

# Package ‘esci’

July 8, 2024

**Type** Package

**Title** Estimation Statistics with Confidence Intervals

**Version** 1.0.3

**Description** A collection of functions and 'jamovi' module for the estimation approach to inferential statistics, the approach which emphasizes effect sizes, interval estimates, and meta-analysis. Nearly all functions are based on 'statpsych' and 'metafor'. This package is still under active development, and breaking changes are likely, especially with the plot and hypothesis test functions. Data sets are included for all examples from Cumming & Calin-Jageman (2024) <ISBN:9780367531508>.

**BugReports** <https://github.com/rcalinjageman/esci>

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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CI_diamond_ratio	<i>Estimate the diamond ratio for a meta-analytic effect, a measure of heterogeneity</i>
------------------	--

---

## Description

CI\_diamond\_ratio returns the diamond ratio and CI for a meta-analytic effect, the ratio of the random-effects CI width to the fixed-effects CI width. The diamond ratio is a measure of effect-size heterogeneity.

## Usage

```
CI_diamond_ratio(RE, FE, vi, conf_level = 0.95)
```

## Arguments

RE	metafor object with random effects result
FE	metafor object with fixed effects result
vi	vector of effect size variances
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

## Details

Calculation of the CI is based on code provided by Maxwell Cairns (see Cairns et al., 2022). Specifically, this function implements what Cairns et al (2022) called the Sub-Q approach, which provides the best CI coverage in simulations. For comparison, this function also returns the CI produced by the bWT-DL approach (which generally has worse performance).

**Value**

Returns a list with 3 properties:

- diamond\_ratio
- LL - lower limit of the conf\_level% CI, Sub-Q approach
- UL - upper limit of the conf\_level% CI, Sub-Q approach
- LL\_bWT\_DL - lower limit of the conf\_level% CI, bWT-DL approach
- UL\_bWT\_DL - upper limit of the conf\_level% CI, bWT-DL approach

**Source**

Cairns, Maxwell, Geoff Cumming, Robert Calin-Jageman, and Luke A. Prendergast. "The Diamond Ratio: A Visual Indicator of the Extent of Heterogeneity in Meta-analysis." *British Journal of Mathematical and Statistical Psychology* 75, no. 2 (May 2022): 201–19. <https://doi.org/10.1111/bmsp.12258>.

**Examples**

```
mydata <- esci::data_mccabemichael_brain

# Use esci to obtain effect sizes and sample variances, storing only raw_data
mydata <- esci::meta_mdifftwo(
  data = mydata,
  comparison_means = "M Brain",
  comparison_ns = "n Brain",
  comparison_sds = "s Brain",
  reference_means = "M No Brain",
  reference_ns = "n No Brain",
  reference_sds = "s No Brain",
  random_effects = FALSE
)$raw_data

# Conduct fixed effects meta-analysis
FE <- metafor::rma(
  data = mydata,
  yi = effect_size,
  vi = sample_variance,
  method="FE"
)
# Conduct random effect meta-analysis
RE <- metafor::rma(
  data = mydata,
  yi = effect_size,
  vi = sample_variance,
  method="DL"
)

# Get the diamond ratio
res <- esci::CI_diamond_ratio(
  RE = RE,
  FE = FE,
```

```

vi = mydata$sample_variance
)

```

---

CI\_smd\_ind\_contrast     *Estimate standardized mean difference (Cohen's d) for an independent groups contrast*

---

### Description

CI\_smd\_ind\_contrast returns the point estimate and confidence interval for a standardized mean difference (smd aka Cohen's  $d$  aka Hedges  $g$ ). A standardized mean difference is a difference in means standardized to a standard deviation:

$$d = \frac{\psi}{s}$$

### Usage

```

CI_smd_ind_contrast(
  means,
  sds,
  ns,
  contrast,
  conf_level = 0.95,
  assume_equal_variance = FALSE,
  correct_bias = TRUE
)

```

### Arguments

means	A vector of 2 or more means
sds	A vector of standard deviations, same length as means
ns	A vector of sample sizes, same length as means
contrast	A vector of group weights, same length as means
conf_level	The confidence level for the confidence interval, in decimal form. Defaults to 0.95.
assume_equal_variance	Defaults to FALSE
correct_bias	Defaults to TRUE; attempts to correct the slight upward bias in $d$ derived from a sample. As of 8/9/2023 - Bias correction has been added for more than 2 groups when equal variance is not assumed, based on recent updates to statspsych

**Value**

Returns a list with these named elements:

- effect\_size - the point estimate from the sample
- lower - lower bound of the CI
- upper - upper bound of the CI
- numerator - the numerator for Cohen's  $d_{\text{biased}}$ ; the mean difference in the contrast
- denominator - the denominator for Cohen's  $d_{\text{biased}}$ ; if equal variance is assumed this is  $sd_{\text{pooled}}$ , otherwise  $sd_{\text{avg}}$
- df - the degrees of freedom used for correction and CI calculation
- se - the standard error of the estimate; **warning** not totally sure about this yet
- moe - margin of error; 1/2 length of the CI
- d\_biased - Cohen's  $d$  without correction applied
- properties - a list of properties for the result
  - Properties
  - effect\_size\_name - if equal variance assumed  $d_s$ , otherwise  $d_{\text{avg}}$
  - effect\_size\_name\_html - html representation of  $d_{\text{name}}$
  - denominator\_name - if equal variance assumed  $sd_{\text{pooled}}$  otherwise  $sd_{\text{avg}}$
  - denominator\_name\_html - html representation of denominator name
  - bias\_corrected - TRUE/FALSE if bias correction was applied
  - message - a message explaining denominator and correction status
  - message\_html - html representation of message

**Details****It's a bit complicated:**

A standardized mean difference turns out to be complicated.

First, it has many names:

- standardized mean difference (smd)
- Cohen's  $d$
- When bias in a sample  $d$  has been corrected, also called Hedge's  $g$

Second, the choice of the standardizer requires thought:

- $sd_{\text{pooled}}$  - used when assuming all groups have exact same variance
- $sd_{\text{avg}}$  - does not require assumption of equal variance
- other possibilities, too, but not dealt with in this function

The choice of standardizer is important, so it's noted in the subscript:

- $d_s$  - assumes equal variance, standardized to  $sd_{\text{pooled}}$
- $d_{\text{avg}}$  - does not assume equal variance, standardized to  $sd_{\text{avg}}$

A third complication is the issue of bias:  $d$  estimated from a sample has a slight upward bias at smaller sample sizes. With total sample size  $> 30$ , this slight bias becomes fairly negligible (kind of like the small upward bias in a sample standard deviation).

This bias can be corrected when equal variance is assumed or when the design of the study is simple (2 groups). For complex designs ( $> 2$  groups) without the assumption of equal variance, there is now also an approximate approach to correcting bias from Bonett.

Corrections for bias produce a long-run reduction in average bias. Corrections for bias are approximate.

### How are $d$ and its CI calculated?:

*When equal variance is assumed:*

When equal variance is assumed, the standardized mean difference is  $d_s$ , defined in Kline, p. 196:

$$d_s = \frac{\psi}{sd_{pooled}}$$

where  $\psi$  is defined in Kline, equation 7.8:

$$\psi = \sum_{i=1}^a c_i M_i$$

and where  $sd_{pooled}$  is defined in Kline, equation 3.11

$$sd_{pooled} = \frac{\sum_{i=1}^a (n_i - 1) s_i^2}{\sum_{i=1}^a (n_i - 1)}$$

The CI for  $d_s$  is derived from lambda-prime transformation from Lecoutre, 2007 with code adapted from Cousineau & Goulet-Pelletier, 2020. Kelley, 2007 explains the general approach for linear contrasts.

This approach to generating the CI is 'exact', meaning coverage should be as desired *if* all assumptions are met (ha!).

Correction of upward bias can be applied.

*When equal variance is not assumed:*

When equal variance is not assumed, the standardized mean difference is  $d_{avg}$ , defined in Bonett, equation 6:

$$d_{avg} = \frac{\psi}{sd_{avg}}$$

Where  $sd_{avg}$  is the square root of the average of the group variances, as given in Bonett, explanation of equation 6:

$$sd_{avg} = \sqrt{\frac{\sum_{i=1}^a s_i^2}{a}}$$

*If only 2 groups:*

- The CI is derived from lambda-prime transformation using  $df$  and  $se$  from Huynh, 1989 – see especially Delacre et al., 2021
- This is also an 'exact' approach, and correction can be applied

*If more than 2 groups:*

- CI is approximated using the approach from Bonett, 2008
- An approximate correction developed by Bonett is used



## References

- Bonett D. G. (2023). statspsych: Statistical Methods for Psychologists. R package version 1.4.0. <https://dgbonett.github.io/statspsych>
- Bonett, D. G. (2018). R code posted to personal website (now removed). Formally at <https://people.ucsc.edu/~dgbonett/>
- Bonett, D. G. (2008). Confidence Intervals for Standardized Linear Contrasts of Means. *Psychological Methods*, 13(2), 99–109. doi:10.1037/1082989X.13.2.99
- Cousineau & Goulet-Pelletier (2020) <https://osf.io/preprints/psyarxiv/s2597>
- Delacre et al., 2021, <https://osf.io/preprints/psyarxiv/tu6mp/>
- Huynh, C.-L. (1989). A unified approach to the estimation of effect size in meta-analysis. NBER Working Paper Series, 58(58), 99–104.
- Kelley, K. (2007). Confidence intervals for standardized effect sizes: Theory, application, and implementation. *Journal of Statistical Software*, 20(8), 1–24. doi:10.18637/jss.v020.i08
- Lecoutre, B. (2007). Another Look at the Confidence Intervals for the Noncentral T Distribution. *Journal of Modern Applied Statistical Methods*, 6(1), 107–116. doi:10.22237/jmasm/1177992600

## See Also

- [estimate\\_mdif\\_ind\\_contrast](#) for friendly version that also returns raw score effect sizes for this design

## Examples

```
# Example from Kline, 2013
# Data in Table 3.4
# Worked out in Chapter 7
# See p. 202, non-central approach
# With equal variance assumed and no correction, should give:
# d_s = -0.8528028 [-2.121155, 0.4482578]

res <- esci::CI_smd_ind_contrast(
  means = c(13, 11, 15),
  sds = c(2.738613, 2.236068, 2.000000),
  ns = c(5, 5, 5),
  contrast = contrast <- c(1, 0, -1),
  conf_level = 0.95,
  assume_equal_variance = TRUE,
  correct_bias = FALSE
)

# Example from [statspsych::ci.lc.stdmean.bs()] should give:
# Estimate      SE      LL      UL
# Unweighted standardizer: -1.273964 0.3692800 -2.025039 -0.5774878
# Weighted standardizer:   -1.273964 0.3514511 -1.990095 -0.6124317
# Group 1 standardizer:    -1.273810 0.4849842 -2.343781 -0.4426775
```

```

res <- esci::CI_smd_ind_contrast(
  means = c(33.5, 37.9, 38.0, 44.1),
  sds = c(3.84, 3.84, 3.65, 4.98),
  ns = c(10,10,10,10),
  contrast = c(.5, .5, -.5, -.5),
  conf_level = 0.95,
  assume_equal_variance = FALSE,
  correct_bias = TRUE
)

```

---

CI\_smd\_one

*Estimate standardized mean difference (Cohen's d1) for a single group*


---

### Description

CI\_smd\_one STILL NEEDS WORK TO VERIFY APPROACH FOR SE and MoE

### Usage

```
CI_smd_one(mean, sd, n, reference_mean, conf_level = 0.95, correct_bias = TRUE)
```

### Arguments

mean	Mean for a single group for the outcome measure
sd	Standard deviation, > 0
n	Sample size, an integer > 2
reference_mean	defaults to 0
conf_level	The confidence level for the confidence interval, in decimal form. Defaults to 0.95.
correct_bias	Defaults to TRUE

### Value

Returns a list with these named elements:

- effect\_size - the point estimate from the sample
- lower - lower bound of the CI
- upper - upper bound of the CI
- numerator - the numerator for Cohen's d\_biased; the mean difference in the contrast
- denominator - the denominator for Cohen's d\_biased; if equal variance is assumed this is sd\_pooled, otherwise sd\_avg
- df - the degrees of freedom used for correction and CI calculation

- se - the standard error of the estimate; **warning** not totally sure about this yet
- moe - margin of error; 1/2 length of the CI
- d\_biased - Cohen's d without correction applied
- properties - a list of properties for the result

#### Properties

- effect\_size\_name - if equal variance assumed d\_s, otherwise d\_avg
- effect\_size\_name\_html - html representation of d\_name
- denominator\_name - if equal variance assumed sd\_pooled otherwise sd\_avg
- denominator\_name\_html - html representation of denominator name
- bias\_corrected - TRUE/FALSE if bias correction was applied
- message - a message explaining denominator and correction status
- message\_html - html representation of message

#### Examples

```
# example code
res <- esci::CI_smd_one(24.5, 3.65, 40, 20)
```

---

data\_altruism\_happiness

*Altruism Happiness - Ch12 - from Brethel-Haurwitz and Marsh (2014)*

---

#### Description

Happiness may not be important just for the person feeling it; happiness may also promote kind, altruistic behavior. Brethel-Haurwitz and Marsh (2014) examined this idea by collecting data on U.S. states. A Gallup poll in 2010 was used to measure each state's well-being index, a measure of mean happiness for the state's residents on a scale from 0 to 100. Next, a kidney donation database for 1999-2010 was used to figure out each state's rate (number of donations per 1 million people) of non-directed kidney donations-that's giving one kidney to a stranger, an extremely generous and altruistic thing to do!

#### Usage

data\_altruism\_happiness

**Format**

data\_altruism\_happiness:

A data frame with 50 rows and 6 columns:

**State** factor - State where data was collected

**Abbreviation** factor - State where data was collected

**Well\_Being\_2010** numeric - State where data was collected

**Well\_Being\_2013** numeric - State where data was collected

**Kidney\_Rate, per million population** numeric - State where data was collected

**WB Change 2013-2010** numeric - State where data was collected

**Source**

<https://journals.sagepub.com/doi/full/10.1177/0956797613516148>

---

data\_anchor\_estimate\_ma

*Anchor Estimate ma - Ch9 - Many Labs replications of Jacowitz and Kahneman (1995)*

---

**Description**

To what extent does the wording of a question influence one's judgment? In their classic study, Jacowitz and Kahneman (1995) asked participants to estimate how many babies are born each day in the United States. Participants were given either a low anchor (more than 100 babies/day) or a high anchor (less than 50,000 babies/day). Those who saw the low anchor estimated many fewer births/day than those who saw the high anchor, which suggests that the wording can have a profound influence. The correct answer, as it happens, is ~11,000 births/day in 2014. To investigate the extent that these results are replicable, the Many Labs project repeated this classic study at many different labs around the world. You can find the summary data for 30 of these labs in the Anchor Estimate ma data file

**Usage**

data\_anchor\_estimate\_ma

**Format**

data\_anchor\_estimate\_ma:

A data frame with 30 rows and 9 columns:

**Location** factor

**M Low** numeric

**s Low** numeric

**n Low** integer

**M High** numeric

**s High** numeric  
**n High** integer  
**USAorNot** factor  
**Country** factor

### Source

<https://econtent.hogrefe.com/doi/10.1027/1864-9335/a000178>

---

data\_basol\_badnews      *Basol badnews - Ch07 - from Basol et al. (2020)*

---

### Description

Climate change? Vaccines? Fake news and conspiracy theories on these and numerous other issues can be highly damaging, but are thriving in this social media age. Trying to debunk a conspiracy theory by presenting facts and evidence often doesn't work, alas. Psychological inoculation, also similar to prebunking, presents a mild form of misinformation, preferably with explanation, in the hope of building resistance to real-life fake news—a sort of vaccine for fake news. The Bad News game is a spin-off from research on psychological inoculation. Basol et al. (2020) assessed the possible effectiveness of this game as a fake news vaccine. At [getbadnews.com](http://getbadnews.com) you can click 'About' for information, or just start playing the game— it's easy and maybe even fun. You encounter mock Twitter (now X) fake news messages that illustrate common strategies for making fake news memorable or believable. You make choices between messages and decide which ones to 'forward' as you try to spread fake news while building your credibility score and number of 'followers'— rather like real life for a conspiracy theorist wanting to spread the word. Compete with your friends for credibility and number of followers. Basol's online participants first saw 18 fictitious fake news tweets and rated each for reliability (accuracy, believability), and also rated their confidence in that reliability rating. Both ratings were on a 1 to 7 scale. Those in the BadNews group then played the game for 15 minutes, whereas those in the Control group played Tetris. Then all once again gave reliability and confidence ratings for the 18 tweets.

### Usage

data\_basol\_badnews

### Format

data\_basol\_badnews:  
 A data frame with 198 rows and 3 columns:  
**Diff reliability** numeric  
**Diff confidence** numeric  
**Condition** factor

### Source

<https://journalofcognition.org/articles/10.5334/joc.91>

---

`data_bem_psychic`*Bem Psychic - Ch13 - from Bem and Honorton (1994)*

---

### Description

Daryl Bem was an experienced mentalist and research psychologist, who, a decade earlier, had been one of several outside experts invited to scrutinize the laboratory and experimental procedures of parapsychology researcher Charles Honorton. Bem not only judged them adequate, but joined the research effort and became a coauthor with Honorton. Bem and Honorton (1994) first reviewed early ganzfeld studies and described how the experimental procedure had been improved to reduce the chance that results could be influenced by various possible biases, or leakages of information from sender to receiver. For example, the randomization procedure was carried out automatically by computer, and all stimuli were presented under computer control. Bem and Honorton then presented data from studies conducted with the improved procedure. Table 13.1 presents basic data from 10 studies reported by Bem and Honorton (1994). Participants each made a single judgment, so in Pilot 1, for example, 22 participants responded, with 8 of them giving a correct response. Three pilot studies helped refine the procedures, then four studies used novice receivers. Study 5 used 20 students of music, drama, or dance as receivers, in response to suggestions that creative people might be more likely to show telepathy. Studies 6 and 7 used receivers who had participated in an earlier study. The proportion of hits expected by chance is .25, and Table 13.1 shows that all but Study 1 found proportions higher than .25.

### Usage

`data_bem_psychic`

### Format

`data_bem_psychic:`

A data frame with 10 rows and 5 columns:

**Study** factor**Participants** factor**N(Trials)** integer**N(Hits)** integer**Proportion Hits** numeric

### Source

<https://psycnet.apa.org/record/1994-20286-001>

---

data_bodywellf	<i>BodyWellF - Ch12 - Body Satisfaction and Well-being data for females from Figure 11.24 right panel</i>
----------------	---

---

**Description**

A subset of data\_bodywell\_fm, reports only for those participants who identified as female. Data is Subjective Wellbeing and Body Satisfaction.

**Usage**

data\_bodywellf

**Format**

data\_bodywellf:

A data frame with 59 rows and 2 columns:

**Body Satisfaction** numeric

**Well-being** numeric

---

data_bodywellfm	<i>BodyWellFM - Ch12 - Body Satisfaction and Well-being data from Figure 11.1</i>
-----------------	---

---

**Description**

Survey data from a convenience sample Dominican University students. Reported are measures of Subjective Wellbeing and Body Satisfaction.

**Usage**

data\_bodywellfm

**Format**

data\_bodywellfm:

A data frame with 106 rows and 2 columns:

**Body Satisfaction** numeric

**Well-being** numeric

---

data_bodywellm	<i>BodyWellM - Ch12 - Body Satisfaction and Well-being data for males from Figure 11.24 left panel</i>
----------------	--

---

**Description**

A subset of data\_bodywell\_fm, reports only for those participants who identified as male. Data is Subjective Wellbeing and Body Satisfaction.

**Usage**

data\_bodywellm

**Format**

data\_bodywellm:

A data frame with 47 rows and 2 columns:

**Body Satisfaction** numeric

**Well-being** numeric

---

data\_campus\_involvement

*Campus Involvement - Ch11 - for End-of-Chapter Exercise 11.7*

---

**Description**

Clinton conducted a survey of college students to determine the extent to which subjective well-being is related to campus involvement (Campus Involvement data set on the book website). Participants completed a measure of subjective well-being (scale from 1 to 5) and a measure of campus involvement (scale from 1 to 5). Participants also reported gender (male or female) and commuter status (resident or commuter). Synthetic data simulated to mimic survey data from a class project.

**Usage**

data\_campus\_involvement

**Format**

data\_campus\_involvement:

A data frame with 113 rows and 6 columns:

**ID** integer

**Gender** factor

**GPA** numeric

**CommuterStatus** factor

**SWB** numeric

**Campus Involvement** numeric



---

 data\_chap\_8\_paired\_ex\_8.18

*Fictitious data from an unrealistically small HEAT study comparing scores for a single group of students before and after a workshop on climate change.*

---

### Description

*Fictitious* data from an unrealistically small HEAT study comparing scores for a single group of students before and after a workshop on climate change.

### Usage

data\_chap\_8\_paired\_ex\_8.18

### Format

data\_chap\_8\_paired\_ex\_8.18:

A data frame with 8 rows and 2 columns:

**Before** numeric

**After** numeric

---

 data\_clean\_moral

*Clean moral - Ch07 - from Schnall et al. (2008), Study 1, and Johnson et al. (2014)*

---

### Description

Some researchers claim that moral judgments are based not only on rational considerations but also on one's current emotional state. To what extent can recent emotional experiences influence moral judgments? Schnall et al. (2008) examined this question by manipulating feelings of cleanliness and purity and then observing the extent that this changes how harshly participants judge the morality of others. In Study 1, Schnall et al. asked participants to complete a word scramble task with either neutral words (neutral prime) or words related to cleanliness (cleanliness prime). All students then completed a set of moral judgments about controversial scenarios: Moral judgment is the average of six items, each rated on a scale from 0 to 9, with high meaning harsh. The data from this study are in the Clean moral file, which also contains data from a replication by Johnson et al. (2014)

### Usage

data\_clean\_moral

**Format**

data\_clean\_moral:

A data frame with 208 rows and 4 columns:

**Schnall Condition** factor

**Schnall Moral judgment** numeric

**Johnson Condition** factor

**Johnson Moral judgment** numeric

**Source**

<https://econtent.hogrefe.com/doi/full/10.1027/1864-9335/a000186>

---

data\_college\_survey\_1 *College survey 1 - Ch03 - for End-of-Chapter Exercise 3.3*

---

**Description**

Data from an additional survey of Dominican University students; reports various psychological and behavioral measures.

**Usage**

data\_college\_survey\_1

**Format**

data\_college\_survey\_1:

A data frame with 243 rows and 23 columns:

**ID** integer

**Gender** factor

**Gender\_Code** factor

**Age** integer

**Shool\_Year** factor

**School\_Year\_Code** factor

**Transfer** factor

**Transfer\_Code** logical

**Student\_Athlete** factor

**Student\_Athlete\_Code** logical

**Wealth\_SR** numeric

**GPA** numeric

**ACT** integer

**Subjective\_Well\_Being** numeric

**Positive\_Affect** numeric

**Negative\_Affect** numeric  
**Relationship\_Confidence** numeric  
**Exercise** numeric  
**Academic\_Motivation\_Intrinsic** numeric  
**Academic\_Motivation\_Extrinsic** numeric  
**Academic\_Motivation\_Amotivation** numeric  
**Intelligence\_Value** numeric  
**Raven\_Score** numeric

---

data\_college\_survey\_2 *College survey 2 - Ch05 - for End-of-Chapter Exercise 5.4*

---

### Description

College survey 2 - Ch05 - for End-of-Chapter Exercise 5.4

### Usage

data\_college\_survey\_2

### Format

data\_college\_survey\_2:  
A data frame with 138 rows and 17 columns:  
**ID** integer  
**Gender** factor  
**Gender\_Code** factor  
**Age** numeric  
**Wealth\_SR** numeric  
**School\_Year** factor  
**School\_Year\_Code** factor  
**Transfer** factor  
**Transfer\_Code** logical  
**GPA** numeric  
**Subjective\_Well\_Being** numeric  
**Positive\_Affect** numeric  
**Negative\_Affect** numeric  
**Academic\_Engagement** numeric  
**Religious\_Meaning** numeric  
**Health** numeric  
**Emotion\_Recognition** factor

---

data_damischrcj	<i>DamischRCJ - Ch9 - from 6 Damisch studies, and Calin-Jageman and Caldwell (2014)</i>
-----------------	---

---

### Description

DamischRCJ - Ch9 - from 6 Damisch studies, and Calin-Jageman and Caldwell (2014)

### Usage

data\_damischrcj

### Format

data\_damischrcj:  
 A data frame with 8 rows and 5 columns:  
**Study** factor  
**Cohen's d unbiased** numeric  
**n Control** integer  
**n Lucky** integer  
**Research Group** factor

---

data_effronraj_fakenews	<i>EffronRaj fakenews - Ch8 - from Effron and Raj (2020)</i>
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---

### Description

*Synthetic data* meant to represent Experiment 1 of Effron & Raj, 2020. 138 U.S. adults, recruited in August 2018 on Prolific Academic, worked online. First, they saw six fake headlines four times, each time being asked to rate how interesting/engaging/ funny/well-written the headline was. This rating task simply ensured that the participants paid some attention to each headline. The stimuli were 12 actual fake-news headlines about American politics, with accompanying photographs. Half appealed to Republicans and half to Democrats. Later, 12 fake headlines were presented one at a time, a random mix of the six Old headlines-those seen before-and six New headlines not seen previously. It was stated very clearly that independent, non-partisan fact-checking had established that all the headlines were not true. Participants first rated, on a 0 (not at all) to 100 (extremely) scale, the degree to which to which they judged it unethical to publish that headline. That's the Unethicality DV. They also rated how likely they would be to share the headline if they saw it posted by an acquaintance on social media; there were three further similar ratings. Finally, they rated how accurate they believed the headline to be.

### Usage

data\_effronraj\_fakenews

**Format**

data\_effronraj\_fakenews:  
A data frame with 138 rows and 5 columns:

**ID** factor  
**UnethOld** numeric  
**UnethNew** numeric  
**AccurOld** numeric  
**AccurNew** numeric

**Source**

<https://journals.sagepub.com/doi/full/10.1177/0956797619887896>

---

data\_emotion\_hearttrate

*Emotion hearttrate - Ch8 - from Lakens (2013)*

---

**Description**

Anger is a powerful emotion. To what extent can feeling angry actually change your heart rate? To investigate, Lakens (2013) asked students to record their heart rate (in beats per minute) at rest before (baseline) and then while recalling a time of intense anger. This is a conceptual replication of a classic study by Ekman et al. (1983). Load the Emotion hearttrate data set from the book website.

**Usage**

data\_emotion\_hearttrate

**Format**

data\_emotion\_hearttrate:  
A data frame with 68 rows and 3 columns:

**ID** integer  
**HR\_baseline** numeric  
**HR\_anger** numeric

**Source**

<https://ieeexplore.ieee.org/abstract/document/6464255>

---

data_exam_scores	<i>Exam Scores - Ch11 - for End-of-Chapter Exercise 11.2</i>
------------------	--

---

### Description

To what extent does initial performance in a class relate to performance on a final exam? First exam and final exam scores for nine students enrolled in an introductory psychology course. Exam scores are percentages, where 0 = no answers correct and 100 = all answers correct. Data is synthetic to represent patterns found in a previous psych stats course.

### Usage

data\_exam\_scores

### Format

data\_exam\_scores:

A data frame with 9 rows and 3 columns:

**StudentID** factor

**First Exam** numeric

**Final Exam** numeric

---

data_flag_priming_ma	<i>Flag Priming ma - Ch9 - Many Labs replications of Carter et al. (2011)</i>
----------------------	---

---

### Description

To what extent does being exposed to the American flag influence political attitudes? One seminal study (Carter et al., 2011) explored this issue by subtly exposing participants either to images of the American flag or to control images. Next, participants were asked about their political attitudes, using a 1-7 rating scale where high scores indicate conservative attitudes. Participants exposed to the flag were found to express substantially more conservative attitudes. The Many Labs project replicated this finding at 25 different locations in the United States.

### Usage

data\_flag\_priming\_ma

**Format**

data\_flag\_priming\_ma:  
 A data frame with 25 rows and 7 columns:  
**Location** factor  
**M Flag** numeric  
**s Flag** numeric  
**n Flag** integer  
**M Noflag** numeric  
**s Noflag** numeric  
**n Noflag** integer

**Source**

<https://openpsychologydata.metajnl.com/articles/10.5334/jopd.ad>

---

data\_gender\_math\_iat    *Gender math IAT - Ch07 - Ithaca and SDSU replications of Nosek et al. (2002)*

---

**Description**

To what extent do men and women differ in their attitudes towards mathematics? To investigate, Nosek et al. (2002) asked male and female students to complete an Implicit Association Test (IAT)- this is a task designed to measure a participant's implicit (non-conscious) feelings towards a topic. (If you've never heard of the IAT, try it out here: [tiny.cc/harvardiat](http://tiny.cc/harvardiat)) On this IAT, students were tested for negative feelings towards mathematics and art. Scores reflect the degree to which a student had more negative implicit attitudes about mathematics than art (positive score: more negative feelings about mathematics; 0: same level of negativity to both; negative score: more negative feelings about art). data\_gender\_math\_iat has data from two labs that participated in a large-scale replication of the original study (Klein et al., 2014a, 2014b)

**Usage**

data\_gender\_math\_iat

**Format**

data\_gender\_math\_iat:  
 A data frame with 155 rows and 4 columns:  
**Ithaca gender** factor  
**Ithaca IAT** numeric  
**SDSU gender** factor  
**SDSU IAT** numeric

**Source**

<https://psycnet.apa.org/fulltext/2014-20922-002.html>

---

data\_gender\_math\_iat\_ma

*Gender math IAT ma - Ch9 - Many Labs replications of Nosek et al. (2002)*

---

### Description

In EOC Exercise 4 in Chapter 7 we encountered the classic study of Nosek et al. (2002), in which male and female participants completed an Implicit Association Test (IAT) that measured the extent of negative attitudes towards mathematics, compared with art. The study found that women, compared with men, tended to have more negative implicit attitudes towards mathematics. The Many Labs project repeated this study at locations around the world (Klein et al., 2014a, 2014b). Summary data for 30 of these labs are available in Gender math IAT ma. Higher scores indicate more implicit bias against mathematics. See also data\_gender\_math\_iat for raw data from two specific sites from this replication effort.

### Usage

data\_gender\_math\_iat\_ma

### Format

data\_gender\_math\_iat\_ma:  
A data frame with 30 rows and 9 columns:

**Location** factor

**M Male** numeric

**s Male** numeric

**n Male** integer

**M Female** numeric

**s Female** numeric

**n Female** integer

**USAorNot** factor

**Country** factor

### Source

<https://psycnet.apa.org/fulltext/2014-20922-002.html>



---

`data_halagappa`*Halagappa - Ch14 - from Halagappa et al. (2007)*

---

**Description**

Could eating much less delay Alzheimer's? If so, that would be great news. Halagappa et al. (2007) investigated the possibility by using a mouse model, meaning they used Alzheimer-prone mice, which were genetically predisposed to develop neural degeneration typical of Alzheimer's. The researchers used six independent groups of mice, three tested in mouse middle age when 10 months old, and three in mouse old age when 17 months. At each age there was a control group of normal mice that ate freely (the NFree10 and NFree17 groups), a group of Alzheimer-prone mice that also ate freely (the AFree10 and AFree17 groups), and another Alzheimer-prone group restricted to 40% less food than normal (the ADiet10 and ADiet17 groups). Table 14.2 lists the factors that define the groups, and group labels. I'll discuss one measure of mouse cognition: the percent time spent near the target of a water maze, with higher values indicating better learning and memory. Table 14.2 reports the means and standard deviations for this measure, and group sizes.

**Usage**`data_halagappa`**Format**`data_halagappa:`

A data frame with 6 rows and 4 columns:

**Groups** factor**Mean** numeric**SD** numeric**n** integer**Source**<https://www.sciencedirect.com/science/article/abs/pii/S0969996106003251>

---

`data_home_prices`*Home Prices - Ch12 - for End-of-Chapter Exercise 12.2*

---

**Description**

Maybe you're thinking about buying a house after college? Regression can help you hunt for a bargain. Download the Home Prices data set. This file contains real estate listings from 1997 to 2003 in a city in California. Let's explore the extent to which the size of the home (in square meters) predicts the sale price.

