 Package ‘SingleCaseES’

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**Type**  Package
**Title**  A Calculator for Single-Case Effect Sizes
**Version**  0.7.1

**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>. 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

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**RoxygenNote**  7.2.3

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

Arguments

dat data frame containing SCD series for which effect sizes will be calculated.
grouping A variable name or list of (unquoted) variable names that uniquely identify each data series.
condition A variable name that identifies the treatment condition for each observation in the series.
outcome A variable name for the outcome data. Default is
aggregate A variable name of 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).
weighting character string specifying the weighting scheme for use when variables are specified in aggregate. Available is "1/V", "equal" (the default), "Equal", "nA", "n_A", "nB", "n_B", "nA*nB", "nA*nB", "n_A*n_B", "n_A*n_B", "1/nA+1/nB", "1/nA + 1/nB", or "1/nA + 1/nB". Note that "1/V" can only be used for effect sizes with known standard errors.

session_number A variable name used to order the data within each series.

baseline_phase character string specifying which value of condition corresponds to the baseline phase. If NULL (the default), the first observed value of condition within the series will be used.

intervention_phase character string specifying which value of condition corresponds to the intervention phase. If NULL (the default), the second unique value of condition within the series will be used.

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", "PAND", "PoGO", "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 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".

scale 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.

goal Used for the percent of goal obtained. Either a numeric common goal level across all series in the dataset or a variable name containing the goal level for each series. If a variable name, the mean goal level within each series will be used. Missing values will be ignored. Defaults to NULL.

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,
Description

Data from an ABAB design that evaluated the effectiveness of functional assessment and functional communication training on the Rett syndrome (RTT) of three individuals with RTT novel communicative behaviors. The dependent variable, communicative behavior, was measured using frequency counting for a five minute observation session. A single outcome (percent of switch activated responses) was calculated with appropriate responses per minute divided by inappropriate responses per minute, multiplied by 100. The variables are as follows:

- **StudyID**: Study identifier.
- **StudyID_CaseID**: Participant identifier.
- **Session_number**: Within-series session-number.
- **Condition**: Indicates condition, (A for baseline, B for treatment).
- **Outcome**: Value for the percent of switch activated responses.
- **Session_length**: Length of the session.
- **Procedure**: Scale of the outcome variable.
- **Goal_level**: Indicates the goal level for each series.
- **phase_pair_calculated**: Indicates the unique phase number of each sequential occurrence of a phase for each participant of ABAB design.

Format

A data frame with 54 rows and 9 variables

Source

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", "PoGO", "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.
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, session = seq_along(x))

Arguments

x vector of phase/condition labels.

session numeric vector of measurement occasions, used to sort x before calculating phase pairs.
Value

A vector containing an integer phase number for every observation.

Examples

```r
# Basic use-case
x <- rep(c("A","B","C","B","C","A","C"), c(4:10))
calc_phase_pairs(x)

# Using session argument to handle sort order
session <- sample(seq_along(x))
x_scrambled <- x[session]
dat <- data.frame(
x = x_scrambled,
  session = session,
  phase_pair = calc_phase_pairs(x_scrambled, session = session)
)
dat_sorted <- dat[order(session),]
identical(x, dat_sorted$x)

# With a grouped data.frame
library(dplyr)
Schmidt2007 %>%
  group_by(Behavior_type, Case_pseudonym) %>%
  mutate(phase_pair = calc_phase_pairs(Condition, session = Session_number))
```

Description

Data from a multiple baseline design across participant that evaluated the effectiveness of use of manual signs with verbalizations in improving appropriate communicative behavior and reducing inappropriate behavior. The study aimed to increase positive communicative behavior to 1 and reduce the proportion of intervals engaged in problem behavior to 0. These two outcomes were combined to create the dependent variable: proportion of communicative opportunities with a signed request. The variables are as follows:

- **StudyID.** Study identifier.
- **StudyID_CaseID.** Participant identifier.
- **Session_number.** Within-series session-number.
- **Condition.** Indicates condition, (A for baseline, B for treatment).
- **Outcome.** Value for the outcome variable.
- **Session_length.** Length of the session.
- **Procedure.** Scale of the outcome variable.
- **Goal_level.** Indicates the goal level for each series.
**Format**

A data frame with 100 rows and 8 variables

**Source**


**Description**

Data from an ABAB design that evaluated a social story intervention on the disruptive behavior of a preschool child with autism. The dependent variable, number of disruptions, was measured using frequency counting for a thirty minute observation session. The variables are as follows:

- **session.** Within-series session-number.
- **phase.** Label for each unique phase (e.g., A1 is the first baseline phase, B2 is the second treatment phase).
- **score.** Value for the outcome.

