Package: respondeR (via r-universe)

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Title Imputing Responder Proportions from Continuous Outcomes

Version 0.1.0

Description Express meta-analyses of continuous trial outcomes in terms of responder risks, following the interpretability tutorial of Thorlund, Walter, Johnston, Furukawa and Guyatt (2011) <doi:10.1002/jrsm.46>. Given the mean change, standard deviation and sample size per arm across studies, respondeR estimates the proportion of patients who cross a minimal important difference (MID) threshold under a parametric model for the change scores, and contrasts the arms as a risk difference, risk ratio, odds ratio or number needed to treat. It provides median, unweighted-mean, weighted-mean and per-study (fixed- or random-effects) pooling, the standardized-mean-difference to odds-ratio bridge of Anzures-Cabrera, Sarpatwari and Higgins (2011) <doi:10.1002/sim.4298>, a threshold-free common-language effect size, and a point-and-click 'Shiny' application. The estimation methods were evaluated in a simulation study by Sofi-Mahmudi (2024) <https://hdl.handle.net/11375/30210>.

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URL https://github.com/choxos/respondeR, https://choxos.github.io/respondeR/

BugReports https://github.com/choxos/respondeR/issues

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Contents

`format_responder_results`
Format responder-analysis results for display

Description

Turns the numeric output of `responder_analysis()` into a compact, display-ready data frame: proportions and risk differences as percentages, the risk ratio and odds ratio with intervals, and a combined "RD (CI)" string. Used by the bundled Shiny app and handy for reports.

Usage

```
format_responder_results(results, digits = 1)
```

Arguments

`results`	A data frame returned by `responder_analysis()`.
`digits`	Number of decimal places (default 1).

Value

A data frame with character columns `Method`, `PE`, `PC`, `RD`, `RR` and `OR` (percentages for proportions/RD; ratios for RR/OR). Methods without a variance model show point estimates only.

Examples

```
format_responder_results(responder_analysis(sample_responder_data, mid = 1))
```

`launch_responder_analysis` *Launch the Responder Analysis Shiny application*

Description

Starts the bundled Shiny application, a point-and-click front end to `responder_analysis()`: upload data (or load the example), set the MID and direction of benefit, and view, plot and download the results.

Usage

```
launch_responder_analysis(...)
```

Arguments

`...`	Additional arguments passed to `shiny::runApp()`.

Value

Called for its side effect of launching the app; invisibly returns the value of `shiny::runApp()`.

Examples

```
launch_responder_analysis()
```

`responder_analysis` *Responder analysis of continuous trial outcomes*

Description

Converts continuous outcomes (mean change, SD and sample size per arm, across studies) into responder proportions and a range of between-arm effect measures: the risk difference (RD), risk ratio (RR), odds ratio (OR) and number needed to treat (NNT), under a parametric model for the change scores. Responders are defined by a minimal important difference (MID) threshold (the cut-point / "dichotomization" approach of Anzures-Cabrera, Sarpatwari and Higgins, 2011). For a threshold-free alternative see `responder_cles()`.

Usage

```
responder_analysis(
  data,
  mid,
  direction = c("higher", "lower"),
  method = c("individual", "weighted", "unweighted", "median", "smd"),
  se_method = c("binomial", "delta"),
  pooling = c("fixed", "random"),
  control = c("matched", "median"),
  tau_method = c("DL", "REML"),
  dist = c("normal", "lognormal", "t"),
  df = NULL,
  mid_sd = 0,
  ci_type = c("wald", "logit"),
  ci_method = c("wald", "hksj"),
  conf_level = 0.95
)
```

Arguments

`data`	A data frame with one row per study and columns `study`, `change_e`, `sd_e`, `n_e`, `change_c`, `sd_c`, `n_c`. See sample_responder_data.
`mid`	Single finite number: the minimal important difference threshold.
`direction`	`"higher"` (a larger change indicates response) or `"lower"`.
`method`	Methods to compute: any of `"individual"`, `"weighted"`, `"unweighted"`, `"median"`, `"smd"`. Defaults to the first four.
`se_method`	Per-study SE model for `"individual"`: `"binomial"` (default) or `"delta"`. The `"binomial"` variance `p(1 - p) / n` is a pseudo-binomial approximation: `p` is a probability implied by the estimated mean and SD, not a proportion of observed dichotomized patients, so it does not include the uncertainty in the reported mean and SD. `"delta"` propagates that uncertainty and is generally preferable for summary-statistic inputs; `"binomial"` is the default only for continuity with earlier results.

