

# Package ‘SingleCaseES’

September 30, 2021

**Type** Package

**Title** A Calculator for Single-Case Effect Sizes

**Version** 0.5.0

**Description** Provides R functions for calculating basic effect size indices for single-case designs, including several non-overlap measures and parametric effect size measures, and for estimating the gradual effects model developed by Swan and Pustejovsky (2018) <[DOI:10.1080/00273171.2018.1466681](https://doi.org/10.1080/00273171.2018.1466681)>. Standard errors and confidence intervals (based on the assumption that the outcome measurements are mutually independent) are provided for the subset of effect sizes indices with known sampling distributions.

**URL** <https://jepusto.github.io/SingleCaseES/>

**BugReports** <https://github.com/jepusto/SingleCaseES/issues>

**License** GPL-3

**Imports** stats, purrr, magrittr, dplyr, tidyr, rlang, tidyselect, utils

**Suggests** spelling, shiny, ggplot2, purrrlyr, testthat, markdown, knitr, rmarkdown, prettydoc, Kendall, kableExtra, covr, readxl, glue, janitor, rclipboard

**LazyData** TRUE

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**Language** en-US

**VignetteBuilder** knitr, rmarkdown, prettydoc

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-09-30 10:00:02 UTC

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batch_calc_ES	<i>Calculate effect sizes from a dataset for multiple series</i>
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### Description

Calculates one or more effect size estimates, along with associated standard errors and confidence intervals, if available, for a single-case data series.

### Usage

```
batch_calc_ES(
  dat,
  grouping,
  condition,
  outcome,
  aggregate = NULL,
  weighting = "1/V",
  session_number = NULL,
  baseline_phase = NULL,
```

```

intervention_phase = NULL,
ES = c("LRRd", "LRRi", "SMD", "Tau"),
improvement = "increase",
scale = "other",
intervals = NA,
observation_length = NA,
confidence = 0.95,
format = "long",
warn = TRUE,
...
)

```

### Arguments

<code>dat</code>	data frame containing SCD series for which effect sizes will be calculated.
<code>grouping</code>	A variable name or list of (unquoted) variable names that uniquely identify each data series.
<code>condition</code>	A variable name that identifies the treatment condition for each observation in the series.
<code>outcome</code>	A variable name for the outcome data. Default is
<code>aggregate</code>	A variable name or list of (unquoted) variable names that identify additional grouping variables. Effect sizes will be calculated separately for each unique value of these variables, after which the effect size estimates will be averaged across values of these variables (but not across the values of the grouping variables).
<code>weighting</code>	character string specifying the weighting scheme for use when variables are specified in <code>aggregate</code> . Either "1/V" (the default) or "equal".
<code>session_number</code>	A variable name used to order the data within each series.
<code>baseline_phase</code>	character string specifying which value of <code>condition</code> corresponds to the baseline phase. If <code>NULL</code> (the default), the first observed value of <code>condition</code> within the series will be used.
<code>intervention_phase</code>	character string specifying which value of <code>condition</code> corresponds to the intervention phase. If <code>NULL</code> (the default), the second unique value of <code>condition</code> within the series will be used.
<code>ES</code>	character string or character vector specifying which effect size index or indices to calculate. Available effect sizes are "LRRd", "LRRi", "LRM", "LOR", "SMD", "NAP", "IRD", "PND", "PEM", "PAND", "Tau", "Tau-U", and "Tau-BC". Set to "all" for all available effect sizes. Set to "parametric" for all parametric effect sizes. Set to "NOM" for all non-overlap measures. Defaults to calculating the LRRd, LRRi, SMD, and Tau indices.
<code>improvement</code>	character string either indicating the direction of uniform improvement ("increase" or "decrease") or the variable name of a variable identifying the direction of improvement for each series. Default is "increase".
<code>scale</code>	character string indicating the common scale of the outcome variable across all of the series in the data set or the name of a variable within the dataset that

	identifies the outcome scale within each series. Possible values for the scale are "percentage" for a percentage with range 0-100, "proportion" for a proportion with range 0-1, "count" for a frequency count (0 or positive integers), "rate" for a standardized rate per minute. If a vector, the most frequent unique value will be used and missing values will be ignored. Defaults to NA.
intervals	for interval recording procedures. Either the total number of intervals per observation session common to all series in the dataset, or the name of a variable within the dataset that identifies the number of intervals for each observation. If a variable name, the mean number of intervals within each series will be used. Missing values will be ignored. Defaults to NA.
observation_length	Used for the log-response ratio. Either the common observation session length (in minutes) across all series in the dataset or a variable name containing the observation session length for each observation. If a variable name, the mean observation session length within each series will be used. Missing values will be ignored. Defaults to NA.
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.
format	character string specifying whether to organize the results in "long" format or "wide" format. Defaults to "long".
warn	logical indicating whether warnings should be displayed. Default is TRUE.
...	further arguments used for calculating some of the effect size indices.

### Details

Calculates one or more effect size indices for each series in a dataset

### Value

A tibble containing the estimate, standard error, and/or confidence interval for each specified effect size.