**Usage**

```
data_home_prices
```

**Format**

```
data_home_prices:
A data frame with 300 rows and 8 columns:
MLS integer
Location factor
Price integer
Bedrooms integer
Bathrooms integer
Size (m2) numeric
Status factor
Status_Code logical
```

---

```
data_kardas_expt_3    Kardas Expt 3 - Ch07 - from Kardas and O'Brien (2018), Experiment
                      3
```

---

**Description**

Suppose you want to change the battery in your phone, cook the perfect soufflé, or perform a three-ball juggle. Just as numerous people do every day, you might search online to find a video that shows what to do. Suppose you watch such a video just once. First question: How well would you then predict you could perform the task? Second question: How well would you actually perform the task, the first time you tried? Now suppose you watch the video many times: Again consider the two questions. These questions were investigated in a series of studies by Kardas and O'Brien (2018). Let's first do some quick analyses of Kardas Experiments 3 and 4—let's call them Expt 3 and Expt 4—focusing on the effect of watching a video many times rather than once. In Expt 3, participants first watched a brief video of a person performing the moonwalk. The Low Exposure group watched the video once, the High Exposure group 20 times. Then participants predicted, on a 1 to 10 scale, how well they felt they would be able to perform the moonwalk themselves. Finally, they attempted a single performance of the moonwalk, which was videoed. These videos were rated, on the same 1 to 10 scale, by independent raters.

**Usage**

```
data_kardas_expt_3
```

**Format**

```
data_kardas_expt_3:
A data frame with 100 rows and 3 columns:
Exposure factor
Prediction numeric
Performance numeric
```

**Source**

<https://journals.sagepub.com/doi/abs/10.1177/0956797617740646>

---

data_kardas_expt_4	<i>Kardas Expt 4 - Ch07 - from Kardas and O'Brien (2018), Experiment 4</i>
--------------------	--

---

**Description**

Suppose you want to change the battery in your phone, cook the perfect souffle, or perform a three-ball juggle. Just as numerous people do every day, you might search online to find a video that shows what to do. Suppose you watch such a video just once. First question: How well would you then predict you could perform the task? Second question: How well would you actually perform the task, the first time you tried? Now suppose you watch the video many times: Again consider the two questions. These questions were investigated in a series of studies by Kardas and O'Brien (2018). Let's first do some quick analyses of Kardas Experiments 3 and 4-let's call them Expt 3 and Expt 4-focusing on the effect of watching a video many times rather than once. Expt 4 was conducted online with participants recruited from Amazon's Mechanical Turk, who are typically more diverse than students. The online task was based on a mirror-drawing game developed by Bob and students (Cusack et al., 2015, [tiny.cc/bobmirrortrace](http://tiny.cc/bobmirrortrace)). Participants first read a description of the game and the scoring procedure. To play, you use your computer trackpad to trace a target line, as accurately and quickly as you can. The task is tricky because you can see only a mirror image of the path you are tracing with a finger on the trackpad. A running score is displayed. The final score is the percentage match between the target line and the path you traced, so scores can range from 0 to 100

**Usage**

data\_kardas\_expt\_4

**Format**

data\_kardas\_expt\_4:

A data frame with 270 rows and 4 columns:

**Exposure** factor

**Prediction** integer

**Performance** integer

**Time** numeric

**Source**

<https://journals.sagepub.com/doi/abs/10.1177/0956797617740646>

---

data\_labels\_flavor      *Labels flavor - Ch8 - from Floretta-Schiller et al. (2015)*

---

### Description

To what extent do brand labels influence perceptions of a product? To investigate, participants were asked to participate in a taste test. All participants were actually given the same grape juice, but one glass was poured from a bottle labeled 'Organic' and the other glass from a bottle labeled 'Generic'. After each tasting (in counterbalanced order), participants were asked to rate how much they enjoyed the juice on a scale from 1 (not at all) to 10 (very much). Participants were also asked to say how much they'd be willing to pay for a large container of that juice on a scale from \$1 to \$10. Load the Labels flavor data set from the book website. These data were collected as part of a class project by Floretta-Schiller et al. (2015), whose work was inspired by a very clever study looking at the effects of fast-food wrappers on children's enjoyment of food (Robinson et al., 2007).

### Usage

data\_labels\_flavor

### Format

data\_labels\_flavor:

A data frame with 51 rows and 6 columns:

**ParticipantID** integer

**Enjoy\_Generic** numeric

**Enjoy\_Organic** numeric

**Pay\_Generic** numeric

**Pay\_Organic** numeric

**Suspicious** logical

---

data\_latimier\_3groups      *Latimier 3Groups - Ch14 - 3 groups in Latimier et al. (2019)*

---

### Description

The researchers were interested in how different study approaches might impact learning. Working in France, they created three independent groups, each comprising 95 adults. Participants worked online through seven learning modules about DNA. The Reread group worked through a module, then worked through it a second time before going on to the next module. The Quiz group worked through a module, then had to complete a quiz before going on to the next module. The Prequiz group had to work through the quiz before seeing the presentation of a module, then went on to the quiz and presentation of the next module. Participants received feedback and a brief explanation after answering each question in a quiz, and could take as long as they wished to work through each module and quiz. Seven days later, participants completed a final test. data\_latimier\_3groups

is the full data set. To facilitate different student exercises, there are also separate data entities for each group (data\_latimier\_prequiz, data\_latimier\_reread, etc.), and for every *pair* of groups (data\_latimier\_quiz\_prequiz, etc.).

### Usage

```
data_latimier_3groups
```

### Format

```
data_latimier_3groups:
```

A data frame with 285 rows and 3 columns:

**Group** factor

**Test%** numeric

**Time** numeric

---

data\_latimier\_prequiz *Latimier Prequiz - Ch03 - Prequiz group in Latimier et al. (2019)*

---

### Description

Just the Prequiz group from Latimier et al., 2019 See full details in data\_latimier\_3\_groups

### Usage

```
data_latimier_prequiz
```

### Format

```
data_latimier_prequiz:
```

A data frame with 95 rows and 3 columns:

**Group** factor

**Test%** numeric

**Time** numeric

### Source

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/XPYPMF>

---

data\_latimier\_quiz      *Latimier Quiz - Ch03 - Quiz group in Latimier et al. (2019)*

---

**Description**

Just the Quiz group from Latimier et al., 2019 See full details in data\_latimier\_3\_groups

**Usage**

data\_latimier\_quiz

**Format**

data\_latimier\_quiz:  
A data frame with 95 rows and 3 columns:  
**Group** factor  
**Test%** numeric  
**Time** numeric

**Source**

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/XPYPMF>

---

data\_latimier\_quiz\_prequiz  
*Latimier Quiz Prequiz - Ch07 - Quiz and Prequiz groups in Latimier et al. (2019)*

---

**Description**

Just the Quiz (RQ) an Prequiz (QR) groups from Latimier et al., 2019 See full details in data\_latimier\_3\_groups

**Usage**

data\_latimier\_quiz\_prequiz

**Format**

data\_latimier\_quiz\_prequiz:  
A data frame with 190 rows and 3 columns:  
**Group** factor  
**Test%** numeric  
**Time** numeric

**Source**

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/XPYPMF>

---

data\_latimier\_reread *Latimier Reread - Ch03 - Reread group in Latimier et al. (2019)*

---

**Description**

Just the Reread group from Latimier et al., 2019 See full details in data\_latimier\_3\_groups

**Usage**

data\_latimier\_reread

**Format**

data\_latimier\_reread:  
A data frame with 95 rows and 3 columns:  
**Group** factor  
**Test%** numeric  
**Time** numeric

**Source**

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/XPYPMF>

---

data\_latimier\_reread\_prequiz  
*Latimier Reread Prequiz - Ch07 - Reread and Prequiz groups in Latimier et al. (2019)*

---

**Description**

Just the Reread (RR) an Prequiz (QR) groups from Latimier et al., 2019 See full details in data\_latimier\_3\_groups

**Usage**

data\_latimier\_reread\_prequiz

**Format**

data\_latimier\_reread\_prequiz:  
A data frame with 190 rows and 3 columns:  
**Group** factor  
**Test%** numeric  
**Time** numeric

**Source**

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/XPYPMF>

---

data\_latimier\_reread\_quiz

*Latimier Reread Quiz - Ch07 - Reread and Quiz groups in Latimier et al. (2019)*

---

### Description

Just the Reread Quiz groups from Latimier et al., 2019 See full details in data\_latimier\_3\_groups

### Usage

data\_latimier\_reread\_quiz

### Format

data\_latimier\_reread\_quiz:

A data frame with 190 rows and 3 columns:

**Group** factor

**Test%** numeric

**Time** numeric

### Source

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/XPYPMF>

---

data\_macnamara\_r\_ma *Macnamara r ma - Ch11 - from Macnamara et al. (2014)*

---

### Description

Is genius born or made? Could any of us be Michael Jordan or Mozart if we worked sufficiently hard to develop the requisite skills? Meta-analysis of correlations can help answer such questions. The issue here is the extent that practice and effort may be sufficient for achieving the highest levels of expertise. Ericsson et al. (1993) argued that years of effort is what matters most: 'Many characteristics once believed to reflect innate talent are actually the result of intense practice extended for a minimum of 10 years' (p. 363). This view was enormously popularized by Malcolm Gladwell (2008), who argued in his book *Outliers* that 10,000 hours of focused practice is the key to achieving expertise. However, this view is now being challenged, with one important contribution being a large meta-analysis of correlations between amount of intense practice and level of achievement: Macnamara et al. (2014) combined 157 correlations reported in a wide range of fields, from sports to music and education, and found correlation of only  $r = .35$  (.30, .39). Table 11.1 shows the 16 main correlations for music, from Macnamara et al. (2014).

### Usage

data\_macnamara\_r\_ma



**Format**

data\_macnamara\_r\_ma:

A data frame with 16 rows and 4 columns:

**Study** factor

**r** numeric

**N** integer

**Instrument\_Type** factor

**Source**

<https://journals.sagepub.com/doi/full/10.1177/0956797614535810>

---

data\_mccabemichael\_brain

*McCabeMichael brain - Ch9 - from Michael et al. (2013)*

---

**Description**

You've probably seen cross sections of the brain with brightly colored areas indicating which brain regions are most active during a particular type of cognition or emotion. Search online for fMRI (functional magnetic resonance imaging) brain scans to see such pictures and learn how they are made. They can be fascinating—are we at last able to see how thinking works? In 2008, McCabe and Castel published studies that investigated how adding a brain picture might alter judgments of the credibility of a scientific article. For one group of participants, an article was accompanied by a brain image that was irrelevant to the article. For a second, independent group, there was no image. Participants read the article, then gave a rating of the statement 'The scientific reasoning in the article made sense'. The response options were 1 (strongly disagree), 2 (disagree), 3 (agree), and 4 (strongly agree). The researchers reported that mean ratings were higher with a brain picture than without, but that the difference was small. It seemed that an irrelevant brain picture may have some, but only a small influence. The authors drew appropriately cautious conclusions, but the result quickly attracted attention and there were many media reports that greatly overstated it. At least according to the popular media, it seemed that adding a brain picture made any story convincing. Search on 'McCabe seeing is believing', or similar, to find media reports and blog posts. Some warned readers to watch out for brain pictures, which, they said, can trick you into believing things that aren't true. The result intrigued some New Zealander colleagues of mine who discovered that, despite its wide recognition, the finding hadn't been replicated. They ran replication studies using the materials used by the original researchers, and found generally small ESs. I joined the team at the data analysis stage and the research was published (Michael et al., 2013). I'll discuss here a meta-analysis of two of the original studies and eight replications by our team. The studies were sufficiently similar for meta-analysis, especially considering that all the Michael studies were designed to have many features that matched the original studies. This data set does *not* include two additional critique studies run by the Michael team. See also data\_mccabemichael\_brain2

**Usage**

data\_mccabemichael\_brain

**Format**

data\_mccabemichael\_brain:  
A data frame with 10 rows and 9 columns:  
**Study name** factor  
**M No Brain** numeric  
**s No Brain** numeric  
**n No Brain** numeric  
**M Brain** numeric  
**s Brain** numeric  
**n Brain** numeric  
**SimpleCritique** factor  
**Research group** factor

**Source**

<https://link.springer.com/article/10.3758/s13423-013-0391-6>

---

data\_mccabemichael\_brain2

*McCabeMichael brain2 - Ch9 - from Michael et al. (2013)*

---

**Description**

Same as data\_mccabemichael\_brain but includes two additional critique studies run by the Michael team.

**Usage**

data\_mccabemichael\_brain2

**Format**

data\_mccabemichael\_brain2:  
A data frame with 12 rows and 9 columns:  
**Study name** factor  
**M No Brain** numeric  
**s No Brain** numeric  
**n No Brain** numeric  
**M Brain** numeric  
**s Brain** numeric  
**n Brain** numeric  
**SimpleCritique** factor  
**Research group** factor

**Source**

<https://link.springer.com/article/10.3758/s13423-013-0391-6>

---

data\_meditationbrain *MeditationBrain - Ch15 - from Holzel et al. (2011)*

---

**Description**

My example is a well-known study of mindfulness meditation by Holzel et al. (2011). People who wanted to reduce stress, and were not experienced meditators, were assigned to a Meditation (n = 16) or a Control (n = 17) group. The Meditation group participated in 8 weeks of intensive training and practice of mindfulness meditation. The researchers used a questionnaire to assess a range of emotional and cognitive variables both before (Pretest) and after (Posttest) the 8-week period. All assessment was conducted while the participants were not meditating. The study is notable for including brain imaging to assess possible changes in participants' brains from Pretest to Posttest. The researchers measured gray matter concentration, which increases in brain regions that experience higher and more frequent activation. The researchers expected that the hippocampus may be especially responsive to meditation because it has been implicated in the regulation of emotion, arousal, and general responsiveness. They therefore included in their planned analysis the assessment of any changes to gray matter concentration in the hippocampus.

**Usage**

data\_meditationbrain

**Format**

data\_meditationbrain:

A data frame with 33 rows and 7 columns:

**Pretest** numeric

**Posttest** numeric

**Group** factor

**ControlPre** numeric

**ControlPost** numeric

**MeditationPre** numeric

**MeditationPost** numeric

**Source**

[https://link.springer.com/chapter/10.1007/978-94-007-2079-4\\_9](https://link.springer.com/chapter/10.1007/978-94-007-2079-4_9)

---

data_organicmoral	<i>OrganicMoral - Ch14 - from Eskine (2013)</i>
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---

## Description

To what extent might choosing organic foods make us morally smug? To investigate, Eskine (2013) asked participants to rate images of organic food, neutral (control) food, or comfort food. Next, under the guise of a different study, all participants completed a moral judgment scale in which they read different controversial scenarios and rated how morally wrong they judged them to be (scale of 1-7, high judgments mean more wrong). Table 14.7 shows summary data, which are also available in the first four variables in the *OrganicMoral* file. In that file you can see two further variables, which report full data—we'll come to these shortly. Here we use the summary data. After the results of Eskine (2013) were published, Moery and Calin-Jageman (2016) conducted a series of close replications. We obtained original materials from Eskine, piloted the procedure, and preregistered our sampling and analysis plan. The OSF page, [osf.io/atkn7](https://osf.io/atkn7), has all the details. The data from one of these close replications are in the last two variables of the *OrganicMoral* file. For this replication study, group names are in the variable *ReplicationGroup* and moral judgments in *MoralJudgment*. (You may need to scroll right to see these variables.)

## Usage

```
data_organicmoral
```

## Format

```
data_organicmoral:
```

A data frame with 106 rows and 6 columns:

**Group** factor

**Mean** numeric

**SD** numeric

**N** integer

**ReplicationGroup** factor

**MoralJudgmentment** numeric

## Source

<https://journals.sagepub.com/doi/full/10.1177/1948550616639649>

---

data_penlaptop1	<i>% transcription scores from pen and laptop group of Mueller et al., 2014</i>
-----------------	---

---

**Description**

*% transcription scores from pen and laptop group of Mueller et al., 2014*

**Usage**

data\_penlaptop1

**Format**

data\_penlaptop1:

A data frame with 65 rows and 2 columns:

**condition** factor

**transcription** numeric

**Source**

<https://journals.sagepub.com/doi/full/10.1177/0956797614524581>

---

data_powerperformance_ma
--------------------------

*PowerPerformance ma - Ch9 - from Burgmer and Englich (2012), and Cusack et al. (2015)*

---

**Description**

To what extent could feeling powerful affect your performance at motor skills? To investigate, Burgmer and Englich (2012) assigned German participants to either power or control conditions and then asked them to play golf (Experiment 1) or darts (Experiment 2). They found that participants manipulated to feel powerful performed substantially better than those in the control condition. To study this finding further, Cusack et al. (2015) conducted five replications in the United States. Across these replications they tried different ways of manipulating power, different types of tasks (golf, mirror tracing, and a cognitive task), different levels of difficulty, and different types of participant pools (undergraduates and online). Summary data from all seven studies are available in PowerPerformance ma.

**Usage**

data\_powerperformance\_ma

**Format**

data\_powerperformance\_ma:

A data frame with 8 rows and 12 columns:

**StudyName** factor

**Country** factor

**Population** factor

**Difficulty** factor

**Task** factor

**M Control** numeric

**s Control** numeric

**M Power** numeric

**s Power** numeric

**Cohen d unb** numeric

**n Control** integer

**n Power** integer

**Source**

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0140806>

---

data\_rattanmotivation *RattanMotivation - Ch14 - from Rattan et al. (2012)*

---

**Description**

How do you think you would react to feedback that gave encouragement and reassurance, or, instead, encouragement and challenge? Carol Dweck and her colleagues have investigated many such questions about how people respond to different types of feedback. My next example comes from Dweck's research group and illustrates data analysis that starts with the full data, rather than only summary statistics. Rattan et al. (2012) asked their college student participants to imagine they were undertaking a mathematics course and had just received a low score (65%) on the first test of the year. Participants were assigned randomly into three groups, which received different feedback along with the low score. The Comfort group received positive encouragement and also reassurance, the Challenge group received positive encouragement and also challenge, and the Control group received just the positive encouragement. Participants then responded to a range of questions about how they felt about the course and their professor. I'll discuss data for their ratings of their own motivation toward mathematics, made after they had received the feedback.

**Usage**

data\_rattanmotivation

**Format**

data\_rattanmotivation:

A data frame with 54 rows and 2 columns:

**Group** factor

**Motivation** numeric

**Source**

<https://www.sciencedirect.com/science/article/pii/S0022103111003027>

---

data\_religionsharing *ReligionSharing - Ch14 - for End-of-Chapter Exercise 14.3*

---

**Description**

To what extent is a religious upbringing related to prosocial behavior in childhood? To investigate, a large international sample of children was asked to play a game in which they were given 10 stickers but then asked if they would give some of these stickers away to another child who had not been able to be tested that day. The number of stickers donated was considered a measure of altruistic sharing. In addition, the parents of each child reported the family's religion. Summary data provided.

**Usage**

```
data_religionsharing
```

**Format**

data\_religionsharing:

A data frame with 3 rows and 4 columns:

**Group** factor

**Mean** numeric

**SD** numeric

**N** integer

data\_religious\_belief *Religious belief - Ch03 - for End-of-Chapter Exercise 3.5*

---

### Description

Let's look at some data about religious beliefs. The Religious belief file has data from a large online survey in which participants were asked to report, on a scale from 0 to 100, their belief in the existence of God. Age was also reported.

### Usage

```
data_religious_belief
```

### Format

data\_religious\_belief:

A data frame with 213 rows and 3 columns:

**Response\_ID** character

**Belief\_in\_God** factor

**Age** integer

---

data\_selfexplain *SelfExplain - Ch15 - from McEldoon et al. (2013)*

---

### Description

Self-explaining is a learning strategy where students write or say their own explanations of the material they are studying. Self-explaining has generally been found to be more effective than standard studying, but it may also take more time. This raises the question of whether it's the study strategy or the extra time that benefits learning. To explore this issue, grade school children took a pretest of mathematics conceptual knowledge, studied mathematics problems, and then took a similar posttest (McEldoon et al., 2013). Participants were randomly assigned to one of two study conditions: normal study + more practice (More Practice group), or self-explaining (Self-Explain group). The first condition was intended to make time spent learning to be similar for the two groups. You can find part of the data from this study in SelfExplain, the scores being percent correct.

### Usage

```
data_selfexplain
```



**Format**

data\_selfexplain:

A data frame with 52 rows and 4 columns:

**Student ID** factor

**Condition** factor

**Pretest** numeric

**Posttest** numeric

**Source**

<https://bpspsychub.onlinelibrary.wiley.com/doi/abs/10.1111/j.2044-8279.2012.02083.x>

---

data\_simmonscredibility

*SimmonsCredibility - Ch14 - from Simmons and Nelson (2020)*

---

**Description**

You're excited! Your company has developed a wonderful new weight-loss program, and now it's your job to develop the ad campaign. Should you choose a BeforeAfter pair of pictures, as in Figure 14.1, top panel? Or might a Progressive sequence of pictures of the same person, as in the bottom panel, be more effective? Pause, think, and discuss. Which would you choose, and why? You might think that BeforeAfter is simpler and more dramatic. On the other hand, Progressive highlights the steady improvement that you claim the program will deliver. You're probably not surprised to learn that BeforeAfter is used often and has long been a favorite of the advertising industry, whereas Progressive is used only rarely. Luca Cian and colleagues (Cian et al., 2020) were curious to know the extent to which BeforeAfter is actually more effective, appealing, and credible than Progressive, or, indeed, whether Progressive might score more highly. They reported seven studies of various aspects of that question. I'll focus on their Study 2, in which they used three independent groups to compare all three conditions illustrated in Figure 14.1. The BeforeAfterInfo condition, in the middle panel, comprises three BeforeAfter pairs, thus providing extra information about the before and after endpoints. The researchers included this condition in case any advantage of Progressive might stem simply from having more images, rather than because it illustrates a clear progressive sequence. They randomly assigned 213 participants from MTurk to one of the three groups. Participants were asked to 'imagine that you have decided to lose some weight', then saw one of the three ads for a weight loss program called MRMDiets. They then answered the question 'How would you evaluate MRMDiets?' by choosing a 1-7 response on several scales, including Unlikeable-Likable, Ineffective-Effective, and Not credible-Credible. The researchers averaged six such scores to give an overall Credibility score, on the 1-7 scale, with 7 being the most credible. Simmons and Nelson (2020) were sufficiently intrigued to carry out two substantial very close replications. With the cooperation of the original researchers, they used the same materials and procedure. They used much larger groups and preregistered their research plan, including data analysis plan. I'll focus on their first replication, in which 761 participants from MTurk were randomized to the three groups.

**Usage**

```
data_simmonscredibility
```

**Format**

```
data_simmonscredibility:  
A data frame with 3 rows and 4 columns:
```

**Groups** factor

**Mean** numeric

**SD** numeric

**n** integer

**Source**

<http://datacolada.org/94>

---

data\_sleep\_beauty

*Sleep Beauty - Ch11 - for End-of-Chapter Exercise 11.6*

---

**Description**

Is there really such a thing as beauty sleep? To investigate, researchers decided to examine the extent to which sleep relates to attractiveness. Each of 70 college students self-reported the amount of sleep they had the night before. In addition, a photograph was taken of each participant and rated for attractiveness on a scale from 1 to 10 by two judges of the opposite gender. The average rating score was used. You can download this data set (Sleep Beauty) from the book website.

**Usage**

```
data_sleep_beauty
```

**Format**

```
data_sleep_beauty:  
A data frame with 70 rows and 2 columns:
```

**Sleep (hours)** numeric

**Rated\_Attractiveness** numeric

---

data_smithrecall	<i>SmithRecall - Ch15 - from Smith et al. (2016)</i>
------------------	--

---

**Description**

SmithRecall - Ch15 - from Smith et al. (2016)

**Usage**

data\_smithrecall

**Format**

data\_smithrecall:

A data frame with 120 rows and 6 columns:

**ID** integer

**Study Technique** factor

**Stress Status** factor

**%Recalled** numeric

**Items Recalled** numeric

**Group** factor

---

data_stickgold	<i>Stickgold - Ch06 - from Stickgold et al. (2000)</i>
----------------	--

---

**Description**

Stickgold et al. (2000) found that, remarkably, performance on a visual discrimination task actually improved over the 48-96 hours after initial training, even without practice during that time. However, what if participants were sleep deprived during that period? They trained 11 participants in that new skill, then all were sleep deprived. The data were (-14.7, -10.7, -10.7, 2.2, 2.4, 4.5, 7.2, 9.6, 10, 21.3, 21.8)-or download the Stickgold data set from the book website. The data are the changes in performance scores from immediately after training to after the night without sleep: 0 represents no change, positive scores represent improvement, and negative scores represent decline. Data set courtesy of DataCrunch ([tiny.cc/Stickgold](http://tiny.cc/Stickgold))

**Usage**

data\_stickgold

**Format**

data\_stickgold:

A data frame with 11 rows and 3 columns:

**Sleep deprived** numeric

**B** factor

**C** factor

**Source**

<https://www.statcrunch.com/app/index.html?dataid=1053539>

---

data\_studystrategies *StudyStrategies - Ch14 - from O'Reilly et al. (1998)*

---

**Description**

To what extent does study strategy influence learning? To investigate, psychology students were randomly assigned to three groups and asked to learn biology facts using one of three different strategies: a) Self-Explain (explaining for each fact what new knowledge is gained and how it relates to what is already known), b) Elab Interrogation (elaborative interrogation: stating for each fact why it makes sense), or c) Repetition Control (stating each fact over and over). After studying, students took a 25-point fill-the-blank test (O'Reilly et al., 1998)

**Usage**

data\_studystrategies

**Format**

data\_studystrategies:

A data frame with 3 rows and 10 columns:

**Group** factor

**TestMean** numeric

**TestSD** numeric

**TestN** integer

**PrevKnowMean** numeric

**PrevKnowSD** numeric

**PrevKnowN** integer

**EaseUseMean** numeric

**EaseUseSD** numeric

**EaseUseN** integer

**Source**

<https://www.sciencedirect.com/science/article/abs/pii/S0361476X97909772>

---

`data_thomason_1`*Thomason 1 - Ch11 - from Thomason 1*

---

**Description**

Summary data from an unpublished study by Neil Thomason and colleagues, who were interested in ways to enhance students' critical thinking. They were investigating argument mapping, which is a promising way to use diagrams to represent the structure of arguments. Students in their study completed an established test of critical thinking (the Pretest), then a critical thinking course based on argument mapping, then a second version of the test (the Posttest).

**Usage**`data_thomason_1`**Format**`data_thomason_1:`

A data frame with 12 rows and 3 columns:

**Participant ID** factor**Pretest** numeric**Posttest** numeric

---

`data_videogameaggression`*VideogameAggression - Ch15 - from Hilgard (2015)*

---

**Description**

Video games can be violent and they can also be challenging. To what extent might these factors cause aggressive behavior? To explore, Hilgard (2015) asked male participants to play one of four versions of a video game for 15 minutes. The game was customized so that it could vary in violence (shooting zombies or helping aliens) and difficulty (targets controlled by tough AI or dumb AI). After the game, players were provoked by being given an insulting evaluation by a confederate. Participants then got to decide how long the confederate should hold their hand in painfully cold ice water (between 0 and 80 seconds), and this was taken as a measure of aggressive behavior. You can find the materials and analysis plan for this study on the Open Science Framework: [osf.io/cwenz](https://osf.io/cwenz). This is a simplified version of the full data set.

**Usage**`data_videogameaggression`

**Format**

data\_videogameaggression:

A data frame with 223 rows and 3 columns:

**Violence** factor

**Difficulty** factor

**Agression** numeric

**Source**

<https://journals.sagepub.com/doi/10.1177/0956797619829688>

---

esci\_plot\_difference\_axis\_x

*Add a difference axis to the x axis of an esci forest plot*

---

**Description**

esci\_plot\_difference\_axis\_x can be used to redraw the difference axis from a forest plot created with `plot_meta`. You must pass the plot returned from `plot_meta` and the effect size table containing the estimated difference.

**Usage**

```
esci_plot_difference_axis_x(  
  myplot,  
  difference_table,  
  dlim = c(NA, NA),  
  d_n.breaks = NULL,  
  d_lab = NULL  
)
```

**Arguments**

myplot	required ggplot2 plot returned from a plot_meta function
difference_table	required data frame from an esci-estimate that has a difference-based effect size
dlim	Optional 2-item vector to provide the lower and upper boundaries of the difference axis. Defaults to c(NA, NA) which is to auto-set both boundaries.
d_n.breaks	Optional numeric > 2 to suggest number of breaks for the difference axis; defaults to NULL in which case number of breaks is handled automatically by ggplot
d_lab	Optional character to serve as the label for the difference axis; defaults to NULL

---

estimate_magnitude	<i>Estimates for a continuous variable with no grouping (single-group design)</i>
--------------------	---

---

### Description

estimate\_magnitude is suitable for a single group design with a continuous outcome variable. It estimates the population mean and population median (raw data only) with confidence intervals. You can pass raw data or summary data.

### Usage

```
estimate_magnitude(
  data = NULL,
  outcome_variable = NULL,
  mean = NULL,
  sd = NULL,
  n = NULL,
  outcome_variable_name = "My outcome variable",
  conf_level = 0.95,
  save_raw_data = TRUE
)
```

### Arguments

data	For raw data - A data frame or tibble
outcome_variable	For raw data - The column name of the outcome variable, or a vector of numeric data
mean	For summary data - A numeric representing the mean of the outcome variable
sd	For summary data - A numeric > 0, standard deviation of the outcome variable
n	For summary data - An integer > 0, sample size of the outcome variable
outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
save_raw_data	For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

### Details

Reach for this function in place of a one-sample *t*-test or *z*-test.

Once you generate an estimate with this function, you can visualize it with [plot\\_magnitude\(\)](#).

If you want to compare your sample to a known value or reference, then use [estimate\\_mdifff\\_one\(\)](#).

The estimated mean is from `statspsych::ci.mean1()` (renamed `ci.mean` as of `statspsych` 1.6).

The estimated median is from `statspsych::ci.median1()` (renamed `ci.median` as of `statspsych` 1.6)

## Value

Returns an object of class `esci_estimate`

- **overview**

- *outcome\_variable\_name* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

- **es\_mean**

- *outcome\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *df* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_median**

- *outcome\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *df* -



- *ta\_LL* -
- *ta\_UL* -

- **raw\_data**

- *grouping\_variable* -
- *outcome\_variable* -

## Examples

```
# From raw data
data("data_penlaptop1")

estimate_from_raw <- esci::estimate_magnitude(
  data = data_penlaptop1[data_penlaptop1$condition == "Pen", ],
  outcome_variable = transcription
)

# To visualize the estimate
myplot_from_raw <- esci::plot_magnitude(
  estimate_from_raw,
  effect_size = "median"
)

# From summary data
mymean <- 24.5
mysd <- 3.65
myn <- 40

estimate_from_summary <- esci::estimate_magnitude(
  mean = mymean,
  sd = mysd,
  n = myn
)

# To visualize the estimate
myplot_from_summary <- esci::plot_magnitude(
  estimate_from_summary,
  effect_size = "mean"
)
```

---

estimate\_mdif\_2x2\_between

*Estimates for a 2x2 between-subjects design with a continuous outcome variable*

---

**Description**

Returns object `estimate_mdif_2x2_between` is suitable for a 2x2 between-subjects design with a continuous outcome variable. It estimates each main effect, the simple effects for the first factor, and the interaction. It can express these estimates as mean differences, standardized mean differences (Cohen's *d*), and as median differences (raw data only). You can pass raw data or or summary data (summary data does not return medians).

**Usage**

```
estimate_mdif_2x2_between(
  data = NULL,
  outcome_variable = NULL,
  grouping_variable_A = NULL,
  grouping_variable_B = NULL,
  means = NULL,
  sds = NULL,
  ns = NULL,
  grouping_variable_A_levels = NULL,
  grouping_variable_B_levels = NULL,
  outcome_variable_name = "My outcome variable",
  grouping_variable_A_name = "A",
  grouping_variable_B_name = "A",
  conf_level = 0.95,
  assume_equal_variance = FALSE,
  save_raw_data = TRUE
)
```

**Arguments**

<code>data</code>	For raw data - a data frame or tibble
<code>outcome_variable</code>	For raw data - The column name of the outcome variable, or a vector of numeric data
<code>grouping_variable_A</code>	For raw data - The column name of the grouping variable, or a vector of group names, only 2 levels allowed
<code>grouping_variable_B</code>	For raw data - The column name of the grouping variable, or a vector of group names, only 2 levels allowed
<code>means</code>	For summary data - A vector of 4 means: A1B1, A1B2, A2B1, A2B2
<code>sds</code>	For summary data - A vector of 4 standard deviations, same order
<code>ns</code>	For summary data - A vector of 4 sample sizes
<code>grouping_variable_A_levels</code>	For summary data - An optional vector of 2 group labels
<code>grouping_variable_B_levels</code>	For summary data - An optional vector of 2 group labels

outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
grouping_variable_A_name	Optional friendly name for the grouping variable. Defaults to 'A' or the grouping variable column name if a data.frame is passed.
grouping_variable_B_name	Optional friendly name for the grouping variable. Defaults to 'A' or the grouping variable column name if a data.frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
assume_equal_variance	Defaults to FALSE
save_raw_data	For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

## Details

Reach for this function in place of a 2x2 between-subjects ANOVA.

