

# 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.

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

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## 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 supports bare-bones, individual-correction, and artifact-distribution methods for meta-analyzing correlations and  $d$  values.

## 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_uvdrr`, `data_r_uvirr`, `data_r_bvdrr`, `data_r_bvirr`, `data_r_meas_multi`, and `data_d_meas_multi`). Additional simulation functions are also available.

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---

adjust\_n\_d

*Adjusted sample size for a non-Cohen d value for use in a meta-analysis of Cohen's d values*

---

**Description**

This function is used to convert a non-Cohen  $d$  value (e.g., Glass'  $\Delta$ ) 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-Pearsonian 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 functions 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 the 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  $\rho_{XX}$  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      *Matrix formula to estimate the correlation between two weighted or unweighted composite variables*

---

## 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  $\rho_{XY}$  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**

```
r_mat <- matrix(.4, 3, 3)
r_mat[,1] <- r_mat[1,] <- .3
diag(r_mat) <- 1
composite_r_matrix(r_mat = r_mat, x_col = 2:3, 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\_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 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"> <li>• <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>.</li> </ul>
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 = TRUE,
```

```

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	<i>Function for computing non-parametric <math>d_{Mod}</math> effect sizes for a single focal group</i>
-------------------	---

---

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

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

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

*Function for computing parametric  $d_{Mod}$  effect sizes for any number of focal groups*

---

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

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

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  $d_{Mod_{Under}}$  and  $d_{Mod_{Over}}$  effect sizes are computed using the same equation as  $d_{Mod_{Signed}}$ , but  $d_{Mod_{Under}}$  is the weighted average of all scores in the area of underprediction (i.e., the differences in prediction with negative signs) and  $d_{Mod_{Over}}$  is the weighted average of all scores in the area of overprediction (i.e., the differences in prediction with negative 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, sd = NULL, k = 1, conf_level = 0.95,
  conf_method = "t")
```

### Arguments

mean	Mean effect size (if used in a meta-analysis) or observed effect size (if used on individual statistics).
se	For individual statistic.: standard error of the statistic.
sd	For meta-analyses: Observed standard deviation of effect sizes, before accounting for variance from artifacts.
k	For meta-analyses: Number of studies in the meta-analysis.
conf_level	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 <i>t</i> distribution or "norm" for normal distribution.

### Details

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

### Value

A matrix of confidence intervals of the specified width.

### Examples

```
confidence(mean = .3, sd = .15, k = 10, conf_level = .95)
confidence(mean = c(.3, .5), sd = c(.15, .2), k = c(10, 5), conf_level = .95)
confidence(mean = c(.3, .5), se = c(.15, .2), conf_level = .95)
```



---

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)
```

---

convert_es	<i>Convert effect sizes and compute confidence intervals</i>
------------	--

---

### 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 $\chi^2$ 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 $\chi^2$ ) 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	<i>Function to convert meta-analysis of correlations to d values or vice-versa</i>
------------	--

---

## Description

Takes a meta-analysis class object of  $d$  values or correlations (classes `ma_r_as_r`, `ma_d_as_d`, `ma_r_as_d`, and `ma_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)
```

## Arguments

`ma_obj` A meta-analysis object of class `ma_r_as_r`, `ma_d_as_d`, `ma_r_as_d`, or `ma_d_as_r`

## 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

*Correct d values for range restriction and/or measurement error*

---

## 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", sign_rgz = 1, sign_ryz = 1, n1 = NULL, n2 = NA,
  conf_level = 0.95, correct_bias = FALSE)
```

## Arguments

<code>correction</code>	Type of correction to be applied. Options are "meas", "uvdrr_g", "uvdrr_y", "uvirr_g", "uvirr_y", "bvdr", "bvirr"
<code>d</code>	Vector of $d$ values.
<code>ryy</code>	Vector of reliability coefficients for Y (the continuous variable).
<code>uy</code>	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 <code>ma_r</code> for a full list of acceptable reliability types.
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 (dgp<sub>i</sub>), operational range-restricted  $d$  values corrected for measurement error in the grouping only (dGy<sub>i</sub>), and range-restricted true-score  $d$  values (dGp<sub>i</sub>), range-corrected observed-score  $d$  values (dgy<sub>a</sub>), operational range-corrected  $d$  values corrected for measurement error in Y only (dgp<sub>a</sub>), operational range-corrected  $d$  values corrected for measurement error in the grouping only (dGy<sub>a</sub>), and range-corrected true-score  $d$  values (dGp<sub>a</sub>).

## 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. (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.

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	<i>Correct for small-sample bias in Cohen's d values</i>
----------------	--

---

### 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

<code>d</code>	Vector of Cohen's $d$ values.
<code>n</code>	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'  $\Delta$  values*

---

### Description

Correct for small-sample bias in Glass'  $\Delta$  values

### Usage

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

### Arguments

delta                  Vector of Glass'  $\Delta$  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  $\Delta$  is the observed effect size,  $\Delta_c$  is the corrected estimate of  $\Delta$ , 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 <- matrix(.2, 5, 5)
diag(Sigma_i) <- 1
Sigma_xx_a <- matrix(.4, 2, 2)
diag(Sigma_xx_a) <- .8
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", ryy_restricted = TRUE, ryy_type = "alpha",
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.
rxx_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.
rxx_type, ryy_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for <a href="#">ma_r</a> for a full list of acceptable reliability types.

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.
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  $\lambda$  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  $\lambda$  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. (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.
- 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, p_x = NA, p_y = NA, n = NULL)
```

## Arguments

r	Vector of correlations attenuated by artificial dichotomization.
p_x	Vector of proportions of the distribution on either side of the split applied to X (set as NA if X is continuous).
p_y	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.

## 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 dichotomization (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, p_x = .5, p_y = .5, n = 100)
```

---

correct_r_split	<i>Correct correlations for uneven/unrepresentative splits</i>
-----------------	--

---

## 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	<i>Generate an artifact distribution object for use in artifact-distribution meta-analysis programs.</i>
-----------	--

---

## Description

This function generates `ad_obj` class 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_d_ad` functions to apply psychometric corrections to barebones meta-analysis objects via artifact distribution methods.

## Usage

```
create_ad(ad_type = "tsa", rxxi = NULL, n_rxxi = NULL, wt_rxxi = n_rxxi,
  rxxi_type = rep("alpha", length(rxxi)), rxxa = NULL, n_rxxa = NULL,
  wt_rxxa = n_rxxa, rxxa_type = rep("alpha", length(rxxa)), ux = NULL,
  ni_ux = NULL, na_ux = NULL, wt_ux = ni_ux, dep_sds_ux_obs = FALSE,
  ut = NULL, ni_ut = NULL, na_ut = NULL, wt_ut = ni_ut,
  dep_sds_ut_obs = FALSE, mean_qxi = NULL, var_qxi = NULL, k_qxi = NULL,
  mean_n_qxi = NULL, qxi_dist_type = rep("alpha", 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_qxa = NULL,
  var_qxa = NULL, k_qxa = NULL, mean_n_qxa = NULL,
  qxa_dist_type = rep("alpha", 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_ux = NULL,
  var_ux = NULL, k_ux = NULL, mean_ni_ux = NULL, mean_na_ux = NA,
  dep_sds_ux_spec = FALSE, mean_ut = NULL, var_ut = NULL, k_ut = NULL,
  mean_ni_ut = NULL, mean_na_ut = NA, dep_sds_ut_spec = FALSE,
  estimate_rxxa = TRUE, estimate_rxxi = TRUE, estimate_ux = TRUE,
  estimate_ut = TRUE, var_unbiased = TRUE, ...)
```

## Arguments

ad_type	Type of artifact distribution to be computed: Either "tsa" for Taylor series approximation or "int" for interactive.
rxxi	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 <a href="#">ma_r</a> for a full list of acceptable reliability types.
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.

### Details

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.

### 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

*Generate an artifact distribution object for a dichotomous grouping variable.*

---

## Description

This function generates `ad_obj` class 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.

## Usage