### Examples

```
data(McKissick)
batch_calc_ES(McKissick,
              grouping = Case_pseudonym,
              condition = Condition,
              outcome = Outcome,
              ES = c("LRRd", "LRRi"),
              improvement = "decrease",
              scale = "count",
              observation_length = 20,
              format = "long")

data(Schmidt2007)
batch_calc_ES(dat = Schmidt2007,
              grouping = c(Behavior_type, Case_pseudonym, Phase_num),
```

```

        condition = Condition,
        outcome = Outcome,
        ES = c("LRRi", "LRRd"),
        improvement = direction,
        scale = Metric,
        bias_correct = TRUE,
        confidence = NULL,
        format = "wide")

# Aggregate across phase-pairs
batch_calc_ES(dat = Schmidt2007,
              grouping = c(Behavior_type, Case_pseudonym),
              aggregate = Phase_num,
              weighting = "1/V",
              condition = Condition,
              outcome = Outcome,
              ES = c("LRRi", "LRRd", "SMD", "Tau"),
              improvement = direction,
              scale = "count",
              bias_correct = TRUE,
              confidence = NULL,
              format = "long")

```

---

calc\_ES

*Calculate effect sizes*


---

### Description

Calculates one or more effect size estimates, along with associated standard errors and confidence intervals, if available, for a single-case data series.

### Usage

```

calc_ES(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  ES = c("LRRd", "LRRi", "SMD", "Tau"),
  improvement = "increase",
  ...,
  confidence = 0.95,
  format = "long"
)

```

**Arguments**

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
intervention_phase	character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique value of condition.
ES	character string or character vector specifying which effect size index or indices to calculate. Available effect sizes are "LRRd", "LRRi", "LRM", "LOR", "SMD", "NAP", "IRD", "PND", "PEM", "PAND", "Tau", "Tau-U", and "Tau-BC". Set to "all" for all available effect sizes. Set to "parametric" for all parametric effect sizes. Set to "NOM" for all non-overlap measures. Defaults to calculating the LRRd, LRRi, SMD, and Tau indices.
improvement	character string indicating direction of improvement. Default is "increase".
...	further arguments used for calculating some of the effect size indices.
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.
format	character string specifying whether to organize the results in "long" format or "wide" format. Defaults to "long".

**Details**

Calculates one or more effect size indices

**Value**

A data.frame containing the estimate, standard error, and/or confidence interval for each specified effect size.

**Examples**

```
# Using the A_data and B_data arguments
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 29)
calc_ES(A_data = A, B_data = B)

# Using the condition and outcome arguments
phase <- c(rep("A", length(A)), rep("B", length(B)))
outcome <- c(A, B)
calc_ES(condition = phase, outcome = outcome, baseline_phase = "A")

# Example from Parker & Vannest (2009)
yA <- c(4, 3, 4, 3, 4, 7, 5, 2, 3, 2)
yB <- c(5, 9, 7, 9, 7, 5, 9, 11, 11, 10, 9)
```

```
calc_ES(yA, yB)
```

---

calc\_phase\_pairs      *Calculate phase pair numbers*

---

### Description

Calculates a vector containing a unique phase number for every sequential occurrence of a phase or treatment condition. This is useful for creating a grouping variable to be used in calculating effect sizes for each pair of A-B phases within treatment reversal designs.

### Usage

```
calc_phase_pairs(x)
```

### Arguments

x                      vector of phase/condition labels.

### Value

A vector containing an integer phase number for every observation.

### Examples

```
x <- rep(c("A", "B", "C", "B", "C", "A", "C"), c(4:10))
calc_phase_pairs(x)

library(dplyr)
Schmidt2007 %>%
  group_by(Behavior_type, Case_pseudonym) %>%
  mutate(phase_pair = calc_phase_pairs(Condition))
```

---

gem\_scd                      *A function to estimate the gradual effects model for an SCD*

---

### Description

A function to estimate the gradual effects model for an SCD

### Usage

```
gem_scd(Trt, outcome, m, fam)
```

**Arguments**

Trt	A vector of treatment assignments where 0 = untreated and 1 = treated.
outcome	A vector of outcomes.
m	The number of treatment occasions to estimate a treatment effect for.
fam	A description of the error distribution and link function to be used in the model. This can be supplied in any way that 'glm' will accept. (See <a href="#">family</a> for details of family functions.)

**Value**

'gem\_scd' returns an object of class `glm`. In addition to the normal contents of a `glm` object, it also contains an estimate of 'omega' and a variance covariance matrix called 'varcov'.

---

IRD	<i>Robust improvement rate difference</i>
-----	-------------------------------------------

---

**Description**

Calculates the robust improvement rate difference index (Parker, Vannest, & Brown, 2009). The range of IRD depends on the number of observations in each phase.

**Usage**

```
IRD(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase"
)
```

**Arguments**

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".