pooling	"fixed" (default) or "random" effects, for the "individual" and "smd" methods.
control	Baseline-risk rule for the summary methods (median, unweighted, weighted): "matched" (default) pools the control arm the same way as the experimental arm; "median" always takes the control responder proportion from the median control arm (the Sofi-Mahmudi 2024 baseline), which yields point estimates only. Ignored by "individual" and "smd".
tau_method	Between-study variance estimator when pooling = "random": "DL" (DerSimonian-Laird, default) or "REML" (needs the metafor package; falls back to DL with a warning if unavailable).
dist	Change-score distribution: "normal" (default), "lognormal" or "t".
df	Degrees of freedom when dist = "t".
mid_sd	Optional standard deviation of the MID threshold; when > 0 its uncertainty is propagated into the effect-measure variances.
ci_type	"wald" (default) or "logit" (keeps proportion and risk-difference intervals within valid bounds via the logit transform and Newcombe's MOVER method).
ci_method	Random-effects interval method: "wald" (Normal, default) or "hksj" (Hartung-Knapp-Sidik-Jonkman, a t-based interval that is better calibrated when the number of studies is small).
conf_level	Confidence level (default 0.95).

Value

A data frame with one row per requested method and columns: method, pooling, k, p_e, p_c, rd/rd_lb/rd_ub, rr/rr_lb/rr_ub, or/or_lb/or_ub, nnt/nnt_lb/nnt_ub, var_rd, and the heterogeneity statistics tau2, i2, q, q_p, pi_lb, pi_ub (for the pooled methods). Proportions, risk differences and CLES are on the proportion scale; multiply by 100 for percentages.

Methods

individual Dichotomize each study, then pool the per-study effect measures (fixed or random effects). The most defensible option; the per-study SE follows se_method.

weighted Pool the mean change by inverse variance and the SD by the within-study pooled SD, dichotomize the pooled summaries, and obtain variances by the delta method.

unweighted, median Dichotomize the arithmetic mean / median of the study means and SDs. Summaries with no variance model: intervals are NA.

smd Pool the standardized mean difference (Hedges' g), bridge to an odds ratio via the logistic link (lnOR = (pi / sqrt(3)) g), and combine with the weighted-pooled control responder rate to recover risks. The second approach of the reference; not included by default.

For the summary methods (median, unweighted, weighted) the control proportion is, by default, pooled the same way as the experimental arm (control = "matched"). Set control = "median" to instead take the baseline risk from the median control arm for every summary method, as in the Sofi-Mahmudi (2024) simulation study; the experimental arm is still pooled by the chosen method. Because the median control arm carries no sampling-variance model, control = "median" reports point estimates only (no intervals) for the summary methods. The individual and smd methods pool per-study contrasts and ignore control.

References

Sofi-Mahmudi A (2024). Identifying an optimal strategy for converting pain as a continuous outcome to a responder analysis. Master's thesis, McMaster University. https://hdl.handle.net/11375/30210

Thorlund K, Walter SD, Johnston BC, Furukawa TA, Guyatt GH (2011). Pooling health-related quality of life outcomes in meta-analysis: a tutorial and review of methods for enhancing interpretability. *Research Synthesis Methods*, 2(3), 188 to 203. doi:10.1002/jrsm.46

Anzures-Cabrera J, Sarpatwari A, Higgins JPT (2011). Expressing findings from meta-analyses of continuous outcomes in terms of risks. *Statistics in Medicine*, 30(25), 2867 to 2880. doi:10.1002/sim.4298