```
create_ad_group(ad_type = "tsa", 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

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

**Details**

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

**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 = 300,
               var_unbiased = 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 = "t")
```

**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.

### **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 <a href="#">ma_r</a> 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:

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

#### 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  $\rho_{XX}$  is the initial reliability,  $\rho_{XX}^*$  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  $\rho_{XX}^*$ .

### 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-rootreliability 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  $\rho_{XX}$  is the initial reliability,  $k$  is the multiplier by which the measure is to be lengthened (or shortened), and  $\rho_{XX}^*$  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 usable 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](#) 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 <a href="#">ma_r</a> 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 rxx_as_qx 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 rxx_as_qx 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:

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

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

Direct range restriction:

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

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

#### Partial derivatives to estimate the variance of rxxi using ut ####

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

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

#### 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  $\rho$  corrected for psychometric artifacts using numeric integration*

---

### Description

Functions to estimate the variance of  $\rho$  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  $\rho$ .

Available functions include:

- estimate\_var\_rho\_int\_meas  
Variance of  $\rho$  corrected for measurement error only
- estimate\_var\_rho\_int\_uvdr  
Variance of  $\rho$  corrected for univariate direct range restriction (i.e., Case II) and measurement error
- estimate\_var\_rho\_int\_bvdr  
Variance of  $\rho$  corrected for bivariate direct range restriction and measurement error
- estimate\_var\_rho\_int\_uvirr  
Variance of  $\rho$  corrected for univariate indirect range restriction (i.e., Case IV) and measurement error
- estimate\_var\_rho\_int\_bvirr  
Variance of  $\rho$  corrected for bivariate indirect range restriction (i.e., Case V) and measurement error
- estimate\_var\_rho\_int\_rb  
Variance of  $\rho$  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_bvirr(mean_qxa, mean_qya, mean_ux, mean_uy, var_res)
```

```
estimate_var_rho_int_bvdr(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>

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estimate\_var\_rho\_tsa    *Taylor Series Approximation of variance of  $\rho$  corrected for psychometric artifacts*

---

**Description**

Functions to estimate the variance of  $\rho$  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  $\rho$  corrected for measurement error only

- `estimate_var_rho_tsa_uvdr`  
Variance of  $\rho$  corrected for univariate direct range restriction (i.e., Case II) and measurement error
- `estimate_var_rho_tsa_bvdr`  
Variance of  $\rho$  corrected for bivariate direct range restriction and measurement error
- `estimate_var_rho_tsa_uvirr`  
Variance of  $\rho$  corrected for univariate indirect range restriction (i.e., Case IV) and measurement error
- `estimate_var_rho_tsa_bvirr`  
Variance of  $\rho$  corrected for bivariate indirect range restriction (i.e., Case V) and measurement error
- `estimate_var_rho_tsa_rb1`  
Variance of  $\rho$  corrected using Raju and Burke's TSA1 correction for direct range restriction and measurement error
- `estimate_var_rho_tsa_rb2`  
Variance of  $\rho$  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.
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

$$\rho_{XY} = \rho_{TP}q_Xq_Y$$

where  $\rho_{XY}$  is an observed correlation,  $\rho_{TP}$  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  $\rho_{TP}$  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  $\rho_{TP}$ , 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  $\rho_{TP_a}$  can be computed using the following linear equation,

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

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  $\rho_{TP_a}$ , 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  $\rho_{XY_i}$  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  $\rho_{TP_a}$  can be computed using the following linear equation,

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

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  $\rho_{TP_a}$ , 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  $\rho_{XY_i}$  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  $\rho_{TP_a}$  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  $\rho_{XY_i}$  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  $\rho_{TP_a}$  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:

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

##### 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  $\rho_{TP_a}$  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:

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

##### 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  $\rho_{TP_a}$  can be computed using the following linear equation,

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

where E, F, G, and H are first-order partial derivatives of the attenuation formula with respect to  $\rho_{TP_a}$ ,  $q_{X_a}$ ,  $q_{Y_a}$ , 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. (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.
- 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)

```

---

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.

---

heterogeneity	<i>Supplemental heterogeneity statistics for meta-analyses</i>
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**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  $SD_{res}$ ,  $SD_{\rho}$ , and  $SD_{\delta}$  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> .
<code>rel_es_obs</code>	$1 - \frac{\text{var}_{pre}}{\text{var}_{es}}$ , 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 <code>rel_es_obs</code> expressed as a percentage rather than a decimal.
Q	Cochran's $\chi^2$ 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	$\tau^2$ , an estimator of the random effects variance component (analogous to the Hunter-Schmidt $SD_{res}^2$ , $SD_{\rho}^2$ , or $SD_{\delta}^2$ 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 $SD_{res}$ , $SD_{\rho}$ , and $SD_{\delta}$ 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

```
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 <- heterogeneity(ma_obj = ma_obj)
ma_obj$follow_up_analyses$heterogeneity$barebones$`Analysis ID = 1`
ma_obj$follow_up_analyses$heterogeneity$individual_correction$true_score$`Analysis ID = 1`
```

---

 ma\_d

---

 Master framework for meta-analysis of d values
 

---

## Description

This is the master function for meta-analyses of  $d$  values - it facilitates the computation of barebones, 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, this function 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). This function is also equipped with the capability to clean databases containing inconsistently recorded artifact data, to 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 are employed when `sample_ids` and/or construct names are provided. When multiple meta-analyses are computed within this program, the result of this function takes on the class `ma_master`, which means that it is a list of meta-analyses. Follow-up analyses (e.g., sensitivity, heterogeneity, meta-regression) performed on `ma_master` objects will analyze data from all meta-analyses recorded in the object.