**Value**

Numeric value



## References

Parker, R. I., Vannest, K. J., & Brown, L. (2009). The improvement rate difference for single-case research. *Exceptional Children*, 75(2), 135–150. doi:doi: [10.1177/001440290907500201](https://doi.org/10.1177/001440290907500201)

## See Also

[PAND](#)

## Examples

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
IRD(A_data = A, B_data = B)
```

---

LOR

*Log-odds ratio*

---

## Description

Calculates the log-odds ratio effect size index, with or without bias correction (Pustejovsky, 2015)

## Usage

```
LOR(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase,
  improvement = "increase",
  scale = "percentage",
  intervals = NULL,
  D_const = NULL,
  bias_correct = TRUE,
  confidence = 0.95
)
```

## Arguments

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.

improvement	character string indicating direction of improvement. Default is "increase".
scale	character string indicating the scale of the outcome variable. Must be either "percentage" for percentages with range 0-100 or "proportion" for proportions with range 0-1. If a vector, the most frequent unique value will be used. "percentage" is assumed by default.
intervals	for interval recording procedures, the total number of intervals per observation session. If a vector, the mean number of intervals will be used.
D_const	constant used for calculating the truncated sample mean (see Pustejovsky, 2015). If a vector, the mean value will be used.
bias_correct	logical value indicating whether to use bias-correction. Default is TRUE.
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.

### Details

The odds ratio parameter is the ratio of the odds of the outcome. The log-odds ratio is the natural logarithm of the odds ratio. This effect size is appropriate for outcomes measured on a percentage or proportion scale. Unlike the LRRd and LRRi, the LOR is symmetric in valence, so that the LOR for an positively-valenced outcome is equal to -1 times the LOR calculated after reversing the scale of the outcome so that it is negatively valenced.

Without bias correction, the log-odds ratio is estimated by substituting the sample mean level in each phase in place of the corresponding parameter. A delta-method bias correction to the estimator is used by default.

The standard error of LOR is calculated based on a delta-method approximation, allowing for the possibility of different degrees of dispersion in each phase. The confidence interval for LOR is based on a large-sample ( $z$ ) approximation.

To account for the possibility of sample means of zero, a truncated mean is calculated following the method described in Pustejovsky (2015). Truncated sample variances are also calculated to ensure that standard errors will be strictly larger than zero. The truncation constant depends on the total number of intervals per session (or the total number of items for other percentage/proportion scales). The arguments `scale` and `intervals` must be specified in order to calculate an appropriate truncation constant. For outcomes measured using continuous recording procedures, set `intervals` equal to 60 times the length of the observation session in minutes.

### Value

A data.frame containing the estimate, standard error, and approximate confidence interval.

### References

Pustejovsky, J. E. (2015). Measurement-comparable effect sizes for single-case studies of free-operant behavior. *Psychological Methods*, 20(3), 342–359. doi:doi: [10.1037/met0000019](https://doi.org/10.1037/met0000019)

### Examples

```
A_pct <- c(20, 20, 25, 25, 20, 25)
B_pct <- c(30, 25, 25, 25, 35, 30, 25)
```

```

LOR(A_data = A_pct, B_data = B_pct,
    scale = "percentage", intervals = 20, bias_correct = FALSE)
LOR(A_data = A_pct, B_data = B_pct,
    scale = "percentage", intervals = 20)

LOR(A_data = A_pct, B_data = B_pct, scale = "percentage")
LOR(A_data = A_pct / 100, B_data = B_pct / 100, scale = "proportion")
LOR(A_data = A_pct, B_data = B_pct, scale = "percentage", improvement = "decrease")

```

---

LRM

*Log ratio of medians*


---

### Description

Calculates the log ratio of medians effect size index

### Usage

```

LRM(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase,
  improvement = "increase",
  delta_method = FALSE,
  confidence = 0.95
)

```

### Arguments

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".
delta_method	logical value indicating whether to use delta method to approximate variance of log ratio of medians. Default is FALSE, which estimates the variance based on the fact that the logarithm of a median is the same as the median of the log-transformed outcomes. If TRUE, the variance of log ratio of medians is approximated using delta method.
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.

### Details

The ratio of medians effect size parameter is defined as the ratio of the medians of the outcomes in different phases. The log ratio of the medians is the natural logarithm of the ratio of medians. This effect size is appropriate for outcomes that are skewed, symmetric but highly leptokurtic, or right-censored (Bonett & Price Jr, 2020).

### Value

A data frame containing the estimate, standard error, and confidence interval.

### References

Bonett, D. G. & Price Jr, R. M. (2020). Confidence Intervals for Ratios of Means and Medians. *Journal of Educational and Behavioral Statistics*, 45(6), 750–770. doi:doi: [10.3102/1076998620934125](https://doi.org/10.3102/1076998620934125)

Bonett, D. G., & Price, R. M. (2020). Interval estimation for linear functions of medians in within-subjects and mixed designs. *British Journal of Mathematical and Statistical Psychology*, 73(2), 333-346. doi:doi: [10.1111/bmsp.12171](https://doi.org/10.1111/bmsp.12171)

### Examples

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
LRM(A_data = A, B_data = B)
```