**Format**

A data frame with 24 rows and 3 variables

**Source**


**Description**

Data from a Repeated acquisition single-case experimental design evaluating vocabulary knowledge using an expressive definition task. The variables are as follows:

- **Participant.** Participant identifier.
- **Condition.** Indicates condition, application (App) or teacher (TCH).
- **Observation.** Within-series session-number
- **Pre.** Pre-intervention score on the expressive definition task.
- **Post.** Post-intervention score on the expressive definition task.
Description

Data from a multiple baseline design across participants conducted by English, et al. (1997), which evaluated the effects of peer-training on interaction skills. This dependent variable, number of communicative acts directed by the participant to their peers, was measured using frequency counting for a 10-minute observation session. The variables are as follows:

- case. Participant pseudonym given by author
- session. Within-series session-number
- phase. Label for each unique phase (A for baseline, B for treatment)
- score. Value for the outcome.

Format

A data frame with 90 rows and 5 variables

Source


Description

Data from a changing criterion design conducted by Facon, et al. (2008), which evaluated two operant learning procedures, shaping and fading, for treating selective mutism. The dependent variable, average speech loudness in dB, was measured during 15-minute observation sessions. The variables are as follows:

- **session.** Within-series session-number
- **phase.** Label for each unique phase (A for baseline, each following for a change in criteria.
- **score.** Value for the outcome.
- **criterion.** The fixed criterion value for each of the phases. The student moved to the next criterion when 80

Format

A data frame with 49 rows and 4 variables

Source


---

**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 `family` for details of family functions.)
IRD

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  
Robust improvement rate difference

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

```r
IRD(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  improvement = "increase"
)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>A_data</td>
<td>vector of numeric data for A phase. Missing values are dropped.</td>
</tr>
<tr>
<td>B_data</td>
<td>vector of numeric data for B phase. Missing values are dropped.</td>
</tr>
<tr>
<td>condition</td>
<td>vector identifying the treatment condition for each observation in the series.</td>
</tr>
<tr>
<td>outcome</td>
<td>vector of outcome data for the entire series.</td>
</tr>
<tr>
<td>baseline_phase</td>
<td>character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.</td>
</tr>
<tr>
<td>intervention_phase</td>
<td>character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique value of condition.</td>
</tr>
<tr>
<td>improvement</td>
<td>character string indicating direction of improvement. Default is “increase”.</td>
</tr>
</tbody>
</table>

Value

Numeric value

References

See Also

PAND

Examples

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

Description

Data from a randomized control trial with embedded repeated acquisition single-case experimental design evaluating vocabulary knowledge using an expressive definition task. The variables are as follows:

- **condition.** Indicates whether control or treatment group.
- **observation.** Identifier for participant
- **unit.** Classroom unit.
- **Pre.** Pre-intervention score on the expressive definition task.
- **Post.** Post-intervention score on the expressive definition task.

Format

A data frame with 54 rows and 5 variables

Source

**LOR**  

*Log-odds ratio*

**Description**

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

**Usage**

```r
LOR(
    A_data,  
    B_data,  
    condition,  
    outcome,  
    baseline_phase = NULL,  
    intervention_phase = NULL,  
    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.
- **intervention_phase** character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique 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


Examples

```r
A_pct <- c(20, 20, 25, 25, 20, 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 / 100, B_data = B_pct / 100, scale = "proportion")
LOR(A_data = A_pct, B_data = B_pct, scale = "percentage", improvement = "decrease")
```
Description

Calculates the log ratio of medians effect size index

Usage

LRM(
    A_data,
    B_data,
    condition,
    outcome,
    baseline_phase = NULL,
    intervention_phase = NULL,
    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.
intervention_phase character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique 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).
A data frame containing the estimate, standard error, and confidence interval.

References


Examples

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

Description

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

Usage

```r
LRRd(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  improvement = "decrease",
  scale = "count",
  observation_length = NULL,
  intervals = NULL,
  D_const = NULL,
  bias_correct = TRUE,
  pct_change = FALSE,
  confidence = 0.95
)
```

```r
LRRi(
  A_data,
```
B_data,
condition,
outcome,
baseline_phase = NULL,
treatment_phase = NULL,
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.
treatment_phase character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique 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 Percentage change = 100 * (exp(LRR) - 1).