## Usage

```
ma_d(d, n1, n2 = NULL, n_adj = NULL, sample_id = NULL,
  treat_as_d = TRUE, ma_method = "bb", ad_type = "tsa",
  correction_method = "auto", group_id = NULL, group1 = NULL,
  group2 = NULL, group_order = NULL, construct_y = NULL,
  measure_y = NULL, construct_order = NULL, wt_type = "inv_var_mean",
  error_type = "mean", correct_bias = TRUE, correct_rGg = FALSE,
  correct_ryy = TRUE, correct_rr_g = TRUE, 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",
uy = NULL, uy_observed = TRUE, sign_rgz = 1, sign_ryz = 1,
conf_level = 0.95, cred_level = 0.8, conf_method = "t",
cred_method = "t", var_unbiased = TRUE, moderators = NULL,
cat_moderators = TRUE, moderator_type = "simple", pairwise_ads = FALSE,
residual_ads = TRUE, check_dependence = TRUE,
collapse_method = "composite", intercor = 0.5, partial_intercor = FALSE,
clean_artifacts = TRUE, impute_artifacts = ifelse(ma_method == "ad",
FALSE, TRUE), impute_method = "bootstrap_mod", decimals = 2,
hs_override = FALSE, use_all_arts = FALSE, supplemental_ads = NULL,
data = NULL, ...)

```

## 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.
treat_as_d	Logical scalar determining whether <i>d</i> values are to be meta-analyzed as <i>d</i> values (TRUE) or whether they should be meta-analyzed as correlations (FALSE).
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	When ma_method is "ad", select one of the following methods for correcting artifacts: "auto", "meas", "uvdr", "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 <a href="#">ma_d_ad</a> for descriptions of the available methods.
group_id	Vector of group comparison IDs (e.g., Treatment1-Control, Treatment2-Control). The group_id argument supercedes 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 names for groups in a comparison (e.g., group1 = "Control" and group2 = "Treatment", group1 = "Majority" and group2 = "Minority"). The group1 and group2 arguments are superceded by the group_id argument. If group_id is NULL, the values supplied to the group_order argument must correspond to individual group1 and group2 values - the order of group pairings will be determined internally. IMPORTANT: Groups whose names appear before other groups' names in the group_order vector will be treated as referent groups for the focal groups whose names occur later in the group_order vector



(the referent group is the group from whose mean the focal group's mean is subtracted when computing a  $d$  value). If a group2 value comes before a group1 value according to the group\_order vector, the groups' positions in all other arguments will be swapped and the sign of the  $d$  value will be reversed so that group1 is always the referent group.

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 initially designated as Y.
measure_y	Vector of names names for measures associated with constructs initially 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 <b>metafor</b> documentation for details about the <b>metafor</b> methods).
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.
correct_bias	Logical scalar that determines whether to correct correlations for small-sample bias (TRUE) or not (FALSE).
correct_rGg	Logical scalar that determines whether to correct the grouping variable variable for measurement error (TRUE) or not (FALSE).
correct_ryy	Logical scalar that determines whether to correct the Y variable for measurement error (TRUE) or not (FALSE).
correct_rr_g	Logical scalar or vector or column name determining whether each $d$ 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 $d$ should be corrected for range restriction in Y (TRUE) or not (FALSE).
indirect_rr_g	Logical vector or column name determining whether each $d$ 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 $d$ 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).
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 $d$ values or (2) be named so as to match with levels of the group_id 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 group_id argument.
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).
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.
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_rgz	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).
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).
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, "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.
pairwise_ads	Logical value that determines whether to compute artifact distributions in a construct-pair-wise fashion (TRUE) or separately by construct (FALSE, default).
residual_ads	Logical argument that determines whether to use residualized variances (TRUE) or observed variances (FALSE) of artifact distributions to estimate sd_delta.
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 or a named vector with element named according to the names of constructs.
partial_intercor	Logical value that determines whether to compute artifact distributions in a construct-pair-wise fashion (TRUE) or separately by construct (FALSE, default).
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 <code>impute_method</code> 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 <code>impute_method</code> for imputation procedures). Default is FALSE for artifact-distribution meta-analyses and TRUE otherwise. When imputation is performed, <code>clean_artifacts</code> 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. See the documentation for <code>ma_r</code> for a list of available imputation methods.
decimals	Number of decimal places to which results should be rounded (default is to perform no rounding).
hs_override	When TRUE, this will override settings for <code>wt_type</code> (will set to "sample_size"), <code>error_type</code> (will set to "mean"), <code>correct_bias</code> (will set to TRUE), <code>conf_method</code> (will set to "norm"), <code>cred_method</code> (will set to "norm"), and <code>var_unbiased</code> (will set to FALSE).
use_all_arts	Logical scalar that determines whether artifact values from studies without valid effect sizes should be used in artifact distributions (TRUE) or not (FALSE).
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.
...	Further arguments to be passed to functions called within the meta-analysis.

### Value

A list object of the classes `psychmeta`, `ma_d_as_r` or `ma_d_as_d`, `ma_bb` (and `ma_ic` or `ma_ad`, as appropriate).

### 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 3.

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.

## Examples

```
## Not run:
## 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)

## End(Not run)
```

---

ma\_d\_ad

*Artifact-distribution meta-analysis of d values*

---

## Description

This function computes artifact distribution meta-analyses of  $d$  values. It supports interactive methods as well as Taylor series methods for all available corrections.

## Usage

```
ma_d_ad(ma_obj, ad_obj_g = NULL, ad_obj_y = NULL,
         correction_method = "auto", use_ic_ads = "tsa", correct_rGg = FALSE,
         correct_ryy = TRUE, correct_rr_g = TRUE, correct_rr_y = TRUE,
         indirect_rr_g = TRUE, indirect_rr_y = TRUE, residual_ads = TRUE,
         sign_rgz = 1, sign_ryz = 1, decimals = 2, ...)
```

## Arguments

ma_obj	Meta-analysis object of correlations or $d$ values (regardless of input metric, output metric will be $d$ ).
ad_obj_g	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	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.
correction_method	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" for descriptions of the available methods.
use_ic_ads	Determines whether artifact distributions should be extracted from the individual correction results in ma_obj. Only evaluated when ad_obj_g 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.
correct_rGg	Logical argument that determines whether to correct the grouping variable for measurement error (TRUE) or not (FALSE).
correct_ryy	Logical argument that determines whether to correct the Y variable for measurement error (TRUE) or not (FALSE).
correct_rr_g	Logical argument that determines whether to correct the grouping variable for range restriction (TRUE) or not (FALSE).
correct_rr_y	Logical argument that determines whether to correct the Y variable for range restriction (TRUE) or not (FALSE).
indirect_rr_g	If correct_rr_g = TRUE: Logical argument that determines whether to correct for indirect range restriction in the grouping variable (TRUE) or not (FALSE).
indirect_rr_y	If correct_rr_y = TRUE: Logical argument that determines whether to correct for indirect range restriction in Y (TRUE) or not (FALSE).
residual_ads	Logical argument that determines whether to use residualized variances (TRUE) or observed variances (FALSE) of artifact distributions to estimate sd_delta.
sign_rgz	Sign of the relationship between the grouping variable and the selection mechanism (for use with the bvirr correction_method only).
sign_ryz	Sign of the relationship between Y and the selection mechanism (for use with the bvirr correction_method only).
decimals	Number of decimal places to which interactive artifact distributions should be rounded (default is 2 decimal places). Rounding artifact distributions can help to consolidate trivially different values and speed up the computation of meta-analyses (especially in simulations).
...	Additional arguments.