Once you generate an estimate with this function, you can visualize it with `plot_mdif()` and you can visualize the interaction specifically with `plot_interaction()`. You can test hypotheses with `test_mdif()`.

The estimated mean differences are from `statspsych::ci.2x2.mean.bs()`.

The estimated SMDs are from `statspsych::ci.2x2.stdmean.bs()`.

The estimated median differences are from `statspsych::ci.2x2.median.bs()`

## Value

Returns object of class `esci_estimate`

- **es\_mean\_difference**
  - *type* -
  - *outcome\_variable\_name* -
  - *grouping\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *df* -
  - *ta\_LL* -
  - *ta\_UL* -
  - *effect\_type* -
  - *effects\_complex* -
- **es\_median\_difference**

- *type* -
- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *ta\_LL* -
- *ta\_UL* -
- *effect\_type* -
- *effects\_complex* -

- **es\_smd**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *numerator* -
- *denominator* -
- *SE* -
- *df* -
- *d\_biased* -
- *effect\_type* -
- *effects\_complex* -

- **overview**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -

- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -
- **raw\_data**
  - *grouping\_variable* -
  - *outcome\_variable* -
  - *grouping\_variable\_A* -
  - *grouping\_variable\_B* -

## Examples

```

data("data_videogameaggression")

estimates_from_raw <- esci::estimate_mdif_2x2_between(
  esci::data_videogameaggression,
  Agression,
  Violence,
  Difficulty
)

# To visualize the estimated mean difference for the interaction
myplot_from_raw <- esci::plot_mdif(
  estimates_from_raw$interaction,
  effect_size = "median"
)

# To conduct a hypothesis test on the mean difference
res_hstest_from_raw <- esci::test_mdif(
  estimates_from_raw$interaction,
  effect_size = "median"
)

# From summary data
means <- c(1.5, 1.14, 1.38, 2.22)
sds <- c(1.38, .96, 1.5, 1.68)
ns <- c(26, 26, 25, 26)
grouping_variable_A_levels <- c("Evening", "Morning")
grouping_variable_B_levels <- c("Sleep", "No Sleep")

estimates_from_summary <- esci::estimate_mdif_2x2_between(
  means = means,
  sds = sds,
  ns = ns,
  grouping_variable_A_levels = grouping_variable_A_levels,
  grouping_variable_B_levels = grouping_variable_B_levels,
  grouping_variable_A_name = "Testing Time",
  grouping_variable_B_name = "Rest",

```

```

  outcome_variable_name = "False Memory Score",
  assume_equal_variance = TRUE
)

# To visualize the estimated mean difference for the interaction
plot_mdif_interaction <- esci::plot_mdif(
  estimates_from_summary$interaction,
  effect_size = "mean"
)

# To visualize the interaction as a line plot
plot_interaction_line <- esci::plot_interaction(estimates_from_summary)

# Same but with fan effect representing each simple-effect CI
plot_interaction_line_CI <- esci::plot_interaction(
  estimates_from_summary,
  show_CI = TRUE
)

# To conduct a hypothesis test on the mean difference
res_hstest_from_raw <- esci::test_mdif(
  estimates_from_summary$interaction,
  effect_size = "mean"
)

```

---

```
estimate_mdif_2x2_mixed
```

*Estimates for a 2x2 mixed factorial design with a continuous outcome variable*

---

## Description

Returns object `estimate_mdif_2x2_mixed` is suitable for a 2x2 mixed-factorial design with a continuous outcome variable. It estimates each main effect, the simple effects for the repeated-measures factor, and the interaction. It can express these estimates as mean differences. This function accepts raw data only. Standardized mean differences are not (yet) available; stay tuned. Median differences are also not yet available.

## Usage

```

estimate_mdif_2x2_mixed(
  data,
  outcome_variable_level1,
  outcome_variable_level2,
  grouping_variable,
  outcome_variable_name = "My outcome variable",
  repeated_measures_name = "Time",

```

```

  conf_level = 0.95,
  save_raw_data = TRUE
)

```

### Arguments

**data** For raw data - a dataframe or tibble

**outcome\_variable\_level1**  
The column name of the outcome variable for level 1 of the repeated-measures factor

**outcome\_variable\_level2**  
The column name of the outcome variable for level 2 of the repeated-measures factor

**grouping\_variable**  
The column name of the grouping variable; only 2 levels allowed; must be a factor

**outcome\_variable\_name**  
Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.

**repeated\_measures\_name**  
Optional friendly name for the repeated measures factor. Defaults to 'Time'

**conf\_level** The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

**save\_raw\_data** For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

### Details

Reach for this function in place of a 2x2 mixed-factorial ANOVA.

Once you generate an estimate with this function, you can visualize it with [plot\\_mdif\(\)](#) and you can visualize the interaction specifically with [plot\\_interaction\(\)](#). You can test hypotheses with [test\\_mdif\(\)](#).

The estimated mean differences are from [statspsych::ci.2x2.mean.mixed\(\)](#).

### Value

Returns object of class `esci_estimate`

- **es\_mean\_difference**
  - *type* -
  - *outcome\_variable\_name* -
  - *grouping\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -

- *SE* -
- *df* -
- *ta\_LL* -
- *ta\_UL* -
- *effect\_type* -
- *effects\_complex* -
- *t* -
- *p* -

- **es\_smd**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *numerator* -
- *denominator* -
- *SE* -
- *df* -
- *d\_biased* -
- *effect\_type* -
- *effects\_complex* -

- **overview**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -



- *median\_SE* -

- **raw\_data**

- *grouping\_variable* -

- *outcome\_variable* -

- *grouping\_variable\_A* -

- *grouping\_variable\_B* -

- *paired* -

## Examples

```
# From raw data (summary data mode not available for this function)
example_data <- data.frame(
  pretest = c(
    19, 18, 19, 20, 17, 16, 16, 10, 12, 9, 13, 15
  ),
  posttest = c(
    18, 19, 20, 17, 20, 16, 19, 16, 16, 14, 16, 18
  ),
  condition = as.factor(
    c(
      rep("Control", times = 6),
      rep("Treated", times = 6)
    )
  )
)

estimates <- esci::estimate_mdif_2x2_mixed(
  data = example_data,
  outcome_variable_level1 = pretest,
  outcome_variable_level2 = posttest,
  grouping_variable = condition,
  repeated_measures_name = "Time"
)

# To visualize the estimated mean difference for the interaction
myplot <- esci::plot_mdif(estimates$interaction, effect_size = "mean")

# Line-plot of the interaction with fan effect representing each simple-effect CI
plot_interaction_line_CI <- esci::plot_interaction(
  estimates,
  show_CI = TRUE
)

# To conduct a hypothesis test
res_htest_from_raw <- esci::test_mdif(
  estimates$interaction,
  effect_size = "mean"
)
```

---

```
estimate_mdif_ind_contrast
```

*Estimates for a multi-group design with a continuous outcome variable*

---

## Description

Returns object `estimate_mdif_ind_contrast` is suitable for a multi-group design (between subjects) with a continuous outcome variable. It accepts a user-defined set of contrast weights that allows estimation of any 1-df contrast. It can express estimates as mean differences, standardized mean differences (Cohen's *d*) or median differences (raw data only). You can pass raw data or summary data.

## Usage

```
estimate_mdif_ind_contrast(
  data = NULL,
  outcome_variable = NULL,
  grouping_variable = NULL,
  means = NULL,
  sds = NULL,
  ns = NULL,
  contrast = NULL,
  grouping_variable_levels = NULL,
  outcome_variable_name = "My outcome variable",
  grouping_variable_name = "My grouping variable",
  conf_level = 0.95,
  assume_equal_variance = FALSE,
  save_raw_data = TRUE
)
```

## Arguments

<code>data</code>	For raw data - a data frame or tibble
<code>outcome_variable</code>	For raw data - The column name of the outcome variable, or a vector of numeric data
<code>grouping_variable</code>	For raw data - The column name of the grouping variable, or a vector of group names
<code>means</code>	For summary data - A vector of 2 or more means
<code>sds</code>	For summary data - A vector of standard deviations, same length as means
<code>ns</code>	For summary data - A vector of sample sizes, same length as means
<code>contrast</code>	A vector of group weights, same length as number of groups.
<code>grouping_variable_levels</code>	For summary data - An optional vector of group labels, same length as means

outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
grouping_variable_name	Optional friendly name for the grouping variable. Defaults to 'My grouping variable' or the grouping variable column name if a data.frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
assume_equal_variance	Defaults to FALSE
save_raw_data	For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

### Details

Reach for this function in place of a one-way ANOVA.

Once you generate an estimate with this function, you can visualize it with `plot_mdif()` and you can test hypotheses with `test_mdif()`.

The estimated mean differences are from `statspsych::ci.lc.mean.bs()`.

The estimated SMDs are from `CI_smd_ind_contrast()` which relies on `statspsych::ci.lc.stdmean.bs()` unless there are only 2 groups.

The estimated median differences are from `statspsych::ci.lc.median.bs()`

### Value

Returns object of class `esci_estimate`

- **es\_mean\_difference**
  - *type* -
  - *outcome\_variable\_name* -
  - *grouping\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *df* -
  - *ta\_LL* -
  - *ta\_UL* -
- **es\_median\_difference**
  - *type* -
  - *outcome\_variable\_name* -
  - *grouping\_variable\_name* -
  - *effect* -

- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_smd**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *numerator* -
- *denominator* -
- *SE* -
- *df* -
- *d\_biased* -

- **overview**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

- **raw\_data**

- *grouping\_variable* -
- *outcome\_variable* -

**Examples**

```

# From raw data
data("data_rattanmotivation")

estimate_from_raw <- esci::estimate_mdif_ind_contrast(
  esci::data_rattanmotivation,
  Motivation,
  Group,
  contrast = c("Challenge" = 1, "Control" = -1/2, "Comfort" = -1/2)
)

# To visualize the estimate
myplot_from_raw <- esci::plot_mdif(
  estimate_from_raw,
  effect_size = "median"
)

# To conduct a hypothesis test
res_htest_from_raw <- esci::test_mdif(
  estimate_from_raw,
  effect_size = "median"
)

# From summary data
data("data_halagappa")

estimate_from_summary <- estimate_mdif_ind_contrast(
  means = data_halagappa$Mean,
  sds = data_halagappa$SD,
  ns = data_halagappa$n,
  grouping_variable_levels = as.character(data_halagappa$Groups),
  assume_equal_variance = TRUE,
  contrast = c(
    "NFree10" = 1/3,
    "AFree10" = 1/3,
    "ADiet10" = -1/3,
    "NFree17" = -1/3,
    "AFree17" = 1/3,
    "ADiet17" = -1/3
  ),
  grouping_variable_name = "Diet",
  outcome_variable_name = "% time near target"
)

# To visualize the estimate
myplot <- esci::plot_mdif(estimate_from_summary, effect_size = "mean")

# To conduct a hypothesis test
res_htest_from_raw <- esci::test_mdif(
  estimate_from_summary,
  effect_size = "mean"
)

```

)

---

estimate_mdif_one	<i>Estimates for a single-group design with a continuous outcome variable compared to a reference or population value</i>
-------------------	---

---

### Description

Returns object estimate\_mdif\_one is suitable for a single-group design with a continuous outcome variable that is compared to a reference or population value. It can express estimates as mean differences, standardized mean differences (Cohen's d) or median differences (raw data only). You can pass raw data or summary data.

### Usage

```
estimate_mdif_one(
  data = NULL,
  outcome_variable = NULL,
  comparison_mean = NULL,
  comparison_sd = NULL,
  comparison_n = NULL,
  reference_mean = 0,
  outcome_variable_name = "My outcome variable",
  conf_level = 0.95,
  save_raw_data = TRUE
)
```

### Arguments

data	For raw data - a data frame or tibble
outcome_variable	For raw data - The column name of the outcome variable, or a vector of numeric data
comparison_mean	For summary data, a numeric
comparison_sd	For summary data, numeric > 0
comparison_n	For summary data, a numeric integer > 0
reference_mean	Reference value, defaults to 0
outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
save_raw_data	For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

## Details

Reach for this function in place of a  $z$ -test or one-sample  $t$ -test.

Once you generate an estimate with this function, you can visualize it with `plot_mdif()` and you can test hypotheses with `test_mdif()`.

The estimated mean differences are from `statspsych::ci.mean1()` (renamed `ci.mean` as of `statspsych` 1.6).

The estimated SMDs are from `CI_smd_one()`.

The estimated median differences are from `statspsych::ci.median1()` (renamed `ci.median` as of `statspsych` 1.6)

## Value

Returns object of class `esci_estimate`

- **overview**

- *outcome\_variable\_name* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

- **es\_mean**

- *outcome\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *df* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_median**
  - *outcome\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *df* -
  - *ta\_LL* -
  - *ta\_UL* -
- **raw\_data**
  - *grouping\_variable* -
  - *outcome\_variable* -
- **es\_mean\_difference**
  - *outcome\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *df* -
  - *ta\_LL* -
  - *ta\_UL* -
  - *type* -
- **es\_median\_difference**
  - *outcome\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *df* -
  - *ta\_LL* -
  - *ta\_UL* -
  - *type* -
- **es\_smd**
  - *outcome\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -



- *numerator* -
- *denominator* -
- *SE* -
- *df* -
- *d\_biased* -

## Examples

```
# From raw data
data("data_penlaptop1")
estimate_from_raw <- esci::estimate_mdif_one(
  data = data_penlaptop1[data_penlaptop1$condition == "Pen", ],
  outcome_variable = transcription,
  reference_mean = 10
)

# To visualize the mean difference estimate
myplot_from_raw <- esci::plot_mdif(estimate_from_raw, effect_size = "mean")

# To conduct a hypothesis test
res_htest_from_raw <- esci::test_mdif(
  estimate_from_raw,
  effect_size = "mean",
  rope = c(-2, 2)
)

# From summary data
mymean <- 12.09
mysd <- 5.52
myn <- 103

estimate_from_summary <- esci::estimate_mdif_one(
  comparison_mean = mymean,
  comparison_sd = mysd,
  comparison_n = myn,
  reference_mean = 12
)

# To visualize the estimate
myplot_from_summary <- esci::plot_mdif(
  estimate_from_summary,
  effect_size = "mean"
)

# To conduct a hypothesis test
res_htest_from_summary <- esci::test_mdif(
  estimate_from_summary,
  effect_size = "mean",
  rope = c(-2, 2)
)
```

---

estimate\_mdifff\_paired *Estimates for a repeated-measures study with two measures of a continuous variable*

---

### Description

Returns object estimate\_mdifff\_paired is suitable for a simple paired design with a continuous outcome variable. It provides estimates and CIs for the population mean difference between the repeated measures, the standardized mean difference (SMD; Cohen's d) between the repeated measures, and the median difference between the repeated measures (raw data only). You can pass raw data or summary data.

### Usage

```
estimate_mdifff_paired(
  data = NULL,
  comparison_measure = NULL,
  reference_measure = NULL,
  comparison_mean = NULL,
  comparison_sd = NULL,
  reference_mean = NULL,
  reference_sd = NULL,
  n = NULL,
  correlation = NULL,
  comparison_measure_name = "Comparison measure",
  reference_measure_name = "Reference measure",
  conf_level = 0.95,
  save_raw_data = TRUE
)
```

### Arguments

data	For raw data - a data frame or tibble
comparison_measure	For raw data - The column name of comparison measure of the outcome variable, or a vector of numeric data
reference_measure	For raw data - The column name of the reference measure of the outcome variable, or a vector of numeric data
comparison_mean	For summary data, a numeric
comparison_sd	For summary data, numeric > 0
reference_mean	For summary data, a numeric
reference_sd	For summary data, numeric > 0
n	For summary data, a numeric integer > 0

correlation	For summary data, correlation between measures, a numeric that is > -1 and < 1
comparison_measure_name	For summary data - An optional character label for the comparison measure. Defaults to 'Comparison measure'
reference_measure_name	For summary data - An optional character label for the reference measure. Defaults to 'Reference measure'
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
save_raw_data	For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

## Details

Reach for this function in place of a paired-samples *t*-test.

Once you generate an estimate with this function, you can visualize it with `plot_mdif()` and you can test hypotheses with `test_mdif()`.

The estimated mean differences are from `statspsych::ci.mean.ps()`.

The estimated SMDs are from `CI_smd_ind_contrast()`.

The estimated median differences are from `statspsych::ci.median.ps()`.

## Value

Returns object of class `esci_estimate`

- **overview**

- *outcome\_variable\_name* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

- **es\_mean\_difference**

- *type* -
- *comparison\_measure\_name* -
- *reference\_measure\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *df* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_smd**

- *comparison\_measure\_name* -
- *reference\_measure\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *numerator* -
- *denominator* -
- *SE* -
- *d\_biased* -
- *df* -

- **es\_r**

- *x\_variable\_name* -
- *y\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *n* -
- *df* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_median\_difference**

- *type* -
- *comparison\_measure\_name* -
- *reference\_measure\_name* -
- *effect* -
- *effect\_size* -

- *LL* -
- *UL* -
- *SE* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_mean\_ratio**

- *comparison\_measure\_name* -
- *reference\_measure\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *comparison\_mean* -
- *reference\_mean* -

- **es\_median\_ratio**

- *comparison\_measure\_name* -
- *reference\_measure\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *comparison\_median* -
- *reference\_median* -

- **raw\_data**

- *comparison\_measure* -
- *reference\_measure* -

## Examples

```
# From raw data
data("data_thomason_1")

estimate_from_raw <- esci::estimate_mdiff_paired(
  data = esci::data_thomason_1,
  comparison_measure = Posttest,
  reference_measure = Pretest
)

# To visualize the estimated median difference (raw data only)
myplot_from_raw <- esci::plot_mdiff(estimate_from_raw, effect_size = "median")

# To conduct a hypothesis test
res_hptest_from_raw <- esci::test_mdiff(
  estimate_from_raw,
  effect_size = "median",
```

```

    rope = c(-2, 2)
  )

sd1 <- 4.28
sd2 <- 3.4
sdiff <- 2.13

cor <- (sd1^2 + sd2^2 - sdiff^2) / (2*sd1*sd2)

estimate_from_summary <- esci::estimate_mdif_paired(
  comparison_mean = 14.25,
  comparison_sd = 4.28,
  reference_mean = 12.88,
  reference_sd = 3.4,
  n = 16,
  correlation = 0.87072223749,
  comparison_measure_name = "After",
  reference_measure_name = "Before"
)

# To visualize the estimated mean difference
myplot_from_summary <- esci::plot_mdif(
  estimate_from_summary,
  effect_size = "mean"
)

# To conduct a hypothesis test
res_hstest_from_summary <- esci::test_mdif(
  estimate_from_summary,
  effect_size = "mean",
  rope = c(-2, 2)
)

```

---

estimate\_mdif\_two      *Estimates for a two-group study with a continuous outcome variable*

---

### Description

Returns object `estimate_mdif_two` is suitable for a simple two-group design with a continuous outcome variable. It provides estimates and CIs for the population mean difference between the repeated measures, the standardized mean difference (SMD; Cohen's *d*) between the repeated measures, and the median difference between the repeated measures (raw data only). You can pass raw data or summary data.

### Usage

```
estimate_mdif_two(
```

```

data = NULL,
outcome_variable = NULL,
grouping_variable = NULL,
comparison_mean = NULL,
comparison_sd = NULL,
comparison_n = NULL,
reference_mean = NULL,
reference_sd = NULL,
reference_n = NULL,
grouping_variable_levels = NULL,
outcome_variable_name = "My outcome variable",
grouping_variable_name = "My grouping variable",
conf_level = 0.95,
assume_equal_variance = FALSE,
save_raw_data = TRUE,
switch_comparison_order = FALSE
)

```

### Arguments

data	For raw data - a data.frame or tibble
outcome_variable	For raw data - The column name of the outcome variable, or a vector of numeric data
grouping_variable	For raw data - The column name of the grouping variable, or a vector of group names
comparison_mean	For summary data, a numeric
comparison_sd	For summary data, numeric > 0
comparison_n	For summary data, a numeric integer > 0
reference_mean	For summary data, a numeric
reference_sd	For summary data, numeric > 0
reference_n	For summary data, a numeric integer > 0
grouping_variable_levels	For summary data - An optional vector of 2 group labels
outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
grouping_variable_name	Optional friendly name for the grouping variable. Defaults to 'My grouping variable' or the grouping variable column name if a data.frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
assume_equal_variance	Defaults to FALSE

save\_raw\_data For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

switch\_comparison\_order  
Defaults to FALSE

## Details

Reach for this function in place of an independent-samples *t*-test.

Once you generate an estimate with this function, you can visualize it with `plot_mdif()` and you can test hypotheses with `test_mdif()`.

The estimated mean differences are from `statspsych::ci.mean2()`.

The estimated SMDs are from `CI_smd_ind_contrast()`.

The estimated median differences are from `statspsych::ci.median2()`.

## Value

Returns object of class `esci_estimate`

- **es\_mean\_difference**
  - *type* -
  - *outcome\_variable\_name* -
  - *grouping\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *df* -
  - *ta\_LL* -
  - *ta\_UL* -
- **es\_median\_difference**
  - *type* -
  - *outcome\_variable\_name* -
  - *grouping\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *ta\_LL* -
  - *ta\_UL* -
- **es\_smd**
  - *outcome\_variable\_name* -



- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *numerator* -
- *denominator* -
- *SE* -
- *df* -
- *d\_biased* -

- **es\_mean\_ratio**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *comparison\_mean* -
- *reference\_mean* -

- **es\_median\_ratio**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *comparison\_median* -
- *reference\_median* -

- **overview**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -

- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

- **raw\_data**

- *grouping\_variable* -
- *outcome\_variable* -

## Examples

```
# From raw data
data("data_penlaptop1")

estimate_from_raw <- esci::estimate_mdif_two(
  data = data_penlaptop1,
  outcome_variable = transcription,
  grouping_variable = condition,
  switch_comparison_order = TRUE,
  assume_equal_variance = TRUE
)

# To visualize the estimated median difference (raw data only)
myplot_from_raw <- esci::plot_mdif(
  estimate_from_raw,
  effect_size = "median"
)

# To conduct a hypothesis test
res_hstest_from_raw <- esci::test_mdif(
  estimate_from_raw,
  effect_size = "median",
  rope = c(-2, 2)
)

# From summary data
estimate_from_summary <- esci::estimate_mdif_two(
  comparison_mean = 12.09,
  comparison_sd = 5.52,
  comparison_n = 103,
  reference_mean = 6.88,
  reference_sd = 4.22,
  reference_n = 48,
  grouping_variable_levels = c("Ref-Laptop", "Comp-Pen"),
  outcome_variable_name = "% Transcription",
  grouping_variable_name = "Note-taking type",
  assume_equal_variance = TRUE
)
```

```
)

# To visualize the estimated mean difference
myplot <- esci::plot_mdif(
  estimate_from_summary,
  effect_size = "mean"
)

# To conduct a hypothesis test
res_hstest_from_summary <- esci::test_mdif(
  estimate_from_summary,
  effect_size = "mean",
  rope = c(-2, 2)
)
```

---

estimate\_pdiff\_ind\_contrast

*Estimates for a multi-group study with a categorical outcome variable*

---

## Description

Returns object `estimate_pdiff_ind_contrast` is suitable for a multi-group design (between subjects) with a categorical outcome variable. It accepts a user-defined set of contrast weights that allows estimation of any 1-df contrast. It can express estimates as a difference in proportions and as an odds ratio (2-group designs only). You can pass raw data or summary data.

## Usage

```
estimate_pdiff_ind_contrast(
  data = NULL,
  outcome_variable = NULL,
  grouping_variable = NULL,
  cases = NULL,
  ns = NULL,
  contrast = NULL,
  case_label = 1,
  grouping_variable_levels = NULL,
  outcome_variable_name = "My outcome variable",
  grouping_variable_name = "My grouping variable",
  conf_level = 0.95,
  count_NA = FALSE
)
```

## Arguments

`data` For raw data - a data frame or tibble

outcome_variable	For raw data - The column name of the outcome variable which is a factor, or a vector that is a factor
grouping_variable	For raw data - The column name of the grouping variable which is a factor, or a vector that is a factor
cases	For summary data - A numeric vector of 2 or more event counts, each an integer $\geq 0$
ns	For summary data - A numeric vector of sample sizes, same length as counts, each an integer $\geq$ corresponding event count
contrast	A vector of group weights, same length as number of groups.
case_label	An optional numeric or character label For summary data, used as the label and defaults to 'Affected'. For raw data, used to specify the level used for the proportion.
grouping_variable_levels	For summary data - An optional vector of group labels, same length as cases
outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
grouping_variable_name	Optional friendly name for the grouping variable. Defaults to 'My grouping variable' or the grouping variable column name if a data.frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
count_NA	Logical to count NAs (TRUE) in total N or not (FALSE)

### Details

Once you generate an estimate with this function, you can visualize it with `plot_mdifff()` and you can test hypotheses with `test_mdifff()`.

The estimated proportion differences are from `statpsych::ci.lc.prop.bs()`.

The estimated odds ratios (if returned) are from `statpsych::ci.oddsratio()`.

### Value

Returns object of class `esci_estimate`

- **es\_proportion\_difference**
  - *type* -
  - *outcome\_variable\_name* -
  - *case\_label* -
  - *grouping\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -

- *UL* -
- *SE* -
- *effect\_size\_adjusted* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_odds\_ratio**

- *outcome\_variable\_name* -
- *case\_label* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *SE* -
- *LL* -
- *UL* -
- *ta\_LL* -
- *ta\_UL* -

- **overview**

- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *outcome\_variable\_name* -
- *outcome\_variable\_level* -
- *cases* -
- *n* -
- *P* -
- *P\_LL* -
- *P\_UL* -
- *P\_SE* -
- *P\_adjusted* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_phi**

- *grouping\_variable\_name* -
- *outcome\_variable\_name* -
- *effect* -
- *effect\_size* -
- *SE* -
- *LL* -
- *UL* -

**Examples**

```

# From raw data
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_pdiff_ind_contrast(
  esci::data_campus_involvement,
  CommuterStatus,
  Gender,
  contrast = c("Male" = -1, "Female" = 1)
)

# To visualize the estimate
myplot_from_raw <- esci::plot_pdiff(estimate_from_raw)

# To conduct a hypothesis test
res_hstest_from_raw <- esci::test_pdiff(estimate_from_raw)

# From summary data
estimate_from_summary <- esci::estimate_pdiff_ind_contrast(
  cases = c(78, 10),
  ns = c(252, 20),
  case_label = "egocentric",
  grouping_variable_levels = c("Original", "Replication"),
  contrast = c(-1, 1),
  conf_level = 0.95
)

# To visualize the estimate
myplot_from_summary <- esci::plot_pdiff(estimate_from_summary)

# To conduct a hypothesis test
res_hstest_from_summary <- esci::test_pdiff(estimate_from_summary)

```

---

estimate_pdiff_one	<i>Estimates for a single-group design with a categorical outcome variable compared to a reference or population value.</i>
--------------------	---

---

**Description**

Returns object `estimate_pdiff_one` is suitable for a single-group design (between subjects) with a categorical outcome variable. It calculates the effect sizes with respect to a reference or population proportion (default value of 0). It returns the estimated difference between the in proportion from the reference/population value. You can pass raw data or summary data.

**Usage**

```
estimate_pdiff_one(
  data = NULL,
  outcome_variable = NULL,
  comparison_cases = NULL,
  comparison_n = NULL,
  reference_p = 0,
  case_label = 1,
  outcome_variable_name = "My outcome variable",
  conf_level = 0.95,
  count_NA = FALSE
)
```

**Arguments**

<code>data</code>	For raw data - a dataframe or tibble
<code>outcome_variable</code>	For raw data - The column name of the outcome variable, which must be a factor, or a vector that is a factor
<code>comparison_cases</code>	For summary data, a numeric integer > 0
<code>comparison_n</code>	For summary data, a numeric integer >= count
<code>reference_p</code>	Reference proportion, numeric >=0 and <=1
<code>case_label</code>	An optional numeric or character label for the count level.
<code>outcome_variable_name</code>	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
<code>conf_level</code>	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
<code>count_NA</code>	Logical to count NAs (TRUE) in total N or not (FALSE)

**Details**

Once you generate an estimate with this function, you can visualize it with [plot\\_pdiff\(\)](#) and you can test hypotheses with [test\\_pdiff\(\)](#).

The estimated proportion differences are from [statspsych::ci.prop1\(\)](#) (renamed `ci.prop` as of `statspsych` 1.6).

**Value**

Returns an object of class `esci_estimate`

- **overview**
  - `outcome_variable_name` -
  - `outcome_variable_level` -
  - `cases` -

- *n* -
- *P* -
- *P\_LL* -
- *P\_UL* -
- *P\_SE* -
- *P\_adjusted* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_proportion\_difference**

- *outcome\_variable\_name* -
- *case\_label* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *effect\_size\_adjusted* -
- *ta\_LL* -
- *ta\_UL* -
- *cases* -
- *n* -
- *type* -

## Examples

```
# From raw data
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_pdiff_one(
  esci::data_campus_involvement,
  CommuterStatus,
  reference_p = 0.50
)

# To visualize the estimate
myplot_from_raw <- esci::plot_pdiff(estimate_from_raw)

# To conduct a hypothesis test
res_hstest_from_raw <- esci::test_pdiff(estimate_from_raw)

# From summary data
estimate_from_summary <- esci::estimate_pdiff_one(
  comparison_cases = 8,
  comparison_n = 22,
  reference_p = 0.5
)
```



```
# To visualize the estimate
myplot_from_summary <- esci::plot_pdiff(estimate_from_summary)

# To conduct a hypothesis test
res_hstest_from_summary <- esci::test_pdiff(estimate_from_summary)
```

---

estimate\_pdiff\_paired *Estimates for a repeated-measures study with two measures of a categorical variable*

---

### Description

Returns object estimate\_pdiff\_paired is suitable for a simple paired design with a categorical outcome variable. It provides estimates and CIs for the population proportion difference between the repeated measures. You can pass raw data or summary data.

### Usage

```
estimate_pdiff_paired(
  data = NULL,
  comparison_measure = NULL,
  reference_measure = NULL,
  cases_consistent = NULL,
  cases_inconsistent = NULL,
  not_cases_consistent = NULL,
  not_cases_inconsistent = NULL,
  case_label = 1,
  not_case_label = NULL,
  comparison_measure_name = "Comparison measure",
  reference_measure_name = "Reference measure",
  conf_level = 0.95,
  count_NA = FALSE
)
```

### Arguments

**data** For raw data - a data.frame or tibble

**comparison\_measure**  
For raw data - The comparison measure, a factor. Can be the column name of a data frame or a vector.

**reference\_measure**  
For raw data - The reference measure, a factor. Can be the column name of a data frame or a vector.

**cases\_consistent**      Count of *cases* in measure 1 that *are* also cases at measure 2; measure 1 = 0, measure 2 = 0; cell 0\_0  
**cases\_inconsistent**      Count of *cases* in measure 1 that are *not* cases at measure 2; measure 1 = 0, measure 2 = 1; cell 0\_1  
**not\_cases\_consistent**      Count of *not cases* in measure 1 that *are* also not cases at measure 2; measure 1 = 1, measure 2 = 1, cell 1\_1  
**not\_cases\_inconsistent**      Count of *not cases* in measure 1 that are *not* cases at measure 2; measure 1 = 1, measure 2 = 0, cell 1\_0  
**case\_label**      An optional numeric or character label for the case level.  
**not\_case\_label**      An optional numeric or character label for the not case level.  
**comparison\_measure\_name**      For summary data - An optional character label for the comparison measure. Defaults to 'Comparison measure'  
**reference\_measure\_name**      For summary data - An optional character label for the reference measure. Defaults to 'Reference measure'  
**conf\_level**      The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.  
**count\_NA**      Logical to count NAs (TRUE) in total N or not (FALSE)

## Details

Once you generate an estimate with this function, you can visualize it with `plot_pdiff()` and you can test hypotheses with `test_pdiff()`.

The estimated proportion differences are from `statpsych::ci.prop.ps()`.