Value

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

References


Examples

```r
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)
```
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

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

Usage
```R
NAP(  
A_data,
B_data,
condition,
outcome,
baseline_phase = NULL,
intervention_phase = NULL,
improvement = "increase",
SE = "unbiased",
confidence = .95,
trunc_const = 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.
intervention_phase character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique 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.
trunc_const logical value indicating whether to return the truncation constant used to calculate the standard error.

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


**Examples**

```r
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)
```

**Description**

Data from a multiple baseline design across behavior looking at four fluency measures (blends, segmenting, first part ID, first sound ID). The dependent variable is a score on a subtest, with a maximum score of 20. The variables are as follows:

- **behavior**: Outcome measure description (blends, segmenting, first part ID, or first sound ID)
- **session**: Within-series session-number
- **phase**: Label for each unique phase (A for baseline, B for treatment)
- **score**: Value for the outcome.
- **Include**: Value for inclusion in POGO calculation (0 if included in article, 1 if not included)

**Format**

A data frame with 72 rows and 4 variables

**Source**

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 = NULL,
    intervention_phase = NULL,
    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.
intervention_phase  character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique 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


Examples

```r
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

```r
PEM(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  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.
intervention_phase
character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique 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

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)

Description
Data from a Repeated acquisition single-case experimental design evaluating vocabulary knowledge using an expressive definition task. The variables are as follows:

- observation. Identifier for participant
- Book. Book used for evaluation.
- Pre. Pre-intervention score on the expressive definition task.
- Post. Post-intervention score on the expressive definition task.

Format
A data frame with 153 rows and 4 variables
**Source**


---

**PND**

Percentage of non-overlapping data

---

**Description**

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

**Usage**

```r
PND(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  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`.
- `intervention_phase`: character string specifying which value of `condition` corresponds to the intervention phase. Defaults to second unique 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


Examples

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

---

PoGO  Percent of Goal Obtained

Description

Calculates the percent of goal obtained effect size index

Usage

```r
PoGO(
  A_data,
  B_data,
  condition,
  outcome,
  goal,
  baseline_phase = NULL,
  intervention_phase = NULL,
  improvement = "increase",
  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.
- **goal**: a numerical value indicating the goal level of behavior.
- **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.

improvement
character string indicating direction of improvement. Default is "increase".

certainty
confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.

Details
The percent of goal obtained (PoGO) effect size parameter is defined as the ratio of the difference in the mean level of behavior during phase B versus during phase A to the difference between the goal level of behavior and the mean level of behavior during phase A, multiplied by 100.

The standard error of PoGO is calculated based on Dunlap and Silver’s (1986) approximation for the standard error of a ratio. The confidence interval for LRR is based on a large-sample (z) approximation.

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

References


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

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.

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

Note

Data were reconstructed from figures in the source document. Consequently, outcome measurements in this dataset include additional error from the reconstruction process and may not exactly match the original source data.

In earlier versions of the package (0.5.0 and earlier), the Case_Pseudonym variable contained incorrect labels for each case, which did not match the labels in the source document. Specifically, Faith was incorrectly labeled as Albert; Lilly was incorrectly labeled as Faith; and Albert was incorrectly labeled as Lilly.
Source


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


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

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

<table>
<thead>
<tr>
<th>Shogren</th>
<th>Shogren et al. (2004)</th>
</tr>
</thead>
</table>

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.
- **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

References

---

**SMD**

*Within-case standardized mean difference*

**Description**
Calculates the within-case standardized mean difference effect size index

**Usage**

```r
SMD(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  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`.
- `intervention_phase` character string specifying which value of `condition` corresponds to the intervention phase. Defaults to second unique 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")

Description

Data from a repeated acquisition single-case experimental design evaluating vocabulary knowledge using an expressive definition task. The variables are as follows:

- Observation. Participant number.
- Book. Book used for evaluation.
- Pre. Pre-intervention score on the expressive definition task.
- Post. Post-intervention score on the expressive definition task.

Format

A data frame with 81 rows and 4 variables
Source


Description

Data from a multiple baseline design across participant that evaluated the effectiveness of an iPod-based speech generating device and a peer mediated intervention on improving sophisticated communication skills of children with autism. The variables are as follows:

- **StudyID**: Study identifier.
- **StudyID_CaseID**: Participant identifier.
- **Session_number**: Within-series session-number.
- **Condition**: Indicates condition, (A for baseline, B for intervention).
- **Outcome**: The number of independent 2-step mands.
- **Session_length**: Length of the session.
- **Procedure**: Scale of the outcome variable.
- **Goal_level**: Indicates the goal level for each series.