### 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 list object of the classes `psychmeta`, `ma_r_as_d` or `ma_d_as_d`, `ma_bb`, and `ma_ad` (and that inherits class `ma_ic` from `ma_obj`)

**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**

- 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. (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.
- 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>

ma\_d\_bb

*Bare-bones meta-analysis of d values***Description**

This function computes bare-bones meta-analyses of  $d$  values.

**Usage**

```
ma_d_bb(d, n1, n2 = rep(NA, length(d)), n_adj = NULL, sample_id = NULL,
  wt_type = "sample_size", error_type = "mean", correct_bias = FALSE,
  conf_level = 0.95, cred_level = 0.8, conf_method = "t",
  cred_method = "t", var_unbiased = TRUE, moderators = NULL,
  cat_moderators = TRUE, moderator_type = "simple", hs_override = FALSE,
  data = NULL, ...)
```

**Arguments**

- |    |   |
|----|---|
| d  | Vector of $d$ values.   |
| n1 | Vector or column name of primary sample sizes (if subgroup sample sizes are not known, these values are total sample sizes; if subgroup sample sizes are known, these values are sample sizes for the first of the two groups). |
| n2 | Optional: Vector or column name of secondary sample sizes. If subgroup sample sizes are known, these values are sample sizes for the second of the two groups. NULL by default.   |

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. 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.
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).
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.
correct_bias	Logical argument that determines whether to correct effect sizes and error variances for small-sample bias (TRUE) or not (FALSE).
conf_level	Width of confidence interval. Set to .95 by default.
cred_level	Width of credibility interval. Set to .80 by default.
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).
moderators	Matrix of moderator variables or column names of data 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").
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"), and var_unbiased (will set to FALSE).
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
...	Further arguments to be passed to functions called within the meta-analysis.

### Value

A list object of the classes psychmeta, ma\_d\_as\_d, and ma\_bb.

### 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.



## Examples

```
## 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",])
```

---

ma\_d\_ic

*Individual-correction meta-analysis of d values*


---

## Description

This function computes individual-correction meta-analyses of  $d$  values.

## Usage

```
ma_d_ic(d, n1, n2 = NULL, n_adj = NULL, sample_id = NULL,
        treat_as_d = TRUE, wt_type = "inv_var_mean", error_type = "mean",
        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", uy = NULL,
        uy_observed = TRUE, sign_rgz = 1, sign_ryz = 1, conf_level = 0.95,
        cred_level = 0.8, conf_method = "t", cred_method = "t",
        var_unbiased = TRUE, moderators = NULL, cat_moderators = TRUE,
        moderator_type = "simple", impute_method = "bootstrap_mod",
        decimals = 2, hs_override = FALSE, use_all_arts = FALSE,
        supplemental_ads_y = NULL, data = NULL, ...)
```

## Arguments

<code>d</code>	Vector or column name of observed $d$ values.
<code>n1</code>	Vector or column name of sample sizes.
<code>n2</code>	Vector or column name of sample sizes.
<code>n_adj</code>	Optional: Vector or column name of sample sizes adjusted for sporadic artifact corrections.
<code>sample_id</code>	Optional vector of identification labels for samples/studies in the meta-analysis.
<code>treat_as_d</code>	Logical scalar determining whether $d$ values are to be meta-analyzed as $d$ values (TRUE) or whether they should be meta-analyzed as correlations (FALSE).
<code>wt_type</code>	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).

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.
correct_bias	Logical scalar that determines whether to correct correlations for small-sample bias (TRUE) or not (FALSE).
correct_rGg	Logical scalar that determines whether to correct the grouping variable variable for measurement error (TRUE) or not (FALSE).
correct_ryy	Logical scalar that determines whether to correct the Y variable for measurement error (TRUE) or not (FALSE).
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_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_x (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 correct_rr_y (i.e., if correct_rr_y == FALSE, the value supplied for indirect_rr_y 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 have as many elements as there are <i>d</i> values.
pa	Scalar or vector containing the unrestricted-group proportions of group membership. If a vector, it must either have as many elements as there are <i>d</i> values.
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).
ryy_type	String vector identifying the types of reliability estimates supplied (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for <a href="#">ma_r</a> for a full list of acceptable reliability types.
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_rgz	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).
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).
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, "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.
impute_method	Method to use for imputing artifacts. See the documentation for <code>ma_r</code> for a list of available imputation methods.
decimals	Number of decimal places to which results should be rounded (default is to perform no rounding).
hs_override	When TRUE, this will override settings for <code>wt_type</code> (will set to "sample_size"), <code>error_type</code> (will set to "mean"), <code>correct_bias</code> (will set to TRUE), <code>conf_method</code> (will set to "norm"), <code>cred_method</code> (will set to "norm"), and <code>var_unbiased</code> (will set to FALSE).
use_all_arts	Logical scalar that determines whether artifact values from studies without valid effect sizes should be used in artifact distributions (TRUE) or not (FALSE).
supplemental_ads_y	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.
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
...	Further arguments to be passed to functions called within the meta-analysis.

### Value

A list object of the classes `psychmeta`, `ma_d_as_r` or `ma_d_as_d`, `ma_bb`, and `ma_ic`.

### 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 3.
- 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.

## Examples

```
## 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",])
```

---

ma\_d\_order2

*Second-order meta-analysis function for d values*


---

## 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(d = NULL, delta = NULL, var_d = NULL, var_d_c = NULL,
            k = NULL, ma_type = c("bb", "ic", "ad"), sample_id = NULL,
            moderators = NULL, moderator_type = "simple", construct_x = NULL,
            construct_y = NULL, conf_level = 0.95, cred_level = 0.8,
            conf_method = "t", cred_method = "t", var_unbiased = TRUE,
            hs_override = FALSE, data = NULL)
```

## Arguments

d	Vector or column name of mean observed $d$ values.
delta	Vector or column name of mean corrected $d$ values.
var_d	Vector or column name of observed variances of observed $d$ values.
var_d_c	Vector or column name of observed variances of corrected $d$ values.
k	Vector or column name of meta-analyses' $k$ values.
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.
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.
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 $t$ 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).
hs_override	When TRUE, this will override settings for conf_method (will set to "norm"), cred_method (will set to "norm"), and var_unbiased (will set to FALSE).
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.

**Value**

An object of the classes psychmeta, ma\_d\_as\_d, ma\_order2, and ma\_bb, ma\_ic, and/or ma\_ad.

---

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, wt_type = "sample_size",
  conf_level = 0.95, cred_level = 0.8, conf_method = "t",
  cred_method = "t", var_unbiased = TRUE, moderators = NULL,
  cat_moderators = TRUE, moderator_type = "simple", hs_override = FALSE,
  data = NULL, ...)
```

**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. 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.
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).
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).
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").
hs_override	When TRUE, this will override settings for wt_type (will set to "sample_size"), conf_method (will set to "norm"), cred_method (will set to "norm"), and var_unbiased (will set to FALSE).
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
...	Further arguments to be passed to functions called within the meta-analysis.

### Value

A list object of the classes `psychmeta`, `ma_generic`, and `ma_bb`.

