

Package ‘psychmeta’

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Description

Tools for computing bare-bones and psychometric meta-analyses and for generating psychometric data for use in meta-analysis simulations. Supports bare-bones, individual-correction, and artifact-distribution methods for meta-analyzing correlations and d values. Includes tools for converting effect sizes, computing sporadic artifact corrections, reshaping meta-analytic databases, computing multivariate corrections for range variation, and more. Bugs can be reported to <<https://github.com/psychmeta/psychmeta/issues>> or <issues@psychmeta.com>.

License GPL (>= 3)

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R topics documented:

psychmeta-package	4
adjust_n_d	7
adjust_n_r	8
composite_d_matrix	9
composite_d_scalar	10
composite_rel_matrix	11
composite_rel_scalar	12
composite_r_matrix	13
composite_r_scalar	14
composite_u_matrix	15
composite_u_scalar	16
compute_alpha	17
compute_dmod	18
compute_dmod_npar	20
compute_dmod_par	23
confidence	25
confidence_r	26
confint	27
control_intercor	27
control_psychmeta	29
convert_es	31
convert_ma	33
correct_d	35
correct_d_bias	37
correct_glass_bias	38
correct_matrix_mvrr	39
correct_means_mvrr	40
correct_r	41
correct_r_bias	44
correct_r_coarseness	45
correct_r_dich	46
correct_r_split	47
create_ad	48
create_ad_group	53
create_ad_tibble	55
credibility	58
data_d_bb_multi	59
data_d_meas_multi	59
data_r_bvdr	60
data_r_bvirr	60
data_r_gonzalez_mule_2014	61
data_r_mcdaniel_1994	61

data_r_mcleod_2007	62
data_r_meas	62
data_r_meas_multi	63
data_r_oh_2009	63
data_r_roth_2015	64
data_r_uvdr	65
data_r_uvirr	65
estimate_artifacts	66
estimate_length_sb	70
estimate_prod	71
estimate_q_dist	72
estimate_rel_dist	73
estimate_rel_sb	74
estimate_u	75
estimate_var_artifacts	76
estimate_var_rho_int	85
estimate_var_rho_tsa	86
estimate_var_tsa	94
filter_ma	97
format_num	98
generate_bib	100
generate_directory	101
get_stuff	102
heterogeneity	106
lm_mat	108
ma_d	110
ma_d_order2	121
ma_generic	123
ma_r	124
ma_r_order2	140
merge_simdat_d	142
merge_simdat_r	142
metabulate	143
metabulate_rmd_helper	146
metareg	148
mix_dist	149
mix_matrix	151
mix_r_2group	152
plot_forest	153
plot_funnel	154
predict	155
print	156
psychmeta_news	157
reattribute	157
reshape_mat2dat	158
reshape_vec2mat	159
reshape_wide2long	160
sensitivity	162

simulate_alpha	164
simulate_d_database	165
simulate_d_sample	168
simulate_matrix	169
simulate_psych	170
simulate_r_database	171
simulate_r_sample	174
sparsify_simdat_d	176
sparsify_simdat_r	176
summary	177
truncate_dist	177
truncate_mean	178
truncate_var	179
unmix_matrix	179
unmix_r_2group	180
var_error_A	181
var_error_alpha	182
var_error_d	183
var_error_delta	185
var_error_g	185
var_error_q	186
var_error_r	187
var_error_rel	188
var_error_r_bvirr	189
var_error_u	193
wt_cov	194
wt_dist	195

Index	197
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psychmeta-package **psychmeta**: *Psychometric meta-analysis toolkit*

Description

Overview of the **psychmeta** package.

Details

The **psychmeta** package provides tools for computing bare-bones and psychometric meta-analyses and for generating psychometric data for use in meta-analysis simulations. Currently, **psychmeta** supports bare-bones, individual-correction, and artifact-distribution methods for meta-analyzing correlations and d values. Please refer to the overview tutorial vignette for an introduction to **psychmeta**'s functions and workflows.

Running a meta-analysis

The main functions for conducting meta-analyses in **psychmeta** are `ma_r` for correlations and `ma_d` for d values. These functions take meta-analytic dataframes including effect sizes and sample sizes (and, optionally, study labels, moderators, construct and measure labels, and psychometric artifact information) and return the full results of psychometric meta-analyses for all of the specified variable pairs. Examples of correctly formatted meta-analytic datasets for ma functions are `data_r_roth_2015`, `data_r_gonzalezmu_2014`, and `data_r_mcdaniel_1994`. Individual parts of the meta-analysis process can also be run separately; these functions are described in detail below.

Preparing a database for meta-analysis

The `convert_es` function can be used to convert a variety of effect sizes to either correlations or d values. Sporadic psychometric artifacts, such as artificial dichotomization or uneven splits for a *truly* dichotomous variable, can be individually corrected using `correct_r` and `correct_d`. These functions can also be used to compute confidence intervals for observed, converted, and corrected effect sizes. 'Wide' meta-analytic coding sheets can be reformatted to the 'long' data frames used by **psychmeta** with `reshape_wide2long`. A correlation matrix and accompanying vectors of information can be similarly reformatted using `reshape_mat2dat`.

Meta-analytic models

psychmeta can compute barebones meta-analyses (no corrections for psychometric artifacts), as well as models correcting for measurement error in one or both variables, univariate direct (Case II) range restriction, univariate indirect (Case IV) range restriction, bivariate direct range restriction, bivariate indirect (Case V) range restriction, and multivariate range restriction. Artifacts can be corrected individually or using artifact distributions. Artifact distribution corrections can be applied using either Schmidt and Hunter's (2015) interactive method or Taylor series approximation models. Meta-analyses can be computed using various weights, including sample size (default for correlations), inverse variance (computed using either sample or mean effect size; error based on mean effect size is the default for d values), and weight methods imported from **metafor**.

Preparing artifact distributions meta-analyses

For individual-corrections meta-analyses, reliability and range restriction (u) values should be supplied in the same data frame as the effect sizes and sample sizes. Missing artifact data can be imputed using either bootstrap or other imputation methods. For artifact distribution meta-analyses, artifact distributions can be created automatically by `ma_r` or `ma_d` or manually by the `create_ad` family of functions.

Moderator analyses

Subgroup moderator analyses are run by supplying a moderator matrix to the `ma_r` or `ma_d` families of functions. Both simple and fully hierarchical moderation can be computed. Subgroup moderator analysis results are shown by passing an `ma_obj` to `print()`. Meta-regression analyses can be run using `metareg`.

Reporting results and supplemental analyses

Meta-analysis results can be viewed by passing an `ma` object to `print()`. Bootstrap confidence intervals, leave one out analyses, and other sensitivity analyses are available in [sensitivity](#). Supplemental heterogeneity statistics (e.g., Q , I^2) can be computed using [heterogeneity](#). Meta-analytic results can be converted between the r and d metrics using [convert_ma](#). Each `ma_obj` contains a **metafor** `escalc` object in `ma$.escalc` that can be passed to **metafor**'s functions for plotting, publication/availability bias, and other supplemental analyses. Second-order meta-analyses of correlations can be computed using [ma_r_order2](#). Example second-order meta-analysis datasets from Schmidt and Oh (2013) are available. Tables of meta-analytic results can be written as rich text files using the [metabulate](#) function, which exports near publication-quality tables that will typically require only minor customization by the user.

Simulating psychometric meta-analyses

psychmeta can be used to run Monte Carlo simulations for different meta-analytic models. [simulate_r_sample](#) and [simulate_d_sample](#) simulate samples of correlations and d values, respectively, with measurement error and/or range restriction artifacts. [simulate_r_database](#) and [simulate_d_database](#) can be used to simulate full meta-analytic databases of sample correlations and d values, respectively, with artifacts. Example datasets fitting different meta-analytic models simulated using these functions are available ([data_r_meas](#), [data_r_uvdr](#), [data_r_uvirr](#), [data_r_bvdr](#), [data_r_bvirr](#), [data_r_meas_multi](#), and [data_d_meas_multi](#)). Additional simulation functions are also available.

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- Jack Kostal (Code for `reshape_mat2dat` function) [contributor]
- Sean Potter (Testing; Code for cumulative and leave1out plots) [contributor]
- John Sakaluk (Code for funnel and forest plots) [contributor]
- Yuejia (Mandy) Teng (Testing) [contributor]

See Also

Useful links:

- Report bugs at <https://github.com/psychmeta/psychmeta/issues>

adjust_n_d	<i>Adjusted sample size for a non-Cohen d value for use in a meta-analysis of Cohen's d values</i>
------------	--

Description

This function is used to convert a non-Cohen d value (e.g., Glass' Δ) to a Cohen's d value by identifying the sample size of a Cohen's d that has the same standard error as the non-Cohen d . This function permits users to account for the influence of sporadic corrections on the sampling variance of d prior to use in a meta-analysis.

Usage

```
adjust_n_d(d, var_e, p = NA)
```

Arguments

d	Vector of non-Cohen d standardized mean differences.
var_e	Vector of error variances of standardized mean differences.
p	Proportion of participants in a study belonging to one of the two groups being contrasted.

Details

The adjusted sample size is computed as:

$$n_{adjusted} = \frac{d^2 p(1-p) + 2}{2p(1-p)var_e}$$

Value

A vector of adjusted sample sizes.

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. Chapter 7 (Equations 7.23 and 7.23a).

Examples

```
adjust_n_d(d = 1, var_e = .03, p = NA)
```

adjust_n_r	<i>Adjusted sample size for a non-Pearson correlation coefficient for use in a meta-analysis of Pearson correlations</i>
------------	--

Description

This function is used to compute the adjusted sample size of a non-Pearson correlation (e.g., a tetrachoric correlation) based on the correlation and its estimated error variance. This function allows users to adjust the sample size of a correlation corrected for sporadic artifacts (e.g., unequal splits of dichotomous variables, artificial dichotomization of continuous variables) prior to use in a meta-analysis.

Usage

```
adjust_n_r(r, var_e)
```

Arguments

r	Vector of correlations.
var_e	Vector of error variances.

Details

The adjusted sample size is computed as:

$$n_{adjusted} = \frac{(r^2 - 1)^2 + var_e}{var_e}$$

Value

A vector of adjusted sample sizes.

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. Equation 3.7.

Examples

```
adjust_n_r(r = .3, var_e = .01)
```

composite_d_matrix	<i>Matrix formula to estimate the standardized mean difference associated with a weighted or unweighted composite variable</i>
--------------------	--

Description

This function is a wrapper for [composite_r_matrix](#) that converts d values to correlations, computes the composite correlation implied by the d values, and transforms the result back to the d metric.

Usage

```
composite_d_matrix(d_vec, r_mat, wt_vec, p = 0.5)
```

Arguments

d_vec	Vector of standardized mean differences associated with variables in the composite to be formed.
r_mat	Correlation matrix from which the composite is to be computed.
wt_vec	Weights to be used in forming the composite (by default, all variables receive equal weight).
p	The proportion of cases in one of the two groups used to compute the standardized mean differences.

Details

The composite d value is computed by converting the vector of d values to correlations, computing the composite correlation (see [composite_r_matrix](#)), and transforming that composite back into the d metric. See "Details" of [composite_r_matrix](#) for the composite computations.

Value

The estimated standardized mean difference associated with the composite variable.

Examples

```
composite_d_matrix(d_vec = c(1, 1), r_mat = matrix(c(1, .7, .7, 1), 2, 2),  
                  wt_vec = c(1, 1), p = .5)
```

composite_d_scalar	<i>Scalar formula to estimate the standardized mean difference associated with a composite variable</i>
--------------------	---

Description

This function estimates the d value of a composite of X variables, given the mean d value of the individual X values and the mean correlation among those variables.

Usage

```
composite_d_scalar(mean_d, mean_intercor, k_vars, p = 0.5,
  partial_intercor = FALSE)
```

Arguments

mean_d	The mean standardized mean differences associated with variables in the composite to be formed.
mean_intercor	The mean correlation among the variables in the composite.
k_vars	The number of variables in the composite.
p	The proportion of cases in one of the two groups used to compute the standardized mean differences.
partial_intercor	Logical scalar determining whether the intercor represents the partial (i.e., within-group) correlation among variables (TRUE) or the overall correlation between variables (FALSE).

Details

There are two different methods available for computing such a composite, one that uses the partial intercorrelation among the X variables (i.e., the average within-group correlation) and one that uses the overall correlation among the X variables (i.e., the total or mixture correlation across groups).

If a partial correlation is provided for the interrelationships among variables, the following formula is used to estimate the composite d value:

$$d_X = \frac{\bar{d}_{x_i} k}{\sqrt{\bar{\rho}_{x_i x_j} k^2 + (1 - \bar{\rho}_{x_i x_j}) k}}$$

where d_X is the composite d value, \bar{d}_{x_i} is the mean d value, $\bar{\rho}_{x_i x_j}$ is the mean intercorrelation among the variables in the composite, and k is the number of variables in the composite. Otherwise, the composite d value is computed by converting the mean d value to a correlation, computing the composite correlation (see [composite_r_scalar](#) for formula), and transforming that composite back into the d metric.

Value

The estimated standardized mean difference associated with the composite variable.

References

Rosenthal, R., & Rubin, D. B. (1986). Meta-analytic procedures for combining studies with multiple effect sizes. *Psychological Bulletin*, 99(3), 400–406.

Examples

```
composite_d_scalar(mean_d = 1, mean_intercor = .7, k_vars = 2, p = .5)
```

composite_rel_matrix *Matrix formula to estimate the reliability of a weighted or unweighted composite variable*

Description

This function computes the reliability of a variable that is a weighted or unweighted composite of other variables.

Usage

```
composite_rel_matrix(rel_vec, r_mat, sd_vec, wt_vec = rep(1,
  length(rel_vec)))
```

Arguments

rel_vec	Vector of reliabilities associated with variables in the composite to be formed.
r_mat	Correlation matrix from which the composite is to be computed.
sd_vec	Vector of standard deviations associated with variables in the composite to be formed.
wt_vec	Weights to be used in forming the composite (by default, all variables receive equal weight).

Details

This function treats measure-specific variance as reliable.

The Mosier composite formula is computed as:

$$\rho_{XX} = \frac{\mathbf{w}^T (\mathbf{r} \circ \mathbf{s}) + \mathbf{w}^T \mathbf{S} \mathbf{w} - \mathbf{w}^T \mathbf{s}}{\mathbf{w}^T \mathbf{S} \mathbf{w}}$$

where ρ_{XX} is a composite reliability estimate, \mathbf{r} is a vector of reliability estimates, \mathbf{w} is a vector of weights, \mathbf{S} is a covariance matrix, and \mathbf{s} is a vector of variances (i.e., the diagonal elements of \mathbf{S}).

Value

The estimated reliability of the composite variable.

References

Mosier, C. I. (1943). On the reliability of a weighted composite. *Psychometrika*, 8(3), 161–168. <https://doi.org/10.1007/BF02288700>

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: Sage. <https://doi.org/10/b6mg>. pp. 441 - 447.

Examples

```
composite_rel_matrix(rel_vec = c(.8, .8),
r_mat = matrix(c(1, .4, .4, 1), 2, 2), sd_vec = c(1, 1))
```

composite_rel_scalar *Scalar formula to estimate the reliability of a composite variable*

Description

This function computes the reliability of a variable that is a unit-weighted composite of other variables.

Usage

```
composite_rel_scalar(mean_rel, mean_intercor, k_vars)
```

Arguments

mean_rel	The mean reliability of variables in the composite.
mean_intercor	The mean correlation among the variables in the composite.
k_vars	The number of variables in the composite.

Details

The Mosier composite formula is computed as:

$$\rho_{XX} = \frac{\bar{\rho}_{x_i x_i} k + k(k-1)\bar{\rho}_{x_i x_j}}{k + k(k-1)\bar{\rho}_{x_i x_j}}$$

where $\bar{\rho}_{x_i x_i}$ is the mean reliability of variables in the composite, $\bar{\rho}_{x_i x_j}$ is the mean intercorrelation among variables in the composite, and k is the number of variables in the composite.

Value

The estimated reliability of the composite variable.

References

- Mosier, C. I. (1943). On the reliability of a weighted composite. *Psychometrika*, 8(3), 161–168. <https://doi.org/10.1007/BF02288700>
- Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: Sage. <https://doi.org/10/b6mg>. pp. 441 - 447.

Examples

```
composite_rel_scalar(mean_rel = .8, mean_intercor = .4, k_vars = 2)
```

composite_r_matrix	<i>Matrix formula to estimate the correlation between two weighted or unweighted composite variables</i>
--------------------	--

Description

This function computes the weighted (or unweighted, by default) composite correlation between a set of X variables and a set of Y variables.

Usage

```
composite_r_matrix(r_mat, x_col, y_col, wt_vec_x = rep(1, length(x_col)),
  wt_vec_y = rep(1, length(y_col)))
```

Arguments

- | | |
|----------|---|
| r_mat | Correlation matrix from which composite correlations are to be computed. |
| x_col | Column indices of variables from 'r_mat' in the X composite (specify a single variable if Y is an observed variable rather than a composite). |
| y_col | Column indices of variables from 'r_mat' in the Y composite (specify a single variable if Y is an observed variable rather than a composite). |
| wt_vec_x | Weights to be used in forming the X composite (by default, all variables receive equal weight). |
| wt_vec_y | Weights to be used in forming the Y composite (by default, all variables receive equal weight). |

Details

This is computed as:

$$\rho_{XY} = \frac{\mathbf{w}_X^T \mathbf{R}_{XY} \mathbf{w}_Y}{\sqrt{(\mathbf{w}_X^T \mathbf{R}_{XX} \mathbf{w}_X) (\mathbf{w}_Y^T \mathbf{R}_{YY} \mathbf{w}_Y)}}$$

where ρ_{XY} is the composite correlation, \mathbf{w} is a vector of weights, and \mathbf{R} is a correlation matrix. The subscripts of \mathbf{w} and \mathbf{R} indicate the variables indexed within the vector or matrix.

Value

A composite correlation

References

Mulaik, S. A. (2010). *Foundations of factor analysis*. Boca Raton, FL: CRC Press. pp. 83–84.

Examples

```
composite_r_scalar(mean_rxy = .3, k_vars_x = 4, mean_intercor_x = .4)
R <- reshape_vec2mat(.4, order = 5)
R[-1,1] <- R[1,-1] <- .3
composite_r_matrix(r_mat = R, x_col = 2:5, y_col = 1)
```

composite_r_scalar	<i>Scalar formula to estimate the correlation between a composite and another variable or between two composite variables</i>
--------------------	---

Description

This function estimates the correlation between a set of X variables and a set of Y variables using a scalar formula.

Usage

```
composite_r_scalar(mean_rxy, k_vars_x = NULL, mean_intercor_x = NULL,
  k_vars_y = NULL, mean_intercor_y = NULL)
```

Arguments

mean_rxy	Mean correlation between sets of X and Y variables.
k_vars_x	Number of X variables.
mean_intercor_x	Mean correlation among X variables.
k_vars_y	Number of Y variables.
mean_intercor_y	Mean correlation among Y variables.

Details

The formula to estimate a correlation between one composite variable and one external variable is:

$$\rho_{Xy} = \frac{\bar{\rho}_{x_iy}}{\sqrt{\frac{1}{k_x} + \frac{k_x-1}{k_x} \bar{\rho}_{x_ix_j}}}$$

and the formula to estimate the correlation between two composite variables is:

$$\rho_{XY} = \frac{\bar{\rho}_{x_i y_j}}{\sqrt{\frac{1}{k_x} + \frac{k_x - 1}{k_x} \bar{\rho}_{x_i x_j}} \sqrt{\frac{1}{k_y} + \frac{k_y - 1}{k_y} \bar{\rho}_{y_i y_j}}}$$

where $\bar{\rho}_{x_i y_j}$ and $\bar{\rho}_{x_i x_j}$ are mean correlations between the x variables and the y variable(s), $\bar{\rho}_{x_i x_j}$ is the mean correlation among x variables, $\bar{\rho}_{y_i y_j}$ is the mean correlation among y variables, k_x is the number of x variables, and k_y is the number of y variables.

Value

A vector of composite correlations

References

Ghiselli, E. E., Campbell, J. P., & Zedeck, S. (1981). *Measurement theory for the behavioral sciences*. San Francisco, CA: Freeman. p. 163-164.

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: Sage. <https://doi.org/10/b6mg>. pp. 441 - 447.

Examples

```
## Composite correlation between 4 variables and an outside variable with which
## the four variables correlate .3 on average:
composite_r_scalar(mean_rxy = .3, k_vars_x = 4, mean_intercor_x = .4)
```

```
## Correlation between two composites:
composite_r_scalar(mean_rxy = .3, k_vars_x = 2, mean_intercor_x = .5,
                  k_vars_y = 2, mean_intercor_y = .2)
```

composite_u_matrix *Matrix formula to estimate the u ratio of a composite variable*

Description

This function estimates the u ratio of a composite variable when at least one matrix of correlations (restricted or unrestricted) among the variables is available.

Usage

```
composite_u_matrix(ri_mat = NULL, ra_mat = NULL, u_vec,
                  wt_vec = rep(1, length(u_vec)), sign_r_vec = 1)
```

Arguments

ri_mat	Range-restricted correlation matrix from which the composite is to be computed (if NULL, ri_mat is estimated from ra_mat).
ra_mat	Unrestricted correlation matrix from which the composite is to be computed (if NULL, ra_mat is estimated from ri_mat).
u_vec	Vector of u ratios associated with variables in the composite to be formed.
wt_vec	Weights to be used in forming the composite (by default, all variables receive equal weight).
sign_r_vec	The signs of the relationships between the variables in the composite and the variable by which range restriction was induced.

Details

This is computed as:

$$u_{composite} = \sqrt{\frac{(\mathbf{w} \circ \mathbf{u})^T \mathbf{R}_i (\mathbf{w} \circ \mathbf{u})}{\mathbf{w}^T \mathbf{R}_a \mathbf{w}}}$$

where $u_{composite}$ is the composite u ratio, \mathbf{u} is a vector of u ratios, \mathbf{R}_i is a range-restricted correlation matrix, \mathbf{R}_a is an unrestricted correlation matrix, and \mathbf{w} is a vector of weights.

Value

The estimated u ratio of the composite variable.

Examples

```
composite_u_matrix(ri_mat = matrix(c(1, .3, .3, 1), 2, 2), u_vec = c(.8, .8))
```

composite_u_scalar *Scalar formula to estimate the u ratio of a composite variable*

Description

This function provides an approximation of the u ratio of a composite variable based on the u ratios of the component variables, the mean restricted intercorrelation among those variables, and the mean unrestricted correlation among those variables. If only one of the mean intercorrelations is known, the other will be estimated using the bivariate indirect range-restriction formula. This tends to compute a conservative estimate of the u ratio associated with a composite.

Usage

```
composite_u_scalar(mean_ri = NULL, mean_ra = NULL, mean_u, k_vars)
```


Arguments

mean_ri	The mean range-restricted correlation among variables in the composite.
mean_ra	The mean unrestricted correlation among variables in the composite.
mean_u	The mean u ratio of variables in the composite.
k_vars	The number of variables in the composite.

Details

This is computed as:

$$u_{composite} = \sqrt{\frac{\bar{\rho}_i \bar{u}^2 k(k-1) + k \bar{u}^2}{\bar{\rho}_a k(k-1) + k}}$$

where $u_{composite}$ is the composite u ratio, \bar{u} is the mean univariate u ratio, $\bar{\rho}_i$ is the mean restricted correlation among variables, $\bar{\rho}_a$ is the mean unrestricted correlation among variables, and k is the number of variables in the composite.

Value

The estimated u ratio of the composite variable.

Examples

```
composite_u_scalar(mean_ri = .3, mean_ra = .4, mean_u = .8, k_vars = 2)
```

compute_alpha	<i>Compute coefficient alpha</i>
---------------	----------------------------------

Description

Compute coefficient alpha

Usage

```
compute_alpha(sigma = NULL, data = NULL, standardized = FALSE, ...)
```

Arguments

sigma	Covariance matrix (must be supplied if data argument is not supplied)
data	Data matrix or data frame (must be supplied if sigma argument is not supplied)
standardized	Logical scalar determining whether alpha should be computed from an unstandardized covariance matrix (TRUE) or a correlation matrix (FALSE).
...	Additional arguments to be passed to cov() function.

Value

Coefficient alpha

Examples

```
compute_alpha(sigma = reshape_vec2mat(cov = .4, order = 10))
```

compute_dmod

Comprehensive d_{Mod} calculator

Description

This is a general-purpose function to compute d_{Mod} effect sizes from raw data and to perform bootstrapping. It subsumes the functionalities of the `compute_dmod_par` (for parametric computations) and `compute_dmod_npar` (for non-parametric computations) functions and automates the generation of regression equations and descriptive statistics for computing d_{Mod} effect sizes. Please see documentation for `compute_dmod_par` and `compute_dmod_npar` for details about how the effect sizes are computed.

Usage

```
compute_dmod(data, group, predictors, criterion, referent_id,
  focal_id_vec = NULL, conf_level = 0.95, rescale_cdf = TRUE,
  parametric = TRUE, bootstrap = TRUE, boot_iter = 1000,
  stratify = FALSE, empirical_ci = FALSE, cross_validate_wts = FALSE)
```

Arguments

- | | |
|------------|--|
| data | Data frame containing the data to be analyzed (if not a data frame, must be an object convertible to a data frame via the <code>as.data.frame</code> function). The data set must contain a criterion variable, at least one predictor variable, and a categorical variable that identifies the group to which each case (i.e., row) in the data set belongs. |
| group | Name or column-index number of the variable that identifies group membership in the data set. |
| predictors | Name(s) or column-index number(s) of the predictor variable(s) in the data set. No predictor can be a factor-type variable. If multiple predictors are specified, they will be combined into a regression-weighted composite that will be carried forward to compute d_{Mod} effect sizes. <ul style="list-style-type: none"> • <i>Note:</i> If weights other than regression weights should be used to combine the predictors into a composite, the user must manually compute such a composite, include the composite in the <code>dat</code> data set, and identify the composite variable in <code>predictors</code>. |
| criterion | Name or column-index number of the criterion variable in the data set. The criterion cannot be a factor-type variable. |

referent_id	Label used to identify the referent group in the group variable.
focal_id_vec	Label(s) to identify the focal group(s) in the group variable. If NULL (the default), the specified referent group will be compared to all other groups.
conf_level	Confidence level (between 0 and 1) to be used in generating confidence intervals. Default is .95
rescale_cdf	Logical argument that indicates whether parametric d_{Mod} results should be rescaled to account for using a cumulative density < 1 in the computations (TRUE; default) or not (FALSE).
parametric	Logical argument that indicates whether d_{Mod} should be computed using an assumed normal distribution (TRUE; default) or observed frequencies (FALSE).
bootstrap	Logical argument that indicates whether d_{Mod} should be bootstrapped (TRUE; default) or not (FALSE).
boot_iter	Number of bootstrap iterations to compute (default = 1000).
stratify	Logical argument that indicates whether the random bootstrap sampling should be stratified (TRUE) or unstratified (FALSE; default).
empirical_ci	Logical argument that indicates whether the bootstrapped confidence intervals should be computed from the observed empirical distributions (TRUE) or computed using bootstrapped means and standard errors via the normal-theory approach (FALSE).
cross_validate_wts	Only relevant when multiple predictors are specified and bootstrapping is performed. Logical argument that indicates whether regression weights derived from the full sample should be used to combine predictors in the bootstrapped samples (TRUE) or if a new set of weights should be derived during each iteration of the bootstrapping procedure (FALSE; default).

Value

If bootstrapping is selected, the list will include:

- `point_estimate` A matrix of effect sizes ($d_{ModSigned}$, $d_{ModUnsigned}$, $d_{ModUnder}$, $d_{ModOver}$), proportions of under- and over-predicted criterion scores, minimum and maximum differences, and the scores associated with minimum and maximum differences. All of these values are computed using the full data set.
- `bootstrap_mean` A matrix of the same statistics as the `point_estimate` matrix, but the values in this matrix are the means of the results from bootstrapped samples.
- `bootstrap_se` A matrix of the same statistics as the `point_estimate` matrix, but the values in this matrix are bootstrapped standard errors (i.e., the standard deviations of the results from bootstrapped samples).
- `bootstrap_CI_Lo` A matrix of the same statistics as the `point_estimate` matrix, but the values in this matrix are the lower confidence bounds of the results from bootstrapped samples.
- `bootstrap_CI_Hi` A matrix of the same statistics as the `point_estimate` matrix, but the values in this matrix are the upper confidence bounds of the results from bootstrapped samples.

If no bootstrapping is performed, the output will be limited to the `point_estimate` matrix.

References

Nye, C. D., & Sackett, P. R. (2016). New effect sizes for tests of categorical moderation and differential prediction. *Organizational Research Methods*, <https://doi.org/10.1177/1094428116644505>.

Examples

```
# Generate some hypothetical data for a referent group and three focal groups:
set.seed(10)
refDat <- MASS::mvrnorm(n = 1000, mu = c(.5, .2),
  Sigma = matrix(c(1, .5, .5, 1), 2, 2), empirical = TRUE)
foc1Dat <- MASS::mvrnorm(n = 1000, mu = c(-.5, -.2),
  Sigma = matrix(c(1, .5, .5, 1), 2, 2), empirical = TRUE)
foc2Dat <- MASS::mvrnorm(n = 1000, mu = c(0, 0),
  Sigma = matrix(c(1, .3, .3, 1), 2, 2), empirical = TRUE)
foc3Dat <- MASS::mvrnorm(n = 1000, mu = c(-.5, -.2),
  Sigma = matrix(c(1, .3, .3, 1), 2, 2), empirical = TRUE)
colnames(refDat) <- colnames(foc1Dat) <- colnames(foc2Dat) <- colnames(foc3Dat) <- c("X", "Y")
dat <- rbind(cbind(G = 1, refDat), cbind(G = 2, foc1Dat),
  cbind(G = 3, foc2Dat), cbind(G = 4, foc3Dat))

# Compute point estimates of parametric d_mod effect sizes:
compute_dmod(data = dat, group = "G", predictors = "X", criterion = "Y",
  referent_id = 1, focal_id_vec = 2:4,
  conf_level = .95, rescale_cdf = TRUE, parametric = TRUE,
  bootstrap = FALSE)

# Compute point estimates of non-parametric d_mod effect sizes:
compute_dmod(data = dat, group = "G", predictors = "X", criterion = "Y",
  referent_id = 1, focal_id_vec = 2:4,
  conf_level = .95, rescale_cdf = TRUE, parametric = FALSE,
  bootstrap = FALSE)

# Compute unstratified bootstrapped estimates of parametric d_mod effect sizes:
compute_dmod(data = dat, group = "G", predictors = "X", criterion = "Y",
  referent_id = 1, focal_id_vec = 2:4,
  conf_level = .95, rescale_cdf = TRUE, parametric = TRUE,
  boot_iter = 10, bootstrap = TRUE, stratify = FALSE, empirical_ci = FALSE)

# Compute unstratified bootstrapped estimates of non-parametric d_mod effect sizes:
compute_dmod(data = dat, group = "G", predictors = "X", criterion = "Y",
  referent_id = 1, focal_id_vec = 2:4,
  conf_level = .95, rescale_cdf = TRUE, parametric = FALSE,
  boot_iter = 10, bootstrap = TRUE, stratify = FALSE, empirical_ci = FALSE)
```

compute_dmod_npar

Function for computing non-parametric d_Mod effect sizes for a single focal group

Description

This function computes non-parametric d_{Mod} effect sizes from user-defined descriptive statistics and regression coefficients, using a distribution of observed scores as weights. This non-parametric function is best used when the assumption of normally distributed predictor scores is not reasonable and/or the distribution of scores observed in a sample is likely to represent the distribution of scores in the population of interest. If one has access to the full raw data set, the `dMod` function may be used as a wrapper to this function so that the regression equations and descriptive statistics can be computed automatically within the program.

Usage

```
compute_dmod_npar(referent_int, referent_slope, focal_int, focal_slope,
  focal_x, referent_sd_y)
```

Arguments

`referent_int` Referent group's intercept.
`referent_slope` Referent group's slope.
`focal_int` Focal group's intercept.
`focal_slope` Focal group's slope.
`focal_x` Focal group's vector of predictor scores.
`referent_sd_y` Referent group's criterion standard deviation.

Details

The $d_{Mod_{Signed}}$ effect size (i.e., the average of differences in prediction over the range of predictor scores) is computed as

$$d_{Mod_{Signed}} = \frac{\sum_{i=1}^m n_i [X_i (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}]}{SD_{Y_1} \sum_{i=1}^m n_i},$$

where

- SD_{Y_1} is the referent group's criterion standard deviation;
- m is the number of unique scores in the distribution of focal-group predictor scores;
- X is the vector of unique focal-group predictor scores, indexed $i = 1$ through m ;
- X_i is the i^{th} unique score value;
- n is the vector of frequencies associated with the elements of X ;
- n_i is the number of cases with a score equal to X_i ;
- b_{1_1} and b_{1_2} are the slopes of the regression of Y on X for the referent and focal groups, respectively; and
- b_{0_1} and b_{0_2} are the intercepts of the regression of Y on X for the referent and focal groups, respectively.

The $d_{ModUnder}$ and $d_{ModOver}$ effect sizes are computed using the same equation as $d_{ModSigned}$, but $d_{ModUnder}$ is the weighted average of all scores in the area of underprediction (i.e., the differences in prediction with negative signs) and $d_{ModOver}$ is the weighted average of all scores in the area of overprediction (i.e., the differences in prediction with positive signs).

The $d_{ModUnsigned}$ effect size (i.e., the average of absolute differences in prediction over the range of predictor scores) is computed as

$$d_{ModUnsigned} = \frac{\sum_{i=1}^m n_i |X_i (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}|}{SD_{Y_1} \sum_{i=1}^m n_i}.$$

The d_{Min} effect size (i.e., the smallest absolute difference in prediction observed over the range of predictor scores) is computed as

$$d_{Min} = \frac{1}{SD_{Y_1}} \text{Min} [|X (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}|].$$

The d_{Max} effect size (i.e., the largest absolute difference in prediction observed over the range of predictor scores) is computed as

$$d_{Max} = \frac{1}{SD_{Y_1}} \text{Max} [|X (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}|].$$

Note: When d_{Min} and d_{Max} are computed in this package, the output will display the signs of the differences (rather than the absolute values of the differences) to aid in interpretation.

Value

A vector of effect sizes ($d_{ModSigned}$, $d_{ModUnsigned}$, $d_{ModUnder}$, $d_{ModOver}$), proportions of under- and over-predicted criterion scores, minimum and maximum differences (i.e., $d_{ModUnder}$ and $d_{ModOver}$), and the scores associated with minimum and maximum differences.

Examples

```
# Generate some hypothetical data for a referent group and three focal groups:
set.seed(10)
refDat <- MASS::mvrnorm(n = 1000, mu = c(.5, .2),
  Sigma = matrix(c(1, .5, .5, 1), 2, 2), empirical = TRUE)
foc1Dat <- MASS::mvrnorm(n = 1000, mu = c(-.5, -.2),
  Sigma = matrix(c(1, .5, .5, 1), 2, 2), empirical = TRUE)
foc2Dat <- MASS::mvrnorm(n = 1000, mu = c(0, 0),
  Sigma = matrix(c(1, .3, .3, 1), 2, 2), empirical = TRUE)
foc3Dat <- MASS::mvrnorm(n = 1000, mu = c(-.5, -.2),
  Sigma = matrix(c(1, .3, .3, 1), 2, 2), empirical = TRUE)
colnames(refDat) <- colnames(foc1Dat) <- colnames(foc2Dat) <- colnames(foc3Dat) <- c("X", "Y")

# Compute a regression model for each group:
refRegMod <- lm(Y ~ X, data.frame(refDat))$coef
foc1RegMod <- lm(Y ~ X, data.frame(foc1Dat))$coef
foc2RegMod <- lm(Y ~ X, data.frame(foc2Dat))$coef
foc3RegMod <- lm(Y ~ X, data.frame(foc3Dat))$coef
```

```

# Use the subgroup regression models to compute d_mod for each referent-focal pairing:

# Focal group #1:
compute_dmod_npar(referent_int = refRegMod[1], referent_slope = refRegMod[2],
                  focal_int = foc1RegMod[1], focal_slope = foc1RegMod[2],
                  focal_x = foc1Dat[, "X"], referent_sd_y = 1)

# Focal group #2:
compute_dmod_npar(referent_int = refRegMod[1], referent_slope = refRegMod[2],
                  focal_int = foc2RegMod[1], focal_slope = foc2RegMod[2],
                  focal_x = foc2Dat[, "X"], referent_sd_y = 1)

# Focal group #3:
compute_dmod_npar(referent_int = refRegMod[1], referent_slope = refRegMod[2],
                  focal_int = foc3RegMod[1], focal_slope = foc3RegMod[2],
                  focal_x = foc3Dat[, "X"], referent_sd_y = 1)

```

compute_dmod_par	<i>Function for computing parametric d_{Mod} effect sizes for any number of focal groups</i>
------------------	---

Description

This function computes d_{Mod} effect sizes from user-defined descriptive statistics and regression coefficients. If one has access to a raw data set, the dMod function may be used as a wrapper to this function so that the regression equations and descriptive statistics can be computed automatically within the program.

Usage

```

compute_dmod_par(referent_int, referent_slope, focal_int, focal_slope,
                 focal_mean_x, focal_sd_x, referent_sd_y, focal_min_x, focal_max_x,
                 focal_names = NULL, rescale_cdf = TRUE)

```

Arguments

referent_int	Referent group's intercept.
referent_slope	Referent group's slope.
focal_int	Focal groups' intercepts.
focal_slope	Focal groups' slopes.
focal_mean_x	Focal groups' predictor-score means.
focal_sd_x	Focal groups' predictor-score standard deviations.
referent_sd_y	Referent group's criterion standard deviation.
focal_min_x	Focal groups' minimum predictor scores.
focal_max_x	Focal groups' maximum predictor scores.

focal_names	Focal-group names. If NULL (the default), the focal groups will be given numeric labels ranging from 1 through the number of groups.
rescale_cdf	Logical argument that indicates whether parametric d_{Mod} results should be rescaled to account for using a cumulative density < 1 in the computations (TRUE; default) or not (FALSE).

Details

The $d_{ModSigned}$ effect size (i.e., the average of differences in prediction over the range of predictor scores) is computed as

$$d_{ModSigned} = \frac{1}{SD_{Y_1}} \int f_2(X) [X (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}] dX,$$

where

- SD_{Y_1} is the referent group's criterion standard deviation;
- $f_2(X)$ is the normal-density function for the distribution of focal-group predictor scores;
- b_{1_1} and b_{1_0} are the slopes of the regression of Y on X for the referent and focal groups, respectively;
- b_{0_1} and b_{0_0} are the intercepts of the regression of Y on X for the referent and focal groups, respectively; and
- the integral spans all X scores within the operational range of predictor scores for the focal group.

The $d_{ModUnder}$ and $d_{ModOver}$ effect sizes are computed using the same equation as $d_{ModSigned}$, but $d_{ModUnder}$ is the weighted average of all scores in the area of underprediction (i.e., the differences in prediction with negative signs) and $d_{ModOver}$ is the weighted average of all scores in the area of overprediction (i.e., the differences in prediction with positive signs).

The $d_{ModUnsigned}$ effect size (i.e., the average of absolute differences in prediction over the range of predictor scores) is computed as

$$d_{ModUnsigned} = \frac{1}{SD_{Y_1}} \int f_2(X) |X (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}| dX.$$

The d_{Min} effect size (i.e., the smallest absolute difference in prediction observed over the range of predictor scores) is computed as

$$d_{Min} = \frac{1}{SD_{Y_1}} \text{Min} [|X (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}|].$$

The d_{Max} effect size (i.e., the largest absolute difference in prediction observed over the range of predictor scores) is computed as

$$d_{Max} = \frac{1}{SD_{Y_1}} \text{Max} [|X (b_{1_1} - b_{1_2}) + b_{0_1} - b_{0_2}|].$$

Note: When d_{Min} and d_{Max} are computed in this package, the output will display the signs of the differences (rather than the absolute values of the differences) to aid in interpretation.

If d_{Mod} effect sizes are to be rescaled to compensate for a cumulative density less than 1 (see the `rescale_cdf` argument), the result of each effect size involving integration will be divided by the ratio of the cumulative density of the observed range of scores (i.e., the range bounded by the `focal_min_x` and `focal_max_x` arguments) to the cumulative density of scores bounded by `-Inf` and `Inf`.

Value

A matrix of effect sizes ($d_{ModSigned}$, $d_{ModUnsigned}$, $d_{ModUnder}$, $d_{ModOver}$), proportions of under- and over-predicted criterion scores, minimum and maximum differences (i.e., $d_{ModUnder}$ and $d_{ModOver}$), and the scores associated with minimum and maximum differences. Note that if the regression lines are parallel and infinite `focal_min_x` and `focal_max_x` values were specified, the extrema will be defined using the scores 3 focal-group SDs above and below the corresponding focal-group means.

References

Nye, C. D., & Sackett, P. R. (2016). New effect sizes for tests of categorical moderation and differential prediction. *Organizational Research Methods*, <https://doi.org/10.1177/1094428116644505>.

Examples

```
compute_dmod_par(referent_int = -.05, referent_slope = .5,
                 focal_int = c(.05, 0, -.05), focal_slope = c(.5, .3, .3),
                 focal_mean_x = c(-.5, 0, -.5), focal_sd_x = rep(1, 3),
                 referent_sd_y = 1,
                 focal_min_x = rep(-Inf, 3), focal_max_x = rep(Inf, 3),
                 focal_names = NULL, rescale_cdf = TRUE)
```

confidence

Construct a confidence interval

Description

Function to construct a confidence interval around an effect size or mean effect size.

Usage

```
confidence(mean, se = NULL, df = NULL, conf_level = 0.95,
           conf_method = c("t", "norm"), ...)
```

Arguments

<code>mean</code>	Mean effect size (if used in a meta-analysis) or observed effect size (if used on individual statistics).
<code>se</code>	Standard error of the statistic.
<code>df</code>	Degrees of freedom of the statistic (necessary if using the t distribution).
<code>conf_level</code>	Confidence level that defines the width of the confidence interval (default = .95).

conf_method Distribution to be used to compute the width of confidence intervals. Available options are "t" for t distribution or "norm" for normal distribution.

... Additional arguments

Details

$$CI = mean_{es} \pm quantile \times SE_{es}$$

Value

A matrix of confidence intervals of the specified width.

Examples

```
confidence(mean = c(.3, .5), se = c(.15, .2), df = c(100, 200), conf_level = .95, conf_method = "t")
confidence(mean = c(.3, .5), se = c(.15, .2), conf_level = .95, conf_method = "norm")
```

confidence_r	<i>Construct a confidence interval for correlations using Fisher's z transformation</i>
--------------	---

Description

Construct a confidence interval for correlations using Fisher's z transformation

Usage

```
confidence_r(r, n, conf_level = 0.95)
```

Arguments

r A vector of correlations

n A vector of sample sizes

conf_level Confidence level that defines the width of the confidence interval (default = .95).

Value

A confidence interval of the specified width (or matrix of confidence intervals)

Examples

```
confidence_r(r = .3, n = 200, conf_level = .95)
```

confint	<i>Confidence interval method for objects of classes deriving from "lm_mat"</i>
---------	---

Description

Confidence interval method for objects of classes deriving from "lm_mat." Returns lower and upper bounds of confidence intervals for regression coefficients.

Arguments

object	Matrix regression object.
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	Confidence level
...	further arguments passed to or from other methods.

control_intercor	<i>Control function to curate intercorrelations to be used in automatic compositing routine</i>
------------------	---

Description

Control function to curate intercorrelations to be used in automatic compositing routine

Usage

```
control_intercor(rxyi = NULL, n = NULL, sample_id = NULL,
  construct_x = NULL, construct_y = NULL, construct_names = NULL,
  facet_x = NULL, facet_y = NULL, intercor_vec = NULL,
  intercor_scalar = 0.5, dx = NULL, dy = NULL, p = 0.5,
  partial_intercor = FALSE, data = NULL, ...)
```

Arguments

rxyi	Vector or column name of observed correlations.
n	Vector or column name of sample sizes.
sample_id	Vector of identification labels for samples/studies in the meta-analysis.
construct_x, construct_y	Vector of construct names for constructs designated as "X" or "Y".
construct_names	Vector of all construct names to be included in the meta-analysis.

facet_x, facet_y	Vector of facet names for constructs designated as "X" or "Y".
intercor_vec	Named vector of pre-specified intercorrelations among measures of constructs in the meta-analysis.
intercor_scalar	Generic scalar intercorrelation that can stand in for unobserved or unspecified values.
dx, dy	d values corresponding to construct_x and construct_y. These values only need to be supplied for cases in which rxyi represents a correlation between two measures of the same construct.
p	Scalar or vector containing the proportions of group membership corresponding to the d values.
partial_intercor	For meta-analyses of d values only: Logical scalar, vector, or column corresponding to values in rxyi that determines whether the correlations are to be treated as within-group correlations (i.e., partial correlation controlling for group membership; TRUE) or not (FALSE; default). Note that this only converts correlation values from the rxyi argument - any values provided in the intercor_vec or intercor_scalar arguments must be total correlations or converted to total correlations using the mix_r_2group() function prior to running control_intercor.
data	Data frame containing columns whose names may be provided as arguments to vector arguments.
...	Further arguments to be passed to functions called within the meta-analysis.

