Package ‘phacking’

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Title Sensitivity Analysis for p-Hacking in Meta-Analyses

Version 0.0.1

Description Fits right-truncated meta-analysis (RTMA), a bias correction for the joint effects of p-hacking (i.e., manipulation of results within studies to obtain significant, positive estimates) and traditional publication bias (i.e., the selective publication of studies with significant, positive results) in meta-analyses [see Mathur MB (2022). ``Sensitivity analysis for p-hacking in meta-analyses.'' <doi:10.31219/osf.io/ezjsx>.]. Unlike publication bias alone, p-hacking that favors significant, positive results (termed ``affirmative'') can distort the distribution of affirmative results. To bias-correct results from affirmative studies would require strong assumptions on the exact nature of p-hacking. In contrast, joint p-hacking and publication bias do not distort the distribution of published nonaffirmative results when there is stringent p-hacking (e.g., investigators who hack always eventually obtain an affirmative result) or when there is stringent publication bias (e.g., nonaffirmative results from hacked studies are never published). This means that any published nonaffirmative results are from unhacked studies. Under these assumptions, RTMA involves analyzing only the published nonaffirmative results to essentially impute the full underlying distribution of all results prior to selection due to p-hacking and/or publication bias. The package also provides diagnostic plots described in Mathur (2022).

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URL `https://github.com/mikabr/phacking`

BugReports `https://github.com/mikabr/phacking/issues`

Encoding UTF-8

RoxygenNote 7.1.2

RdMacros Rdpack

Biarch true

Depends R (>= 3.4.0)

Imports dplyr, ggplot2, methods, purrr, rlang, stats, stats4, truncnorm, Rcpp (>= 0.12.0), RcppParallel (>= 5.0.1), Rdpack, rstan (>= 2.18.1), rstantools (>= 2.2.0)

LinkingTo BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

SystemRequirements GNU make

LazyData true

Suggests testthat (>= 3.0.0)

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R topics documented:

`lodder` *Meta-analysis of money priming studies*

Description

Dataset from a meta-analysis of experimental studies on the effect of money primes on a variety of psychological and behavioral outcomes, in which some studies were preregistered (Lodder et al. 2019).

Usage

```
lodder
```

Format

A data frame with 287 rows and 4 variables:

study Code identifying the study

yi Point estimate on the Hedges' g scale

vi Variance of point estimate

zi Z-score

preregistered Logical indicating whether study was preregistered

References

Lodder P, Ong HH, Grasman RPPP, Wicherts JM (2019). "A comprehensive meta-analysis of money priming." *Journal of Experimental Psychology: General*, **148**(4), 688.

Lodder P, Ong HH, Grasman RPPP, Wicherts JM (2020). "A comprehensive meta-analysis of money priming." OSF. `https://osf.io/dhp63`.

`phacking_rtma` *Right-truncated meta-analysis*

Description

Fits right-truncated meta-analysis (RTMA), a bias correction for the joint effects of p-hacking (i.e., manipulation of results within studies to obtain significant, positive estimates) and traditional publication bias (i.e., the selective publication of studies with significant, positive results) in meta-analyses.

Usage

```
phacking_rtma(
  yi,
  vi,
  sei,
  favor_positive = TRUE,
  alpha_select = 0.05,
  stan_control = list(adapt_delta = 0.98, max_treedepth = 20),
  parallelize = TRUE
)
```

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).
`favor_positive`	`TRUE` if p-hacking and 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 p-hacking and/or by publication bias is assumed to change (i.e., the threshold at which study investigators, journal editors, etc., consider an estimate to be significant).
`stan_control`	List passed to `rstan::sampling()` as the `control` argument.
`parallelize`	Logical indicating whether to parallelize sampling.

Value

An object of class `metabias`, which is list with four elements:

data A tibble with one row per study and the columns `yi`, `vi`, `sei`, and `affirm` (logical indicating whether the study result is affirmative).

values A vector with the elements `k` (number of studies), `k_affirmative` (number of affirmative studies), `k_nonaffirmative` (number of nonaffirmative studies), `favor_positive` (as passed to `phacking_rtma()`), `alpha_select` (as passed to `phacking_rtma()`), `tcrit` (critical t-value based on `alpha_select`), and `optim_converged` (logical indicating whether the optimization to find the posterior mode converged).

stats A tibble with two rows and the columns `param` (mu, tau), `mode`, `median`, `mean`, `se`, `ci_lower`, `ci_upper`, `n_eff`, and `r_hat`. We recommend reporting the `mode` for the point estimate; `median` and `mean` represent posterior medians and means respectively.

fit A `stanfit` object (the result of fitting the RTMA model).

References

Mathur MB (2022). “Sensitivity analysis for p-hacking in meta-analyses.” doi: 10.31219/osf.io/ezjsx.

Examples

```
set.seed(22)
phacking_rtma(lodder$yi, lodder$vi, parallelize = FALSE)
```

`rtma_cdf` *Compute theoretical and empirical CDFs for a right-truncated meta-analysis*

Description

Compute theoretical and empirical CDFs for a right-truncated meta-analysis

Usage

```
rtma_cdf(rtma)
```

Arguments

`rtma`	Output of `phacking_rtma()`.

Value

A tibble with the columns `yi` (effect sizes), `cdfi` (their fitted CDF) and `ecdfi` (their empirical CDF).

References

Mathur MB (2022). "Sensitivity analysis for p-hacking in meta-analyses." doi: 10.31219/osf.io/ezjsx.

Examples

```
set.seed(22)
lodder_rtma <- phacking_rtma(lodder$yi, lodder$vi, parallelize = FALSE)
rtma_cdf(lodder_rtma)
```

`rtma_qqplot` *Diagnostic quantile-quantile plot for a right-truncated meta-analysis*

Description

To assess the fit of right-truncated meta-analysis and possible violations of its distributional assumptions, plots the fitted cumulative distribution function (CDF) of the published nonaffirmative estimates versus their empirical CDF. If the points do not adhere fairly closely to a 45-degree line, the right-truncated meta-analysis may not fit adequately.

Usage

```
rtma_qqplot(rtma)
```

Arguments

`rtma`	Output of `phacking_rtma()`.

Value

No return value, draws a plot.

Examples

```
set.seed(22)
lodder_rtma <- phacking_rtma(lodder$yi, lodder$vi, parallelize = FALSE)
rtma_qqplot(lodder_rtma)
```

`z_density` *Z-score density plot*

Description

Plots the Z-scores of all published point estimates. When p-hacking favors affirmative estimates over nonaffirmative estimates, as our methods and others assume, Z-scores may disproportionately concentrate just above the critical value (e.g., 1.96). Importantly, the presence of p-hacking does not *guarantee* a concentration of Z-scores just above the critical value, so it is prudent to proceed with the fitting RTMA even if no such concentration is apparent. In contrast, if Z-scores also concentrate just *below* the critical value, or if they also concentrate below the sign-reversed critical value (e.g., -1.96), this could indicate forms of p-hacking that violate the assumptions of RTMA.

Usage

```
z_density(yi, vi, sei, alpha_select = 0.05, crit_color = "red")
```

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).
`alpha_select`	Alpha level at which an estimate's probability of being favored by p-hacking and/or by publication bias is assumed to change (i.e., the threshold at which study investigators, journal editors, etc., consider an estimate to be significant).
`crit_color`	Color for line and text are critical z-score.

Value

No return value, draws a plot.

Examples

```
z_density(lodder$yi, lodder$vi)
```

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