### Examples

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

---

ma\_r

*Master framework for meta-analysis of correlations*

---

### Description

This 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, this function 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). This function is also equipped with the capability to clean databases containing inconsistently recorded artifact data, to 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 are employed when `sample_ids` and/or construct names are provided. When multiple construct pairs are meta-analyzed, the result of this function takes on the class `ma_master`, which means that it is a list of meta-analyses. Follow-up analyses (e.g., sensitivity, heterogeneity, meta-regression) performed on `ma_master` objects will analyze data from all meta-analyses recorded in the object.

**Usage**

```
ma_r(rxyi, n, n_adj = NULL, sample_id = NULL, ma_method = "bb",
     ad_type = "tsa", correction_method = "auto", construct_x = NULL,
     construct_y = NULL, measure_x = NULL, measure_y = NULL,
     construct_order = NULL, wt_type = "sample_size", error_type = "mean",
     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", ryy = NULL, ryy_restricted = TRUE,
     ryy_type = "alpha", ux = NULL, ux_observed = TRUE, uy = NULL,
     uy_observed = TRUE, sign_rxz = 1, sign_ryz = 1, conf_level = 0.95,
     cred_level = 0.8, conf_method = "t", cred_method = "t",
     var_unbiased = TRUE, moderators = NULL, cat_moderators = TRUE,
     moderator_type = "simple", pairwise_ads = FALSE, residual_ads = TRUE,
     check_dependence = TRUE, collapse_method = "composite", intercor = 0.5,
     clean_artifacts = TRUE, impute_artifacts = ifelse(ma_method == "ad",
     FALSE, TRUE), impute_method = "bootstrap_mod", decimals = 2,
     hs_override = FALSE, use_all_arts = FALSE, supplemental_ads = NULL,
     data = NULL, ...)
```

**Arguments**

rxyi	Vector or column name of observed correlations
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.
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	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 iterative artifact distributions are provided). See "Details" of <a href="#">ma_r_ad</a> for descriptions of the available methods.
construct_x	Vector of construct names for construct initially designated as X.
construct_y	Vector of construct names for construct initially designated as Y.
measure_x	Vector of names names for measures associated with constructs initially designated as "X".
measure_y	Vector of names names for measures associated with constructs initially designated 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 <b>metafor</b> documentation for details about the <b>metafor</b> methods).
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.
correct_bias	Logical scalar that determines whether to correct correlations for small-sample bias (TRUE) or not (FALSE).
correct_rxx	Logical scalar that determines whether to correct the X variable for measurement error (TRUE) or not (FALSE).
correct_ryy	Logical scalar that determines whether to correct the Y variable for measurement error (TRUE) or not (FALSE).
correct_rr_x	Logical scalar, logical vector or column name determining whether each correlation in $r_{xyi}$ 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 $r_{xyi}$ 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_x	Logical vector or column name determining whether each correlation in $r_{xyi}$ should be corrected for indirect range restriction in X (TRUE) or not (FALSE). Superseded in evaluation by <code>correct_rr_x</code> (i.e., if <code>correct_rr_x == FALSE</code> , the value supplied for <code>indirect_rr_x</code> is disregarded).
indirect_rr_y	Logical vector or column name determining whether each correlation in $r_{xyi}$ 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).
rxx	Vector or column name of reliability estimates for X.
rxx_restricted	Logical vector or column name determining whether each element of <code>rxx</code> 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"> <li>• <code>internal_consistency</code> A generic designation for internal-consistency reliability estimates derived from responses to a single test administration.</li> <li>• <code>multiple_administrations</code> A generic designation for reliability estimates derived from multiple administrations of a test.</li> <li>• <code>alpha</code> Coefficient alpha.</li> </ul>



- 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.
- 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).
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).
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).
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.
pairwise_ads	Logical value that determines whether to compute artifact distributions in a construct-pair-wise fashion (TRUE) or separately by construct (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 or a named vector with element named according to the names of constructs.
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.

<code>impute_artifacts</code>	If TRUE, artifact imputation will be performed (see <code>impute_method</code> for imputation procedures). Default is FALSE for artifact-distribution meta-analyses and TRUE otherwise. When imputation is performed, <code>clean_artifacts</code> is treated as TRUE so as to resolve all discrepancies among artifact entries before and after imputation.
<code>impute_method</code>	<p>Method to use for imputing artifacts. Choices are:</p> <ul style="list-style-type: none"> <li>• <code>bootstrap_mod</code> Select random values from the most specific moderator categories available (default).</li> <li>• <code>bootstrap_full</code> Select random values from the full vector of artifacts.</li> <li>• <code>simulate_mod</code> Generate random values from the distribution with the mean and variance of observed artifacts from the most specific moderator categories available. (uses <code>rnorm</code> for u ratios and <code>rbeta</code> for reliability values).</li> <li>• <code>simulate_full</code> Generate random values from the distribution with the mean and variance of all observed artifacts (uses <code>rnorm</code> for u ratios and <code>rbeta</code> for reliability values).</li> <li>• <code>wt_mean_mod</code> Replace missing values with the sample-size weighted mean of the distribution of artifacts from the most specific moderator categories available (not recommended).</li> <li>• <code>wt_mean_full</code> Replace missing values with the sample-size weighted mean of the full distribution of artifacts (not recommended).</li> <li>• <code>unwt_mean_mod</code> Replace missing values with the unweighted mean of the distribution of artifacts from the most specific moderator categories available (not recommended).</li> <li>• <code>unwt_mean_full</code> Replace missing values with the unweighted mean of the full distribution of artifacts (not recommended).</li> <li>• <code>replace_unity</code> Replace missing values with 1 (not recommended).</li> <li>• <code>stop</code> Stop evaluations when missing artifacts are encountered.</li> </ul> <p>If an imputation method ending in "mod" is selected but no moderators are provided, the "mod" suffix will internally be replaced with "full".</p>
<code>decimals</code>	Number of decimal places to which interactive artifact distributions should be rounded (default is 2 decimal places).
<code>hs_override</code>	When TRUE, this will override settings for <code>wt_type</code> (will set to "sample_size"), <code>error_type</code> (will set to "mean"), <code>correct_bias</code> (will set to TRUE), <code>conf_method</code> (will set to "norm"), <code>cred_method</code> (will set to "norm"), and <code>var_unbiased</code> (will set to FALSE).

use_all_arts	Logical scalar that determines whether artifact values from studies without valid effect sizes should be used in artifact distributions (TRUE) or not (FALSE).
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 and/or moderators.
...	Further arguments to be passed to functions called within the meta-analysis.

### Value

A list object of the classes psychmeta, ma\_r\_as\_r, ma\_bb (and ma\_ic or ma\_ad, as appropriate).

### 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 3.

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.

### Examples

```
## The 'ma_r' function can compute multi-construct bare-bones meta-analyses:
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)

## It can also perform multiple individual-correction meta-analyses:
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)

## And 'ma_r' can also curate artifact distributions and compute multiple
## artifact-distribution meta-analyses:
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, data = data_r_meas_multi)

## 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_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)))

## 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
dat <- rbind(dat1, dat2)
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)

```

---

ma\_r\_ad

*Artifact-distribution meta-analysis of correlations*


---

## Description

This function computes artifact distribution meta-analyses of correlations. It supports interactive methods as well as Taylor series methods for all available corrections.