Value

A vector of intercorrelations

Examples

```
## Create a dataset in which constructs correlate with themselves
rxyi <- seq(.1, .5, length.out = 27)
construct_x <- rep(rep(c("X", "Y", "Z"), 3), 3)
construct_y <- c(rep("X", 9), rep("Y", 9), rep("Z", 9))
dat <- data.frame(rxyi = rxyi,
                  construct_x = construct_x,
                  construct_y = construct_y)
dat <- rbind(cbind(sample_id = "Sample 1", dat),
            cbind(sample_id = "Sample 2", dat),
            cbind(sample_id = "Sample 3", dat))

## Identify some constructs for which intercorrelations are not
## represented in the data object:
construct_names = c("U", "V", "W")

## Specify some externally determined intercorrelations among measures:
intercor_vec <- c(W = .4, X = .1)
```

```
## Specify a generic scalar intercorrelation that can stand in for missing values:
intercor_scalar <- .5

control_intercor(rxyi = rxyi, sample_id = sample_id,
                construct_x = construct_x, construct_y = construct_y,
                construct_names = construct_names,
                intercor_vec = intercor_vec, intercor_scalar = intercor_scalar, data = dat)
```

control_psychmeta *Control for psychmeta meta-analyses*

Description

Control for **psychmeta** meta-analyses

Usage

```
control_psychmeta(error_type = c("mean", "sample"), conf_level = 0.95,
                 cred_level = 0.8, conf_method = c("t", "norm"),
                 cred_method = c("t", "norm"), var_unbiased = TRUE,
                 pairwise_ads = FALSE, moderated_ads = FALSE, residual_ads = TRUE,
                 check_dependence = TRUE, collapse_method = c("composite", "average",
                 "stop"), intercor = control_intercor(), clean_artifacts = TRUE,
                 impute_artifacts = TRUE, impute_method = c("bootstrap_mod",
                 "bootstrap_full", "simulate_mod", "simulate_full", "wt_mean_mod",
                 "wt_mean_full", "unwt_mean_mod", "unwt_mean_full", "replace_unity",
                 "stop"), seed = 42, use_all_arts = TRUE, estimate_pa = FALSE,
                 decimals = 2, hs_override = FALSE, ...)
```

Arguments

error_type	Method to be used to estimate error variances: "mean" uses the mean effect size to estimate error variances and "sample" uses the sample-specific effect sizes.
conf_level	Confidence level to define the width of the confidence interval (default = .95).
cred_level	Credibility level to define the width of the credibility interval (default = .80).
conf_method	Distribution to be used to compute the width of confidence intervals. Available options are "t" for <i>t</i> distribution or "norm" for normal distribution.
cred_method	Distribution to be used to compute the width of credibility intervals. Available options are "t" for <i>t</i> distribution or "norm" for normal distribution.
var_unbiased	Logical scalar determining whether variances should be unbiased (TRUE) or maximum-likelihood (FALSE).
pairwise_ads	Logical value that determines whether to compute artifact distributions in a construct-pair-wise fashion (TRUE) or separately by construct (FALSE, default).
moderated_ads	Logical value that determines whether to compute artifact distributions separately for each moderator combination (TRUE) or for overall analyses only (FALSE, default).

- `residual_ads` Logical argument that determines whether to use residualized variances (TRUE) or observed variances (FALSE) of artifact distributions to estimate `sd_rho`.
- `check_dependence` Logical scalar that determines whether database should be checked for violations of independence (TRUE) or not (FALSE).
- `collapse_method` Character argument that determines how to collapse dependent studies. Options are "composite" (default), "average," and "stop."
- `intercor` The intercorrelation(s) among variables to be combined into a composite. Can be a scalar, a named vector with element named according to the names of constructs, or output from the `control_intercor` function. Default scalar value is .5.
- `clean_artifacts` If TRUE, multiple instances of the same construct (or construct-measure pair, if measure is provided) in the database are compared and reconciled with each other in the case that any of the matching entries within a study have different artifact values. When `impute_method` is anything other than "stop", this method is always implemented to prevent discrepancies among imputed values.
- `impute_artifacts` If TRUE, artifact imputation will be performed (see `impute_method` for imputation procedures). Default is FALSE for artifact-distribution meta-analyses and TRUE otherwise. When imputation is performed, `clean_artifacts` is treated as TRUE so as to resolve all discrepancies among artifact entries before and after imputation.
- `impute_method` Method to use for imputing artifacts. Choices are:
- `bootstrap_mod`
Select random values from the most specific moderator categories available (default).
 - `bootstrap_full`
Select random values from the full vector of artifacts.
 - `simulate_mod`
Generate random values from the distribution with the mean and variance of observed artifacts from the most specific moderator categories available. (uses `rnorm` for u ratios and `rbeta` for reliability values).
 - `simulate_full`
Generate random values from the distribution with the mean and variance of all observed artifacts (uses `rnorm` for u ratios and `rbeta` for reliability values).
 - `wt_mean_mod`
Replace missing values with the sample-size weighted mean of the distribution of artifacts from the most specific moderator categories available (not recommended).
 - `wt_mean_full`
Replace missing values with the sample-size weighted mean of the full distribution of artifacts (not recommended).

- unwt_mean_mod
Replace missing values with the unweighted mean of the distribution of artifacts from the most specific moderator categories available (not recommended).
- unwt_mean_full
Replace missing values with the unweighted mean of the full distribution of artifacts (not recommended).
- replace_unity
Replace missing values with 1 (not recommended).
- stop
Stop evaluations when missing artifacts are encountered.

If an imputation method ending in "mod" is selected but no moderators are provided, the "mod" suffix will internally be replaced with "full".

seed	Seed value to use for imputing artifacts in a reproducible way. Default value is 42.
use_all_arts	Logical scalar that determines whether artifact values from studies without valid effect sizes should be used in artifact distributions (TRUE; default) or not (FALSE).
estimate_pa	Logical scalar that determines whether the unrestricted subgroup proportions associated with univariate-range-restricted effect sizes should be estimated by rescaling the range-restricted subgroup proportions as a function of the range-restriction correction (TRUE) or not (FALSE; default).
decimals	Number of decimal places to which interactive artifact distributions should be rounded (default is 2 decimal places).
hs_override	When TRUE, this will override settings for wt_type (will set to "sample_size"), error_type (will set to "mean"), correct_bias (will set to TRUE), conf_method (will set to "norm"), cred_method (will set to "norm"), var_unbiased (will set to FALSE), residual_ads (will be set to FALSE), and use_all_arts (will set to FALSE).
...	Further arguments to be passed to functions called within the meta-analysis.

Value

A list of control arguments in the package environment.

Examples

```
control_psychmeta()
```

 convert_es

Convert effect sizes and compute confidence intervals

Description

This function converts a variety of effect sizes to either correlations or Cohen's d values. The function also computes and prints confidence intervals for the output effect sizes.

Usage

```
convert_es(es, input_es = c("r", "d", "delta", "g", "t", "p.t", "F",
  "p.F", "chisq", "p.chisq", "or", "lor", "Fisherz", "A", "auc", "cles"),
  output_es = c("r", "d", "A", "auc", "cles"), n1 = NULL, n2 = NULL,
  df1 = NULL, df2 = NULL, sd1 = NULL, sd2 = NULL,
  correct_bias = TRUE, conf_level = 0.95)
```

Arguments

es	Vector of effect sizes to convert.
input_es	Metric of input effect sizes. Currently supports correlations, Cohen's <i>d</i> , independent samples <i>t</i> values (or their <i>p</i> values), two-group one-way ANOVA <i>F</i> values (or their <i>p</i> values), 1df χ^2 values (or their <i>p</i> values), odds ratios, log odds ratios, Fisher <i>z</i> , and the common language effect size (CLES, A, AUC).
output_es	Metric of output effect sizes. Currently supports correlations, Cohen's <i>d</i> values, and common language effect sizes (CLES, A, AUC).
n1	Vector of total sample sizes or sample sizes of group 1 of the two groups being contrasted.
n2	Vector of sample sizes of group 2 of the two groups being contrasted.
df1	Vector of input test statistic degrees of freedom (for <i>t</i> and χ^2) or between-groups degree of freedom (for <i>F</i>).
df2	Vector of input test statistic within-group degrees of freedom (for <i>F</i>).
sd1	Vector of pooled (within-group) standard deviations or standard deviations of group 1 of the two groups being contrasted.
sd2	Vector of standard deviations of group 2 of the two groups being contrasted.
correct_bias	Logical argument that determines whether to correct output effect sizes and error-variance estimates for small-sample bias (TRUE) or not (FALSE) when computing confidence intervals.
conf_level	Confidence level that defines the width of the confidence interval (default = .95).

Value

A **psychmeta** effect size es object containing:

meta_input	A matrix of converted effect sizes and adjusted sample sizes for use in subsequent meta-analyses.
original_es	The input data.
confidence	The output data with computed confidence intervals (for printing).

Notes

To use converted effect sizes in a meta-analysis, add the values from `es$meta_input` to your meta-analytic input data frame.

References

- Chinn, S. (2000). A simple method for converting an odds ratio to effect size for use in meta-analysis. *Statistics in Medicine*, *19*(22), 3127–3131. <https://doi.org/10/c757hm>
- Lipsey, M. W., & Wilson, D. B. (2001). *Practical meta-analysis*. Thousand Oaks, CA: SAGE.
- Ruscio, J. (2008). A probability-based measure of effect size: Robustness to base rates and other factors. *Psychological Methods*, *13*(1), 19–30. <https://doi.org/10.1037/1082-989X.13.1.19>
- Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>

Examples

```
## To convert a statistic to r or d metric:
convert_es(es = 1, input_es="d", output_es="r", n1=100)
convert_es(es = 1, input_es="d", output_es="r", n1=50, n2 = 50)
convert_es(es = .2, input_es="r", output_es="d", n1=100, n2=150)
convert_es(es = -1.3, input_es="t", output_es="r", n1 = 100, n2 = 140)
convert_es(es = 10.3, input_es="F", output_es="d", n1 = 100, n2 = 150)
convert_es(es = 1.3, input_es="chisq", output_es="r", n1 = 100, n2 = 100)
convert_es(es = .021, input_es="p.chisq", output_es="d", n1 = 100, n2 = 100)
convert_es(es = 4.37, input_es="or", output_es="r", n1=100, n2=100)
convert_es(es = 4.37, input_es="or", output_es="d", n1=100, n2=100)
convert_es(es = 1.47, input_es="lor", output_es="r", n1=100, n2=100)
convert_es(es = 1.47, input_es="lor", output_es="d", n1=100, n2=100)

## To simply compute a confidence interval for r, d, or A:
convert_es(es = .3, input_es="r", output_es="r", n1=100)
convert_es(es = .8, input_es="d", output_es="d", n1=64, n2=36)
convert_es(es = .8, input_es="A", output_es="A", n1=64, n2=36)
```

convert_ma

Function to convert meta-analysis of correlations to d values or vice-versa

Description

Takes a meta-analysis class object of *d* values or correlations (classes *r_as_r*, *d_as_d*, *r_as_d*, and *d_as_r*; second-order meta-analyses are currently not supported) as an input and uses conversion formulas and Taylor series approximations to convert effect sizes and variance estimates, respectively.

Usage

```
convert_ma(ma_obj, ...)
```

```
convert_meta(ma_obj, ...)
```

Arguments

ma_obj A meta-analysis object of class r_as_r, d_as_d, r_as_d, or d_as_r
 ... Additional arguments.

Details

The formula used to convert correlations to d values is:

$$d = \frac{r \sqrt{\frac{1}{p(1-p)}}}{\sqrt{1-r^2}}$$

The formula used to convert d values to correlations is:

$$r = \frac{d}{\sqrt{d^2 + \frac{1}{p(1-p)}}}$$

To approximate the variance of correlations from the variance of d values, the function computes:

$$\text{var}_r \approx a_d^2 \text{var}_d$$

where a_d is the first partial derivative of the d -to- r transformation with respect to d :

$$a_d = -\frac{1}{[d^2 p(1-p) - 1] \sqrt{d^2 + \frac{1}{p-p^2}}}$$

To approximate the variance of d values from the variance of correlations, the function computes:

$$\text{var}_d \approx a_r^2 \text{var}_r$$

where a_r is the first partial derivative of the r -to- d transformation with respect to r :

$$a_r = \frac{\sqrt{\frac{1}{p-p^2}}}{(1-r^2)^{1.5}}$$

Value

A meta-analysis converted to the d value metric (if ma_obj was a meta-analysis in the correlation metric) or converted to the correlation metric (if ma_obj was a meta-analysis in the d value metric).

correct_d	<i>Correct d values for range restriction and/or measurement error</i>
-----------	--

Description

This function is a wrapper for the [correct_r](#) function to correct d values for statistical and psychometric artifacts.

Usage

```
correct_d(correction = c("meas", "uvdrr_g", "uvdrr_y", "uvirr_g",
  "uvirr_y", "bvdr", "bvirr"), d, ryy = 1, uy = 1, rGg = 1,
  pi = NULL, pa = NULL, uy_observed = TRUE, ryy_restricted = TRUE,
  ryy_type = "alpha", k_items_y = NA, sign_rgz = 1, sign_ryz = 1,
  n1 = NULL, n2 = NA, conf_level = 0.95, correct_bias = FALSE)
```

Arguments

correction	Type of correction to be applied. Options are "meas", "uvdrr_g", "uvdrr_y", "uvirr_g", "uvirr_y", "bvdr", "bvirr"
d	Vector of d values.
ryy	Vector of reliability coefficients for Y (the continuous variable).
uy	Vector of u ratios for Y (the continuous variable).
rGg	Vector of reliabilities for the group variable (i.e., the correlations between observed group membership and latent group membership).
pi	Proportion of cases in one of the groups in the observed data (not necessary if n1 and n2 reflect this proportionality).
pa	Proportion of cases in one of the groups in the population.
uy_observed	Logical vector in which each entry specifies whether the corresponding uy value is an observed-score u ratio (TRUE) or a true-score u ratio. All entries are TRUE by default.
ryy_restricted	Logical vector in which each entry specifies whether the corresponding rxx value is an incumbent reliability (TRUE) or an applicant reliability. All entries are TRUE by default.
ryy_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for ma_r for a full list of acceptable reliability types.
k_items_y	Numeric vector identifying the number of items in each scale.
sign_rgz	Vector of signs of the relationships between grouping variables and the selection mechanism.
sign_ryz	Vector of signs of the relationships between Y variables and the selection mechanism.

n1	Optional vector of sample sizes associated with group 1 (or the total sample size, if n2 is NULL).
n2	Optional vector of sample sizes associated with group 2.
conf_level	Confidence level to define the width of the confidence interval (default = .95).
correct_bias	Logical argument that determines whether to correct error-variance estimates for small-sample bias in correlations (TRUE) or not (FALSE). For sporadic corrections (e.g., in mixed artifact-distribution meta-analyses), this should be set to FALSE (the default).

Value

Data frame(s) of observed d values (dgyi), operational range-restricted d values corrected for measurement error in Y only (dgpi), operational range-restricted d values corrected for measurement error in the grouping only (dGyi), and range-restricted true-score d values (dGpi), range-corrected observed-score d values (dgya), operational range-corrected d values corrected for measurement error in Y only (dgpa), operational range-corrected d values corrected for measurement error in the grouping only (dGya), and range-corrected true-score d values (dGpa).

References

- Alexander, R. A., Carson, K. P., Alliger, G. M., & Carr, L. (1987). Correcting doubly truncated correlations: An improved approximation for correcting the bivariate normal correlation when truncation has occurred on both variables. *Educational and Psychological Measurement*, 47(2), 309–315. <https://doi.org/10.1177/0013164487472002>
- Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.
- Hunter, J. E., Schmidt, F. L., & Le, H. (2006). Implications of direct and indirect range restriction for meta-analysis methods and findings. *Journal of Applied Psychology*, 91(3), 594–612. <https://doi.org/10.1037/0021-9010.91.3.594>
- Le, H., Oh, I.-S., Schmidt, F. L., & Wooldridge, C. D. (2016). Correction for range restriction in meta-analysis revisited: Improvements and implications for organizational research. *Personnel Psychology*, 69(4), 975–1008. <https://doi.org/10.1111/peps.12122>
- Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. pp. 43–44, 140–141.

Examples

```
## Correction for measurement error only
correct_d(correction = "meas", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
correct_d(correction = "meas", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

## Correction for direct range restriction in the continuous variable
correct_d(correction = "uvdrr_y", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
```

```

correct_d(correction = "uvdrr_y", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

## Correction for direct range restriction in the grouping variable
correct_d(correction = "uvdrr_g", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
correct_d(correction = "uvdrr_g", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

## Correction for indirect range restriction in the continuous variable
correct_d(correction = "uvdrr_y", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
correct_d(correction = "uvdrr_y", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

## Correction for indirect range restriction in the grouping variable
correct_d(correction = "uvirr_g", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
correct_d(correction = "uvirr_g", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

## Correction for indirect range restriction in the continuous variable
correct_d(correction = "uvdrr_y", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
correct_d(correction = "uvdrr_y", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

## Correction for direct range restriction in both variables
correct_d(correction = "bvdr", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
correct_d(correction = "bvdr", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

## Correction for indirect range restriction in both variables
correct_d(correction = "bvirr", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = .7, pa = .5)
correct_d(correction = "bvirr", d = .5, ryy = .8, uy = .7,
          rGg = .9, pi = NULL, pa = .5, n1 = 100, n2 = 200)

```

correct_d_bias

Correct for small-sample bias in Cohen's d values

Description

Corrects a vector of Cohen's d values for small-sample bias, as Cohen's d has a slight positive bias.

Usage

```
correct_d_bias(d, n)
```

Arguments

d Vector of Cohen's d values.
n Vector of sample sizes.

Details

The bias correction is estimated as:

$$d_c = \frac{d_{obs}}{1 + \frac{.75}{n-3}}$$

where d_{obs} is the observed effect size, d_c is the corrected estimate of d , and n is the total sample size.

Value

Vector of d values corrected for small-sample bias.

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. pp. 293–295.

Examples

```
correct_d_bias(d = .3, n = 30)
correct_d_bias(d = .3, n = 300)
correct_d_bias(d = .3, n = 3000)
```

correct_glass_bias *Correct for small-sample bias in Glass' Δ values*

Description

Correct for small-sample bias in Glass' Δ values

Usage

```
correct_glass_bias(delta, nc, ne, use_pooled_sd = rep(FALSE,
length(delta)))
```

Arguments

delta Vector of Glass' Δ values.
nc Vector of control-group sample sizes.
ne Vector of experimental-group sample sizes.
use_pooled_sd Logical vector determining whether the pooled standard deviation was used (TRUE) or not (FALSE; default).

Details

The bias correction is estimated as:

$$\Delta_c = \Delta_{obs} \frac{\Gamma\left(\frac{n_{control}-1}{2}\right)}{\Gamma\left(\frac{n_{control}-1}{2}\right) \Gamma\left(\frac{n_{control}-2}{2}\right)}$$

where Δ is the observed effect size, Δ_c is the corrected estimate of Δ , and $n_{control}$ is the control-group sample size.

Value

Vector of d values corrected for small-sample bias.

References

Hedges, L. V. (1981). Distribution theory for Glass's estimator of effect size and related estimators. *Journal of Educational Statistics*, 6(2), 107–128. <https://doi.org/10.2307/1164588>

Examples

```
correct_glass_bias(delta = .3, nc = 30, ne = 30)
```

```
correct_matrix_mvrr    Multivariate select/correction for covariance matrices
```

Description

Correct (or select upon) a covariance matrix using the Pearson-Aitken-Lawley multivariate selection theorem.

Usage

```
correct_matrix_mvrr(Sigma_i, Sigma_xx_a, x_col, y_col = NULL,
  standardize = FALSE, var_names = NULL)
```

Arguments

Sigma_i	The complete range-restricted (unrestricted) covariance matrix to be corrected (selected upon).
Sigma_xx_a	The matrix of unrestricted (range-restricted) covariances among of selection variables.
x_col	The row/column indices of the variables in Sigma_i that correspond, in order, to the variables in Sigma_xx_a.
y_col	Optional: The variables in Sigma_i not listed in x_col that are to be manipulated by the multivariate range-restriction formula.
standardize	Should the function's output matrix be returned in standardized form (TRUE) or in unstandardized form (FALSE; the default).
var_names	Optional vector of names for the variables in Sigma_i, in order of appearance in the matrix.

Value

A matrix that has been manipulated by the multivariate range-restriction formula.

References

Aitken, A. C. (1934). Note on selection from a multivariate normal population. *Proceedings of the Edinburgh Mathematical Society (Series 2)*, 4(2), 106–110.

Lawley, D. N. (1943). A note on Karl Pearson's selection formulae. *Proceedings of the Royal Society of Edinburgh. Section A. Mathematical and Physical Sciences*, 62(1), 28–30.

Examples

```
Sigma_i <- reshape_vec2mat(cov = .2, var = .8, order = 4)
Sigma_xx_a <- reshape_vec2mat(cov = .5, order = 2)
correct_matrix_mvrr(Sigma_i = Sigma_i, Sigma_xx_a = Sigma_xx_a, x_col = 1:2, standardize = TRUE)
```

correct_means_mvrr *Multivariate select/correction for vectors of means*

Description

Correct (or select upon) a vector of means using principles from the Pearson-Aitken-Lawley multivariate selection theorem.

Usage

```
correct_means_mvrr(Sigma, means_i = rep(0, ncol(Sigma)), means_x_a,
  x_col, y_col = NULL, var_names = NULL)
```

Arguments

Sigma	The complete covariance matrix to be used to manipulate means: This matrix may be entirely unrestricted or entirely range restricted, as the regression weights estimated from this matrix are expected to be invariant to the effects of selection.
means_i	The complete range-restricted (unrestricted) vector of means to be corrected (selected upon).
means_x_a	The vector of unrestricted (range-restricted) means of selection variables
x_col	The row/column indices of the variables in Sigma that correspond, in order, to the variables in means_x_a
y_col	Optional: The variables in Sigma not listed in x_col that are to be manipulated by the multivariate range-restriction formula.
var_names	Optional vector of names for the variables in Sigma, in order of appearance in the matrix.

Value

A vector of means that has been manipulated by the multivariate range-restriction formula.

References

Aitken, A. C. (1934). Note on selection from a multivariate normal population. *Proceedings of the Edinburgh Mathematical Society (Series 2)*, 4(2), 106–110.

Lawley, D. N. (1943). A note on Karl Pearson's selection formulae. *Proceedings of the Royal Society of Edinburgh. Section A. Mathematical and Physical Sciences*, 62(1), 28–30.

Examples

```
Sigma <- diag(.5, 4)
Sigma[lower.tri(Sigma)] <- c(.2, .3, .4, .3, .4, .4)
Sigma <- Sigma + t(Sigma)
diag(Sigma) <- 1
correct_means_mvrr(Sigma = Sigma, means_i = c(.3, .3, .1, .1),
means_x_a = c(-.1, -.1), x_col = 1:2)
```

correct_r

Correct correlations for range restriction and/or measurement error

Description

Correct correlations for range restriction and/or measurement error

Usage

```
correct_r(correction = c("meas", "uvdrr_x", "uvdrr_y", "uvirr_x",
"uvirr_y", "bvdr", "bvirr"), rxyi, ux = 1, uy = 1, rxx = 1,
ryy = 1, ux_observed = TRUE, uy_observed = TRUE,
rxx_restricted = TRUE, rxx_type = "alpha", k_items_x = NA,
ryy_restricted = TRUE, ryy_type = "alpha", k_items_y = NA,
sign_rxz = 1, sign_ryz = 1, n = NULL, conf_level = 0.95,
correct_bias = FALSE)
```

Arguments

correction	Type of correction to be applied. Options are "meas", "uvdrr_x", "uvdrr_y", "uvirr_x", "uvirr_y", "bvdr", "bvirr"
rxyi	Vector of observed correlations.
ux	Vector of u ratios for X.
uy	Vector of u ratios for Y.
rxx	Vector of reliability coefficients for X.
ryy	Vector of reliability coefficients for Y.

ux_observed	Logical vector in which each entry specifies whether the corresponding ux value is an observed-score u ratio (TRUE) or a true-score u ratio. All entries are TRUE by default.
uy_observed	Logical vector in which each entry specifies whether the corresponding uy value is an observed-score u ratio (TRUE) or a true-score u ratio. All entries are TRUE by default.
rxr_restricted	Logical vector in which each entry specifies whether the corresponding rxr value is an incumbent reliability (TRUE) or an applicant reliability. All entries are TRUE by default.
rxr_type, ryr_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for <code>ma_r</code> for a full list of acceptable reliability types.
k_items_x, k_items_y	Numeric vector identifying the number of items in each scale.
ryr_restricted	Logical vector in which each entry specifies whether the corresponding rxr value is an incumbent reliability (TRUE) or an applicant reliability. All entries are TRUE by default.
sign_rxz	Vector of signs of the relationships between X variables and the selection mechanism.
sign_ryz	Vector of signs of the relationships between Y variables and the selection mechanism.
n	Optional vector of sample sizes associated with the rxyi correlations.
conf_level	Confidence level to define the width of the confidence interval (default = .95).
correct_bias	Logical argument that determines whether to correct error-variance estimates for small-sample bias in correlations (TRUE) or not (FALSE). For sporadic corrections (e.g., in mixed artifact-distribution meta-analyses), this should be set to FALSE, the default).

Details

The correction for measurement error is:

$$\rho_{TP} = \frac{\rho_{XY}}{\sqrt{\rho_{XX}\rho_{YY}}}$$

The correction for univariate direct range restriction is:

$$\rho_{TP_a} = \left[\frac{\rho_{XY_i}}{u_X \sqrt{\rho_{YY_i}} \sqrt{\left(\frac{1}{u_X^2} - 1\right) \frac{\rho_{XY_i}^2}{\rho_{YY_i}} + 1}} \right] / \sqrt{\rho_{XX_a}}$$

The correction for univariate indirect range restriction is:

$$\rho_{TP_a} = \frac{\rho_{XY_i}}{u_T \sqrt{\rho_{XX_i}\rho_{YY_i}} \sqrt{\left(\frac{1}{u_T^2} - 1\right) \frac{\rho_{XY_i}^2}{\rho_{XX_i}\rho_{YY_i}} + 1}}$$

The correction for bivariate direct range restriction is:

$$\rho_{TP_a} = \frac{\frac{\rho_{XY_i}^2 - 1}{2\rho_{XY_i}} u_X u_Y + \text{sign}(\rho_{XY_i}) \sqrt{\frac{(1 - \rho_{XY_i}^2)^2}{4\rho_{XY_i}} u_X^2 u_Y^2 + 1}}{\sqrt{\rho_{XX_a} \rho_{YY_a}}}$$

The correction for bivariate indirect range restriction is:

$$\rho_{TP_a} = \frac{\rho_{XY_i} u_X u_Y + \lambda \sqrt{|1 - u_X^2| |1 - u_Y^2|}}{\sqrt{\rho_{XX_a} \rho_{YY_a}}}$$

where the λ value allows u_X and u_Y to fall on either side of unity so as to function as a two-stage correction for mixed patterns of range restriction and range enhancement. The λ value is computed as:

$$\lambda = \text{sign}[\rho_{ST_a} \rho_{SP_a} (1 - u_X) (1 - u_Y)] \frac{\text{sign}(1 - u_X) \min\left(u_X, \frac{1}{u_X}\right) + \text{sign}(1 - u_Y) \min\left(u_Y, \frac{1}{u_Y}\right)}{\min\left(u_X, \frac{1}{u_X}\right) \min\left(u_Y, \frac{1}{u_Y}\right)}$$

Value

Data frame(s) of observed correlations (r_{xyi}), operational range-restricted correlations corrected for measurement error in Y only (r_{xpi}), operational range-restricted correlations corrected for measurement error in X only (r_{tyi}), and range-restricted true-score correlations (r_{tpi}), range-corrected observed-score correlations (r_{xya}), operational range-corrected correlations corrected for measurement error in Y only (r_{xpa}), operational range-corrected correlations corrected for measurement error in X only (r_{tya}), and range-corrected true-score correlations (r_{tpa}).

References

- Alexander, R. A., Carson, K. P., Alliger, G. M., & Carr, L. (1987). Correcting doubly truncated correlations: An improved approximation for correcting the bivariate normal correlation when truncation has occurred on both variables. *Educational and Psychological Measurement*, 47(2), 309–315. <https://doi.org/10.1177/0013164487472002>
- Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.
- Hunter, J. E., Schmidt, F. L., & Le, H. (2006). Implications of direct and indirect range restriction for meta-analysis methods and findings. *Journal of Applied Psychology*, 91(3), 594–612. <https://doi.org/10.1037/0021-9010.91.3.594>
- Le, H., Oh, I.-S., Schmidt, F. L., & Wooldridge, C. D. (2016). Correction for range restriction in meta-analysis revisited: Improvements and implications for organizational research. *Personnel Psychology*, 69(4), 975–1008. <https://doi.org/10.1111/peps.12122>
- Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. pp. 43-44, 140–141.

Examples

```

## Correction for measurement error only
correct_r(correction = "bvirr", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE)
correct_r(correction = "meas", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE, n = 100)

## Correction for direct range restriction in X
correct_r(correction = "uvdrr_x", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE)
correct_r(correction = "uvdrr_x", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE, n = 100)

## Correction for indirect range restriction in X
correct_r(correction = "uvirr_x", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE)
correct_r(correction = "uvirr_x", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE, n = 100)

## Correction for direct range restriction in X and Y
correct_r(correction = "bvdr", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE)
correct_r(correction = "bvdr", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE, n = 100)

## Correction for indirect range restriction in X and Y
correct_r(correction = "bvirr", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE)
correct_r(correction = "bvirr", rxyi = .3, ux = .8, uy = .8, rxx = .8, ryy = .8,
          ux_observed = TRUE, uy_observed = TRUE, rxx_restricted = TRUE, ryy_restricted = TRUE, n = 100)

```

correct_r_bias

Correct correlations for small-sample bias

Description

Correct correlations for small-sample bias

Usage

```
correct_r_bias(r, n)
```

Arguments

r Vector of correlations.
n Vector of sample sizes.

Details

$$r_c = \frac{r_{obs}}{\left(\frac{2n-2}{2n-1}\right)}$$

Value

Vector of correlations corrected for small-sample bias.

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. pp. 140–141.

Examples

```
correct_r_bias(r = .3, n = 30)
correct_r_bias(r = .3, n = 300)
correct_r_bias(r = .3, n = 3000)
```

correct_r_coarseness *Correct correlations for scale coarseness*

Description

Correct correlations for scale coarseness

Usage

```
correct_r_coarseness(r, kx = NULL, ky = NULL, n = NULL,
  dist_x = "norm", dist_y = "norm", bin_value_x = c("median", "mean",
  "index"), bin_value_y = c("median", "mean", "index"), width_x = 3,
  width_y = 3, lbound_x = NULL, ubound_x = NULL, lbound_y = NULL,
  ubound_y = NULL, index_values_x = NULL, index_values_y = NULL)
```

Arguments

r	Observed correlation.
kx, ky	Number of scale points used to measure the x and y variables. Set to NULL to treat as continuously measured.
n	Optional sample size.
dist_x, dist_y	Assumed latent distribution of the x and y variables.
bin_value_x, bin_value_y	Are the scale points used to measure the of the x and y variables assumed to represent bin medians, means, or index values?

width_x, width_y	For symmetrically distributed variables, how many standard deviations above/below the latent mean should be used for the latent variable range to make the correction? (Note: Setting width > 3 produces erratic results.) The latent variable range can alternatively be set using lbound and ubound.
lbound_x, lbound_y	What lower bound of the range for the latent x and y variables should be used to make the correction? (Note: For normally distributed variables, setting lbound < -3 produces erratic results.)
ubound_x, ubound_y	What upper bound of the range for the latent x and y variables should be used to make the correction? (Note: For normally distributed variables, setting ubound > 3 produces erratic results.)
index_values_x, index_values_y	Optional. If bin_value = "index", the bin index values. If unspecified, values 1:k are used.

Value

Vector of correlations corrected for scale coarseness (if n is supplied, corrected error variance and adjusted sample size is also reported).

References

- Aguinis, H., Pierce, C. A., & Culpepper, S. A. (2009). Scale coarseness as a methodological artifact: Correcting correlation coefficients attenuated from using coarse scales. *Organizational Research Methods, 12*(4), 623–652. <https://doi.org/10.1177/1094428108318065>
- Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. pp. 287-288.
- Peters, C. C., & Van Voorhis, W. R. (1940). *Statistical procedures and their mathematical bases*. New York, NY: McGraw-Hill. <https://doi.org/10.1037/13596-000>. pp. 393–399.

Examples

```
correct_r_coarseness(r = .35, kx = 5, ky = 4, n = 100)
correct_r_coarseness(r = .35, kx = 5, n = 100)
correct_r_coarseness(r = .35, kx = 5, ky = 4, n = 100, dist_x="unif", dist_y="norm")
```

correct_r_dich	<i>Correct correlations for artificial dichotomization of one or both variables</i>
----------------	---

Description

Correct correlations for artificial dichotomization of one or both variables

Usage

```
correct_r_dich(r, px = NA, py = NA, n = NULL, ...)
```

Arguments

r Vector of correlations attenuated by artificial dichomization.

px Vector of proportions of the distribution on either side of the split applied to X (set as NA if X is continuous).

py Vector of proportions of the distribution on either side of the split applied to Y (set as NA if Y is continuous).

n Optional vector of sample sizes.

... Additional arguments.

Details

$$r_c = \frac{r_{obs}}{\left[\frac{\phi(p_X)}{p_X(1-p_X)} \right] \left[\frac{\phi(p_Y)}{p_Y(1-p_Y)} \right]}$$

Value

Vector of correlations corrected for artificial dichomization (if n is supplied, corrected error variance and adjusted sample size is also reported).

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>, pp. 43–44.

Examples

```
correct_r_dich(r = 0.32, px = .5, py = .5, n = 100)
```

correct_r_split *Correct correlations for uneven/unrepresentative splits*

Description

This correction is mathematically equivalent to correcting the correlation for direct range restriction in the split variable.

Usage

```
correct_r_split(r, pi, pa = 0.5, n = NULL)
```

Arguments

r	Vector of correlations affected by an uneven or unrepresentative split of a dichotomous variable.
pi	Vector of proportions of incumbent/sample cases in one of the categories of the dichotomous variable.
pa	Vector of proportions of applicant/population cases in one of the categories of the dichotomous variable.
n	Optional vector of sample sizes.

Details

$$r_c = \frac{r_{obs}}{u \sqrt{\left(\frac{1}{u^2} - 1\right) r_{obs}^2 + 1}}$$

where $u = \sqrt{\frac{p_i(1-p_i)}{p_a(1-p_a)}}$, the ratio of the dichotomous variance in the sample (p_i is the incumbent/sample proportion in one of the two groups) to the dichotomous variance in the population (p_a is the applicant/population proportion in one of the two groups). This correction is identical to the correction for univariate direct range restriction, applied to a dichotomous variable.

Value

Vector of correlations corrected for unrepresentative splits (if n is supplied, corrected error variance and adjusted sample size is also reported).

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: SAGE. <https://doi.org/10/b6mg>. pp. 287-288.

Examples

```
correct_r_split(r = 0.3, pi = .9, pa = .5, n = 100)
```

create_ad

Generate an artifact distribution object for use in artifact-distribution meta-analysis programs.

Description

This function generates artifact-distribution objects containing either interactive or Taylor series artifact distributions. Use this to create objects that can be supplied to the `ma_r_ad` and `ma_r_ad` functions to apply psychometric corrections to barebones meta-analysis objects via artifact distribution methods.

Allows consolidation of observed and estimated artifact information by cross-correcting artifact distributions and forming weighted artifact summaries.

For u ratios, error variances can be computed for independent samples (i.e., settings in which the unrestricted standard deviation comes from an external study) or dependent samples (i.e., settings in which the range-restricted standard deviation comes from a sample that represents a subset of the applicant sample that provided the unrestricted standard deviation). The former circumstance is presumed to be more common, so error variances are computed for independent samples by default.

Usage

```
create_ad(ad_type = c("tsa", "int"), rxxi = NULL, n_rxxi = NULL,
  wt_rxxi = n_rxxi, rxxi_type = rep("alpha", length(rxxi)),
  k_items_rxxi = rep(NA, length(rxxi)), rxxa = NULL, n_rxxa = NULL,
  wt_rxxa = n_rxxa, rxxa_type = rep("alpha", length(rxxa)),
  k_items_rxxa = rep(NA, length(rxxa)), ux = NULL, ni_ux = NULL,
  na_ux = NULL, wt_ux = ni_ux, dep_sds_ux_obs = rep(FALSE,
  length(ux)), ut = NULL, ni_ut = NULL, na_ut = NULL,
  wt_ut = ni_ut, dep_sds_ut_obs = rep(FALSE, length(ut)),
  mean_qxi = NULL, var_qxi = NULL, k_qxi = NULL, mean_n_qxi = NULL,
  qxi_dist_type = rep("alpha", length(mean_qxi)),
  mean_k_items_qxi = rep(NA, length(mean_qxi)), mean_rxxi = NULL,
  var_rxxi = NULL, k_rxxi = NULL, mean_n_rxxi = NULL,
  rxxi_dist_type = rep("alpha", length(mean_rxxi)),
  mean_k_items_rxxi = rep(NA, length(mean_rxxi)), mean_qxa = NULL,
  var_qxa = NULL, k_qxa = NULL, mean_n_qxa = NULL,
  qxa_dist_type = rep("alpha", length(mean_qxa)),
  mean_k_items_qxa = rep(NA, length(mean_qxa)), mean_rxxa = NULL,
  var_rxxa = NULL, k_rxxa = NULL, mean_n_rxxa = NULL,
  rxxa_dist_type = rep("alpha", length(mean_rxxa)),
  mean_k_items_rxxa = rep(NA, length(mean_rxxa)), mean_ux = NULL,
  var_ux = NULL, k_ux = NULL, mean_ni_ux = NULL,
  mean_na_ux = rep(NA, length(mean_ux)), dep_sds_ux_spec = rep(FALSE,
  length(mean_ux)), mean_ut = NULL, var_ut = NULL, k_ut = NULL,
  mean_ni_ut = NULL, mean_na_ut = rep(NA, length(mean_ut)),
  dep_sds_ut_spec = rep(FALSE, length(mean_ut)), estimate_rxxa = TRUE,
  estimate_rxxi = TRUE, estimate_ux = TRUE, estimate_ut = TRUE,
  var_unbiased = TRUE, ...)
```

Arguments

<code>ad_type</code>	Type of artifact distribution to be computed: Either "tsa" for Taylor series approximation or "int" for interactive.
<code>rxxi</code>	Vector of incumbent reliability estimates.

n_rxxi	Vector of sample sizes associated with the elements of rxxi.
wt_rxxi	Vector of weights associated with the elements of rxxi (by default, sample sizes will be used as weights).
rxxi_type, rxxa_type, qxi_dist_type, rxxi_dist_type, qxa_dist_type, rxxa_dist_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for ma_r for a full list of acceptable reliability types.
k_items_rxxi, mean_k_items_qxi, mean_k_items_rxxi, k_items_rxxa, mean_k_items_qxa, mean_k_items_rxxa	Numeric vector of the number of items in each scale (or mean number of items, for pre-specified distributions).
rxxa	Vector of applicant reliability estimates.
n_rxxa	Vector of sample sizes associated with the elements of rxxa.
wt_rxxa	Vector of weights associated with the elements of rxxa (by default, sample sizes will be used as weights).
ux	Vector of observed-score u ratios.
ni_ux	Vector of incumbent sample sizes associated with the elements of ux.
na_ux	Vector of applicant sample sizes that can be used in estimating the sampling error of supplied ux values. NULL by default. Only used when ni_ux is not NULL. If supplied, must be either a scalar or the same length as ni_ux.
wt_ux	Vector of weights associated with the elements of ux (by default, sample sizes will be used as weights).
dep_sds_ux_obs	Logical scalar or vector determining whether supplied ux values were computed using dependent samples (TRUE) or independent samples (FALSE).
ut	Vector of true-score u ratios.
ni_ut	Vector of incumbent sample sizes associated with the elements of ut.
na_ut	Vector of applicant sample sizes that can be used in estimating the sampling error of supplied ut values. NULL by default. Only used when ni_ut is not NULL. If supplied, must be either a scalar or the same length as ni_ut.
wt_ut	Vector of weights associated with the elements of ut (by default, sample sizes will be used as weights).
dep_sds_ut_obs	Logical scalar or vector determining whether supplied ut values were computed using dependent samples (TRUE) or independent samples (FALSE).
mean_qxi	Vector that can be used to supply the means of externally computed distributions of incumbent square-root reliabilities.
var_qxi	Vector that can be used to supply the variances of externally computed distributions of incumbent square-root reliabilities.
k_qxi	Vector that can be used to supply the number of studies included in externally computed distributions of incumbent square-root reliabilities.
mean_n_qxi	Vector that can be used to supply the mean sample sizes of externally computed distributions of incumbent square-root reliabilities.
mean_rxxi	Vector that can be used to supply the means of externally computed distributions of incumbent reliabilities.

var_rxxi	Vector that can be used to supply the variances of externally computed distributions of incumbent reliabilities.
k_rxxi	Vector that can be used to supply the number of studies included in externally computed distributions of incumbent reliabilities.
mean_n_rxxi	Vector that can be used to supply the mean sample sizes of externally computed distributions of incumbent reliabilities.
mean_qxa	Vector that can be used to supply the means of externally computed distributions of applicant square-root reliabilities.
var_qxa	Vector that can be used to supply the variances of externally computed distributions of applicant square-root reliabilities.
k_qxa	Vector that can be used to supply the number of studies included in externally computed distributions of applicant square-root reliabilities.
mean_n_qxa	Vector that can be used to supply the mean sample sizes of externally computed distributions of applicant square-root reliabilities.
mean_rxxa	Vector that can be used to supply the means of externally computed distributions of applicant reliabilities.
var_rxxa	Vector that can be used to supply the variances of externally computed distributions of applicant reliabilities.
k_rxxa	Vector that can be used to supply the number of studies included in externally computed distributions of applicant reliabilities.
mean_n_rxxa	Vector that can be used to supply the mean sample sizes of externally computed distributions of applicant reliabilities.
mean_ux	Vector that can be used to supply the means of externally computed distributions of observed-score u ratios.
var_ux	Vector that can be used to supply the variances of externally computed distributions of observed-score u ratios.
k_ux	Vector that can be used to supply the number of studies included in externally computed distributions of observed-score u ratios.
mean_ni_ux	Vector that can be used to supply the mean incumbent sample sizes of externally computed distributions of observed-score u ratios.
mean_na_ux	Vector or scalar that can be used to supply the mean applicant sample size(s) of externally computed distributions of observed-score u ratios.
dep_sds_ux_spec	Logical scalar or vector determining whether externally computed ux distributions were computed using dependent samples (TRUE) or independent samples (FALSE).
mean_ut	Vector that can be used to supply the means of externally computed distributions of true-score u ratios.
var_ut	Vector that can be used to supply the variances of externally computed distributions of true-score u ratios.
k_ut	Vector that can be used to supply the number of studies included in externally computed distributions of true-score u ratios.

mean_ni_ut	Vector that can be used to supply the mean sample sizes for of externally computed distributions of true-score u ratios.
mean_na_ut	Vector or scalar that can be used to supply the mean applicant sample size(s) of externally computed distributions of true-score u ratios.
dep_sds_ut_spec	Logical scalar or vector determining whether externally computed ut distributions were computed using dependent samples (TRUE) or independent samples (FALSE).
estimate_rxxa	Logical argument to estimate rxxa values from other artifacts (TRUE) or to only used supplied rxxa values (FALSE). TRUE by default.
estimate_rxxi	Logical argument to estimate rxxi values from other artifacts (TRUE) or to only used supplied rxxi values (FALSE). TRUE by default.
estimate_ux	Logical argument to estimate ux values from other artifacts (TRUE) or to only used supplied ux values (FALSE). TRUE by default.
estimate_ut	Logical argument to estimate ut values from other artifacts (TRUE) or to only used supplied ut values (FALSE). TRUE by default.
var_unbiased	Logical scalar determining whether variance should be unbiased (TRUE) or maximum-likelihood (FALSE).
...	Further arguments.

Value

Artifact distribution object (matrix of artifact-distribution means and variances) for use artifact-distribution meta-analyses.

Examples

```
## Example computed using observed values only:
create_ad(ad_type = "tsa", rxxa = c(.9, .8), n_rxxa = c(50, 150),
          rxxi = c(.8, .7), n_rxxi = c(50, 150),
          ux = c(.9, .8), ni_ux = c(50, 150))

create_ad(ad_type = "int", rxxa = c(.9, .8), n_rxxa = c(50, 150),
          rxxi = c(.8, .7), n_rxxi = c(50, 150),
          ux = c(.9, .8), ni_ux = c(50, 150))

## Example computed using all possible input arguments (arbitrary values):
rxxa <- rxxi <- ux <- ut <- c(.7, .8)
n_rxxa <- n_rxxi <- ni_ux <- ni_ut <- c(50, 100)
na_ux <- na_ut <- c(200, 200)
mean_qxa <- mean_qxi <- mean_ux <- mean_ut <- mean_rxxi <- mean_rxxa <- c(.7, .8)
var_qxa <- var_qxi <- var_ux <- var_ut <- var_rxxi <- var_rxxa <- c(.1, .05)
k_qxa <- k_qxi <- k_ux <- k_ut <- k_rxxa <- k_rxxi <- 2
mean_n_qxa <- mean_n_qxi <- mean_ni_ux <- mean_ni_ut <- mean_n_rxxa <- mean_n_rxxi <- c(100, 100)
dep_sds_ux_obs <- dep_sds_ux_spec <- dep_sds_ut_obs <- dep_sds_ut_spec <- FALSE
mean_na_ux <- mean_na_ut <- c(200, 200)

wt_rxxa <- n_rxxa
```

```

wt_rxxi <- n_rxxi
wt_ux <- ni_ux
wt_ut <- ni_ut

estimate_rxxa <- TRUE
estimate_rxxi <- TRUE
estimate_ux <- TRUE
estimate_ut <- TRUE
var_unbiased <- TRUE

create_ad(rxxa = rxxa, n_rxxa = n_rxxa, wt_rxxa = wt_rxxa,
          mean_qxa = mean_qxa, var_qxa = var_qxa,
          k_qxa = k_qxa, mean_n_qxa = mean_n_qxa,
          mean_rxxa = mean_rxxa, var_rxxa = var_rxxa,
          k_rxxa = k_rxxa, mean_n_rxxa = mean_n_rxxa,

          rxxi = rxxi, n_rxxi = n_rxxi, wt_rxxi = wt_rxxi,
          mean_qxi = mean_qxi, var_qxi = var_qxi,
          k_qxi = k_qxi, mean_n_qxi = mean_n_qxi,
          mean_rxxi = mean_rxxi, var_rxxi = var_rxxi,
          k_rxxi = k_rxxi, mean_n_rxxi = mean_n_rxxi,

          ux = ux, ni_ux = ni_ux, na_ux = na_ux, wt_ux = wt_ux,
          dep_sds_ux_obs = dep_sds_ux_obs,
          mean_ux = mean_ux, var_ux = var_ux, k_ux =
            k_ux, mean_ni_ux = mean_ni_ux,
          mean_na_ux = mean_na_ux, dep_sds_ux_spec = dep_sds_ux_spec,

          ut = ut, ni_ut = ni_ut, na_ut = na_ut, wt_ut = wt_ut,
          dep_sds_ut_obs = dep_sds_ut_obs,
          mean_ut = mean_ut, var_ut = var_ut,
          k_ut = k_ut, mean_ni_ut = mean_ni_ut,
          mean_na_ut = mean_na_ut, dep_sds_ut_spec = dep_sds_ut_spec,

          estimate_rxxa = estimate_rxxa, estimate_rxxi = estimate_rxxi,
          estimate_ux = estimate_ux, estimate_ut = estimate_ut, var_unbiased = var_unbiased)

```

create_ad_group	<i>Generate an artifact distribution object for a dichotomous grouping variable.</i>
-----------------	--

Description

This function generates artifact-distribution objects containing either interactive or Taylor series artifact distributions for dichotomous group-membership variables. Use this to create objects that can be supplied to the `ma_r_ad` and `ma_d_ad` functions to apply psychometric corrections to barebones meta-analysis objects via artifact distribution methods.