---

LRR

*Log-response ratio*

---

### Description

Calculates the increasing or decreasing version of the log-response ratio effect size index, with or without bias correction (Pustejovsky, 2015)

### Usage

```
LRRd(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "decrease",
  scale = "count",
  observation_length = NULL,
  intervals = NULL,
  D_const = NULL,
  bias_correct = TRUE,
```

```

    pct_change = FALSE,
    confidence = 0.95
  )

LRRi(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase",
  scale = "count",
  observation_length = NULL,
  intervals = NULL,
  D_const = NULL,
  bias_correct = TRUE,
  pct_change = FALSE,
  confidence = 0.95
)

```

### Arguments

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".
scale	character string indicating the scale of the outcome variable, with possible values "percentage" for a percentage with range 0-100, "proportion" for a proportion with range 0-1, "count" for a frequency count (0 or positive integers), "rate" for a standardized rate per minute. If a vector, the most frequent unique value will be used.
observation_length	length of observation session (in minutes). If a vector, the mean observation session length will be used.
intervals	for interval recording procedures, the total number of intervals per observation session. If a vector, the mean number of intervals will be used.
D_const	constant used for calculating the truncated sample mean (see Pustejovsky, 2018). If a vector, the mean value will be used.
bias_correct	logical value indicating whether to use bias-correction. Default is TRUE.
pct_change	logical value indicating whether to convert the LRR estimate and confidence interval into percentage change.
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.

## Details

The response ratio parameter is the ratio of the mean level of the outcome during phase B to the mean level of the outcome during phase A. The log response ratio is the natural logarithm of the response ratio. This effect size is appropriate for outcomes measured on a ratio scale (so that zero corresponds to the true absence of the outcome). There are two versions of the LRR. The LRR-increasing (LRRi) is defined so that positive values correspond to therapeutic improvements. The LRR-decreasing (LRRd) is defined so that negative values correspond to therapeutic improvements. For outcomes measured as frequency counts or rates, the two versions will have the same magnitude but opposite sign; for outcomes measured as percentages or proportions, the LRRd and LRRi will differ in both sign and magnitude (Pustejovsky, 2018).

Without bias correction, the log response ratio is estimated as the natural logarithm of the phase B sample mean, minus the natural logarithm of the phase A sample mean. A delta-method bias correction to the estimator is used by default.

The standard error of LRR is calculated based on a delta-method approximation, allowing for the possibility of different degrees of dispersion in each phase. The confidence interval for LRR is based on a large-sample ( $z$ ) approximation.

To account for the possibility of sample means of zero, a truncated mean is calculated following the method described in Pustejovsky (2018). Truncated sample variances are also calculated to ensure that standard errors will be strictly larger than zero. The truncation constant depends on the scale of the outcome, the length of the observation sessions used to measure the dependent variable, and (for interval recording procedures) the total number of intervals per session (or the total number of items for other percentage/proportion scales). The argument `scale` must be specified in order to calculate an appropriate truncation constant. For standardized rates, the argument `observation_length` must also be specified; for percentages or proportions, the argument `intervals` must be specified. For outcomes measured using continuous recording procedures, set `intervals` equal to 60 times the length of the observation session in minutes.

If `pct_change` is TRUE, then the LRR estimate and confidence interval are converted into percentage change using the formula  $\text{Percentage change} = 100 * (\exp(\text{LRR}) - 1)$ .

## Value

A data.frame containing the estimate, standard error, and approximate confidence interval.

## References

- Pustejovsky, J. E. (2015). Measurement-comparable effect sizes for single-case studies of free-operant behavior. *Psychological Methods*, 20(3), 342–359. doi:doi: [10.1037/met0000019](https://doi.org/10.1037/met0000019)
- Pustejovsky, J. E. (2018). Using response ratios for meta-analyzing single-case designs with behavioral outcomes. *Journal of School Psychology*, 16, 99-112. doi:doi: [10.1016/j.jsp.2018.02.003](https://doi.org/10.1016/j.jsp.2018.02.003)

## Examples

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
LRRd(A_data = A, B_data = B, bias_correct = FALSE)
LRRd(A_data = A, B_data = B)
LRRd(A_data = A, B_data = B, pct_change = TRUE)
```

---

 McKissick

 McKissick et al. (2010)
 

---

### Description

Disruptive behavior data from a study by McKissick et al. (2010). All data were collected via event counting. The variables are as follows:

- Case\_Pseudonym. Case Pseudonym provided by the authors.
- Session\_number. Within-series session-number
- Condition. Describes whether the outcome is in the baseline (A) or treatment (B) phase.
- Outcome. Value for the outcome.
- Session\_length. Length of the observation session.
- Procedure. The metric in which the outcome measurement is expressed, all "count".
- Session\_length. The length of the observation session.

### Format

A data frame with 35 rows and 4 variables

### Source

McKissick, C., Hawkins, R. O., Lentz, F. E., Hailley, J., & McGuire, S. (2010). Randomizing multiple contingency components to decrease disruptive behaviors and increase student engagement in an urban second-grade classroom. *Psychology in the Schools*, 47(9), 944–959. <https://doi.org/10.1002/pits.20516>

---

 NAP

 Non-overlap of all pairs
 

---

### Description

Calculates the non-overlap of all pairs index (Parker & Vannest, 2009).

### Usage