## Usage

```

ma_r_ad(ma_obj, ad_obj_x = NULL, ad_obj_y = NULL,
        correction_method = "auto", use_ic_ads = "tsa", correct_rxx = TRUE,
        correct_ryy = TRUE, correct_rr_x = TRUE, correct_rr_y = TRUE,
        indirect_rr_x = TRUE, indirect_rr_y = TRUE, residual_ads = TRUE,
        sign_rxz = 1, sign_ryz = 1, decimals = 2, ...)

```

## Arguments

**ma\_obj** Meta-analysis object of correlations or d values (regardless of input metric, output metric will be r).

ad_obj_x	Artifact-distribution object for the X variable (output of the <code>create_ad</code> function). 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_x</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	Artifact-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> .
correction_method	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" for descriptions of the available methods.
use_ic_ads	Determines whether artifact distributions should be extracted from the individual correction results in <code>ma_obj</code> . Only evaluated when <code>ad_obj_x</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>t</code> to use the Taylor series method or <code>i</code> to use the interactive method.
correct_rxx	Logical argument that determines whether to correct the X variable for measurement error (TRUE) or not (FALSE).
correct_ryy	Logical argument that determines whether to correct the Y variable for measurement error (TRUE) or not (FALSE).
correct_rr_x	Logical argument that determines whether to correct the X variable for range restriction (TRUE) or not (FALSE).
correct_rr_y	Logical argument that determines whether to correct the Y variable for range restriction (TRUE) or not (FALSE).
indirect_rr_x	If <code>correct_rr_x = TRUE</code> : Logical argument that determines whether to correct for indirect range restriction in X (TRUE) or not (FALSE).
indirect_rr_y	If <code>correct_rr_y = TRUE</code> : Logical argument that determines whether to correct for indirect range restriction in Y (TRUE) or not (FALSE).
residual_ads	Logical argument that determines whether to use residualized variances (TRUE) or observed variances (FALSE) of artifact distributions to estimate <code>sd_rho</code> .
sign_rxz	Sign of the relationship between X and the selection mechanism (for use with the <code>bvirr</code> <code>correction_method</code> only).
sign_ryz	Sign of the relationship between Y and the selection mechanism (for use with the <code>bvirr</code> <code>correction_method</code> only).
decimals	Number of decimal places to which interactive artifact distributions should be rounded (default is 2 decimal places). Rounding artifact distributions can help to consolidate trivially different values and speed up the computation of meta-analyses (especially in simulations).
...	Additional arguments.

## 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 list object of the classes `psychmeta`, `ma_r_as_r` or `ma_d_as_r`, `ma_bb`, and `ma_ad` (and that inherits class `ma_ic` from `ma_obj`)

## 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, CA: Sage. <https://doi.org/10/b6mg>. 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), 425–438. <https://doi.org/10.1037/0021-9010.79.3.425>

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.

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

```
## 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_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_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 = "uvdr",
        correct_rr_y = FALSE, indirect_rr_x = FALSE)
```



---

ma\_r\_bb

*Bare-bones meta-analysis of correlations*


---

## Description

This function computes bare-bones meta-analyses of correlations.

## Usage

```
ma_r_bb(r, n, n_adj = NULL, sample_id = NULL, wt_type = "sample_size",
        error_type = "mean", correct_bias = TRUE, conf_level = 0.95,
        cred_level = 0.8, conf_method = "t", cred_method = "t",
        var_unbiased = TRUE, moderators = NULL, cat_moderators = TRUE,
        moderator_type = "simple", hs_override = FALSE, data = NULL, ...)
```

## Arguments

r	Vector or column name of observed correlations.
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. 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.
wt_type	Type of weight to use in the meta-analysis: native 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).
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.
correct_bias	Logical argument that determines whether to correct correlations for small-sample bias (TRUE) or not (FALSE).
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).

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").
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"), and var_unbiased (will set to FALSE).
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
...	Further arguments to be passed to functions called within the meta-analysis.

### Value

A list object of the classes psychmeta, ma\_r\_as\_r, and ma\_bb.

### 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 3.

### Examples

```
## 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)
```

---

ma\_r\_ic

*Individual-correction meta-analysis of correlations*

---

### Description

This function computes individual-correction meta-analyses of correlations.

**Usage**

```
ma_r_ic(rxyi, n, n_adj = NULL, sample_id = NULL, wt_type = "sample_size",
  error_type = "mean", 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", ryy = NULL,
  ryy_restricted = TRUE, ryy_type = "alpha", ux = NULL,
  ux_observed = TRUE, uy = NULL, uy_observed = TRUE, sign_rxz = 1,
  sign_ryz = 1, conf_level = 0.95, cred_level = 0.8, conf_method = "t",
  cred_method = "t", var_unbiased = TRUE, moderators = NULL,
  cat_moderators = TRUE, moderator_type = "simple",
  impute_method = "bootstrap_mod", hs_override = FALSE,
  use_all_arts = FALSE, supplemental_ads_x = NULL,
  supplemental_ads_y = NULL, data = NULL, ...)
```

**Arguments**

<code>rxyi</code>	Vector or column name of observed correlations.
<code>n</code>	Vector or column name of sample sizes.
<code>n_adj</code>	Optional: Vector or column name of sample sizes adjusted for sporadic artifact corrections.
<code>sample_id</code>	Optional vector of identification labels for studies in the meta-analysis.
<code>wt_type</code>	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).
<code>error_type</code>	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.
<code>correct_bias</code>	Logical scalar that determines whether to correct correlations for small-sample bias (TRUE) or not (FALSE).
<code>correct_rxx</code>	Logical scalar that determines whether to correct the X variable for measurement error (TRUE) or not (FALSE).
<code>correct_ryy</code>	Logical scalar that determines whether to correct the Y variable for measurement error (TRUE) or not (FALSE).
<code>correct_rr_x</code>	Logical scalar or vector or column name determining whether each correlation in <code>rxyi</code> should be corrected for range restriction in X (TRUE) or not (FALSE).
<code>correct_rr_y</code>	Logical scalar or vector or column name determining whether each correlation in <code>rxyi</code> should be corrected for range restriction in Y (TRUE) or not (FALSE).
<code>indirect_rr_x</code>	Logical vector or column name determining whether each correlation in <code>rxyi</code> should be corrected for indirect range restriction in X (TRUE) or not (FALSE). Superseded in evaluation by <code>correct_rr_x</code> (i.e., if <code>correct_rr_x == FALSE</code> , the value supplied for <code>indirect_rr_x</code> 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 (e.g., "alpha", "retest", "interrater_r", "splithalf"). See the documentation for <a href="#">ma_r</a> for a full list of acceptable reliability types.
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).
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).
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).
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.
impute_method	Method to use for imputing artifacts. See the documentation for <a href="#">ma_r</a> for a list of available imputation methods.

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"), and var_unbiased (will set to FALSE).
use_all_arts	Logical scalar that determines whether artifact values from studies without valid effect sizes should be used in artifact distributions (TRUE) or not (FALSE).
supplemental_ads_x, supplemental_ads_y	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.
data	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.
...	Further arguments to be passed to functions called within the meta-analysis (e.g., create_ad_int and create_ad_tsa).