Allows consolidation of observed and estimated artifact information by cross-correcting artifact distributions and forming weighted artifact summaries.

Usage

```
create_ad_group(ad_type = c("tsa", "int"), rGg = NULL, n_rGg = NULL,
  wt_rGg = n_rGg, pi = NULL, pa = NULL, n_pi = NULL, n_pa = NULL,
  wt_p = n_pi, mean_rGg = NULL, var_rGg = NULL, k_rGg = NULL,
  mean_n_rGg = NULL, var_unbiased = TRUE, ...)
```

Arguments

ad_type	Type of artifact distribution to be computed: Either "tsa" for Taylor series approximation or "int" for interactive.
rGg	Vector of incumbent reliability estimates.
n_rGg	Vector of sample sizes associated with the elements of rGg.
wt_rGg	Vector of weights associated with the elements of rGg (by default, sample sizes will be used as weights if provided).
pi	Vector of incumbent/sample proportions of members in one of the two groups being compared (one or both of pi/pa can be vectors - if both are vectors, they must be of equal length).
pa	Vector of applicant/population proportions of members in one of the two groups being compared (one or both of pi/pa can be vectors - if both are vectors, they must be of equal length).
n_pi	Vector of sample sizes associated with the elements in pi.
n_pa	Vector of sample sizes associated with the elements in pa.
wt_p	Vector of weights associated with the collective element pairs in pi and pa.
mean_rGg	Vector that can be used to supply the means of externally computed distributions of correlations between observed and latent group membership.
var_rGg	Vector that can be used to supply the variances of externally computed distributions of correlations between observed and latent group membership.
k_rGg	Vector that can be used to supply the number of studies included in externally computed distributions of correlations between observed and latent group membership.
mean_n_rGg	Vector that can be used to supply the mean sample sizes of externally computed distributions of correlations between observed and latent group membership.
var_unbiased	Logical scalar determining whether variance should be unbiased (TRUE) or maximum-likelihood (FALSE).
...	Further arguments.

Value

Artifact distribution object (matrix of artifact-distribution means and variances) for use in artifact-distribution meta-analyses.

Examples

```
## Example artifact distribution for a dichotomous grouping variable:
create_ad_group(rGg = c(.8, .9, .95), n_rGg = c(100, 200, 250),
  mean_rGg = .9, var_rGg = .05,
  k_rGg = 5, mean_n_rGg = 100,
  pi = c(.6, .55, .3), pa = .5, n_pi = c(100, 200, 250), n_pa = c(300, 300, 300),
  var_unbiased = TRUE)

create_ad_group(ad_type = "int", rGg = c(.8, .9, .95), n_rGg = c(100, 200, 250),
  mean_rGg = .9, var_rGg = .05,
  k_rGg = 5, mean_n_rGg = 100,
  pi = c(.6, .55, .3), pa = .5, n_pi = c(100, 200, 250), n_pa = c(300, 300, 300),
  var_unbiased = TRUE)
```

create_ad_tibble	<i>Create a tibble of artifact distributions by construct</i>
------------------	---

Description

Create a tibble of artifact distributions by construct

Usage

```
create_ad_tibble(ad_type = c("tsa", "int"), n = NULL,
  sample_id = NULL, construct_x = NULL, facet_x = NULL,
  measure_x = NULL, construct_y = NULL, facet_y = NULL,
  measure_y = NULL, rxx = NULL, rxx_restricted = TRUE,
  rxx_type = "alpha", k_items_x = NA, ryy = NULL,
  ryy_restricted = TRUE, ryy_type = "alpha", k_items_y = NA,
  ux = NULL, ux_observed = TRUE, uy = NULL, uy_observed = TRUE,
  estimate_rxxa = TRUE, estimate_rxxi = TRUE, estimate_ux = TRUE,
  estimate_ut = TRUE, moderators = NULL, cat_moderators = TRUE,
  moderator_type = c("simple", "hierarchical", "none"),
  construct_order = NULL, supplemental_ads = NULL, data = NULL,
  control = control_psychmeta(), ...)

create_ad_list(ad_type = c("tsa", "int"), n = NULL, sample_id = NULL,
  construct_x = NULL, facet_x = NULL, measure_x = NULL,
  construct_y = NULL, facet_y = NULL, measure_y = NULL, rxx = NULL,
  rxx_restricted = TRUE, rxx_type = "alpha", k_items_x = NA,
  ryy = NULL, ryy_restricted = TRUE, ryy_type = "alpha",
  k_items_y = NA, ux = NULL, ux_observed = TRUE, uy = NULL,
  uy_observed = TRUE, estimate_rxxa = TRUE, estimate_rxxi = TRUE,
  estimate_ux = TRUE, estimate_ut = TRUE, moderators = NULL,
  cat_moderators = TRUE, moderator_type = c("simple", "hierarchical",
  "none"), construct_order = NULL, supplemental_ads = NULL,
  data = NULL, control = control_psychmeta(), ...)
```

Arguments

ad_type	Type of artifact distributions to be computed: Either "tsa" for Taylor series approximation or "int" for interactive.
n	Vector or column name of sample sizes.
sample_id	Optional vector of identification labels for samples/studies in the meta-analysis.
construct_x, construct_y	Vector of construct names for constructs initially designated as "X" or "Y".
facet_x, facet_y	Vector of facet names for constructs initially designated as "X" or "Y". Facet names "global", "overall", and "total" are reserved to indicate observations that represent effect sizes that have already been composited or that represent construct-level measurements rather than facet-level measurements. To avoid double-compositing, any observation with one of these reserved names will only be eligible for auto-compositing with other such observations and will not be combined with narrow facets.
measure_x, measure_y	Vector of names for measures associated with constructs initially designated as "X" or "Y".
rxx	Vector or column name of reliability estimates for X.
rxx_restricted	Logical vector or column name determining whether each element of rxx is an incumbent reliability (TRUE) or an applicant reliability (FALSE).
rxx_type, ryy_type	String vector identifying the types of reliability estimates supplied. See documentation of ma_r for a full list of acceptable values.
k_items_x, k_items_y	Numeric vector identifying the number of items in each scale.
ryy	Vector or column name of reliability estimates for Y.
ryy_restricted	Logical vector or column name determining whether each element of ryy is an incumbent reliability (TRUE) or an applicant reliability (FALSE).
ux	Vector or column name of u ratios for X.
ux_observed	Logical vector or column name determining whether each element of ux is an observed-score u ratio (TRUE) or a true-score u ratio (FALSE).
uy	Vector or column name of u ratios for Y.
uy_observed	Logical vector or column name determining whether each element of uy is an observed-score u ratio (TRUE) or a true-score u ratio (FALSE).
estimate_rxxa	Logical argument to estimate rxxa values from other artifacts (TRUE) or to only used supplied rxxa values (FALSE). TRUE by default.
estimate_rxxi	Logical argument to estimate rxxi values from other artifacts (TRUE) or to only used supplied rxxi values (FALSE). TRUE by default.
estimate_ux	Logical argument to estimate ux values from other artifacts (TRUE) or to only used supplied ux values (FALSE). TRUE by default.
estimate_ut	Logical argument to estimate ut values from other artifacts (TRUE) or to only used supplied ut values (FALSE). TRUE by default.

moderators	Matrix or column names of moderator variables to be used in the meta-analysis (can be a vector in the case of one moderator).
cat_moderators	Logical scalar or vector identifying whether variables in the moderators argument are categorical variables (TRUE) or continuous variables (FALSE).
moderator_type	Type of moderator analysis: "none" means that no moderators are to be used, "simple" means that moderators are to be examined one at a time, and "hierarchical" means that all possible combinations and subsets of moderators are to be examined.
construct_order	Vector indicating the order in which variables should be arranged, with variables listed earlier in the vector being preferred for designation as X.
supplemental_ads	Named list (named according to the constructs included in the meta-analysis) of supplemental artifact distribution information from studies not included in the meta-analysis. This is a list of lists, where the elements of a list associated with a construct are named like the arguments of the create_ad() function.
data	Data frame containing columns whose names may be provided as arguments to vector arguments.
control	Output from the control_psychmeta() function or a list of arguments controlled by the control_psychmeta() function. Ellipsis arguments will be screened for internal inclusion in control.
...	Additional arguments

Value

A tibble of artifact distributions

Examples

```
## Examples to create Taylor series artifact distributions:
# Overall artifact distributions (not pairwise, not moderated)
create_ad_tibble(ad_type = "tsa",
  n = n, rxx = rxxi, ryy = ryyi,
  construct_x = x_name, construct_y = y_name,
  sample_id = sample_id, moderators = moderator,
  data = data_r_meas_multi,
  control = control_psychmeta(pairwise_ads = FALSE,
    moderated_ads = FALSE))

# Overall artifact distributions by moderator combination
create_ad_tibble(ad_type = "tsa",
  n = n, rxx = rxxi, ryy = ryyi,
  construct_x = x_name, construct_y = y_name,
  sample_id = sample_id, moderators = moderator,
  data = data_r_meas_multi,
  control = control_psychmeta(pairwise_ads = FALSE,
    moderated_ads = TRUE))

# Pairwise artifact distributions (not moderated)
```

```

create_ad_tibble(ad_type = "tsa",
                 n = n, rxx = rxxi, ryy = ryyi,
                 construct_x = x_name, construct_y = y_name,
                 sample_id = sample_id, moderators = moderator,
                 data = data_r_meas_multi,
                 control = control_psychmeta(pairwise_ads = TRUE,
                                             moderated_ads = FALSE))

# Pairwise artifact distributions by moderator combination
create_ad_tibble(ad_type = "tsa",
                 n = n, rxx = rxxi, ryy = ryyi,
                 construct_x = x_name, construct_y = y_name,
                 sample_id = sample_id, moderators = moderator,
                 data = data_r_meas_multi,
                 control = control_psychmeta(pairwise_ads = TRUE,
                                             moderated_ads = TRUE))

```

credibility

Construct a credibility interval

Description

Function to construct a credibility interval around a mean effect size.

Usage

```
credibility(mean, sd, k = NULL, cred_level = 0.8,
            cred_method = c("t", "norm"))
```

Arguments

mean	Mean effect size.
sd	Residual/true standard deviation of effect sizes, after accounting for variance from artifacts.
k	Number of studies in the meta-analysis.
cred_level	Credibility level that defines the width of the credibility interval (default = .80).
cred_method	Distribution to be used to compute the width of credibility intervals. Available options are "t" for <i>t</i> distribution or "norm" for normal distribution.

Details

$$CV = mean_{es} \pm quantile \times SD_{es}$$

Value

A matrix of credibility intervals of the specified width.

Examples

```
credibility(mean = .3, sd = .15, cred_level = .8)
credibility(mean = .3, sd = .15, cred_level = .8, k = 10)
credibility(mean = c(.3, .5), sd = c(.15, .2), cred_level = .8, k = 10)
```

data_d_bb_multi	<i>Hypothetical d value dataset simulated with sampling error only</i>
-----------------	--

Description

Data set for use in example meta-analyses of multiple variables.

Usage

```
data(data_d_bb_multi)
```

Format

data.frame

Examples

```
data(data_d_bb_multi)
```

data_d_meas_multi	<i>Hypothetical d value dataset simulated to satisfy the assumptions of the correction for measurement error only in multiple constructs</i>
-------------------	--

Description

Data set for use in example meta-analyses correcting for measurement error in multiple variables.

Usage

```
data(data_d_meas_multi)
```

Format

data.frame

Examples

```
data(data_d_meas_multi)
```

data_r_bvdrr	<i>Hypothetical dataset simulated to satisfy the assumptions of the bivariate correction for direct range restriction</i>
--------------	---

Description

Data set for use in example meta-analyses of bivariate direct range restriction. Note that the BVDRR correction is only an approximation of the appropriate range-restriction correction and tends to have a noticeable positive bias when applied in meta-analyses.

Usage

```
data(data_r_bvdrr)
```

Format

```
data.frame
```

Examples

```
data(data_r_bvdrr)
```

data_r_bvirr	<i>Hypothetical dataset simulated to satisfy the assumptions of the bivariate correction for indirect range restriction</i>
--------------	---

Description

Data set for use in example meta-analyses of bivariate indirect range restriction.

Usage

```
data(data_r_bvirr)
```

Format

```
data.frame
```

Examples

```
data(data_r_bvirr)
```

`data_r_gonzalezmule_2014`*Meta-analysis of OCB correlations with other constructs*

Description

Data set to demonstrate corrections for univariate range restriction and measurement error using individual corrections or artifact distributions. NOTE: This is an updated version of the data set reported in the Gonzalez-Mulé, Mount, an Oh (2014) article that was obtained from the first author.

Usage

```
data(data_r_gonzalezmule_2014)
```

Format

```
data.frame
```

References

Gonzalez-Mulé, E., Mount, M. K., & Oh, I.-S. (2014). A meta-analysis of the relationship between general mental ability and nontask performance. *Journal of Applied Psychology*, 99(6), 1222–1243. <https://doi.org/10.1037/a0037547>

Examples

```
data(data_r_gonzalezmule_2014)
```

`data_r_mcdaniel_1994` *Artifact-distribution meta-analysis of the validity of interviews*

Description

Data set to demonstrate corrections for univariate range restriction and criterion measurement error using artifact distributions.

Usage

```
data(data_r_mcdaniel_1994)
```

Format

```
data.frame
```

References

McDaniel, M. A., Whetzel, D. L., Schmidt, F. L., & Maurer, S. D. (1994). The validity of employment interviews: A comprehensive review and meta-analysis. *Journal of Applied Psychology*, 79(4), 599–616. <https://doi.org/10.1037/0021-9010.79.4.599>

Examples

```
data(data_r_mcdaniel_1994)
```

data_r_mcleod_2007	<i>Bare-bones meta-analysis of parenting and childhood depression</i>
--------------------	---

Description

Data set to demonstrate bare-bones meta-analysis.

Usage

```
data(data_r_mcleod_2007)
```

Format

```
data.frame
```

References

McLeod, B. D., Weisz, J. R., & Wood, J. J., (2007). Examining the association between parenting and childhood depression: A meta-analysis. *Clinical Psychology Review*, 27(8), 986–1003. <https://doi.org/10.1016/j.cpr.2007.03.001>

Examples

```
data(data_r_mcleod_2007)
```

data_r_meas	<i>Hypothetical dataset simulated to satisfy the assumptions of the correction for measurement error only</i>
-------------	---

Description

Data set for use in example meta-analyses correcting for measurement error in two variables.

Usage

```
data(data_r_meas)
```

Format

data.frame

Examples

```
data(data_r_meas)
```

data_r_meas_multi	<i>Hypothetical correlation dataset simulated to satisfy the assumptions of the correction for measurement error only in multiple constructs</i>
-------------------	--

Description

Data set for use in example meta-analyses correcting for measurement error in multiple variables.

Usage

```
data(data_r_meas_multi)
```

Format

data.frame

Examples

```
data(data_r_meas_multi)
```

data_r_oh_2009	<i>Second order meta-analysis of operational validities of big five personality measures across East Asian countries</i>
----------------	--

Description

Example of a second-order meta-analysis of correlations corrected using artifact-distribution methods.

Usage

```
data(data_r_oh_2009)
```

Format

data.frame

References

Oh, I. -S. (2009). *The Five-Factor Model of personality and job performance in East Asia: A cross-cultural validity generalization study*. (Doctoral dissertation) Iowa City, IA: University of Iowa. <http://search.proquest.com/dissertations/docview/304903943/>

Schmidt, F. L., & Oh, I.-S. (2013). Methods for second order meta-analysis and illustrative applications. *Organizational Behavior and Human Decision Processes*, 121(2), 204–218. <https://doi.org/10.1016/j.obhdp.2013.03.002>

Examples

```
data(data_r_oh_2009)
```

data_r_roth_2015	<i>Artifact-distribution meta-analysis of the correlation between school grades and cognitive ability</i>
------------------	---

Description

Data set to demonstrate corrections for univariate range restriction and cognitive ability measurement error.

Usage

```
data(data_r_roth_2015)
```

Format

```
data.frame
```

References

Roth, B., Becker, N., Romeyke, S., Schäfer, S., Domnick, F., & Spinath, F. M. (2015). Intelligence and school grades: A meta-analysis. *Intelligence*, 53, 118–137. <https://doi.org/10.1016/j.intell.2015.09.002>

Examples

```
data(data_r_roth_2015)
```

data_r_uvdr	<i>Hypothetical dataset simulated to satisfy the assumptions of the univariate correction for direct range restriction</i>
-------------	--

Description

Data set for use in example meta-analyses correcting for univariate direct range restriction.

Usage

```
data(data_r_uvdr)
```

Format

```
data.frame
```

Examples

```
data(data_r_uvdr)
```

data_r_uvirr	<i>Hypothetical dataset simulated to satisfy the assumptions of the univariate correction for indirect range restriction</i>
--------------	--

Description

Data set for use in example meta-analyses correcting for univariate indirect range restriction.

Usage

```
data(data_r_uvirr)
```

Format

```
data.frame
```

Examples

```
data(data_r_uvirr)
```

estimate_artifacts	<i>Estimation of applicant and incumbent reliabilities and of true- and observed-score u ratios</i>
--------------------	---

Description

Functions to estimate the values of artifacts from other artifacts. These functions allow for reliability estimates to be corrected/attenuated for range restriction and allow u ratios to be converted between observed-score and true-score metrics. Some functions also allow for the extrapolation of an artifact from other available information.

Available functions include:

- estimate_rxxa
Estimate the applicant reliability of variable X from X's incumbent reliability value and X's observed-score or true-score u ratio.
- estimate_rxxa_u
Estimate the applicant reliability of variable X from X's observed-score and true-score u ratios.
- estimate_rxxi
Estimate the incumbent reliability of variable X from X's applicant reliability value and X's observed-score or true-score u ratio.
- estimate_rxxi_u
Estimate the incumbent reliability of variable X from X's observed-score and true-score u ratios.
- estimate_ux
Estimate the true-score u ratio for variable X from X's reliability coefficient and X's observed-score u ratio.
- estimate_uy
Estimate the observed-score u ratio for variable X from X's reliability coefficient and X's true-score u ratio.
- estimate_ryya
Estimate the applicant reliability of variable Y from Y's incumbent reliability value, Y's correlation with X, and X's u ratio.
- estimate_ryyi
Estimate the incumbent reliability of variable Y from Y's applicant reliability value, Y's correlation with X, and X's u ratio.
- estimate_uy
Estimate the observed-score u ratio for variable Y from Y's applicant and incumbent reliability coefficients.
- estimate_up
Estimate the true-score u ratio for variable Y from Y's applicant and incumbent reliability coefficients.

Usage

```

estimate_rxxa(rxxi, ux, ux_observed = TRUE, indirect_rr = TRUE,
  rxxi_type = "alpha")

estimate_rxxi(rxxa, ux, ux_observed = TRUE, indirect_rr = TRUE,
  rxxa_type = "alpha")

estimate_ut(ux, rxx, rxx_restricted = TRUE)

estimate_ux(ut, rxx, rxx_restricted = TRUE)

estimate_ryya(ryyi, rxyi, ux)

estimate_ryyi(ryya, rxyi, ux)

estimate_uy(ryyi, ryya, indirect_rr = TRUE, ryy_type = "alpha")

estimate_up(ryyi, ryya)

estimate_rxxa_u(ux, ut)

estimate_rxxi_u(ux, ut)

```

Arguments

rxxi	Vector of incumbent reliability estimates for X.
ux	Vector of observed-score u ratios for X (if used in the context of estimating a reliability value, a true-score u ratio may be supplied by setting ux_observed to FALSE).
ux_observed	Logical vector determining whether each element of ux is an observed-score u ratio (TRUE) or a true-score u ratio (FALSE).
indirect_rr	Logical vector determining whether each reliability value is associated with indirect range restriction (TRUE) or direct range restriction (FALSE).
rxxi_type, rxxa_type, ryy_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for ma_r for a full list of acceptable reliability types.
rxxa	Vector of applicant reliability estimates for X.
rxx	Vector of reliability estimates for X (used in the context of estimating ux and ut - specify that reliability is an incumbent value by setting rxx_restricted to FALSE).
rxx_restricted	Logical vector determining whether each element of rxx is an incumbent reliability (TRUE) or an applicant reliability (FALSE).
ut	Vector of true-score u ratios for X.
ryyi	Vector of incumbent reliability estimates for Y.
rxyi	Vector of observed-score incumbent correlations between X and Y.
ryya	Vector of applicant reliability estimates for Y.

Details

Formulas to estimate rxxa

Formulas for indirect range restriction:

$$\rho_{XX_a} = 1 - u_X^2 (1 - \rho_{XX_i})$$

$$\rho_{XX_a} = \frac{\rho_{XX_i}}{\rho_{XX_i} + u_T^2 - \rho_{XX_i} u_T^2}$$

Formula for direct range restriction:

$$\rho_{XX_a} = \frac{\rho_{XX_i}}{u_X^2 \left[1 + \rho_{XX_i} \left(\frac{1}{u_X^2} - 1 \right) \right]}$$

Formulas to estimate rxxi

Formulas for indirect range restriction:

$$\rho_{XX_i} = 1 - \frac{1 - \rho_{XX_a}}{u_X^2}$$

$$\rho_{XX_i} = 1 - \frac{1 - \rho_{XX_a}}{\rho_{XX_a} \left[u_T^2 - \left(1 - \frac{1}{\rho_{XX_a}} \right) \right]}$$

Formula for direct range restriction:

$$\rho_{XX_i} = \frac{\rho_{XX_a} u_X^2}{1 + \rho_{XX_i} (u_X^2 - 1)}$$

Formulas to estimate ut

$$u_T = \sqrt{\frac{\rho_{XX_i} u_X^2}{1 + \rho_{XX_i} u_X^2 - u_X^2}}$$

$$u_T = \sqrt{\frac{u_X^2 - (1 - \rho_{XX_a})}{\rho_{XX_a}}}$$

Formulas to estimate ux

$$u_X = \sqrt{\frac{u_T^2}{\rho_{XX_i} \left(1 + \frac{u_T^2}{\rho_{XX_i}} - u_T^2 \right)}}$$

$$u_X = \sqrt{\rho_{XX_a} \left[u_T^2 - \left(1 - \frac{1}{\rho_{XX_a}} \right) \right]}$$

Formula to estimate ryya

$$\rho_{YY_a} = 1 - \frac{1 - \rho_{YY_i}}{1 - \rho_{XY_i}^2 \left(1 - \frac{1}{u_X^2} \right)}$$

Formula to estimate ryyi

$$\rho_{YY_i} = 1 - (1 - \rho_{YY_a}) \left[1 - \rho_{XY_i}^2 \left(1 - \frac{1}{u_X^2} \right) \right]$$

Formula to estimate uy

$$u_Y = \sqrt{\frac{1 - \rho_{YY_a}}{1 - \rho_{YY_i}}}$$

Formula to estimate up

$$u_P = \sqrt{\frac{\frac{1 - \rho_{YY_a}}{1 - \rho_{YY_i}} - (1 - \rho_{YY_a})}{\rho_{YY_a}}}$$

Value

A vector of estimated artifact values.

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: Sage. <https://doi.org/10/b6mg> p. 127.

Le, H., & Schmidt, F. L. (2006). Correcting for indirect range restriction in meta-analysis: Testing a new meta-analytic procedure. *Psychological Methods, 11*(4), 416–438. <https://doi.org/10.1037/1082-989X.11.4.416>

Hunter, J. E., Schmidt, F. L., & Le, H. (2006). Implications of direct and indirect range restriction for meta-analysis methods and findings. *Journal of Applied Psychology, 91*(3), 594–612. <https://doi.org/10.1037/0021-9010.91.3.594>

Le, H., Oh, I.-S., Schmidt, F. L., & Wooldridge, C. D. (2016). Correction for range restriction in meta-analysis revisited: Improvements and implications for organizational research. *Personnel Psychology, 69*(4), 975–1008. <https://doi.org/10.1111/peps.12122>

Examples

```
estimate_rxxa(rxxi = .8, ux = .8, ux_observed = TRUE)
estimate_rxxi(rxxa = .8, ux = .8, ux_observed = TRUE)
estimate_ut(ux = .8, rxx = .8, rxx_restricted = TRUE)
estimate_ux(ut = .8, rxx = .8, rxx_restricted = TRUE)
estimate_ryya(ryyi = .8, rxyi = .3, ux = .8)
estimate_ryyi(ryya = .8, rxyi = .3, ux = .8)
estimate_uy(ryyi = c(.5, .7), ryya = c(.7, .8))
estimate_up(ryyi = c(.5, .7), ryya = c(.7, .8))
estimate_rxxa_u(ux = c(.7, .8), ut = c(.65, .75))
estimate_rxxi_u(ux = c(.7, .8), ut = c(.65, .75))
```

estimate_length_sb	<i>Inverse Spearman-Brown formula to estimate the amount by which a measure would have to be lengthened or shortened to achieve a desired level of reliability</i>
--------------------	--

Description

This function implements the inverse of the Spearman-Brown prophecy formula and answers the question: "How much would I have to increase (do decrease) the length of this measure to obtain a desired reliability level given the current reliability of the measure?" The result of the function is the multiplier by which the length of the original measure should be adjusted. The formula implemented here assumes that all items added to (or subtracted from) the measure will be parallel forms of the original items.

Usage

```
estimate_length_sb(rel_initial, rel_desired)
```

Arguments

rel_initial	Initial reliability of a measure.
rel_desired	Desired reliability of a lengthened or shortened measure.

Details

This is computed as:

$$k^* = \frac{\rho_{XX}^*(\rho_{XX} - 1)}{(\rho_{XX}^* - 1)\rho_{XX}}$$

where ρ_{XX} is the initial reliability, ρ_{XX}^* is the predicted reliability of a measure with a different length, and k^* is the number of times the measure would have to be lengthened to obtain a reliability equal to ρ_{XX}^* .

Value

The estimated number of times by which the number of items in the initial measure would have to be multiplied to achieve the desired reliability.

References

Ghiselli, E. E., Campbell, J. P., & Zedeck, S. (1981). *Measurement theory for the behavioral sciences*. San Francisco, CA: Freeman. p. 236.

Examples

```
## Estimated k to achieve a reliability of .8 from a measure with an initial reliability of .7
estimate_length_sb(rel_initial = .7, rel_desired = .8)

## Estimated k to achieve a reliability of .8 from a measure with an initial reliability of .9
estimate_length_sb(rel_initial = .9, rel_desired = .8)
```

estimate_prod	<i>Estimation of statistics computed from products of random, normal variables</i>
---------------	--

Description

This family of functions computes univariate descriptive statistics for the products of two variables denoted as "x" and "y" (e.g., $\text{mean}(x * y)$ or $\text{var}(x * y)$) and the covariance between the products of "x" and "y" and of "u" and "v" (e.g., $\text{cov}(x * y, u * v)$ or $\text{cor}(x * y, u * v)$). These functions presume all variables are random normal variables.

Available functions include:

- `estimate_mean_prod`
Estimate the mean of the product of two variables: $x * y$.
- `estimate_var_prod`
Estimate the variance of the product of two variables: $x * y$.
- `estimate_cov_prods`
Estimate the covariance between the products of two pairs of variables: $x * y$ and $u * v$.
- `estimate_cor_prods`
Estimate the correlation between the products of two pairs of variables: $x * y$ and $u * v$.

Usage

```
estimate_mean_prod(mu_x, mu_y, cov_xy)

estimate_var_prod(mu_x, mu_y, var_x, var_y, cov_xy)

estimate_cov_prods(mu_x, mu_y, mu_u, mu_v, cov_xu, cov_xv, cov_yu, cov_yv)

estimate_cor_prods(mu_x, mu_y, mu_u, mu_v, var_x, var_y, var_u, var_v,
  cov_xu, cov_xv, cov_yu, cov_yv, cov_xy, cov_uv)
```

Arguments

<code>mu_x</code>	Expected value of variable x.
<code>mu_y</code>	Expected value of variable y.
<code>cov_xy</code>	Covariance between x and y.
<code>var_x</code>	Variance of variable x.

var_y	Variance of variable y.
mu_u	Expected value of variable u.
mu_v	Expected value of variable v.
cov_xu	Covariance between x and u.
cov_xv	Covariance between x and v.
cov_yu	Covariance between y and u.
cov_yv	Covariance between y and v.
var_u	Variance of variable u.
var_v	Variance of variable v.
cov_uv	Covariance between u and v.

Value

An estimated statistic computed from the products of random, normal variables.

References

Bohrnstedt, G. W., & Goldberger, A. S. (1969). On the exact covariance of products of random variables. *Journal of the American Statistical Association*, 64(328), 1439. <https://doi.org/10.2307/2286081>

Goodman, L. A. (1960). On the exact variance of products. *Journal of the American Statistical Association*, 55(292), 708. <https://doi.org/10.2307/2281592>

estimate_q_dist	<i>Estimate descriptive statistics of square-root reliabilities</i>
-----------------	---

Description

Estimate descriptive statistics of square-root reliabilities from descriptive statistics of reliabilities via Taylor series approximation

Usage

```
estimate_q_dist(mean_rel, var_rel)
```

Arguments

mean_rel	Mean reliability value.
var_rel	Variance of reliability values.

Details

$$var_{q_x} = \frac{var_{\rho_{xx}}}{4q_x^2}$$

Value

The estimated mean and variance of a distribution of square-root reliability values.

Examples

```
estimate_q_dist(mean_rel = .8, var_rel = .15)
```

estimate_rel_dist	<i>Estimate descriptive statistics of reliabilities</i>
-------------------	---

Description

Estimate descriptive statistics of reliabilities from descriptive statistics of square-root reliabilities via Taylor series approximation

Usage

```
estimate_rel_dist(mean_q, var_q)
```

Arguments

mean_q	Mean square-root reliability value.
var_q	Variance of square-root reliability values.

Details

$$var_{\rho_{XX}} = 4q_X^2 var_{\rho_{XX}}$$

Value

The estimated mean and variance of a distribution of reliability values.

Examples

```
estimate_rel_dist(mean_q = .9, var_q = .05)
```

estimate_rel_sb	<i>Spearman-Brown prophecy formula to estimate the reliability of a lengthened measure</i>
-----------------	--

Description

This function implements the Spearman-Brown prophecy formula for estimating the reliability of a lengthened (or shortened) measure. The formula implemented here assumes that all items added to (or subtracted from) the measure will be parallel forms of the original items.

Usage

```
estimate_rel_sb(rel_initial, k)
```

Arguments

rel_initial	Initial reliability of a measure.
k	The number of times by which the measure should be lengthened (if $k > 1$) or shortened (if $k < 1$), assuming that all new items are parallel forms of initial items.

Details

This is computed as:

$$\rho_{XX}^* = \frac{k\rho_{XX}}{1 + (k - 1)\rho_{XX}}$$

where ρ_{XX} is the initial reliability, k is the multiplier by which the measure is to be lengthened (or shortened), and ρ_{XX}^* is the predicted reliability of a measure with a different length.

Value

The estimated reliability of the lengthened (or shortened) measure.

References

Ghiselli, E. E., Campbell, J. P., & Zedeck, S. (1981). *Measurement theory for the behavioral sciences*. San Francisco, CA: Freeman. p. 232.

Examples

```
## Double the length of a measure with an initial reliability of .7
estimate_rel_sb(rel_initial = .7, k = 2)

## Halve the length of a measure with an initial reliability of .9
estimate_rel_sb(rel_initial = .9, k = .5)
```

estimate_u	<i>Estimate u ratios from available artifact information</i>
------------	--

Description

Uses information about standard deviations, reliability estimates, and selection ratios to estimate u ratios. Selection ratios are only used to estimate u when no other information is available, but estimates of u computed from SDs and reliabilities will be averaged to reduce error.

Usage

```
estimate_u(measure_id = NULL, sdi = NULL, sda = NULL, rxxi = NULL,
           rxxa = NULL, item_ki = NULL, item_ka = NULL, n = NULL,
           meani = NULL, sr = NULL, rxya_est = NULL, data = NULL)
```

Arguments

measure_id	Vector of measure identifiers.
sdi	Scalar or vector containing restricted standard deviation(s).
sda	Scalar or vector containing unrestricted standard deviation(s).
rxxi	Scalar or vector containing restricted reliability coefficient(s).
rxxa	Scalar or vector containing unrestricted reliability coefficient(s).
item_ki	Scalar or vector containing the number of items used in measures within samples.
item_ka	Scalar or vector indicating the number of items toward which reliability estimates should be adjusted using the Spearman-Brown formula.
n	Vector of sample sizes.
meani	Vector of sample means.
sr	Vector of selection ratios (used only when no other useable u-ratio inputs are available).
rxya_est	Vector of estimated unrestricted correlations between the selection mechanism and the variable of interest (used only when sr is used).
data	Optional data frame containing any or all information for use in other arguments.

Value

A vector of estimated u ratios.

Examples

```

sdi <- c(1.4, 1.2, 1.3, 1.4)
sda <- 2
rxxi <- c(.6, .7, .75, .8)
rxxa <- c(.9, .95, .8, .9)
item_ki <- c(12, 12, 12, NA)
item_ka <- NULL
n <- c(200, 200, 200, 200)
meani <- c(2, 1, 2, 3)
sr <- c(.5, .6, .7, .4)
rxya_est <- .5

## Estimate u from standard deviations only:
estimate_u(sdi = sdi, sda = sda)

## Estimate u from incumbent standard deviations and the
## mixture standard deviation:
estimate_u(sdi = sdi, sda = "mixture", meani = meani, n = n)

## Estimate u from reliability information:
estimate_u(rxxi = rxxi, rxxa = rxxa)

## Estimate u from both standard deviations and reliabilities:
estimate_u(sdi = sdi, sda = sda, rxxi = rxxi, rxxa = rxxa,
           item_ki = item_ki, item_ka = item_ka, n = n,
           meani = meani, sr = sr, rxya_est = rxya_est)

estimate_u(sdi = sdi, sda = "average", rxxi = rxxi, rxxa = "average",
           item_ki = item_ki, item_ka = item_ka, n = n, meani = meani)

## Estimate u from selection ratios as direct range restriction:
estimate_u(sr = sr)

## Estimate u from selection ratios as indirect range restriction:
estimate_u(sr = sr, rxya_est = rxya_est)

```

estimate_var_artifacts

Taylor series approximations for the variances of estimates artifact distributions.

Description

Taylor series approximations to estimate the variances of artifacts that have been estimated from other artifacts. These functions are implemented internally in the `create_ad` function and related functions, but are useful as general tools for manipulating artifact distributions.

Available functions include:

- `estimate_var_qxi`
Estimate the variance of a qxi distribution from a qxa distribution and a distribution of u ratios.

- estimate_var_rxxi
Estimate the variance of an rxxi distribution from an rxxa distribution and a distribution of u ratios.
- estimate_var_qxa
Estimate the variance of a qxa distribution from a qxi distribution and a distribution of u ratios.
- estimate_var_rxxa
Estimate the variance of an rxxa distribution from an rxxi distribution and a distribution of u ratios.
- estimate_var_ut
Estimate the variance of a true-score u ratio distribution from an observed-score u ratio distribution and a reliability distribution.
- estimate_var_ux
Estimate the variance of an observed-score u ratio distribution from a true-score u ratio distribution and a reliability distribution.
- estimate_var_qyi
Estimate the variance of a qyi distribution from the following distributions: qya, rxyi, and ux.
- estimate_var_ryyi
Estimate the variance of an ryyi distribution from the following distributions: ryya, rxyi, and ux.
- estimate_var_qya
Estimate the variance of a qya distribution from the following distributions: qyi, rxyi, and ux.
- estimate_var_ryya
Estimate the variance of an ryya distribution from the following distributions: ryyi, rxyi, and ux.

Usage

```
estimate_var_qxi(qxa, var_qxa = 0, ux, var_ux = 0, cor_qxa_ux = 0,
  ux_observed = TRUE, indirect_rr = TRUE, qxa_type = "alpha")
```

```
estimate_var_qxa(qxi, var_qxi = 0, ux, var_ux = 0, cor_qxi_ux = 0,
  ux_observed = TRUE, indirect_rr = TRUE, qxi_type = "alpha")
```

```
estimate_var_rxxi(rxxa, var_rxxa = 0, ux, var_ux = 0,
  cor_rxxa_ux = 0, ux_observed = TRUE, indirect_rr = TRUE,
  rxxa_type = "alpha")
```

```
estimate_var_rxxa(rxxi, var_rxxi = 0, ux, var_ux = 0,
  cor_rxxi_ux = 0, ux_observed = TRUE, indirect_rr = TRUE,
  rxxi_type = "alpha")
```

```
estimate_var_ut(rxx, var_rxx = 0, ux, var_ux = 0, cor_rxx_ux = 0,
  rxx_restricted = TRUE, rxx_as_qx = FALSE)
```

```
estimate_var_ux(rxx, var_rxx = 0, ut, var_ut = 0, cor_rxx_ut = 0,
  rxx_restricted = TRUE, rxx_as_qx = FALSE)
```

```
estimate_var_ryya(ryyi, var_ryyi = 0, rxyi, var_rxyi = 0, ux,
  var_ux = 0, cor_ryyi_rxyi = 0, cor_ryyi_ux = 0, cor_rxyi_ux = 0)
```

```
estimate_var_qya(qyi, var_qyi = 0, rxyi, var_rxyi = 0, ux,
  var_ux = 0, cor_qyi_rxyi = 0, cor_qyi_ux = 0, cor_rxyi_ux = 0)
```

```
estimate_var_qyi(qya, var_qya = 0, rxyi, var_rxyi = 0, ux,
  var_ux = 0, cor_qya_rxyi = 0, cor_qya_ux = 0, cor_rxyi_ux = 0)
```

```
estimate_var_ryyi(ryya, var_ryya = 0, rxyi, var_rxyi = 0, ux,
  var_ux = 0, cor_ryya_rxyi = 0, cor_ryya_ux = 0, cor_rxyi_ux = 0)
```

Arguments

qxa	Square-root of applicant reliability estimate.
var_qxa	Variance of square-root of applicant reliability estimate.
ux	Observed-score u ratio.
var_ux	Variance of observed-score u ratio.
cor_qxa_ux	Correlation between qxa and ux.
ux_observed	Logical vector determining whether u ratios are observed-score u ratios (TRUE) or true-score u ratios (FALSE).
indirect_rr	Logical vector determining whether reliability values are associated with indirect range restriction (TRUE) or direct range restriction (FALSE).
qxi	Square-root of incumbent reliability estimate.
var_qxi	Variance of square-root of incumbent reliability estimate.
cor_qxi_ux	Correlation between qxi and ux.
rxxa	Incumbent reliability value.
var_rxxa	Variance of incumbent reliability values.
cor_rxxa_ux	Correlation between rxxa and ux.
rxxi	Incumbent reliability value.
var_rxxi	Variance of incumbent reliability values.
cor_rxxi_ux	Correlation between rxxi and ux.
rxxi_type, rxxa_type, qxi_type, qxa_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for <code>ma_r</code> for a full list of acceptable reliability types.
rxx	Generic argument for a reliability estimate (whether this is a reliability or the square root of a reliability is clarified by the <code>rxx_as_qx</code> argument).
var_rxx	Generic argument for the variance of reliability estimates (whether this pertains to reliabilities or the square roots of reliabilities is clarified by the <code>rxx_as_qx</code> argument).
cor_rxx_ux	Correlation between rxx and ux.

rxx_restricted	Logical vector determining whether reliability estimates were incumbent reliabilities (TRUE) or applicant reliabilities (FALSE).
rxx_as_qx	Logical vector determining whether the reliability estimates were reliabilities (TRUE) or square-roots of reliabilities (FALSE).
ut	True-score u ratio.
var_ut	Variance of true-score u ratio.
cor_rxx_ut	Correlation between rxx and ut.
ryyi	Incumbent reliability value.
var_ryyi	Variance of incumbent reliability values.
rxyi	Incumbent correlation between X and Y.
var_rxyi	Variance of incumbent correlations.
cor_ryyi_rxyi	Correlation between ryyi and rxyi.
cor_ryyi_ux	Correlation between ryyi and ux.
cor_rxyi_ux	Correlation between rxyi and ux.
qyi	Square-root of incumbent reliability estimate.
var_qyi	Variance of square-root of incumbent reliability estimate.
cor_qyi_rxyi	Correlation between qyi and rxyi.
cor_qyi_ux	Correlation between qyi and ux.
qya	Square-root of applicant reliability estimate.
var_qya	Variance of square-root of applicant reliability estimate.
cor_qya_rxyi	Correlation between qya and rxyi.
cor_qya_ux	Correlation between qya and ux.
ryya	Applicant reliability value.
var_ryya	Variance of applicant reliability values.
cor_ryya_rxyi	Correlation between ryya and rxyi.
cor_ryya_ux	Correlation between ryya and ux.