```
NAP(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase",
  SE = "unbiased",
  confidence = 0.95
)
```

### Arguments

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".
SE	character value indicating which formula to use for calculating the standard error of NAP, with possible values "unbiased" for the exactly unbiased estimator, "Hanley" for the Hanley-McNeil estimator, "null" for the (known) variance under the null hypothesis of no effect, or "none" to not calculate a standard error. Defaults to "unbiased".
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.

### Details

NAP is calculated as the proportion of all pairs of one observation from each phase in which the measurement from the B phase improves upon the measurement from the A phase, with pairs of data points that are exactly tied being given a weight of 0.5. The range of NAP is [0,1], with a null value of 0.5.

The unbiased variance estimator was described by Sen (1967) and Mee (1990). The Hanley estimator was proposed by Hanley and McNeil (1982). The null variance is a known function of sample size, equal to the exact sampling variance when the null hypothesis of no effect holds. When the null hypothesis does not hold, the null variance will tend to over-estimate the true sampling variance of NAP.

The confidence interval for NAP is calculated based on the symmetrized score-inversion method (Method 5) proposed by Newcombe (2006).

### Value

A data.frame containing the estimate, standard error, and/or confidence interval.

### References

- Hanley, J. A., & McNeil, B. J. (1982). The meaning and use of the area under a receiver operating characteristic (ROC) curve. *Radiology*, *143*, 29–36. doi:doi: [10.1148/radiology.143.1.7063747](https://doi.org/10.1148/radiology.143.1.7063747)
- Mee, W. (1990). Confidence intervals for probabilities and tolerance regions based on a generalization of the Mann-Whitney statistic. *Journal of the American Statistical Association*, *85*(411), 793–800. doi:doi: [10.1080/01621459.1990.10474942](https://doi.org/10.1080/01621459.1990.10474942)
- Newcombe, R. G. (2006). Confidence intervals for an effect size measure based on the Mann-Whitney statistic. Part 2: Asymptotic methods and evaluation. *Statistics in Medicine*, *25*(4), 559–573. doi:doi: [10.1002/sim.2324](https://doi.org/10.1002/sim.2324)



Parker, R. I., & Vannest, K. J. (2009). An improved effect size for single-case research: Nonoverlap of all pairs. *Behavior Therapy*, 40(4), 357–67. doi:doi: [10.1016/j.beth.2008.10.006](https://doi.org/10.1016/j.beth.2008.10.006)

Sen, P. K. (1967). A note on asymptotically distribution-free confidence bounds for  $PX < Y$ , based on two independent samples. *The Annals of Mathematical Statistics*, 29(1), 95-102. <https://www.jstor.org/stable/25049448>

## Examples

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
NAP(A_data = A, B_data = B)

# Example from Parker & Vannest (2009)
yA <- c(4, 3, 4, 3, 4, 7, 5, 2, 3, 2)
yB <- c(5, 9, 7, 9, 7, 5, 9, 11, 11, 10, 9)
NAP(yA, yB)
```

---

PAND

*Percentage of all non-overlapping data (PAND)*

---

## Description

Calculates the percentage of all non-overlapping data index (Parker, Hagan-Burke, & Vannest, 2007; Parker, Vannest, & Davis, 2011).

## Usage

```
PAND(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase"
)
```

## Arguments

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".

### Details

For an outcome where increase is desirable, PAND is calculated as the proportion of observations remaining after removing the fewest possible number of observations from either phase so that the highest remaining point from the baseline phase is less than the lowest remaining point from the treatment phase. For an outcome where decrease is desirable, PAND is calculated as the proportion of observations remaining after removing the fewest possible number of observations from either phase so that the lowest remaining point from the baseline phase is greater than the highest remaining point from the treatment phase. The range of PAND depends on the number of observations in each phase.

### Value

Numeric value

### References

Parker, R. I., Hagan-Burke, S., & Vannest, K. J. (2007). Percentage of all non-overlapping data (PAND): An alternative to PND. *The Journal of Special Education, 40*(4), 194–204. doi:doi: [10.1177/00224669070400040101](https://doi.org/10.1177/00224669070400040101)

Parker, R. I., Vannest, K. J., & Davis, J. L. (2011). Effect size in single-case research: A review of nine nonoverlap techniques. *Behavior Modification, 35*(4), 303–22. doi:doi: [10.1177/0145445511399147](https://doi.org/10.1177/0145445511399147)

### Examples

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
PAND(A_data = A, B_data = B)
```

---

PEM

*Percentage exceeding the median*

---

### Description

Calculates the percentage exceeding the median (PEM) index (Ma, 2006).

### Usage

```
PEM(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase"
)
```

**Arguments**

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".

**Details**

For an outcome where increase is desirable, PEM is calculated as the proportion of observations in the B phase that exceed the median observation from the A phase. For an outcome where decrease is desirable, PEM is calculated as the proportion of observations in the B phase that are less than the median observation from the A phase. Ties are counted with a weight of 0.5. The range of PEM is [0,1].

**Value**

Numeric value

**References**

Ma, H.-H. (2006). An alternative method for quantitative synthesis of single-subject researches: Percentage of data points exceeding the median. *Behavior Modification*, 30(5), 598–617. doi:doi: [10.1177/0145445504272974](https://doi.org/10.1177/0145445504272974)

**Examples**

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
PEM(A_data = A, B_data = B)
```

---

PND

*Percentage of non-overlapping data*

---

**Description**

Calculates the percentage of non-overlapping data index (Scruggs, Mastropieri, & Castro, 1987).