### Value

A list object of the classes psychmeta, ma\_r\_as\_r, ma\_bb, and ma\_ic.

### 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 3.
- 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.

### Examples

```
## 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)

## 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 = Complexity)
```

---

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(r = NULL, rho = NULL, var_r = NULL, var_r_c = NULL,
  k = NULL, ma_type = c("bb", "ic", "ad"), sample_id = NULL,
  moderators = NULL, moderator_type = "simple", construct_x = NULL,
  construct_y = NULL, conf_level = 0.95, cred_level = 0.8,
  conf_method = "t", cred_method = "t", var_unbiased = TRUE,
  hs_override = FALSE, data = NULL)
```

**Arguments**

<code>r</code>	Vector or column name of mean observed correlations.
<code>rho</code>	Vector or column name of mean corrected correlations.
<code>var_r</code>	Vector or column name of observed variances of observed correlations.
<code>var_r_c</code>	Vector or column name of observed variances of corrected correlations.
<code>k</code>	Vector or column name of meta-analyses' <i>k</i> 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>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>conf_level</code>	Confidence level to define the width of the confidence interval (default = .95).
<code>cred_level</code>	Credibility level to define the width of the credibility interval (default = .80).
<code>conf_method</code>	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.
<code>cred_method</code>	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.
<code>var_unbiased</code>	Logical scalar determining whether variances should be unbiased (TRUE) or maximum-likelihood (FALSE).
<code>hs_override</code>	When TRUE, this will override settings for <code>conf_method</code> (will set to "norm"), <code>cred_method</code> (will set to "norm"), and <code>var_unbiased</code> (will set to FALSE).
<code>data</code>	Data frame containing columns whose names may be provided as arguments to vector arguments and/or moderators.

**Value**

An object of the classes `psychmeta`, `ma_r_as_r`, `ma_order2`, and `ma_bb`, `ma_ic`, and/or `ma_ad`.

**Examples**

```
## Analysis of the validity of conscientiousness as a predictor of job performance in East Asia
ma_r_order2(r = r_bar_i, rho = rho_bar_i, var_r = var_r,
            var_r_c = NULL, k = k, ma_type = "ad",
            sample_id = NULL, moderators = NULL,
            construct_x = NULL, construct_y = NULL,
            conf_level = .95, cred_level = .8,
            cred_method = "t", var_unbiased = TRUE,
            data = dplyr::filter(data_r_oh_2009, Predictor == "Conscientiousness"))

## Analysis of the validity of the Big Five traits as predictors of job performance in East Asia
ma_r_order2(r = r_bar_i, rho = rho_bar_i, var_r = var_r,
            var_r_c = NULL, k = k, ma_type = "ad",
            sample_id = NULL, moderators = NULL, construct_x = Predictor,
            conf_level = .95, cred_level = .8,
            cred_method = "t", var_unbiased = TRUE,
            data = data_r_oh_2009)

## Analysis of the average validity of the Big Five traits as predictors of
## job performance by Eastern Asian country
ma_r_order2(r = r_bar_i, rho = rho_bar_i, var_r = var_r,
            var_r_c = NULL, k = k, ma_type = "ad",
            sample_id = NULL, moderators = "Country",
            conf_level = .95, cred_level = .8, cred_method = "t",
            var_unbiased = TRUE, data = data_r_oh_2009)
```

---

merge\_simdat\_d

---

*Merge multiple "simdat\_d" class objects*


---

**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" 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`

---

metabulate	<i>Write a summary table of meta-anlytic results</i>
------------	--

---

**Description**

Write a summary table of meta-anlytic results

**Usage**

```
metabulate(ma_obj, path, show_conf = TRUE, show_cred = TRUE,
           show_se = FALSE)
```

**Arguments**

ma_obj	Meta-analysis object.
path	Path (with file name and .rtf extension) for the ouput file.
show_conf	Logical scalar determining whether to show confidence intervals (TRUE; default) or not (FALSE).
show_cred	Logical scalar determining whether to show credibility intervals (TRUE; default) or not (FALSE).
show_se	Logical scalar determining whether to show standard errors (TRUE) or not (FALSE; default).



**Value**

Saved rich text file containing tables of meta-analytic output.

**Examples**

```
## Not run:
## Create output table for meta-analysis of correlations
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)
ma_r_obj <- ma_r_ad(ma_obj = ma_r_obj, correct_rr_x = FALSE, correct_rr_y = FALSE)
metabulate(ma_obj = ma_r_obj, path = "meta tables correlations.rtf")

## 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, path = "meta tables d values.rtf")

## 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, path = "meta tables generic es.rtf")

## End(Not run)
```

---

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, max_interaction = 1)
```

**Arguments**

ma\_obj            Meta-analysis object.  
 max\_interaction            The maximum level at which interactions should be analyzed. Default is 1 (i.e., main effects only).

**Value**

ma\_obj with meta-regression results added (see ma\_obj\$follow\_up\_analyses\$meta\_regression).

**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$follow_up_analyses$meta_regression$barebones$`Main Effects`
ma_obj$follow_up_analyses$meta_regression$individual_correction$true_score$`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)
```

**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) or maximum-likelihood (FALSE).

**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  $\mu$  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(mat_list, mu_mat, p_vec, N = NULL, group_names = NULL,
           var_names = NULL)
```

**Arguments**

mat_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.

---

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:

$$\rho_{xyWG} = \rho_{xyMix} \sqrt{(d_x^2 p(1-p) + 1)(d_y^2 p(1-p) + 1)} - \sqrt{d_x^2 d_y^2 p^2 (1-p)^2}$$

where  $\rho_{xyWG}$  is the average within-group correlation,  $\rho_{xyMix}$  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 two-group mixture correlationa

**Examples**

```
mix_r_2group(rxy = .375, dx = 1, dy = 1, p = .5)
```

---

psychmeta\_news

*Retrieve the NEWS file for the psychmeta package*

---

**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()
```

---

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:
dat <- 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 = dat)

## Arguments can also provided as raw vectors, matrices, dataframes, etc. without a data argument:
reshape_mat2dat(var_names = dat[,1],
               cor_data = dat[,6:8],
               common_data = dat[,2],
               unique_data = dat[,3:5])

## If data is not null, arguments can be a mix of matrix/dataframe/vector and column-name arguments
reshape_mat2dat(var_names = dat[,1],
               cor_data = dat[,6:8],
               common_data = "n",
               unique_data = c("mean", "sd", "rel"),
               data = dat)

```

---

reshape_vec2mat	<i>Assemble a variance-covariance matrix</i>
-----------------	--

---

## 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)
```

## Arguments

<code>cov</code>	Scalar or vector of covariance information to include the off-diagonal positions of the matrix (default value is zero). If a vector, the elements must be provided in the order associated with concatenated column vectors of the lower triangle of the desired matrix, which is the order or elements that would occur if the lower triangle of the desired matrix were extracted with the following R function: <code>x[lower.tri(x)]</code> .
<code>var</code>	Scalar or vector of variance information to include the diagonal positions of the matrix (default value is 1).
<code>order</code>	If <code>cov</code> and <code>var</code> are scalars, this argument determines the number of variables to create in the output matrix.
<code>var_names</code>	Optional vector of variable names.

**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
c(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, es_design, n_design, other_design,
  es_name = "rxyi")
```

**Arguments**

data	Database of data for use in a meta-analysis in "wide" format.
common_vars	String vector of column names relevant to all variables in data.
es_design	p x p matrix containing the names of columns of intercorrelations among variables in the lower triangle of the matrix.
n_design	Scalar sample-size column name or a p x p matrix containing the names of columns of sample sizes the lower triangle of the matrix.