Details

Partial derivatives to estimate the variance of qxa using ux

Indirect range restriction:

$$b_{u_X} = \frac{(q_{X_i}^2 - 1)u_X}{\sqrt{(q_{X_i}^2 - 1)u_X^2 + 1}}$$

$$b_{q_{X_i}} = \frac{q_{X_i}^2 u_X^2}{\sqrt{(q_{X_i}^2 - 1)u_X^2 + 1}}$$

Direct range restriction:

$$b_{u_X} = \frac{q_{X_i}^2 (q_{X_i}^2 - 1)u_X}{\sqrt{-\frac{q_{X_i}^2}{q_{X_i}^2 (u_X^2 - 1) - u_X^2} (q_{X_i}^2 (u_X^2 - 1) - u_X^2)^2}}$$

$$b_{q_{X_i}} = \frac{q_{X_i} u_X^2}{\sqrt{-\frac{q_{X_i}^2}{q_{X_i}^2 (u_X^2 - 1) - u_X^2} (q_{X_i}^2 (u_X^2 - 1) - u_X^2)^2}}$$

Partial derivatives to estimate the variance of rxxa using ux

Indirect range restriction:

$$b_{u_X} = 2(\rho_{XX_i} - 1) u_X$$

$$\rho_{XX_i} : b_{\rho_{XX_i}} = u_X^2$$

Direct range restriction:

$$b_{u_X} = \frac{2(\rho_{XX_i} - 1)\rho_{XX_i} u_X}{(-\rho_{XX_i} u_X^2 + \rho_{XX_i} + u_X^2)^2}$$

$$b_{\rho_{XX_i}} = \frac{u_X^2}{(-\rho_{XX_i} u_X^2 + \rho_{XX_i} + u_X^2)^2}$$

Partial derivatives to estimate the variance of rxxa using ut

$$b_{u_T} = \frac{2(\rho_{XX_i} - 1) * \rho_{XX_i} u_T}{(-\rho_{XX_i} u_T^2 + \rho_{XX_i} + u_T^2)^2}$$

$$b_{\rho_{XX_i}} = \frac{u_T^2}{(-\rho_{XX_i} u_T^2 + \rho_{XX_i} + u_T^2)^2}$$

Partial derivatives to estimate the variance of qxa using ut

$$b_{u_T} = \frac{q_{X_i}^2 (q_{X_i}^2 - 1) u_T}{\sqrt{\frac{-q_{X_i}^2}{q_{X_i}^2 * (u_T^2 - 1) - u_T^2} (q_{X_i}^2 (u_T^2 - 1) - u_T^2)^2}}$$

$$b_{q_{X_i}} = \frac{q_{X_i} u_T^2}{\sqrt{\frac{q_{X_i}^2}{u_T^2 - q_{X_i}^2 (u_T^2 - 1)} (u_T^2 - q_{X_i}^2 (u_T^2 - 1))^2}}$$

Partial derivatives to estimate the variance of qxi using ux

Indirect range restriction:

$$b_{u_X} = \frac{1 - q_X a^2}{u_X^3 \sqrt{\frac{q_{X_a}^2 + u_X^2 - 1}{u_X^2}}}$$

$$b_{q_{X_a}} = \frac{q_{X_a}}{u_X^2 \sqrt{\frac{q_{X_a}^2 - 1}{u_X^2} + 1}}$$

Direct range restriction:

$$b_{u_X} = -\frac{q_{X_a}^2 (q_{X_a}^2 - 1) u_X}{\sqrt{\frac{q_{X_a}^2 u_X^2}{q_{X_a}^2 (u_X^2 - 1) + 1} (q_{X_a}^2 (u_X^2 - 1) + 1)^2}}$$

$$b_{q_{X_a}} = \frac{q_{X_a} u_X^2}{\sqrt{\frac{q_{X_a}^2 u_X^2}{q_{X_a}^2 (u_X^2 - 1) + 1} (q_{X_a}^2 (u_X^2 - 1) + 1)^2}}$$

Partial derivatives to estimate the variance of rxxi using ux

Indirect range restriction:

$$b_{u_X} = \frac{2 - 2\rho_{XX_a}}{u_X^3}$$

$$b_{\rho_{XX_a}} = \frac{1}{u_X^2}$$

Direct range restriction:

$$b_{u_X} = -\frac{2(\rho_{XX_a} - 1)\rho_{XX_a} u_X}{(\rho_{XX_a} (u_X^2 - 1) + 1)^2}$$

$$b_{\rho_{XX_a}} = \frac{u_X^2}{(\rho_{XX_a} (u_X^2 - 1) + 1)^2}$$

Partial derivatives to estimate the variance of rxxi using ut

$$u_T : b_{u_T} = -\frac{2(\rho_{XX_a} - 1)\rho_{XX_a} u_T}{(\rho_{XX_a} (u_T^2 - 1) + 1)^2}$$

$$b_{\rho_{XX_a}} = \frac{u_T^2}{(\rho_{XX_a} (u_T^2 - 1) + 1)^2}$$

Partial derivatives to estimate the variance of qxi using ut

$$b_{u_T} = -\frac{(q_{X_a} - 1)q_{X_a}^2 (q_{X_a} + 1)u_T}{\sqrt{\frac{q_{X_a}^2 u_T^2}{q_{X_a}^2 u_T^2 - q_{X_a}^2 + 1} (q_{X_a}^2 u_T^2 - q_{X_a}^2 + 1)^2}}$$

$$b_{q_{X_a}} = \frac{q_{X_a} u_T^2}{\sqrt{\frac{q_{X_a}^2 u_T^2}{q_{X_a}^2 u_T^2 - q_{X_a}^2 + 1} (q_{X_a}^2 u_T^2 - q_{X_a}^2 + 1)^2}}$$

Partial derivatives to estimate the variance of ut using qxi

$$b_{u_X} = \frac{q_{X_i}^2 u_X}{\sqrt{\frac{q_{X_i}^2 u_X^2}{(q_{X_i}^2 - 1)u_X^2 + 1} ((q_{X_i}^2 - 1)u_X^2 + 1)^2}}$$

$$b_{q_{X_i}} = -\frac{u_X^2 (u_X^2 - 1)}{\sqrt{\frac{q_{X_i}^2 u_X^2}{(q_{X_i}^2 - 1)u_X^2 + 1} ((q_{X_i}^2 - 1)u_X^2 + 1)^2}}$$

Partial derivatives to estimate the variance of ut using rxxi

$$b_{u_X} = \frac{\rho_{XX_i} u_X}{\sqrt{\frac{\rho_{XX_i} u_X^2}{(\rho_{XX_i} - 1)u_X^2 + 1} ((\rho_{XX_i} - 1)u_X^2 + 1)^2}}$$

$$b_{\rho_{XX_i}} = -\frac{u_X^2 (u_X^2 - 1)}{2\sqrt{\frac{\rho_{XX_i} u_X^2}{(\rho_{XX_i} - 1)u_X^2 + 1} ((\rho_{XX_i} - 1)u_X^2 + 1)^2}}$$

Partial derivatives to estimate the variance of ut using qxa

$$b_{u_X} = \frac{u_X}{q_{X_a}^2 \sqrt{\frac{q_{X_a}^2 + u_X^2 - 1}{q_{X_a}^2}}}$$

$$b_{q_{X_a}} = \frac{1 - u_X^2}{q_{X_a}^3 \sqrt{\frac{q_{X_a}^2 + u_X^2 - 1}{q_{X_a}^2}}}$$

Partial derivatives to estimate the variance of ut using rxxa

$$b_{u_X} = \frac{u_X}{\rho_{XX_a} \sqrt{\frac{\rho_{XX_a} + u_X^2 - 1}{\rho_{XX_a}}}}$$

$$b_{\rho_{XX_a}} = \frac{1 - u_X^2}{2\rho_{XX_a}^2 \sqrt{\frac{\rho_{XX_a} + u_X^2 - 1}{\rho_{XX_a}}}}$$

Partial derivatives to estimate the variance of ux using qxi

$$b_{u_T} = \frac{q_{X_i}^2 u_T}{\sqrt{\frac{u_T^2}{u_T^2 - q_{X_i}^2 (u_T^2 - 1)} (u_T^2 - q_{X_i}^2 (u_T^2 - 1))^2}}$$

$$b_{q_{X_i}} = \frac{q_{X_i} (u_T^2 - 1) \left(\frac{u_T^2}{u_T^2 - q_{X_i}^2 (u_T^2 - 1)} \right)^{1.5}}{u_T^2}$$

Partial derivatives to estimate the variance of ux using rxxi

$$b_{u_T} = \frac{\rho_{XX_i} u_T}{\sqrt{\frac{u_T^2}{-\rho_{XX_i} u_T^2 + \rho_{XX_i} + u_T^2} (-\rho_{XX_i} u_T^2 + \rho_{XX_i} + u_T^2)^2}}$$

$$b_{\rho_{XX_i}} = \frac{(u_T^2 - 1) \left(\frac{u_T^2}{-\rho_{XX_i} u_T^2 + \rho_{XX_i} + u_T^2} \right)^{1.5}}{2u_T^2}$$

Partial derivatives to estimate the variance of ux using qxa

$$b_{u_T} = \frac{q_{X_a}^2 u_T}{\sqrt{q_{X_a}^2 (u_T^2 - 1) + 1}}$$

$$b_{q_{X_a}} = \frac{q_{X_a} (u_T - 1)}{\sqrt{q_{X_a}^2 (u_T^2 - 1) + 1}}$$

Partial derivatives to estimate the variance of ux using rxxa

$$b_{u_T} = \frac{\rho_{X X_a} u_T}{\sqrt{\rho_{X X_a} (u_T^2 - 1) + 1}}$$

$$b_{\rho_{X X_a}} = \frac{u_T^2 - 1}{2\sqrt{\rho_{X X_a} (u_T^2 - 1) + 1}}$$

Partial derivatives to estimate the variance of ryya

$$b_{\rho_{Y Y_i}} = \frac{1}{\rho_{X Y_i}^2 \left(\frac{1}{u_X^2} - 1 \right) + 1}$$

$$b_{u_X} = \frac{2(\rho_{Y Y_i} - 1)\rho_{X Y_i}^2 u_X}{(u_X^2 - \rho_{X Y_i}^2 (u_X^2 - 1))^2}$$

$$b_{\rho_{X Y_i}} = \frac{2(\rho_{Y Y_i} - 1)\rho_{X Y_i} u_X^2 (u_X^2 - 1)}{(u_X^2 - \rho_{X Y_i}^2 (u_X^2 - 1))^2}$$

Partial derivatives to estimate the variance of qya

$$b_{q_{Y_i}} = \frac{q_{Y_i}}{\left[1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_X^2} \right) \right] \sqrt{1 - \frac{1 - q_{Y_i}^2}{1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_X^2} \right)}}$$

$$b_{u_X} = - \frac{(1 - q_{Y_i}^2)\rho_{X Y_i}^2}{u_X^3 \left[1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_X^2} \right) \right] \sqrt{1 - \frac{1 - q_{Y_i}^2}{1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_X^2} \right)}}$$

$$b_{\rho_{X Y_i}} = - \frac{(1 - q_{Y_i}^2)\rho_{X Y_i} \left(1 - \frac{1}{u_X^2} \right)}{\left[1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_X^2} \right) \right] \sqrt{1 - \frac{1 - q_{Y_i}^2}{1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_X^2} \right)}}$$

Partial derivatives to estimate the variance of ryyi

$$\rho_{Y Y_a} : b_{\rho_{Y Y_a}} = \rho_{X Y_i}^2 \left(\frac{1}{u_X^2} - 1 \right) + 1$$

$$b_{u_x} = -\frac{2(\rho_{Y Y_a} - 1)\rho_{X Y_i}^2}{u_x^3}$$

$$b_{\rho_{X Y_i}} = -\frac{2(\rho_{Y Y_a} - 1)\rho_{X Y_i}(u_x^2 - 1)}{u_x^2}$$

Partial derivatives to estimate the variance of qyi

$$b_{q_{Y_a}} = \frac{q_{Y_a} \left[1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_x^2} \right) \right]}{\sqrt{1 - (1 - q_{Y_a}) \left[1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_x^2} \right) \right]}}$$

$$b_{u_x} = \frac{(1 - q_{Y_a}^2)\rho_{X Y_i} \left(1 - \frac{1}{u_x^2} \right)}{\sqrt{1 - (1 - q_{Y_a}) \left[1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_x^2} \right) \right]}}$$

$$b_{\rho_{X Y_i}} = \frac{(1 - q_{Y_a}^2)\rho_{X Y_i}^2}{u_x^3 \sqrt{1 - (1 - q_{Y_a}) \left[1 - \rho_{X Y_i}^2 \left(1 - \frac{1}{u_x^2} \right) \right]}}$$

Examples

```
estimate_var_qxi(qxa = c(.8, .85, .9, .95), var_qxa = c(.02, .03, .04, .05),
  ux = .8, var_ux = 0,
  ux_observed = c(TRUE, TRUE, FALSE, FALSE),
  indirect_rr = c(TRUE, FALSE, TRUE, FALSE))
estimate_var_qxa(qxi = c(.8, .85, .9, .95), var_qxi = c(.02, .03, .04, .05),
  ux = .8, var_ux = 0,
  ux_observed = c(TRUE, TRUE, FALSE, FALSE),
  indirect_rr = c(TRUE, FALSE, TRUE, FALSE))
estimate_var_rxxi(rxxa = c(.8, .85, .9, .95),
  var_rxxa = c(.02, .03, .04, .05), ux = .8, var_ux = 0,
  ux_observed = c(TRUE, TRUE, FALSE, FALSE),
  indirect_rr = c(TRUE, FALSE, TRUE, FALSE))
estimate_var_rxxa(rxxi = c(.8, .85, .9, .95), var_rxxi = c(.02, .03, .04, .05),
  ux = .8, var_ux = 0,
  ux_observed = c(TRUE, TRUE, FALSE, FALSE),
  indirect_rr = c(TRUE, FALSE, TRUE, FALSE))
estimate_var_ut(rxx = c(.8, .85, .9, .95), var_rxx = 0,
  ux = c(.8, .8, .9, .9), var_ux = c(.02, .03, .04, .05),
  rxx_restricted = c(TRUE, TRUE, FALSE, FALSE),
  rxx_as_qx = c(TRUE, FALSE, TRUE, FALSE))
estimate_var_ux(rxx = c(.8, .85, .9, .95), var_rxx = 0,
  ut = c(.8, .8, .9, .9), var_ut = c(.02, .03, .04, .05),
  rxx_restricted = c(TRUE, TRUE, FALSE, FALSE),
  rxx_as_qx = c(TRUE, FALSE, TRUE, FALSE))
estimate_var_ryya(ryyi = .9, var_ryyi = .04, rxyi = .4, var_rxyi = 0, ux = .8, var_ux = 0)
estimate_var_ryya(ryyi = .9, var_ryyi = .04, rxyi = .4, var_rxyi = 0, ux = .8, var_ux = 0)
estimate_var_qyi(qya = .9, var_qya = .04, rxyi = .4, var_rxyi = 0, ux = .8, var_ux = 0)
estimate_var_ryyi(ryya = .9, var_ryya = .04, rxyi = .4, var_rxyi = 0, ux = .8, var_ux = 0)
```

estimate_var_rho_int *Non-linear estimate of variance of ρ corrected for psychometric artifacts using numeric integration*

Description

Functions to estimate the variance of ρ corrected for psychometric artifacts. These functions integrate over the residual distribution of correlations from an interactive artifact-distribution meta-analysis to non-linearly estimate the variance of ρ .

Available functions include:

- estimate_var_rho_int_meas
Variance of ρ corrected for measurement error only
- estimate_var_rho_int_uvdr
Variance of ρ corrected for univariate direct range restriction (i.e., Case II) and measurement error
- estimate_var_rho_int_bvdr
Variance of ρ corrected for bivariate direct range restriction and measurement error
- estimate_var_rho_int_uvirr
Variance of ρ corrected for univariate indirect range restriction (i.e., Case IV) and measurement error
- estimate_var_rho_int_bvirr
Variance of ρ corrected for bivariate indirect range restriction (i.e., Case V) and measurement error
- estimate_var_rho_int_rb
Variance of ρ corrected using Raju and Burke's correction for direct range restriction and measurement error

Usage

```
estimate_var_rho_int_meas(mean_qx, mean_qy, var_res)
```

```
estimate_var_rho_int_uvdr(mean_rxyi, mean_rtpa, mean_qxa, mean_qyi,
  mean_ux, var_res)
```

```
estimate_var_rho_int_uvirr(mean_rxyi, mean_rtpa, mean_qxi, mean_qyi,
  mean_ut, var_res)
```

```
estimate_var_rho_int_bvdr(mean_qxa, mean_qya, mean_ux, mean_uy, var_res)
```

```
estimate_var_rho_int_bvirr(mean_rxyi, mean_rtpa, mean_qxa, mean_qya,
  mean_ux, mean_uy, var_res)
```

```
estimate_var_rho_int_rb(mean_rxyi, mean_rtpa, mean_qx, mean_qy, mean_ux,
  var_res)
```

Arguments

mean_qx	Mean square root of reliability for X.
mean_qy	Mean square root of reliability for Y.
var_res	Residual variance from an interactive artifact distribution (i.e., variance of observed correlations minus predicted error variance and predicted artifact variance).
mean_rxyi	Mean observed correlation.
mean_rtpa	Mean corrected correlation.
mean_qxa	Mean square root of unrestricted reliability for X.
mean_qyi	Mean square root of restricted reliability for Y.
mean_ux	Mean observed-score u ratio for X.
mean_qxi	Mean square root of restricted reliability for X.
mean_ut	Mean true-score u ratio for X.
mean_qya	Mean square root of unrestricted reliability for Y.
mean_uy	Mean observed-score u ratio for Y.

Value

A vector of non-linear estimates of the variance of rho.

Notes

estimate_var_rho_int_meas and estimate_var_rho_int_bvirr do not make use of numeric integration because they are linear functions.

References

Law, K. S., Schmidt, F. L., & Hunter, J. E. (1994). Nonlinearity of range corrections in meta-analysis: Test of an improved procedure. *Journal of Applied Psychology*, 79(3), 425–438. <https://doi.org/10.1037/0021-9010.79.3.425>

estimate_var_rho_tsa *Taylor Series Approximation of variance of ρ corrected for psychometric artifacts*

Description

Functions to estimate the variance of ρ corrected for psychometric artifacts. These functions use Taylor series approximations (i.e., the delta method) to estimate the variance in observed effect sizes predictable from the variance in artifact distributions based on the partial derivatives.

The available Taylor-series functions include:

- estimate_var_rho_tsa_meas
Variance of ρ corrected for measurement error only

- `estimate_var_rho_tsa_uvdr`
Variance of ρ corrected for univariate direct range restriction (i.e., Case II) and measurement error
- `estimate_var_rho_tsa_bvdr`
Variance of ρ corrected for bivariate direct range restriction and measurement error
- `estimate_var_rho_tsa_uvirr`
Variance of ρ corrected for univariate indirect range restriction (i.e., Case IV) and measurement error
- `estimate_var_rho_tsa_bvirr`
Variance of ρ corrected for bivariate indirect range restriction (i.e., Case V) and measurement error
- `estimate_var_rho_tsa_rb1`
Variance of ρ corrected using Raju and Burke's TSA1 correction for direct range restriction and measurement error
- `estimate_var_rho_tsa_rb2`
Variance of ρ corrected using Raju and Burke's TSA2 correction for direct range restriction and measurement error. Note that a typographical error in Raju and Burke's article has been corrected in this function so as to compute appropriate partial derivatives.

Usage

```
estimate_var_rho_tsa_meas(mean_rtp, var_rxy, var_e, mean_qx = 1,
  var_qx = 0, mean_qy = 1, var_qy = 0, ...)
```

```
estimate_var_rho_tsa_uvdr(mean_rtpa, var_rxyi, var_e, mean_ux = 1,
  var_ux = 0, mean_qxa = 1, var_qxa = 0, mean_qyi = 1,
  var_qyi = 0, ...)
```

```
estimate_var_rho_tsa_bvdr(mean_rtpa, var_rxyi, var_e = 0, mean_ux = 1,
  var_ux = 0, mean_uy = 1, var_uy = 0, mean_qxa = 1, var_qxa = 0,
  mean_qya = 1, var_qya = 0, ...)
```

```
estimate_var_rho_tsa_uvirr(mean_rtpa, var_rxyi, var_e, mean_ut = 1,
  var_ut = 0, mean_qxa = 1, var_qxa = 0, mean_qyi = 1,
  var_qyi = 0, ...)
```

```
estimate_var_rho_tsa_bvirr(mean_rtpa, var_rxyi, var_e = 0, mean_ux = 1,
  var_ux = 0, mean_uy = 1, var_uy = 0, mean_qxa = 1, var_qxa = 0,
  mean_qya = 1, var_qya = 0, sign_rxz = 1, sign_ryz = 1, ...)
```

```
estimate_var_rho_tsa_rb1(mean_rtpa, var_rxyi, var_e, mean_ux = 1,
  var_ux = 0, mean_rxx = 1, var_rxx = 0, mean_ryy = 1,
  var_ryy = 0, ...)
```

```
estimate_var_rho_tsa_rb2(mean_rtpa, var_rxyi, var_e, mean_ux = 1,
  var_ux = 0, mean_qx = 1, var_qx = 0, mean_qy = 1, var_qy = 0,
  ...)
```

Arguments

mean_rtp	Mean corrected correlation.
var_rxy	Variance of observed correlations.
var_e	Error variance of observed correlations
mean_qx	Mean square root of reliability for X.
var_qx	Variance of square roots of reliability estimates for X.
mean_qy	Mean square root of reliability for Y.
var_qy	Variance of square roots of reliability estimates for Y.
...	Additional arguments.
mean_rtpa	Mean corrected correlation.
var_rxyi	Variance of observed correlations.
mean_ux	Mean observed-score u ratio for X.
var_ux	Variance of observed-score u ratios for X.
mean_qxa	Mean square root of unrestricted reliability for X.
var_qxa	Variance of square roots of unrestricted reliability estimates for X.
mean_qyi	Mean square root of restricted reliability for Y.
var_qyi	Variance of square roots of restricted reliability estimates for Y.
mean_uy	Mean observed-score u ratio for Y.
var_uy	Variance of observed-score u ratios for Y.
mean_qya	Mean square root of unrestricted reliability for Y.
var_qya	Variance of square roots of unrestricted reliability estimates for Y.
mean_ut	Mean true-score u ratio for X.
var_ut	Variance of true-score u ratios for X.
sign_rxz	Sign of the relationship between X and the selection mechanism.
sign_ryz	Sign of the relationship between Y and the selection mechanism.
mean_rxx	Mean reliability for X.
var_rxx	Variance of reliability estimates for X.
mean_ryy	Mean reliability for Y.
var_ryy	Variance of reliability estimates for Y.

Details

Measurement error only

The attenuation formula for measurement error is

$$\rho_{XY} = \rho_{TP} q_X q_Y$$

where ρ_{XY} is an observed correlation, ρ_{TP} is a true-score correlation, and q_X and q_Y are the square roots of reliability coefficients for X and Y, respectively.

The Taylor series approximation of the variance of ρ_{TP} can be computed using the following linear equation,

$$var_{\rho_{TP}} \approx [var_{r_{XY}} - var_e - (b_1^2 var_{q_X} + b_2^2 var_{q_Y})] / b_3^2$$

where b_1 , b_2 , and b_3 are first-order partial derivatives of the attenuation formula with respect to q_X , q_Y , and ρ_{TP} , respectively. The first-order partial derivatives of the attenuation formula are:

$$b_1 = \frac{\partial \rho_{XY}}{\partial q_X} = \rho_{TP} q_Y$$

$$b_2 = \frac{\partial \rho_{XY}}{\partial q_Y} = \rho_{TP} q_X$$

$$b_3 = \frac{\partial \rho_{XY}}{\partial \rho_{TP}} = q_X q_Y$$

Univariate direct range restriction (UVDRR; i.e., Case II)

The UVDRR attenuation procedure may be represented as

$$\rho_{XY_i} = \frac{\rho_{TP_a} q_{Y_i} q_{X_a} u_X}{\sqrt{\rho_{TP_a}^2 q_{X_a}^2 (u_X^2 - 1) + 1}}$$

The attenuation formula can also be represented as:

$$\rho_{XY_i} = \rho_{TP_a} q_{Y_i} q_{X_a} u_X A$$

where

$$A = \frac{1}{\sqrt{\rho_{TP_a}^2 q_{X_a}^2 (u_X^2 - 1) + 1}}$$

The Taylor series approximation of the variance of ρ_{TP_a} can be computed using the following linear equation,

$$var_{\rho_{TP_a}} \approx [var_{r_{XY_i}} - var_e - (b_1^2 var_{q_{X_a}} + b_2^2 var_{q_{Y_i}} + b_3^2 var_{u_X})] / b_4^2$$

where b_1 , b_2 , b_3 , and b_4 are first-order partial derivatives of the attenuation formula with respect to q_{X_a} , q_{Y_i} , u_X , and ρ_{TP_a} , respectively. The first-order partial derivatives of the attenuation formula are:

$$b_1 = \frac{\partial \rho_{XY_i}}{\partial q_{X_a}} = \rho_{TP_a} q_{Y_i} u_X A^3$$

$$b_2 = \frac{\partial \rho_{XY_i}}{\partial q_{Y_i}} = \frac{\rho_{XY_i}}{q_{Y_i}}$$

$$b_3 = \frac{\partial \rho_{XY_i}}{\partial u_X} = -\rho_{TP_a} q_{Y_i} q_{X_a} (\rho_{TP_a}^2 q_{X_a}^2 - 1) A^3$$

$$b_4 = \frac{\partial \rho_{XY_i}}{\partial \rho_{TP_a}} = q_{Y_i} q_{X_a} u_X A^3$$

Univariate indirect range restriction (UVIRR; i.e., Case IV)

Under univariate indirect range restriction, the attenuation formula yielding ρ_{XY_i} is:

$$\rho_{XY_i} = \frac{u_T q_{X_a}}{\sqrt{u_T^2 q_{X_a}^2 + 1 - q_{X_a}^2}} \frac{u_T \rho_{TP_a}}{\sqrt{u_T^2 \rho_{TP_a}^2 + 1 - \rho_{TP_a}^2}}$$

The attenuation formula can also be represented as:

$$\rho_{XY_i} = q_{X_a} q_{Y_i} \rho_{TP_a} u_T^2 AB$$

where

$$A = \frac{1}{\sqrt{u_T^2 q_{X_a}^2 + 1 - q_{X_a}^2}}$$

and

$$B = \frac{1}{\sqrt{u_T^2 \rho_{TP_a}^2 + 1 - \rho_{TP_a}^2}}$$

The Taylor series approximation of the variance of ρ_{TP_a} can be computed using the following linear equation,

$$\text{var}_{\rho_{TP_a}} \approx [\text{var}_{r_{XY_i}} - \text{var}_e - (b_1^2 \text{var}_{q_{X_a}} + b_2^2 \text{var}_{q_{Y_i}} + b_3^2 \text{var}_{u_T})] / b_4^2$$

where b_1 , b_2 , b_3 , and b_4 are first-order partial derivatives of the attenuation formula with respect to q_{X_a} , q_{Y_i} , u_T , and ρ_{TP_a} , respectively. The first-order partial derivatives of the attenuation formula are:

$$\begin{aligned} b_1 &= \frac{\partial \rho_{XY_i}}{\partial q_{X_a}} = \frac{\rho_{XY_i}}{q_{X_a}} - \rho_{XY_i} q_{X_a} B^2 (u_T^2 - 1) \\ b_2 &= \frac{\partial \rho_{XY_i}}{\partial q_{Y_i}} = \frac{\rho_{XY_i}}{q_{Y_i}} \\ b_3 &= \frac{\partial \rho_{XY_i}}{\partial u_T} = \frac{2\rho_{XY_i}}{u_T} - \rho_{XY_i} u_T q_{X_a}^2 B^2 - \rho_{XY_i} u_T \rho_{TP_a}^2 A^2 \\ b_4 &= \frac{\partial \rho_{XY_i}}{\partial \rho_{TP_a}} = \frac{\rho_{XY_i}}{\rho_{TP_a}} - \rho_{XY_i} \rho_{TP_a} A^2 (u_T^2 - 1) \end{aligned}$$

Bivariate direct range restriction (BVDRR)

Under bivariate direct range restriction, the attenuation formula yielding ρ_{XY_i} is:

$$\rho_{XY_i} = \frac{A + \rho_{TP_a}^2 q_{X_a} q_{Y_a} - \frac{1}{q_{X_a} q_{Y_a}}}{2\rho_{TP_a} u_X u_Y}$$

where

$$A = \sqrt{\left(\frac{1}{q_{X_a} q_{Y_a}} - \rho_{TP_a}^2 q_{X_a} q_{Y_a}\right)^2 + 4\rho_{TP_a} u_X^2 u_Y^2}$$

The Taylor series approximation of the variance of ρ_{TP_a} can be computed using the following linear equation,

$$var_{\rho_{TP_a}} \approx [var_{r_{XY_i}} - var_e - (b_1^2 var_{q_{X_a}} + b_2^2 var_{q_{Y_i}} + b_3^2 var_{u_X} + b_4^2 var_{u_Y})] / b_5^2$$

where $b_1, b_2, b_3, b_4,$ and b_5 are first-order partial derivatives of the attenuation formula with respect to $q_{X_a}, q_{Y_a}, u_X, u_Y,$ and $\rho_{TP_a},$ respectively. First, we define terms to simplify the computation of partial derivatives:

$$B = (\rho_{TP_a}^2 q_{X_a}^2 q_{Y_a}^2 + q_{X_a} q_{Y_a} A - 1)$$

$$C = 2\rho_{TP_a} q_{X_a}^2 q_{Y_a}^2 u_X u_Y A$$

The first-order partial derivatives of the attenuation formula are:

$$b_1 = \frac{\partial \rho_{XY_i}}{\partial q_{X_a}} = \frac{(\rho_{TP_a}^2 q_{X_a}^2 q_{Y_a}^2 + 1) B}{q_{X_a} C}$$

$$b_2 = \frac{\partial \rho_{XY_i}}{\partial q_{Y_i}} = \frac{(\rho_{TP_a}^2 q_{X_a}^2 q_{Y_a}^2 + 1) B}{q_{Y_a} C}$$

$$b_3 = \frac{\partial \rho_{XY_i}}{\partial u_X} = -\frac{(\rho_{TP_a} q_{X_a} q_{Y_a} - 1) (\rho_{TP_a} q_{X_a} q_{Y_a} + 1) B}{u_X C}$$

$$b_4 = \frac{\partial \rho_{XY_i}}{\partial u_Y} = -\frac{(\rho_{TP_a} q_{X_a} q_{Y_a} - 1) (\rho_{TP_a} q_{X_a} q_{Y_a} + 1) B}{u_Y C}$$

$$b_5 = \frac{\partial \rho_{XY_i}}{\partial \rho_{TP_a}} = \frac{(\rho_{TP_a}^2 q_{X_a}^2 q_{Y_a}^2 + 1) B}{\rho_{TP_a} C}$$

Bivariate indirect range restriction (BVIRR; i.e., Case V)

Under bivariate indirect range restriction, the attenuation formula yielding ρ_{XY_i} is:

$$\rho_{XY_i} = \frac{\rho_{TP_a} q_{X_a} q_{Y_a} - \lambda \sqrt{|1 - u_X^2| |1 - u_Y^2|}}{u_X u_Y}$$

The Taylor series approximation of the variance of ρ_{TP_a} can be computed using the following linear equation,

$$var_{\rho_{TP_a}} \approx [var_{r_{XY_i}} - var_e - (b_1^2 var_{q_{X_a}} + b_2^2 var_{q_{Y_i}} + b_3^2 var_{u_X} + b_4^2 var_{u_Y})] / b_5^2$$

where $b_1, b_2, b_3, b_4,$ and b_5 are first-order partial derivatives of the attenuation formula with respect to $q_{X_a}, q_{Y_a}, u_X, u_Y,$ and $\rho_{TP_a},$ respectively. First, we define terms to simplify the computation of partial derivatives:

$$\begin{aligned} b_1 &= \frac{\partial \rho_{XY_i}}{\partial q_{X_a}} = \frac{\rho_{TP_a} q_{Y_a}}{u_X u_Y} \\ b_2 &= \frac{\partial \rho_{XY_i}}{\partial q_{Y_i}} = \frac{\rho_{TP_a} q_{X_a}}{u_X u_Y} \\ b_3 &= \frac{\partial \rho_{XY_i}}{\partial u_X} = \frac{\lambda (1 - u_X^2) \sqrt{|1 - u_Y^2|}}{u_Y |1 - u_X^2|^{1.5}} - \frac{\rho_{XY_i}}{u_X} \\ b_4 &= \frac{\partial \rho_{XY_i}}{\partial u_Y} = \frac{\lambda (1 - u_Y^2) \sqrt{|1 - u_X^2|}}{u_X |1 - u_Y^2|^{1.5}} - \frac{\rho_{XY_i}}{u_Y} \\ b_5 &= \frac{\partial \rho_{XY_i}}{\partial \rho_{TP_a}} = \frac{q_{X_a} q_{Y_a}}{u_X u_Y} \end{aligned}$$

Raju and Burke's TSA1 procedure

Raju and Burke's attenuation formula may be represented as

$$\rho_{XY_i} = \frac{\rho_{TP_a} u_X \sqrt{\rho_{XX_a} \rho_{YY_a}}}{\sqrt{\rho_{TP_a}^2 \rho_{XX_a} \rho_{YY_a} u_X^2 - \rho_{TP_a}^2 \rho_{XX_a} \rho_{YY_a} + 1}}$$

The Taylor series approximation of the variance of ρ_{TP_a} can be computed using the following linear equation,

$$var_{\rho_{TP_a}} \approx [var_{r_{XY_i}} - var_e - (B^2 var_{\rho_{YY_a}} + C^2 var_{\rho_{XX_a}} + D^2 var_{u_X})] / A^2$$

where A, B, C, and D are first-order partial derivatives of the attenuation formula with respect to $\rho_{TP_a}, \rho_{XX_a}, \rho_{YY_a},$ and $u_X,$ respectively. The first-order partial derivatives of the attenuation formula are:

$$\begin{aligned} A &= \frac{\partial \rho_{XY_i}}{\partial \rho_{TP_a}} = \frac{\rho_{XY_i}}{\rho_{TP_a}} + \frac{\rho_{XY_i}^3 (1 - u_X^2)}{\rho_{TP_a} u_X^2} \\ B &= \frac{\partial \rho_{XY_i}}{\partial \rho_{YY_a}} = \frac{1}{2} \left(\frac{\rho_{XY_i}}{\rho_{YY_a}} + \frac{\rho_{XY_i}^3 (1 - u_X^2)}{\rho_{YY_a} u_X^2} \right) \\ C &= \frac{\partial \rho_{XY_i}}{\partial \rho_{XX_a}} = \frac{1}{2} \left(\frac{\rho_{XY_i}}{\rho_{XX_a}} + \frac{\rho_{XY_i}^3 (1 - u_X^2)}{\rho_{XX_a} u_X^2} \right) \end{aligned}$$

$$D = \frac{\partial \rho_{XY_i}}{\partial u_X} = \frac{\rho_{XY_i} - \rho_{XY_i}^3}{u_X}$$

Raju and Burke's TSA2 procedure

Raju and Burke's attenuation formula may be represented as

$$\rho_{XY_i} = \frac{\rho_{TP_a} q_{X_a} q_{Y_a} u_X}{\sqrt{\rho_{TP_a}^2 q_{X_a}^2 q_{Y_a}^2 u_X^2 - \rho_{TP_a}^2 q_{X_a}^2 q_{Y_a}^2 + 1}}$$

The Taylor series approximation of the variance of ρ_{TP_a} can be computed using the following linear equation,

$$var_{\rho_{TP_a}} \approx [var_{r_{XY_i}} - var_e - (F^2 var_{q_{Y_a}} + G^2 var_{q_{X_a}} + H^2 var_{u_X})] / E^2$$

where E, F, G, and H are first-order partial derivatives of the attenuation formula with respect to ρ_{TP_a} , q_{X_a} , q_{Y_a} , and u_X , respectively. The first-order partial derivatives of the attenuation formula (with typographic errors in the original article corrected) are:

$$E = \frac{\partial \rho_{XY_i}}{\partial \rho_{TP_a}} = \frac{\rho_{XY_i}}{\rho_{TP_a}} + \frac{\rho_{XY_i}^3 (1 - u_X^2)}{\rho_{TP_a} u_X^2}$$

$$F = \frac{\partial \rho_{XY_i}}{\partial q_{Y_a}} = \frac{\rho_{XY_i}}{q_{Y_a}} + \frac{\rho_{XY_i}^3 (1 - u_X^2)}{q_{Y_a} u_X^2}$$

$$G = \frac{\partial \rho_{XY_i}}{\partial q_{X_a}} = \frac{\rho_{XY_i}}{q_{X_a}} + \frac{\rho_{XY_i}^3 (1 - u_X^2)}{q_{X_a} u_X^2}$$

$$H = \frac{\partial \rho_{XY_i}}{\partial u_X} = \frac{\rho_{XY_i} - \rho_{XY_i}^3}{u_X}$$

Value

Vector of meta-analytic variances estimated via Taylor series approximation.

Notes

A typographical error in Raju and Burke's article has been corrected in estimate_var_rho_tsa_rb2 so as to compute appropriate partial derivatives.

References

Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.

Hunter, J. E., Schmidt, F. L., & Le, H. (2006). Implications of direct and indirect range restriction for meta-analysis methods and findings. *Journal of Applied Psychology*, 91(3), 594–612. <https://doi.org/10.1037/0021-9010.91.3.594>

Raju, N. S., & Burke, M. J. (1983). Two new procedures for studying validity generalization. *Journal of Applied Psychology*, 68(3), 382–395. <https://doi.org/10.1037/0021-9010.68.3.382>

Examples

```

estimate_var_rho_tsa_meas(mean_rtp = .5, var_rxy = .02, var_e = .01,
                          mean_qx = .8, var_qx = .005,
                          mean_qy = .8, var_qy = .005)
estimate_var_rho_tsa_uvdrd(mean_rtpa = .5, var_rxyi = .02, var_e = .01,
                          mean_ux = .8, var_ux = .005,
                          mean_qxa = .8, var_qxa = .005,
                          mean_qyi = .8, var_qyi = .005)
estimate_var_rho_tsa_bvdrd(mean_rtpa = .5, var_rxyi = .02, var_e = .01,
                          mean_ux = .8, var_ux = .005,
                          mean_uy = .8, var_uy = .005,
                          mean_qxa = .8, var_qxa = .005,
                          mean_qya = .8, var_qya = .005)
estimate_var_rho_tsa_uvirr(mean_rtpa = .5, var_rxyi = .02, var_e = .01,
                          mean_ut = .8, var_ut = .005,
                          mean_qxa = .8, var_qxa = .005,
                          mean_qyi = .8, var_qyi = .005)
estimate_var_rho_tsa_bvirr(mean_rtpa = .5, var_rxyi = .02, var_e = .01,
                          mean_ux = .8, var_ux = .005,
                          mean_uy = .8, var_uy = .005,
                          mean_qxa = .8, var_qxa = .005,
                          mean_qya = .8, var_qya = .005,
                          sign_rxz = 1, sign_ryz = 1)
estimate_var_rho_tsa_rb1(mean_rtpa = .5, var_rxyi = .02, var_e = .01,
                        mean_ux = .8, var_ux = .005,
                        mean_rxx = .8, var_rxx = .005,
                        mean_ryy = .8, var_ryy = .005)
estimate_var_rho_tsa_rb2(mean_rtpa = .5, var_rxyi = .02, var_e = .01,
                        mean_ux = .8, var_ux = .005,
                        mean_qx = .8, var_qx = .005,
                        mean_qy = .8, var_qy = .005)

```

estimate_var_tsa

Taylor Series Approximation of effect-size variances corrected for psychometric artifacts

Description

Functions to estimate the variances corrected for psychometric artifacts. These functions use Taylor series approximations (i.e., the delta method) to estimate the corrected variance of an effect-size distribution.

The available Taylor-series functions include:

- estimate_var_tsa_meas
Variance of ρ corrected for measurement error only
- estimate_var_tsa_uvdrd
Variance of ρ corrected for univariate direct range restriction (i.e., Case II) and measurement error

- `estimate_var_tsa_bvdrr`
Variance of ρ corrected for bivariate direct range restriction and measurement error
- `estimate_var_tsa_uvirr`
Variance of ρ corrected for univariate indirect range restriction (i.e., Case IV) and measurement error
- `estimate_var_tsa_bvirr`
Variance of ρ corrected for bivariate indirect range restriction (i.e., Case V) and measurement error
- `estimate_var_tsa_rb1`
Variance of ρ corrected using Raju and Burke's TSA1 correction for direct range restriction and measurement error
- `estimate_var_tsa_rb2`
Variance of ρ corrected using Raju and Burke's TSA2 correction for direct range restriction and measurement error. Note that a typographical error in Raju and Burke's article has been corrected in this function so as to compute appropriate partial derivatives.

Usage

```
estimate_var_tsa_meas(mean_rtp, var = 0, mean_qx = 1, mean_qy = 1,
  ...)

estimate_var_tsa_uvdrd(mean_rtpa, var = 0, mean_ux = 1, mean_qxa = 1,
  mean_qyi = 1, ...)

estimate_var_tsa_bvdrr(mean_rtpa, var = 0, mean_ux = 1, mean_uy = 1,
  mean_qxa = 1, mean_qya = 1, ...)

estimate_var_tsa_uvirr(mean_rtpa, var = 0, mean_ut = 1, mean_qxa = 1,
  mean_qyi = 1, ...)

estimate_var_tsa_bvirr(mean_rtpa, var = 0, mean_ux = 1, mean_uy = 1,
  mean_qxa = 1, mean_qya = 1, sign_rxz = 1, sign_ryz = 1, ...)

estimate_var_tsa_rb1(mean_rtpa, var = 0, mean_ux = 1, mean_rxx = 1,
  mean_ryy = 1, ...)

estimate_var_tsa_rb2(mean_rtpa, var = 0, mean_ux = 1, mean_qx = 1,
  mean_qy = 1, ...)
```

Arguments

<code>mean_rtp</code>	Mean corrected correlation.
<code>var</code>	Variance to be corrected for artifacts.
<code>mean_qx</code>	Mean square root of reliability for X.
<code>mean_qy</code>	Mean square root of reliability for Y.
<code>...</code>	Additional arguments.

mean_rtpa	Mean corrected correlation.
mean_ux	Mean observed-score u ratio for X.
mean_qxa	Mean square root of unrestricted reliability for X.
mean_qyi	Mean square root of restricted reliability for Y.
mean_uy	Mean observed-score u ratio for Y.
mean_qya	Mean square root of unrestricted reliability for Y.
mean_ut	Mean true-score u ratio for X.
sign_rxz	Sign of the relationship between X and the selection mechanism.
sign_ryz	Sign of the relationship between Y and the selection mechanism.
mean_rxx	Mean reliability for X.
mean_ryy	Mean reliability for Y.

Value

Vector of variances corrected for mean artifacts via Taylor series approximation.

Notes

A typographical error in Raju and Burke's article has been corrected in estimate_var_tsa_rb2 so as to compute appropriate partial derivatives.

References

- Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.
- Hunter, J. E., Schmidt, F. L., & Le, H. (2006). Implications of direct and indirect range restriction for meta-analysis methods and findings. *Journal of Applied Psychology, 91*(3), 594–612. <https://doi.org/10.1037/0021-9010.91.3.594>
- Raju, N. S., & Burke, M. J. (1983). Two new procedures for studying validity generalization. *Journal of Applied Psychology, 68*(3), 382–395. <https://doi.org/10.1037/0021-9010.68.3.382>

Examples

```
estimate_var_tsa_meas(mean_rtp = .5, var = .02,
                     mean_qx = .8,
                     mean_qy = .8)
estimate_var_tsa_uvdr(mean_rtpa = .5, var = .02,
                     mean_ux = .8,
                     mean_qxa = .8,
                     mean_qyi = .8)
estimate_var_tsa_bvdr(mean_rtpa = .5, var = .02,
                     mean_ux = .8,
                     mean_uy = .8,
                     mean_qxa = .8,
                     mean_qya = .8)
```



```

estimate_var_tsa_uvirr(mean_rtpa = .5, var = .02,
  mean_ut = .8,
  mean_qxa = .8,
  mean_qyi = .8)
estimate_var_tsa_bvirr(mean_rtpa = .5, var = .02,
  mean_ux = .8,
  mean_uy = .8,
  mean_qxa = .8,
  mean_qya = .8,
  sign_rxz = 1, sign_ryz = 1)
estimate_var_tsa_rb1(mean_rtpa = .5, var = .02,
  mean_ux = .8,
  mean_rxx = .8,
  mean_ryy = .8)
estimate_var_tsa_rb2(mean_rtpa = .5, var = .02,
  mean_ux = .8,
  mean_qx = .8,
  mean_qy = .8)

```

 filter_ma

Filter meta-analyses

Description

Filter psychmeta meta-analysis objects based on specified criteria.

Usage

```
filter_ma(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)
```

```
filter_meta(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)
```

Arguments

- | | |
|----------|---|
| ma_obj | A psychmeta meta-analysis object. |
| analyses | Which analyses to extract? Can be either "all" to extract references for all meta-analyses in the object (default) or a list containing one or more of the following arguments: <ul style="list-style-type: none"> • <code>construct</code>: A list or vector of construct names to search for. • <code>construct_pair</code>: A list of vectors of construct pairs to search for. (e.g., <code>list(c("X", "Y"), c("X", "Z"))</code>). • <code>pair_id</code>: A list or vector of numeric construct pair IDs (unique construct-pair indices). • <code>analysis_id</code>: A list or vector of numeric analysis IDs (unique analysis indexes). |

	<ul style="list-style-type: none"> • <code>k_min</code>: A numeric value specifying the minimum <code>k</code> for extracted meta-analyses. • <code>N_minv</code>: A numeric value specifying the minimum <code>N</code> for extracted meta-analyses.
<code>match</code>	Should extracted meta-analyses match all (default) or any of the criteria given in analyses?
<code>case_sensitive</code>	Logical scalar that determines whether character values supplied in analyses should be treated as case sensitive (TRUE, default) or not (FALSE).
<code>...</code>	Additional arguments.

Value

A psychmeta meta-analysis object with analyses matching the specified criteria.

Examples

```
ma_obj <- ma_r(ma_method = "ic", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
  construct_x = x_name, construct_y = y_name, sample_id = sample_id, citekey = NULL,
  moderators = moderator, data = data_r_meas_multi,
  impute_artifacts = FALSE, clean_artifacts = FALSE)
ma_obj <- ma_r_ad(ma_obj, correct_rr_x = FALSE, correct_rr_y = FALSE)

filter_ma(ma_obj, analyses="all")
filter_ma(ma_obj, analyses=list(construct="X"), match="all")
filter_ma(ma_obj, analyses=list(construct="X", k_min=21), match="any")
filter_ma(ma_obj, analyses=list(construct="X", k_min=21), match="all")
```

format_num	<i>Format numbers for presentation</i>
------------	--

Description

A function to format numbers and logical values as characters for display purposes. Includes control over formatting of decimal digits, leading zeros, sign characters, and characters to replace logical, NA, NaN, and Inf values. Factors are converted to strings. Strings are returned verbatim.

Usage

```
format_num(x, digits = 2L, decimal.mark = getOption("OutDec"),
  leading0 = "conditional", drop0integer = FALSE,
  neg.sign = "&minus;", pos.sign = "figure", big.mark = "&#8239;",
  big.interval = 3L, small.mark = "&#8239;", small.interval = 3L,
  na.mark = "&mdash;", lgl.mark = c("+", "&minus;"),
  inf.mark = c("+&infin;", "&minus;&infin;"))
```

Arguments

x	A vector, matrix, or data.frame of numbers to format
digits	The number of decimal digits desired (used strictly; default: 2)
decimal.mark	The character to use for the decimal point (defaults to locale default: <code>getOption("OutDec")</code>)
leading0	How to print leading zeros on decimals. Can be logical to print (TRUE) or suppress (FALSE) leading zeros or a character string to substitute for leading zeros. If "conditional" (default), leading zeros are shown if a column contains any absolute values greater than 1 and suppressed otherwise. If "figure", leading zeros are replaced with a figure space (U+2007) if a column contains any absolute values greater than 1 and suppressed otherwise.
drop0integer	Logical. Should trailing decimal zeros be dropped for integers?
neg.sign	Character to use as negative sign. Defaults to minus-sign (U+2212).
pos.sign	Character to use as positive sign. Set to FALSE to suppress. If "figure" (default), the positive sign is a figure-space (U+2007) if a column contains any negative numbers and suppressed otherwise.
big.mark	Character to mark between each big.interval digits <i>before</i> the decimal point. Set to FALSE to suppress. Defaults to the SI/ISO 31-0 standard-recommended thin-spaces (U+202F).
big.interval	See big.mark above; defaults to 3.
small.mark	Character to mark between each small.interval digits <i>after</i> the decimal point. Set to FALSE to suppress. Defaults to the SI/ISO 31-0 standard-recommended thin-spaces (U+202F).
small.interval	See small.mark above; defaults to 3.
na.mark	Character to replace NA and NaN values. Defaults to em-dash (U+2014)
lg1.mark	A length 2 vector containing characters to replace TRUE and FALSE. Defaults to c("+", "U+2212").
inf.mark	A length 2 vector containing characters to replace Inf and -Inf. Defaults to c("+U+221e", "U+2212U+221e").

Examples

```
# format_num() converts numeric values to characters with the specified formatting options.
# By default, thousands digit groups are separated by thin spaces, negative signs are replaced
# with minus signs, and positive signs and leading zeros are replaced with figure spaces
# (which have the same width as numbers and minus signs). These options ensure that all
# results will align neatly in columns when tabled.
format_num(x = c(10000, 1000, 2.41, -1.20, 0.41, -0.20))

# By default, format_num() uses your computer locale's default decimal mark as
# the decimal point. To force the usage of "." instead (e.g., for submission to
# a U.S. journal), set decimal.mark = ".":
format_num(x = .41, decimal.mark = ".")

# By default, format_num() separates groups of large digits using thin spaces.
# This is following the international standard for scientific communication (SI/ISO 31-0),
```

```
# which advises against using "." or "," to separate digits because doing so can lead
# to confusion for human and computer readers because "." and "," are also used
# as decimal marks in various countries. If you prefer to use commas to separate
# large digit groups, set big.mark = ",":
format_num(x = 10000, big.mark = ",")
```

generate_bib

Generate a list of references included in meta-analyses

Description

This function generates a list of studies contributing to a meta-analysis

Usage

```
generate_bib(ma_obj = NULL, bib = NULL, title.bib = NULL,
  style = "apa", additional_citekeys = NULL, file = NULL,
  output_dir = getwd(), output_format = c("word", "html", "pdf",
  "text", "odt", "rmd", "biblatex", "citekeys"), analyses = "all",
  match = c("all", "any"), case_sensitive = TRUE,
  save_build_files = FALSE, header = list(), ...)
```

Arguments

ma_obj	A psychmeta meta-analysis object with citekeys supplied.
bib	A BibTeX file containing the citekeys for the meta-analyses.
title.bib	The title to give to the bibliography. If NULL, defaults to "Sources Contributing to Meta-Analyses"
style	What style should references be formatted in? Can be a file path or URL for a CSL citation style or the style ID for any style available from the Zotero Style Repository . Defaults to APA style. (Retrieving a style by ID requires an internet connection. If unavailable, references will be rendered in Chicago style.)
additional_citekeys	Additional citekeys to include in the reference list.
file	The filename or filepath for the output file. If NULL, function will output directly to the R console (if output_format is "text", the formatted references in BibOptions "authoryear" style; if "citekeys", the citekeys for included sources; otherwise, code to generate the bibliography in an RMarkdown document).
output_dir	The filepath for the output file. Defaults to the current working directory.
output_format	The format of the output reference list. Available options are Word (default), HTML, PDF (requires LaTeX to be installed), ODT, or Rmarkdown, plain text, and BibLaTeX. Returning only the item citekeys is also possible. You can also specify the full name of another RMarkdown output_format .
analyses	Which analyses to extract references for? See filter_ma for details.
match	Match all or any of the filter criteria? See filter_ma for details.

case_sensitive Logical scalar that determines whether character values supplied in analyses should be treated as case sensitive (TRUE, default) or not (FALSE).
save_build_files Should the BibTeX and RMarkdown files used to generate the bibliography be saved (default: FALSE; always TRUE if file is NULL)?
header A list of YAML header parameters to pass to `link{rmarkdown::render}`.
... Additional arguments to pass to [render](#).