**Usage**

```
PND(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase"
)
```

**Arguments**

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".

**Details**

For an outcome where increase is desirable, PND is calculated as the proportion of observations in the B phase that exceed the highest observation from the A phase. For an outcome where decrease is desirable, PND is the proportion of observations in the B phase that are less than the lowest observation from the A phase. The range of PND is [0,1].

**Value**

Numeric value

**References**

Scruggs, T. E., Mastropieri, M. A., & Casto, G. (1987). The quantitative synthesis of single-subject research: Methodology and validation. *Remedial and Special Education*, 8(2), 24–43. doi:doi: [10.1177/074193258700800206](https://doi.org/10.1177/074193258700800206)

**Examples**

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 29)
PND(A_data = A, B_data = B)
```

---

SCD\_effect\_sizes      *SCD effect size calculator*

---

### Description

An interactive tool for calculating effect size indices for single-case designs.

### Usage

```
SCD_effect_sizes(browser = TRUE)
```

### Arguments

browser      logical value indicating whether to launch the app in the system's default web-browser. Defaults to TRUE.

---

Schmidt2007      *Schmidt (2007)*

---

### Description

Data from a study by Schmidt (2007). The variables are as follows:

- Behavior\_type. Outcome measure description (disruptive behavior or on task behavior).
- Procedure. The observation recording procedure used to measure the outcome.
- Metric. The metric in which the outcome measurement is expressed ("count" for natural counts; "percentage" for percentage of intervals)
- Session\_length. Length (in minutes) of the observation sessions
- Interval\_length. If an interval method was used, the length of the intervals (in seconds); NA otherwise.
- Case\_Pseudonym. Case Pseudonym provided by the authors.
- Session\_number. Within-series session-number.
- Phase. Label for each unique phase (e.g., A1 is the first baseline phase, B2 is the second treatment phase).
- Condition. Label indicating whether the outcome is in the baseline (A) or treatment (B) phase.
- Outcome. Outcome measurement.
- Phase\_num. Indicator for each pair of baseline and treatment phases.
- direction. Direction of therapeutic improvement for the outcome.
- n\_Intervals. If an interval method was used, the total number of intervals; NA otherwise.

**Format**

A data frame with 172 rows and 13 variables

**Source**

Schmidt, A. C. (2007). The effects of a group contingency on group and individual behavior in an urban first-grade classroom. Masters Thesis, University of Kansas, Department of Applied Behavioral Sciences. ProQuest Dissertations & Theses Global, thesis number 1443719.

---

Schmidt2012

*Schmidt and Stichter (2012)*

---

**Description**

Data from an ABAB design conducted by Schmidt and Stichter (2012). All data were collected via continuous recording. The variables are as follows:

- Case. Participant identifier.
- Behavior. Behavior type (Conversation, Initiations, or Responses).
- Trt Treatment indicators.
- Outcome. Outcome scores.
- Session\_num. Measurement occasion.
- Session\_length Length of the observation session.
- Procedure The metric in which the outcome measurement is expressed, all "other".

**Format**

A data frame with 180 rows and 5 variables

**Source**

Schmidt, C., & Stichter, J. P. (2012). The use of peer-mediated interventions to promote the generalization of social competence for adolescents with high-functioning autism and Asperger's syndrome. *Exceptionality*, 20(2), 94-113. doi:10.1080/09362835.2012

---

`shine_gem_scd`*Gradual Effects Model SCD Calculator*

---

**Description**

Open an interactive tool for calculating the gradual effects model for SCDs.

**Usage**

```
shine_gem_scd(browser = TRUE)
```

**Arguments**

`browser` logical value indicating whether to launch the app in the system's default web-browser. Defaults to TRUE.

**Examples**

```
## Not run:  
shine_gem_scd()  
  