## Value

Returns object of class `esci_estimate`

## Examples

```

# From summary data
# Example 1 from Bonett & Price, 2012
estimate_from_summary <- esci::estimate_pdiff_paired(
  cases_consistent = 60,
  cases_inconsistent = 50,
  not_cases_inconsistent = 22,
  not_cases_consistent = 68,
  case_label = "Answered True",
  not_case_label = "Answered False",
  reference_measure_name = "9th grade",
  comparison_measure_name = "12th grade",
  conf_level = 0.95

```

```

)

# To visualize the estimate
myplot_from_summary <- esci::plot_pdiff(estimate_from_summary)

# To conduct a hypothesis test
res_hstest_from_summary <- esci::test_pdiff(estimate_from_summary)

```

---

estimate\_pdiff\_two      *Estimates for a two-group study with a categorical outcome variable*

---

### Description

Returns object estimate\_pdiff\_two is suitable for a simple two-group design with a categorical outcome variable. It provides estimates and CIs for the difference in proportions between the two groups, the odds ratio, and phi. You can pass raw data or summary data.

### Usage

```

estimate_pdiff_two(
  data = NULL,
  outcome_variable = NULL,
  grouping_variable = NULL,
  comparison_cases = NULL,
  comparison_n = NULL,
  reference_cases = NULL,
  reference_n = NULL,
  case_label = 1,
  not_case_label = NULL,
  grouping_variable_levels = NULL,
  outcome_variable_name = "My outcome variable",
  grouping_variable_name = "My grouping variable",
  conf_level = 0.95,
  count_NA = FALSE
)

```

### Arguments

data                      For raw data - a data frame or tibble

outcome\_variable                      For raw data - The column name of the outcome variable which is a factor, or a vector that is a factor

grouping\_variable                      For raw data - The column name of the grouping variable which is a factor, or a vector that is a factor

comparison_cases	For summary data, a numeric integer $\geq 0$
comparison_n	For summary data, a numeric integer $\geq$ comparison_events
reference_cases	For summary data, a numeric integer $\geq 0$
reference_n	For summary data, a numeric integer $\geq$ reference_events
case_label	An optional numeric or character label for the case level.
not_case_label	An optional numeric or character label for the not case level.
grouping_variable_levels	For summary data - An optional vector of 2 group labels
outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
grouping_variable_name	Optional friendly name for the grouping variable. Defaults to 'My grouping variable' or the grouping variable column name if a data.frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
count_NA	Logical to count NAs (TRUE) in total N or not (FALSE)

### Details

Once you generate an estimate with this function, you can visualize it with `plot_mdifff()` and you can test hypotheses with `test_mdifff()`.

The estimated mean differences are from `statspsych::ci.prop2()`.

The estimated odds ratio is from `statspsych::ci.oddsratio()`.

The estimated correlation ( $\phi$ ) is from `statspsych::ci.phi()`.

### Value

Returns object of class `esci_estimate`

- **es\_proportion\_difference**

- *type* -
- *outcome\_variable\_name* -
- *case\_label* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *effect\_size\_adjusted* -
- *ta\_LL* -

- *ta\_UL* -

- **es\_odds\_ratio**

- *outcome\_variable\_name* -
- *case\_label* -
- *grouping\_variable\_name* -
- *effect* -
- *effect\_size* -
- *SE* -
- *LL* -
- *UL* -
- *ta\_LL* -
- *ta\_UL* -

- **overview**

- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *outcome\_variable\_name* -
- *outcome\_variable\_level* -
- *cases* -
- *n* -
- *P* -
- *P\_LL* -
- *P\_UL* -
- *P\_SE* -
- *P\_adjusted* -
- *ta\_LL* -
- *ta\_UL* -

- **es\_phi**

- *grouping\_variable\_name* -
- *outcome\_variable\_name* -
- *effect* -
- *effect\_size* -
- *SE* -
- *LL* -
- *UL* -

## Examples

```
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_pdiff_two(
  esci::data_campus_involvement,
  CommuterStatus,
  Gender
```

```

)

# To visualize the estimate
myplot_from_raw <- esci::plot_pdiff(estimate_from_raw)

# To conduct a hypothesis test
res_hstest_from_raw <- esci::test_pdiff(estimate_from_raw)

# From summary_data
estimate_from_summary <- esci::estimate_pdiff_two(
  comparison_cases = 10,
  comparison_n = 20,
  reference_cases = 78,
  reference_n = 252,
  grouping_variable_levels = c("Original", "Replication"),
  conf_level = 0.95
)

# To visualize the estimate
myplot_from_summary <- esci::plot_pdiff(estimate_from_summary)

#' # To conduct a hypothesis test
res_hstest_from_summary <- esci::test_pdiff(estimate_from_summary)

```

---

estimate_proportion	<i>Estimates for a categorical variable with no grouping (single-group design)</i>
---------------------	--

---

## Description

estimate\_proportion is suitable for a single group design with a categorical outcome variable. It estimates the population proportion for the frequency of each level of the outcome variable, with confidence intervals. You can pass raw data or summary data.

## Usage

```

estimate_proportion(
  data = NULL,
  outcome_variable = NULL,
  cases = NULL,
  case_label = 1,
  outcome_variable_levels = NULL,
  outcome_variable_name = "My outcome variable",
  conf_level = 0.95,
  count_NA = FALSE
)

```

**Arguments**

data	For raw data - a data frame or tibble
outcome_variable	For raw data - The column name of the outcome variable, which must be a factor, or a vector that is a factor
cases	For summary data - A vector of cases
case_label	A numeric or string indicating which level of the factor to estimate. Defaults to 1, meaning first level is analyzed
outcome_variable_levels	For summary data - optional vector of 2 characters indicating name of the count level and name of the not count level. Defaults to "Affected" and "Not Affected"
outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My outcome variable' or the outcome variable column name if a data frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
count_NA	Logical to count NAs (TRUE) in total N or not (FALSE)

**Details**

Once you generate an estimate with this function, you can visualize it with [plot\\_proportion\(\)](#).

If you want to compare your estimate to a known value or reference, then use [estimate\\_pdiff\\_one\(\)](#).

The estimated proportions are from [statspsych::ci.prop1\(\)](#) (renamed ci.prop as of statspsych 1.6).

**Value**

Returns an object of class `esci_estimate`

- **overview**

- `outcome_variable_name` -
- `outcome_variable_level` -
- `cases` -
- `n` -
- `P` -
- `P_LL` -
- `P_UL` -
- `P_SE` -
- `P_adjusted` -
- `ta_LL` -
- `ta_UL` -

- **es\_proportion**

- `outcome_variable_name` -
- `case_label` -

- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *effect\_size\_adjusted* -
- *ta\_LL* -
- *ta\_UL* -
- *cases* -
- *n* -

### Examples

```
# From raw data
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_proportion(
  esci::data_campus_involvement,
  CommuterStatus
)

# To visualize the estimate
myplot_from_raw <- esci::plot_proportion(estimate_from_raw)

# From summary data
estimate_from_summary <- esci::estimate_proportion(
  cases = c(8, 22-8),
  outcome_variable_levels = c("Affected", "Not Affected")
)

# To visualize the estimate
myplot_from_summary <- esci::plot_proportion(estimate_from_summary)
```

---

estimate\_r

*Estimates the linear correlation (Pearson's r) between two continuous variables*

---

### Description

estimate\_r is suitable for a design with two continuous variables. It estimates the linear correlation between two variables (Pearson's r) with a confidence interval. You can pass raw data or summary data.



**Usage**

```
estimate_r(
  data = NULL,
  x = NULL,
  y = NULL,
  r = NULL,
  n = NULL,
  x_variable_name = "My x variable",
  y_variable_name = "My y variable",
  conf_level = 0.95,
  save_raw_data = TRUE
)
```

**Arguments**

data	For raw data - A data frame or tibble
x	For raw data - The column name of the outcome variable, or a vector of numeric data
y	For raw data - The column name of the outcome variable, or a vector of numeric data
r	For summary data - A pearson's r correlation coefficient
n	For summary data - Sample size, an integer > 0
x_variable_name	Optional friendly name for the x variable. Defaults to 'My x variable' or the outcome variable column name if a data frame is passed.
y_variable_name	Optional friendly name for the y variable. Defaults to 'My y variable' or the outcome variable column name if a data frame is passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
save_raw_data	For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

**Details**

Reach for this function to conduct simple linear correlation or simple linear regression.

Once you generate an estimate with this function, you can visualize it with [plot\\_correlation\(\)](#) and you can test hypotheses with [test\\_correlation\(\)](#). In addition, you can use [plot\\_scatter\(\)](#) to visualize the raw data and to conduct a regression analysis that r returns predicted Y' values from a given X value.

The estimated correlation is from [statspsych::ci.cor\(\)](#), which uses the Fisher r-to-z approach.

**Value**

Returns object of class `esci_estimate`

- **overview**

- *outcome\_variable\_name* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

- **es\_r**

- *x\_variable\_name* -
- *y\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *n* -
- *df* -
- *ta\_LL* -
- *ta\_UL* -

- **regression**

- *component* -
- *values* -
- *LL* -
- *UL* -

- **raw\_data**

- *x* -
- *y* -
- *fit* -
- *lwr* -
- *upr* -

**Examples**

```

# From raw data
data("data_thomason_1")

estimate_from_raw <- esci::estimate_r(
  esci::data_thomason_1,
  Pretest,
  Posttest
)

# To visualize the value of r
myplot_correlation <- esci::plot_correlation(estimate_from_raw)

# To visualize the data (scatterplot) and use regression to obtain Y' from X
myplot_scatter_from_raw <- esci::plot_scatter(estimate_from_raw, predict_from_x = 10)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
res_htest_from_raw <- esci::test_correlation(
  estimate_from_raw,
  rope = c(-0.1, 0.1)
)

# From summary data
estimate_from_summary <- esci::estimate_r(r = 0.536, n = 50)

# To visualize the value of r
myplot_correlation_from_summary <- esci::plot_correlation(estimate_from_summary)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
res_htest_from_summary <- esci::test_correlation(
  estimate_from_summary,
  rope = c(-0.1, 0.1)
)

```

---

estimate_rdiff_two	<i>Estimates the difference in correlation for a design with two groups and two continuous outcome variables</i>
--------------------	--

---

**Description**

Returns object `estimate_rdiff_two` is suitable for a simple two-group design with two continuous outcome variables where you want to estimate the difference in the strength of the relationship between the two groups. It estimate the linear correlation (Pearson's  $r$ ) for each group and the difference in  $r$ , along with confidence intervals. You can pass raw data or summary data.

Returns effect sizes appropriate for estimating the linear relationship between two quantitative variables

**Usage**

```
estimate_rdiff_two(
  data = NULL,
  x = NULL,
  y = NULL,
  grouping_variable = NULL,
  comparison_r = NULL,
  comparison_n = NULL,
  reference_r = NULL,
  reference_n = NULL,
  grouping_variable_levels = NULL,
  x_variable_name = "My x variable",
  y_variable_name = "My y variable",
  grouping_variable_name = "My grouping variable",
  conf_level = 0.95,
  save_raw_data = TRUE
)
```

**Arguments**

<code>data</code>	For raw data - a dataframe or tibble
<code>x</code>	For raw data - The column name of the outcome variable, or a vector of numeric data
<code>y</code>	For raw data - The column name of the outcome variable, or a vector of numeric data
<code>grouping_variable</code>	For raw data, a vector that is a factor or the name of a factor column from data
<code>comparison_r</code>	For summary data, a pearson's r correlation coefficient
<code>comparison_n</code>	For summary data - An integer > 0
<code>reference_r</code>	For summary data, a pearson's r correlation coefficient
<code>reference_n</code>	For summary data - An integer > 0
<code>grouping_variable_levels</code>	For summary data - An optional vector of 2 group labels
<code>x_variable_name</code>	Optional friendly name for the x variable. Defaults to 'My x variable' or the outcome variable column name if a data frame is passed.
<code>y_variable_name</code>	Optional friendly name for the y variable. Defaults to 'My y variable' or the outcome variable column name if a data frame is passed.
<code>grouping_variable_name</code>	Optional friendly name for the grouping variable. Defaults to 'My grouping variable' or the grouping variable column name if a data.frame is passed.
<code>conf_level</code>	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
<code>save_raw_data</code>	For raw data; defaults to TRUE; set to FALSE to save memory by not returning raw data in estimate object

## Details

Once you generate an estimate with this function, you can visualize it with `plot_rdiff()` and you can test hypotheses with `test_rdiff()`. In addition, you can use `plot_scatter()` to visualize the raw data.

The estimated single-group  $r$  values are from `statspsych::ci.cor()`.

The difference in  $r$  values is from `statspsych::ci.cor2()`.

## Value

Returns object of class `esci_estimate`

- **overview**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

- **es\_r\_difference**

- *type* -
- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *x\_variable\_name* -
- *y\_variable\_name* -
- *effect* -
- *effect\_size* -
- *LL* -
- *UL* -
- *SE* -
- *n* -

- *df* -
- *ta\_LL* -
- *ta\_UL* -
- *rz* -
- *sem* -
- *z* -
- *p* -
- **es\_r**
  - *grouping\_variable\_name* -
  - *grouping\_variable\_level* -
  - *x\_variable\_name* -
  - *y\_variable\_name* -
  - *effect* -
  - *effect\_size* -
  - *LL* -
  - *UL* -
  - *SE* -
  - *n* -
  - *df* -
  - *ta\_LL* -
  - *ta\_UL* -
- **raw\_data**
  - *x* -
  - *y* -
  - *grouping\_variable* -

## Examples

```
# From raw data
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_rdiff_two(
  esci::data_campus_involvement,
  GPA,
  SWB,
  Gender
)

# To visualize the difference in r
myplot_from_raw <- esci::plot_rdiff(estimate_from_raw)

# To visualize the data (scatterplot) by group
myplot_scatter <- esci::plot_scatter(estimate_from_raw)

# To evaluate a hypothesis (by default: point null of exactly 0):
res_htest_from_raw <- esci::test_rdiff(
```

```

    estimate_from_raw
  )

# From summary data
estimate <- esci::estimate_rdiff_two(
  comparison_r = .53,
  comparison_n = 45,
  reference_r = .41,
  reference_n = 59,
  grouping_variable_levels = c("Females", "Males"),
  x_variable_name = "Satisfaction with life",
  y_variable_name = "Body satisfaction",
  grouping_variable_name = "Gender",
  conf_level = .95
)

myplot_from_summary <- esci::plot_rdiff(estimate)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
res_hstest_from_summary <- esci::test_rdiff(
  estimate,
  rope = c(-0.1, 0.1)
)

```

---

geom\_meta\_diamond\_h    *Meta-analysis diamond*

---

## Description

geom\_meta\_diamond\_h creates a horizontal meta-analytic diamond defined by an x value (horizontal center of diamond), xmin and xmax values (for the horizontal ends of the diamond), a y value (for the vertical placement of the diamond) and a height (for the vertical height of the diamond). Note the use of xmin and xmax allows for representation of asymmetric confidence intervals with this geom.

## Usage

```

geom_meta_diamond_h(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

```

**Arguments**

mapping	Set of aesthetic mappings created by <code>aes()</code> . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <code>ggplot()</code>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify()</code> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
stat	<p>The statistical transformation to use on the data for this layer. When using a <code>geom_*()</code> function to construct a layer, the <code>stat</code> argument can be used to override the default coupling between geoms and stats. The <code>stat</code> argument accepts the following:</p> <ul style="list-style-type: none"> <li>• A Stat ggproto subclass, for example <code>StatCount</code>.</li> <li>• A string naming the stat. To give the stat as a string, strip the function name of the <code>stat_</code> prefix. For example, to use <code>stat_count()</code>, give the stat as "count".</li> <li>• For more information and other ways to specify the stat, see the <a href="#">layer stat</a> documentation.</li> </ul>
position	<p>A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following:</p> <ul style="list-style-type: none"> <li>• The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position.</li> <li>• A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter".</li> <li>• For more information and other ways to specify the position, see the <a href="#">layer position</a> documentation.</li> </ul>
...	<p>Other arguments passed to the geom. These are often aesthetics, used to set an aesthetic to a fixed value, like <code>colour = "red"</code> or <code>linewidth = 3</code> (see <b>Aesthetics</b>, below).</p> <p><b>##Aesthetics ## geom_meta_diamond_h understands the following aesthetics (required are in bold):</b></p> <ul style="list-style-type: none"> <li>• <b>x</b> - The horizontal center of the diamond</li> <li>• <b>y</b> - The vertical placement of the diamond</li> <li>• <b>xmin</b> - The left-side start of the diamond</li> <li>• <b>xmax</b> - The right-side start of the diamond</li> <li>• <b>height</b> - The vertical span of the diamond</li> </ul>



<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .

## Examples

```
# example code
library(ggplot2)

my_effects <- data.frame(
  effect_size = c(1, 2, 1, 0),
  UL = c(2, 3, 2, 1),
  LL = c(0, 1, 0, -1),
  y = c(1, 2, 3, 4)
)

myplot <- ggplot2::ggplot()
myplot <- myplot + geom_meta_diamond_h(
  data = my_effects,
  ggplot2::aes(
    x = effect_size,
    xmin = LL,
    xmax = UL,
    y = y
  ),
  height = 0.25,
  color = "black",
  fill = "red",
)
```

## Description

Correlations: Single Group

**Usage**

```
jamovicorrelation(  
  switch = "from_raw",  
  data,  
  x,  
  y,  
  r = " ",  
  n = " ",  
  x_variable_name = "X variable",  
  y_variable_name = "Y variable",  
  conf_level = 95,  
  show_details = FALSE,  
  do_regression = FALSE,  
  show_line = FALSE,  
  show_line_CI = FALSE,  
  show_residuals = FALSE,  
  show_PI = FALSE,  
  show_mean_lines = FALSE,  
  show_r = FALSE,  
  plot_as_z = FALSE,  
  predict_from_x = " ",  
  evaluate_hypotheses = FALSE,  
  null_value = "0",  
  null_boundary = "0",  
  alpha = 0.05,  
  null_color = "#A40122",  
  es_plot_width = "300",  
  es_plot_height = "400",  
  sp_plot_width = "650",  
  sp_plot_height = "650",  
  ymin = "-1",  
  ymax = "1",  
  ybreaks = "auto",  
  ylab = "auto",  
  xlab = "auto",  
  axis.text.y = "14",  
  axis.title.y = "15",  
  axis.text.x = "14",  
  axis.title.x = "15",  
  error_layout = "none",  
  sp_ymin = "auto",  
  sp_ymax = "auto",  
  sp_ybreaks = "auto",  
  sp_xmin = "auto",  
  sp_xmax = "auto",  
  sp_xbreaks = "auto",  
  sp_ylab = "auto",  
  sp_xlab = "auto",
```

```
sp_axis.text.y = "14",
sp_axis.title.y = "15",
sp_axis.text.x = "14",
sp_axis.title.x = "15",
shape_summary = "circle filled",
color_summary = "#008DF9",
fill_summary = "#008DF9",
size_summary = "4",
alpha_summary = "1",
linetype_summary = "solid",
color_interval = "black",
size_interval = "3",
alpha_interval = "1",
alpha_error = "1",
fill_error = "gray75",
sp_shape_raw_reference = "circle filled",
sp_color_raw_reference = "black",
sp_fill_raw_reference = "#008DF9",
sp_size_raw_reference = "3",
sp_alpha_raw_reference = ".25",
sp_linetype_summary_reference = "solid",
sp_color_summary_reference = "#008DF9",
sp_size_summary_reference = "3",
sp_alpha_summary_reference = ".25",
sp_linetype_PI_reference = "dotted",
sp_color_PI_reference = "#E20134",
sp_size_PI_reference = "2",
sp_alpha_PI_reference = "1",
sp_linetype_residual_reference = "solid",
sp_color_residual_reference = "#E20134",
sp_size_residual_reference = "1",
sp_alpha_residual_reference = "1",
sp_prediction_label = "5",
sp_prediction_color = "#E20134",
sp_linetype_CI = "solid",
sp_color_CI = "#008DF9",
sp_size_CI = "4",
sp_alpha_CI = "1",
sp_linetype_ref = "dotted",
sp_color_ref = "gray60",
sp_size_ref = "1",
sp_alpha_ref = "1",
sp_linetype_PI = "solid",
sp_color_PI = "#E20134",
sp_size_PI = "2",
sp_alpha_PI = "1"
)
```

**Arguments**

```

switch          .
data            .
x              .
y              .
r              .
n              .
x_variable_name
y_variable_name
.
conf_level     .
show_details   .
do_regression  .
show_line      .
show_line_CI   .
show_residuals .
show_PI        .
show_mean_lines
.
show_r         .
plot_as_z      .
predict_from_x .
evaluate_hypotheses
.
null_value     .
null_boundary  .
alpha          .
null_color     .
es_plot_width  .
es_plot_height .
sp_plot_width  .
sp_plot_height .
ymin          .
ymax          .
ybreaks       .
ylab           .
xlab           .
axis.text.y    .

```

axis.title.y .  
axis.text.x .  
axis.title.x .  
error\_layout .  
sp\_ymin .  
sp\_ymax .  
sp\_ybreaks .  
sp\_xmin .  
sp\_xmax .  
sp\_xbreaks .  
sp\_ylab .  
sp\_xlab .  
sp\_axis.text.y .  
sp\_axis.title.y .  
sp\_axis.text.x .  
sp\_axis.title.x .  
shape\_summary .  
color\_summary .  
fill\_summary .  
size\_summary .  
alpha\_summary .  
linetype\_summary .  
color\_interval .  
size\_interval .  
alpha\_interval .  
alpha\_error .  
fill\_error .  
sp\_shape\_raw\_reference .  
sp\_color\_raw\_reference .  
sp\_fill\_raw\_reference .  
sp\_size\_raw\_reference .  
sp\_alpha\_raw\_reference .

```
sp_linetype_summary_reference
.
sp_color_summary_reference
.
sp_size_summary_reference
.
sp_alpha_summary_reference
.
sp_linetype_PI_reference
.
sp_color_PI_reference
.
sp_size_PI_reference
.
sp_alpha_PI_reference
.
sp_linetype_residual_reference
.
sp_color_residual_reference
.
sp_size_residual_reference
.
sp_alpha_residual_reference
.
sp_prediction_label
.
sp_prediction_color
.
sp_linetype_CI .
sp_color_CI .
sp_size_CI .
sp_alpha_CI .
sp_linetype_ref
.
sp_color_ref .
sp_size_ref .
sp_alpha_ref .
sp_linetype_PI .
sp_color_PI .
sp_size_PI .
sp_alpha_PI .
```

**Value**

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_r	a table
results\$regression	a table
results\$point_null	a table
results\$interval_null	a table
results\$scatter_plot_warnings	a html
results\$scatter_plots	an image
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$overview$asDF
as.data.frame(results$overview)
```

---

jamovidescribe

*Describe*

---

**Description**

Describe

**Usage**

```
jamovidescribe(
  data,
  outcome_variable,
  show_details = FALSE,
  mark_mean = FALSE,
  mark_median = FALSE,
  mark_sd = FALSE,
  mark_quartiles = FALSE,
  mark_z_lines = FALSE,
  mark_percentile = "0",
  histogram_bins = "12",
  es_plot_width = "500",
  es_plot_height = "400",
  ymin = "auto",
  ymax = "auto",
  breaks = "auto",
```

```

xmin = "auto",
xmax = "auto",
xbreaks = "auto",
ylab = "auto",
xlab = "auto",
axis.text.y = "14",
axis.title.y = "15",
axis.text.x = "14",
axis.title.x = "15",
fill_regular = "#008DF9",
fill_highlighted = "#E20134",
color = "black",
marker_size = "4"
)

```

### Arguments

```

data .
outcome_variable .
.
show_details .
mark_mean .
mark_median .
mark_sd .
mark_quartiles .
mark_z_lines .
mark_percentile .
.
histogram_bins .
es_plot_width .
es_plot_height .
ymin .
ymax .
breaks .
xmin .
xmax .
xbreaks .
ylab .
xlab .
axis.text.y .
axis.title.y .
axis.text.x .

```



```

axis.title.x    .
fill_regular   .
fill_highlighted
               .
color          .
marker_size    .

```

### Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$describe_plot_warnings	a html
results\$describe_plot	an image
results\$describe_dotplot	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```

---

jamovimagnitude	<i>Means and Medians: Single Group</i>
-----------------	--

---

### Description

Means and Medians: Single Group

### Usage

```

jamovimagnitude(
  switch = "from_raw",
  data,
  outcome_variable,
  mean = "",
  sd = "",
  n = "",
  outcome_variable_name = "Outcome variable",
  conf_level = 95,
  effect_size = "mean",
  show_details = FALSE,
  show_calculations = FALSE,
  evaluate_hypotheses = FALSE,

```

```

null_value = "0",
null_boundary = "0",
alpha = 0.05,
null_color = "#A40122",
es_plot_width = "300",
es_plot_height = "400",
ymin = "auto",
ymax = "auto",
breaks = "auto",
ylab = "auto",
xlab = "auto",
axis.text.y = "14",
axis.title.y = "15",
axis.text.x = "14",
axis.title.x = "15",
error_layout = "halfeye",
error_scale = "0.20",
error_nudge = "0.3",
data_layout = "random",
data_spread = "0.25",
shape_raw = "circle filled",
shape_summary = "circle filled",
color_raw = "#008DF9",
color_summary = "#008DF9",
fill_raw = "NA",
fill_summary = "#008DF9",
size_raw = "2",
size_summary = "4",
alpha_raw = "1",
alpha_summary = "1",
linetype_summary = "solid",
color_interval = "black",
size_interval = "3",
alpha_interval = "1",
alpha_error = "1",
fill_error = "gray75"
)

```

### Arguments

```

switch      .
data        .
outcome_variable
            .
mean        .
sd          .
n           .

```

```
outcome_variable_name
.
conf_level      .
effect_size     .
show_details    .
show_calculations
.
evaluate_hypotheses
.
null_value      .
null_boundary   .
alpha           .
null_color      .
es_plot_width   .
es_plot_height  .
ymin            .
ymax            .
breaks          .
ylab            .
xlab            .
axis.text.y     .
axis.title.y    .
axis.text.x     .
axis.title.x    .
error_layout    .
error_scale     .
error_nudge     .
data_layout     .
data_spread     .
shape_raw       .
shape_summary   .
color_raw       .
color_summary   .
fill_raw        .
fill_summary    .
size_raw        .
size_summary    .
alpha_raw       .
```

```

alpha_summary .
linetype_summary
.
color_interval .
size_interval .
alpha_interval .
alpha_error .
fill_error .

```

### Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_smd	a table
results\$point_null	a table
results\$interval_null	a table
results\$magnitude_plot_warnings	a html
results\$magnitude_plot	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```

---

jamovimdiff2x2

*Means and Medians: 2x2 Factorial*

---

### Description

Means and Medians: 2x2 Factorial

### Usage

```

jamovimdiff2x2(
  design = "fully_between",
  switch = "from_raw",
  data,
  outcome_variable,
  grouping_variable_A,
  grouping_variable_B,
  outcome_variable_level1,
  outcome_variable_level2,

```

```
outcome_variable_name_bs = "My outcome variable",
grouping_variable,
repeated_measures_name = "Time",
outcome_variable_name = "My outcome variable",
A1_label = "A1 level",
A2_label = "A2 level",
B1_label = "B1 level",
B2_label = "B2 level",
A_label = "Variable A",
B_label = "Variable B",
A1B1_mean = " ",
A1B1_sd = " ",
A1B1_n = " ",
A1B2_mean = " ",
A1B2_sd = " ",
A1B2_n = " ",
A2B1_mean = " ",
A2B1_sd = " ",
A2B1_n = " ",
A2B2_mean = " ",
A2B2_sd = " ",
A2B2_n = " ",
conf_level = 95,
effect_size = "mean_difference",
assume_equal_variance = TRUE,
show_details = FALSE,
show_interaction_plot = FALSE,
show_CI = FALSE,
evaluate_hypotheses = FALSE,
null_value = "0",
null_boundary = "0",
rope_units = "raw",
alpha = 0.05,
null_color = "#A40122",
es_plot_width = "700",
es_plot_height = "400",
ymin = "auto",
ymax = "auto",
ybreaks = "auto",
ylab = "auto",
xlab = "auto",
axis.text.y = "14",
axis.title.y = "15",
axis.text.x = "14",
axis.title.x = "15",
simple_contrast_labels = FALSE,
error_layout = "halfeye",
error_scale = "0.25",
```

```
error_nudge = "0.5",
data_layout = "random",
data_spread = "0.20",
difference_axis_units = "raw",
difference_axis_breaks = "auto",
shape_raw_reference = "circle filled",
shape_raw_comparison = "circle filled",
shape_raw_unused = "circle filled",
shape_summary_reference = "circle filled",
shape_summary_comparison = "circle filled",
shape_summary_unused = "circle filled",
shape_summary_difference = "triangle filled",
color_raw_reference = "#008DF9",
color_raw_comparison = "#009F81",
color_raw_unused = "gray65",
color_summary_reference = "#008DF9",
color_summary_comparison = "#009F81",
color_summary_unused = "gray65",
color_summary_difference = "black",
fill_raw_reference = "NA",
fill_raw_comparison = "NA",
fill_raw_unused = "NA",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_unused = "gray65",
fill_summary_difference = "black",
size_raw_reference = "2",
size_raw_comparison = "2",
size_raw_unused = "1",
size_summary_reference = "4",
size_summary_comparison = "4",
size_summary_unused = "4",
size_summary_difference = "4",
alpha_raw_reference = "1",
alpha_raw_comparison = "1",
alpha_raw_unused = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_unused = "1",
alpha_summary_difference = "1",
linetype_summary_reference = "solid",
linetype_summary_comparison = "solid",
linetype_summary_unused = "solid",
linetype_summary_difference = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_unused = "gray65",
color_interval_difference = "black",
```

```

    size_interval_reference = "3",
    size_interval_comparison = "3",
    size_interval_unused = "3",
    size_interval_difference = "3",
    alpha_interval_reference = "1",
    alpha_interval_comparison = "1",
    alpha_interval_unused = "1",
    alpha_interval_difference = "1",
    alpha_error_reference = "1",
    alpha_error_comparison = "1",
    alpha_error_unused = "1",
    alpha_error_difference = "1",
    fill_error_reference = "gray75",
    fill_error_comparison = "gray75",
    fill_error_unused = "gray75",
    fill_error_difference = "gray75"
  )

```

### Arguments

```

design          .
switch         .
data           .
outcome_variable
               .
grouping_variable_A
               .
grouping_variable_B
               .
outcome_variable_level1
               .
outcome_variable_level2
               .
outcome_variable_name_bs
               .
grouping_variable
               .
repeated_measures_name
               .
outcome_variable_name
               .
A1_label      .
A2_label      .
B1_label      .
B2_label      .
A_label       .

```

```
B_label .
A1B1_mean .
A1B1_sd .
A1B1_n .
A1B2_mean .
A1B2_sd .
A1B2_n .
A2B1_mean .
A2B1_sd .
A2B1_n .
A2B2_mean .
A2B2_sd .
A2B2_n .
conf_level .
effect_size .
assume_equal_variance .
show_details .
show_interaction_plot .
show_CI .
evaluate_hypotheses .
null_value .
null_boundary .
rope_units .
alpha .
null_color .
es_plot_width .
es_plot_height .
ymin .
ymax .
ybreaks .
ylab .
xlab .
axis.text.y .
axis.title.y .
axis.text.x .
```



```
axis.title.x      .
simple_contrast_labels
.
error_layout     .
error_scale      .
error_nudge      .
data_layout      .
data_spread      .
difference_axis_units
.
difference_axis_breaks
.
shape_raw_reference
.
shape_raw_comparison
.
shape_raw_unused
.
shape_summary_reference
.
shape_summary_comparison
.
shape_summary_unused
.
shape_summary_difference
.
color_raw_reference
.
color_raw_comparison
.
color_raw_unused
.
color_summary_reference
.
color_summary_comparison
.
color_summary_unused
.
color_summary_difference
.
fill_raw_reference
.
fill_raw_comparison
.
fill_raw_unused
.
```

fill\_summary\_reference  
.  
fill\_summary\_comparison  
.  
fill\_summary\_unused  
.  
fill\_summary\_difference  
.  
size\_raw\_reference  
.  
size\_raw\_comparison  
.  
size\_raw\_unused  
.  
size\_summary\_reference  
.  
size\_summary\_comparison  
.  
size\_summary\_unused  
.  
size\_summary\_difference  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_unused  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_unused  
.  
alpha\_summary\_difference  
.  
linetype\_summary\_reference  
.  
linetype\_summary\_comparison  
.  
linetype\_summary\_unused  
.  
linetype\_summary\_difference  
.  
color\_interval\_reference  
.  
color\_interval\_comparison  
.