Value

A list containing the RefManagerR BibEntry object. Additionally, a reference list formatted in the requested style and `output_format` is exported (or printed if file is "console").

See Also

Other output functions: [metabulate_rmd_helper](#), [metabulate](#)

Examples

```

## Not run:
## Run a meta-analysis using ma_r() and include a citekey argument to provide
## citation information for each source contributing to the meta-analyses.
ma_obj <- ma_r(ma_method = "ic", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              moderators = moderator, citekey = citekey, data = data_r_meas_multi)

## Next, use generate_bib() to generate the bibliography for the retained studies.
## The bib argument is the BibTeX or BibLaTeX .bib file containing the full
## reference information for each of the citekeys included in the meta-analysis database.
generate_bib(ma_obj, bib = system.file("templates/sample_bibliography.bib", package="psychmeta"),
            file = "sample bibliography", output_dir = tempdir(), output_format = "word")

## End(Not run)

```

generate_directory *Generate a system of folders from a file path to a new directory*

Description

This function is intended to be helpful in simulations when directories need to be created and named according to values that are used or created within the simulation.

Usage

```
generate_directory(path)
```

Arguments

path The path to the directory to be created

Value

Creates a system of folders to a new directory.

get_stuff

Extract results from a psychmeta meta-analysis object

Description

Functions to extract specific results from a meta-analysis tibble. This family of functions harvests information from meta-analysis objects and returns it as lists or tibbles that are easily navigable.

Available functions include:

- `get_stuff`
Wrapper function for all other "get_" functions.
- `get_metatab`
Retrieve list of meta-analytic tables.
- `get_ad`
Retrieve list of artifact-distribution objects or a summary table of artifact descriptive statistics.
- `get_plots`
Retrieve list of meta-analytic plots.
- `get_escalc`
Retrieve list of escalc objects (i.e., effect-size data) for use with **metafor**.
- `get_metafor`
Alias for `get_escalc`.
- `get_followup`
Retrieve list of follow-up analyses.
- `get_leave1out`
Retrieve list of leave-one-out meta-analyses (special case of `get_followup`).
- `get_cumulative`
Retrieve list of cumulative meta-analyses (special case of `get_followup`).
- `get_bootstrap`
Retrieve list of bootstrap meta-analyses (special case of `get_followup`).
- `get_metareg`
Retrieve list of meta-regression analyses (special case of `get_followup`).
- `get_heterogeneity`
Retrieve list of heterogeneity analyses (special case of `get_followup`).
- `get_matrix`
Retrieve a tibble of matrices summarizing the relationships among constructs (only applicable to meta-analyses with multiple constructs).

Usage

```

get_stuff(ma_obj, what = c("metatab", "escalc", "metafor", "ad",
  "followup", "heterogeneity", "leave1out", "cumulative", "bootstrap",
  "metareg", "matrix", "plots"), analyses = "all", match = c("all",
  "any"), case_sensitive = TRUE, ma_method = c("bb", "ic", "ad"),
  correction_type = c("ts", "vgx", "vgy"), moderators = FALSE,
  as_ad_obj = TRUE, inputs_only = FALSE, ad_type = c("tsa", "int"),
  follow_up = c("heterogeneity", "leave1out", "cumulative", "bootstrap",
  "metareg"), plot_types = c("funnel", "forest", "leave1out",
  "cumulative"), ...)

get_escalc(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, moderators = FALSE, ...)

get_metafor(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, moderators = FALSE, ...)

get_metatab(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ma_method = c("bb", "ic", "ad"),
  correction_type = c("ts", "vgx", "vgy"), ...)

get_ad(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ma_method = c("ad", "ic"),
  ad_type = c("tsa", "int"), as_ad_obj = FALSE, inputs_only = FALSE,
  ...)

get_followup(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, follow_up = c("heterogeneity", "leave1out",
  "cumulative", "bootstrap", "metareg"), ...)

get_heterogeneity(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)

get_leave1out(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)

get_cumulative(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)

get_bootstrap(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)

get_metareg(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)

get_matrix(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, ...)

```

```
get_plots(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, plot_types = c("funnel", "forest",
  "leave1out", "cumulative"), ...)
```

Arguments

ma_obj	A psychmeta meta-analysis object.
what	For the get_stuff() function only: Character scalar telling get_stuff() what to get. All suffixes from functions in the "get_" family can be passed as arguments to what: "metatab", "escalc", "metafor", "ad", "followup", "heterogeneity", "leave1out", "cumulative", "bootstrap", "metareg", "matrix", "plots"
analyses	Which analyses to extract? Can be either "all" to extract references for all meta-analyses in the object (default) or a list containing one or more of the following arguments: <ul style="list-style-type: none"> • construct: A list or vector of construct names to search for. • construct_pair: A list of vectors of construct pairs to search for. (e.g., list(c("X", "Y"), c("X", "Z"))). • pair_id: A list or vector of numeric construct pair IDs (unique construct-pair indices). • analysis_id: A list or vector of numeric analysis IDs (unique analysis indexes). • k_min: A numeric value specifying the minimum k for extracted meta-analyses. • N_minv: A numeric value specifying the minimum N for extracted meta-analyses.
match	Should extracted meta-analyses match all (default) or any of the criteria given in analyses?
case_sensitive	Logical scalar that determines whether character values supplied in analyses should be treated as case sensitive (TRUE, default) or not (FALSE).
ma_method	Meta-analytic methods to be included. Valid options are: "bb", "ic", and "ad"
correction_type	Types of meta-analytic corrections to be included. Valid options are: "ts", "vgx", and "vgy"
moderators	Logical scalar that determines whether moderator information should be included in the escalc list (TRUE) or not (FALSE; default).
as_ad_obj	Logical scalar that determines whether artifact information should be returned as artifact-distribution objects (TRUE) or a summary table of artifact-distribution descriptive statistics (FALSE; default).
inputs_only	Used only if as_ad_obj = TRUE: Logical scalar that determines whether artifact information should be returned as summaries of the raw input values (TRUE) or artifact values that may have been cross-corrected for range restriction and measurement error (FALSE; default).
ad_type	Used only if ma_method = "ic": Character value(s) indicating whether Taylor-series approximation artifact distributions ("tsa") and/or interactive artifact distributions ("int") should be retrieved.

follow_up	Vector of follow-up analysis names (options are: "heterogeneity", "leave1out", "cumulative", "bootstrap", "metareg").
plot_types	Vector of plot types (options are: "funnel", "forest", "leave1out", "cumulative"; multiple allowed).
...	Additional arguments.

Value

Selected set of results.

Examples

```
## Not run:
## Run meta-analysis:
ma_obj <- ma_r(ma_method = "ic", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              construct_x = x_name, construct_y = y_name,
              sample_id = sample_id, citekey = NULL,
              moderators = moderator, data = data_r_meas_multi,
              impute_artifacts = FALSE, clean_artifacts = FALSE)
ma_obj <- ma_r_ad(ma_obj, correct_rr_x = FALSE, correct_rr_y = FALSE)

## Run additional analyses:
ma_obj <- heterogeneity(ma_obj)
ma_obj <- sensitivity(ma_obj, boot_iter = 10, boot_ci_type = "norm")
ma_obj <- metareg(ma_obj)
ma_obj <- plot_funnel(ma_obj)
ma_obj <- plot_forest(ma_obj)

## View summary:
summary(ma_obj)

## Extract selected analyses:
get_metatab(ma_obj)
get_matrix(ma_obj)
get_escalc(ma_obj)
get_bootstrap(ma_obj)
get_cumulative(ma_obj)
get_leave1out(ma_obj)
get_heterogeneity(ma_obj)
get_metareg(ma_obj)
get_plots(ma_obj)
get_ad(ma_obj, ma_method = "ic", as_ad_obj = TRUE)
get_ad(ma_obj, ma_method = "ic", as_ad_obj = FALSE)

## Same extractions as above, but using get_stuff() and the "what" argument:
get_stuff(ma_obj, what = "metatab")
get_stuff(ma_obj, what = "matrix")
get_stuff(ma_obj, what = "escalc")
get_stuff(ma_obj, what = "bootstrap")
get_stuff(ma_obj, what = "cumulative")
get_stuff(ma_obj, what = "leave1out")
get_stuff(ma_obj, what = "heterogeneity")
```

```

get_stuff(ma_obj, what = "metareg")
get_stuff(ma_obj, what = "plots")
get_stuff(ma_obj, what = "ad", ma_method = "ic", as_ad_obj = TRUE)
get_stuff(ma_obj, what = "ad", ma_method = "ic", as_ad_obj = FALSE)

## End(Not run)

```

heterogeneity

Supplemental heterogeneity statistics for meta-analyses

Description

This function computes a variety of supplemental statistics for meta-analyses. The statistics here are included for interested users. It is strongly recommended that heterogeneity in meta-analysis be interpreted using the SD_{res} , SD_{ρ} , and SD_{δ} statistics, along with corresponding credibility intervals, which are reported in the default `ma_obj` output (Wiernik et al., 2017).

Usage

```
heterogeneity(ma_obj, es_failsafe = NULL, conf_level = 0.95, ...)
```

Arguments

<code>ma_obj</code>	Meta-analysis object.
<code>es_failsafe</code>	Failsafe effect-size value for file-drawer analyses.
<code>conf_level</code>	Confidence level to define the width of confidence intervals (default = .95).
<code>...</code>	Additional arguments.

Value

`ma_obj` with heterogeneity statistics added. Included statistics include:

<code>es_type</code>	The effect size metric used.
<code>percent_var_accounted</code>	Percent variance accounted for statistics (by sampling error, by other artifacts, and total). These statistics are widely reported, but not recommended, as they tend to be misinterpreted as suggesting only a small portion of the observed variance is accounted for by sampling error and other artifacts (Schmidt, 2010; Schmidt & Hunter, 2015, p. 15, 425). The square roots of these values are more interpretable and appropriate indices of the relations between observed effect sizes and statistical artifacts (see <code>cor(es, perturbations)</code>).
<code>cor(es, perturbations)</code>	The correlation between observed effect sizes and statistical artifacts in each sample (with sampling error, with other artifacts, and with artifacts in total), computed as $\sqrt{\text{percent var accounted}}$. These indices are more interpretable and appropriate indices of the relations between observed effect sizes and statistical artifacts than <code>percent_var_accounted</code> .

rel_es_obs	$1 - \frac{var_{pre}}{var_{res}}$, the reliability of observed effect size differences as indicators of true effect sizes differences in the sampled studies. This value is useful for correcting correlations between moderators and effect sizes in meta-regression.
H_squared	The ratio of the observed effect size variance to the predicted (error) variance. Also the square root of Q divided by its degrees of freedom.
H	The ratio of the observed effect size standard deviation to the predicted (error) standard deviation.
I_squared	The estimated percent variance not accounted for by sampling error or other artifacts (attributable to moderators and uncorrected artifacts). This statistic is simply rel_es_obs expressed as a percentage rather than a decimal.
Q	Cochran's χ^2 statistic. Significance tests using this statistic are strongly discouraged; heterogeneity should instead be determined by examining the width of the credibility interval and the practical differences between effect sizes contained within it (Wiernik et al., 2017). This value is not accurate when artifact distribution methods are used for corrections.
tau_squared	τ^2 , an estimator of the random effects variance component (analogous to the Hunter-Schmidt SD_{res}^2 , SD_{ρ}^2 , or SD_{δ}^2 statistics), with its confidence interval. This value is not accurate when artifact distribution methods are used for corrections.
tau	$\sqrt{\tau^2}$, analogous to the Hunter-Schmidt SD_{res} , SD_{ρ} , and SD_{δ} statistics, with its confidence interval. This value is not accurate when artifact distribution methods are used for corrections.
Q_r, H_r_squared, H_r, I_r_squared, tau_r_squared, tau_r	Outlier-robust versions of these statistics, computed based on absolute deviations from the weighted mean effect size (see Lin et al., 2017). These values are not accurate when artifact distribution methods are used for corrections.
Q_m, H_m_squared, H_m, I_m_squared, tau_m_squared, tau_m	Outlier-robust versions of these statistics, computed based on absolute deviations from the weighted median effect size (see Lin et al., 2017). These values are not accurate when artifact distribution methods are used for corrections.
file_drawer	Fail-safe N and k statistics (file-drawer analyses). These statistics should not be used to evaluate publication bias, as they counterintuitively suggest <i>less</i> when publication bias is strong (Becker, 2005). However, in the absence of publication bias, they can be used as an index of second-order sampling error (how likely is a mean effect to reduce to the specified value with additional studies?). The confidence interval around the mean effect can be used more directly for the same purpose.

References

- Becker, B. J. (2005). Failsafe N or file-drawer number. In H. R. Rothstein, A. J. Sutton, & M. Borenstein (Eds.), *Publication bias in meta-analysis: Prevention, assessment and adjustments* (pp. 111–125). Hoboken, NJ: Wiley. <https://doi.org/10.1002/0470870168.ch7>
- Higgins, J. P. T., & Thompson, S. G. (2002). Quantifying heterogeneity in a meta-analysis. *Statistics in Medicine*, 21(11), 1539–1558. <https://doi.org/10.1002/sim.1186>

Lin, L., Chu, H., & Hodges, J. S. (2017). Alternative measures of between-study heterogeneity in meta-analysis: Reducing the impact of outlying studies. *Biometrics*, 73(1), 156–166. <https://doi.org/10.1111/biom.12543>

Schmidt, F. (2010). Detecting and correcting the lies that data tell. *Perspectives on Psychological Science*, 5(3), 233–242. <https://doi.org/10.1177/1745691610369339>

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: Sage. <https://doi.org/10/b6mg>. pp. 15, 414, 426, 533–534.

Wiernik, B. M., Kostal, J. W., Wilmot, M. P., Dilchert, S., & Ones, D. S. (2017). Empirical benchmarks for interpreting effect size variability in meta-analysis. *Industrial and Organizational Psychology*, 10(3). <https://doi.org/10.1017/iop.2017.44>

Examples

```
## Correlations
ma_obj <- ma_r_ic(rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi, ux = ux,
                 correct_rr_y = FALSE, data = data_r_uvirr)
ma_obj <- ma_r_ad(ma_obj, correct_rr_y = FALSE)
ma_obj <- heterogeneity(ma_obj = ma_obj)
ma_obj$heterogeneity[[1]]$barebones
ma_obj$heterogeneity[[1]]$individual_correction$true_score
ma_obj$heterogeneity[[1]]$artifact_distribution$true_score

## d values
ma_obj <- ma_d_ic(d = d, n1 = n1, n2 = n2, ryy = ryyi,
                 data = data_d_meas_multi)
ma_obj <- ma_d_ad(ma_obj)
ma_obj <- heterogeneity(ma_obj = ma_obj)
ma_obj$heterogeneity[[1]]$barebones
ma_obj$heterogeneity[[1]]$individual_correction$latentGroup_latentY
ma_obj$heterogeneity[[1]]$artifact_distribution$latentGroup_latentY
```

lm_mat

Compute linear regression models and generate "lm" objects from covariance matrices.

Description

Compute linear regression models and generate "lm" objects from covariance matrices.

Usage

```
lm_mat(formula, cov_mat, mean_vec = rep(0, ncol(cov_mat)), n = Inf,
        se_beta_method = c("lm", "normal"), ...)

matrixreg(formula, cov_mat, mean_vec = rep(0, ncol(cov_mat)), n = Inf,
           se_beta_method = c("lm", "normal"), ...)
```

```
matreg(formula, cov_mat, mean_vec = rep(0, ncol(cov_mat)), n = Inf,
       se_beta_method = c("lm", "normal"), ...)
```

```
lm_matrix(formula, cov_mat, mean_vec = rep(0, ncol(cov_mat)), n = Inf,
          se_beta_method = c("lm", "normal"), ...)
```

Arguments

formula	Regression formula with a single outcome variable on the left-hand side and one or more predictor variables on the right-hand side (e.g., $Y \sim X1 + X2$).
cov_mat	Covariance matrix containing the variables to be used in the regression.
mean_vec	Vector of means corresponding to the variables in cov_mat.
n	Sample size to be used in significance testing
se_beta_method	Method to use to estimate the standard errors of standardized regression (beta) coefficients. Current options include "lm" (estimate standard errors using conventional regression formulas) and "normal" (use the Jones-Waller normal-theory approach from the <code>fungible::seBeta()</code> and <code>fungible::seBetaCor()</code> functions)
...	Additional arguments.

Value

An object with the class "lm_mat" that can be used with `summary`, `print`, `predict`, and `anova` methods.

Examples

```
## Generate data
S <- reshape_vec2mat(cov = c(.3 * 2 * 3,
                             .4 * 2 * 4,
                             .5 * 3 * 4),
                    var = c(2, 3, 4)^2,
                    var_names = c("X", "Y", "Z"))
mean_vec <- setNames(c(1, 2, 3), colnames(S))
dat <- data.frame(MASS::mvrnorm(n = 100, mu = mean_vec,
                               Sigma = S, empirical = TRUE))

## Compute regression models with lm
lm_out1 <- lm(Y ~ X, data = dat)
lm_out2 <- lm(Y ~ X + Z, data = dat)

## Compute regression models with lm_mat
matreg_out1 <- lm_mat(formula = Y ~ X, cov_mat = S, mean_vec = mean_vec, n = nrow(dat))
matreg_out2 <- lm_mat(formula = Y ~ X + Z, cov_mat = S, mean_vec = mean_vec, n = nrow(dat))

## Compare results of lm and lm_mat with one predictor
lm_out1
matreg_out1

## Compare summaries of lm and lm_mat with one predictor
summary(lm_out1)
```

```
summary(matreg_out1)

## Compare results of lm and lm_mat with two predictors
lm_out2
matreg_out2

## Compare summaries of lm and lm_mat with two predictors
summary(lm_out2)
summary(matreg_out2)

## Compare predictions made with lm and lm_mat
predict(object = matreg_out1, newdata = data.frame(X = 1:5))
predict(object = summary(matreg_out1), newdata = data.frame(X = 1:5))
predict(lm_out1, newdata = data.frame(X = 1:5))

## Compare predictions made with lm and lm_mat (with confidence intervals)
predict(object = matreg_out1, newdata = data.frame(X = 1:5),
        se.fit = TRUE, interval = "confidence")
predict(lm_out1, newdata = data.frame(X = 1:5),
        se.fit = TRUE, interval = "confidence")

## Compare predictions made with lm and lm_mat (with prediction intervals)
predict(object = matreg_out1, newdata = data.frame(X = 1:5),
        se.fit = TRUE, interval = "prediction")
predict(lm_out1, newdata = data.frame(X = 1:5),
        se.fit = TRUE, interval = "prediction")

## Compare model comparisons computed using lm and lm_mat objects
anova(lm_out1, lm_out2)
anova(matreg_out1, matreg_out2)

## Model comparisons can be run on lm_mat summaries, too:
anova(summary(matreg_out1), summary(matreg_out2))
## Or summaries and raw models can be mixed:
anova(matreg_out1, summary(matreg_out2))
anova(summary(matreg_out1), matreg_out2)

## Compare confidence intervals computed using lm and lm_mat objects
confint(object = lm_out1)
confint(object = matreg_out1)
confint(object = summary(matreg_out1))

confint(object = lm_out2)
confint(object = matreg_out2)
confint(object = summary(matreg_out2))
```

Description

The `ma_r_bb`, `ma_r_ic`, and `ma_r_ad` functions implement bare-bones, individual-correction, and artifact-distribution correction methods for d values, respectively. The `ma_d` function is the master function for meta-analyses of d values - it facilitates the computation of bare-bones, artifact-distribution, and individual-correction meta-analyses of correlations for any number of group-wise contrasts and any number of dependent variables. When artifact-distribution meta-analyses are performed, `ma_d` will automatically extract the artifact information from a database and organize it into the requested type of artifact distribution object (i.e., either Taylor series or interactive artifact distributions). `ma_d` is also equipped with the capability to clean databases containing inconsistently recorded artifact data, impute missing artifacts (when individual-correction meta-analyses are requested), and remove dependency among samples by forming composites or averaging effect sizes and artifacts. The automatic compositing features in `ma_d` are employed when `sample_ids` and/or construct names are provided.

Usage

```
ma_d(d, n1, n2 = NULL, n_adj = NULL, sample_id = NULL,
     citekey = NULL, treat_as_r = FALSE, ma_method = c("bb", "ic",
     "ad"), ad_type = c("tsa", "int"), correction_method = "auto",
     group_id = NULL, group1 = NULL, group2 = NULL,
     group_order = NULL, construct_y = NULL, facet_y = NULL,
     measure_y = NULL, construct_order = NULL,
     wt_type = c("sample_size", "inv_var_mean", "inv_var_sample", "DL",
     "HE", "HS", "SJ", "ML", "REML", "EB", "PM"), correct_bias = TRUE,
     correct_rel = NULL, correct_rGg = FALSE, correct_ryy = TRUE,
     correct_rr = NULL, correct_rr_g = TRUE, correct_rr_y = TRUE,
     indirect_rr = NULL, indirect_rr_g = TRUE, indirect_rr_y = TRUE,
     rGg = NULL, pi = NULL, pa = NULL, ryy = NULL,
     ryy_restricted = TRUE, ryy_type = "alpha", k_items_y = NULL,
     uy = NULL, uy_observed = TRUE, sign_rz = NULL, sign_rgz = 1,
     sign_ryz = 1, moderators = NULL, cat_moderators = TRUE,
     moderator_type = c("simple", "hierarchical", "none"),
     supplemental_ads = NULL, data = NULL,
     control = control_psychmeta(), ...)

ma_d_ad(ma_obj, ad_obj_g = NULL, ad_obj_y = NULL,
        correction_method = "auto", use_ic_ads = c("tsa", "int"),
        correct_rGg = FALSE, correct_ryy = TRUE, correct_rr_g = TRUE,
        correct_rr_y = TRUE, indirect_rr_g = TRUE, indirect_rr_y = TRUE,
        sign_rgz = 1, sign_ryz = 1, control = control_psychmeta(), ...)

ma_d_bb(d, n1, n2 = rep(NA, length(d)), n_adj = NULL,
        sample_id = NULL, citekey = NULL, wt_type = c("sample_size",
        "inv_var_mean", "inv_var_sample", "DL", "HE", "HS", "SJ", "ML", "REML",
        "EB", "PM"), correct_bias = FALSE, moderators = NULL,
        cat_moderators = TRUE, moderator_type = c("simple", "hierarchical",
        "none"), data = NULL, control = control_psychmeta(), ...)
```

```

ma_d_ic(d, n1, n2 = NULL, n_adj = NULL, sample_id = NULL,
  citekey = NULL, treat_as_r = FALSE, wt_type = c("sample_size",
  "inv_var_mean", "inv_var_sample", "DL", "HE", "HS", "SJ", "ML", "REML",
  "EB", "PM"), correct_bias = TRUE, correct_rGg = FALSE,
  correct_ryy = TRUE, correct_rr_g = FALSE, correct_rr_y = TRUE,
  indirect_rr_g = TRUE, indirect_rr_y = TRUE, rGg = NULL,
  pi = NULL, pa = NULL, ryy = NULL, ryy_restricted = TRUE,
  ryy_type = "alpha", k_items_y = NULL, uy = NULL,
  uy_observed = TRUE, sign_rgz = 1, sign_ryz = 1,
  moderators = NULL, cat_moderators = TRUE,
  moderator_type = c("simple", "hierarchical", "none"),
  supplemental_ads_y = NULL, data = NULL,
  control = control_psychmeta(), ...)

```

Arguments

d	Vector or column name of observed <i>d</i> values.
n1	Vector or column name of sample sizes.
n2	Vector or column name of sample sizes.
n_adj	Optional: Vector or column name of sample sizes adjusted for sporadic artifact corrections.
sample_id	Optional vector of identification labels for samples/studies in the meta-analysis.
citekey	Optional vector of bibliographic citation keys for samples/studies in the meta-analysis (if multiple citekeys pertain to a given effect size, combine them into a single string entry with comma delimiters (e.g., "citekey1,citekey2")).
treat_as_r	Logical scalar determining whether <i>d</i> values are to be meta-analyzed as <i>d</i> values (FALSE; default) or whether they should be meta-analyzed as correlations and have the final results converted to the <i>d</i> metric (TRUE).
ma_method	Method to be used to compute the meta-analysis: "bb" (barebones), "ic" (individual correction), or "ad" (artifact distribution).
ad_type	For when ma_method is "ad", specifies the type of artifact distribution to use: "int" or "tsa".
correction_method	Character scalar or a matrix with group_id levels as row names and construct_y levels as column names. When ma_method is "ad", select one of the following methods for correcting artifacts: "auto", "meas", "uvdrr", "uvirr", "bvdr", "bvirr", "rbOrig", "rb1Orig", "rb2Orig", "rbAdj", "rb1Adj", and "rb2Adj". (note: "rb1Orig", "rb2Orig", "rb1Adj", and "rb2Adj" can only be used when Taylor series artifact distributions are provided and "rbOrig" and "rbAdj" can only be used when interactive artifact distributions are provided). See "Details" of ma_d_ad for descriptions of the available methods.
group_id	Vector of group comparison IDs (e.g., Treatment1-Control, Treatment2-Control). The group_id argument supersedes the group1 and group2 arguments. If group_id is not NULL, the values supplied to the group_order argument must correspond to group_id values.
group1, group2	Vector of group identification labels (e.g., Treatment1, Treatment2, Control)

group_order	Optional vector indicating the order in which (1) group1 and group2 values or (2) group_ids should be arranged. If group_order is NULL, the order of group pairings will be determined internally using alpha-numeric ordering.
construct_y	Vector of construct names for construct designated as "Y".
facet_y	Vector of facet names for constructs designated as "Y". Facet names "global", "overall", and "total" are reserved to indicate observations that represent effect sizes that have already been composited or that represent construct-level measurements rather than facet-level measurements. To avoid double-compositing, any observation with one of these reserved names will only be eligible for auto-compositing with other such observations and will not be combined with narrow facets.
measure_y	Vector of names for measures associated with constructs designated as "Y".
construct_order	Vector indicating the order in which Y variables should be arranged.
wt_type	Type of weight to use in the meta-analysis: options are "sample_size", "inv_var_mean" (inverse variance computed using mean effect size), and "inv_var_sample" (inverse variance computed using sample-specific effect sizes). Supported options borrowed from metafor are "DL", "HE", "HS", "SJ", "ML", "REML", "EB", and "PM" (see metafor documentation for details about the metafor methods).
correct_bias	Logical scalar that determines whether to correct correlations for small-sample bias (TRUE) or not (FALSE).
correct_rel	Optional named vector that supersedes correct_rGg and correct_ryy. Names should correspond to construct names in group_id and construct_y to determine which constructs should be corrected for unreliability.
correct_rGg	Logical scalar or vector that determines whether to correct the grouping variable for measurement error (TRUE) or not (FALSE).
correct_ryy	Logical scalar or vector that determines whether to correct the Y variable for measurement error (TRUE) or not (FALSE).
correct_rr	Optional named vector that supersedes correct_rr_g and correct_rr_y. Names should correspond to construct names in group_id and construct_y to determine which constructs should be corrected for range restriction.
correct_rr_g	Logical scalar or vector or column name determining whether each <i>d</i> value should be corrected for range restriction in the grouping variable (TRUE) or not (FALSE).
correct_rr_y	Logical scalar or vector or column name determining whether each <i>d</i> should be corrected for range restriction in Y (TRUE) or not (FALSE).
indirect_rr	Optional named vector that supersedes indirect_rr_g and indirect_rr_y. Names should correspond to construct names in group_id and construct_y to determine which constructs should be corrected for indirect range restriction.
indirect_rr_g	Logical vector or column name determining whether each <i>d</i> should be corrected for indirect range restriction in the grouping variable (TRUE) or not (FALSE). Superseded in evaluation by correct_rr_g (i.e., if correct_rr_g == FALSE, the value supplied for indirect_rr_g is disregarded).

indirect_rr_y	Logical vector or column name determining whether each <i>d</i> should be corrected for indirect range restriction in Y (TRUE) or not (FALSE). Superseded in evaluation by <code>correct_rr_y</code> (i.e., if <code>correct_rr_y == FALSE</code> , the value supplied for <code>indirect_rr_y</code> is disregarded).
rGg	Vector or column name of reliability estimates for X.
pi	Scalar or vector containing the restricted-group proportions of group membership. If a vector, it must either (1) have as many elements as there are <i>d</i> values or (2) be named so as to match with levels of the <code>group_id</code> argument.
pa	Scalar or vector containing the unrestricted-group proportions of group membership (default = .5). If a vector, it must either (1) have as many elements as there are <i>d</i> values or (2) be named so as to match with levels of the <code>group_id</code> argument.
ryy	Vector or column name of reliability estimates for Y.
ryy_restricted	Logical vector or column name determining whether each element of <code>ryy</code> is an incumbent reliability (TRUE) or an applicant reliability (FALSE).
ryy_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for <code>ma_r</code> for a full list of acceptable reliability types.
k_items_y	Numeric vector identifying the number of items in each scale.
uy	Vector or column name of u ratios for Y.
uy_observed	Logical vector or column name determining whether each element of <code>uy</code> is an observed-score u ratio (TRUE) or a true-score u ratio (FALSE).
sign_rz	Optional named vector that supersedes <code>sign_rgz</code> and <code>sign_ryz</code> . Names should correspond to construct names in <code>group_id</code> and <code>construct_y</code> to determine the sign of each construct's relationship with the selection mechanism.
sign_rgz	Sign of the relationship between X and the selection mechanism (for use with <code>bvrr</code> corrections only).
sign_ryz	Sign of the relationship between Y and the selection mechanism (for use with <code>bvrr</code> corrections only).
moderators	Matrix or column names of moderator variables to be used in the meta-analysis (can be a vector in the case of one moderator).
cat_moderators	Logical scalar or vector identifying whether variables in the <code>moderators</code> argument are categorical variables (TRUE) or continuous variables (FALSE).
moderator_type	Type of moderator analysis: "none" means that no moderators are to be used, "simple" means that moderators are to be examined one at a time, "hierarchical" means that all possible combinations and subsets of moderators are to be examined, and "all" means that simple and hierarchical moderator analyses are to be performed.
supplemental_ads	Named list (named according to the constructs included in the meta-analysis) of supplemental artifact distribution information from studies not included in the meta-analysis. This is a list of lists, where the elements of a list associated with a construct are named like the arguments of the <code>create_ad()</code> function.

data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
control	Output from the <code>control_psychmeta()</code> function or a list of arguments controlled by the <code>control_psychmeta()</code> function. Ellipsis arguments will be screened for internal inclusion in <code>control</code> .
...	Further arguments to be passed to functions called within the meta-analysis.
ma_obj	For <code>ma_d_ad</code> only: Meta-analysis object of correlations or d values (regardless of input metric, output metric will be d).
ad_obj_g	For <code>ma_d_ad</code> only: Artifact-distribution object for the grouping variable (output of the <code>link{create_ad}</code> or <code>link{create_ad_group}</code> functions). If <code>ma_obj</code> is of the class <code>ma_master</code> (i.e., the output of <code>ma_r</code> or <code>ma_d</code>), the object supplied for <code>ad_obj_g</code> must be a named list of artifact distributions with names corresponding to the "X" constructs in the meta-analyses contained within <code>ma_obj</code> .
ad_obj_y	For <code>ma_d_ad</code> only: AArtifact-distribution object for the Y variable (output of the <code>create_ad</code> function). If <code>ma_obj</code> is of the class <code>ma_master</code> , the object supplied for <code>ad_obj_y</code> must be a named list of artifact distributions with names corresponding to the "Y" constructs in the meta-analyses contained within <code>ma_obj</code> .
use_ic_ads	For <code>ma_d_ad</code> only: Determines whether artifact distributions should be extracted from the individual correction results in <code>ma_obj</code> . Only evaluated when <code>ad_obj_g</code> or <code>ad_obj_y</code> is NULL and <code>ma_obj</code> does not contain individual correction results. Use one of the following commands: <code>tsa</code> to use the Taylor series method or <code>int</code> to use the interactive method.
supplemental_ads_y	For <code>ma_d_ic</code> only: List supplemental artifact distribution information from studies not included in the meta-analysis. The elements of this list are named like the arguments of the <code>create_ad()</code> function.

Details

The options for `correction_method` are:

- "auto"
Automatic selection of the most appropriate correction procedure, based on the available artifacts and the logical arguments provided to the function. (default)
- "meas"
Correction for measurement error only.
- "uvdr"
Correction for univariate direct range restriction (i.e., Case II). The choice of which variable to correct for range restriction is made using the `correct_rr_x` and `correct_rr_y` arguments.
- "uvirr"
Correction for univariate indirect range restriction (i.e., Case IV). The choice of which variable to correct for range restriction is made using the `correct_rr_x` and `correct_rr_y` arguments.
- "bvdr"
Correction for bivariate direct range restriction. Use with caution: This correction is an approximation only and is known to have a positive bias.

- "bvirr"
Correction for bivariate indirect range restriction (i.e., Case V).
- "rbOrig"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied interactively. We recommend using "uvdr" instead.
- "rbAdj"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied interactively. Adjusted to account for range restriction in the reliability of the Y variable. We recommend using "uvdr" instead.
- "rb1Orig"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA1 method. We recommend using "uvdr" instead.
- "rb1Adj"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA1 method. Adjusted to account for range restriction in the reliability of the Y variable. We recommend using "uvdr" instead.
- "rb2Orig"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA2 method. We recommend using "uvdr" instead.
- "rb2Adj"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA2 method. Adjusted to account for range restriction in the reliability of the Y variable. We recommend using "uvdr" instead.

Value

A nested tabular object of the class "ma_psychmeta". Components of output tables for bare-bones meta-analyses:

- Pair_ID
Unique identification number for each construct-contrast pairing.
- group_contrast
Name of the variable analyzed as the group-contrast variable.
- construct_y
Name of the variable analyzed as construct Y.
- analysis_id
Unique identification number for each analysis.
- analysis_type
Type of moderator analyses: Overall, Simple Moderator, or Hierarchical Moderator.
- k
Number of effect sizes meta-analyzed.
- N
Total sample size of all effect sizes in the meta-analysis.
- mean_d
Mean observed d value.

- var_d
Weighted variance of observed *d* values.
- var_e
Predicted sampling-error variance of observed *d* values.
- var_res
Variance of observed *d* values after removing predicted sampling-error variance.
- sd_d
Square root of var_r.
- se_d
Standard error of mean_d.
- sd_e
Square root of var_e.
- sd_res
Square root of var_res.
- CI_LL_XX
Lower limit of the confidence interval around mean_d, where "XX" represents the confidence level as a percentage.
- CI_UL_XX
Upper limit of the confidence interval around mean_d, where "XX" represents the confidence level as a percentage.
- CV_LL_XX
Lower limit of the credibility interval around mean_d, where "XX" represents the credibility level as a percentage.
- CV_UL_XX
Upper limit of the credibility interval around mean_d, where "XX" represents the credibility level as a percentage.

Components of output tables for individual-correction meta-analyses:

- pair_id
Unique identification number for each construct-contrast pairing.
- group_contrast
Name of the variable analyzed as the group-contrast variable.
- construct_y
Name of the variable analyzed as construct Y.
- analysis_id
Unique identification number for each analysis.
- analysis_type
Type of moderator analyses: Overall, Simple Moderator, or Hierarchical Moderator.
- k
Number of effect sizes meta-analyzed.
- N
Total sample size of all effect sizes in the meta-analysis.

- mean_d
Mean observed d value.
- var_d
Weighted variance of observed d values.
- var_e
Predicted sampling-error variance of observed d values.
- var_res
Variance of observed d values after removing predicted sampling-error variance.
- sd_d
Square root of var_r.
- se_d
Standard error of mean_d.
- sd_e
Square root of var_e.
- sd_res
Square root of var_res.
- mean_delta
Mean artifact-corrected d value.
- var_d_c
Variance of artifact-corrected d values.
- var_e_c
Predicted sampling-error variance of artifact-corrected d values.
- var_delta
Variance of artifact-corrected d values after removing predicted sampling-error variance.
- sd_d_c
Square root of var_r_c.
- se_d_c
Standard error of mean_delta.
- sd_e_c
Square root of var_e_c.
- sd_delta
Square root of var_delta.
- CI_LL_XX
Lower limit of the confidence interval around mean_delta, where "XX" represents the confidence level as a percentage.
- CI_UL_XX
Upper limit of the confidence interval around mean_delta, where "XX" represents the confidence level as a percentage.
- CV_LL_XX
Lower limit of the credibility interval around mean_delta, where "XX" represents the credibility level as a percentage.
- CV_UL_XX
Upper limit of the credibility interval around mean_delta, where "XX" represents the credibility level as a percentage.

Components of output tables for artifact-distribution meta-analyses:

- pair_id
Unique identification number for each construct-contrast pairing.
- group_contrast
Name of the variable analyzed as the group-contrast variable.
- construct_y
Name of the variable analyzed as construct Y.
- analysis_id
Unique identification number for each analysis.
- analysis_type
Type of moderator analyses: Overall, Simple Moderator, or Hierarchical Moderator.
- k
Number of effect sizes meta-analyzed.
- N
Total sample size of all effect sizes in the meta-analysis.
- mean_d
Mean observed d value.
- var_d
Weighted variance of observed d values.
- var_e
Predicted sampling-error variance of observed d values.
- var_art
Amount of variance in observed d values that is attributable to measurement-error and range-restriction artifacts.
- var_pre
Total predicted artifactual variance (i.e., the sum of var_e and var_art).
- var_res
Variance of observed d values after removing predicted sampling-error variance and predicted artifact variance.
- sd_d
Square root of var_d.
- se_d
Standard error of mean_d.
- sd_e
Square root of var_e.
- sd_art
Square root of var_art.
- sd_pre
Square root of var_pre.
- sd_res
Square root of var_res.
- mean_delta
Mean artifact-corrected d value.

- var_d
Weighted variance of observed d values corrected to the metric of delta.
- var_e
Predicted sampling-error variance of observed d values corrected to the metric of delta.
- var_art
Amount of variance in observed d values that is attributable to measurement-error and range-restriction artifacts corrected to the metric of delta.
- var_pre
Total predicted artifactual variance (i.e., the sum of var_e and var_art) corrected to the metric of delta.
- var_delta
Variance of artifact-corrected d values after removing predicted sampling-error variance and predicted artifact variance.
- sd_d
Square root of var_d corrected to the metric of delta.
- se_d
Standard error of mean_d corrected to the metric of delta.
- sd_e
Square root of var_e corrected to the metric of delta.
- sd_art
Square root of var_art corrected to the metric of delta.
- sd_pre
Square root of var_pre corrected to the metric of delta.
- sd_delta
Square root of var_delta.
- CI_LL_XX
Lower limit of the confidence interval around mean_delta, where "XX" represents the confidence level as a percentage.
- CI_UL_XX
Upper limit of the confidence interval around mean_delta, where "XX" represents the confidence level as a percentage.
- CV_LL_XX
Lower limit of the credibility interval around mean_delta, where "XX" represents the credibility level as a percentage.
- CV_UL_XX
Upper limit of the credibility interval around mean_delta, where "XX" represents the credibility level as a percentage.

Note

The difference between "rb" methods with the "orig" and "adj" suffixes is that the original does not account for the impact of range restriction on criterion reliabilities, whereas the adjusted procedure attempts to estimate the applicant reliability information for the criterion. The "rb" procedures are included for posterity: We strongly recommend using the "uvdr" procedure to appropriately correct for univariate range restriction.

References

- Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings (3rd ed.)*. Thousand Oaks, California: SAGE Publications, Inc. Chapter 4.
- Law, K. S., Schmidt, F. L., & Hunter, J. E. (1994). Nonlinearity of range corrections in meta-analysis: Test of an improved procedure. *Journal of Applied Psychology, 79*(3), 425.
- Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.
- Raju, N. S., & Burke, M. J. (1983). Two new procedures for studying validity generalization. *Journal of Applied Psychology, 68*(3), 382. <https://doi.org/10.1037/0021-9010.68.3.382>

Examples

```
### Demonstration of ma_d ###
## The 'ma_d' function can compute multi-construct bare-bones meta-analyses:
ma_d(d = d, n1 = n1, n2 = n2, construct_y = construct, data = data_d_meas_multi)

## It can also perform multiple individual-correction meta-analyses:
ma_d(ma_method = "ic", d = d, n1 = n1, n2 = n2, ryy = ryyi,
     construct_y = construct, data = data_d_meas_multi)

## And 'ma_d' can also curate artifact distributions and compute multiple
## artifact-distribution meta-analyses:
ma_d(ma_method = "ad", d = d, n1 = n1, n2 = n2,
     ryy = ryyi, correct_rr_y = FALSE,
     construct_y = construct, data = data_d_meas_multi)

### Demonstration of ma_d_bb ###
## Example meta-analyses using simulated data:
ma_d_bb(d = d, n1 = n1, n2 = n2,
        data = data_d_meas_multi[data_d_meas_multi$construct == "Y",])
ma_d_bb(d = d, n1 = n1, n2 = n2,
        data = data_d_meas_multi[data_d_meas_multi$construct == "Z",])

### Demonstration of ma_d_ic ###
## Example meta-analyses using simulated data:
ma_d_ic(d = d, n1 = n1, n2 = n2, ryy = ryyi, correct_rr_y = FALSE,
        data = data_d_meas_multi[data_d_meas_multi$construct == "Y",])
ma_d_ic(d = d, n1 = n1, n2 = n2, ryy = ryyi, correct_rr_y = FALSE,
        data = data_d_meas_multi[data_d_meas_multi$construct == "Z",])
```

Description

This function computes second-order meta-analysis function for d values. It supports second-order analyses of bare-bones, artifact-distribution, and individual-correction meta-analyses.

Usage

```
ma_d_order2(k, N = NULL, d = NULL, delta = NULL, var_d = NULL,
  var_d_c = NULL, ma_type = c("bb", "ic", "ad"), sample_id = NULL,
  citekey = NULL, moderators = NULL, moderator_type = "simple",
  construct_x = NULL, construct_y = NULL, data = NULL,
  control = control_psychmeta(), ...)
```

Arguments

<code>k</code>	Vector or column name of meta-analyses' k values.
<code>N</code>	Vector or column name of meta-analyses' total sample sizes (optional).
<code>d</code>	Vector or column name of mean observed d values.
<code>delta</code>	Vector or column name of mean corrected d values.
<code>var_d</code>	Vector or column name of observed variances of observed d values.
<code>var_d_c</code>	Vector or column name of observed variances of corrected d values.
<code>ma_type</code>	Type of meta-analyses being analyzed: "bb" (barebones), "ic" (individual correction), or "ad" (artifact distribution).
<code>sample_id</code>	Vector or column name of study ID labels.
<code>citekey</code>	Optional vector of bibliographic citation keys for samples/studies in the meta-analysis (if multiple citekeys pertain to a given effect size, combine them into a single string entry with comma delimiters (e.g., "citekey1,citekey2")).
<code>moderators</code>	Matrix or column names of moderator variables to be used in the meta-analysis (can be a vector in the case of one moderator).
<code>moderator_type</code>	Type of moderator analysis ("none", "simple", or "hierarchical").
<code>construct_x</code>	Vector or column name of construct names for X.
<code>construct_y</code>	Vector or column name of construct names for Y.
<code>data</code>	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
<code>control</code>	Output from the <code>control_psychmeta()</code> function or a list of arguments controlled by the <code>control_psychmeta()</code> function. Ellipsis arguments will be screened for internal inclusion in <code>control</code> .
<code>...</code>	Further arguments to be passed to functions called within the meta-analysis.

Value

A nested tabular object of the class "ma_psychmeta".

ma_generic	<i>Bare-bones meta-analysis of generic effect sizes</i>
------------	---

Description

This function computes bare-bones meta-analyses of any effect size using user-supplied effect error variances.

Usage

```
ma_generic(es, n, var_e, sample_id = NULL, citekey = NULL,
  construct_x = NULL, construct_y = NULL, group1 = NULL,
  group2 = NULL, wt_type = c("sample_size", "inv_var", "DL", "HE",
  "HS", "SJ", "ML", "REML", "EB", "PM"), moderators = NULL,
  cat_moderators = TRUE, moderator_type = c("simple", "hierarchical",
  "none"), data = NULL, control = control_psychmeta(), ...)
```

Arguments

es	Vector or column name of observed effect sizes.
n	Vector or column name of sample sizes.
var_e	Vector or column name of error variances.
sample_id	Optional vector of identification labels for samples/studies in the meta-analysis.
citekey	Optional vector of bibliographic citation keys for samples/studies in the meta-analysis (if multiple citekeys pertain to a given effect size, combine them into a single string entry with comma delimiters (e.g., "citekey1,citekey2"). When TRUE, program will use sample-size weights, error variances estimated from the mean effect size, maximum likelihood variances, and normal-distribution confidence and credibility intervals.
construct_x, construct_y	Vector of construct names for constructs designated as "X" and as "Y".
group1, group2	Vector of groups' names associated with effect sizes that represent pairwise contrasts.
wt_type	Type of weight to use in the meta-analysis: native options are "sample_size", and "inv_var" (inverse error variance). Supported options borrowed from metafor are "DL", "HE", "HS", "SJ", "ML", "REML", "EB", and "PM" (see metafor documentation for details about the metafor methods).
moderators	Matrix of moderator variables to be used in the meta-analysis (can be a vector in the case of one moderator).
cat_moderators	Logical scalar or vector identifying whether variables in the moderators argument are categorical variables (TRUE) or continuous variables (FALSE).
moderator_type	Type of moderator analysis ("none", "simple", or "hierarchical").
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.

`control` Output from the `control_psychmeta()` function or a list of arguments controlled by the `control_psychmeta()` function. Ellipsis arguments will be screened for internal inclusion in `control`.

`...` Further arguments to be passed to functions called within the meta-analysis.

Value

A nested tabular object of the class "ma_psychmeta".

Examples

```
es <- c(.3, .5, .8)
n <- c(100, 200, 150)
var_e <- 1 / n
ma_obj <- ma_generic(es = es, n = n, var_e = var_e)
ma_obj
summary(ma_obj)
```

ma_r

Meta-analysis of correlations

Description

The `ma_r_bb`, `ma_r_ic`, and `ma_r_ad` functions implement bare-bones, individual-correction, and artifact-distribution correction methods for correlations, respectively. The `ma_r` function is the master function for meta-analyses of correlations - it facilitates the computation of bare-bones, artifact-distribution, and individual-correction meta-analyses of correlations for any number of construct pairs. When artifact-distribution meta-analyses are performed, `ma_r` will automatically extract the artifact information from a database and organize it into the requested type of artifact distribution object (i.e., either Taylor series or interactive artifact distributions). `ma_r` is also equipped with the capability to clean databases containing inconsistently recorded artifact data, impute missing artifacts (when individual-correction meta-analyses are requested), and remove dependency among samples by forming composites or averaging effect sizes and artifacts. The automatic compositing features in `ma_r` are employed when `sample_ids` and/or construct names are provided.