`other_design` 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.

`es_name` Name of the effect size represented in data.

## 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))))

## Simultate 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 = "weight", boot_iter = 1000, boot_conf_level = 0.95,
  boot_ci_type = "bca", ...)
```

```
sensitivity_bootstrap(ma_obj, boot_iter = 1000, boot_conf_level = 0.95,
  boot_ci_type = "bca", ...)
```

```
sensitivity_cumulative(ma_obj, sort_method = "weight", ...)
```

```
sensitivity_leave1out(ma_obj, ...)
```

### Arguments

<code>ma_obj</code>	Meta-analysis object.
<code>leave1out</code>	Logical scalar determining whether to compute leave-one-out analyses (TRUE) or not (FALSE).
<code>bootstrap</code>	Logical scalar determining whether bootstrapping is to be performed (TRUE) or not (FALSE).
<code>cumulative</code>	Logical scalar determining whether a cumulative meta-analysis is to be computed (TRUE) or not (FALSE).
<code>sort_method</code>	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.
<code>boot_iter</code>	Number of bootstrap iterations to be computed.
<code>boot_conf_level</code>	Width of confidence intervals to be constructed for all bootstrapped statistics.
<code>boot_ci_type</code>	Type of bootstrapped confidence interval (see "type" options for <code>boot::boot.ci</code> for possible arguments). Default is "bca".
<code>...</code>	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**

```
## Run a meta-analysis using simulated UVIRR data:
ma_obj <- ma_r_ic(rxyi = rxyi, n = n, rxx = rxxi, ryy = ryyi, ux = ux,
  correct_rr_y = FALSE, data = data_r_uvirr)

## Pass the meta-analysis object to the sensitivity() function:
ma_obj <- sensitivity(ma_obj = ma_obj, boot_iter = 10, cumulative = TRUE,
  boot_ci_type = "norm", sort_method = "inv_var")

## Examine the tables and plots produced for the meta-analysis:
ma_obj$follow_up_analyses$bootstrap$barebones$`Analysis ID = 1`
ma_obj$follow_up_analyses$bootstrap$individual_correction$true_score$`Analysis ID = 1`
ma_obj$follow_up_analyses$leave1out$individual_correction$true_score$`Analysis ID = 1`
ma_obj$follow_up_analyses$cumulative$individual_correction$true_score$`Analysis ID = 1`
```

---

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, standardized = FALSE)
```

**Arguments**

item_mat	Item intercorrelation/intercovariance 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 samples (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.

group_names	Optional vector of group names.
var_names	Optional vector of variable names for all non-composite variables.
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).
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.
max_iter	Maximum number of iterations to allow in the parameter selection process before terminating with convergence failure. Must be finite.

## 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

```
## Not run:
## 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,
                  group_names = NULL, var_names = c("y1", "y2"),
                  show_applicant = TRUE, keep_vars = c("y1", "y2"), decimals = 2)

## End(Not run)

```

---

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 statistics 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  $\chi^2$  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)), wt_mat = NULL, sr_composites = NULL,
  var_names = NULL, composite_names = NULL)
```

**Arguments**

n	Number of cases to simulate before performing selection. If Inf, function will simulate parameter values.
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).

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, and 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))
```

---

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 samples (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.
<code>composite_names</code>	Optional vector of names for composite variables.
<code>n_as_ni</code>	Logical argument determining whether <code>n</code> 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.
<code>show_applicant</code>	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.

### 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 $\text{Inf}$ , 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 paramters 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      *Create sparse artifact information in a "simdat\_d" class object*

---

### 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" 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      *Create sparse artifact information in a "simdat\_r" class object*

---

**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" 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

---

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, mu_mat, p_vec, N = NULL, group_names = NULL,
             var_names = NULL)
```

**Arguments**

sigma	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.

---

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**

rxy	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  $\rho_{xyWG}$  is the average within-group correlation,  $\rho_{xyMix}$  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

**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	<i>Analytic estimate of the sampling variance of alpha</i>
-----------------	--

---

**Description**

Analytic estimate of the sampling variance of alpha

**Usage**

```
var_error_alpha(item_mat = NULL, alpha = NULL, k_items = NULL, ncases)
```

**Arguments**

item_mat	Item intercorrelation/intercovariance 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.
ncases	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, ncases = 50)
var_error_alpha(alpha = alpha, k_items = k_items, ncases = 50)
var_error_alpha(alpha = c(alpha, alpha), k_items = c(k_items, k_items), ncases = 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)
```

**Arguments**

q                      Vector of of square roots of reliability estimates.  
n                      Vector of sample sizes.

**Details**

The sampling variance of the square root of a reliability coefficient is:

$$var_e = \frac{(1 - q_X^2)^2}{n - 1}$$

**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.

**Examples**

```
var_error_q(q = .8, n = 100)
```



---

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)
```

**Arguments**

rel	Vector of reliability estimates.
n	Vector of sample sizes.

**Details**

The sampling variance of a reliability coefficient is:

$$var_e = \frac{4r_{XX}(1 - r_{XX})^2}{n - 1}$$

**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.

**Examples**

```
var_error_rel(rel = .8, n = 100)
```

---

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, uy, qx,
  qx_restricted = TRUE, qy, qy_restricted = TRUE, 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.
uy	Vector of observed-score u ratios for Y.
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).
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  $\rho_{XY_i}$ , are independent, we can derive a linear approximation of the sampling error of  $\rho_{TP_a}$ . 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  $\rho_{TP_a}$ :

$$SE_{\rho_{TP_a}}^2 = b_1^2 SE_{q_{X_a}}^2 + b_2^2 SE_{q_{Y_a}}^2 + b_3^2 SE_{u_X}^2 + b_4^2 SE_{u_Y}^2 + b_5^2 SE_{\rho_{XY_i}}^2$$

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  $\rho_{XY_i}$ , 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. (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.

## 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, n_i, n_a = NA, dependent_sds = FALSE)
```

### Arguments

u	Vector of u ratios.
n_i	Vector of incumbent-group sample sizes.
n_a	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 deviations 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. (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.

**Examples**

```
var_error_u(u = .8, n_i = 100, n_a = 200)
var_error_u(u = .8, n_i = 100, n_a = 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 = "everything")
```

```
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.

**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\_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)
```

```
wt_mean(x, wt = rep(1, length(x)))
```

```
wt_var(x, wt = rep(1, length(x)), unbiased = TRUE)
```

**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).

**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))
```



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