See Also

`responder_rd_individual()`, `responder_cles()`, `responder_proportions()`

Examples

```
responder_analysis(sample_responder_data, mid = 1)

# Random-effects individual method with relative measures:
responder_analysis(sample_responder_data, mid = 1,
  method = "individual", pooling = "random")
```

`responder_cles` *Common-language effect size (probabilistic index)*

Description

A threshold-free responder-type measure: the probability that a randomly chosen treated patient has a better change score than a randomly chosen control. Under a Normal model this is exact, $\mathrm{CLES} = \Phi(\delta)$ with $\delta = (\mu_e - \mu_c)/\sqrt{\sigma_e^2 + \sigma_c^2}$ (the sign is flipped when `direction = "lower"`). Per-study δ values are pooled by fixed- or random-effect inverse variance and back-transformed, so no minimal important difference is required.

Usage

```
responder_cles(
  data,
  direction = c("higher", "lower"),
  pooling = c("fixed", "random"),
  tau_method = c("DL", "REML"),
  ci_method = c("wald", "hksj"),
  conf_level = 0.95
)
```

Arguments

`data`	A data frame with columns `study`, `change_e`, `sd_e`, `n_e`, `change_c`, `sd_c`, `n_c`. See sample_responder_data.
`direction`	`"higher"` (a larger change is better) or `"lower"`.
`pooling`	`"fixed"` (default) or `"random"` effects.
`tau_method`	Between-study variance estimator for random effects: `"DL"` (default) or `"REML"`.
`ci_method`	Random-effects interval method: `"wald"` (default) or `"hksj"` (Hartung-Knapp-Sidik-Jonkman, better for small numbers of studies).
`conf_level`	Confidence level (default `0.95`).

Value

A list with:

studies Per-study data frame: `study`, `delta`, `cles`, `cles_lb`, `cles_ub`.

cles, cles_lb, cles_ub Pooled CLES and its interval.

delta, se_delta Pooled standardized difference and its SE.

tau2, i2, q, q_p, pi_lb, pi_ub Heterogeneity statistics; the prediction interval is back-transformed to the CLES scale.

pooling, k Settings echoed back.

References

McGraw KO, Wong SP (1992). A common language effect size statistic. *Psychological Bulletin*, 111(2), 361 to 365.

Examples

```
cles <- responder_cles(sample_responder_data)
cles$cles
```

`responder_proportions` *Responder proportions from continuous arm summaries*

Description

Estimates, for each study arm, the probability that a patient's change score crosses the minimal important difference (MID) threshold under a parametric model for the change scores, together with a delta-method (sampling) variance for that probability.

Usage

```
responder_proportions(
  change,
  sd,
  n,
  mid,
  direction = c("higher", "lower"),
  dist = c("normal", "lognormal", "t"),
  df = NULL
)
```

Arguments

change	Numeric vector of mean change scores.
sd	Numeric vector of standard deviations (> 0).
n	Numeric vector of sample sizes (>= 2).
mid	Single finite number: the minimal important difference threshold.
direction	"higher" (a larger change indicates response) or "lower".
dist	Change-score distribution: "normal" (default), "lognormal" or "t".
df	Degrees of freedom when dist = "t".

Value

A data frame with one row per input element and columns p (responder probability) and var_p (delta-method variance).

References

Thorlund K, Walter SD, Johnston BC, Furukawa TA, Guyatt GH (2011). Pooling health-related quality of life outcomes in meta-analysis: a tutorial and review of methods for enhancing interpretability. *Research Synthesis Methods*, 2(3), 188 to 203. doi:10.1002/jrsm.46

Anzures-Cabrera J, Sarpatwari A, Higgins JPT (2011). Expressing findings from meta-analyses of continuous outcomes in terms of risks. *Statistics in Medicine*, 30(25), 2867 to 2880. doi:10.1002/sim.4298

Examples

```
responder_proportions(
  change = c(0.96, 0.79, 1.02), sd = c(1.26, 1.28, 1.34),
  n = c(43, 139, 156), mid = 1
)
```

`responder_rd_individual` *Per-study responder risk differences*

Description

Dichotomizes each study at the MID threshold and returns the per-study responder risk difference (experimental minus control) with a confidence interval. Building block for the `"individual"` method of `responder_analysis()`; also feeds the forest plot and per-study table.