## End(Not run)
```

---

`Shogren`*Shogren et al. (2004)*

---

**Description**

Data from a systematic review by Shogren et al. (2004) on the effects of choice-making interventions. These data were compiled and re-analyzed in Pustejovsky (2015). The variables are as follows:

- Study. An ID for each study in the systematic review.
- Case. Case Pseudonym provided by the authors.
- Measure. Type of behavior observed as the outcome measure
- Phase. Phase indicator, baseline phase is "No Choice" and treatment phase is "Choice."
- Percentage. For those outcomes measured as percentage, outcomes value. NA for count outcomes.
- Observed. For those outcomes measured as count, outcome value. NA for percentage outcomes.
- Possible. For counts out of a maximum, lists the maximum value.

- Recording\_procedure Recording procedure. CDR = "Continuous Duration Recording", EC = "Event Counting", "MTS = "Momentary Time Sampling", and PIR = "Partial Interval Recording."
- Session\_length. Length of the observation session in minutes.
- interval\_length. Length of the observation intervals for data observed using MTS or PIR.
- outcome. Value for the outcome for all outcome types.
- direction. Direction of therapeutic improvement for the outcome.

### Format

A data frame with 634 rows and 15 variables

### Source

Shogren, K. A., Faggella-Luby, M. N., Bae, S. J., & Wehmeyer, M. L. (2004). The effect of choice-making as an intervention for problem behavior. *Journal of Positive Behavior Interventions*, 6(4), 228–237.

### References

Pustejovsky, J.E. (2015). Measurement-comparable effect sizes for single-case studies of free-operand behavior. *Psychological Methods*, 20(3), 342–359.

---

SMD

*Within-case standardized mean difference*

---

### Description

Calculates the within-case standardized mean difference effect size index

### Usage

```
SMD(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase,
  improvement = "increase",
  std_dev = "baseline",
  bias_correct = TRUE,
  confidence = 0.95
)
```



**Arguments**

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".
std_dev	character string controlling how to calculate the standard deviation in the denominator of the effect size. Set to "baseline" (the default) to use the baseline standard deviation. Set to "pool" to use the pooled standard deviation.
bias_correct	logical value indicating whether to use bias-correction (i.e., Hedges' g). Default is TRUE
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.

**Details**

The standardized mean difference parameter is defined as the difference between the mean level of the outcome in phase B and the mean level of the outcome in phase A, scaled by the within-case standard deviation of the outcome in phase A. The parameter is estimated using sample means and sample standard deviations and (optionally) making a small-sample correction.

By default, the scaling factor is estimated using the sample standard deviation in phase A (the baseline phase) only. Set `std_dev = "pool"` to use the sample standard deviation pooled across both phases. Hedges' (1981) small-sample bias correction is applied by default.

**Value**

A list containing the estimate, standard error, and confidence interval.

**Examples**

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
SMD(A_data = A, B_data = B, bias_correct = FALSE)
SMD(A_data = A, B_data = B)
SMD(A_data = A, B_data = B, std_dev = "pool")
```

---

Tau	<i>Tau (non-overlap)</i>
-----	--------------------------

---

### Description

Calculates the Tau (non-overlap) index (Parker, Vannest, Davis, & Sauber 2011).

### Usage

```
Tau(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase",
  SE = "unbiased",
  confidence = 0.95
)
```

### Arguments

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".
SE	character value indicating which formula to use for calculating the standard error of NAP, with possible values "unbiased" for the exactly unbiased estimator, "Hanley" for the Hanley-McNeil estimator, "null" for the (known) variance under the null hypothesis of no effect, or "none" to not calculate a standard error. Defaults to "unbiased".
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.

### Details

Tau (non-overlap) a linear re-scaling of [NAP](#) to the range [-1,1], with a null value of 0.

Standard errors and confidence intervals for Tau are based on transformations of the corresponding SEs and CIs for [NAP](#).

### Value

A list containing the estimate, standard error, and/or confidence interval.

## References

Parker, R. I., Vannest, K. J., Davis, J. L., & Sauber, S. B. (2011). Combining nonoverlap and trend for single-case research: Tau-U. *Behavior Therapy*, *42*(2), 284–299. doi:doi: [10.1016/j.beth.2010.08.006](https://doi.org/10.1016/j.beth.2010.08.006)

## Examples

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
Tau(A_data = A, B_data = B)
```

---

Tau\_BC

*Tau-BC*

---

## Description

Calculates the baseline-corrected Tau index (Tarlow 2017).

## Usage