Usage

```
ma_r(rxyi, n, n_adj = NULL, sample_id = NULL, citekey = NULL,
     ma_method = c("bb", "ic", "ad"), ad_type = c("tsa", "int"),
     correction_method = "auto", construct_x = NULL, construct_y = NULL,
     facet_x = NULL, facet_y = NULL, measure_x = NULL,
     measure_y = NULL, construct_order = NULL,
     wt_type = c("sample_size", "inv_var_mean", "inv_var_sample", "DL",
                "HE", "HS", "SJ", "ML", "REML", "EB", "PM"), correct_bias = TRUE,
     correct_rel = NULL, correct_rxx = TRUE, correct_ryy = TRUE,
     correct_rr = NULL, correct_rr_x = TRUE, correct_rr_y = TRUE,
     indirect_rr = NULL, indirect_rr_x = TRUE, indirect_rr_y = TRUE,
     rxx = NULL, rxx_restricted = TRUE, rxx_type = "alpha",
```

```

k_items_x = NULL, ryy = NULL, ryy_restricted = TRUE,
ryy_type = "alpha", k_items_y = NULL, ux = NULL,
ux_observed = TRUE, uy = NULL, uy_observed = TRUE,
sign_rz = NULL, sign_rxz = 1, sign_ryz = 1, moderators = NULL,
cat_moderators = TRUE, moderator_type = c("simple", "hierarchical",
"none"), supplemental_ads = NULL, data = NULL,
control = control_psychmeta(), ...)

```

```

ma_r_ad(ma_obj, ad_obj_x = NULL, ad_obj_y = NULL,
correction_method = "auto", use_ic_ads = c("tsa", "int"),
correct_rxx = TRUE, correct_ryy = TRUE, correct_rr_x = TRUE,
correct_rr_y = TRUE, indirect_rr_x = TRUE, indirect_rr_y = TRUE,
sign_rxz = 1, sign_ryz = 1, control = control_psychmeta(), ...)

```

```

ma_r_bb(r, n, n_adj = NULL, sample_id = NULL, citekey = NULL,
wt_type = c("sample_size", "inv_var_mean", "inv_var_sample", "DL",
"HE", "HS", "SJ", "ML", "REML", "EB", "PM"), correct_bias = TRUE,
moderators = NULL, cat_moderators = TRUE,
moderator_type = c("simple", "hierarchical", "none"), data = NULL,
control = control_psychmeta(), ...)

```

```

ma_r_ic(rxyi, n, n_adj = NULL, sample_id = NULL, citekey = NULL,
wt_type = c("sample_size", "inv_var_mean", "inv_var_sample", "DL",
"HE", "HS", "SJ", "ML", "REML", "EB", "PM"), correct_bias = TRUE,
correct_rxx = TRUE, correct_ryy = TRUE, correct_rr_x = TRUE,
correct_rr_y = TRUE, indirect_rr_x = TRUE, indirect_rr_y = TRUE,
rxx = NULL, rxx_restricted = TRUE, rxx_type = "alpha",
k_items_x = NULL, ryy = NULL, ryy_restricted = TRUE,
ryy_type = "alpha", k_items_y = NULL, ux = NULL,
ux_observed = TRUE, uy = NULL, uy_observed = TRUE, sign_rxz = 1,
sign_ryz = 1, moderators = NULL, cat_moderators = TRUE,
moderator_type = c("simple", "hierarchical", "none"),
supplemental_ads_x = NULL, supplemental_ads_y = NULL, data = NULL,
control = control_psychmeta(), ...)

```

Arguments

rxyi, r	Vector or column name of observed correlations. The r argument is used with the ma_r_bb (i.e., the barebones function) function and the rxyi argument is used with ma_r and ma_r_ic (i.e., the function in which corrections are applied).
n	Vector or column name of sample sizes.
n_adj	Optional: Vector or column name of sample sizes adjusted for sporadic artifact corrections.
sample_id	Optional vector of identification labels for samples/studies in the meta-analysis.
citekey	Optional vector of bibliographic citation keys for samples/studies in the meta-analysis (if multiple citekeys pertain to a given effect size, combine them into a single string entry with comma delimiters (e.g., "citekey1,citekey2")).

ma_method	Method to be used to compute the meta-analysis: "bb" (barebones), "ic" (individual correction), or "ad" (artifact distribution).
ad_type	For when ma_method is "ad". Dpecifies the type of artifact distribution to use: "int" or "tsa".
correction_method	For when ma_method is "ad". Character scalar or a square matrix with the collective levels of construct_x and construct_y as row names and column names. Select one of the following methods for correcting artifacts: "auto", "meas", "uvdrr", "uvirr", "bvdrr", "bvirr", "rbOrig", "rb1Orig", "rb2Orig", "rbAdj", "rb1Adj", and "rb2Adj". (note: "rb1Orig", "rb2Orig", "rb1Adj", and "rb2Adj" can only be used when Taylor series artifact distributions are provided and "rbOrig" and "rbAdj" can only be used when interative artifact distributions are provided). See "Details" of ma_r_ad for descriptions of the available methods.
construct_x, construct_y	Vector of construct names for constructs initially designated as "X" or as "Y".
facet_x, facet_y	Vector of facet names for constructs initially designated as "X" or as "Y". Facet names "global", "overall", and "total" are reserved to indicate observations that represent effect sizes that have already been composited or that represent construct-level measurements rather than facet-level measurements. To avoid double-compositing, any observation with one of these reserved names will only be eligible for auto-compositing with other such observations and will not be combined with narrow facets.
measure_x, measure_y	Vector of names for measures associated with constructs initially designated as "X" or as "Y".
construct_order	Vector indicating the order in which variables should be arranged, with variables listed earlier in the vector being preferred for designation as X.
wt_type	Type of weight to use in the meta-analysis: options are "sample_size", "inv_var_mean" (inverse variance computed using mean effect size), and "inv_var_sample" (inverse variance computed using sample-specific effect sizes). Supported options borrowed from metafor are "DL", "HE", "HS", "SJ", "ML", "REML", "EB", and "PM" (see metafor documentation for details about the metafor methods).
correct_bias	Logical scalar that determines whether to correct correlations for small-sample bias (TRUE) or not (FALSE).
correct_rel	Optional named vector that supersedes correct_rxx and correct_ryy. Names should correspond to construct names in construct_x and construct_y to determine which constructs should be corrected for unreliability.
correct_rxx, correct_ryy	Logical scalar or vector that determines whether to correct the X or Y variable for measurement error (TRUE) or not (FALSE).
correct_rr	Optional named vector that supersedes correct_rr_x and correct_rr_y. Names should correspond to construct names in construct_x and construct_y to determine which constructs should be corrected for range restriction.

correct_rr_x	Logical scalar, logical vector, or column name determining whether each correlation in rxyi should be corrected for range restriction in X (TRUE) or not (FALSE). If using artifact distribution methods, this must be a scalar value.
correct_rr_y	Logical scalar, logical vector, or column name determining whether each correlation in rxyi should be corrected for range restriction in Y (TRUE) or not (FALSE). If using artifact distribution methods, this must be a scalar value.
indirect_rr	Optional named vector that supersedes indirect_rr_x and indirect_rr_y. Names should correspond to construct names in construct_x and construct_y to determine which constructs should be corrected for indirect range restriction.
indirect_rr_x	Logical vector or column name determining whether each correlation in rxyi should be corrected for indirect range restriction in X (TRUE) or not (FALSE). Superseded in evaluation by correct_rr_x (i.e., if correct_rr_x == FALSE, the value supplied for indirect_rr_x is disregarded).
indirect_rr_y	Logical vector or column name determining whether each correlation in rxyi should be corrected for indirect range restriction in Y (TRUE) or not (FALSE). Superseded in evaluation by correct_rr_y (i.e., if correct_rr_y == FALSE, the value supplied for indirect_rr_y is disregarded).
rxx	Vector or column name of reliability estimates for X.
rxx_restricted	Logical vector or column name determining whether each element of rxx is an incumbent reliability (TRUE) or an applicant reliability (FALSE).
rxx_type, ryy_type	String vector identifying the types of reliability estimates supplied. Acceptable reliability types are: <ul style="list-style-type: none"> • internal_consistency A generic designation for internal-consistency reliability estimates derived from responses to a single test administration. • multiple_administrations A generic designation for reliability estimates derived from multiple administrations of a test. • alpha Coefficient alpha. • lambda Generic designation for a Guttman's lambda coefficient. • lambda1 Guttman's lambda 1 coefficient. • lambda2 Guttman's lambda 2 coefficient. • lambda3 Guttman's lambda 3 coefficient. • lambda4 Guttman's lambda 4 coefficient. • lambda5 Guttman's lambda 5 coefficient. • lambda6 Guttman's lambda 6 coefficient.

- omega
Omega coefficient indicating the proportion variance in a variable accounted for by modeled latent factors.
- icc
Intraclass correlation coefficient.
- interrater_r
Inter-rater correlation coefficient.
- interrater_r_sb
Inter-rater correlation coefficient, stepped up with the Spearman-Brown formula.
- splithalf
Split-half reliability coefficient.
- splithalf_sb
Split-half reliability coefficient, corrected toward the full test length with the Spearman-Brown formula.
- retest
Test-retest reliability coefficient.
- parallel
Parallel-forms reliability coefficient with tests taken during the same testing session.
- alternate
Alternate-forms reliability coefficient with tests taken during the same testing session.
- parallel_delayed
Parallel-forms reliability coefficient with tests taken during separate testing sessions with a time delay in between.
- alternate_delayed
Alternate-forms reliability coefficient with tests taken during separate testing sessions with a time delay in between.

k_items_x, k_items_y	Numeric vector identifying the number of items in each scale.
ryy	Vector or column name of reliability estimates for Y.
ryy_restricted	Logical vector or column name determining whether each element of coderyy is an incumbent reliability (TRUE) or an applicant reliability (FALSE).
ux	Vector or column name of u ratios for X.
ux_observed	Logical vector or column name determining whether each element of ux is an observed-score u ratio (TRUE) or a true-score u ratio (FALSE).
uy	Vector or column name of u ratios for Y.
uy_observed	Logical vector or column name determining whether each element of uy is an observed-score u ratio (TRUE) or a true-score u ratio (FALSE).
sign_rz	Optional named vector that supersedes sign_rxz and sign_ryz. Names should correspond to construct names in construct_x and construct_y to determine the sign of each construct's relationship with the selection mechanism.
sign_rxz	Sign of the relationship between X and the selection mechanism (for use with bvirr corrections only).

sign_ryz	Sign of the relationship between Y and the selection mechanism (for use with bvirr corrections only).
moderators	Matrix or column names of moderator variables to be used in the meta-analysis (can be a vector in the case of one moderator).
cat_moderators	Logical scalar or vector identifying whether variables in the moderators argument are categorical variables (TRUE) or continuous variables (FALSE).
moderator_type	Type of moderator analysis: "none" means that no moderators are to be used, "simple" means that moderators are to be examined one at a time, and "hierarchical" means that all possible combinations and subsets of moderators are to be examined.
supplemental_ads	For ma_r only: Named list (named according to the constructs included in the meta-analysis) of supplemental artifact distribution information from studies not included in the meta-analysis. This is a list of lists, where the elements of a list associated with a construct are named like the arguments of the create_ad() function.
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
control	Output from the control_psychmeta() function or a list of arguments controlled by the control_psychmeta() function. Ellipsis arguments will be screened for internal inclusion in control.
...	Further arguments to be passed to functions called within the meta-analysis.
ma_obj	For ma_r_ad only: Meta-analysis object of correlations or <i>d</i> values (regardless of input metric, output metric will be <i>r</i>).
ad_obj_x	For ma_r_ad only: Artifact-distribution object for the X variable (output of the create_ad function). If ma_obj is of the class ma_master (i.e., the output of ma_r or ma_d), the object supplied for ad_obj_x must be a named list of artifact distributions with names corresponding to the "X" constructs in the meta-analyses contained within ma_obj.
ad_obj_y	For ma_r_ad only: Artifact-distribution object for the Y variable (output of the create_ad function). If ma_obj is of the class ma_master, the object supplied for ad_obj_y must be a named list of artifact distributions with names corresponding to the "Y" constructs in the meta-analyses contained within ma_obj.
use_ic_ads	For ma_r_ad only: Determines whether artifact distributions should be extracted from the individual correction results in ma_obj. Only evaluated when ad_obj_x or ad_obj_y is NULL and ma_obj does not contain individual correction results. Use one of the following commands: tsa to use the Taylor series method or int to use the interactive method.
supplemental_ads_x, supplemental_ads_y	For ma_r_ic only: List supplemental artifact distribution information from studies not included in the meta-analysis. The elements of this list are named like the arguments of the create_ad() function.

Details

The options for correction_method are:

- "auto"
Automatic selection of the most appropriate correction procedure, based on the available artifacts and the logical arguments provided to the function. (default)
- "meas"
Correction for measurement error only.
- "uvdr"
Correction for univariate direct range restriction (i.e., Case II). The choice of which variable to correct for range restriction is made using the `correct_rr_x` and `correct_rr_y` arguments.
- "uvirr"
Correction for univariate indirect range restriction (i.e., Case IV). The choice of which variable to correct for range restriction is made using the `correct_rr_x` and `correct_rr_y` arguments.
- "bvdr"
Correction for bivariate direct range restriction. Use with caution: This correction is an approximation only and is known to have a positive bias.
- "bvirr"
Correction for bivariate indirect range restriction (i.e., Case V).
- "rbOrig"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied interactively. We recommend using "uvdr" instead.
- "rbAdj"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied interactively. Adjusted to account for range restriction in the reliability of the Y variable. We recommend using "uvdr" instead.
- "rb1Orig"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA1 method. We recommend using "uvdr" instead.
- "rb1Adj"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA1 method. Adjusted to account for range restriction in the reliability of the Y variable. We recommend using "uvdr" instead.
- "rb2Orig"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA2 method. We recommend using "uvdr" instead.
- "rb2Adj"
Not recommended: Raju and Burke's version of the correction for direct range restriction, applied using their TSA2 method. Adjusted to account for range restriction in the reliability of the Y variable. We recommend using "uvdr" instead.

Value

A nested tabular object of the class "ma_psychmeta". Components of output tables for bare-bones meta-analyses:

- `pair_id`
Unique identification number for each construct pairing.

- `construct_x`
Name of the variable analyzed as construct X.
- `construct_y`
Name of the variable analyzed as construct Y.
- `analysis_id`
Unique identification number for each analysis.
- `analysis_type`
Type of moderator analyses: Overall, Simple Moderator, or Hierarchical Moderator.
- `k`
Number of effect sizes meta-analyzed.
- `N`
Total sample size of all effect sizes in the meta-analysis.
- `mean_r`
Mean observed correlation.
- `var_r`
Weighted variance of observed correlations.
- `var_e`
Predicted sampling-error variance of observed correlations.
- `var_res`
Variance of observed correlations after removing predicted sampling-error variance.
- `sd_r`
Square root of `var_r`.
- `se_r`
Standard error of `mean_r`.
- `sd_e`
Square root of `var_e`.
- `sd_res`
Square root of `var_res`.
- `CI_LL_XX`
Lower limit of the confidence interval around `mean_r`, where "XX" represents the confidence level as a percentage.
- `CI_UL_XX`
Upper limit of the confidence interval around `mean_r`, where "XX" represents the confidence level as a percentage.
- `CV_LL_XX`
Lower limit of the credibility interval around `mean_r`, where "XX" represents the credibility level as a percentage.
- `CV_UL_XX`
Upper limit of the credibility interval around `mean_r`, where "XX" represents the credibility level as a percentage.

Components of output tables for individual-correction meta-analyses:

- `pair_id`
Unique identification number for each construct pairing.

- `construct_x`
Name of the variable analyzed as construct X.
- `construct_y`
Name of the variable analyzed as construct Y.
- `analysis_id`
Unique identification number for each analysis.
- `analysis_type`
Type of moderator analyses: Overall, Simple Moderator, or Hierarchical Moderator.
- `k`
Number of effect sizes meta-analyzed.
- `N`
Total sample size of all effect sizes in the meta-analysis.
- `mean_r`
Mean observed correlation.
- `var_r`
Weighted variance of observed correlations.
- `var_e`
Predicted sampling-error variance of observed correlations.
- `var_res`
Variance of observed correlations after removing predicted sampling-error variance.
- `sd_r`
Square root of `var_r`.
- `se_r`
Standard error of `mean_r`.
- `sd_e`
Square root of `var_e`.
- `sd_res`
Square root of `var_res`.
- `mean_rho`
Mean artifact-corrected correlation.
- `var_r_c`
Variance of artifact-corrected correlations.
- `var_e_c`
Predicted sampling-error variance of artifact-corrected correlations.
- `var_rho`
Variance of artifact-corrected correlations after removing predicted sampling-error variance.
- `sd_r_c`
Square root of `var_r_c`.
- `se_r_c`
Standard error of `mean_rho`.
- `sd_e_c`
Square root of `var_e_c`.

- sd_rho
Square root of var_rho.
- CI_LL_XX
Lower limit of the confidence interval around mean_rho, where "XX" represents the confidence level as a percentage.
- CI_UL_XX
Upper limit of the confidence interval around mean_rho, where "XX" represents the confidence level as a percentage.
- CV_LL_XX
Lower limit of the credibility interval around mean_rho, where "XX" represents the credibility level as a percentage.
- CV_UL_XX
Upper limit of the credibility interval around mean_rho, where "XX" represents the credibility level as a percentage.

Components of output tables for artifact-distribution meta-analyses:

- pair_id
Unique identification number for each construct pairing.
- construct_x
Name of the variable analyzed as construct X.
- construct_y
Name of the variable analyzed as construct Y.
- analysis_id
Unique identification number for each analysis.
- analysis_type
Type of moderator analyses: Overall, Simple Moderator, or Hierarchical Moderator.
- k
Number of effect sizes meta-analyzed.
- N
Total sample size of all effect sizes in the meta-analysis.
- mean_r
Mean observed correlation.
- var_r
Weighted variance of observed correlations.
- var_e
Predicted sampling-error variance of observed correlations.
- var_art
Amount of variance in observed correlations that is attributable to measurement-error and range-restriction artifacts.
- var_pre
Total predicted artifactual variance (i.e., the sum of var_e and var_art).
- var_res
Variance of observed correlations after removing predicted sampling-error variance and predicted artifact variance.

- sd_r
Square root of var_r.
- se_r
Standard error of mean_r.
- sd_e
Square root of var_e.
- sd_art
Square root of var_art.
- sd_pre
Square root of var_pre.
- sd_res
Square root of var_res.
- mean_rho
Mean artifact-corrected correlation.
- var_r_c
Weighted variance of observed correlations corrected to the metric of rho.
- var_e_c
Predicted sampling-error variance of observed correlations corrected to the metric of rho.
- var_art_c
Amount of variance in observed correlations that is attributable to measurement-error and range-restriction artifacts corrected to the metric of rho.
- var_pre_c
Total predicted artifactual variance (i.e., the sum of var_e and var_art) corrected to the metric of rho.
- var_rho
Variance of artifact-corrected correlations after removing predicted sampling-error variance and predicted artifact variance.
- sd_r_c
Square root of var_r corrected to the metric of rho.
- se_r_c
Standard error of mean_r corrected to the metric of rho.
- sd_e_c
Square root of var_e corrected to the metric of rho.
- sd_art_c
Square root of var_art corrected to the metric of rho.
- sd_pre_c
Square root of var_pre corrected to the metric of rho.
- sd_rho
Square root of var_rho.
- CI_LL_XX
Lower limit of the confidence interval around mean_rho, where "XX" represents the confidence level as a percentage.

- CI_UL_XX
Upper limit of the confidence interval around mean_rho, where "XX" represents the confidence level as a percentage.
- CV_LL_XX
Lower limit of the credibility interval around mean_rho, where "XX" represents the credibility level as a percentage.
- CV_UL_XX
Upper limit of the credibility interval around mean_rho, where "XX" represents the credibility level as a percentage.

Note

The difference between "rb" methods with the "orig" and "adj" suffixes is that the original does not account for the impact of range restriction on criterion reliabilities, whereas the adjusted procedure attempts to estimate the applicant reliability information for the criterion. The "rb" procedures are included for posterity: We strongly recommend using the "uvdrr" procedure to appropriately correct for univariate range restriction.

References

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- Law, K. S., Schmidt, F. L., & Hunter, J. E. (1994). Nonlinearity of range corrections in meta-analysis: Test of an improved procedure. *Journal of Applied Psychology*, 79(3), 425–438. <https://doi.org/10.1037/0021-9010.79.3.425>
- Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.
- Raju, N. S., & Burke, M. J. (1983). Two new procedures for studying validity generalization. *Journal of Applied Psychology*, 68(3), 382–395. <https://doi.org/10.1037/0021-9010.68.3.382>

Examples

```
## Not run:
## The 'ma_r' function can compute multi-construct bare-bones meta-analyses:
ma_obj <- ma_r(rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              moderators = moderator, data = data_r_meas_multi)
summary(ma_obj)

## It can also perform multiple individual-correction meta-analyses:
ma_obj <- ma_r(ma_method = "ic", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              moderators = moderator, data = data_r_meas_multi)
summary(ma_obj)
ma_obj$meta_tables[[1]]$individual_correction$true_score

## And 'ma_r' can also curate artifact distributions and compute multiple
```

```
## artifact-distribution meta-analyses:
ma_obj <- ma_r(ma_method = "ad", ad_type = "int", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              correct_rr_x = FALSE, correct_rr_y = FALSE,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              clean_artifacts = FALSE, impute_artifacts = FALSE,
              moderators = moderator, data = data_r_meas_multi)
summary(ma_obj)
ma_obj$meta_tables[[1]]$artifact_distribution$true_score
```

```
## Even if no studies in the database provide artifact information,
## pre-specified artifact distributions from previous meta-analyses
## can still be used! (These results should match the previous example.)
ma_obj <- ma_r(ma_method = "ad", rxyi = rxyi, n = n,
              correct_rr_x = FALSE, correct_rr_y = FALSE,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              clean_artifacts = FALSE, impute_artifacts = FALSE,
              moderators = moderator, data = data_r_meas_multi,
              supplemental_ads =
                list(X = list(mean_qxi = 0.8927818, var_qxi = 0.0008095520, k_qxi = 40,
                              mean_n_qxi = 11927 / 40, qxi_dist_type = "alpha"),
                    Y = list(mean_qxi = 0.8941266, var_qxi = 0.0009367234, k_qxi = 40,
                              mean_n_qxi = 11927 / 40, qxi_dist_type = "alpha"),
                    Z = list(mean_qxi = 0.8962108, var_qxi = 0.0007840593, k_qxi = 40,
                              mean_n_qxi = 11927 / 40, qxi_dist_type = "alpha")))
summary(ma_obj)
ma_obj$meta_tables[[1]]$artifact_distribution$true_score
```

```
## Artifact information may also be supplied by passing "ad_obj" class objects with the
## "supplemental_ads" argument.
## Create a list of artifact-distribution objects:
ad_list <- create_ad_list(n = n, rxx = rxxi, ryy = ryyi,
                        construct_x = x_name, construct_y = y_name,
                        sample_id = sample_id,
                        data = data_r_meas_multi)
ad_list <- setNames(ad_list$ad_x, ad_list$construct_x)
```

```
## Run the artifact-distribution meta-analysis:
ma_obj <- ma_r(ma_method = "ad", rxyi = rxyi, n = n,
              correct_rr_x = FALSE, correct_rr_y = FALSE,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              clean_artifacts = FALSE, impute_artifacts = FALSE,
              moderators = moderator, data = data_r_meas_multi,
              supplemental_ads = ad_list)
summary(ma_obj)
ma_obj$meta_tables[[1]]$artifact_distribution$true_score
```

```
## Artifact information from studies not included in the meta-analysis can also be used to make
## corrections. Passing artifact information with the 'supplemental_ads' argument allows for
## additional artifact values and/or means and variances of artifacts to be used.
## The 'supplemental_ads' analysis below gives the same results as the prior meta-analysis.
x_ids <- c(data_r_meas_multi$x_name, data_r_meas_multi$y_name) == "X"
rxxi <- c(data_r_meas_multi$rxxi, data_r_meas_multi$ryyi)[x_ids]
```



```

n_rxxi = c(data_r_meas_multi$n, data_r_meas_multi$n)[x_ids]

y_ids <- c(data_r_meas_multi$x_name, data_r_meas_multi$y_name) == "Y"
ryyi <- c(data_r_meas_multi$rxxi, data_r_meas_multi$ryyi)[y_ids]
n_ryyi = c(data_r_meas_multi$n, data_r_meas_multi$n)[y_ids]

z_ids <- c(data_r_meas_multi$x_name, data_r_meas_multi$y_name) == "Z"
rzzi <- c(data_r_meas_multi$rxxi, data_r_meas_multi$ryyi)[z_ids]
n_rzzi = c(data_r_meas_multi$n, data_r_meas_multi$n)[z_ids]

ma_obj <- ma_r(ma_method = "ad", rxyi = rxyi, n = n,
              correct_rr_x = FALSE, correct_rr_y = FALSE,
              construct_x = x_name, construct_y = y_name,
              moderators = moderator, sample_id = sample_id, data = data_r_meas_multi,
              supplemental_ads = list(X = list(rxxi = rxxi, n_rxxi = n_rxxi, wt_rxxi = n_rxxi),
                                      Y = list(rxxi = ryyi, n_rxxi = n_ryyi, wt_rxxi = n_ryyi),
                                      Z = list(rxxi = rzzi, n_rxxi = n_rzzi, wt_rxxi = n_rzzi)))

summary(ma_obj)
ma_obj$meta_tables[[1]]$artifact_distribution$true_score

## If 'use_all_arts' is set to TRUE, artifacts from studies without valid correlations
## will be used to inform artifact distributions. Below, correlations and artifacts
## are provided by non-overlapping sets of studies.
dat1 <- dat2 <- data_r_meas_multi
dat1$rxxi <- dat1$ryyi <- NA
dat2$rxyi <- NA
dat2$sample_id <- dat2$sample_id + 40
dat <- rbind(dat1, dat2)
ma_obj <- ma_r(ma_method = "ad", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              correct_rr_x = FALSE, correct_rr_y = FALSE,
              construct_x = x_name, construct_y = y_name,
              sample_id = sample_id, moderators = moderator,
              use_all_arts = TRUE, data = dat)

summary(ma_obj)
ma_obj$meta_tables[[1]]$artifact_distribution$true_score

### Demonstration of ma_r_bb ###
## Example analysis using data from Gonzalez-Mule et al. (2014):

## Not correcting for bias and using normal distributions to compute uncertainty intervals
## allows for exact replication of the results reported in the text:
ma_r_bb(r = rxyi, n = n, correct_bias = FALSE, conf_method = "norm", cred_method = "norm",
        data = data_r_gonzalez_mule_2014)

## Using hs_override = TRUE allows one to easily implement the traditional Hunter-Schmidt method:
ma_r_bb(r = rxyi, n = n, hs_override = TRUE, data = data_r_gonzalez_mule_2014)

## With hs_override = FALSE, the program defaults will compute unbiased variances and use
## t-distributions to estimate confidence and credibility intervals - these settings make
## a noticeable difference for small studies like the textbook example:
ma_r_bb(r = rxyi, n = n, hs_override = FALSE, data = data_r_gonzalez_mule_2014)

```

```

### Demonstration of ma_r_ic ###
## Simulated example satisfying the assumptions of the Case IV
## range-restriction correction (parameter values: mean_rho = .3, sd_rho = .15):
ma_r_ic(rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi, ux = ux, data = data_r_uvirr)

## Simulated example satisfying the assumptions of the Case V
## range-restriction correction
ma_r_ic(rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
        rxx_type = "parallel", ryy_type = "parallel",
        ux = ux, uy = uy, data = data_r_bvirr)

## Published example from Gonzalez-Mule et al. (2014)
ma_r_ic(rxyi = rxyi, n = n, hs_override = TRUE, data = data_r_gonzalez_mule_2014,
        rxx = rxxi, ryy = ryyi, ux = ux, indirect_rr_x = TRUE,
        moderators = c("Rating source", "Published", "Type", "Complexity"))

### Demonstration of ma_r_ad ###
## Compute barebones meta-analysis
ma_obj <- ma_r_bb(r = rxyi, n = n, correct_bias = FALSE,
                conf_method = "norm", cred_method = "norm", data = data_r_mcdaniel_1994)

## Construct artifact distribution for X
ad_obj_x <- create_ad(ad_type = "tsa", mean_rxxi = data_r_mcdaniel_1994$Mrxxi[1],
                    var_rxxi = data_r_mcdaniel_1994$SDrxxi[1]^2,
                    ux = data_r_mcdaniel_1994$ux,
                    wt_ux = data_r_mcdaniel_1994$ux frequency)

## Construct artifact distribution for Y
ad_obj_y <- create_ad(ad_type = "tsa", rxxi = data_r_mcdaniel_1994$ryyi,
                    wt_rxxi = data_r_mcdaniel_1994$ryyi frequency)

## Compute artifact-distribution meta-analysis, correcting for measurement error only
ma_r_ad(ma_obj = ma_obj, ad_obj_x = ad_obj_x, ad_obj_y = ad_obj_y, correction_method = "meas")

## Compute artifact-distribution meta-analysis, correcting for univariate direct range restriction
ma_r_ad(ma_obj = ma_obj, ad_obj_x = ad_obj_x, ad_obj_y = ad_obj_y, correction_method = "uvdrr",
        correct_rr_y = FALSE, indirect_rr_x = FALSE)

# The results of ma_r() can also be corrected using artifact distributions
ma_obj <- ma_r(ma_method = "bb", rxyi = rxyi, n = n,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              moderators = moderator, data = data_r_meas_multi)

# The create_ad_list function can be used to generate batches of artifact-distribution objects.
# Here is an example in which one distribution is created per construct.
ad_tibble <- create_ad_list(n = n, rxx = rxxi, ryy = ryyi,
                           construct_x = x_name, construct_y = y_name,

```

```

        sample_id = sample_id,
        data = data_r_meas_multi)
# Passing that collection of distributions to ma_r_ad() corrects 'ma_obj' for artifacts:
ma_obj_tibble <- ma_r_ad(ma_obj = ma_obj,
                        ad_obj_x = ad_tibble, ad_obj_y = ad_tibble)
summary(ma_obj_tibble)
ma_obj_tibble$meta_tables[[1]]$artifact_distribution$true_score

# The same outcomes as the previous example can be achieved by passing a named list of
# artifact information, with each element bearing the name of a construct:
ad_list <- setNames(ad_tibble$ad_x, ad_tibble$construct_x)
ma_obj_list <- ma_r_ad(ma_obj = ma_obj,
                      ad_obj_x = ad_list, ad_obj_y = ad_list)
summary(ma_obj_list)
ma_obj_list$meta_tables[[1]]$artifact_distribution$true_score

# It is also possible to construct artifact distributions in a pairwise fashion.
# For example, if correlations between X and Y and between X and Z are being analyzed,
# X will get a different distribution for its relationships with Y than with Z.
# These pairwise distributions are based only on artifact data from specific construct pairs.
ad_tibble_pair <- create_ad_list(n = n, rxx = rxxi, ryy = ryyi,
                                construct_x = x_name, construct_y = y_name,
                                sample_id = sample_id,
                                control = control_psychmeta(pairwise_ads = TRUE),
                                data = data_r_meas_multi)
# Passing these pairwise distributions to ma_r_ad() corrects 'ma_obj' for artifacts:
ma_obj_pair <- ma_r_ad(ma_obj = ma_obj,
                      ad_obj_x = ad_tibble_pair, ad_obj_y = ad_tibble_pair)
summary(ma_obj_pair)
ma_obj_pair$meta_tables[[1]]$artifact_distribution$true_score

# Sometimes moderators have important influences on artifact distributions as well as
# distributions of effect sizes. When this occurs, moderated artifact distributions
# can be created to make more appropriate corrections.
ad_tibble_mod <- create_ad_list(n = n, rxx = rxxi, ryy = ryyi,
                                construct_x = x_name, construct_y = y_name,
                                sample_id = sample_id,
                                control = control_psychmeta(moderated_ads = TRUE),
                                moderators = moderator,
                                data = data_r_meas_multi)
# Passing these moderated distributions to ma_r_ad() corrects 'ma_obj' for artifacts:
ma_obj_mod <- ma_r_ad(ma_obj = ma_obj,
                      ad_obj_x = ad_tibble_mod, ad_obj_y = ad_tibble_mod)
summary(ma_obj_mod)
ma_obj_mod$meta_tables[[1]]$artifact_distribution$true_score

# It is also possible to create pairwise moderated artifact distributions.
ad_tibble_pairmod <- create_ad_list(n = n, rxx = rxxi, ryy = ryyi,
                                    construct_x = x_name, construct_y = y_name,

```

```

        sample_id = sample_id,
        control = control_psychmeta(moderated_ads = TRUE,
                                   pairwise_ads = TRUE),
        moderators = moderator,
        data = data_r_meas_multi)
# Passing these pairwise moderated distributions to ma_r_ad() corrects 'ma_obj' for artifacts:
ma_obj_pairmod <- ma_r_ad(ma_obj = ma_obj,
                        ad_obj_x = ad_tibble_pairmod, ad_obj_y = ad_tibble_pairmod)
summary(ma_obj_pairmod)
ma_obj_pairmod$meta_tables[[1]]$artifact_distribution$true_score

# For even more control over which artifact distributions are used in corrections, you can supply
# un-named list of distributions in which the order of distributions corresponds to the order of
# meta-analyses in ma_obj. It is important for the elements to be un-named, as the absence of names
# and the length of the list are the two ways in which ma_r_ad() validates the lists.
ad_list_pairmod_x <- ad_tibble_pairmod$ad_x
ad_list_pairmod_y <- ad_tibble_pairmod$ad_y
# Passing these lists of distributions to ma_r_ad() corrects 'ma_obj' for artifacts:
ma_obj_pairmodlist <- ma_r_ad(ma_obj = ma_obj,
                             ad_obj_x = ad_list_pairmod_x, ad_obj_y = ad_list_pairmod_y)
summary(ma_obj_pairmodlist)
ma_obj_pairmodlist$meta_tables[[1]]$artifact_distribution$true_score

## End(Not run)

```

ma_r_order2

Second-order meta-analysis function for correlations

Description

This function computes second-order meta-analysis function for correlations. It supports second-order analyses of bare-bones, artifact-distribution, and individual-correction meta-analyses.

Usage

```

ma_r_order2(k, N = NULL, r = NULL, rho = NULL, var_r = NULL,
            var_r_c = NULL, ma_type = c("bb", "ic", "ad"), sample_id = NULL,
            citekey = NULL, moderators = NULL, moderator_type = "simple",
            construct_x = NULL, construct_y = NULL, data = NULL,
            control = control_psychmeta(), ...)

```

Arguments

k	Vector or column name of meta-analyses' k values.
N	Vector or column name of meta-analyses' total sample sizes (optional).
r	Vector or column name of mean observed correlations.
rho	Vector or column name of mean corrected correlations.

var_r	Vector or column name of observed variances of observed correlations.
var_r_c	Vector or column name of observed variances of corrected correlations.
ma_type	Type of meta-analyses being analyzed: "bb" (barebones), "ic" (individual correction), or "ad" (artifact distribution).
sample_id	Vector or column name of study ID labels.
citekey	Optional vector of bibliographic citation keys for samples/studies in the meta-analysis (if multiple citekeys pertain to a given effect size, combine them into a single string entry with comma delimiters (e.g., "citekey1,citekey2")).
moderators	Matrix or column names of moderator variables to be used in the meta-analysis (can be a vector in the case of one moderator).
moderator_type	Type of moderator analysis ("none", "simple", or "hierarchical").
construct_x	Vector or column name of construct names for X.
construct_y	Vector or column name of construct names for Y.
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
control	Output from the control_psychmeta() function or a list of arguments controlled by the control_psychmeta() function. Ellipsis arguments will be screened for internal inclusion in control.
...	Further arguments to be passed to functions called within the meta-analysis.

Value

A nested tabular object of the class "ma_psychmeta".

Examples

```
## Analysis of the validity of conscientiousness as a predictor of job performance in East Asia
out <- ma_r_order2(k = k, r = r_bar_i, rho = rho_bar_i, var_r = var_r,
  var_r_c = NULL, ma_type = c("bb", "ad"),
  sample_id = NULL, moderators = NULL,
  construct_x = NULL, construct_y = NULL,
  data = dplyr::filter(data_r_oh_2009, Predictor == "Conscientiousness"))
summary(out)

## Analysis of the validity of the Big Five traits as predictors of job performance in East Asia
out <- ma_r_order2(k = k, r = r_bar_i, rho = rho_bar_i, var_r = var_r,
  var_r_c = NULL, ma_type = c("bb", "ad"),
  sample_id = NULL, moderators = NULL, construct_x = Predictor,
  data = data_r_oh_2009)
summary(out)

## Analysis of the average validity of the Big Five traits as predictors of
## job performance by Eastern Asian country
out <- ma_r_order2(k = k, r = r_bar_i, rho = rho_bar_i, var_r = var_r,
  var_r_c = NULL, ma_type = c("bb", "ad"),
  sample_id = NULL, moderators = "Country", data = data_r_oh_2009)
summary(out)
```

merge_simdat_d	<i>Merge multiple "simdat_d_database" class objects</i>
----------------	---

Description

This function allows for multiple simulated databases from [simulate_d_database](#) to be merged together into a single database. Merged databases will be assigned moderator variable codes.

Usage

```
merge_simdat_d(...)
```

Arguments

... Collection of objects created by the "simulate_d_database" function. Simply enter the database objects as `merge_simdat_d(data_obj1, data_obj2, data_obj3)`.

Value

A merged database of class `simdat_d`

merge_simdat_r	<i>Merge multiple "simdat_r_database" class objects</i>
----------------	---

Description

This function allows for multiple simulated databases from [simulate_r_database](#) to be merged together into a single database. Merged databases will be assigned moderator variable codes.

Usage

```
merge_simdat_r(...)
```

Arguments

... Collection of objects created by the "simulate_r_database" function. Simply enter the database objects as `merge_simdat_r(data_obj1, data_obj2, data_obj3)`.

Value

A merged database of class `simdat_r_database`

metabulate	<i>Write a summary table of meta-analytic results</i>
------------	---

Description

Write a summary table of meta-analytic results

Usage

```
metabulate(ma_obj, file = NULL, output_dir = getwd(),
  output_format = c("word", "html", "pdf", "odt", "text", "rmd"),
  show_msd = TRUE, show_conf = TRUE, show_cred = TRUE,
  show_se = FALSE, show_var = FALSE, analyses = "all",
  match = c("all", "any"), case_sensitive = TRUE, ma_method = "ad",
  correction_type = "ts", collapse_construct_labels = TRUE,
  bold_headers = TRUE, digits = 2L,
  decimal.mark = getOption("OutDec"), leading0 = "conditional",
  drop0integer = FALSE, neg.sign = "&minus;", pos.sign = "figure",
  big.mark = "&#8239;", big.interval = 3L, small.mark = "&#8239;",
  small.interval = 3L, na.mark = "&mdash;", lgl.mark = c("+",
  "&minus;"), inf.mark = c("+&infin;", "&minus;&infin;"),
  conf_format = "parentheses", cred_format = "parentheses",
  symbol_es = "ES", caption = "Results of meta-analyses",
  header = NULL, verbose = FALSE, unicode = NULL, bib = NULL,
  title.bib = NULL, style = "apa", additional_citekeys = NULL,
  save_build_files = FALSE, ...)
```

Arguments

ma_obj	A psychmeta meta-analysis object.
file	The filename (optionally with a subfolder path) for the output file. If NULL, the function will output directly to the R console (also useful if you want to include psychmeta results in a larger RMarkdown document).
output_dir	The filepath for the output directory/folder. Defaults to the current working directory.
output_format	The format of the output tables. Available options are Word (default), HTML, PDF (requires LaTeX and the unicode-math LaTeX package to be installed), ODT, rmd (Rmarkdown), and text (plain text). You can also specify the full name of another RMarkdown output_format .
show_msd	Logical. Should means and standard deviations of effect sizes be shown (default TRUE)
show_conf	Logical. Should confidence intervals be shown (default: TRUE)?
show_cred	Logical. Should credibility intervals be shown (default: TRUE)?
show_se	Logical. Should standard errors be shown (default: FALSE)?
show_var	Logical. Should variances be shown (default: FALSE)?

analyses	Which analyses to extract references for? See filter_ma for details.
match	Match all or any of the filter criteria? See filter_ma for details.
case_sensitive	Logical scalar that determines whether character values supplied in analyses should be treated as case sensitive (TRUE, default) or not (FALSE).
ma_method	Meta-analytic methods to be included. Valid options are: "ad", "ic", and "bb". Multiple methods are permitted. By default, results are given for one method with order of priority: 1. "ad", 2. "ic", 3. "bb".
correction_type	Type of meta-analytic corrections to be included. Valid options are: "ts" (default), "vgx", and "vgy". Multiple options are permitted.
collapse_construct_labels	Should the construct labels for construct pairs with multiple rows of results be simplified so that only the first occurrence of each set of construct names is shown (TRUE; default) or should construct labels be shown for each row of the table (FALSE).
bold_headers	Logical. Should column headers be bolded (default: TRUE)?
digits, decimal.mark, leading0, drop0integer, neg.sign, pos.sign, big.mark, big.interval, small.mar	Number formatting arguments. See format_num for details.
conf_format	How should confidence intervals be formatted? Options are: <ul style="list-style-type: none"> • parentheses: Bounds are enclosed in parentheses and separated by a comma: (LO, UP). • brackets: Bounds are enclosed in square brackets and separated by a comma: [LO, UP]. • columns: Bounds are shown in individual columns.
cred_format	How should credibility intervals be formatted? Options are the same as for conf_format above.
symbol_es	For meta-analyses of generic (non-r, non-d) effect sizes, the symbol used for the effect sizes (default: symbol_es = "ES").
caption	Caption to print before tables. Either a character scalar or a named character vector with names corresponding to combinations of ma_method and correction_type (i.e., bb, ic_ts, ad_vgx, etc.).
header	A list of YAML header parameters to pass to <code>link[rmarkdown]{render}</code> .
verbose	Logical. Should detailed SD and variance components be shown (default: FALSE)?
unicode	Logical. If output_format is "text", should UTF-8 characters be used (defaults to system default).
bib	A BibTeX file containing the citekeys for the meta-analyses. If provided and file is not NULL, a bibliography will be included with the meta-analysis table. See generate_bib for additional arguments controlling the bibliography.
title.bib	The title to give to the bibliography (see bib above). If NULL, defaults to "Sources Contributing to Meta-Analyses"
style	What style should the bibliography (see bib above) be formatted in? Can be a file path or URL for a CSL citation style or the style ID for any style available from the Zotero Style Repository). Defaults to APA style. (Retrieving a style by ID requires an internet connection. If unavailable, references will be rendered in Chicago style.).


```

additional_citekeys
    Additional citekeys to include in the reference list (see bib above).
save_build_files
    Should the RMarkdown and BibLaTeX (if any) files used to generate the output
    be saved (default: FALSE)?
...
    Additional arguments to pass to render.

```

Value

A list of meta-analysis results [tibbles](#) with "caption" and "footnote" attributes.
 If file is specified, formatted tables and bibliographies are exported in the requested output_format.
 Formatted tables of meta-analytic output.

See Also

Other output functions: [generate_bib](#), [metabulate_rmd_helper](#)

Examples

```

## Not run:
## Create a results table for meta-analysis of correlations and output to Word:
ma_r_obj <- ma_r(ma_method = "ic", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
               construct_x = x_name, construct_y = y_name,
               moderators = moderator, data = data_r_meas_multi)
metabulate(ma_obj = ma_r_obj, file = "meta tables correlations",
           output_format = "word", output_dir = tempdir())

## Output to PDF:
metabulate(ma_obj = ma_r_obj, file = "meta tables correlations",
           output_format = "pdf", output_dir = tempdir())

## Output to ODT (LibreOffice):
metabulate(ma_obj = ma_r_obj, file = "meta tables correlations",
           output_format = "odt", output_dir = tempdir())

## To produce Markdown tables to include inline in an RMarkdown report,
## leave file == NULL and output_format to anything but "text":
ma_table <- metabulate(ma_obj = ma_r_obj, file = NULL, output_format = "rmd")

## Use the metabulate_rmd_helper() function to ensure all symbols render properly.
## Insert the following code as 'as-is' output:
metabulate_rmd_helper()

## Then, add the formatted table to your document using your preferred table
## formatting functions:

#### Using just the 'knitr' package, include the following as 'as-is' output:
knitr::kable(ma_table[[1]], caption = attr(ma_table[[1]], "caption"))
cat("\n", attr(ma_table[[1]], "footnote"))

```

```
#### Using 'knitr' plus the 'kableExtra' package:
knitr::kable(ma_table[[1]], "latex", booktabs = TRUE,
             caption = attr(ma_table[[1]], "caption")) %>%
  kableExtra::kable_styling(latex_options = c("striped", "hold_position")) %>%
  kableExtra::footnote(general = attr(ma_table[[1]], "footnote"))

# !!! Note: On Windows, R currently can only handle Unicode characters if kables
# are printed at top-level (e.g., not in an if() statement, in a for() loop,
# or in lapply() or map() ). To correctly print Unicode metabulate tables, call
# kable() as a top-level function (as above).

## Create output table for meta-analysis of d values:
ma_d_obj <- ma_d(ma_method = "ic", d = d, n1 = n1, n2 = n2, ryy = ryyi,
                construct_y = construct, data = data_d_meas_multi)
ma_d_obj <- ma_d_ad(ma_obj = ma_d_obj, correct_rr_g = FALSE, correct_rr_y = FALSE)
metabulate(ma_obj = ma_d_obj, file = "meta tables d values", output_dir = tempdir())

## Create output table for meta-analysis of generic effect sizes:
dat <- data.frame(es = data_r_meas_multi$rxyi,
                 n = data_r_meas_multi$n,
                 var_e = (1 - data_r_meas_multi$rxyi^2)^2 / (data_r_meas_multi$n - 1))
ma_obj <- ma_generic(es = es, n = n, var_e = var_e, data = dat)
metabulate(ma_obj = ma_obj, file = "meta tables generic es", output_dir = tempdir())

## End(Not run)
```

metabulate_rmd_helper *Add metabulate equation commands and LaTeX dependencies*

Description

`metabulate` requires several lines of code to correctly render meta-analysis results table column headings and footnotes. If `metabulate` is used to render files directly, these are added to the internal RMarkdown document. If you use `metabulate` output in a larger RMarkdown document, use this function to automatically add the necessary lines of code based on your chosen output format.