```

color_interval_unused
.
color_interval_difference
.
size_interval_reference
.
size_interval_comparison
.
size_interval_unused
.
size_interval_difference
.
alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_unused
.
alpha_interval_difference
.
alpha_error_reference
.
alpha_error_comparison
.
alpha_error_unused
.
alpha_error_difference
.
fill_error_reference
.
fill_error_comparison
.
fill_error_unused
.
fill_error_difference
.

```

**Value**

A results object containing:

results\$analysis_type	a html
results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_median_difference	a table
results\$es_mean_difference	a table
results\$es_smd	a table

results\$point_null	a table
results\$interval_null	a table
results\$estimation_plot_warnings	a html
results\$main_effect_A	an image
results\$main_effect_B	an image
results\$interaction	an image
results\$interaction_plot	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$overview$asDF
as.data.frame(results$overview)
```

---

jamovimdiffindcontrast

*Means and Medians: Independent Groups Contrast*

---

## Description

Means and Medians: Independent Groups Contrast

## Usage

```
jamovimdiffindcontrast(
  switch = "from_raw",
  data,
  outcome_variable,
  grouping_variable,
  means,
  sds,
  ns,
  grouping_variable_levels,
  outcome_variable_name = "Outcome variable",
  grouping_variable_name = "Grouping variable",
  comparison_labels = " ",
  reference_labels = " ",
  conf_level = 95,
  effect_size = "mean_difference",
  assume_equal_variance = TRUE,
  show_details = FALSE,
  evaluate_hypotheses = FALSE,
  null_value = "0",
  null_boundary = "0",
  rope_units = "raw",
  alpha = 0.05,
  null_color = "#A40122",
```

```
es_plot_width = "550",
es_plot_height = "450",
ymin = "auto",
ymax = "auto",
ybreaks = "auto",
ylab = "auto",
xlab = "auto",
axis.text.y = "14",
axis.title.y = "15",
axis.text.x = "14",
axis.title.x = "15",
simple_contrast_labels = TRUE,
error_layout = "halfeye",
error_scale = "0.25",
error_nudge = "0.5",
data_layout = "random",
data_spread = "0.20",
difference_axis_units = "raw",
difference_axis_breaks = "auto",
shape_raw_reference = "circle filled",
shape_raw_comparison = "circle filled",
shape_raw_unused = "circle filled",
shape_summary_reference = "circle filled",
shape_summary_comparison = "circle filled",
shape_summary_unused = "circle filled",
shape_summary_difference = "triangle filled",
color_raw_reference = "#008DF9",
color_raw_comparison = "#009F81",
color_raw_unused = "gray65",
color_summary_reference = "#008DF9",
color_summary_comparison = "#009F81",
color_summary_unused = "gray65",
color_summary_difference = "black",
fill_raw_reference = "NA",
fill_raw_comparison = "NA",
fill_raw_unused = "NA",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_unused = "gray65",
fill_summary_difference = "black",
size_raw_reference = "2",
size_raw_comparison = "2",
size_raw_unused = "1",
size_summary_reference = "4",
size_summary_comparison = "4",
size_summary_unused = "4",
size_summary_difference = "4",
alpha_raw_reference = "1",
```

```

alpha_raw_comparison = "1",
alpha_raw_unused = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_unused = "1",
alpha_summary_difference = "1",
linetype_summary_reference = "solid",
linetype_summary_comparison = "solid",
linetype_summary_unused = "solid",
linetype_summary_difference = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_unused = "gray65",
color_interval_difference = "black",
size_interval_reference = "3",
size_interval_comparison = "3",
size_interval_unused = "3",
size_interval_difference = "3",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
alpha_interval_unused = "1",
alpha_interval_difference = "1",
alpha_error_reference = "1",
alpha_error_comparison = "1",
alpha_error_unused = "1",
alpha_error_difference = "1",
fill_error_reference = "gray75",
fill_error_comparison = "gray75",
fill_error_unused = "gray75",
fill_error_difference = "gray75"
)

```

### Arguments

```

switch      .
data        .
outcome_variable
            .
grouping_variable
            .
means       .
sds         .
ns          .
grouping_variable_levels
            .
outcome_variable_name
            .

```

```
grouping_variable_name
.
comparison_labels
.
reference_labels
.
conf_level      .
effect_size     .
assume_equal_variance
.
show_details    .
evaluate_hypotheses
.
null_value      .
null_boundary   .
rope_units      .
alpha           .
null_color      .
es_plot_width   .
es_plot_height  .
ymin            .
ymax            .
ybreaks         .
ylab            .
xlab            .
axis.text.y     .
axis.title.y    .
axis.text.x     .
axis.title.x    .
simple_contrast_labels
.
error_layout    .
error_scale     .
error_nudge     .
data_layout     .
data_spread     .
difference_axis_units
.
difference_axis_breaks
.
```

```
shape_raw_reference
.
shape_raw_comparison
.
shape_raw_unused
.
shape_summary_reference
.
shape_summary_comparison
.
shape_summary_unused
.
shape_summary_difference
.
color_raw_reference
.
color_raw_comparison
.
color_raw_unused
.
color_summary_reference
.
color_summary_comparison
.
color_summary_unused
.
color_summary_difference
.
fill_raw_reference
.
fill_raw_comparison
.
fill_raw_unused
.
fill_summary_reference
.
fill_summary_comparison
.
fill_summary_unused
.
fill_summary_difference
.
size_raw_reference
.
size_raw_comparison
.
size_raw_unused
.
```



size\_summary\_reference  
.  
size\_summary\_comparison  
.  
size\_summary\_unused  
.  
size\_summary\_difference  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_unused  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_unused  
.  
alpha\_summary\_difference  
.  
linetype\_summary\_reference  
.  
linetype\_summary\_comparison  
.  
linetype\_summary\_unused  
.  
linetype\_summary\_difference  
.  
color\_interval\_reference  
.  
color\_interval\_comparison  
.  
color\_interval\_unused  
.  
color\_interval\_difference  
.  
size\_interval\_reference  
.  
size\_interval\_comparison  
.  
size\_interval\_unused  
.  
size\_interval\_difference  
.  
alpha\_interval\_reference  
.  
.

```

alpha_interval_comparison
.
alpha_interval_unused
.
alpha_interval_difference
.
alpha_error_reference
.
alpha_error_comparison
.
alpha_error_unused
.
alpha_error_difference
.
fill_error_reference
.
fill_error_comparison
.
fill_error_unused
.
fill_error_difference
.

```

## Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_median_difference	a table
results\$es_mean_difference	a table
results\$es_smd	a table
results\$point_null	a table
results\$interval_null	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an array of images

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```

---

jamovimdiffpaired      *Means and Medians: Paired*

---

## Description

Means and Medians: Paired

## Usage

```
jamovimdiffpaired(  
  switch = "from_raw",  
  data,  
  reference_measure,  
  comparison_measure,  
  comparison_mean = " ",  
  comparison_sd = " ",  
  reference_mean = " ",  
  reference_sd = " ",  
  n = " ",  
  enter_r_or_sdiff = "enter_r",  
  correlation = " ",  
  sdiff = " ",  
  comparison_measure_name = "Comparison measure",  
  reference_measure_name = "Reference measure",  
  conf_level = 95,  
  effect_size = "mean_difference",  
  show_ratio = FALSE,  
  show_details = FALSE,  
  show_calculations = FALSE,  
  evaluate_hypotheses = FALSE,  
  null_value = "0",  
  null_boundary = "0",  
  rope_units = "raw",  
  alpha = 0.05,  
  null_color = "#A40122",  
  es_plot_width = "600",  
  es_plot_height = "400",  
  ymin = "auto",  
  ymax = "auto",  
  ybreaks = "auto",  
  ylab = "auto",  
  xlab = "auto",  
  axis.text.y = "14",  
  axis.title.y = "15",  
  axis.text.x = "14",  
  axis.title.x = "15",  
  simple_contrast_labels = TRUE,
```

```
error_layout = "halfeye",
error_scale = "0.25",
error_nudge = "0.5",
data_layout = "random",
data_spread = "0.20",
difference_axis_units = "raw",
difference_axis_breaks = "auto",
shape_raw_reference = "circle filled",
shape_raw_comparison = "circle filled",
shape_raw_difference = "triangle filled",
shape_summary_reference = "circle filled",
shape_summary_comparison = "circle filled",
shape_summary_difference = "triangle filled",
color_raw_reference = "#008DF9",
color_raw_comparison = "#008DF9",
color_raw_difference = "#E20134",
color_summary_reference = "#008DF9",
color_summary_comparison = "#008DF9",
color_summary_difference = "black",
fill_raw_reference = "NA",
fill_raw_comparison = "NA",
fill_raw_difference = "NA",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#008DF9",
fill_summary_difference = "black",
size_raw_reference = "2",
size_raw_comparison = "2",
size_raw_difference = "2",
size_summary_reference = "4",
size_summary_comparison = "4",
size_summary_difference = "4",
alpha_raw_reference = "1",
alpha_raw_comparison = "1",
alpha_raw_difference = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_difference = "1",
linetype_summary_reference = "solid",
linetype_summary_comparison = "solid",
linetype_summary_difference = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_difference = "black",
size_interval_reference = "3",
size_interval_comparison = "3",
size_interval_difference = "3",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
```

```

    alpha_interval_difference = "1",
    alpha_error_reference = "1",
    alpha_error_comparison = "1",
    alpha_error_difference = "1",
    fill_error_reference = "gray75",
    fill_error_comparison = "gray75",
    fill_error_difference = "gray75"
)

```

### Arguments

```

switch          .
data            .
reference_measure .
               .
comparison_measure .
               .
comparison_mean .
               .
comparison_sd   .
reference_mean  .
reference_sd    .
n              .
enter_r_or_sdiff .
               .
correlation     .
sdiff          .
comparison_measure_name .
               .
reference_measure_name .
               .
conf_level     .
effect_size    .
show_ratio     .
show_details   .
show_calculations .
               .
evaluate_hypotheses .
               .
null_value     .
null_boundary  .
rope_units     .
alpha         .

```

```
null_color      .
es_plot_width   .
es_plot_height  .
ymin            .
ymax            .
ybreaks         .
ylab            .
xlab            .
axis.text.y     .
axis.title.y    .
axis.text.x     .
axis.title.x    .
simple_contrast_labels
                .
error_layout    .
error_scale     .
error_nudge     .
data_layout     .
data_spread     .
difference_axis_units
                .
difference_axis_breaks
                .
shape_raw_reference
                .
shape_raw_comparison
                .
shape_raw_difference
                .
shape_summary_reference
                .
shape_summary_comparison
                .
shape_summary_difference
                .
color_raw_reference
                .
color_raw_comparison
                .
color_raw_difference
                .
color_summary_reference
                .
```

color\_summary\_comparison  
.  
color\_summary\_difference  
.  
fill\_raw\_reference  
.  
fill\_raw\_comparison  
.  
fill\_raw\_difference  
.  
fill\_summary\_reference  
.  
fill\_summary\_comparison  
.  
fill\_summary\_difference  
.  
size\_raw\_reference  
.  
size\_raw\_comparison  
.  
size\_raw\_difference  
.  
size\_summary\_reference  
.  
size\_summary\_comparison  
.  
size\_summary\_difference  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_difference  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_difference  
.  
linetype\_summary\_reference  
.  
linetype\_summary\_comparison  
.  
linetype\_summary\_difference  
.  
color\_interval\_reference  
.

```

color_interval_comparison
.
color_interval_difference
.
size_interval_reference
.
size_interval_comparison
.
size_interval_difference
.
alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_difference
.
alpha_error_reference
.
alpha_error_comparison
.
alpha_error_difference
.
fill_error_reference
.
fill_error_comparison
.
fill_error_difference
.

```

### Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_r	a table
results\$es_mean_difference	a table
results\$es_smd	a table
results\$es_mean_ratio	a table
results\$es_median_difference	a table
results\$es_median_ratio	a table
results\$point_null	a table
results\$interval_null	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:



```
results$overview$asDF
as.data.frame(results$overview)
```

---

jamovimdifftwo

*Means and Medians: Two Groups*

---

## Description

Means and Medians: Two Groups

## Usage

```
jamovimdifftwo(
  switch = "from_raw",
  data,
  outcome_variable,
  grouping_variable,
  reference_level_name = "Reference group",
  reference_mean = " ",
  reference_sd = " ",
  reference_n = " ",
  comparison_level_name = "Comparison group",
  comparison_mean = " ",
  comparison_sd = " ",
  comparison_n = " ",
  outcome_variable_name = "Outcome variable",
  grouping_variable_name = "Grouping variable",
  conf_level = 95,
  assume_equal_variance = TRUE,
  effect_size = "mean_difference",
  show_ratio = FALSE,
  switch_comparison_order = FALSE,
  show_details = FALSE,
  show_calculations = FALSE,
  evaluate_hypotheses = FALSE,
  null_value = "0",
  null_boundary = "0",
  rope_units = "raw",
  alpha = 0.05,
  null_color = "#A40122",
  es_plot_width = "600",
  es_plot_height = "400",
  ymin = "auto",
  ymax = "auto",
  ybreaks = "auto",
  ylab = "auto",
  xlab = "auto",
```

```
axis.text.y = "14",
axis.title.y = "15",
axis.text.x = "14",
axis.title.x = "15",
simple_contrast_labels = TRUE,
error_layout = "halfeye",
error_scale = "0.25",
error_nudge = "0.5",
data_layout = "random",
data_spread = "0.20",
difference_axis_units = "raw",
difference_axis_breaks = "auto",
shape_raw_reference = "circle filled",
shape_raw_comparison = "circle filled",
shape_summary_reference = "circle filled",
shape_summary_comparison = "circle filled",
shape_summary_difference = "triangle filled",
color_raw_reference = "#008DF9",
color_raw_comparison = "#009F81",
color_summary_reference = "#008DF9",
color_summary_comparison = "#009F81",
color_summary_difference = "black",
fill_raw_reference = "NA",
fill_raw_comparison = "NA",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_difference = "black",
size_raw_reference = "2",
size_raw_comparison = "2",
size_summary_reference = "4",
size_summary_comparison = "4",
size_summary_difference = "4",
alpha_raw_reference = "1",
alpha_raw_comparison = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_difference = "1",
linetype_summary_reference = "solid",
linetype_summary_comparison = "solid",
linetype_summary_difference = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_difference = "black",
size_interval_reference = "3",
size_interval_comparison = "3",
size_interval_difference = "3",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
```

```

    alpha_interval_difference = "1",
    alpha_error_reference = "1",
    alpha_error_comparison = "1",
    alpha_error_difference = "1",
    fill_error_reference = "gray75",
    fill_error_comparison = "gray75",
    fill_error_difference = "gray75"
)

```

### Arguments

```

switch          .
data            .
outcome_variable
               .
grouping_variable
               .
reference_level_name
               .
reference_mean  .
reference_sd    .
reference_n     .
comparison_level_name
               .
comparison_mean
               .
comparison_sd   .
comparison_n    .
outcome_variable_name
               .
grouping_variable_name
               .
conf_level     .
assume_equal_variance
               .
effect_size    .
show_ratio     .
switch_comparison_order
               .
show_details   .
show_calculations
               .
evaluate_hypotheses
               .
null_value     .

```

```
null_boundary .
rope_units .
alpha .
null_color .
es_plot_width .
es_plot_height .
ymin .
ymax .
ybreaks .
ylab .
xlab .
axis.text.y .
axis.title.y .
axis.text.x .
axis.title.x .
simple_contrast_labels
.
error_layout .
error_scale .
error_nudge .
data_layout .
data_spread .
difference_axis_units
.
difference_axis_breaks
.
shape_raw_reference
.
shape_raw_comparison
.
shape_summary_reference
.
shape_summary_comparison
.
shape_summary_difference
.
color_raw_reference
.
color_raw_comparison
.
color_summary_reference
.
```

color\_summary\_comparison  
.  
color\_summary\_difference  
.  
fill\_raw\_reference  
.  
fill\_raw\_comparison  
.  
fill\_summary\_reference  
.  
fill\_summary\_comparison  
.  
fill\_summary\_difference  
.  
size\_raw\_reference  
.  
size\_raw\_comparison  
.  
size\_summary\_reference  
.  
size\_summary\_comparison  
.  
size\_summary\_difference  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_difference  
.  
linetype\_summary\_reference  
.  
linetype\_summary\_comparison  
.  
linetype\_summary\_difference  
.  
color\_interval\_reference  
.  
color\_interval\_comparison  
.  
color\_interval\_difference  
.  
size\_interval\_reference  
.  
.

```

size_interval_comparison
.
size_interval_difference
.
alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_difference
.
alpha_error_reference
.
alpha_error_comparison
.
alpha_error_difference
.
fill_error_reference
.
fill_error_comparison
.
fill_error_difference
.

```

## Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_mean_difference	a table
results\$es_smd	a table
results\$es_mean_ratio	a table
results\$es_median_difference	a table
results\$es_median_ratio	a table
results\$point_null	a table
results\$interval_null	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an array of images

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```

---

jamovimetamdiff      *Meta-Analysis: Difference in Means*

---

## Description

Meta-Analysis: Difference in Means

## Usage

```
jamovimetamdiff(  
  switch = "from_raw",  
  data,  
  comparison_means,  
  comparison_sds,  
  comparison_ns,  
  reference_means,  
  reference_sds,  
  reference_ns,  
  r,  
  labels,  
  moderator,  
  d,  
  dcomparison_ns,  
  dreference_ns,  
  dr,  
  dlabels,  
  dmoderator,  
  conf_level = 95,  
  effect_label = "My effect",  
  reported_effect_size = "mean_difference",  
  assume_equal_variance = TRUE,  
  random_effects = "random_effects",  
  include_PIs = FALSE,  
  show_details = FALSE,  
  es_plot_width = "600",  
  es_plot_height = "750",  
  size_base = "2",  
  size_multiplier = "3",  
  axis.text.y = "14",  
  report_CIs = FALSE,  
  meta_diamond_height = ".25",  
  xlab = "auto",  
  xmin = "auto",  
  xmax = "auto",  
  xbreaks = "auto",  
  mark_zero = TRUE,  
  axis.text.x = "14",
```

```
axis.title.x = "15",
dlab = "auto",
dmin = "auto",
dmax = "auto",
dbreaks = "auto",
shape_raw_reference = "square filled",
shape_raw_comparison = "square filled",
shape_summary_difference = "triangle filled",
shape_raw_unused = "square filled",
color_raw_reference = "#008DF9",
color_raw_comparison = "#009F81",
color_raw_unused = "gray65",
color_summary_reference = "#008DF9",
color_summary_comparison = "#009F81",
color_summary_unused = "gray75",
color_summary_difference = "black",
color_summary_overall = "black",
fill_raw_reference = "#008DF9",
fill_raw_comparison = "#009F81",
fill_raw_unused = "gray65",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_unused = "gray75",
fill_summary_difference = "black",
fill_summary_overall = "black",
alpha_raw_reference = "1",
alpha_raw_comparison = "1",
alpha_raw_unused = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_unused = "1",
alpha_summary_difference = "1",
alpha_summary_overall = "1",
linetype_raw_reference = "solid",
linetype_raw_comparison = "solid",
linetype_summary_difference = "solid",
linetype_raw_unused = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_difference = "black",
color_interval_unused = "black",
size_interval_reference = ".50",
size_interval_comparison = ".50",
size_interval_difference = ".50",
size_interval_unused = ".50",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
alpha_interval_difference = "1",
```



```

    alpha_interval_unused = "1"
  )

```

### Arguments

```

switch          .
data            .
comparison_means .
               .
comparison_sds  .
comparison_ns   .
reference_means .
               .
reference_sds   .
reference_ns    .
r              .
labels         .
moderator      .
d              .
dcomparison_ns .
dreference_ns  .
dr            .
dlabels       .
dmoderator    .
conf_level    .
effect_label  .
reported_effect_size
               .
assume_equal_variance
               .
random_effects .
include_PIs    .
show_details   .
es_plot_width  .
es_plot_height .
size_base      .
size_multiplier
               .
axis.text.y    .
report_CIs     .

```

```
meta_diamond_height
      .
xlab      .
xmin      .
xmax      .
xbreaks   .
mark_zero .
axis.text.x .
axis.title.x .
dlab      .
dmin      .
dmax      .
dbreaks   .
shape_raw_reference
      .
shape_raw_comparison
      .
shape_summary_difference
      .
shape_raw_unused
      .
color_raw_reference
      .
color_raw_comparison
      .
color_raw_unused
      .
color_summary_reference
      .
color_summary_comparison
      .
color_summary_unused
      .
color_summary_difference
      .
color_summary_overall
      .
fill_raw_reference
      .
fill_raw_comparison
      .
fill_raw_unused
      .
fill_summary_reference
      .
```

fill\_summary\_comparison  
.  
fill\_summary\_unused  
.  
fill\_summary\_difference  
.  
fill\_summary\_overall  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_unused  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_unused  
.  
alpha\_summary\_difference  
.  
alpha\_summary\_overall  
.  
linetype\_raw\_reference  
.  
linetype\_raw\_comparison  
.  
linetype\_summary\_difference  
.  
linetype\_raw\_unused  
.  
color\_interval\_reference  
.  
color\_interval\_comparison  
.  
color\_interval\_difference  
.  
color\_interval\_unused  
.  
size\_interval\_reference  
.  
size\_interval\_comparison  
.  
size\_interval\_difference  
.  
size\_interval\_unused  
.

```

alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_difference
.
alpha_interval_unused
.

```

### Value

A results object containing:

results\$debug	a html
results\$help	a html
results\$raw_data	a table
results\$es_meta	a table
results\$es_heterogeneity	a table
results\$es_meta_difference	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$raw_data$asDF
as.data.frame(results$raw_data)

```

---

jamovimetamean

*Meta-Analysis: Means*

---

### Description

Meta-Analysis: Means

### Usage

```

jamovimetamean(
  switch = "from_raw",
  data,
  means,
  sds,
  ns,
  labels,
  moderator,
  ds,
  dns,

```

```
dlabels,  
dmoderator,  
conf_level = 95,  
effect_label = "My effect",  
reference_mean = "",  
reported_effect_size = "mean_difference",  
random_effects = "random_effects",  
include_PIs = FALSE,  
show_details = FALSE,  
es_plot_width = "600",  
es_plot_height = "750",  
size_base = "2",  
size_multiplier = "3",  
axis.text.y = "14",  
report_CIs = FALSE,  
meta_diamond_height = ".25",  
xlab = "auto",  
xmin = "auto",  
xmax = "auto",  
xbreaks = "auto",  
mark_zero = TRUE,  
axis.text.x = "14",  
axis.title.x = "15",  
dlab = "auto",  
dmin = "auto",  
dmax = "auto",  
dbreaks = "auto",  
shape_raw_reference = "square filled",  
shape_raw_comparison = "square filled",  
shape_summary_difference = "triangle filled",  
shape_raw_unused = "square filled",  
color_raw_reference = "#008DF9",  
color_raw_comparison = "#009F81",  
color_raw_unused = "gray65",  
color_summary_reference = "#008DF9",  
color_summary_comparison = "#009F81",  
color_summary_unused = "gray75",  
color_summary_difference = "black",  
color_summary_overall = "black",  
fill_raw_reference = "#008DF9",  
fill_raw_comparison = "#009F81",  
fill_raw_unused = "gray65",  
fill_summary_reference = "#008DF9",  
fill_summary_comparison = "#009F81",  
fill_summary_unused = "gray75",  
fill_summary_difference = "black",  
fill_summary_overall = "black",  
alpha_raw_reference = "1",
```

```

alpha_raw_comparison = "1",
alpha_raw_unused = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_unused = "1",
alpha_summary_difference = "1",
alpha_summary_overall = "1",
linetype_raw_reference = "solid",
linetype_raw_comparison = "solid",
linetype_summary_difference = "solid",
linetype_raw_unused = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_difference = "black",
color_interval_unused = "black",
size_interval_reference = ".50",
size_interval_comparison = ".50",
size_interval_difference = ".50",
size_interval_unused = ".50",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
alpha_interval_difference = "1",
alpha_interval_unused = "1"
)

```

### Arguments

```

switch      .
data        .
means       .
sds         .
ns          .
labels      .
moderator   .
ds          .
dns         .
dlabels     .
dmoderator  .
conf_level  .
effect_label .
reference_mean .
reported_effect_size
            .
random_effects .

```

```
include_PIs      .
show_details    .
es_plot_width   .
es_plot_height  .
size_base       .
size_multiplier .
                .
axis.text.y     .
report_CIs      .
meta_diamond_height
                .
xlab            .
xmin           .
xmax           .
xbreaks        .
mark_zero      .
axis.text.x     .
axis.title.x   .
dlab           .
dmin           .
dmax           .
dbreaks        .
shape_raw_reference
                .
shape_raw_comparison
                .
shape_summary_difference
                .
shape_raw_unused
                .
color_raw_reference
                .
color_raw_comparison
                .
color_raw_unused
                .
color_summary_reference
                .
color_summary_comparison
                .
color_summary_unused
                .
```

color\_summary\_difference  
.  
color\_summary\_overall  
.  
fill\_raw\_reference  
.  
fill\_raw\_comparison  
.  
fill\_raw\_unused  
.  
fill\_summary\_reference  
.  
fill\_summary\_comparison  
.  
fill\_summary\_unused  
.  
fill\_summary\_difference  
.  
fill\_summary\_overall  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_unused  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_unused  
.  
alpha\_summary\_difference  
.  
alpha\_summary\_overall  
.  
linetype\_raw\_reference  
.  
linetype\_raw\_comparison  
.  
linetype\_summary\_difference  
.  
linetype\_raw\_unused  
.  
color\_interval\_reference  
.  
color\_interval\_comparison  
.



```

color_interval_difference
.
color_interval_unused
.
size_interval_reference
.
size_interval_comparison
.
size_interval_difference
.
size_interval_unused
.
alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_difference
.
alpha_interval_unused
.

```

## Value

A results object containing:

results\$debug	a html
results\$help	a html
results\$raw_data	a table
results\$es_meta	a table
results\$es_heterogeneity	a table
results\$es_meta_difference	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$raw_data$asDF
as.data.frame(results$raw_data)

```

---

`jamovimetapdiff`*Meta-Analysis: Difference in Proportions*

---

**Description**

Meta-Analysis: Difference in Proportions

**Usage**

```
jamovimetapdiff(  
  data,  
  reference_cases,  
  reference_ns,  
  comparison_cases,  
  comparison_ns,  
  labels,  
  moderator,  
  effect_label = "My effect",  
  reported_effect_size = "RD",  
  conf_level = 95,  
  random_effects = "random_effects",  
  include_PIs = FALSE,  
  show_details = FALSE,  
  es_plot_width = "600",  
  es_plot_height = "750",  
  size_base = "2",  
  size_multiplier = "3",  
  axis.text.y = "14",  
  report_CIs = FALSE,  
  meta_diamond_height = ".25",  
  xlab = "auto",  
  xmin = "auto",  
  xmax = "auto",  
  xbreaks = "auto",  
  mark_zero = FALSE,  
  axis.text.x = "14",  
  axis.title.x = "15",  
  dlab = "auto",  
  dmin = "auto",  
  dmax = "auto",  
  dbreaks = "auto",  
  shape_raw_reference = "square filled",  
  shape_raw_comparison = "square filled",  
  shape_summary_difference = "triangle filled",  
  shape_raw_unused = "square filled",  
  color_raw_reference = "#008DF9",  
  color_raw_comparison = "#009F81",
```

```

color_raw_unused = "gray65",
color_summary_reference = "#008DF9",
color_summary_comparison = "#009F81",
color_summary_unused = "gray75",
color_summary_difference = "black",
color_summary_overall = "black",
fill_raw_reference = "#008DF9",
fill_raw_comparison = "#009F81",
fill_raw_unused = "gray65",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_unused = "gray75",
fill_summary_difference = "black",
fill_summary_overall = "black",
alpha_raw_reference = "1",
alpha_raw_comparison = "1",
alpha_raw_unused = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_unused = "1",
alpha_summary_difference = "1",
alpha_summary_overall = "1",
linetype_raw_reference = "solid",
linetype_raw_comparison = "solid",
linetype_summary_difference = "solid",
linetype_raw_unused = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_difference = "black",
color_interval_unused = "black",
size_interval_reference = ".50",
size_interval_comparison = ".50",
size_interval_difference = ".50",
size_interval_unused = ".50",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
alpha_interval_difference = "1",
alpha_interval_unused = "1"
)

```

### Arguments

```

data          .
reference_cases
              .
reference_ns   .
comparison_cases
              .

```

```
comparison_ns .
labels .
moderator .
effect_label .
reported_effect_size
.
conf_level .
random_effects .
include_PIs .
show_details .
es_plot_width .
es_plot_height .
size_base .
size_multiplier
.
axis.text.y .
report_CIs .
meta_diamond_height
.
xlab .
xmin .
xmax .
xbreaks .
mark_zero .
axis.text.x .
axis.title.x .
dlab .
dmin .
dmax .
dbreaks .
shape_raw_reference
.
shape_raw_comparison
.
shape_summary_difference
.
shape_raw_unused
.
color_raw_reference
.
```

color\_raw\_comparison  
.  
color\_raw\_unused  
.  
color\_summary\_reference  
.  
color\_summary\_comparison  
.  
color\_summary\_unused  
.  
color\_summary\_difference  
.  
color\_summary\_overall  
.  
fill\_raw\_reference  
.  
fill\_raw\_comparison  
.  
fill\_raw\_unused  
.  
fill\_summary\_reference  
.  
fill\_summary\_comparison  
.  
fill\_summary\_unused  
.  
fill\_summary\_difference  
.  
fill\_summary\_overall  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_unused  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_unused  
.  
alpha\_summary\_difference  
.  
alpha\_summary\_overall  
.  
linetype\_raw\_reference  
.

```

linetype_raw_comparison
.
linetype_summary_difference
.
linetype_raw_unused
.
color_interval_reference
.
color_interval_comparison
.
color_interval_difference
.
color_interval_unused
.
size_interval_reference
.
size_interval_comparison
.
size_interval_difference
.
size_interval_unused
.
alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_difference
.
alpha_interval_unused
.

```

## Value

A results object containing:

results\$debug	a html
results\$help	a html
results\$raw_data	a table
results\$es_meta	a table
results\$es_heterogeneity	a table
results\$es_meta_difference	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$raw_data$asDF
as.data.frame(results$raw_data)

```

---

jamovimetaproportion *Meta-Analysis: Proportions*

---

## Description

Meta-Analysis: Proportions

## Usage

```
jamovimetaproportion(  
  data,  
  cases,  
  ns,  
  labels,  
  moderator,  
  effect_label = "My effect",  
  conf_level = 95,  
  random_effects = "random_effects",  
  include_PIs = FALSE,  
  show_details = FALSE,  
  es_plot_width = "600",  
  es_plot_height = "750",  
  size_base = "2",  
  size_multiplier = "3",  
  axis.text.y = "14",  
  report_CIs = FALSE,  
  meta_diamond_height = ".25",  
  xlab = "auto",  
  xmin = "auto",  
  xmax = "auto",  
  xbreaks = "auto",  
  mark_zero = FALSE,  
  axis.text.x = "14",  
  axis.title.x = "15",  
  dlab = "auto",  
  dmin = "auto",  
  dmax = "auto",  
  dbreaks = "auto",  
  shape_raw_reference = "square filled",  
  shape_raw_comparison = "square filled",  
  shape_summary_difference = "triangle filled",  
  shape_raw_unused = "square filled",  
  color_raw_reference = "#008DF9",  
  color_raw_comparison = "#009F81",  
  color_raw_unused = "gray65",  
  color_summary_reference = "#008DF9",  
  color_summary_comparison = "#009F81",
```

```

color_summary_unused = "gray75",
color_summary_difference = "black",
color_summary_overall = "black",
fill_raw_reference = "#008DF9",
fill_raw_comparison = "#009F81",
fill_raw_unused = "gray65",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_unused = "gray75",
fill_summary_difference = "black",
fill_summary_overall = "black",
alpha_raw_reference = "1",
alpha_raw_comparison = "1",
alpha_raw_unused = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_unused = "1",
alpha_summary_difference = "1",
alpha_summary_overall = "1",
linetype_raw_reference = "solid",
linetype_raw_comparison = "solid",
linetype_summary_difference = "solid",
linetype_raw_unused = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_difference = "black",
color_interval_unused = "black",
size_interval_reference = ".50",
size_interval_comparison = ".50",
size_interval_difference = ".50",
size_interval_unused = ".50",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
alpha_interval_difference = "1",
alpha_interval_unused = "1"
)

```

### Arguments

```

data          .
cases         .
ns            .
labels        .
moderator     .
effect_label  .
conf_level    .
random_effects .

```



```
include_PIs      .
show_details     .
es_plot_width    .
es_plot_height   .
size_base        .
size_multiplier  .
                .
axis.text.y      .
report_CIs       .
meta_diamond_height
                .
xlab             .
xmin            .
xmax            .
xbreaks         .
mark_zero       .
axis.text.x     .
axis.title.x    .
dlab            .
dmin            .
dmax            .
dbreaks         .
shape_raw_reference
                .
shape_raw_comparison
                .
shape_summary_difference
                .
shape_raw_unused
                .
color_raw_reference
                .
color_raw_comparison
                .
color_raw_unused
                .
color_summary_reference
                .
color_summary_comparison
                .
color_summary_unused
                .
```

color\_summary\_difference  
.  
color\_summary\_overall  
.  
fill\_raw\_reference  
.  
fill\_raw\_comparison  
.  
fill\_raw\_unused  
.  
fill\_summary\_reference  
.  
fill\_summary\_comparison  
.  
fill\_summary\_unused  
.  
fill\_summary\_difference  
.  
fill\_summary\_overall  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_unused  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_unused  
.  
alpha\_summary\_difference  
.  
alpha\_summary\_overall  
.  
linetype\_raw\_reference  
.  
linetype\_raw\_comparison  
.  
linetype\_summary\_difference  
.  
linetype\_raw\_unused  
.  
color\_interval\_reference  
.  
color\_interval\_comparison  
.  
.