Format

A data frame with 47 rows and 8 variables

Source

Description

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

Usage

```r
Tau(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  improvement = "increase",
  SE = "unbiased",
  confidence = 0.95,
  trunc_const = 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`.
- `intervention_phase`: character string specifying which value of `condition` corresponds to the intervention phase. Defaults to second unique 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.
- `trunc_const`: logical value indicating whether to return the truncation constant used to calculate the standard error.
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


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)

Description

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

Usage

Tau_BC(
  A_data,
  B_data,
  condition,
  outcome,
  baseline_phase = NULL,
  intervention_phase = NULL,
  improvement = "increase",
  SE = "unbiased",
  confidence = 0.95,
  trunc_const = FALSE,
  Kendall = FALSE,
  pretest_trend = FALSE,
  report_correction = FALSE,
  warn = TRUE
)
**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>A_data</td>
<td>vector of numeric data for A phase. Missing values are dropped.</td>
</tr>
<tr>
<td>B_data</td>
<td>vector of numeric data for B phase. Missing values are dropped.</td>
</tr>
<tr>
<td>condition</td>
<td>vector identifying the treatment condition for each observation in the series.</td>
</tr>
<tr>
<td>outcome</td>
<td>vector of outcome data for the entire series.</td>
</tr>
<tr>
<td>baseline_phase</td>
<td>character string specifying which value of condition corresponds to the baseline phase. Defaults to first observed value of condition.</td>
</tr>
<tr>
<td>intervention_phase</td>
<td>character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique value of condition.</td>
</tr>
<tr>
<td>improvement</td>
<td>character string indicating direction of improvement. Default is &quot;increase&quot;.</td>
</tr>
<tr>
<td>SE</td>
<td>character value indicating which formula to use for calculating the standard error of Tau-BC, with possible values &quot;unbiased&quot; for the exactly unbiased estimator, &quot;Hanley&quot; for the Hanley-McNeil estimator, &quot;null&quot; for the (known) variance under the null hypothesis of no effect, or &quot;none&quot; to not calculate a standard error. Defaults to &quot;unbiased&quot;. Note that the &quot;unbiased&quot; standard error is unbiased for Tau, but not necessarily unbiased for Tau_BC. None of the standard error formulas account for the additional uncertainty due to use of the baseline trend correction.</td>
</tr>
<tr>
<td>confidence</td>
<td>confidence level for the reported interval estimate. Set to NULL to omit confidence interval calculations.</td>
</tr>
<tr>
<td>trunc_const</td>
<td>logical value indicating whether to return the truncation constant used to calculate the standard error.</td>
</tr>
<tr>
<td>Kendall</td>
<td>logical value indicating whether to use Kendall’s rank correlation to calculate the Tau effect size measure. If TRUE, the Kendall’s rank correlation (with adjustment for ties) is calculated between the data and a dummy coded phase variable, which is consistent with the method used in Tarlow (2017). Default is FALSE, which calculates Tau (non-overlap) index (without adjustment for ties).</td>
</tr>
<tr>
<td>pretest_trend</td>
<td>significance level for the initial baseline trend test. The raw data are corrected and Tau_BC is calculated only if the baseline trend is statistically significant. Otherwise, Tau_BC is equal to Tau. Default is FALSE, which always adjusts for the baseline trend.</td>
</tr>
<tr>
<td>report_correction</td>
<td>logical value indicating whether to report the baseline corrected slope and intercept values. Default is FALSE.</td>
</tr>
<tr>
<td>warn</td>
<td>logical value indicating whether to print a message regarding the outcome of the baseline trend test. Default is TRUE.</td>
</tr>
</tbody>
</table>

**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 (using either Kendall’s rank correlation, with adjustment for ties, or computing Tau directly, without adjustment for ties).
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 index. If the slope is significantly different from zero, then in the second step, the outcomes are adjusted for baseline trend using Theil-Sen regression. Then, in the third step, the residuals from Theil-Sen regression are used to calculate the Tau index. If Kendall = FALSE (the default), then Tau (non-overlap) index is calculated. If Kendall = TRUE, then Kendall’s rank correlation is calculated, including adjustment for ties, as in Tarlow (2017).

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

See Also
Tau, Tau_U

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)

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 = NULL,
intervention_phase = NULL,
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.
intervention_phase: character string specifying which value of condition corresponds to the intervention phase. Defaults to second unique 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


Examples

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


References


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
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