Usage

```
metabulate_rmd_helper(latex = TRUE, html = TRUE, word_proc = TRUE)
```

Arguments

latex	Should required commands be included when converting to PDF, LaTeX, and related formats?
html	Should required commands be included when converting to HTML and related formats?
word_proc	Should required commands be included when converting to Word, ODT, and related formats?

Value

Requested commands are printed to the console.

PDF and LaTeX output

If `latex` is `TRUE` and you render to PDF, LaTeX, or other output formats requiring LaTeX (e.g., `beamer_presentation`, see [is_latex_output](#)), a YAML metadata block with a `header-includes` argument calling the required `unicode-math` LaTeX package is printed.

An RMarkdown file can only include one `header-includes` metadata entry. If your document already has one, set `latex` to `FALSE` and manually add the `unicode-math` package to your LaTeX header instead.

(Note that `header-includes` is generally discouraged in favor of adding an `include` argument to specific output formats, see http://rmarkdown.rstudio.com/pdf_document_format.html#includes.)

HTML output

If `html` is `TRUE` and you render to HTML (or related formats, see [is_html_output](#)), the following LaTeX math commands are defined:

- `symit`
- `symup`
- `symbfit`
- `symbfup`

If you define your own LaTeX or MathJax macros for these commands, set `html` to `FALSE`.

Microsoft Office and LibreOffice output

If `word_proc` is `TRUE` and you render to Word or ODT (or related formats such as PowerPoint), the following LaTeX math commands are defined:

- `symit`
- `symup`
- `symbfit`
- `symbfup`

If you define your own LaTeX, Office, or OpenDocument macros for these commands, set `word_proc` to `FALSE`.

See Also

Other output functions: [generate_bib](#), [metabulate](#)

Examples

```
## Include this line as 'asis' output in your RMarkdown document:
metabulate_rmd_helper()

## If you've already included \\usepackage{unicode-math} in your RMarkdown header
## for PDF (and related formats) header, set latex to FALSE:
metabulate_rmd_helper(latex = FALSE)
```

metareg

Compute meta-regressions

Description

This function is a wrapper for **metafor**'s `rma` function that computes meta-regressions for all bare-bones and individual-correction meta-analyses within an object. It makes use of both categorical and continuous moderator information stored in the meta-analysis object and allows for interaction effects to be included in the regression model. Output from this function will be added to the meta-analysis object in a list called `follow_up_analyses`. If using this function with a multi-construct meta-analysis object from `ma_r` or `ma_d`, note that the `follow_up_analyses` list is appended to the meta-analysis object belonging to a specific construct pair within the `construct_pairs` list.

Usage

```
metareg(ma_obj, formula_list = NULL, ...)
```

Arguments

<code>ma_obj</code>	Meta-analysis object.
<code>formula_list</code>	Optional list of regression formulas to evaluate. NOTE: If there are spaces in your moderator names, replace them with underscores (i.e., "_") so that the formula(s) will perform properly. The function will remove spaces in the data, you only have to account for this in <code>formula_list</code> when you supply your own formula(s).
<code>...</code>	Additional arguments.

Value

`ma_obj` with meta-regression results added (see `ma_obj$follow_up_analyses$metareg`).

Examples

```
## Meta-analyze the data from Gonzalez-Mule et al. (2014)
## Note: These are corrected data and we have confirmed with the author that
## these results are accurate:
ma_obj <- ma_r_ic(rxyi = rxyi, n = n, hs_override = TRUE, data = data_r_gonzalez_mule_2014,
                 rxx = rxxi, ryy = ryyi, ux = ux, indirect_rr_x = TRUE,
                 correct_rr_x = TRUE, moderators = Complexity)
```

```

## Pass the meta-analysis object to the meta-regression function:
ma_obj <- metareg(ma_obj)

## Examine the meta-regression results for the bare-bones and corrected data:
ma_obj$metareg[[1]]$barebones$`Main Effects`
ma_obj$metareg[[1]]$individual_correction$true_score$`Main Effects`

## Meta-analyze simulated d-value data
dat <- data_d_meas_multi
## Simulate a random moderator
set.seed(100)
dat$moderator <- sample(1:2, nrow(dat), replace = TRUE)
ma_obj <- ma_d(ma_method = "ic", d = d, n1 = n1, n2 = n2, ryy = ryyi,
              construct_y = construct, sample_id = sample_id,
              moderators = moderator, data = dat)

## Pass the meta-analysis object to the meta-regression function:
ma_obj <- metareg(ma_obj)

## Examine the meta-regression results for the bare-bones and corrected data:
ma_obj$metareg[[1]]$barebones$`Main Effects`
ma_obj$metareg[[1]]$individual_correction$latentGroup_latentY$`Main Effects`

```

mix_dist

Descriptive statistics for a mixture distribution

Description

Compute descriptive statistics for a mixture distribution. This function returns the grand mean, the pooled sample (within-sample) variance, variance of sample means (between-groups), and mixture (total sample) variance of the mixture sample data.

Usage

```
mix_dist(mean_vec, var_vec, n_vec, unbiased = TRUE, na.rm = FALSE)
```

Arguments

mean_vec	Vector of sample means.
var_vec	Vector of sample variances.
n_vec	Vector of sample sizes.
unbiased	Logical scalar determining whether variance should be unbiased (TRUE; default) or maximum-likelihood (FALSE).
na.rm	Logical scalar determining whether to remove missing values prior to computing output (TRUE) or not (FALSE; default)

Details

The grand mean of a mixture distribution is computed as:

$$\mu = \frac{\sum_{i=1}^k \bar{x}_i n_i}{\sum_{i=1}^k n_i}$$

where μ is the grand mean, \bar{x}_i represents the sample means, and n_i represents the sample sizes.

Maximum-likelihood mixture variances are computed as:

$$var_{BG_{ML}} = \frac{\sum_{i=1}^k (\bar{x}_i - \mu) n_i}{\sum_{i=1}^k n_i}$$

$$var_{WG_{ML}} = \frac{\sum_{i=1}^k v_i n_i}{\sum_{i=1}^k n_i}$$

$$var_{mix_{ML}} = var_{BG_{ML}} + var_{WG_{ML}}$$

where v_i represents the sample variances.

Unbiased mixture variances are computed as:

$$var_{BG_{Unbiased}} = \frac{\sum_{i=1}^k (\bar{x}_i - \mu) n_i}{(\sum_{i=1}^k n_i) - 1}$$

$$var_{WG_{Unbiased}} = \frac{\sum_{i=1}^k v_i (n_i - 1)}{(\sum_{i=1}^k n_i) - 1}$$

$$var_{mix_{Unbiased}} = var_{BG_{Unbiased}} + var_{WG_{Unbiased}}$$

Value

The mean, pooled sample (within-sample) variance, variance of sample means (between-groups), and mixture (total sample) variance of the mixture sample data.

Examples

```
mix_dist(mean_vec = c(-.5, 0, .5), var_vec = c(.9, 1, 1.1), n_vec = c(100, 100, 100))
```

mix_matrix	<i>Estimate mixture covariance matrix from within-group covariance matrices</i>
------------	---

Description

Estimate mixture covariance matrix from within-group covariance matrices

Usage

```
mix_matrix(sigma_list, mu_mat, p_vec, N = Inf, group_names = NULL,
           var_names = NULL)
```

Arguments

sigma_list	List of covariance matrices.
mu_mat	Matrix of mean parameters, with groups on the rows and variables on the columns.
p_vec	Vector of proportion of cases in each group.
N	Optional total sample size across all groups (used to compute unbiased covariance estimates).
group_names	Optional vector of group names.
var_names	Optional vector of variable names.

Value

List of mixture covariances and means.

Examples

```
out <- unmix_matrix(sigma_mat = reshape_vec2mat(.5, order = 2),
                   mu_mat = rbind(c(0, 0), c(.5, 1)),
                   p_vec = c(.3, .7), N = 100)

mix_matrix(sigma_list = out$cov_group_unbiased,
           mu_mat = out$means_raw[-3,],
           p_vec = out$p_group, N = out$N)
```

mix_r_2group	<i>Estimate the mixture correlation for two groups</i>
--------------	--

Description

Estimate the mixture correlation for two groups

Usage

```
mix_r_2group(rxy, dx, dy, p = 0.5)
```

Arguments

rxy	Average within-group correlation
dx	Standardized mean difference between groups on X.
dy	Standardized mean difference between groups on Y.
p	Proportion of cases in one of the two groups.

Details

The average within-group correlation is estimated as:

$$\rho_{xy_{WG}} = \rho_{xy_{Mix}} \sqrt{(d_x^2 p(1-p) + 1)(d_y^2 p(1-p) + 1)} - \sqrt{d_x^2 d_y^2 p^2 (1-p)^2}$$

where $\rho_{xy_{WG}}$ is the average within-group correlation, $\rho_{xy_{Mix}}$ is the overall mixture correlation, d_x is the standardized mean difference between groups on X, d_y is the standardized mean difference between groups on Y, and p is the proportion of cases in one of the two groups.

Value

A vector of two-group mixture correlations

Examples

```
mix_r_2group(rxy = .375, dx = 1, dy = 1, p = .5)
```

plot_forest	<i>Create forest plots</i>
-------------	----------------------------

Description

Create forest plots

Usage

```
plot_forest(ma_obj, analyses = "all", match = c("all", "any"),
  case_sensitive = TRUE, show_filtered = FALSE,
  ma_facetname = "Summary", facet_levels = NULL, conf_level = 0.95,
  conf_method = "t", x_limits = NULL, x_breaks = NULL,
  x_lab = NULL, y_lab = "Reference")
```

Arguments

ma_obj	Meta-analysis object.
analyses	Which analyses to extract? Can be either "all" to extract references for all meta-analyses in the object (default) or a list containing one or more of the following arguments: <ul style="list-style-type: none"> • construct A list or vector of construct names to search for. • construct_pair A list of vectors of construct pairs to search for (e.g., list(c("Construct A", "Construct B"), list(1, 2))). • pair_id A list or vector of numeric construct Pair IDs. • analysis_id A list or vector of analysis IDs (combinations of moderator levels). • k_min A numeric value specifying the minimum k for extracted meta-analyses. • N_min A numeric value specifying the minimum N for extracted meta-analyses.
match	Should extracted meta-analyses match all (default) or any of the criteria given in analyses?
case_sensitive	Logical scalar that determines whether character values supplied in analyses should be treated as case sensitive (TRUE, default) or not (FALSE).
show_filtered	Logical scalar that determines whether the meta-analysis object given in the output should be the modified input object (FALSE, default) or the filtered object (TRUE).
ma_facetname	Label to use for meta-analysis results in the facet_grid() function from ggplot2.
facet_levels	Order in which moderator levels should be displayed.
conf_level	Confidence level to define the width of the confidence interval (default = .95).
conf_method	Distribution to be used to compute the width of confidence intervals. Available options are "t" for t distribution or "norm" for normal distribution.
x_limits	Span of the X values to be plotted.
x_breaks	Breaks for the X values to be plotted.
x_lab	Label to use for the X axis.
y_lab	Label to use for the Y axis.

Value

A list of forest plots.

Author(s)

Based on code by John Sakaluk

Examples

```
ma_obj <- ma_r(ma_method = "ic", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              moderators = moderator, data = data_r_meas_multi)
plot_forest(ma_obj = ma_obj)
plot_forest(ma_obj = ma_obj, analyses = list(pair_id = 2))
plot_forest(ma_obj = ma_obj, analyses = list(pair_id = 1), show_filtered = TRUE)

## d values
ma_obj <- ma_d(ma_method = "ic", d = d, n1 = n1, n2 = n2, ryy = ryyi,
              construct_y = construct, sample_id = sample_id,
              data = data_d_meas_multi)
plot_forest(ma_obj = ma_obj)
plot_forest(ma_obj = ma_obj, analyses = list(pair_id = 2))
plot_forest(ma_obj = ma_obj, analyses = list(pair_id = 1, analysis_id = 1), show_filtered = TRUE)
```

plot_funnel

Create funnel plots

Description

Create funnel plots

Usage

```
plot_funnel(ma_obj, analyses = "all", match = c("all", "any"),
            case_sensitive = TRUE, show_filtered = FALSE)
```

Arguments

ma_obj	Meta-analysis object.
analyses	Which analyses to extract? Can be either "all" to extract references for all meta-analyses in the object (default) or a list containing one or more of the following arguments: <ul style="list-style-type: none"> • constructA list or vector of construct names to search for. • construct_pairA list of vectors of construct pairs to search for (e.g., list(c("Construct A", "Construct B"))). • pair_idA list or vector of numeric construct Pair IDs. • analysis_idA list or vector of analysis IDs (combinations of moderator levels).

- `k_minA` numeric value specifying the minimum `k` for extracted meta-analyses.
 - `N_minA` numeric value specifying the minimum `N` for extracted meta-analyses.
- `match` Should extracted meta-analyses match all (default) or any of the criteria given in analyses?
- `case_sensitive` Logical scalar that determines whether character values supplied in analyses should be treated as case sensitive (TRUE, default) or not (FALSE).
- `show_filtered` Logical scalar that determines whether the meta-analysis object given in the output should be the modified input object (FALSE, default) or the filtered object (TRUE).

Value

A list of funnel plots.

Author(s)

Based on code by John Sakaluk

Examples

```
## Correlations
ma_obj <- ma_r(ma_method = "ic", rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi,
              construct_x = x_name, construct_y = y_name, sample_id = sample_id,
              moderators = moderator, data = data_r_meas_multi)
plot_funnel(ma_obj = ma_obj)
plot_funnel(ma_obj = ma_obj, analyses = list(pair_id = 2))
plot_funnel(ma_obj = ma_obj, analyses = list(pair_id = 1, analysis_id = 1), show_filtered = TRUE)

## d values
ma_obj <- ma_d(ma_method = "ic", d = d, n1 = n1, n2 = n2, ryy = ryyi,
              construct_y = construct, sample_id = sample_id,
              data = data_d_meas_multi)
plot_funnel(ma_obj = ma_obj)
plot_funnel(ma_obj = ma_obj, analyses = list(pair_id = 2))
plot_funnel(ma_obj = ma_obj, analyses = list(pair_id = 1, analysis_id = 1), show_filtered = TRUE)
```

predict

Prediction method for objects of classes deriving from "lm_mat"

Description

Prediction method for objects of classes deriving from "lm_mat"

Arguments

object	Object of class inheriting from "lm_mat"
newdata	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
se.fit	A switch indicating if standard errors are required.
df	Degrees of freedom for scale.
interval	Type of interval calculation. Can be abbreviated.
level	Tolerance/confidence level.
...	further arguments passed to or from other methods.

Value

An set of predicted values

print *Print methods for psychmeta*

Description

Print methods for **psychmeta** output objects with classes exported from **psychmeta**.

Arguments

x	Object to be printed (object is used to select a method).
...	Additional arguments.
digits	Number of digits to which results should be rounded.
ma_methods	Meta-analytic methods to be included. Valid options are: "bb", "ic", and "ad"
correction_types	Types of meta-analytic corrections to be included. Valid options are: "ts", "vgx", and "vgy"
verbose	Logical scalar that determines whether printed object should contain verbose information (e.g., non-standard columns of meta-analytic output; TRUE) or not (FALSE).
symbolic.cor	For lm_mat output: logical. If TRUE, print the correlations in a symbolic form (see symnum) rather than as numbers.
signif.stars	For lm_mat output: logical. If TRUE, 'significance stars' are printed for each coefficient.

psychmeta_news	<i>Retrieve the NEWS file for the psychmeta package</i>
----------------	---

Description

This function gives a shortcut to the `utils::news(package = "psychmeta")` function and displays psychmeta's NEWS file, which contains version information, outlines additions and changes to the package, and describes other updates.

Usage

```
psychmeta_news()
```

Examples

```
psychmeta_news()
```

reattribute	<i>Copy class and attributes from the original version of an object to a modified version.</i>
-------------	--

Description

Copy class and attributes from the original version of an object to a modified version.

Usage

```
reattribute(x, result)
```

Arguments

x	The original object, which has a class/attributes to copy
result	The modified object, which is / might be missing the class/attributes.

Value

result, now with class/attributes restored.

reshape_mat2dat	<i>Extract a long-format correlation database from a correlation matrix and its supporting vectors/matrices of variable information</i>
-----------------	---

Description

This function is designed to extract data from a correlation matrix that is in the format commonly published in journals, with leading columns of construct names and descriptive statistics being listed along with correlation data.

Usage

```
reshape_mat2dat(var_names, cor_data, common_data = NULL,
               unique_data = NULL, diag_label = NULL, lower_tri = TRUE,
               data = NULL)
```

Arguments

var_names	Vector (or scalar column name to match with data) containing variable names.
cor_data	Square matrix (or vector of column names to match with data) containing correlations among variables.
common_data	Vector or matrix (or vector of column names to match with data) of data common to both X and Y variables (e.g., sample size, study-wise moderators).
unique_data	Vector or matrix (or vector of column names to match with data) of data unique to X and Y variables (e.g., mean, SD, reliability).
diag_label	Optional name to attribute to values extracted from the diagonal of the matrix (if NULL, no values are extracted from the diagonal).
lower_tri	Logical scalar that identifies whether the correlations are in the lower triangle (TRUE) or in the upper triangle FALSE of the matrix.
data	Matrix, dataframe, or tibble containing study data (when present, column names of data will be matched to column names provided as other arguments).

Value

Long-format dataframe of correlation data, variable names, and supporting information

Author(s)

Jack W. Kostal

Examples

```
## Create a hypothetical matrix of data from a small study:
mat <- data.frame(var_names = c("X", "Y", "Z"),
                 n = c(100, 100, 100),
                 mean = c(4, 5, 3),
                 sd = c(2.4, 2.6, 2),
                 rel = c(.8, .7, .85),
                 reshape_vec2mat(cov = c(.3, .4, .5)))

## Arguments can be provided as quoted characters or as the unquoted names of data's columns:
reshape_mat2dat(var_names = var_names,
               cor_data = c("Var1", "Var2", "Var3"),
               common_data = "n",
               unique_data = c("mean", "sd", "rel"),
               data = mat)

## Arguments can also provided as raw vectors, matrices, dataframes, etc. without a data argument:
reshape_mat2dat(var_names = mat[,1],
               cor_data = mat[,6:8],
               common_data = mat[,2],
               unique_data = mat[,3:5])

## If data is not null, arguments can be a mix of matrix/dataframe/vector and column-name arguments
reshape_mat2dat(var_names = mat[,1],
               cor_data = mat[,6:8],
               common_data = "n",
               unique_data = c("mean", "sd", "rel"),
               data = mat)
```

 reshape_vec2mat

Assemble a variance-covariance matrix

Description

The `reshape_vec2mat` function facilitates the creation of square correlation/covariance matrices from scalars or vectors of variances/covariances. It allows the user to supply a vector of covariances that make up the lower triangle of a matrix, determines the order of the matrix necessary to hold those covariances, and constructs a matrix accordingly.

Usage

```
reshape_vec2mat(cov = NULL, var = NULL, order = NULL,
               var_names = NULL, by_row = FALSE, diag = FALSE)
```

Arguments

`cov` Scalar or vector of covariance information to include the lower-triangle positions of the matrix (default value is zero). If a vector, the elements must be provided in the order associated with concatenated column (`by_row = FALSE`; default)

	or row (by_row = TRUE) vectors of the lower triangle of the desired matrix. If variances are included in these values, set the diag argument to TRUE.
var	Scalar or vector of variance information to include the diagonal positions of the matrix (default value is 1).
order	If cov and var are scalars, this argument determines the number of variables to create in the output matrix.
var_names	Optional vector of variable names.
by_row	Logical scalar indicating whether cov values should fill the lower triangle by row (TRUE) or by column (FALSE; default).
diag	Logical scalar indicating whether cov values include variances (FALSE by default; if TRUE, the variance values supplied with the cov argument will supersede the var argument).

Value

A variance-covariance matrix

Examples

```
## Specify the lower triangle covariances
## Can provide names for the variables
reshape_vec2mat(cov = c(.3, .2, .4), var_names = c("x", "y", "z"))

## Specify scalar values to repeat for the covariances and variances
reshape_vec2mat(cov = .3, var = 2, order = 3)

## Give a vector of variances to create a diagonal matrix
reshape_vec2mat(var = 1:5)

## Specify order only to create identity matrix
reshape_vec2mat(order = 3)

## Specify order and scalar variance to create a scalar matrix
reshape_vec2mat(var = 2, order = 3)

## A quick way to make a 2x2 matrix for bivariate correlations
reshape_vec2mat(cov = .2)
```

 reshape_wide2long

Reshape database from wide format to long format

Description

This function automates the process of converting a wide-format database (i.e., a database in which intercorrelations between construct pairs define the columns, such that there are multiple columns of correlations) to a long-format database (i.e., a database with just one column of correlations). The meta-analysis functions in **psychmeta** work best with long-format databases, so this function can be a helpful addition to one's workflow when data are organized in a wide format.

Usage

```
reshape_wide2long(data, common_vars = NULL, es_design = NULL,
  n_design = NULL, other_design = NULL, es_name = "rxyi",
  missing_col_action = c("warn", "ignore", "stop"))
```

Arguments

<code>data</code>	Database of data for use in a meta-analysis in "wide" format.
<code>common_vars</code>	String vector of column names relevant to all variables in data.
<code>es_design</code>	$p \times p$ matrix containing the names of columns of intercorrelations among variables in the lower triangle of the matrix.
<code>n_design</code>	Scalar sample-size column name or a $p \times p$ matrix containing the names of columns of sample sizes the lower triangle of the matrix.
<code>other_design</code>	A matrix with variable names on the rows and names of long-format variables to create on the columns. Elements of this matrix must be column names of data.
<code>es_name</code>	Name of the effect size represented in data.
<code>missing_col_action</code>	Character scalar indicating how missing columns should be handled. Options are: "warn", "ignore", and "stop"

Value

A long-format database

Examples

```
n_params = c(mean = 150, sd = 20)
rho_params <- list(c(.1, .3, .5),
  c(mean = .3, sd = .05),
  rbind(value = c(.1, .3, .5), weight = c(1, 2, 1)))
rel_params = list(c(.7, .8, .9),
  c(mean = .8, sd = .05),
  rbind(value = c(.7, .8, .9), weight = c(1, 2, 1)))
sr_params = c(list(1, 1, c(.5, .7)))
sr_composite_params = list(1, c(.5, .6, .7))
wt_params = list(list(c(1, 2, 3),
  c(mean = 2, sd = .25),
  rbind(value = c(1, 2, 3), weight = c(1, 2, 1))),
  list(c(1, 2, 3),
  c(mean = 2, sd = .25),
  rbind(value = c(1, 2, 3), weight = c(1, 2, 1))))

## Simulate with wide format
data <- simulate_r_database(k = 10, n_params = n_params, rho_params = rho_params,
  rel_params = rel_params, sr_params = sr_params,
  sr_composite_params = sr_composite_params, wt_params = wt_params,
  var_names = c("X", "Y", "Z"), format = "wide")$statistics

## Define values to abstract from the data object
```

```

common_vars <- "sample_id"
es_design <- matrix(NA, 3, 3)
var_names <- c("X", "Y", "Z")
es_design[lower.tri(es_design)] <- c("rxyi_X_Y", "rxyi_X_Z", "rxyi_Y_Z")
rownames(es_design) <- colnames(es_design) <- var_names
n_design <- "ni"
other_design <- cbind(rxxi = paste0("parallel_rxxi_", var_names),
                     ux_local = paste0("ux_local_", var_names),
                     ux_external = paste0("ux_external_", var_names))
rownames(other_design) <- var_names

## Reshape the data to "long" format
reshape_wide2long(data = data, common_vars = common_vars, es_design = es_design,
                 n_design = n_design, other_design = other_design)

```

sensitivity

Sensitivity analyses for meta-analyses

Description

Wrapper function to compute bootstrap analyses, leave-one-out analyses, and cumulative meta-analyses. This function helps researchers to examine the stability/fragility of their meta-analytic results with bootstrapping and leave-one-out analyses, as well as detect initial evidence of publication bias with cumulative meta-analyses.

Usage

```

sensitivity(ma_obj, leave1out = TRUE, bootstrap = TRUE,
           cumulative = TRUE, sort_method = c("weight", "n", "inv_var"),
           boot_iter = 1000, boot_conf_level = 0.95, boot_ci_type = c("bca",
                             "norm", "basic", "stud", "perc"), ...)

sensitivity_bootstrap(ma_obj, boot_iter = 1000, boot_conf_level = 0.95,
                    boot_ci_type = c("bca", "norm", "basic", "stud", "perc"), ...)

sensitivity_cumulative(ma_obj, sort_method = c("weight", "n", "inv_var"),
                      ...)

sensitivity_leave1out(ma_obj, ...)

```

Arguments

ma_obj	Meta-analysis object.
leave1out	Logical scalar determining whether to compute leave-one-out analyses (TRUE) or not (FALSE).
bootstrap	Logical scalar determining whether bootstrapping is to be performed (TRUE) or not (FALSE).

cumulative	Logical scalar determining whether a cumulative meta-analysis is to be computed (TRUE) or not (FALSE).
sort_method	Method to sort samples in the cumulative meta-analysis. Options are "weight" to sort by weight (default), "n" to sort by sample size, and "inv_var" to sort by inverse variance.
boot_iter	Number of bootstrap iterations to be computed.
boot_conf_level	Width of confidence intervals to be constructed for all bootstrapped statistics.
boot_ci_type	Type of bootstrapped confidence interval. Options are "bca", "norm", "basic", "stud", and "perc" (these are "type" options from the <code>boot::boot.ci</code> function). Default is "bca". Note: If you have too few iterations, the "bca" method will not work and you will need to either increase the iterations or choose a different method.
...	Additional arguments.

Value

An updated meta-analysis object with sensitivity analyses added.

- When bootstrapping is performed, the `bootstrap` section of the `follow_up_analyses` section of the updated `ma_obj` returned by this function will contain both a matrix summarizing the mean, variance, and confidence intervals of the bootstrapped samples and a table of meta-analytic results from all bootstrapped samples.
- When leave-one-out analyses are performed, the `ma_obj` will acquire a list of leave-one-out results in its `follow_up_analyses` section that contains a table of all leave-one-out meta-analyses along with plots of the mean and residual variance of the effect sizes in the meta-analyses.
- When cumulative meta-analysis is performed, the `ma_obj` will acquire a list of cumulative meta-analysis results in its `follow_up_analyses` section that contains a table of all meta-analyses computed along with plots of the mean and residual variance of the effect sizes in the meta-analyses, sorted by the order in which studies were added to the meta-analysis.

Examples

```
## Not run:
## Run a meta-analysis using simulated correlation data:
ma_obj <- ma_r_ic(rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi, ux = ux,
                correct_rr_y = FALSE, data = data_r_uvirr)
ma_obj <- ma_r_ad(ma_obj, correct_rr_y = FALSE)

## Pass the meta-analysis object to the sensitivity() function:
ma_obj <- sensitivity(ma_obj = ma_obj, boot_iter = 10,
                    boot_ci_type = "norm", sort_method = "inv_var")

## Examine the tables and plots produced for the IC meta-analysis:
ma_obj$bootstrap[[1]]$barebones
ma_obj$bootstrap[[1]]$individual_correction$true_score
ma_obj$leave1out[[1]]$individual_correction$true_score
```

```

ma_obj$cumulative[[1]]$individual_correction$true_score

## Examine the tables and plots produced for the AD meta-analysis:
ma_obj$bootstrap[[1]]$artifact_distribution$true_score
ma_obj$leave1out[[1]]$artifact_distribution$true_score
ma_obj$cumulative[[1]]$artifact_distribution$true_score

## Run a meta-analysis using simulated d-value data:
ma_obj <- ma_d_ic(d = d, n1 = n1, n2 = n2, ryy = ryyi,
                 data = filter(data_d_meas_multi, construct == "Y"))
ma_obj <- ma_d_ad(ma_obj)

## Pass the meta-analysis object to the sensitivity() function:
ma_obj <- sensitivity(ma_obj = ma_obj, boot_iter = 10,
                     boot_ci_type = "norm", sort_method = "inv_var")

## Examine the tables and plots produced for the IC meta-analysis:
ma_obj$bootstrap[[1]]$barebones
ma_obj$bootstrap[[1]]$individual_correction$latentGroup_latentY
ma_obj$leave1out[[1]]$individual_correction$latentGroup_latentY
ma_obj$cumulative[[1]]$individual_correction$latentGroup_latentY

## Examine the tables and plots produced for the AD meta-analysis:
ma_obj$bootstrap[[1]]$artifact_distribution$latentGroup_latentY
ma_obj$leave1out[[1]]$artifact_distribution$latentGroup_latentY
ma_obj$cumulative[[1]]$artifact_distribution$latentGroup_latentY

## End(Not run)

```

simulate_alpha

Generate a vector of simulated sample alpha coefficients

Description

This function generates inter-item covariance matrices from a population matrix and computes a coefficient alpha reliability estimate for each matrix.

Usage

```
simulate_alpha(item_mat = NULL, alpha = NULL, k_items = NULL,
              n_cases, k_samples, standarized = FALSE)
```

Arguments

item_mat	Item correlation/covariance matrix. If item_mat is not supplied, the user must supply both alpha and k_items. If item_mat is NULL, the program will assume that all item intercorrelations are equal.
alpha	Population alpha value. Must be supplied if item_mat is NULL.

k_items	Number of items on the test to be simulated. Must be supplied if item_mat is NULL.
n_cases	Number of cases to simulate in sampling distribution of alpha.
k_samples	Number of samples to simulate.
standarized	Should alpha be computed from correlation matrices (TRUE) or unstandardized covariance matrices (FALSE)?

Value

A vector of simulated sample alpha coefficients

Examples

```
## Define a hypothetical matrix:
item_mat <- reshape_vec2mat(cov = .3, order = 12)

## Simulations of unstandardized alphas
set.seed(100)
simulate_alpha(item_mat = item_mat, n_cases = 50, k_samples = 10, standarized = FALSE)
set.seed(100)
simulate_alpha(alpha = mean(item_mat[lower.tri(item_mat)]) / mean(item_mat),
k_items = ncol(item_mat), n_cases = 50, k_samples = 10, standarized = FALSE)

## Simulations of standardized alphas
set.seed(100)
simulate_alpha(item_mat = item_mat, n_cases = 50, k_samples = 10, standarized = TRUE)
set.seed(100)
simulate_alpha(alpha = mean(item_mat[lower.tri(item_mat)]) / mean(item_mat),
k_items = ncol(item_mat), n_cases = 50, k_samples = 10, standarized = TRUE)
```

simulate_d_database *Simulate d value databases of primary studies*

Description

The `simulate_d_database` function generates databases of psychometric *d* value data from sample-size parameters, correlation parameters, mean parameters, standard deviation parameters, reliability parameters, and selection-ratio parameters. The output database can be provided in a long format. If composite variables are to be formed, parameters can also be defined for the weights used to form the composites as well as the selection ratios applied to the composites. This function will return a database of statistics as well as a database of parameters - the parameter database contains the actual study parameters for each simulated sample (without sampling error) to allow comparisons between meta-analytic results computed from the statistics and the actual means and variances of parameters. The `merge_simdat_d` function can be used to merge multiple simulated databases and the `sparsify_simdat_d` function can be used to randomly delete artifact information (a procedure commonly done in simulations of artifact-distribution methods).

Usage

```
simulate_d_database(k, n_params, rho_params, mu_params = NULL,
  sigma_params = 1, rel_params = 1, sr_params = 1,
  k_items_params = 1, wt_params = NULL, allow_neg_wt = FALSE,
  sr_composite_params = NULL, group_names = NULL, var_names = NULL,
  composite_names = NULL, diffs_as_obs = FALSE,
  show_applicant = FALSE, keep_vars = NULL, decimals = 2,
  max_iter = 100, ...)
```

Arguments

<code>k</code>	Number of studies to simulate.
<code>n_params</code>	List of parameter distributions (or data-generation function; see details) for subgroup sample sizes.
<code>rho_params</code>	List containing a list of parameter distributions (or data-generation functions; see details) for correlations for each simulated group. If simulating data from a single fixed population matrix in each group, supply a list of those matrices for this argument (if the diagonals contains non-unity values and 'sigma_params' argument is not specified, those values will be used as variances).
<code>mu_params</code>	List containing a list of parameter distributions (or data-generation functions; see details) for means for each simulated group. If NULL, all means will be set to zero.
<code>sigma_params</code>	List containing a list of parameter distributions (or data-generation functions; see details) for standard deviations for each simulated group. If NULL, all standard deviations will be set to unity.
<code>rel_params</code>	List containing a list of parameter distributions (or data-generation functions; see details) for reliabilities for each simulated group. If NULL, all reliabilities will be set to unity.
<code>sr_params</code>	List of parameter distributions (or data-generation functions; see details) for selection ratios. If NULL, all selection ratios will be set to unity.
<code>k_items_params</code>	List of parameter distributions (or data-generation functions; see details) for the number of test items comprising each of the variables to be simulated (all are single-item variables by default).
<code>wt_params</code>	List of parameter distributions (or data-generation functions; see details) to create weights for use in forming composites. If multiple composites are formed, the list should be a list of lists, with the general format: <code>list(comp1_params = list(...params...), c</code>
<code>allow_neg_wt</code>	Logical scalar that determines whether negative weights should be allowed (TRUE) or not (FALSE).
<code>sr_composite_params</code>	Parameter distributions (or data-generation functions; see details) for composite selection ratios.
<code>group_names</code>	Optional vector of group names.
<code>var_names</code>	Optional vector of variable names for all non-composite variables.
<code>composite_names</code>	Optional vector of names for composite variables.

<code>diffs_as_obs</code>	Logical scalar that determines whether standard deviation parameters represent standard deviations of observed scores (TRUE) or of true scores (FALSE; default).
<code>show_applicant</code>	Should applicant data be shown for sample statistics (TRUE) or suppressed (FALSE)?
<code>keep_vars</code>	Optional vector of variable names to be extracted from the simulation and returned in the output object. All variables are returned by default. Use this argument when only some variables are of interest and others are generated solely to serve as selection variables.
<code>decimals</code>	Number of decimals to which statistical results (not parameters) should be rounded. Rounding to 2 decimal places best captures the precision of data available from published primary research.
<code>max_iter</code>	Maximum number of iterations to allow in the parameter selection process before terminating with convergence failure. Must be finite.
<code>...</code>	Additional arguments.

Details

Values supplied as any argument with the suffix "params" can take any of three forms (see Examples for a demonstration of usage):

- A vector of values from which study parameters should be sampled.
- A vector containing a mean with a variance or standard deviation. These values must be named "mean," "var," and "sd", respectively, for the program to recognize which value is which.
- A matrix containing a row of values (this row must be named "values") from which study parameters should be sampled and a row of weights (this row must be labeled 'weights') associated with the values to be sampled.
- A matrix containing a column of values (this column must be named "values") from which study parameters should be sampled and a column of weights (this column must be labeled 'weights') associated with the values to be sampled.
- A function that is configured to generate data using only one argument that defines the number of cases to generate, e.g., `fun(n = 10)`.

Value

A database of simulated primary studies' statistics and analytically determined parameter values.

Examples

```
## Define sample sizes, means, and other parameters for each of two groups:
n_params <- list(c(mean = 200, sd = 20),
                c(mean = 100, sd = 20))
rho_params <- list(list(c(.3, .4, .5)),
                  list(c(.3, .4, .5)))
mu_params <- list(list(c(mean = .5, sd = .5), c(-.5, 0, .5)),
                  list(c(mean = 0, sd = .5), c(-.2, 0, .2)))
sigma_params <- list(list(1, 1),
                    list(1, 1))
rel_params <- list(list(.8, .8),
                  list(.8, .8))
```

```

sr_params <- list(1, .5)

simulate_d_database(k = 5, n_params = n_params, rho_params = rho_params,
  mu_params = mu_params, sigma_params = sigma_params,
  rel_params = rel_params, sr_params = sr_params,
  k_items = c(4, 4),
  group_names = NULL, var_names = c("y1", "y2"),
  show_applicant = TRUE, keep_vars = c("y1", "y2"), decimals = 2)

```

simulate_d_sample	<i>Simulate a sample of psychometric d value data with measurement error, direct range restriction, and/or indirect range restriction</i>
-------------------	---

Description

This function generates a simulated psychometric sample consisting of any number of groups and computes the d values that result after introducing measurement error and/or range restriction.

Usage

```

simulate_d_sample(n_vec, rho_mat_list, mu_mat, sigma_mat = 1,
  rel_mat = 1, sr_vec = 1, k_items_vec = 1, wt_mat = NULL,
  sr_composites = NULL, group_names = NULL, var_names = NULL,
  composite_names = NULL, diffs_as_obs = FALSE)

```

Arguments

n_vec	Vector of sample sizes (or a vector of proportions, if parameters are to be estimated).
rho_mat_list	List of true-score correlation matrices.
mu_mat	Matrix of mean parameters, with groups on the rows and variables on the columns.
sigma_mat	Matrix of standard-deviation parameters, with groups on the rows and variables on the columns.
rel_mat	Matrix of reliability parameters, with groups on the rows and variables on the columns.
sr_vec	Vector of selection ratios.
k_items_vec	Number of test items comprising each of the variables to be simulated (all are single-item variables by default).
wt_mat	Optional matrix of weights to use in forming a composite of the variables in rho_mat. Matrix should have as many rows (or vector elements) as there are variables in rho_mat.
sr_composites	Optional vector selection ratios for composite variables. If not NULL, sr_composites must have as many elements as there are columns in wt_mat.
group_names	Optional vector of group names.
var_names	Optional vector of variable names.

composite_names Optional vector of names for composite variables.

diffs_as_obs Logical scalar that determines whether standard deviation parameters represent standard deviations of observed scores (TRUE) or of true scores (FALSE; default).

Value

A sample of simulated mean differences.

Examples

```
## Simulate statistics by providing integers as "n_vec":
simulate_d_sample(n_vec = c(200, 100), rho_mat_list = list(reshape_vec2mat(.5),
                                                         reshape_vec2mat(.4)),
                 mu_mat = rbind(c(1, .5), c(0, 0)), sigma_mat = rbind(c(1, 1), c(1, 1)),
                 rel_mat = rbind(c(.8, .7), c(.7, .7)), sr_vec = c(1, .5),
                 group_names = c("A", "B"))

## Simulate parameters by providing proportions as "n_vec":
simulate_d_sample(n_vec = c(2/3, 1/3), rho_mat_list = list(reshape_vec2mat(.5),
                                                         reshape_vec2mat(.4)),
                 mu_mat = rbind(c(1, .5), c(0, 0)), sigma_mat = rbind(c(1, 1), c(1, 1)),
                 rel_mat = rbind(c(.8, .7), c(.7, .7)), sr_vec = c(1, .5),
                 group_names = c("A", "B"))
```

simulate_matrix	<i>Generate a list of simulated sample matrices sampled from the Wishart distribution</i>
-----------------	---

Description

This function generates simulated sample matrices based on a population matrix and a sample size. It uses the Wishart distribution (i.e., the multivariate χ^2 distribution) to obtain data, rescales the data into the input metric, and can be standardized into a correlation matrix by setting `as_cor` to TRUE. The function can produce a list of matrices for any number of samples.

Usage

```
simulate_matrix(sigma, n, k = 1, as_cor = FALSE)
```

Arguments

sigma Population covariance matrix. May be standardized or unstandardized.

n Sample size for simulated sample matrices.

k Number of sample matrices to generate.

as_cor Should the simulated matrices be standardized (TRUE) or unstandardized (FALSE)?

Value

A list of simulated sample matrices.

Examples

```
## Define a hypothetical matrix:
sigma <- reshape_vec2mat(cov = .4, order = 5)

## Simualte a list of unstandardized covariance matrices:
simulate_matrix(sigma = sigma, n = 50, k = 10, as_cor = FALSE)

## Simualte a list of correlation matrices:
simulate_matrix(sigma = sigma, n = 50, k = 10, as_cor = TRUE)
```

simulate_psych	<i>Simulate Monte Carlo psychometric data (observed, true, and error scores)</i>
----------------	--

Description

Simulate Monte Carlo psychometric data (observed, true, and error scores)

Usage

```
simulate_psych(n, rho_mat, mu_vec = rep(0, ncol(rho_mat)),
  sigma_vec = rep(1, ncol(rho_mat)), rel_vec = rep(1, ncol(rho_mat)),
  sr_vec = rep(1, ncol(rho_mat)), k_items_vec = rep(1, ncol(rho_mat)),
  wt_mat = NULL, sr_composites = NULL, var_names = NULL,
  composite_names = NULL)
```

Arguments

n	Number of cases to simulate before performing selection.
rho_mat	Matrix of true-score correlations.
mu_vec	Vector of means.
sigma_vec	Vector of observed-score standard deviations.
rel_vec	Vector of reliabilities corresponding to the variables in rho_mat.
sr_vec	Vector of selection ratios corresponding to the variables in rho_mat. (set selection ratios to 1 for variables that should not be used in selection).
k_items_vec	Number of test items comprising each of the variables to be simulated (all are single-item variables by default).
wt_mat	Optional matrix of weights to use in forming a composite of the variables in rho_mat. Matrix should have as many rows (or vector elements) as there are variables in rho_mat.

sr_composites Optional vector selection ratios for composite variables. If not NULL, **sr_composites** must have as many elements as there are columns in **wt_mat**.
var_names Vector of variable names corresponding to the variables in **rho_mat**.
composite_names Optional vector of names for composite variables.
... Further arguments.

Value

A list of observed-score, true-score, and error-score data frames. If selection is requested, the data frames will include logical variables indicating whether each case would be selected on the basis of observed scores, true scores, or error scores.

Examples

```

## Generate data for a simple sample with two variables without selection:
simulate_psych(n = 1000, rho_mat = matrix(c(1, .5, .5, 1), 2, 2), sigma_vec = c(1, 1),
  rel_vec = c(.8, .8), var_names = c("Y", "X"))

## Generate data for a simple sample with two variables with selection:
simulate_psych(n = 1000, rho_mat = matrix(c(1, .5, .5, 1), 2, 2), sigma_vec = c(1, 1),
  rel_vec = c(.8, .8), sr_vec = c(1, .5), var_names = c("Y", "X"))

## Generate data for samples with five variables, of which subsets are used to form composites:
rho_mat <- matrix(.5, 5, 5)
diag(rho_mat) <- 1
simulate_psych(n = 1000, rho_mat = rho_mat,
  rel_vec = rep(.8, 5), sr_vec = c(1, 1, 1, 1, .5),
  wt_mat = cbind(c(0, 0, 0, .3, 1), c(1, .3, 0, 0, 0)), sr_composites = c(.7, .5))

## Generate data for similar scenario as above, but with scales consisting of 1-5 items:
rho_mat <- matrix(.5, 5, 5)
diag(rho_mat) <- 1
simulate_psych(n = 1000, rho_mat = rho_mat,
  rel_vec = rep(.8, 5), sr_vec = c(1, 1, 1, 1, .5),
  k_items_vec = 1:5,
  wt_mat = cbind(c(0, 0, 0, .3, 1), c(1, .3, 0, 0, 0)), sr_composites = c(.7, .5))

```

simulate_r_database *Simulate correlation databases of primary studies*

Description

The `simulate_r_database` function generates databases of psychometric correlation data from sample-size parameters, correlation parameters, reliability parameters, and selection-ratio parameters. The output database can be provided in either a long format or a wide format. If composite variables are to be formed, parameters can also be defined for the weights used to form the composites as well as the selection ratios applied to the composites. This function will return a database

of statistics as well as a database of parameters - the parameter database contains the actual study parameters for each simulated sample (without sampling error) to allow comparisons between meta-analytic results computed from the statistics and the actual means and variances of parameters. The `merge_simdat_r` function can be used to merge multiple simulated databases and the `sparsify_simdat_r` function can be used to randomly delete artifact information (a procedure commonly done in simulations of artifact-distribution methods).

Usage

```
simulate_r_database(k, n_params, rho_params, mu_params = 0,
  sigma_params = 1, rel_params = 1, sr_params = 1,
  k_items_params = 1, wt_params = NULL, allow_neg_wt = FALSE,
  sr_composite_params = NULL, var_names = NULL,
  composite_names = NULL, n_as_ni = FALSE, show_applicant = FALSE,
  keep_vars = NULL, decimals = 2, format = "long", max_iter = 100,
  ...)
```

Arguments

<code>k</code>	Number of studies to simulate.
<code>n_params</code>	Parameter distribution (or data-generation function; see details) for sample size.
<code>rho_params</code>	List of parameter distributions (or data-generation functions; see details) for correlations. If simulating data from a single fixed population matrix, that matrix can be supplied for this argument (if the diagonal contains non-unity values and 'sigma_params' is not specified, those values will be used as variances).
<code>mu_params</code>	List of parameter distributions (or data-generation functions; see details) for means.
<code>sigma_params</code>	List of parameter distributions (or data-generation functions; see details) for standard deviations.
<code>rel_params</code>	List of parameter distributions (or data-generation functions; see details) for reliabilities.
<code>sr_params</code>	List of parameter distributions (or data-generation functions; see details) for selection ratios.
<code>k_items_params</code>	List of parameter distributions (or data-generation functions; see details) for the number of test items comprising each of the variables to be simulated (all are single-item variables by default).
<code>wt_params</code>	List of parameter distributions (or data-generation functions; see details) to create weights for use in forming composites. If multiple composites are formed, the list should be a list of lists, with the general format: <code>list(comp1_params = list(...params...), c</code>
<code>allow_neg_wt</code>	Logical scalar that determines whether negative weights should be allowed (TRUE) or not (FALSE).
<code>sr_composite_params</code>	Parameter distributions (or data-generation functions; see details) for composite selection ratios.
<code>var_names</code>	Optional vector of variable names for all non-composite variables.

composite_names	Optional vector of names for composite variables.
n_as_ni	Logical argument determining whether n specifies the incumbent sample size (TRUE) or the applicant sample size (FALSE; default). This can only be TRUE when only one variable is involved in selection.
show_applicant	Should applicant data be shown for sample statistics (TRUE) or suppressed (FALSE)?
keep_vars	Optional vector of variable names to be extracted from the simulation and returned in the output object. All variables are returned by default. Use this argument when only some variables are of interest and others are generated solely to serve as selection variables.
decimals	Number of decimals to which statistical results (not parameters) should be rounded. Rounding to 2 decimal places best captures the precision of data available from published primary research.
format	Database format: "long" or "wide."
max_iter	Maximum number of iterations to allow in the parameter selection process before terminating with convergence failure. Must be finite.
...	Additional arguments.