```
Tau_BC(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase",
  SE = "unbiased",
  confidence = 0.95,
  pretest_trend = FALSE,
  report_correction = FALSE
)
```

## Arguments

A_data	vector of numeric data for A phase. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".

SE	character value indicating which formula to use for calculating the standard error of Tau-BC, with possible values "unbiased" for the exactly unbiased estimator, "Hanley" for the Hanley-McNeil estimator, "null" for the (known) variance under the null hypothesis of no effect, or "none" to not calculate a standard error. Defaults to "unbiased". Note that the "unbiased" standard error is unbiased for <a href="#">Tau</a> , but not necessarily unbiased for <a href="#">Tau_BC</a> . None of the standard error formulas account for the additional uncertainty due to use of the baseline trend correction.
confidence	confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.
pretest_trend	significance level for the initial baseline trend test. The raw data are corrected and <a href="#">Tau_BC</a> is calculated only if the baseline trend is statistically significant. Otherwise, <a href="#">Tau_BC</a> is equal to <a href="#">Tau</a> . Default is FALSE, which always adjusts for the baseline trend.
report_correction	logical value indicating whether to report the baseline corrected slope and intercept values. Default is FALSE.

## Details

Tau-BC is an elaboration of the [Tau](#) that includes a correction for baseline trend. The calculation of Tau-BC involves two or three steps, depending on the `pretest_trend` argument.

If `pretest_trend = FALSE` (the default), the first step involves adjusting the outcomes for baseline trend estimated using Theil-Sen regression. In the second step, the residuals from Theil-Sen regression are used to calculate the [Tau](#) (non-overlap) index.

Alternately, `pretest_trend` can be set equal to a significance level between 0 and 1 (e.g. `pretest_trend = .05`, as suggested by Tarlow, 2017). In this case, the first step involves a significance test for the slope of the baseline trend based on Kendall's rank correlation. If the slope is not significantly different from zero, then no baseline trend adjustment is made and Tau-BC is set equal to [Tau](#). If the slope is significantly different from zero, then in the second step, the outcomes are adjusted for baseline trend using Theil-Sen regression and, in the third step, the residuals from Theil-Sen regression are used to calculate the [Tau](#) (non-overlap) index.

Note that the standard error formulas are based on the standard errors for [Tau](#) (non-overlap) and they do not account for the additional uncertainty due to use of the baseline trend correction (nor to the pre-test for statistical significance of baseline trend, if used).

## Value

A list containing the estimate, standard error, and/or confidence interval.

## References

Tarlow, K. R. (2017). An improved rank correlation effect size statistic for single-case designs: Baseline corrected Tau. *Behavior modification*, 41(4), 427-467. doi:doi: [10.1177/0145445516676750](https://doi.org/10.1177/0145445516676750)

**Examples**

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 30, 29)
Tau_BC(A_data = A, B_data = B)
```

---

 Tau\_U
 

---

*Tau-U***Description**

Calculates the Tau-U index with baseline trend correction (Parker, Vannest, Davis, & Sauber 2011).

**Usage**

```
Tau_U(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = unique(condition)[1],
  improvement = "increase"
)
```

**Arguments**

A_data	vector of numeric data for A phase, sorted in order of session number. Missing values are dropped.
B_data	vector of numeric data for B phase. Missing values are dropped.
condition	vector identifying the treatment condition for each observation in the series.
outcome	vector of outcome data for the entire series.
baseline_phase	character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.
improvement	character string indicating direction of improvement. Default is "increase".

**Details**

Tau-U is an elaboration of the [Tau](#) that includes a correction for baseline trend. It is calculated as Kendall's S statistic for the comparison between the phase B data and the phase A data, plus Kendall's S statistic for the A phase observations, scaled by the product of the number of observations in each phase.

Note that A\_data must be ordered by session number.

**Value**

Numeric value

## References

Parker, R. I., Vannest, K. J., Davis, J. L., & Sauber, S. B. (2011). Combining nonoverlap and trend for single-case research: Tau-U. *Behavior Therapy*, 42(2), 284–299. doi:doi: [10.1016/j.beth.2010.08.006](https://doi.org/10.1016/j.beth.2010.08.006)

## Examples

```
A <- c(20, 20, 26, 25, 22, 23)
B <- c(28, 25, 24, 27, 30, 29)
Tau_U(A_data = A, B_data = B)
```

---

Thorne

*Thorne and Kamps (2008)*

---

## Description

Data from an ABAB design conducted by Thorne and Kamps (2008). These data were used as an example in Swan and Pustejovsky (2017). Academic engagement was collected via continuous recording (marked as "other") and inappropriate verbalizations were collected via event counting (marked as "count"). The variables are as follows:

- Measure. Outcome measure description (academic engagement or inappropriate verbalizations).
- Case. Participant identifier.
- Session\_number. Measurement occasion.
- Outcome. Outcome scores
- Trt. Treatment indicators.
- Session\_length. Length of the observation session.
- Measure. The metric in which the outcome measurement is expressed (count or other).

## Format

A data frame with 776 rows and 5 variables

## Source

Thorne, S., & Kamps, D. (2008). The effects of a group contingency intervention on academic engagement and problem behavior of at-risk students. *Behavior Analysis in Practice*, 1(2), 12-18.

## References

Swan, D. M., & Pustejovsky, J. E. (2017). A gradual effects model for single-case designs. <http://doi.org/10.17605/OSF.IO/G>

---

Wright2012

*Wright & McCathren (2012)*

---

**Description**

Data from a multiple baseline design conducted by Wright and McCathren (2012), which evaluated the effects of two types of social story interventions (a basic social story and a modified social story) on the behavior of four children with autism. Both dependent variables were measured using frequency counting for 10 minute observation sessions. The variables are as follows:

- Participant Participant identifier.
- Session Session number.
- Condition Phase of the design (baseline, intervention A, or intervention B).
- Problem\_behavior Outcome scores.

**Format**

A data frame with 97 rows and 5 variables

**Source**

Wright, L. A., & McCathren, R. B. (2012). Utilizing social stories to increase prosocial behavior and reduce problem behavior in young children with autism. *Child Development Research*, 2012, 1-13. doi:10.1155/2012/357291

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