less than `alpha_select` and estimates in the direction indicated by `favor_positive`).
`bias_affirmative`	Mean internal bias, on the additive scale, among published affirmative studies. The bias has the same units as `yi`.
`bias_nonaffirmative`	Mean internal bias, on the additive scale, among published nonaffirmative studies. The bias has the same units as `yi`.
`favor_positive`	`TRUE` if publication bias are assumed to favor significant positive estimates; `FALSE` if assumed to favor significant negative estimates.
`alpha_select`	Alpha level at which an estimate's probability of being favored by publication bias is assumed to change (i.e., the threshold at which study investigators, journal editors, etc., consider an estimate to be significant).
`ci_level`	Confidence interval level (as proportion) for the corrected point estimate. (The alpha level for inference on the corrected point estimate will be calculated from `ci_level`.)
`small`	Should inference allow for a small meta-analysis? We recommend always using `TRUE`.
`return_worst_meta`	Boolean indicating whether the worst-case meta-analysis of only the nonaffirmative studies be returned.
`return_pubbias_meta`	Boolean indicating whether a meta-analysis correcting for publication but not for confounding be returned.

Value

An object of class `metabias::metabias()`, a list containing:

data A tibble with one row per study and the columns `yi`, `vi`, `sei`, `biased`, `cluster`, `affirmative`, `yi_adj`, `weight`, `userweight`.

values A list with the elements `selection_ratio`, `bias_affirmative`, `bias_nonaffirmative`, `favor_positive`, `alpha_select`, `ci_level`, `small`.

stats A tibble with the columns `model`, `estimate`, `se`, `ci_lower`, `ci_upper`, `p_value`.

fit A list of fitted models.

References

Mathur MB (2022). “Sensitivity analysis for the interactive effects of internal bias and publication bias in meta-analyses.” doi:10.31219/osf.io/u7vcb.

Examples

```
# publication bias without internal bias
meta_0 <- multibias_meta(yi = meta_meat$yi,
                         vi = meta_meat$vi,
                         selection_ratio = 4,
                         bias_affirmative = 0,
                         bias_nonaffirmative = 0)
meta_0$stats

# publication bias and internal bias in the non-randomized studies
meta_4 <- multibias_meta(yi = meta_meat$yi,
                         vi = meta_meat$vi,
                         biased = !meta_meat$randomized,
                         selection_ratio = 4,
                         bias_affirmative = log(1.5),
                         bias_nonaffirmative = log(1.1))
meta_4$stats

# treat all studies as biased, not just non-randomized ones
meta_all <- multibias_meta(yi = meta_meat$yi,
                           vi = meta_meat$vi,
                           biased = TRUE,
                           selection_ratio = 4,
                           bias_affirmative = log(1.5),
                           bias_nonaffirmative = log(1.1))
meta_all$stats
```

Index