Details

Values supplied as any argument with the suffix "params" can take any of three forms (see Examples for a demonstration of usage):

- A vector of values from which study parameters should be sampled.
- A vector containing a mean with a variance or standard deviation. These values must be named "mean," "var," and "sd", respectively, for the program to recognize which value is which.
- A matrix containing a row of values (this row must be named "values") from which study parameters should be sampled and a row of weights (this row must be labeled 'weights') associated with the values to be sampled.
- A matrix containing a column of values (this column must be named "values") from which study parameters should be sampled and a column of weights (this column must be labeled 'weights') associated with the values to be sampled.
- A function that is configured to generate data using only one argument that defines the number of cases to generate, e.g., fun(n = 10).

Value

A database of simulated primary studies' statistics and analytically determined parameter values.

Examples

```
## Note the varying methods for defining parameters:
n_params = function(n) rgamma(n, shape = 100)
rho_params <- list(c(.1, .3, .5),
                  c(mean = .3, sd = .05),
                  rbind(value = c(.1, .3, .5), weight = c(1, 2, 1)))
rel_params = list(c(.7, .8, .9),
```

```

        c(mean = .8, sd = .05),
        rbind(value = c(.7, .8, .9), weight = c(1, 2, 1)))
sr_params = c(list(1, 1, c(.5, .7)))
sr_composite_params = list(1, c(.5, .6, .7))
wt_params = list(list(c(1, 2, 3),
        c(mean = 2, sd = .25),
        rbind(value = c(1, 2, 3), weight = c(1, 2, 1))),
list(c(1, 2, 3),
        c(mean = 2, sd = .25),
        cbind(value = c(1, 2, 3), weight = c(1, 2, 1))))

## Simulate with long format
simulate_r_database(k = 10, n_params = n_params, rho_params = rho_params,
        rel_params = rel_params, sr_params = sr_params,
        sr_composite_params = sr_composite_params, wt_params = wt_params,
        var_names = c("X", "Y", "Z"), format = "long")

## Simulate with wide format
simulate_r_database(k = 10, n_params = n_params, rho_params = rho_params,
        rel_params = rel_params, sr_params = sr_params,
        sr_composite_params = sr_composite_params, wt_params = wt_params,
        var_names = c("X", "Y", "Z"), format = "wide")

```

simulate_r_sample	<i>Simulation of data with measurement error and range-restriction artifacts</i>
-------------------	--

Description

This function simulates a psychometric sample and produces correlation matrices, artifact information, and other descriptive statistics that have been affected by measurement error and/or range restriction. It allows the formation of composite variables within the simulation and allows selection to be performed on any or all variables, including composites. By setting the sample size to $n = \text{Inf}$, users can explore the effects of measurement error and/or range restriction on parameters without the influence of sampling error. To generate multiple samples and compile a database of simulated statistics, see the [simulate_r_database](#) function.

Usage

```

simulate_r_sample(n, rho_mat, rel_vec = rep(1, ncol(rho_mat)),
        mu_vec = rep(0, ncol(rho_mat)), sigma_vec = rep(1, ncol(rho_mat)),
        sr_vec = rep(1, ncol(rho_mat)), k_items_vec = rep(1, ncol(rho_mat)),
        wt_mat = NULL, sr_composites = NULL, var_names = NULL,
        composite_names = NULL, n_as_ni = FALSE, ...)

```

Arguments

n Number of cases to simulate before performing selection. If Inf , function will simulate parameter values.

rho_mat	Matrix of true-score correlations.
rel_vec	Vector of reliabilities corresponding to the variables in rho_mat.
mu_vec	Vector of means.
sigma_vec	Vector of observed-score standard deviations.
sr_vec	Vector of selection ratios corresponding to the variables in rho_mat (set selection ratios to 1 for variables that should not be used in selection).
k_items_vec	Number of test items comprising each of the variables to be simulated (all are single-item variables by default).
wt_mat	Optional matrix of weights to use in forming a composite of the variables in rho_mat. Matrix should have as many rows (or vector elements) as there are variables in rho_mat.
sr_composites	Optional vector selection ratios for composite variables. If not NULL, sr_composites must have as many elements as there are columns in wt_mat.
var_names	Vector of variable names corresponding to the variables in rho_mat.
composite_names	Optional vector of names for composite variables.
n_as_ni	Logical argument determining whether n specifies the incumbent sample size (TRUE) or the applicant sample size (FALSE; default). This can only be TRUE when only one variable is involved in selection.
...	Further arguments.

Value

A list of study information, including correlations, reliabilities, standard deviations, means, and u ratios for true scores and for observed scores.

Examples

```
## Generate data for a simple sample with two variables:
simulate_r_sample(n = 1000, rho_mat = matrix(c(1, .5, .5, 1), 2, 2),
               rel_vec = c(.8, .8), sr_vec = c(1, .5), var_names = c("Y", "X"))

## Generate data for samples with five variables, of which subsets are used to form composites:
rho_mat <- matrix(.5, 5, 5)
diag(rho_mat) <- 1

## Simulate parameters by supply n = Inf
simulate_r_sample(n = Inf, rho_mat = rho_mat,
               rel_vec = rep(.8, 5), sr_vec = c(1, 1, 1, 1, .5),
               wt_mat = cbind(c(0, 0, 0, .3, 1), c(1, .3, 0, 0, 0)), sr_composites = c(.7, .5))

## Finite sample sizes allow the generation of sample data
simulate_r_sample(n = 1000, rho_mat = rho_mat,
               rel_vec = rep(.8, 5), sr_vec = c(1, 1, 1, 1, .5),
               wt_mat = cbind(c(0, 0, 0, .3, 1), c(1, .3, 0, 0, 0)), sr_composites = c(.7, .5))
```

sparsify_simdat_d	<i>Create sparse artifact information in a "simdat_d_database" class object</i>
-------------------	---

Description

This function can be used to randomly delete artifact from databases produced by the [simulate_d_database](#) function. Deletion of artifacts can be performed in either a study-wise fashion for complete missingness within randomly selected studies or element-wise missingness for completely random deletion of artifacts in the database. Deletion can be applied to reliability estimates and/or u ratios.

Usage

```
sparsify_simdat_d(data_obj, prop_missing, sparify_arts = c("rel", "u"),
  study_wise = TRUE)
```

Arguments

data_obj	Object created by the "simdat_d_database" function.
prop_missing	Proportion of studies in from which artifact information should be deleted.
sparify_arts	Vector of codes for the artifacts to be sparsified: "rel" for reliabilities, "u" for u ratios, or c("rel", "u") for both.
study_wise	Logical scalar argument determining whether artifact deletion should occur for all variables in a study (TRUE) or randomly across variables within studies (FALSE).

Value

A sparsified database

sparsify_simdat_r	<i>Create sparse artifact information in a "simdat_r_database" class object</i>
-------------------	---

Description

This function can be used to randomly delete artifact from databases produced by the [simulate_r_database](#) function. Deletion of artifacts can be performed in either a study-wise fashion for complete missingness within randomly selected studies or element-wise missingness for completely random deletion of artifacts in the database. Deletion can be applied to reliability estimates and/or u ratios.

Usage

```
sparsify_simdat_r(data_obj, prop_missing, sparify_arts = c("rel", "u"),
  study_wise = TRUE)
```


Arguments

data_obj	Object created by the "simdat_r_database" function.
prop_missing	Proportion of studies in from which artifact information should be deleted.
sparify_arts	Vector of codes for the artifacts to be sparsified: "rel" for reliabilities, "u" for u ratios, or c("rel", "u") for both.
study_wise	Logical scalar argument determining whether artifact deletion should occur for all variables in a study (TRUE) or randomly across variables within studies (FALSE).

Value

A sparsified database

summary	<i>Summary methods for psychmeta</i>
---------	---

Description

Summary methods for **psychmeta** output objects with classes exported from **psychmeta**.

Arguments

object	Object to be printed (object is used to select a method).
...	Additional arguments.

Value

Summary object.

truncate_dist	<i>Truncation function for normal distributions (truncates both mean and variance)</i>
---------------	--

Description

This function computes the mean and variance of a normal distributions that has been truncated at one or both ends.

Usage

```
truncate_dist(a = -Inf, b = Inf, mean = 0, sd = 1)
```

Arguments

a	Quantile (i.e., cut score) below which scores should be censored from the distribution.
b	Quantile (i.e., cut score) above which scores should be censored from the distribution.
mean	Scalar mean or vector of means.
sd	Scalar standard deviation or vector of standard deviations.

Value

A matrix of truncated means (column 1) and truncated variances (column 2).

Examples

```
truncate_dist(a = -1, b = 3, mean = 0, sd = 1)
truncate_dist(a = 1, b = Inf, mean = 0, sd = 1)
truncate_dist(a = c(-1, 1), b = c(3, Inf), mean = 0, sd = 1)
```

truncate_mean	<i>Truncation function for means</i>
---------------	--------------------------------------

Description

This function computes the mean of a normal distributions that has been truncated at one or both ends.

Usage

```
truncate_mean(a = -Inf, b = Inf, mean = 0, sd = 1)
```

Arguments

a	Quantile (i.e., cut score) below which scores should be censored from the distribution.
b	Quantile (i.e., cut score) above which scores should be censored from the distribution.
mean	Scalar mean or vector of means.
sd	Scalar standard deviation or vector of standard deviations.

Value

A vector of truncated means.

Examples

```
truncate_mean(a = -1, b = 3, mean = 0, sd = 1)
truncate_mean(a = 1, b = Inf, mean = 0, sd = 1)
truncate_mean(a = c(-1, 1), b = c(3, Inf), mean = 0, sd = 1)
```

truncate_var	<i>Truncation function for variances</i>
--------------	--

Description

This function computes the variance of a normal distributions that has been truncated at one or both ends.

Usage

```
truncate_var(a = -Inf, b = Inf, mean = 0, sd = 1)
```

Arguments

a	Quantile (i.e., cut score) below which scores should be censored from the distribution.
b	Quantile (i.e., cut score) above which scores should be censored from the distribution.
mean	Scalar mean or vector of means.
sd	Scalar standard deviation or vector of standard deviations.

Value

A vector of truncated variances

Examples

```
truncate_var(a = -1, b = 3, mean = 0, sd = 1)
truncate_var(a = 1, b = Inf, mean = 0, sd = 1)
truncate_var(a = c(-1, 1), b = c(3, Inf), mean = 0, sd = 1)
```

unmix_matrix	<i>Estimate average within-group covariance matrices from a mixture covariance matrix</i>
--------------	---

Description

Estimate average within-group covariance matrices from a mixture covariance matrix

Usage

```
unmix_matrix(sigma_mat, mu_mat, p_vec, N = Inf, group_names = NULL,
  var_names = NULL)
```

Arguments

sigma_mat	Mixture covariance matrix.
mu_mat	Matrix of mean parameters, with groups on the rows and variables on the columns.
p_vec	Vector of proportion of cases in each group.
N	Optional total sample size across all groups (used to compute unbiased covariance estimates).
group_names	Optional vector of group names.
var_names	Optional vector of variable names.

Value

List of within-group covariances and means.

Examples

```

out <- unmix_matrix(sigma_mat = reshape_vec2mat(.5, order = 2),
                   mu_mat = rbind(c(0, 0), c(.5, 1)),
                   p_vec = c(.3, .7), N = 100)

## Result of unmix_matrix:
out

## Simulated data reproduce the total parameter matrix:
dat <- NULL
for(i in 1:2){
  dat <- rbind(dat, cbind(group = i,
                          data.frame(MASS::mvrnorm(n = round(out$p_group[i] * out$N),
                                                    mu = out$means_raw[i,],
                                                    Sigma = out$cov_group_unbiased[[i]],
                                                    empirical = TRUE))))
}
cov(dat[, -1])

```

unmix_r_2group	<i>Estimate the average within-group correlation from a mixture correlation for two groups</i>
----------------	--

Description

Estimate the average within-group correlation from a mixture correlation for two groups

Usage

```
unmix_r_2group(rxy, dx, dy, p = 0.5)
```

Arguments

rx _y	Overall mixture correlation.
dx	Standardized mean difference between groups on X.
dy	Standardized mean difference between groups on Y.
p	Proportion of cases in one of the two groups.

Details

The mixture correlation for two groups is estimated as:

$$r_{xyMix} = \frac{\rho_{xyWG} + \sqrt{d_x^2 d_y^2 p^2 (1-p)^2}}{\sqrt{(d_x^2 p(1-p) + 1)(d_y^2 p(1-p) + 1)}}$$

where ρ_{xyWG} is the average within-group correlation, ρ_{xyMix} is the overall mixture correlation, d_x is the standardized mean difference between groups on X, d_y is the standardized mean difference between groups on Y, and p is the proportion of cases in one of the two groups.

Value

A vector of average within-group correlations

References

Oswald, F. L., Converse, P. D., & Putka, D. J. (2014). Generating race, gender and other subgroup data in personnel selection simulations: A pervasive issue with a simple solution. *International Journal of Selection and Assessment*, 22(3), 310-320.

Examples

```
unmix_r_2group(rxy = .5, dx = 1, dy = 1, p = .5)
```

var_error_A	<i>Estimate the error variance of the probability-based effect size (A, AUC, the common language effect size [CLES])</i>
-------------	--

Description

Estimate the error variance of the probability-based effect size (A, AUC, the common language effect size [CLES])

Usage

```
var_error_A(A, n1, n2 = NA)
```

```
var_error_auc(A, n1, n2 = NA)
```

```
var_error_cles(A, n1, n2 = NA)
```

Arguments

A	Vector of probability-based effect sizes (common language effect sizes)
n1	Vector of sample sizes from group 1 (or the total sample size with the assumption that groups are of equal size, if no group 2 sample size is supplied).
n2	Vector of sample sizes from group 2.

Details

The sampling variance of a A (also called AUC [area under curve] or $CLES$ [common-language effect size]) value is:

$$\left[\left(\frac{1}{n_1} \right) + \left(\frac{1}{n_2} \right) + \left(\frac{1}{n_1 n_2} \right) \right]$$

12

When groups 1 and 2 are of equal size, this reduces to

$$\left[\left(\frac{1}{n} \right) + \left(\frac{1}{n^2} \right) \right]$$

3

Value

A vector of sampling-error variances.

References

Ruscio, J. (2008). A probability-based measure of effect size: Robustness to base rates and other factors. *Psychological Methods*, 13(1), 19–30. <https://doi.org/10.1037/1082-989X.13.1.19>

Examples

```
var_error_A(A = 1, n1 = 30, n2 = 30)
var_error_auc(A = 1, n1 = 60, n2 = NA)
var_error_cles(A = 1, n1 = 30, n2 = 30)
```

var_error_alpha

Analytic estimate of the sampling variance of alpha

Description

Analytic estimate of the sampling variance of alpha

Usage

```
var_error_alpha(item_mat = NULL, alpha = NULL, k_items = NULL,
  n_cases)
```

Arguments

item_mat	Item correlation/covariance matrix. If item_mat is not supplied, the user must supply both alpha and k_items. If item_mat is NULL, the program will assume that all item intercorrelations are equal.
alpha	Vector of population alpha values. Must be supplied if item_mat is NULL.
k_items	Vector of numbers of items to be simulated. Must be supplied if item_mat is NULL.
n_cases	Vector of sample sizes to simulate in sampling distribution of alpha.

Value

Vector of sampling variances of the supplied alpha(s).

References

Duhachek, A., & Iacobucci, D. (2004). Alpha's standard error (ASE): An accurate and precise confidence interval estimate. *Journal of Applied Psychology*, 89(5), 792–808. <https://doi.org/10.1037/0021-9010.89.5.792>

Examples

```

item_mat <- matrix(.3, 5, 5)
diag(item_mat) <- 1
alpha <- mean(item_mat[lower.tri(item_mat)]) / mean(item_mat)
k_items <- nrow(item_mat)

var_error_alpha(item_mat = item_mat, n_cases = 50)
var_error_alpha(alpha = alpha, k_items = k_items, n_cases = 50)
var_error_alpha(alpha = c(alpha, alpha), k_items = c(k_items, k_items), n_cases = 50)

```

var_error_d

Estimate the error variance Cohen's d values

Description

Allows for error variance to be estimated using total sample size of both groups being compared (in this case, supply sample sizes using only the n1 argument) or using separate sample sizes for group 1 and group 2 (i.e., the groups being compared; in this case, supply sample sizes using both the n1 and n2 arguments).

Usage

```
var_error_d(d, n1, n2 = NA, correct_bias = TRUE)
```

Arguments

d	Vector of Cohen's d values.
n1	Vector of sample sizes from group 1 (or the total sample size with the assumption that groups are of equal size, if no group 2 sample size is supplied).
n2	Vector of sample sizes from group 2.
correct_bias	Logical argument that determines whether to correct error-variance estimates for small-sample bias in d values (TRUE) or not (FALSE).

Details

The sampling variance of a d value is:

$$\left(\frac{n-1}{n-3}\right) \left(\frac{n_1+n_2}{n_1n_2} + \frac{d^2}{2(n_1+n_2)}\right)$$

When groups 1 and 2 are of equal size, this reduces to

$$var_e = \left(\frac{n-1}{n-3}\right) \left(\frac{4}{n}\right) \left(1 + \frac{d^2}{8}\right)$$

The estimated error variance can be divided by the following term to correct for small-sample bias:

$$bias\ factor = \left(1 + \frac{.75}{n-3}\right)^2$$

Value

A vector of sampling-error variances.

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: Sage. <https://doi.org/10/b6mg>. pp. 292–295.

Examples

```
var_error_d(d = 1, n1 = 30, n2 = 30, correct_bias = TRUE)
var_error_d(d = 1, n1 = 60, n2 = NA, correct_bias = TRUE)
```

var_error_delta	<i>Estimate the error variance of Glass' delta values</i>
-----------------	---

Description

Estimate the error variance of Glass' delta values

Usage

```
var_error_delta(delta, nc, ne = NA, use_pooled_sd = FALSE,
  correct_bias = TRUE)
```

Arguments

delta	Vector of Glass' delta values.
nc	Vector of control-group sample sizes (or the total sample size with the assumption that groups are of equal size, if no experimental-group sample size is supplied).
ne	Vector of experimental-group sample sizes.
use_pooled_sd	Logical vector determining whether the pooled standard deviation was used (TRUE) or not (FALSE). FALSE by default.
correct_bias	Logical argument that determines whether to correct error-variance estimates for small-sample bias in d values (TRUE) or not (FALSE).

Value

A vector of sampling-error variances.

Examples

```
var_error_delta(delta = .3, nc = 30, ne = 30)
var_error_delta(delta = .3, nc = 60, ne = NA)
```

var_error_g	<i>Estimate the error variance Hedge's g values</i>
-------------	---

Description

Allows for error variance to be estimated using total sample size of both groups being compared (in this case, supply sample sizes using only the n1 argument) or using separate sample sizes for group 1 and group 2 (i.e., the groups being compared; in this case, supply sample sizes using both the n1 and n2 arguments).

Usage

```
var_error_g(g, n1, n2 = NA)
```

Arguments

g Vector of Hedge's g values.

n1 Vector of sample sizes from group 1 (or the total sample size with the assumption that groups are of equal size, if no group 2 sample size is supplied).

n2 Vector of sample sizes from group 2.

Value

A vector of sampling-error variances.

References

Borenstein, M., Hedges, L. V., Higgins, J. P. T., & Rothstein, H. R. (2009). *Introduction to meta-analysis*. Chichester, UK: Wiley. Chapter 4.

Examples

```
var_error_g(g = 1, n1 = 30, n2 = 30)
var_error_g(g = 1, n1 = 60, n2 = NA)
```

var_error_q

Estimate the error variance of square roots of reliability estimates

Description

Estimate the error variance of square roots of reliability estimates

Usage

```
var_error_q(q, n, rel_type = "alpha", k_items = NULL)
```

Arguments

q Vector of square roots of reliability estimates.

n Vector of sample sizes.

rel_type Character vector indicating the type(s) of reliabilities being analyzed. See documentation for `ma_r` for a full list of acceptable reliability types. NOTE: Currently, only alpha has its own dedicated error-variance estimate; the error variance of other reliability types is estimated using the generic definition of reliability as the squared correlation between observed scores and true scores.

k_items Optional numeric vector indicating the number of items in each scale for which reliabilities are being analyzed.

Details

The sampling variance of the square root of a reliability coefficient is:

$$var_e = \frac{(1 - q_X^2)^2}{n - 1}$$

For the equation to estimate the variance of coefficient alpha, see Duhachek and Iacobucci (2004).

Value

A vector of sampling-error variances.

References

Dahlke, J. A., & Wiernik, B. M. (2017). *One of these artifacts is not like the others: New methods to account for the unique implications of indirect range-restriction corrections in organizational research*. Unpublished manuscript.

Duhachek, A., & Iacobucci, D. (2004). Alpha's standard error (ASE): An accurate and precise confidence interval estimate. *Journal of Applied Psychology*, 89(5), 792–808. <https://doi.org/10.1037/0021-9010.89.5.792>

Examples

```
var_error_q(q = .8, n = 100)
var_error_q(q = .8, n = 100, rel_type = "alpha", k_items = 10)
```

var_error_r

Estimate the error variance of correlations

Description

Estimate the error variance of correlations

Usage

```
var_error_r(r, n, correct_bias = TRUE)
```

Arguments

r	Vector of correlations.
n	Vector of sample sizes.
correct_bias	Logical argument that determines whether to correct error-variance estimates for small-sample bias in correlations (TRUE) or not (FALSE).

Details

The sampling variance of a correlation is:

$$var_e = \frac{(1 - r^2)^2}{n - 1}$$

which can be corrected for bias by dividing the sampling variance by the bias factor:

$$bias\ factor = \left(\frac{2n - 2}{2n - 1}\right)^2$$

Value

A vector of sampling-error variances.

References

Schmidt, F. L., & Hunter, J. E. (2015). *Methods of meta-analysis: Correcting error and bias in research findings* (3rd ed.). Thousand Oaks, CA: Sage. <https://doi.org/10/b6mg>. p. 99.

Examples

```
var_error_r(r = .3, n = 30, correct_bias = TRUE)
var_error_r(r = .3, n = 30, correct_bias = FALSE)
```

var_error_rel	<i>Estimate the error variance of reliability estimates</i>
---------------	---

Description

Estimate the error variance of reliability estimates

Usage

```
var_error_rel(rel, n, rel_type = "alpha", k_items = NULL)
```

Arguments

rel	Vector of reliability estimates.
n	Vector of sample sizes.
rel_type	Character vector indicating the type(s) of reliabilities being analyzed. See documentation for ma_r for a full list of acceptable reliability types. NOTE: Currently, only alpha has its own dedicated error-variance estimate; the error variance of other reliability types is estimated using the generic definition of reliability as the squared correlation between observed scores and true scores.
k_items	Optional numeric vector indicating the number of items in each scale for which reliabilities are being analyzed.

Details

The sampling variance of a reliability coefficient is:

$$var_e = \frac{4r_{XX}(1 - r_{XX})^2}{n - 1}$$

For the equation to estimate the variance of coefficient alpha, see Duhachek and Iacobucci (2004).

Value

A vector of sampling-error variances.

References

Dahlke, J. A., & Wiernik, B. M. (2017). *One of these artifacts is not like the others: New methods to account for the unique implications of indirect range-restriction corrections in organizational research*. Unpublished manuscript.

Duhachek, A., & Iacobucci, D. (2004). Alpha's standard error (ASE): An accurate and precise confidence interval estimate. *Journal of Applied Psychology*, 89(5), 792–808. <https://doi.org/10.1037/0021-9010.89.5.792>

Examples

```
var_error_rel(rel = .8, n = 100)
var_error_rel(rel = .8, n = 100, rel_type = "alpha", k_items = 10)
```

var_error_r_bvirr	<i>Taylor series approximation of the sampling variance of correlations corrected using the Case V correction for indirect range restriction</i>
-------------------	--

Description

This function propagates error in the bivariate indirect range-restriction correction formula to allow for the computation of a pseudo compound attenuation factor in individual-correction meta-analysis. Traditional methods for estimating compound attenuation factors (i.e., dividing the observed correlation by the corrected correlation) do not work with the BVIRR correction because BVIRR has an additive term that makes the corrected correlation inappropriate for use in estimating the effect of the correction on the variance of the sampling distribution of correlations. The equation-implied adjustment for the BVIRR correction (i.e., the first derivative of the correction equation with respect to the observed correlation) underestimates the error of corrected correlations, so this function helps to account for that additional error.

Usage

```
var_error_r_bvirr(rxyi, var_e = NULL, ni, na = NA, ux = rep(1,
  length(rxyi)), ux_observed = rep(TRUE, length(rxyi)), uy = rep(1,
  length(rxyi)), uy_observed = rep(TRUE, length(rxyi)), qx = rep(1,
  length(rxyi)), qx_restricted = rep(TRUE, length(rxyi)),
  qx_type = rep("alpha", length(rxyi)), k_items_x = rep(NA,
  length(rxyi)), qy = rep(1, length(rxyi)), qy_restricted = rep(TRUE,
  length(rxyi)), qy_type = rep("alpha", length(rxyi)),
  k_items_y = rep(NA, length(rxyi)), mean_rxyi = NULL,
  mean_ux = NULL, mean_uy = NULL, mean_qxa = NULL, mean_qya = NULL,
  var_rxyi = NULL, var_ux = NULL, var_uy = NULL, var_qxa = NULL,
  var_qya = NULL, cor_rxyi_ux = 0, cor_rxyi_uy = 0,
  cor_rxyi_qxa = 0, cor_rxyi_qya = 0, cor_ux_uy = 0,
  cor_ux_qxa = 0, cor_ux_qya = 0, cor_uy_qxa = 0, cor_uy_qya = 0,
  cor_qxa_qya = 0, sign_rxz = 1, sign_ryz = 1,
  r_deriv_only = FALSE)
```

Arguments

rxyi	Vector of observed correlations.
var_e	Vector of estimated sampling variances for rxyi values.
ni	Vector of incumbent sample sizes (necessary when variances of correlations/artifacts are not supplied).
na	Optional vector of applicant sample sizes (for estimating error variance of u ratios and applicant reliabilities).
ux	Vector of observed-score u ratios for X.
ux_observed	Logical vector in which each entry specifies whether the corresponding ux value is an observed-score u ratio (TRUE) or a true-score u ratio. All entries are TRUE by default.
uy	Vector of observed-score u ratios for Y.
uy_observed	Logical vector in which each entry specifies whether the corresponding uy value is an observed-score u ratio (TRUE) or a true-score u ratio. All entries are TRUE by default.
qx	Vector of square roots of reliability estimates for X.
qx_restricted	Logical vector determining whether each element of qx is derived from an incumbent reliability (TRUE) or an applicant reliability (FALSE).
qx_type, qy_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for ma_r for a full list of acceptable reliability types.
k_items_x, k_items_y	Numeric vector identifying the number of items in each scale.
qy	Vector of square roots of reliability estimates for X.
qy_restricted	Logical vector determining whether each element of qy is derived from an incumbent reliability (TRUE) or an applicant reliability (FALSE).

mean_rxyi	Mean observed correlation.
mean_ux	Mean observed-score u ratio for X (for use in estimating sampling errors in the context of a meta-analysis).
mean_uy	Mean observed-score u ratio for Y (for use in estimating sampling errors in the context of a meta-analysis).
mean_qxa	Mean square-root applicant reliability estimate for X (for use in estimating sampling errors in the context of a meta-analysis).
mean_qya	Mean square-root applicant reliability estimate for Y (for use in estimating sampling errors in the context of a meta-analysis).
var_rxyi	Optional pre-specified variance of correlations.
var_ux	Optional pre-specified variance of observed-score u ratios for X.
var_uy	Optional pre-specified variance of observed-score u ratios for Y.
var_qxa	Optional pre-specified variance of square-root applicant reliability estimate for X.
var_qya	Optional pre-specified variance of square-root applicant reliability estimate for Y.
cor_rxyi_ux	Correlation between rxyi and ux (zero by default).
cor_rxyi_uy	Correlation between rxyi and uy (zero by default).
cor_rxyi_qxa	Correlation between rxyi and qxa (zero by default).
cor_rxyi_qya	Correlation between rxyi and qya (zero by default).
cor_ux_uy	Correlation between ux and uy (zero by default).
cor_ux_qxa	Correlation between ux and qxa (zero by default).
cor_ux_qya	Correlation between ux and qya (zero by default).
cor_uy_qxa	Correlation between uy and qxa (zero by default).
cor_uy_qya	Correlation between uy and qya (zero by default).
cor_qxa_qya	Correlation between qxa and qya (zero by default).
sign_rxz	Sign of the relationship between X and the selection mechanism.
sign_ryz	Sign of the relationship between Y and the selection mechanism.
r_deriv_only	Logical scalar determining whether to use the partial derivative with respect to rxyi only (TRUE) or a full Taylor series approximation of the disattenuation formula (FALSE).

Details

Per the principles of propagation of uncertainty and assuming that q_{X_a} , q_{Y_a} , u_X , u_Y , and ρ_{XY_i} , are independent, we can derive a linear approximation of the sampling error of ρ_{TP_a} . We begin with the bivariate indirect range restriction formula,

$$\rho_{TP_a} = \frac{\rho_{XY_i} u_X u_Y + \lambda \sqrt{|1 - u_X^2| |1 - u_Y^2|}}{q_{X_a} q_{Y_a}}$$

which implies the following linear approximation of the sampling variance of ρ_{TP_a} :

$$SE_{\rho_{TP_a}}^2 = b_1^2 SE_{q_{X_a}}^2 + b_2^2 SE_{q_{Y_a}}^2 + b_3^2 SE_{u_X}^2 + b_4^2 SE_{u_Y}^2 + b_5^2 SE_{\rho_{XY_i}}^2$$

where b_1 , b_2 , b_3 , b_4 , and b_5 are the first-order partial derivatives of the disattenuation formula with respect to q_{X_a} , q_{Y_a} , u_X , u_Y , and ρ_{XY_i} , respectively. These partial derivatives are computed as follows:

$$b_1 = \frac{\partial \rho_{TP_a}}{\partial q_{X_a}} = -\frac{\rho_{TP_a}}{q_{X_a}}$$

$$b_2 = \frac{\partial \rho_{TP_a}}{\partial q_{Y_a}} = -\frac{\rho_{TP_a}}{q_{Y_a}}$$

$$b_3 = \frac{\partial \rho_{TP_a}}{\partial u_X} = \left[\rho_{XY_i} u_Y - \frac{\lambda u_X (1 - u_X^2) \sqrt{|1 - u_Y^2|}}{|1 - u_X^2|^{1.5}} \right] / (q_{X_a} q_{Y_a})$$

$$b_4 = \frac{\partial \rho_{TP_a}}{\partial u_Y} = \left[\rho_{XY_i} u_X - \frac{\lambda u_Y (1 - u_Y^2) \sqrt{|1 - u_X^2|}}{|1 - u_Y^2|^{1.5}} \right] / (q_{X_a} q_{Y_a})$$

$$b_5 = \frac{\partial \rho_{TP_a}}{\partial \rho_{XY_i}} = \frac{u_X u_Y}{q_{X_a} q_{Y_a}}$$

Value

A vector of corrected correlations' sampling-error variances.

References

Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.

Examples

```
var_error_r_bvirr(rxyi = .3, var_e = var_error_r(r = .3, n = 100), ni = 100,
  ux = .8, uy = .8,
  qx = .9, qx_restricted = TRUE,
  qy = .9, qy_restricted = TRUE,
  sign_rxz = 1, sign_ryz = 1)
```

var_error_u	<i>Estimate the error variance of u ratios</i>
-------------	--

Description

Estimate the error variance of u ratios

Usage

```
var_error_u(u, ni, na = NA, dependent_sds = FALSE)
```

Arguments

u	Vector of u ratios.
ni	Vector of incumbent-group sample sizes.
na	Vector of applicant-group sample sizes.
dependent_sds	Logical vector identifying whether each u ratio is based on standard deviations from independent samples (FALSE) or based on standard deviations from an applicant sample and an incumbent sample that is a subset of that applicant sample (TRUE).

Details

The sampling variance of a u ratio is computed differently for independent samples (i.e., settings where the referent unrestricted standard deviation comes from an different sample than the range-restricted standard deviation) than for dependent samples (i.e., unrestricted samples from which a subset of individuals are selected to be in the incumbent sample).

The sampling variance for independent samples (the more common case) is:

$$var_e = \frac{u^2}{2} \left(\frac{1}{n_i - 1} + \frac{1}{n_a - 1} \right)$$

and the sampling variance for dependent samples is:

$$var_e = \frac{u^2}{2} \left(\frac{1}{n_i - 1} - \frac{1}{n_a - 1} \right)$$

where u is the u ratio, n_i is the incumbent sample size, and n_a is the applicant sample size.

Value

A vector of sampling-error variances.

References

Dahlke, J. A., & Wiernik, B. M. (2018). *One of these artifacts is not like the others: Accounting for indirect range restriction in organizational and psychological research*. Manuscript submitted for review.

Examples

```
var_error_u(u = .8, ni = 100, na = 200)
var_error_u(u = .8, ni = 100, na = NA)
```

wt_cov

*Compute weighted covariances***Description**

Compute the weighted covariance among variables in a matrix or between the variables in two separate matrices/vectors.

Usage

```
wt_cov(x, y = NULL, wt = NULL, as_cor = FALSE,
       use = c("everything", "listwise", "pairwise"), unbiased = TRUE,
       df_type = c("count", "sum_wts"))
```

```
wt_cor(x, y = NULL, wt = NULL, use = "everything")
```

Arguments

x	Vector or matrix of x variables.
y	Vector or matrix of y variables
wt	Vector of weights
as_cor	Logical scalar that determines whether the covariances should be standardized (TRUE) or unstandardized (FALSE).
use	Method for handling missing values. "everything" uses all values and does not account for missingness, "listwise" uses only complete cases, and "pairwise" uses pairwise deletion.
unbiased	Logical scalar determining whether variance should be unbiased (TRUE) or maximum-likelihood (FALSE).
df_type	Character scalar determining whether the degrees of freedom for unbiased estimates should be based on numbers of cases ("count"; default) or sums of weights ("sum_wts").

Value

Scalar, vector, or matrix of covariances.

Examples

```
wt_cov(x = c(1, 0, 2), y = c(1, 2, 3), wt = c(1, 2, 2), as_cor = FALSE, use = "everything")
wt_cov(x = c(1, 0, 2), y = c(1, 2, 3), wt = c(1, 2, 2), as_cor = TRUE, use = "everything")
wt_cov(x = cbind(c(1, 0, 2), c(1, 2, 3)), wt = c(1, 2, 2), as_cor = FALSE, use = "everything")
wt_cov(x = cbind(c(1, 0, 2), c(1, 2, 3)), wt = c(1, 2, 2), as_cor = TRUE, use = "everything")
wt_cov(x = cbind(c(1, 0, 2, NA), c(1, 2, 3, 3)),
       wt = c(1, 2, 2, 1), as_cor = FALSE, use = "listwise")
wt_cov(x = cbind(c(1, 0, 2, NA), c(1, 2, 3, 3)),
       wt = c(1, 2, 2, 1), as_cor = TRUE, use = "listwise")
```

wt_dist

*Weighted descriptive statistics for a vector of numbers***Description**

Compute the weighted mean and variance of a vector of numeric values. If no weights are supplied, defaults to computing the unweighted mean and the unweighted maximum-likelihood variance.

Usage

```
wt_dist(x, wt = rep(1, length(x)), unbiased = TRUE,
       df_type = c("count", "sum_wts"))

wt_mean(x, wt = rep(1, length(x)))

wt_var(x, wt = rep(1, length(x)), unbiased = TRUE,
      df_type = c("count", "sum_wts"))
```

Arguments

x	Vector of values to be analyzed.
wt	Weights associated with the values in x.
unbiased	Logical scalar determining whether variance should be unbiased (TRUE) or maximum-likelihood (FALSE).
df_type	Character scalar determining whether the degrees of freedom for unbiased estimates should be based on numbers of cases ("count"; default) or sums of weights ("sum_wts").

Details

The weighted mean is computed as

$$\bar{x}_w = \frac{\sum_{i=1}^k x_i w_i}{\sum_{i=1}^k w_i}$$

where x is a numeric vector and w is a vector of weights.

The weighted variance is computed as

$$var_w(x) = \frac{\sum_{i=1}^k (x_i - \bar{x}_w)^2 w_i}{\sum_{i=1}^k w_i}$$

and the unbiased weighted variance is estimated by multiplying $var_w(x)$ by $\frac{k}{k-1}$.

Value

A weighted mean and variance if weights are supplied or an unweighted mean and variance if weights are not supplied.

Examples

```
wt_dist(x = c(.1, .3, .5), wt = c(100, 200, 300))  
wt_mean(x = c(.1, .3, .5), wt = c(100, 200, 300))  
wt_var(x = c(.1, .3, .5), wt = c(100, 200, 300))
```

Index

- *Topic **datagen**
 - simulate_d_database, 165
 - simulate_psych, 170
 - simulate_r_database, 171
 - simulate_r_sample, 174
- *Topic **datasets**
 - data_d_bb_multi, 59
 - data_d_meas_multi, 59
 - data_r_bvdrr, 60
 - data_r_bvirr, 60
 - data_r_gonzalezmu_2014, 61
 - data_r_mcdaniel_1994, 61
 - data_r_mcleod_2007, 62
 - data_r_meas, 62
 - data_r_meas_multi, 63
 - data_r_oh_2009, 63
 - data_r_roth_2015, 64
 - data_r_uvdr, 65
 - data_r_uvirr, 65
- *Topic **distribution**
 - simulate_alpha, 164
 - simulate_matrix, 169
- *Topic **regression**
 - metareg, 148
- *Topic **univar**
 - mix_dist, 149
 - truncate_dist, 177
 - truncate_mean, 178
 - truncate_var, 179
 - wt_dist, 195
- *Topic **utilities**
 - generate_directory, 101
- adjust_n_d, 7
- adjust_n_r, 8
- BibOptions, 100
- composite_d_matrix, 9
- composite_d_scalar, 10
- composite_r_matrix, 9, 13
- composite_r_scalar, 10, 14
- composite_rel_matrix, 11
- composite_rel_scalar, 12
- composite_u_matrix, 15
- composite_u_scalar, 16
- compute_alpha, 17
- compute_dmod, 18
- compute_dmod_npar, 20
- compute_dmod_par, 23
- confidence, 25
- confidence_r, 26
- confint, 27
- control_intercor, 27
- control_psychmeta, 29
- convert_es, 5, 31
- convert_ma, 6, 33
- convert_meta (convert_ma), 33
- correct_d, 5, 35
- correct_d_bias, 37
- correct_glass_bias, 38
- correct_matrix_mvrr, 39
- correct_means_mvrr, 40
- correct_r, 5, 35, 41
- correct_r_bias, 44
- correct_r_coarseness, 45
- correct_r_dich, 46
- correct_r_split, 47
- create_ad, 5, 48, 76, 129
- create_ad_group, 53
- create_ad_list (create_ad_tibble), 55
- create_ad_tibble, 55
- credibility, 58
- data_d_bb_multi, 59
- data_d_meas_multi, 6, 59
- data_r_bvdrr, 6, 60
- data_r_bvirr, 6, 60
- data_r_gonzalezmu_2014, 5, 61
- data_r_mcdaniel_1994, 5, 61

- data_r_mcleod_2007, 62
- data_r_meas, 6, 62
- data_r_meas_multi, 6, 63
- data_r_oh_2009, 63
- data_r_roth_2015, 5, 64
- data_r_uvdr, 6, 65
- data_r_uvirr, 6, 65

- estimate_artifacts, 66
- estimate_cor_prods (estimate_prod), 71
- estimate_cov_prods (estimate_prod), 71
- estimate_length_sb, 70
- estimate_mean_prod (estimate_prod), 71
- estimate_prod, 71
- estimate_q_dist, 72
- estimate_rel_dist, 73
- estimate_rel_sb, 74
- estimate_rxxa (estimate_artifacts), 66
- estimate_rxxa_u (estimate_artifacts), 66
- estimate_rxxi (estimate_artifacts), 66
- estimate_rxxi_u (estimate_artifacts), 66
- estimate_ryya (estimate_artifacts), 66
- estimate_ryyi (estimate_artifacts), 66
- estimate_u, 75
- estimate_up (estimate_artifacts), 66
- estimate_ut (estimate_artifacts), 66
- estimate_ux (estimate_artifacts), 66
- estimate_uy (estimate_artifacts), 66
- estimate_var_artifacts, 76
- estimate_var_prod (estimate_prod), 71
- estimate_var_qxa
(estimate_var_artifacts), 76
- estimate_var_qxi
(estimate_var_artifacts), 76
- estimate_var_qya
(estimate_var_artifacts), 76
- estimate_var_qyi
(estimate_var_artifacts), 76
- estimate_var_rho_int, 85
- estimate_var_rho_int_bvdr
(estimate_var_rho_int), 85
- estimate_var_rho_int_bvirr
(estimate_var_rho_int), 85
- estimate_var_rho_int_meas
(estimate_var_rho_int), 85
- estimate_var_rho_int_rb
(estimate_var_rho_int), 85
- estimate_var_rho_int_uvdr
(estimate_var_rho_int), 85

- estimate_var_rho_int_uvirr
(estimate_var_rho_int), 85
- estimate_var_rho_tsa, 86
- estimate_var_rho_tsa_bvdr
(estimate_var_rho_tsa), 86
- estimate_var_rho_tsa_bvirr
(estimate_var_rho_tsa), 86
- estimate_var_rho_tsa_meas
(estimate_var_rho_tsa), 86
- estimate_var_rho_tsa_rb1
(estimate_var_rho_tsa), 86
- estimate_var_rho_tsa_rb2
(estimate_var_rho_tsa), 86
- estimate_var_rho_tsa_uvdr
(estimate_var_rho_tsa), 86
- estimate_var_rho_tsa_uvirr
(estimate_var_rho_tsa), 86
- estimate_var_rxxa
(estimate_var_artifacts), 76
- estimate_var_rxxi
(estimate_var_artifacts), 76
- estimate_var_ryya
(estimate_var_artifacts), 76
- estimate_var_ryyi
(estimate_var_artifacts), 76
- estimate_var_tsa, 94
- estimate_var_tsa_bvdr
(estimate_var_tsa), 94
- estimate_var_tsa_bvirr
(estimate_var_tsa), 94
- estimate_var_tsa_meas
(estimate_var_tsa), 94
- estimate_var_tsa_rb1
(estimate_var_tsa), 94
- estimate_var_tsa_rb2
(estimate_var_tsa), 94
- estimate_var_tsa_uvdr
(estimate_var_tsa), 94
- estimate_var_tsa_uvirr
(estimate_var_tsa), 94
- estimate_var_ut
(estimate_var_artifacts), 76
- estimate_var_ux
(estimate_var_artifacts), 76

- filter_ma, 97, 100, 144
- filter_meta (filter_ma), 97
- format_num, 98, 144

- generate_bib, [100](#), [144](#), [145](#), [147](#)
- generate_directory, [101](#)
- get_ad (get_stuff), [102](#)
- get_bootstrap (get_stuff), [102](#)
- get_cumulative (get_stuff), [102](#)
- get_escalc (get_stuff), [102](#)
- get_followup (get_stuff), [102](#)
- get_heterogeneity (get_stuff), [102](#)
- get_leave1out (get_stuff), [102](#)
- get_matrix (get_stuff), [102](#)
- get_metafor (get_stuff), [102](#)
- get_metareg (get_stuff), [102](#)
- get_metatab (get_stuff), [102](#)
- get_plots (get_stuff), [102](#)
- get_stuff, [102](#)

- heterogeneity, [6](#), [106](#)

- is_html_output, [147](#)
- is_latex_output, [147](#)

- lm_mat, [108](#)
- lm_matrix (lm_mat), [108](#)

- ma_d, [5](#), [110](#), [115](#), [129](#), [148](#)
- ma_d_ad, [112](#)
- ma_d_ad (ma_d), [110](#)
- ma_d_barebones (ma_d), [110](#)
- ma_d_bb (ma_d), [110](#)
- ma_d_ic (ma_d), [110](#)
- ma_d_order2, [121](#)
- ma_generic, [123](#)
- ma_r, [5](#), [35](#), [42](#), [50](#), [56](#), [67](#), [78](#), [114](#), [115](#), [124](#), [129](#), [148](#), [190](#)
- ma_r_ad, [49](#), [126](#)
- ma_r_ad (ma_r), [124](#)
- ma_r_barebones (ma_r), [124](#)
- ma_r_bb (ma_r), [124](#)
- ma_r_ic (ma_r), [124](#)
- ma_r_order2, [6](#), [140](#)
- matreg (lm_mat), [108](#)
- matrixreg (lm_mat), [108](#)
- merge_simdat_d, [142](#), [165](#)
- merge_simdat_r, [142](#), [172](#)
- metabulate, [6](#), [101](#), [143](#), [146](#), [147](#)
- metabulate_rmd_helper, [101](#), [145](#), [146](#)
- metareg, [5](#), [148](#)
- mix_dist, [149](#)
- mix_matrix, [151](#)

- mix_r_2group, [152](#)

- output_format, [100](#), [143](#)

- plot_forest, [153](#)
- plot_funnel, [154](#)
- predict, [155](#)
- print, [156](#)
- psychmeta (psychmeta-package), [4](#)
- psychmeta-package, [4](#)
- psychmeta_news, [157](#)

- reattribute, [157](#)
- render, [101](#), [145](#)
- reshape_mat2dat, [5](#), [158](#)
- reshape_vec2mat, [159](#)
- reshape_wide2long, [5](#), [160](#)

- sensitivity, [6](#), [162](#)
- sensitivity_bootstrap (sensitivity), [162](#)
- sensitivity_cumulative (sensitivity), [162](#)
- sensitivity_leave1out (sensitivity), [162](#)
- simulate_alpha, [164](#)
- simulate_d_database, [6](#), [142](#), [165](#), [176](#)
- simulate_d_sample, [6](#), [168](#)
- simulate_matrix, [169](#)
- simulate_psych, [170](#)
- simulate_r_database, [6](#), [142](#), [171](#), [174](#), [176](#)
- simulate_r_sample, [6](#), [174](#)
- sparsify_simdat_d, [165](#), [176](#)
- sparsify_simdat_r, [172](#), [176](#)
- summary, [177](#)

- tibble, [145](#)
- truncate_dist, [177](#)
- truncate_mean, [178](#)
- truncate_var, [179](#)

- unmix_matrix, [179](#)
- unmix_r_2group, [180](#)

- var_error_A, [181](#)
- var_error_alpha, [182](#)
- var_error_auc (var_error_A), [181](#)
- var_error_cles (var_error_A), [181](#)
- var_error_d, [183](#)
- var_error_delta, [185](#)
- var_error_g, [185](#)
- var_error_q, [186](#)

[var_error_r](#), 187
[var_error_r_bvirr](#), 189
[var_error_rel](#), 188
[var_error_u](#), 193

[wt_cor \(wt_cov\)](#), 194
[wt_cov](#), 194
[wt_dist](#), 195
[wt_mean \(wt_dist\)](#), 195
[wt_var \(wt_dist\)](#), 195