Usage

```
responder_rd_individual(
  data,
  mid,
  direction = c("higher", "lower"),
  se_method = c("binomial", "delta"),
  conf_level = 0.95,
  dist = c("normal", "lognormal", "t"),
  df = NULL,
  mid_sd = 0
)
```

Arguments

`data`	A data frame with one row per study and columns `study`, `change_e`, `sd_e`, `n_e`, `change_c`, `sd_c`, `n_c`. See sample_responder_data.
`mid`	Single finite number: the minimal important difference threshold.
`direction`	`"higher"` (a larger change indicates response) or `"lower"`.
`se_method`	Per-study SE model for `"individual"`: `"binomial"` (default) or `"delta"`. The `"binomial"` variance `p(1 - p) / n` is a pseudo-binomial approximation: `p` is a probability implied by the estimated mean and SD, not a proportion of observed dichotomized patients, so it does not include the uncertainty in the reported mean and SD. `"delta"` propagates that uncertainty and is generally preferable for summary-statistic inputs; `"binomial"` is the default only for continuity with earlier results.
`conf_level`	Confidence level (default `0.95`).
`dist`	Change-score distribution: `"normal"` (default), `"lognormal"` or `"t"`.
`df`	Degrees of freedom when `dist = "t"`.
`mid_sd`	Optional standard deviation of the MID threshold; when `> 0` its uncertainty is propagated into the effect-measure variances.

Value

A data frame with one row per study and columns `study`, `p_e`, `p_c`, `rd`, `se`, `ci_lb`, `ci_ub` (proportion scale).

See Also

responder_analysis()

Examples

```
responder_rd_individual(sample_responder_data, mid = 1)
```

`sample_responder_data` *Example responder-analysis dataset*

Description

A small illustrative dataset of three trials reporting continuous change scores per arm. Used in examples, the bundled Shiny app and the package tests. Values are fictional but plausible.

Usage

```
sample_responder_data
```

Format

A data frame with 3 rows and 7 columns:

study Study identifier.

change_e Mean change in the experimental arm.

sd_e Standard deviation of change in the experimental arm.

n_e Sample size of the experimental arm.

change_c Mean change in the control arm.

sd_c Standard deviation of change in the control arm.

n_c Sample size of the control arm.

Examples

```
responder_analysis(sample_responder_data, mid = 1)
```

vas_pain *VAS pain change scores from a spinal-health exercise meta-analysis*

Description

Per-study change in pain on a 0-10 cm visual analogue scale (VAS) for an exercise-therapy arm versus a control arm, from the 20 randomized trials pooled for the VAS outcome by Li, Bao, Wang and Zhao (2025). The change scores are post minus baseline VAS, so a more negative value is a larger pain reduction; analyze with `direction = "lower"` and a negative MID equal to the required reduction (for example `mid = -1.5` for a 1.5 cm responder threshold).

Usage

```
vas_pain
```

Format

A data frame with 20 rows and 7 columns:

study Study label (first author and year).

change_e Mean VAS change in the exercise (experimental) arm.

sd_e Standard deviation of the change in the exercise arm.

n_e Exercise-arm sample size.

change_c Mean VAS change in the control arm.

sd_c Standard deviation of the change in the control arm.

n_c Control-arm sample size.

Source

Li Z, Bao Z, Wang S, Zhao M (2025). Meta-analysis of the best exercise mode and dose study for improving spinal health. *Frontiers in Sports and Active Living*, 7, 1614906. doi:10.3389/fspor.2025.1614906. Figure 3 (VAS pain). Reproduced under the Creative Commons Attribution License (CC BY 4.0); the original authors and journal are credited as required.

Examples

```
# Proportion achieving at least a 1.5 cm VAS reduction (responder),
# exercise versus control, random-effects with HKSJ intervals.
responder_analysis(vas_pain, mid = -1.5, direction = "lower",
  pooling = "random", ci_method = "hksj")
```

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