```

color_interval_difference
.
color_interval_unused
.
size_interval_reference
.
size_interval_comparison
.
size_interval_difference
.
size_interval_unused
.
alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_difference
.
alpha_interval_unused
.

```

## Value

A results object containing:

results\$debug	a html
results\$help	a html
results\$raw_data	a table
results\$es_meta	a table
results\$es_heterogeneity	a table
results\$es_meta_difference	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$raw_data$asDF
as.data.frame(results$raw_data)

```

---

jamovimetar

*Meta-Analysis: Correlations*

---

## Description

Meta-Analysis: Correlations

## Usage

```
jamovimetar(  
  data,  
  rs,  
  ns,  
  labels,  
  moderator,  
  effect_label = "My effect",  
  conf_level = 95,  
  random_effects = "random_effects",  
  include_PIs = FALSE,  
  show_details = FALSE,  
  es_plot_width = "600",  
  es_plot_height = "750",  
  size_base = "2",  
  size_multiplier = "3",  
  axis.text.y = "14",  
  report_CIs = FALSE,  
  meta_diamond_height = ".25",  
  xlab = "auto",  
  xmin = "-1",  
  xmax = "1",  
  xbreaks = "auto",  
  mark_zero = TRUE,  
  axis.text.x = "14",  
  axis.title.x = "15",  
  dlab = "auto",  
  dmin = "auto",  
  dmax = "auto",  
  dbreaks = "auto",  
  shape_raw_reference = "square filled",  
  shape_raw_comparison = "square filled",  
  shape_summary_difference = "triangle filled",  
  shape_raw_unused = "square filled",  
  color_raw_reference = "#008DF9",  
  color_raw_comparison = "#009F81",  
  color_raw_unused = "gray65",  
  color_summary_reference = "#008DF9",  
  color_summary_comparison = "#009F81",
```

```

color_summary_unused = "gray75",
color_summary_difference = "black",
color_summary_overall = "black",
fill_raw_reference = "#008DF9",
fill_raw_comparison = "#009F81",
fill_raw_unused = "gray65",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_unused = "gray75",
fill_summary_difference = "black",
fill_summary_overall = "black",
alpha_raw_reference = "1",
alpha_raw_comparison = "1",
alpha_raw_unused = "1",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_unused = "1",
alpha_summary_difference = "1",
alpha_summary_overall = "1",
linetype_raw_reference = "solid",
linetype_raw_comparison = "solid",
linetype_summary_difference = "solid",
linetype_raw_unused = "solid",
color_interval_reference = "black",
color_interval_comparison = "black",
color_interval_difference = "black",
color_interval_unused = "black",
size_interval_reference = ".50",
size_interval_comparison = ".50",
size_interval_difference = ".50",
size_interval_unused = ".50",
alpha_interval_reference = "1",
alpha_interval_comparison = "1",
alpha_interval_difference = "1",
alpha_interval_unused = "1"
)

```

### Arguments

```

data      .
rs        .
ns        .
labels    .
moderator .
effect_label .
conf_level .
random_effects .

```

```

include_PIs      .
show_details    .
es_plot_width   .
es_plot_height  .
size_base       .
size_multiplier .
                .
axis.text.y     .
report_CIs      .
meta_diamond_height
                .
xlab            .
xmin           .
xmax           .
xbreaks        .
mark_zero      .
axis.text.x     .
axis.title.x    .
dlab           .
dmin           .
dmax           .
dbreaks        .
shape_raw_reference
                .
shape_raw_comparison
                .
shape_summary_difference
                .
shape_raw_unused
                .
color_raw_reference
                .
color_raw_comparison
                .
color_raw_unused
                .
color_summary_reference
                .
color_summary_comparison
                .
color_summary_unused
                .

```

color\_summary\_difference  
.  
color\_summary\_overall  
.  
fill\_raw\_reference  
.  
fill\_raw\_comparison  
.  
fill\_raw\_unused  
.  
fill\_summary\_reference  
.  
fill\_summary\_comparison  
.  
fill\_summary\_unused  
.  
fill\_summary\_difference  
.  
fill\_summary\_overall  
.  
alpha\_raw\_reference  
.  
alpha\_raw\_comparison  
.  
alpha\_raw\_unused  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_unused  
.  
alpha\_summary\_difference  
.  
alpha\_summary\_overall  
.  
linetype\_raw\_reference  
.  
linetype\_raw\_comparison  
.  
linetype\_summary\_difference  
.  
linetype\_raw\_unused  
.  
color\_interval\_reference  
.  
color\_interval\_comparison  
.

```

color_interval_difference
.
color_interval_unused
.
size_interval_reference
.
size_interval_comparison
.
size_interval_difference
.
size_interval_unused
.
alpha_interval_reference
.
alpha_interval_comparison
.
alpha_interval_difference
.
alpha_interval_unused
.

```

## Value

A results object containing:

results\$debug	a html
results\$help	a html
results\$raw_data	a table
results\$es_meta	a table
results\$es_heterogeneity	a table
results\$es_meta_difference	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$raw_data$asDF
as.data.frame(results$raw_data)

```



---

jamovipdiffpaired      *Proportions: Paired*

---

## Description

Proportions: Paired

## Usage

```
jamovipdiffpaired(  
  switch = "from_raw",  
  data,  
  reference_measure,  
  comparison_measure,  
  cases_consistent = " ",  
  cases_inconsistent = " ",  
  not_cases_consistent = " ",  
  not_cases_inconsistent = " ",  
  case_label = "Sick",  
  not_case_label = "Well",  
  comparison_measure_name = "Post-test",  
  reference_measure_name = "Pre-test",  
  conf_level = 95,  
  show_details = FALSE,  
  evaluate_hypotheses = FALSE,  
  null_value = "0",  
  null_boundary = "0",  
  alpha = 0.05,  
  null_color = "#A40122",  
  es_plot_width = "400",  
  es_plot_height = "450",  
  ymin = "auto",  
  ymax = "auto",  
  ybreaks = "auto",  
  ylab = "auto",  
  xlab = "auto",  
  axis.text.y = "14",  
  axis.title.y = "15",  
  axis.text.x = "14",  
  axis.title.x = "15",  
  simple_contrast_labels = TRUE,  
  error_layout = "none",  
  difference_axis_breaks = "auto",  
  shape_summary_reference = "circle filled",  
  shape_summary_comparison = "circle filled",  
  shape_summary_difference = "triangle filled",  
  color_summary_reference = "#008DF9",
```

```

    color_summary_comparison = "#009F81",
    color_summary_difference = "black",
    fill_summary_reference = "#008DF9",
    fill_summary_comparison = "#009F81",
    fill_summary_difference = "black",
    size_summary_reference = "4",
    size_summary_comparison = "4",
    size_summary_difference = "4",
    alpha_summary_reference = "1",
    alpha_summary_comparison = "1",
    alpha_summary_difference = "1",
    linetype_summary_reference = "solid",
    linetype_summary_comparison = "solid",
    linetype_summary_difference = "solid"
)

```

### Arguments

```

switch          .
data            .
reference_measure
               .
comparison_measure
               .
cases_consistent
               .
cases_inconsistent
               .
not_cases_consistent
               .
not_cases_inconsistent
               .
case_label      .
not_case_label  .
comparison_measure_name
               .
reference_measure_name
               .
conf_level      .
show_details    .
evaluate_hypotheses
               .
null_value      .
null_boundary   .
alpha           .
null_color      .

```

```
es_plot_width .
es_plot_height .
ymin .
ymax .
ybreaks .
ylab .
xlab .
axis.text.y .
axis.title.y .
axis.text.x .
axis.title.x .
simple_contrast_labels
.
error_layout .
difference_axis_breaks
.
shape_summary_reference
.
shape_summary_comparison
.
shape_summary_difference
.
color_summary_reference
.
color_summary_comparison
.
color_summary_difference
.
fill_summary_reference
.
fill_summary_comparison
.
fill_summary_difference
.
size_summary_reference
.
size_summary_comparison
.
size_summary_difference
.
alpha_summary_reference
.
alpha_summary_comparison
.
```

```

alpha_summary_difference
.
linetype_summary_reference
.
linetype_summary_comparison
.
linetype_summary_difference
.

```

## Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_proportion_difference	a table
results\$point_null	a table
results\$interval_null	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```

---

jamovipdifftwo

*Proportions: Two Groups*

---

## Description

Proportions: Two Groups

## Usage

```

jamovipdifftwo(
  switch = "from_raw",
  data,
  outcome_variable,
  grouping_variable,
  comparison_cases = " ",
  comparison_not_cases = " ",
  reference_cases = " ",
  reference_not_cases = " ",
  case_label = "Sick",

```

```
not_case_label = "Well",
grouping_variable_level1 = "Treated",
grouping_variable_level2 = "Control",
outcome_variable_name = "Outcome variable",
grouping_variable_name = "Grouping variable",
count_NA = FALSE,
show_ratio = FALSE,
show_chi_square = FALSE,
chi_table_option = "both",
show_phi = FALSE,
conf_level = 95,
show_details = FALSE,
evaluate_hypotheses = FALSE,
null_value = "0",
null_boundary = "0",
alpha = 0.05,
null_color = "#A40122",
es_plot_width = "400",
es_plot_height = "450",
ymin = "auto",
ymax = "auto",
ybreaks = "auto",
ylab = "auto",
xlab = "auto",
axis.text.y = "14",
axis.title.y = "15",
axis.text.x = "14",
axis.title.x = "15",
simple_contrast_labels = TRUE,
error_layout = "none",
difference_axis_breaks = "auto",
shape_summary_reference = "circle filled",
shape_summary_comparison = "circle filled",
shape_summary_difference = "triangle filled",
color_summary_reference = "#008DF9",
color_summary_comparison = "#009F81",
color_summary_difference = "black",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_difference = "black",
size_summary_reference = "4",
size_summary_comparison = "4",
size_summary_difference = "4",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_difference = "1",
linetype_summary_reference = "solid",
linetype_summary_comparison = "solid",
```

```

    linetype_summary_difference = "solid"
  )

```

### Arguments

```

switch          .
data            .
outcome_variable
               .
grouping_variable
               .
comparison_cases
               .
comparison_not_cases
               .
reference_cases
               .
reference_not_cases
               .
case_label     .
not_case_label .
grouping_variable_level1
               .
grouping_variable_level2
               .
outcome_variable_name
               .
grouping_variable_name
               .
count_NA       .
show_ratio     .
show_chi_square
               .
chi_table_option
               .
show_phi       .
conf_level     .
show_details   .
evaluate_hypotheses
               .
null_value     .
null_boundary  .
alpha          .
null_color     .

```

```
es_plot_width .
es_plot_height .
ymin .
ymax .
ybreaks .
ylab .
xlab .
axis.text.y .
axis.title.y .
axis.text.x .
axis.title.x .
simple_contrast_labels
.
error_layout .
difference_axis_breaks
.
shape_summary_reference
.
shape_summary_comparison
.
shape_summary_difference
.
color_summary_reference
.
color_summary_comparison
.
color_summary_difference
.
fill_summary_reference
.
fill_summary_comparison
.
fill_summary_difference
.
size_summary_reference
.
size_summary_comparison
.
size_summary_difference
.
alpha_summary_reference
.
alpha_summary_comparison
.
```

```

alpha_summary_difference
.
linetype_summary_reference
.
linetype_summary_comparison
.
linetype_summary_difference
.

```

## Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_proportion_difference	a table
results\$contingency_table	a table
results\$es_phi	a table
results\$es_odds_ratio	a table
results\$point_null	a table
results\$interval_null	a table
results\$estimation_plot_warnings	a html
results\$estimation_plots	an array of images

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```

---

jamoviproportion      *Proportions: Single Group*

---

## Description

Proportions: Single Group

## Usage

```

jamoviproportion(
  switch = "from_raw",
  data,
  outcome_variable,
  cases = " ",
  not_cases = " ",
  case_label = "Affected",

```



```

not_case_label = "Not Affected",
outcome_variable_name = "My outcome variable",
count_NA = FALSE,
conf_level = 95,
show_details = FALSE,
plot_possible = FALSE,
evaluate_hypotheses = FALSE,
null_value = "0",
null_boundary = "0",
alpha = 0.05,
null_color = "#A40122",
es_plot_width = "300",
es_plot_height = "400",
ymin = "0",
ymax = "1",
breaks = "auto",
ylab = "auto",
xlab = "auto",
axis.text.y = "14",
axis.title.y = "15",
axis.text.x = "14",
axis.title.x = "15",
error_layout = "none",
shape_summary = "circle filled",
color_summary = "#008DF9",
fill_summary = "#008DF9",
size_summary = "4",
alpha_summary = "1",
linetype_summary = "solid"
)

```

### Arguments

```

switch      .
data        .
outcome_variable
           .
cases       .
not_cases   .
case_label  .
not_case_label .
outcome_variable_name
           .
count_NA    .
conf_level  .
show_details .

```

```

plot_possible .
evaluate_hypotheses
.
null_value .
null_boundary .
alpha .
null_color .
es_plot_width .
es_plot_height .
ymin .
ymax .
breaks .
ylab .
xlab .
axis.text.y .
axis.title.y .
axis.text.x .
axis.title.x .
error_layout .
shape_summary .
color_summary .
fill_summary .
size_summary .
alpha_summary .
linetype_summary
.

```

### Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$point_null	a table
results\$interval_null	a table
results\$magnitude_plot_warnings	a html
results\$estimation_plots	an array of images

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```

**Description**

Correlations: Two Groups

**Usage**

```
jamovirdifftwo(  
  switch = "from_raw",  
  data,  
  x,  
  y,  
  grouping_variable,  
  comparison_r = " ",  
  comparison_n = " ",  
  reference_r = " ",  
  reference_n = " ",  
  x_variable_name = "X variable",  
  y_variable_name = "Y variable",  
  comparison_level_name = "Comparison level",  
  reference_level_name = "Reference level",  
  grouping_variable_name = "Grouping variable",  
  conf_level = 95,  
  show_details = FALSE,  
  show_line = TRUE,  
  show_line_CI = TRUE,  
  evaluate_hypotheses = FALSE,  
  null_value = "0",  
  null_boundary = "0",  
  alpha = 0.05,  
  null_color = "#A40122",  
  es_plot_width = "600",  
  es_plot_height = "400",  
  sp_plot_width = "650",  
  sp_plot_height = "650",  
  ymin = "auto",  
  ymax = "auto",  
  ybreaks = "auto",  
  ylab = "auto",  
  xlab = "auto",  
  axis.text.y = "14",  
  axis.title.y = "15",  
  axis.text.x = "14",  
  axis.title.x = "15",  
  sp_ymin = "auto",
```

```
sp_ymax = "auto",
sp_ybreaks = "auto",
sp_xmin = "auto",
sp_xmax = "auto",
sp_xbreaks = "auto",
sp_ylab = "auto",
sp_xlab = "auto",
sp_axis.text.y = "14",
sp_axis.title.y = "15",
sp_axis.text.x = "14",
sp_axis.title.x = "15",
difference_axis_breaks = "auto",
shape_summary_reference = "circle filled",
shape_summary_comparison = "circle filled",
shape_summary_difference = "triangle filled",
color_summary_reference = "#008DF9",
color_summary_comparison = "#009F81",
color_summary_difference = "black",
fill_summary_reference = "#008DF9",
fill_summary_comparison = "#009F81",
fill_summary_difference = "black",
size_summary_reference = "4",
size_summary_comparison = "4",
size_summary_difference = "4",
alpha_summary_reference = "1",
alpha_summary_comparison = "1",
alpha_summary_difference = "1",
linetype_summary_reference = "solid",
linetype_summary_comparison = "solid",
linetype_summary_difference = "solid",
sp_shape_raw_reference = "circle filled",
sp_shape_raw_comparison = "circle filled",
sp_shape_raw_unused = "circle filled",
sp_color_raw_reference = "black",
sp_color_raw_comparison = "black",
sp_color_raw_unused = "black",
sp_fill_raw_reference = "#008DF9",
sp_fill_raw_comparison = "#009F81",
sp_fill_raw_unused = "NA",
sp_size_raw_reference = "3",
sp_size_raw_comparison = "3",
sp_size_raw_unused = "2",
sp_alpha_raw_reference = ".25",
sp_alpha_raw_comparison = ".25",
sp_alpha_raw_unused = ".25",
sp_linetype_summary_reference = "solid",
sp_linetype_summary_comparison = "solid",
sp_color_summary_reference = "#008DF9",
```

```

    sp_color_summary_comparison = "#009F81",
    sp_size_summary_reference = "2",
    sp_size_summary_comparison = "2",
    sp_alpha_summary_reference = ".25",
    sp_alpha_summary_comparison = ".25"
)

```

### Arguments

```

switch          .
data            .
x               .
y               .
grouping_variable
                .
comparison_r    .
comparison_n    .
reference_r     .
reference_n     .
x_variable_name
                .
y_variable_name
                .
comparison_level_name
                .
reference_level_name
                .
grouping_variable_name
                .
conf_level      .
show_details    .
show_line       .
show_line_CI    .
evaluate_hypotheses
                .
null_value      .
null_boundary   .
alpha           .
null_color      .
es_plot_width   .
es_plot_height  .
sp_plot_width   .

```

```
sp_plot_height .
ymin .
ymax .
ybreaks .
ylab .
xlab .
axis.text.y .
axis.title.y .
axis.text.x .
axis.title.x .
sp_ymin .
sp_ymax .
sp_ybreaks .
sp_xmin .
sp_xmax .
sp_xbreaks .
sp_ylab .
sp_xlab .
sp_axis.text.y .
sp_axis.title.y
.
sp_axis.text.x .
sp_axis.title.x
.
difference_axis_breaks
.
shape_summary_reference
.
shape_summary_comparison
.
shape_summary_difference
.
color_summary_reference
.
color_summary_comparison
.
color_summary_difference
.
fill_summary_reference
.
fill_summary_comparison
.
```

fill\_summary\_difference  
.  
size\_summary\_reference  
.  
size\_summary\_comparison  
.  
size\_summary\_difference  
.  
alpha\_summary\_reference  
.  
alpha\_summary\_comparison  
.  
alpha\_summary\_difference  
.  
linetype\_summary\_reference  
.  
linetype\_summary\_comparison  
.  
linetype\_summary\_difference  
.  
sp\_shape\_raw\_reference  
.  
sp\_shape\_raw\_comparison  
.  
sp\_shape\_raw\_unused  
.  
sp\_color\_raw\_reference  
.  
sp\_color\_raw\_comparison  
.  
sp\_color\_raw\_unused  
.  
sp\_fill\_raw\_reference  
.  
sp\_fill\_raw\_comparison  
.  
sp\_fill\_raw\_unused  
.  
sp\_size\_raw\_reference  
.  
sp\_size\_raw\_comparison  
.  
sp\_size\_raw\_unused  
.  
sp\_alpha\_raw\_reference  
.  
sp\_alpha\_raw\_comparison  
.

```

sp_alpha_raw_unused
.
sp_linetype_summary_reference
.
sp_linetype_summary_comparison
.
sp_color_summary_reference
.
sp_color_summary_comparison
.
sp_size_summary_reference
.
sp_size_summary_comparison
.
sp_alpha_summary_reference
.
sp_alpha_summary_comparison
.

```

## Value

A results object containing:

results\$debug	a preformatted
results\$help	a html
results\$overview	a table
results\$es_r	a table
results\$es_r_difference	a table
results\$point_null	a table
results\$interval_null	a table
results\$scatter_plot_warnings	a html
results\$scatter_plots	an image
results\$estimation_plot_warnings	a html
results\$estimation_plots	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```

results$overview$asDF
as.data.frame(results$overview)

```



---

meta_any	<i>Estimate any meta effect.</i>
----------	----------------------------------

---

### Description

meta\_any is suitable for synthesizing any effect size across multiple studies. You must provide the effect size for each study and the predicted sampling variance for each study.

### Usage

```
meta_any(
  data,
  yi,
  vi,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  effect_size_name = "Effect size",
  moderator_variable_name = "My moderator",
  random_effects = TRUE,
  conf_level = 0.95
)
```

### Arguments

data	A data frame or tibble with columns
yi	Name a column in data containing the effect size for each study
vi	Name of a column in data containing the expected sampling variance for each study
labels	Name of a column in data containing a label for each study
moderator	Optional name of a column in data containing a factor as a categorical moderator
contrast	Optional vector specifying a contrast analysis for the categorical moderator. Only define if a moderator is defined; vector length should match number of levels in the moderator
effect_label	Optional human-friendly name for the effect being synthesized; defaults to 'My effect'
effect_size_name	Optional human-friendly name of the effect size being synthesized; defaults to 'Effect size'
moderator_variable_name	Optional human-friendly name of the moderator, if defined; If not passed but a moderator is defined, will be set to the quoted name of the moderator column or 'My moderator'

`random_effects` Use TRUE to obtain a random effect meta-analysis (usually recommended); FALSE for fixed effect.

`conf_level` The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

### Details

#' Once you generate an estimate with this function, you can visualize it with `plot_meta()`.  
 The meta-analytic effect size, confidence interval and heterogeneity estimates all come from `metafor::rma()`.  
 The diamond ratio and its confidence interval come from `CI_diamond_ratio()`.

### Value

An esci-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - *effect\_label* - Study label
  - *effect\_size* - Effect size
  - *LL* - Lower bound of `conf_level%` confidence interval
  - *UL* - Upper bound of `conf_level%` confidence interval
  - *SE* - Expected standard error
  - *k* - Number of studies
  - *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
  - *diamond\_ratio\_LL* - lower bound of `conf_level%` confidence interval for diamond ratio
  - *diamond\_ratio\_UL* - upper bound of `conf_level%` confidence interval for diamond ratio
  - *I2* - I2 measure of heterogeneity
  - *I2\_LL* - Lower bound of `conf_level%` confidence interval for I2
  - *I2\_UL* - upper bound of `conf_level%` confidence interval for I2
  - *PI\_LL* - lower bound of `conf_level%` of prediction interval
  - *PI\_UL* - upper bound of `conf_level%` of prediction interval
  - *p* - p value for the meta-analytic effect size, based on null of exactly 0
  - *\*width* - width of the effect-size confidence interval
  - *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
  - *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
  - *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
  - *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- **es\_heterogeneity** - A data frame of of heterogeneity values and `conf_level%` CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label

- *moderator\_variable\_name* - if moderator passed, gives name of the moderator
- *moderator\_level* - 'Overall' and each level of moderator, if passed
- *measure* - Name of the measure of heterogeneity
- *estimate* - Value of the heterogeneity estimate
- *LL* - lower bound of *conf\_level%* confidence interval
- *UL* - upper bound of *conf\_level%* confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis
  - *sample\_variance* - expected level of sampling variation
  - *SE* - expected standard error
  - *LL* - lower bound of *conf\_level%* confidence interval
  - *UL* - upper bound of *conf\_level%* confidence interval
  - *mean* - used to calculate study p value; this is the d value entered for the study
  - *sd* - use to calculate study p value; set to 1 for each study
  - *n* - study sample size
  - *p* - p value for the study, based on null of exactly 0

## Examples

```
#' # Data set -- see Introduction to the New Statistics, 2nd edition
data("data_mccabemichael_brain")

# Fixed effect, 95% CI
esizes <- esci::meta_mean(
  data = esci::data_mccabemichael_brain,
  means = "M Brain",
  sds = "s Brain",
  ns = "n Brain",
  labels = "Study name",
  random_effects = FALSE
)$raw_data

estimate <- esci::meta_any(
  data = esizes,
  yi = effect_size,
  vi = sample_variance,
  labels = label,
  effect_size_name = "Mean",
  random_effects = FALSE
)

myplot_forest <- esci::plot_meta(estimate)
```

meta\_d1

*Estimate a meta-analytic Cohen's d1 across multiple studies***Description**

meta\_d1 is suitable for synthesizing across multiple single-group studies with a continuous outcome variable, but where the outcome is not measured on the same scale in all studies

**Usage**

```
meta_d1(
  data,
  ds,
  ns,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  random_effects = TRUE,
  conf_level = 0.95
)
```

**Arguments**

data	A data frame or tibble
ds	Set of bias-adjusted cohen's d1 values, 1 for each study
ns	Set of sample sizes, positive integers, 1 for each study
labels	Optional set of labels, 1 for each study
moderator	Optional factor as a categorical moderator; should have $k > 2$ per group
contrast	Optional vector specifying a contrast between moderator levels
effect_label	Optional character providing a human-friendly label for the effect
random_effects	Boolean; TRUE for a random effects model; otherwise fixed effects
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

**Details**

Once you generate an estimate with this function, you can visualize it with [plot\\_meta\(\)](#).

Each study's effect size should be expressed as Cohen's d1:  $(\text{mean} - \text{reference}) / \text{sd}$ .

And the d1 values should all be corrected for bias. The function [CI\\_smd\\_one\(\)](#) can assist with converting raw data from each study to d1\_unbiased.

The meta-analytic effect size, confidence interval and heterogeneity estimates all come from [metafor::rma\(\)](#).

The diamond ratio and its confidence interval come from [CI\\_diamond\\_ratio\(\)](#).

**Value**

An esci-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - *effect\_label* - Study label
  - *effect\_size* - Effect size
  - *LL* - Lower bound of *conf\_level%* confidence interval
  - *UL* - Upper bound of *conf\_level%* confidence interval
  - *SE* - Expected standard error
  - *k* - Number of studies
  - *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
  - *diamond\_ratio\_LL* - lower bound of *conf\_level%* confidence interval for diamond ratio
  - *diamond\_ratio\_UL* - upper bound of *conf\_level%* confidence interval for diamond ratio
  - *I2* - I2 measure of heterogeneity
  - *I2\_LL* - Lower bound of *conf\_level%* confidence interval for I2
  - *I2\_UL* - upper bound of *conf\_level%* confidence interval for I2
  - *PI\_LL* - lower bound of *conf\_level%* of prediction interval
  - *PI\_UL* - upper bound of *conf\_level%* of prediction interval
  - *p* - p value for the meta-analytic effect size, based on null of exactly 0
  - *\*width* - width of the effect-size confidence interval
  - *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
  - *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
  - *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
  - *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- **es\_heterogeneity** - A data frame of of heterogeneity values and *conf\_level%* CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label
  - *moderator\_variable\_name* - if moderator passed, gives name of the moderator
  - *moderator\_level* - 'Overall' and each level of moderator, if passed
  - *measure* - Name of the measure of heterogeneity
  - *estimate* - Value of the heterogeneity estimate
  - *LL* - lower bound of *conf\_level%* confidence interval
  - *UL* - upper bound of *conf\_level%* confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis

- *sample\_variance* - expected level of sampling variation
- *SE* - expected standard error
- *LL* - lower bound of *conf\_level%* confidence interval
- *UL* - upper bound of *conf\_level%* confidence interval
- *mean* - used to calculate study p value; this is the d value entered for the study
- *sd* - use to calculate study p value; set to 1 for each study
- *n* - study sample size
- *p* - p value for the study, based on null of exactly 0

### Examples

```
# example code
original_7 <- data.frame(
  study_name = c(
    "Aden (1993)" ,
    "Buggs (1995)" ,
    "Crazed (1999)" ,
    "Dudley (2003)" ,
    "Evers (2005)" ,
    "Fox (2009)",
    "Mine (2011)"
  ),
  rt_mean = c(
    454 ,
    317 ,
    430 ,
    525 ,
    479 ,
    387,
    531
  ),
  rt_sd = c(
    142 ,
    158 ,
    137 ,
    260 ,
    144 ,
    165,
    233
  ),
  rt_n = c(
    24 ,
    7 ,
    20 ,
    8 ,
    14 ,
    13,
    18
  ),
  subset = as.factor(
    c(
```

```
      "90s",
      "90s",
      "90s",
      "00s",
      "00s",
      "00s",
      "00s"
    )
  ),
  d1_unbiased = c(
    3.091587,
    1.742751,
    3.012857,
    1.793487,
    3.130074,
    2.195209,
    2.17667
  )
)

# Fixed effect, 95% CI
estimate <- esci::meta_d1(
  original_7,
  d1_unbiased,
  rt_n,
  study_name,
  random_effects = FALSE
)

# Forest plot
myplot_forest <- esci::plot_meta(estimate)

# Add a moderator
estimate_moderator <- esci::meta_d1(
  data = original_7,
  ds = d1_unbiased,
  ns = rt_n,
  moderator = subset,
  labels = study_name,
  random_effects = FALSE
)

# Forest plot
myplot_forest_moderator <- esci::plot_meta(estimate_moderator)
```

---

meta\_d2

*Estimate meta-analytic standardized mean difference across multiple two group studies (all paired, all independent, or a mix).*

---

## Description

meta\_d2 is suitable for synthesizing across multiple two-group studies (paired or independent) with a continuous outcome measure but where not all studies are measured on the same scale, and instead the magnitude of difference for each study is expressed as d\_s or d\_avg.

## Usage

```
meta_d2(
  data,
  ds,
  comparison_ns,
  reference_ns,
  r = NULL,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  assume_equal_variance = FALSE,
  random_effects = TRUE,
  conf_level = 0.95
)
```

## Arguments

data	A data frame or tibble
ds	Set of bias-adjusted cohen's d_s or d_avg values, 1 for each study
comparison_ns	Set of comparison_group sample sizes, positive integers, 1 for each study
reference_ns	Set of reference_groups sample sizes, positive integers, 1 for each study
r	optional correlation between measures for w-s studies, NA otherwise
labels	Optional set of labels, 1 for each study
moderator	Optional factor as a categorical moderator; should have k > 2 per group
contrast	Optional vector specifying a contrast between moderator levels
effect_label	Optional character providing a human-friendly label for the effect
assume_equal_variance	Defaults to FALSE
random_effects	Boolean; TRUE for a random effects model; otherwise fixed effects
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.



## Details

Once you generate an estimate with this function, you can visualize it with `plot_meta()`.

Each study's effect size should be expressed as: Cohen's  $d_s$ :  $(\text{comparison\_mean} - \text{reference\_mean}) / \text{sd\_pooled}$  or Cohen's  $d_{avg}$ :  $(\text{comparison\_mean} - \text{reference\_mean}) / \text{sd\_avg}$

To enter  $d_s$ , set `assume_equal_variance` to TRUE To enter  $d_{avg}$ , set `assume_equal_variance` to FALSE

And the  $d$  values should all be corrected for bias. The function `CI_smd_ind_contrast()` can assist with converting raw data from each study to  $d_s$  or  $d_{avg}$  with bias correction. It also has more details on calculation of these forms of  $d$  and their CIs.

The meta-analytic effect size, confidence interval and heterogeneity estimates all come from `metafor::rma()`.

The diamond ratio and its confidence interval come from `CI_diamond_ratio()`.

## Value

An esci-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - *effect\_label* - Study label
  - *effect\_size* - Effect size
  - *LL* - Lower bound of `conf_level%` confidence interval
  - *UL* - Upper bound of `conf_level%` confidence interval
  - *SE* - Expected standard error
  - *k* - Number of studies
  - *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
  - *diamond\_ratio\_LL* - lower bound of `conf_level%` confidence interval for diamond ratio
  - *diamond\_ratio\_UL* - upper bound of `conf_level%` confidence interval for diamond ratio
  - *I2* - I2 measure of heterogeneity
  - *I2\_LL* - Lower bound of `conf_level%` confidence interval for I2
  - *I2\_UL* - upper bound of `conf_level%` confidence interval for I2
  - *PI\_LL* - lower bound of `conf_level%` of prediction interval
  - *PI\_UL* - upper bound of `conf_level%` of prediction interval
  - *p* - p value for the meta-analytic effect size, based on null of exactly 0
  - *\*width* - width of the effect-size confidence interval
  - *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
  - *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
  - *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
  - *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio

- **es\_heterogeneity** - A data frame of of heterogeneity values and conf\_level% CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label
  - *moderator\_variable\_name* - if moderator passed, gives name of the moderator
  - *moderator\_level* - 'Overall' and each level of moderator, if passed
  - *measure* - Name of the measure of heterogeneity
  - *estimate* - Value of the heterogeneity estimate
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis
  - *sample\_variance* - expected level of sampling variation
  - *SE* - expected standard error
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
  - *mean* - used to calculate study p value; this is the d value entered for the study
  - *sd* - use to calculate study p value; set to 1 for each study
  - *n* - study sample size
  - *p* - p value for the study, based on null of exactly 0

## Examples

```
# Data set -- see Introduction to the New Statistics, 1st edition
data("data_damischrcj")

# Meta-analysis, random effects, assuming equal variance, no moderator
estimate <- esci::meta_d2(
  data = esci::data_damischrcj,
  ds = "Cohen's d unbiased",
  comparison_ns = "n Control",
  reference_ns = "n Lucky",
  labels = Study,
  assume_equal_variance = TRUE,
  random_effects = TRUE
)

# Forest plot
myplot_forest <- esci::plot_meta(estimate)

# Add a categorical moderator
estimate_moderator <- esci::meta_d2(
  data = esci::data_damischrcj,
  ds = "Cohen's d unbiased",
```

```

    comparison_ns = "n Control",
    reference_ns = "n Lucky",
    labels = "Study",
    moderator = "Research Group",
    assume_equal_variance = TRUE,
    random_effects = TRUE
  )

# Forest plot
myplot_forest_moderator <- esci::plot_meta(estimate_moderator)

```

---

meta_mdifftwo	<i>Estimate meta-analytic difference in means across multiple two-group studies.</i>
---------------	--

---

## Description

meta\_mdifftwo is suitable for synthesizing across multiple two-group studies (paired or independent) with a continuous outcome measure. It takes in raw data from each study. If all studies used the same measurement scale, a meta-analytic raw-score difference can be returned. If studies used different scales, a standardized mean difference can be returned. Studies can be all paired, all independent, or a mix. Equal variance can be assumed, or not. If standardized mean difference is the output, it is d\_s when equal variance is assumed and d\_avg when equal variance is not assumed.

## Usage

```

meta_mdifftwo(
  data,
  comparison_means,
  comparison_sds,
  comparison_ns,
  reference_means,
  reference_sds,
  reference_ns,
  r = NULL,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  reported_effect_size = c("mean_difference", "smd_unbiased", "smd"),
  assume_equal_variance = FALSE,
  random_effects = TRUE,
  conf_level = 0.95
)

```

**Arguments**

<code>data</code>	A data frame or tibble
<code>comparison_means</code>	Set of <code>comparison_group</code> means, 1 per study
<code>comparison_sds</code>	Set of <code>comparison_group</code> standard deviations, 1 per study, all > 0
<code>comparison_ns</code>	Set of <code>comparison_group</code> sample sizes, positive integers, 1 for each study
<code>reference_means</code>	Set of <code>reference_group</code> means, 1 per study
<code>reference_sds</code>	Set of <code>reference_group</code> standard deviations, 1 per study, all > 0
<code>reference_ns</code>	Set of <code>reference_group</code> sample sizes, positive integers, 1 for each study
<code>r</code>	Optional correlation between measures for w-s studies, NA otherwise
<code>labels</code>	An optional collection of study labels
<code>moderator</code>	An optional factor to analyze as a categorical moderator, must have $k > 2$ per groups
<code>contrast</code>	An optional contrast to estimate between moderator levels; express as a vector of contrast weights with 1 weight per moderator level.
<code>effect_label</code>	Optional character giving a human-friendly name of the effect being synthesized
<code>reported_effect_size</code>	Character specifying effect size to return: Must be one of 'mean_difference', 'smd_unbiased' (to return an unbiased Cohen's $d_s$ or $d_{avg}$ ) or 'smd' (to return $d_s$ or $d_{avg}$ without correction for bias). Defaults to <code>mean_difference</code> .
<code>assume_equal_variance</code>	Defaults to FALSE
<code>random_effects</code>	TRUE for random effect model; FALSE for fixed effects
<code>conf_level</code>	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

**Details**

Once you generate an estimate with this function, you can visualize it with `plot_meta()`.

The meta-analytic effect size, confidence interval and heterogeneity estimates all come from `metafor::rma()`.

The diamond ratio and its confidence interval come from `CI_diamond_ratio()`.

If `reported_effect_size` is `smd_unbiased` or `smd` the conversion to Cohen's  $d$  is handled by `CI_smd_ind_contrast()`.

**Value**

An `esci`-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - `effect_label` - Study label
  - `effect_size` - Effect size
  - `LL` - Lower bound of `conf_level%` confidence interval

- *UL* - Upper bound of conf\_level% confidence interval
- *SE* - Expected standard error
- *k* - Number of studies
- *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
- *diamond\_ratio\_LL* - lower bound of conf\_level% confidence interval for diamond ratio
- *diamond\_ratio\_UL* - upper bound of conf\_level% confidence interval for diamond ratio
- *I2* - I2 measure of heterogeneity
- *I2\_LL* - Lower bound of conf\_level% confidence interval for I2
- *I2\_UL* - upper bound of conf\_level% confidence interval for I2
- *PI\_LL* - lower bound of conf\_level% of prediction interval
- *PI\_UL* - upper bound of conf\_level% of prediction interval
- *p* - p value for the meta-analytic effect size, based on null of exactly 0
- *\*width* - width of the effect-size confidence interval
- *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
- *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
- *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- **es\_heterogeneity** - A data frame of of heterogeneity values and conf\_level% CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label
  - *moderator\_variable\_name* - if moderator passed, gives name of the moderator
  - *moderator\_level* - 'Overall' and each level of moderator, if passed
  - *measure* - Name of the measure of heterogeneity
  - *estimate* - Value of the heterogeneity estimate
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis
  - *sample\_variance* - expected level of sampling variation
  - *SE* - expected standard error
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
  - *mean* - used to calculate study p value; this is the d value entered for the study
  - *sd* - use to calculate study p value; set to 1 for each study
  - *n* - study sample size
  - *p* - p value for the study, based on null of exactly 0

## Examples

```
# Data set -- see Introduction to the New Statistics, 2nd edition
data("data_mccabemichael_brain")

# Meta-analysis: random effects, no moderator
estimate <- esci::meta_mdifftwo(
  data = esci::data_mccabemichael_brain,
  comparison_means = "M Brain",
  comparison_sds = "s Brain",
  comparison_ns = "n Brain",
  reference_means = "M No Brain",
  reference_sds = "s No Brain",
  reference_ns = "n No Brain",
  labels = "Study name",
  effect_label = "Brain Photo Rating - No Brain Photo Rating",
  assume_equal_variance = TRUE,
  random_effects = TRUE
)
# Forest plot
myplot_forest <- esci::plot_meta(estimate)

# Meta-analysis: random effects, moderator
estimate_moderator <- esci::meta_mdifftwo(
  data = esci::data_mccabemichael_brain,
  comparison_means = "M Brain",
  comparison_sds = "s Brain",
  comparison_ns = "n Brain",
  reference_means = "M No Brain",
  reference_sds = "s No Brain",
  reference_ns = "n No Brain",
  labels = "Study name",
  moderator = "Research group",
  effect_label = "Brain Photo Rating - No Brain Photo Rating",
  assume_equal_variance = TRUE,
  random_effects = TRUE
)
# Forest plot
myplot_forest_moderator <- esci::plot_meta(estimate_moderator)

# Meta-analysis: random effects, moderator, output d_s
estimate_moderator_d <- esci::meta_mdifftwo(
  data = esci::data_mccabemichael_brain,
  comparison_means = "M Brain",
  comparison_sds = "s Brain",
  comparison_ns = "n Brain",
  reference_means = "M No Brain",
  reference_sds = "s No Brain",
  reference_ns = "n No Brain",
  labels = "Study name",
  moderator = "Research group",
```

```

effect_label = "Brain Photo Rating - No Brain Photo Rating",
assume_equal_variance = TRUE,
random_effects = TRUE
)
# Forest plot
myplot_forest_moderator_d <- esci::plot_meta(estimate_moderator_d)

```

---

meta\_mean

*Estimate a meta-analytic mean across multiple single-group studies.*


---

### Description

meta\_mean is suitable for synthesizing across multiple single-group studies with a continuous outcome variable when all studies are measured on the same scale.

### Usage

```

meta_mean(
  data,
  means,
  sds,
  ns,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  reference_mean = 0,
  reported_effect_size = c("mean_difference", "smd_unbiased", "smd"),
  random_effects = TRUE,
  conf_level = 0.95
)

```

### Arguments

data	A dataframe or tibble
means	A collection of study means, 1 per study
sds	A collection of study standard deviations, 1 per study, all >0
ns	A collection of sample sizes, 1 per study, all integers > 2
labels	An optional collection of study labels
moderator	An optional factor to analyze as a categorical moderator, must have k > 2 per groups
contrast	An optional contrast to estimate between moderator levels; express as a vector of contrast weights with 1 weight per moderator level.
effect_label	Optional character giving a human-friendly name of the effect being synthesized

reference\_mean Optional reference mean, defaults to 0

reported\_effect\_size Character specifying effect size to return; Must be one of 'mean\_difference', 'smd\_unbiased' (to return an unbiased Cohen's d1) or 'smd' (to return Cohen's d1 without correction for bias)

random\_effects TRUE for random effect model; FALSE for fixed effects

conf\_level The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

### Details

The meta-analytic effect size, confidence interval and heterogeneity estimates all come from `metafor::rma()`.

The diamond ratio and its confidence interval come from `CI_diamond_ratio()`.

If reported\_effect\_size is smd\_unbiased or smd the conversion to d1 is handled by `CI_smd_one()`.

### Value

An esci-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - *effect\_label* - Study label
  - *effect\_size* - Effect size
  - *LL* - Lower bound of conf\_level% confidence interval
  - *UL* - Upper bound of conf\_level% confidence interval
  - *SE* - Expected standard error
  - *k* - Number of studies
  - *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
  - *diamond\_ratio\_LL* - lower bound of conf\_level% confidence interval for diamond ratio
  - *diamond\_ratio\_UL* - upper bound of conf\_level% confidence interval for diamond ratio
  - *I2* - I2 measure of heterogeneity
  - *I2\_LL* - Lower bound of conf\_level% confidence interval for I2
  - *I2\_UL* - upper bound of conf\_level% confidence interval for I2
  - *PI\_LL* - lower bound of conf\_level% of prediction interval
  - *PI\_UL* - upper bound of conf\_level% of prediction interval
  - *p* - p value for the meta-analytic effect size, based on null of exactly 0
  - *\*width* - width of the effect-size confidence interval
  - *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
  - *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
  - *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
  - *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio



- **es\_heterogeneity** - A data frame of of heterogeneity values and conf\_level% CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label
  - *moderator\_variable\_name* - if moderator passed, gives name of the moderator
  - *moderator\_level* - 'Overall' and each level of moderator, if passed
  - *measure* - Name of the measure of heterogeneity
  - *estimate* - Value of the heterogeneity estimate
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis
  - *sample\_variance* - expected level of sampling variation
  - *SE* - expected standard error
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
  - *mean* - used to calculate study p value; this is the d value entered for the study
  - *sd* - use to calculate study p value; set to 1 for each study
  - *n* - study sample size
  - *p* - p value for the study, based on null of exactly 0

## Examples

```
# Data set -- see Introduction to the New Statistics, 2nd edition
data("data_mccabemichael_brain")
```

```
# Fixed effect, 95% CI
estimate <- esci::meta_mean(
  data = esci::data_mccabemichael_brain,
  means = "M Brain",
  sds = "s Brain",
  ns = "n Brain",
  labels = "Study name",
  random_effects = FALSE
)
```

```
myplot_forest <- esci::plot_meta(estimate)
```

```
# Add a moderator, report cohen's d1
estimate_moderator_d <- esci::meta_mean(
  data = esci::data_mccabemichael_brain,
  means = "M Brain",
  sds = "s Brain",
  ns = "n Brain",
```

```

labels = "Study name",
moderator = "Research group",
reported_effect_size = "smd_unbiased",
random_effects = FALSE
)

# Forest plot
myplot_forest_moderator_d <- esci::plot_meta(estimate_moderator_d)

```

---

meta_pdiff_two	<i>Estimate meta-analytic difference in proportions over multiple studies with two independent groups and a categorical outcome variable.</i>
----------------	---

---

## Description

meta\_pdiff\_two is suitable for synthesizing across multiple two-group studies with a categorical outcome variable. It takes as input the the number of cases/events in the comparison and reference groups as well as the total number of samples in the comparison and reference groups.

## Usage

```

meta_pdiff_two(
  data,
  comparison_cases,
  comparison_ns,
  reference_cases,
  reference_ns,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  reported_effect_size = c("RD", "RR", "OR", "AS", "PETO"),
  random_effects = TRUE,
  conf_level = 0.95
)

```

## Arguments

data	A dataframe or tibble
comparison_cases	A collection of case/event counts for the comparison groups, 1 per study, all integers $\geq 0$
comparison_ns	A collection of sample sizes for the comparison groups, 1 per study, all integers $> 2$

reference_cases	A collection of case/event counts for the reference groups, 1 per study, all integers $\geq 0$
reference_ns	A collection of sample sizes for the reference groups, 1 per study, all integers $> 2$
labels	An optional collection of study labels
moderator	An optional factor to analyze as a categorical moderator, must have $k > 2$ per groups
contrast	An optional contrast to estimate between moderator levels; express as a vector of contrast weights with 1 weight per moderator level.
effect_label	Optional character giving a human-friendly name of the effect being synthesized
reported_effect_size	Character specifying effect size to return: Must be one of 'RD' (risk difference, default), 'RR' (log risk ratio), 'OR' (log odds ratio), 'AS' (arcsine square root transformed risk difference), or 'PETO' (log odds ratio estimated using Peto's method). See <code>metafor::escalc()</code> for details.
random_effects	TRUE for random effect model; FALSE for fixed effects
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

## Details

Once you generate an estimate with this function, you can visualize it with `plot_meta()`.

The meta-analytic effect size, confidence interval and heterogeneity estimates all come from `metafor::rma()`.

The conversion of events into suitable effect sizes is handled by `metafor::escalc()`

## Value

An esci-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - *effect\_label* - Study label
  - *effect\_size* - Effect size
  - *LL* - Lower bound of *conf\_level*% confidence interval
  - *UL* - Upper bound of *conf\_level*% confidence interval
  - *SE* - Expected standard error
  - *k* - Number of studies
  - *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
  - *diamond\_ratio\_LL* - lower bound of *conf\_level*% confidence interval for diamond ratio
  - *diamond\_ratio\_UL* - upper bound of *conf\_level*% confidence interval for diamond ratio
  - *I2* - I2 measure of heterogeneity
  - *I2\_LL* - Lower bound of *conf\_level*% confidence interval for I2
  - *I2\_UL* - upper bound of *conf\_level*% confidence interval for I2

- *PI\_LL* - lower bound of conf\_level% of prediction interval
- *PI\_UL* - upper bound of conf\_level% of prediction interval
- *p* - p value for the meta-analytic effect size, based on null of exactly 0
- *\*width* - width of the effect-size confidence interval
- *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
- *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
- *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- **es\_heterogeneity** - A data frame of of heterogeneity values and conf\_level% CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label
  - *moderator\_variable\_name* - if moderator passed, gives name of the moderator
  - *moderator\_level* - 'Overall' and each level of moderator, if passed
  - *measure* - Name of the measure of heterogeneity
  - *estimate* - Value of the heterogeneity estimate
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis
  - *sample\_variance* - expected level of sampling variation
  - *SE* - expected standard error
  - *LL* - lower bound of conf\_level% confidence interval
  - *UL* - upper bound of conf\_level% confidence interval
  - *mean* - used to calculate study p value; this is the d value entered for the study
  - *sd* - use to calculate study p value; set to 1 for each study
  - *n* - study sample size
  - *p* - p value for the study, based on null of exactly 0

## Examples

```
# Data set: Replications of power on egocentric behavior
esci_meta_pdiff_two <- data.frame(
  studies = c(
    "Online",
    "Original",
    "Online Pilot",
    "Exact replication"
  ),
```

```
control_egocentric = c(
  33,
  4,
  4,
  7
),
control_sample_size = c(
  101,
  33,
  10,
  53
),
power_egocentric = c(
  48,
  8,
  4,
  11
),
power_sample_size = c(
  105,
  24,
  12,
  56
),
setting = as.factor(
  c(
    "Online",
    "In-Person",
    "Online",
    "In-Person"
  )
)
)

# Meta-analysis, risk difference as effect size
estimate <- esci::meta_pdiff_two(
  esci_meta_pdiff_two,
  power_egocentric,
  power_sample_size,
  control_egocentric,
  control_sample_size,
  studies,
  reported_effect_size = "RD"
)

# Forest plot
myplot_forst <- esci::plot_meta(estimate)

# Add a categorical moderator (setting)
estimate_moderator <- esci::meta_pdiff_two(
  esci_meta_pdiff_two,
  power_egocentric,
```

```

power_sample_size,
control_egocentric,
control_sample_size,
studies,
moderator = setting,
reported_effect_size = "RD"
)

# Forest plot
myplot_forest_moderator <- esci::plot_meta(estimate_moderator)

```

---

meta_proportion	<i>Estimate a meta-analytic proportion of outcomes over multiple studies with a categorical outcome variable.</i>
-----------------	---

---

### Description

meta\_proportion is suitable for synthesizing across multiple studies with a categorical outcome variable. It takes as input the number of cases/events and the number of samples in each study.

### Usage

```

meta_proportion(
  data,
  cases,
  ns,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  random_effects = TRUE,
  conf_level = 0.95
)

```

### Arguments

data	A dataframe or tibble
cases	A collection of cases/event counts, 1 per study, all integers, all > 0
ns	A collection of sample sizes, 1 per study, all integers > 2
labels	An optional collection of study labels
moderator	An optional factor to analyze as a categorical moderator, must have k > 2 per groups
contrast	An optional contrast to estimate between moderator levels; express as a vector of contrast weights with 1 weight per moderator level.

effect\_label    Optional character giving a human-friendly name of the effect being synthesized  
 random\_effects    TRUE for random effect model; FALSE for fixed effects  
 conf\_level    The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

## Details

Once you generate an estimate with this function, you can visualize it with `plot_meta()`.

The meta-analytic effect size, confidence interval and heterogeneity estimates all come from `metafor::rma()`.

## Value

An esci-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - *effect\_label* - Study label
  - *effect\_size* - Effect size
  - *LL* - Lower bound of *conf\_level%* confidence interval
  - *UL* - Upper bound of *conf\_level%* confidence interval
  - *SE* - Expected standard error
  - *k* - Number of studies
  - *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
  - *diamond\_ratio\_LL* - lower bound of *conf\_level%* confidence interval for diamond ratio
  - *diamond\_ratio\_UL* - upper bound of *conf\_level%* confidence interval for diamond ratio
  - *I2* - I2 measure of heterogeneity
  - *I2\_LL* - Lower bound of *conf\_level%* confidence interval for I2
  - *I2\_UL* - upper bound of *conf\_level%* confidence interval for I2
  - *PI\_LL* - lower bound of *conf\_level%* of prediction interval
  - *PI\_UL* - upper bound of *conf\_level%* of prediction interval
  - *p* - p value for the meta-analytic effect size, based on null of exactly 0
  - *\*width* - width of the effect-size confidence interval
  - *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
  - *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
  - *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
  - *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- **es\_heterogeneity** - A data frame of of heterogeneity values and *conf\_level%* CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label

- *moderator\_variable\_name* - if moderator passed, gives name of the moderator
- *moderator\_level* - 'Overall' and each level of moderator, if passed
- *measure* - Name of the measure of heterogeneity
- *estimate* - Value of the heterogeneity estimate
- *LL* - lower bound of *conf\_level*% confidence interval
- *UL* - upper bound of *conf\_level*% confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis
  - *sample\_variance* - expected level of sampling variation
  - *SE* - expected standard error
  - *LL* - lower bound of *conf\_level*% confidence interval
  - *UL* - upper bound of *conf\_level*% confidence interval
  - *mean* - used to calculate study p value; this is the d value entered for the study
  - *sd* - use to calculate study p value; set to 1 for each study
  - *n* - study sample size
  - *p* - p value for the study, based on null of exactly 0

### Examples

```
# Data set: Replications of power on egocentric behavior
esci_meta_pdiff_two <- data.frame(
  studies = c(
    "Online",
    "Original",
    "Online Pilot",
    "Exact replication"
  ),
  control_egocentric = c(
    33,
    4,
    4,
    7
  ),
  control_sample_size = c(
    101,
    33,
    10,
    53
  ),
  power_egocentric = c(
    48,
    8,
    4,
    11
  ),
  power_sample_size = c(
```



```

    105,
    24,
    12,
    56
  ),
  setting = as.factor(
    c(
      "Online",
      "In-Person",
      "Online",
      "In-Person"
    )
  )
)

# Meta-analysis, risk difference as effect size
estimate <- esci::meta_proportion(
  esci_meta_pdiff_two,
  power_egocentric,
  power_sample_size,
  studies
)

# Forest plot
myplot_forest <- esci::plot_meta(estimate)

# Meta-analysis, risk difference as effect size, moderator (setting)
estimate_moderator <- esci::meta_proportion(
  esci_meta_pdiff_two,
  power_egocentric,
  power_sample_size,
  studies,
  moderator = setting
)

# Forest plot
myplot_forest_moderator <- esci::plot_meta(estimate_moderator)

```

---

 meta\_r

*Estimate meta-analytic Pearson's r across multiple studies with two continuous outcome variables.*

---

### Description

meta\_r is suitable for synthesizing across multiple studies that have measured a linear correlation (Pearson's r) from two continuous variables.

**Usage**

```
meta_r(
  data,
  rs,
  ns,
  labels = NULL,
  moderator = NULL,
  contrast = NULL,
  effect_label = "My effect",
  random_effects = TRUE,
  conf_level = 0.95
)
```

**Arguments**

data	A dataframe or tibble
rs	A collection of Pearson's r values, 1 per study, all between -1 and 1, inclusive
ns	A collection of study sample sizes, all integers > 2
labels	An optional collection of study labels
moderator	An optional factor to analyze as a categorical moderator, must have k > 2 per groups
contrast	An optional contrast to estimate between moderator levels; express as a vector of contrast weights with 1 weight per moderator level.
effect_label	Optional character giving a human-friendly name of the effect being synthesized
random_effects	TRUE for random effect model; FALSE for fixed effects
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.

**Details**

Once you generate an estimate with this function, you can visualize it with [plot\\_meta\(\)](#).

The meta-analytic effect size, confidence interval and heterogeneity estimates all come from [metafor::rma\(\)](#).

**Value**

An esci-estimate object; a list of data frames and properties. Returned tables include:

- **es\_meta** - A data frame of meta-analytic effect sizes. If a moderator was defined, there is an additional row for each level of the moderator.
  - *effect\_label* - Study label
  - *effect\_size* - Effect size
  - *LL* - Lower bound of conf\_level% confidence interval
  - *UL* - Upper bound of conf\_level% confidence interval
  - *SE* - Expected standard error
  - *k* - Number of studies

- *diamond\_ratio* - ratio of random to fixed effects meta-analytic effect sizes
- *diamond\_ratio\_LL* - lower bound of *conf\_level%* confidence interval for diamond ratio
- *diamond\_ratio\_UL* - upper bound of *conf\_level%* confidence interval for diamond ratio
- *I2* - I2 measure of heterogeneity
- *I2\_LL* - Lower bound of *conf\_level%* confidence interval for I2
- *I2\_UL* - upper bound of *conf\_level%* confidence interval for I2
- *PI\_LL* - lower bound of *conf\_level%* of prediction interval
- *PI\_UL* - upper bound of *conf\_level%* of prediction interval
- *p* - p value for the meta-analytic effect size, based on null of exactly 0
- *\*width* - width of the effect-size confidence interval
- *FE\_effect\_size* - effect size of the fixed-effects model (regardless of if fixed effects was selected)
- *RE\_effect\_size* - effect size of the random-effects model (regardless of if random effects was selected)
- *FE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- *RE\_CI\_width* - width of the fixed-effects confidence interval, used to calculate diamond ratio
- **es\_heterogeneity** - A data frame of of heterogeneity values and *conf\_level%* CIs for the meta-analytic effect size. If a moderator was defined also reports heterogeneity estimates for each level of the moderator.
  - *effect\_label* - study label
  - *moderator\_variable\_name* - if moderator passed, gives name of the moderator
  - *moderator\_level* - 'Overall' and each level of moderator, if passed
  - *measure* - Name of the measure of heterogeneity
  - *estimate* - Value of the heterogeneity estimate
  - *LL* - lower bound of *conf\_level%* confidence interval
  - *UL* - upper bound of *conf\_level%* confidence interval
- **raw\_data** - A data from with one row for each study that was passed
  - *label* - study label
  - *effect\_size* - effect size
  - *weight* - study weight in the meta analysis
  - *sample\_variance* - expected level of sampling variation
  - *SE* - expected standard error
  - *LL* - lower bound of *conf\_level%* confidence interval
  - *UL* - upper bound of *conf\_level%* confidence interval
  - *mean* - used to calculate study p value; this is the d value entered for the study
  - *sd* - use to calculate study p value; set to 1 for each study
  - *n* - study sample size
  - *p* - p value for the study, based on null of exactly 0

**Examples**

```
# Data: See Introduction to the New Statistics, first edition
esci_single_r <- data.frame(
  studies = c(
    'Violin, viola' ,
    'Strings' ,
    'Piano' ,
    'Piano' ,
    'Piano' ,
    'Piano' ,
    'Piano' ,
    'Piano' ,
    'Piano' ,
    'All' ,
    'Piano' ,
    'Piano' ,
    'Band' ,
    'Music majors' ,
    'Music majors' ,
    'All'
  ),
  rvalues = c(
    .67,
    .51,
    .4,
    .46,
    .47,
    .228,
    -.224,
    .104,
    .322,
    .231,
    .67,
    .41,
    .34,
    .31,
    .54,
    .583
  ),
  sample_size = c(
    109,
    55,
    19,
    30,
    19,
    52,
    24,
    52,
    16,
    97,
    57,
    107,
```



overview

*Calculates descriptive statistics for a continuous variable***Description**

This function calculates basic descriptive statistics for a numerical variable. It can calculate an overall summary, or broken down by the levels of a grouping variable. Inputs can be summary data, vectors, or a data frame.

**Usage**

```
overview(
  data = NULL,
  outcome_variable = NULL,
  grouping_variable = NULL,
  means = NULL,
  sds = NULL,
  ns = NULL,
  grouping_variable_levels = NULL,
  outcome_variable_name = "My Outcome Variable",
  grouping_variable_name = NULL,
  conf_level = 0.95,
  assume_equal_variance = FALSE
)
```

**Arguments**

<code>data</code>	• for raw data, a data frame or tibble
<code>outcome_variable</code>	• for raw data, either a vector containing numerical data or the name of a data-frame column containing a factor
<code>grouping_variable</code>	• optional; for raw data either a vector containing a factor or the name of a data frame column containing a factor
<code>means</code>	For summary data - A vector of 1 or more numerical means
<code>sds</code>	For summary data - A vector of standard deviations, same length as means
<code>ns</code>	For summary data - A vector of sample sizes, same length as means
<code>grouping_variable_levels</code>	For summary data - An optional vector of group labels, same length as means. If not passed, auto-generated.
<code>outcome_variable_name</code>	Optional friendly name for the outcome variable. Defaults to 'My Outcome Variable'. Ignored if a data-frame is passed, this argument is ignored.

<code>grouping_variable_name</code>	Optional friendly name for the grouping variable. If a data frame is passed, this argument is ignored.
<code>conf_level</code>	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
<code>assume_equal_variance</code>	Defaults to FALSE

## Details

If equal variance is not assumed, each group is treated independently. In that case, the estimated mean, CI, and SE is from `statspsych::ci.mean1()`, and the estimated median, CI, and SE is from `statspsych::ci.median1()`. If equal variance is assumed, each group CI is calculated as with respect to all group data, using `statspsych::ci.lc.mean.bs()` and `statspsych::ci.lc.median.bs()`

## Value

Returns a table of descriptive statistics

- **overview**

- *outcome\_variable\_name* -
- *grouping\_variable\_name* -
- *grouping\_variable\_level* -
- *mean* -
- *mean\_LL* -
- *mean\_UL* -
- *median* -
- *median\_LL* -
- *median\_UL* -
- *sd* -
- *min* -
- *max* -
- *q1* -
- *q3* -
- *n* -
- *missing* -
- *df* -
- *mean\_SE* -
- *median\_SE* -

## Examples

```
# example code
esci::overview(data_latimier_3groups, "Test%", "Group")
```

---

overview_nominal	<i>Calculates descriptive statistics for a numerical variable</i>
------------------	---

---

### Description

This function calculated basic descriptive statistics for a categorical/ nominal variable. Inputs can be summary data, vectors, or a data frame.

### Usage

```
overview_nominal(
  data = NULL,
  outcome_variable = NULL,
  grouping_variable = NULL,
  cases = NULL,
  outcome_variable_levels = NULL,
  outcome_variable_name = "My Outcome Variable",
  grouping_variable_name = "My Grouping Variable",
  conf_level = 0.95,
  count_NA = FALSE
)
```

### Arguments

data	• for raw data, a data frame or tibble
outcome_variable	• for raw data, either a vector containing factor data or the name of a data-frame column containing a factor
grouping_variable	• for raw data, either NULL (default), or the vector of a factor or a data-frame column containing a factor
cases	For summary data - A vector of 1 or more counts, integers>0
outcome_variable_levels	For summary data - An optional vector of group labels, same length as cases. If not passed, auto-generated.
outcome_variable_name	Optional friendly name for the outcome variable. Defaults to 'My Outcome Variable'. Ignored if a data-frame is passed, this argument is ignored.
grouping_variable_name	Optional friendly name for the grouping variable. Defaults to 'My Grouping Variable'. Ignored for summary data and for data frames – only used if vectors of data are passed.
conf_level	The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
count_NA	Logical to count NAs (TRUE) in total N or not (FALSE)



**Value**

Returns a table of descriptive statistics

- **overview\_nominal**

- *outcome\_variable\_name* -
- *outcome\_variable\_level* -
- *cases* -
- *n* -
- *P* -
- *P\_LL* -
- *P\_UL* -
- *P\_SE* -
- *P\_adjusted* -
- *ta\_LL* -
- *ta\_UL* -

**Examples**

```
# example code
esci::overview_nominal(esci::data_latimier_3groups, "Group")
```

---

plot_correlation	<i>Plot an estimated Pearson's r value</i>
------------------	--

---

**Description**

plot\_correlation creates a ggplot2 plot suitable for visualizing an estimate correlation between two continuous variables (Pearson's  $r$ ). This function can be passed an esci\_estimate object generated by `estimate_r()`

**Usage**

```
plot_correlation(
  estimate,
  error_layout = c("halfeye", "eye", "gradient", "none"),
  error_scale = 0.3,
  error_normalize = c("groups", "all", "panels"),
  rope = c(NA, NA),
  ggtheme = NULL
)
```

## Arguments

- |                 |  |
|-----------------|--|
| estimate        | • An <code>esci_estimate</code> object generated by <code>estimate_r()</code>  |
| error_layout    | • Optional; One of 'halfeye', 'eye', 'gradient' or 'none' for how expected sampling error of the measure of central tendency should be displayed.<br><b>Caution - the displayed error distributions do not seem correct yet</b>  |
| error_scale     | • Optional real number > 0 specifying width of the expected sampling error visualization; default is 0.3   |
| error_normalize | • Optional; One of 'groups' (default), 'all', or 'panels' specifying how width of expected sampling error distributions should be calculated.  |
| rope            | • Optional two-item vector specifying a region of practical equivalence (ROPE) to be highlighted on the plot. For a point null hypothesis, pass the same value (e.g. <code>c(0, 0)</code> ) to test a point null of exactly 0); for an interval null pass ascending values (e.g. <code>c(-1, 1)</code> ) |
| ggtheme         | • Optional ggplot2 theme object to control overall styling; defaults to <code>ggplot2::theme_classic()</code>  |

## Details

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

## Value

Returns a ggplot object

## Examples

```
# From raw data
data("data_thomason_1")

estimate_from_raw <- esci::estimate_r(
  esci::data_thomason_1,
  Pretest,
  Posttest
)

# To visualize the value of r
myplot_correlation <- esci::plot_correlation(estimate_from_raw)

# To visualize the data (scatterplot) and use regression to obtain Y' from X
myplot_scatter_from_raw <- esci::plot_scatter(estimate_from_raw, predict_from_x = 10)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
```

```

res_hstest_from_raw <- esci::test_correlation(
  estimate_from_raw,
  rope = c(-0.1, 0.1)
)

# From summary data
estimate_from_summary <- esci::estimate_r(r = 0.536, n = 50)

# To visualize the value of r
myplot_correlation_from_summary <- esci::plot_correlation(estimate_from_summary)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
res_hstest_from_summary <- esci::test_correlation(
  estimate_from_summary,
  rope = c(-0.1, 0.1)
)

```

---

plot\_describe

*Plot a histogram or dotplot of an estimated magnitude with raw data*


---

## Description

plot\_describe Takes an estimate produced from [estimate\\_magnitude](#) and produces a dotplot or histogram. It can mark various descriptive statistics on the plot, including mean, median, sd, quartiles, and z lines. If a percentile is passed, it color-codes data based on if it is above or below that percentile.

## Usage

```

plot_describe(
  estimate,
  type = c("histogram", "dotplot"),
  mark_mean = FALSE,
  mark_median = FALSE,
  mark_sd = FALSE,
  mark_quartiles = FALSE,
  mark_z_lines = FALSE,
  mark_percentile = NULL,
  histogram_bins = 12,
  ylim = c(0, NA),
  ybreaks = NULL,
  xlim = c(NA, NA),
  xbreaks = NULL,
  fill_regular = "#008DF9",
  fill_highlighted = "#E20134",

```

```

    color = "black",
    marker_size = 5,
    ggtheme = NULL
  )

```

### Arguments

estimate	A <code>esci_estimate</code> object with raw data and an <code>es_mean</code>
type	histogram or dotplot
mark_mean	should mean be marked?
mark_median	should median be marked?
mark_sd	should mean be marked?
mark_quartiles	should mean be marked?
mark_z_lines	should z lines be marked?
mark_percentile	a percentile (0 to 1) to be marked
histogram_bins	number of bins if a histogram
ylim	2-length numeric vector
ybreaks	numeric $\geq 1$
xlim	2-length numeric vector
xbreaks	numeric $\geq 1$
fill_regular	color for
fill_highlighted	color for
color	outline color
marker_size	Size of markers
ggtheme	theme to apply, if any

### Details

This function was developed primarily for student use within jamovi when learning along with the text book *Introduction to the New Statistics*, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

### Value

Returns a ggplot object

**Examples**

```
# example code
# Generate an estimate on a single continuous variable
estimate <- esci::estimate_magnitude(esci::data_latimier_3groups, `Test%`)

# Now describe the result, with a histogram
myplot_hist <- plot_describe(estimate)

# Same, but as a dotplot and mark the mean
myplot_dots <- plot_describe(estimate, type = "dotplot", mark_mean = TRUE)
```

---

plot_interaction	<i>Plot the interaction from a 2x2 design</i>
------------------	---

---

**Description**

plot\_interaction helps visualize the interaction from a 2x2 design. It plots the 2 simple effects for the first factor and can also help visualize the CIs on those simple effects. It is the comparison between those simple effects that represents an interaction (the difference in the difference). You can pass esci-estimate objects generated [estimate\\_mdifff\\_2x2\\_between\(\)](#) or [estimate\\_mdifff\\_2x2\\_mixed\(\)](#). This function returns a ggplot2 object.

**Usage**

```
plot_interaction(
  estimate,
  effect_size = c("mean", "median"),
  show_CI = FALSE,
  ggtheme = NULL,
  line_count = 100,
  line_alpha = 0.02
)
```

**Arguments**

estimate	A esci_estimate object with raw data an es_mdifff_2x2_ function
effect_size	Optional; one of 'mean' or 'median' to determine the measure of central tendency plotted. Note that median is only available if the estimate was generated from raw data. Defaults to 'mean'
show_CI	Optional logical; set to TRUE to visualize the confidence intervals on each simple effect; defaults to FALSE
ggtheme	Optional ggplot2 theme object to specify the visual style of the plot. Defaults to <a href="#">ggplot2::theme_classic()</a>

<code>line_count</code>	Optional integer > 0 to specify the number of lines used to visualize the simple-effect confidence intervals; defaults to 100
<code>line_alpha</code>	Optional numeric between 0 and 1 to specify the alpha (transparency) of the confidence interval lines; defaults to 0.02

### Details

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

### Value

Returns a ggplot object

### Examples

```
data("data_videogameaggression")

estimates_from_raw <- esci::estimate_mdifff_2x2_between(
  esci::data_videogameaggression,
  Agression,
  Violence,
  Difficulty
)

# To visualize the estimated mean difference for the interaction
myplot_from_raw <- esci::plot_mdifff(
  estimates_from_raw$interaction,
  effect_size = "median"
)

# To conduct a hypothesis test on the mean difference
res_htest_from_raw <- esci::test_mdifff(
  estimates_from_raw$interaction,
  effect_size = "median"
)

# From summary data
means <- c(1.5, 1.14, 1.38, 2.22)
sds <- c(1.38, .96, 1.5, 1.68)
ns <- c(26, 26, 25, 26)
grouping_variable_A_levels <- c("Evening", "Morning")
grouping_variable_B_levels <- c("Sleep", "No Sleep")

estimates_from_summary <- esci::estimate_mdifff_2x2_between(
```

```

means = means,
sds = sds,
ns = ns,
grouping_variable_A_levels = grouping_variable_A_levels,
grouping_variable_B_levels = grouping_variable_B_levels,
grouping_variable_A_name = "Testing Time",
grouping_variable_B_name = "Rest",
outcome_variable_name = "False Memory Score",
assume_equal_variance = TRUE
)

# To visualize the estimated mean difference for the interaction
plot_mdif_interaction <- esci::plot_mdif(
  estimates_from_summary$interaction,
  effect_size = "mean"
)

# To visualize the interaction as a line plot
plot_interaction_line <- esci::plot_interaction(estimates_from_summary)

# Same but with fan effect representing each simple-effect CI
plot_interaction_line_CI <- esci::plot_interaction(
  estimates_from_summary,
  show_CI = TRUE
)

# To conduct a hypothesis test on the mean difference
res_htest_from_raw <- esci::test_mdif(
  estimates_from_summary$interaction,
  effect_size = "mean"
)

```

---

plot\_magnitude

*Plot the mean or median for a continuous variable*


---

### Description

plot\_magnitude creates a ggplot2 plot suitable for visualizing the results of a study with one group and one or more continuous outcome variables. It can highlight either the mean or median of each outcome variable. This function can be passed an esci\_estimate object generated by [estimate\\_magnitude\(\)](#)

### Usage

```

plot_magnitude(
  estimate,
  effect_size = c("mean", "median"),
  data_layout = c("random", "swarm", "none"),

```

```

data_spread = 0.25,
error_layout = c("halfeye", "eye", "gradient", "none"),
error_scale = 0.3,
error_nudge = 0.35,
error_normalize = c("groups", "all", "panels"),
rope = c(NA, NA),
ggtheme = NULL
)

```

### Arguments

estimate	• An <code>esci_estimate</code> object generated by <code>estimate_magnitude()</code>
effect_size	• Optional; One of 'mean' (default) or 'median'; specifies which measure of central tendency to highlight; note medians are only available if the <code>esci_estimate</code> object was generated from raw data
data_layout	• Optional; One of 'random' (default), 'swarm', or 'none' for how raw data (if available) will be displayed
data_spread	• Optional real number > 0 specifying width raw data (if available) should take on the graph; default is 0.25; default spacing between two groups on the graph is 1
error_layout	• Optional; One of 'halfeye', 'eye', 'gradient' or 'none' for how expected sampling error of the measure of central tendency should be displayed. Currently, only applies if 'mean' is selected as measure of central tendency
error_scale	• Optional real number > 0 specifying width of the expected sampling error visualization; default is 0.3
error_nudge	• Optional amount by which error distribution should be offset; default is 0.35
error_normalize	• Optional; One of 'groups' (default), 'all', or 'panels' specifying how width of expected sampling error distributions should be calculated.
rope	• Optional two-item vector specifying a region of practical equivalence (ROPE) to be highlighted on the plot. For a point null hypothesis, pass the same value (e.g. <code>c(0, 0)</code> to test a point null of exactly 0); for an interval null pass ascending values (e.g. <code>c(-1, 1)</code> )
ggtheme	• Optional <code>ggplot2</code> theme object to control overall styling; defaults to <code>ggplot2::theme_classic()</code>

### Details

This function was developed primarily for student use within jamovi when learning along with the text book *Introduction to the New Statistics*, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated `ggplot` features
- Revise for consistent ability to control aesthetics and consistent layer names



**Value**

Returns a ggplot object

**Examples**

```
# From raw data
data("data_penlaptop1")

estimate_from_raw <- esci::estimate_magnitude(
  data = data_penlaptop1[data_penlaptop1$condition == "Pen", ],
  outcome_variable = transcription
)

# To visualize the estimate
myplot_from_raw <- esci::plot_magnitude(
  estimate_from_raw,
  effect_size = "median"
)

# From summary data
mymean <- 24.5
mysd <- 3.65
myn <- 40

estimate_from_summary <- esci::estimate_magnitude(
  mean = mymean,
  sd = mysd,
  n = myn
)

# To visualize the estimate
myplot_from_summary <- esci::plot_magnitude(
  estimate_from_summary,
  effect_size = "mean"
)
```

---

plot\_mdif

*Plots for comparing continuous outcome variables between conditions*

---

**Description**

plot\_mdif helps visualize comparisons of a continuous outcome variable between conditions. It can plot raw data (if available) for each condition, the mean or median (raw data only) for each condition, and it emphasizes a 1-df comparison among conditions, plotting the estimated difference and its confidence interval with a difference axis. You can pass esci-estimate objects generated by [estimate\\_mdif\\_one\(\)](#), [estimate\\_mdif\\_two\(\)](#), [estimate\\_mdif\\_paired\(\)](#), [estimate\\_mdif\\_ind\\_contrast\(\)](#),

`estimate_mdif_2x2_between()`, and `estimate_mdif_2x2_mixed()`. This function returns a `ggplot2` object.

### Usage

```
plot_mdif(
  estimate,
  effect_size = c("mean", "median"),
  data_layout = c("random", "swarm", "none"),
  data_spread = 0.15,
  error_layout = c("halfeye", "eye", "gradient", "none"),
  error_scale = 0.3,
  error_nudge = 0.4,
  error_normalize = c("groups", "all", "panels"),
  difference_axis_units = c("raw", "sd"),
  difference_axis_breaks = 5,
  difference_axis_space = 1,
  simple_contrast_labels = TRUE,
  ylim = c(NA, NA),
  ybreaks = 5,
  rope = c(NA, NA),
  rope_units = c("raw", "sd"),
  ggtheme = NULL
)
```

### Arguments

<code>estimate</code>	An <code>esci-estimate</code> object generated by an <code>estimate_mdif_</code> function
<code>effect_size</code>	Optional; one of 'mean' or 'median' to determine the measure of central tendency plotted. Note that median is only available if the estimate was generated from raw data. Defaults to 'mean'
<code>data_layout</code>	Optional; one of 'random', 'swarm', or 'none' to determine how raw data (if available) will be displayed. Defaults to 'random'
<code>data_spread</code>	Optional numeric determining width raw data will use in each condition. Defaults to 0.15 (relative to 1 unit per condition)
<code>error_layout</code>	Optional; one of 'halfeye', 'eye', 'gradient' or 'none' to determine how expected error distribution will be displayed for each estimated parameter. Defaults to 'halfeye'. Currently does not apply if 'median' is selected as effect size, in which case a simple error bar will be used
<code>error_scale</code>	Optional numeric determining width of the expected error distribution. Defaults to 0.3
<code>error_nudge</code>	Optional numeric determining degree to which measures of central tendency will be shifted to the right of the raw data; defaults to 0.4
<code>error_normalize</code>	Optional; one of 'groups', 'all', or 'panels' to determine how width of the expected error distributions will be normalized. Defaults to 'groups'. See documentation in <code>ggdist</code>

difference_axis_units	Optional; one of 'raw' or 'sd' to determine if markings on the difference axis will be in raw-score units or in standard-deviation units. For 'sd' the standard deviation of the mean difference is used, and this is true even if 'median' is selected as the effect size
difference_axis_breaks	Optional numeric > 1 of suggested number of breaks for the difference axis. Defaults to 5
difference_axis_space	Optional numeric > 0 to indicate spacing to the difference axis. Defaults to 1
simple_contrast_labels	Optional logical to determine if contrasts are given simple labels ('Reference', 'Comparison', 'Difference') or more descriptive labels based on the contrast specified.
ylim	Optional 2-item vector specifying y-axis limits. Defaults to c(NA NA); Use NA to specify auto-limit.
ybreaks	Optional numeric > 2 for suggested number of y-axis breaks; defaults to 5
rope	Optional 2-item vector with item 2 >= item 1. Use to specify a range of values to use to visualize a hypothesis test. If both values are the same, a point-null hypothesis test will be visualized. If item2 > item1 an interval-null hypothesis test will be visualized. Defaults to c(NA, NA), which is to not visualize a hypothesis test
rope_units	Optional; one of 'raw' or 'sd' to indicate units of the rope passed. Defaults to 'raw'
ggtheme	Optional ggplot2 theme object to specify the visual style of the plot. Defaults to <code>ggplot2::theme_classic()</code>

## Details

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

## Value

Returns a ggplot object

## Examples

```
# From raw data
data("data_penlaptop1")

estimate_from_raw <- esci::estimate_mdif_two(
  data = data_penlaptop1,
```

```
outcome_variable = transcription,
grouping_variable = condition,
switch_comparison_order = TRUE,
assume_equal_variance = TRUE
)

# To visualize the estimated median difference (raw data only)
myplot_from_raw <- esci::plot_mdifff(
  estimate_from_raw,
  effect_size = "median"
)

# To conduct a hypothesis test
res_htest_from_raw <- esci::test_mdifff(
  estimate_from_raw,
  effect_size = "median",
  rope = c(-2, 2)
)

# From summary data
estimate_from_summary <- esci::estimate_mdifff_two(
  comparison_mean = 12.09,
  comparison_sd = 5.52,
  comparison_n = 103,
  reference_mean = 6.88,
  reference_sd = 4.22,
  reference_n = 48,
  grouping_variable_levels = c("Ref-Laptop", "Comp-Pen"),
  outcome_variable_name = "% Transcription",
  grouping_variable_name = "Note-taking type",
  assume_equal_variance = TRUE
)

# To visualize the estimated mean difference
myplot <- esci::plot_mdifff(
  estimate_from_summary,
  effect_size = "mean"
)

# To conduct a hypothesis test
res_htest_from_summary <- esci::test_mdifff(
  estimate_from_summary,
  effect_size = "mean",
  rope = c(-2, 2)
)
```

## Description

'plot\_meta' returns a ggplot2 object visualizing the results of a meta-analysis, showing each study effect size and CI, the overall effect size and CI as a diamond, effect sizes estimated at each moderator level (if defined), and (optionally) prediction intervals for subsequent studies. This function requires as input an esci\_estimate object generated by an esci meta-analysis function: [meta\\_any\(\)](#), [meta\\_d1\(\)](#), [meta\\_d2\(\)](#), [meta\\_mdif\\_two\(\)](#), [meta\\_mean\(\)](#), [meta\\_pdif\\_two\(\)](#), [meta\\_proportion\(\)](#), and [meta\\_r\(\)](#).

## Usage

```
plot_meta(
  estimate,
  mark_zero = TRUE,
  include_PIs = FALSE,
  report_CIs = FALSE,
  explain_DR = FALSE,
  meta_diamond_height = 0.35,
  ggtheme = ggplot2::theme_classic()
)
```

## Arguments

estimate	• an esci_estimate object generated by an esci meta_ function
mark_zero	• Boolean; defaults to TRUE to include a dotted line indicated no effect (effect_size = 0)
include_PIs	• Boolean; defaults to FALSE; set to TRUE to include prediction intervals for the overall effect and each moderator level (if defined)
report_CIs	• Boolean; defaults to FALSE; set to TRUE to include printed representation of each study effect size and CI along the right- hand of the figure
explain_DR	• Boolean; defaults to FALSE; set to TRUE if no moderator is defined to show both the RE and FE effect sizes to represent how the diamond ration measure of effect-size heterogeneity is calculated
meta_diamond_height	• Optional real number > 0 to indicate height that each meta-analytic diamond should be drawn; defaults to 0.35
ggtheme	• Optional ggplot2 theme object to control overall styling; defaults to <a href="#">ggplot2::theme_classic()</a>

## Details

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

**Value**

Returns a ggplot object

**Examples**

```
# Data set -- see Introduction to the New Statistics, 2nd edition
data("data_mccabemichael_brain")
```

```
# Meta-analysis: random effects, no moderator
estimate <- esci::meta_mdifftwo(
  data = esci::data_mccabemichael_brain,
  comparison_means = "M Brain",
  comparison_sds = "s Brain",
  comparison_ns = "n Brain",
  reference_means = "M No Brain",
  reference_sds = "s No Brain",
  reference_ns = "n No Brain",
  labels = "Study name",
  effect_label = "Brain Photo Rating - No Brain Photo Rating",
  assume_equal_variance = TRUE,
  random_effects = TRUE
)
# Forest plot
myplot_forest <- esci::plot_meta(estimate)
```

```
# Meta-analysis: random effects, moderator
estimate_moderator <- esci::meta_mdifftwo(
  data = esci::data_mccabemichael_brain,
  comparison_means = "M Brain",
  comparison_sds = "s Brain",
  comparison_ns = "n Brain",
  reference_means = "M No Brain",
  reference_sds = "s No Brain",
  reference_ns = "n No Brain",
  labels = "Study name",
  moderator = "Research group",
  effect_label = "Brain Photo Rating - No Brain Photo Rating",
  assume_equal_variance = TRUE,
  random_effects = TRUE
)
# Forest plot
myplot_forest_moderator <- esci::plot_meta(estimate_moderator)
```

```
# Meta-analysis: random effects, moderator, output d_s
estimate_moderator_d <- esci::meta_mdifftwo(
  data = esci::data_mccabemichael_brain,
  comparison_means = "M Brain",
  comparison_sds = "s Brain",
  comparison_ns = "n Brain",
  reference_means = "M No Brain",
```

```

reference_sds = "s No Brain",
reference_ns = "n No Brain",
labels = "Study name",
moderator = "Research group",
effect_label = "Brain Photo Rating - No Brain Photo Rating",
assume_equal_variance = TRUE,
random_effects = TRUE
)
# Forest plot
myplot_forest_moderator_d <- esci::plot_meta(estimate_moderator_d)

```

---

plot_pdiff	<i>Plots for comparing categorical outcome variables between conditions</i>
------------	---

---

### Description

plot\_pdiff helps visualize comparisons of a categorical outcome variable between conditions. It plots proportions of cases for each level of grouping variable and emphasizes a 1-df comparison among conditions, plotting the estimated difference and its confidence interval with a difference axis. You can pass esci-estimate objects generated by [estimate\\_pdiff\\_one\(\)](#), [estimate\\_pdiff\\_two\(\)](#), [estimate\\_pdiff\\_paired\(\)](#), [estimate\\_pdiff\\_ind\\_contrast\(\)](#). This function returns a ggplot2 object.

### Usage

```

plot_pdiff(
  estimate,
  error_layout = c("halfeye", "eye", "gradient", "none"),
  error_scale = 0.3,
  error_normalize = c("groups", "all", "panels"),
  difference_axis_breaks = 5,
  difference_axis_space = 1,
  simple_contrast_labels = TRUE,
  ylim = c(NA, NA),
  ybreaks = 5,
  rope = c(NA, NA),
  ggtheme = NULL
)

```

### Arguments

estimate	An esci-estimate object generated by an estimate_pdiff_ function
error_layout	Optional; one of 'halfeye', 'eye', 'gradient' or 'none' to determine how expected error distribution will be displayed for each estimated parameter. Defaults to 'halfeye'. Currently does not apply if 'median' is selected as effect size, in which case a simple error bar will be used

error_scale	Optional numeric determining width of the expected error distribution. Defaults to 0.3
error_normalize	Optional; one of 'groups', 'all', or 'panels' to determine how width of the expected error distributions will be normalized. Defaults to 'groups'. See documentation in ggdist
difference_axis_breaks	Optional numeric > 1 of suggested number of breaks for the difference axis. Defaults to 5
difference_axis_space	Optional numeric > 0 to indicate spacing to the difference axis. Defaults to 1
simple_contrast_labels	Optional logical to determine if contrasts are given simple labels ('Reference', 'Comparison', 'Difference') or more descriptive labels based on the contrast specified.
ylim	Optional 2-item vector specifying y-axis limits. Defaults to c(NA NA); Use NA to specify auto-limit.
ybreaks	Optional numeric > 2 for suggested number of y-axis breaks; defaults to 5
rope	Optional 2-item vector with item 2 >= item 1. Use to specify a range of values to use to visualize a hypothesis test. If both values are the same, a point-null hypothesis test will be visualized. If item2 > item1 an interval-null hypothesis test will be visualized. Defaults to c(NA, NA), which is to not visualize a hypothesis test
ggtheme	Optional ggplot2 theme object to specify the visual style of the plot. Defaults to <code>ggplot2::theme_classic()</code>

## Details

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

## Value

Returns a ggplot object

## Examples

```
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_pdiff_two(
  esci::data_campus_involvement,
  CommuterStatus,
  Gender
```



```
)

# To visualize the estimate
myplot_from_raw <- esci::plot_pdiff(estimate_from_raw)

# To conduct a hypothesis test
res_hstest_from_raw <- esci::test_pdiff(estimate_from_raw)

# From summary_data
estimate_from_summary <- esci::estimate_pdiff_two(
  comparison_cases = 10,
  comparison_n = 20,
  reference_cases = 78,
  reference_n = 252,
  grouping_variable_levels = c("Original", "Replication"),
  conf_level = 0.95
)

# To visualize the estimate
myplot_from_summary <- esci::plot_pdiff(estimate_from_summary)

#' # To conduct a hypothesis test
res_hstest_from_summary <- esci::test_pdiff(estimate_from_summary)
```

---

plot\_proportion

*Plot an estimated proportion*

---

## Description

`plot_proportion` creates a `ggplot2` plot suitable for visualizing an estimated proportion from a categorical variable. This function can be passed an `esci_estimate` object generated by [estimate\\_proportion\(\)](#)

## Usage

```
plot_proportion(
  estimate,
  error_layout = c("halfeye", "eye", "gradient", "none"),
  error_scale = 0.3,
  error_normalize = c("groups", "all", "panels"),
  rope = c(NA, NA),
  plot_possible = FALSE,
  ggtheme = NULL
)
```

**Arguments**

- estimate • An `esci_estimate` object generated by `estimate_proportion()`
- error\_layout • Optional; One of 'halfeye', 'eye', 'gradient' or 'none' for how expected sampling error of the measure of central tendency should be displayed. **Caution - the displayed error distributions do not seem correct yet**
- error\_scale • Optional real number > 0 specifying width of the expected sampling error visualization; default is 0.3
- error\_normalize • Optional; One of 'groups' (default), 'all', or 'panels' specifying how width of expected sampling error distributions should be calculated.
- rope • Optional two-item vector specifying a region of practical equivalence (ROPE) to be highlighted on the plot. For a point null hypothesis, pass the same value (e.g. `c(0, 0)` to test a point null of exactly 0); for an interval null pass ascending values (e.g. `c(-1, 1)`)
- plot\_possible • Boolean; defaults to FALSE; TRUE to plot lines at each discrete proportion possible given the sample size (e.g for a proportion with 10 total cases, would draw lines at 0, .1, .2, etc.)
- ggtheme • Optional ggplot2 theme object to control overall styling; defaults to `ggplot2::theme_classic()`

**Details**

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

**Value**

Returns a ggplot object

**Examples**

```
# From raw data
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_proportion(
  esci::data_campus_involvement,
  CommuterStatus
)

# To visualize the estimate
myplot_from_raw <- esci::plot_proportion(estimate_from_raw)
```

```
# From summary data
estimate_from_summary <- esci::estimate_proportion(
  cases = c(8, 22-8),
  outcome_variable_levels = c("Affected", "Not Affected")
)

# To visualize the estimate
myplot_from_summary<- esci::plot_proportion(estimate_from_summary)
```

---

plot\_rdiff

*Plots for comparing Pearson r values between conditions*


---

### Description

plot\_rdiff helps visualize comparisons of Pearson's r estimates between conditions. It plots the Pearson's r value for each level of a grouping variable and emphasizes a 1-df comparison among conditions, plotting the estimated difference and its confidence interval with a difference axis. You can pass esci-estimate objects generated by `estimate_rdiff_two()`. This function returns a ggplot2 object.

### Usage

```
plot_rdiff(
  estimate,
  error_layout = c("halfeye", "eye", "gradient", "none"),
  error_scale = 0.3,
  error_normalize = c("groups", "all", "panels"),
  difference_axis_breaks = 5,
  simple_contrast_labels = TRUE,
  ylim = c(NA, NA),
  ybreaks = 5,
  rope = c(NA, NA),
  ggtheme = NULL
)
```

### Arguments

estimate	An esci-estimate object generated by an estimate_pdiff_ function
error_layout	Optional; one of 'halfeye', 'eye', 'gradient' or 'none' to determine how expected error distribution will be displayed for each estimated parameter. Defaults to 'halfeye'. Currently does not apply if 'median' is selected as effect size, in which case a simple error bar will be used
error_scale	Optional numeric determining width of the expected error distribution. Defaults to 0.3

<code>error_normalize</code>	Optional; one of 'groups', 'all', or 'panels' to determine how width of the expected error distributions will be normalized. Defaults to 'groups'. See documentation in <code>ggdist</code>
<code>difference_axis_breaks</code>	Optional numeric > 1 of suggested number of breaks for the difference axis. Defaults to 5
<code>simple_contrast_labels</code>	Optional logical to determine if contrasts are given simple labels ('Reference', 'Comparison', 'Difference') or more descriptive labels based on the contrast specified.
<code>ylim</code>	Optional 2-item vector specifying y-axis limits. Defaults to <code>c(NA NA)</code> ; Use NA to specify auto-limit.
<code>ybreaks</code>	Optional numeric > 2 for suggested number of y-axis breaks; defaults to 5
<code>rope</code>	Optional 2-item vector with item 2 >= item 1. Use to specify a range of values to use to visualize a hypothesis test. If both values are the same, a point-null hypothesis test will be visualized. If item2 > item1 an interval-null hypothesis test will be visualized. Defaults to <code>c(NA, NA)</code> , which is to not visualize a hypothesis test
<code>ggtheme</code>	Optional <code>ggplot2</code> theme object to specify the visual style of the plot. Defaults to <code>ggplot2::theme_classic()</code>

## Details

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated `ggplot` features
- Revise for consistent ability to control aesthetics and consistent layer names

## Value

Returns a `ggplot` object

## Examples

```
# From raw data
data("data_campus_involvement")

estimate_from_raw <- esci::estimate_rdiff_two(
  esci::data_campus_involvement,
  GPA,
  SWB,
  Gender
)
```

```

# To visualize the difference in r
myplot_from_raw <- esci::plot_rdiff(estimate_from_raw)

# To visualize the data (scatterplot) by group
myplot_scatter <- esci::plot_scatter(estimate_from_raw)

# To evaluate a hypothesis (by default: point null of exactly 0):
res_hstest_from_raw <- esci::test_rdiff(
  estimate_from_raw
)

# From summary data
estimate <- esci::estimate_rdiff_two(
  comparison_r = .53,
  comparison_n = 45,
  reference_r = .41,
  reference_n = 59,
  grouping_variable_levels = c("Females", "Males"),
  x_variable_name = "Satisfaction with life",
  y_variable_name = "Body satisfaction",
  grouping_variable_name = "Gender",
  conf_level = .95
)

myplot_from_summary <- esci::plot_rdiff(estimate)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
res_hstest_from_summary <- esci::test_rdiff(
  estimate,
  rope = c(-0.1, 0.1)
)

```

---

plot\_scatter

*Generates a scatter plot of data for two continuous variables*


---

### Description

plot\_scatter returns a ggplot2 object of data from two continuous variables. Can indicate regression line and its confidence interval, prediction intervals, regression residuals and more. This function requires as input an esci\_estimate object generated by [estimate\\_r\(\)](#)

### Usage

```

plot_scatter(
  estimate,
  show_line = FALSE,
  show_line_CI = FALSE,

```

```

show_PI = FALSE,
show_residuals = FALSE,
show_mean_lines = FALSE,
show_r = FALSE,
predict_from_x = NULL,
plot_as_z = FALSE,
ggtheme = ggplot2::theme_classic()
)

```

### Arguments

estimate	• an <code>esci_estimate</code> object generated by <code>estimate_r()</code>
show_line	• Boolean; defaults to FALSE; set to TRUE to show the regression line
show_line_CI	• Boolean; defaults to FALSE; set to TRUE to show the confidence interval on the regression line
show_PI	• Boolean; defaults to FALSE; set to TRUE to show prediction intervals
show_residuals	• Boolean; defaults to FALSE; set to TRUE to show residuals of prediction
show_mean_lines	• Boolean; defaults to FALSE; set to TRUE to plot lines showing the mean of each variable
show_r	• Boolean; defaults to FALSE; set to TRUE to print the <i>r</i> value and its CI on the plot
predict_from_x	• Optional real number in the range of the x variable for the plot; Defaults to NULL; if passed, the graph shows the predicted Y' for this x value
plot_as_z	• Boolean; defaults to FALSE; set to TRUE to convert x and y scores to z scores prior to plotting
ggtheme	• Optional ggplot2 theme object to control overall styling; defaults to <code>ggplot2::theme_classic()</code>

### Details

This function was developed primarily for student use within jamovi when learning along with the text book Introduction to the New Statistics, 2nd edition (Cumming & Calin-Jageman, 2024).

Expect breaking changes as this function is improved for general use. Work still do be done includes:

- Revise to avoid deprecated ggplot features
- Revise for consistent ability to control aesthetics and consistent layer names

### Value

Returns a ggplot object

## Examples

```
# From raw data
data("data_thomason_1")

estimate_from_raw <- esci::estimate_r(
  esci::data_thomason_1,
  Pretest,
  Posttest
)

# To visualize the value of r
myplot_correlation <- esci::plot_correlation(estimate_from_raw)

# To visualize the data (scatterplot) and use regression to obtain Y' from X
myplot_scatter_from_raw <- esci::plot_scatter(estimate_from_raw, predict_from_x = 10)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
res_htest_from_raw <- esci::test_correlation(
  estimate_from_raw,
  rope = c(-0.1, 0.1)
)

# From summary data
estimate_from_summary <- esci::estimate_r(r = 0.536, n = 50)

# To visualize the value of r
myplot_correlation_from_summary <- esci::plot_correlation(estimate_from_summary)

# To evaluate a hypothesis (interval null from -0.1 to 0.1):
res_htest_from_summary <- esci::test_correlation(
  estimate_from_summary,
  rope = c(-0.1, 0.1)
)
```

---

print.esci\_estimate    *Print an esci\_estimate*

---

## Description

Pretties up the printing of a complex `esci_estimate` object.

## Usage

```
## S3 method for class 'esci_estimate'
print(x, ..., verbose = FALSE)
```

**Arguments**

- x • object to print; must be of class `esci_estimate`
- ... S3 signature for generic plot function.
- verbose • optional logical print all details; defaults to false

---

<code>test_correlation</code>	<i>Test a hypothesis about the strength of a Pearson's <math>r</math> correlation</i>
-------------------------------	---

---

**Description**

`test_correlation` is suitable for testing a hypothesis about a the strength of correlation between two continuous variables (designs in which Pearson's  $r$  is a suitable measure of correlation).

**Usage**

```
test_correlation(estimate, rope = c(0, 0), output_html = FALSE)
```

**Arguments**

- `estimate` • An `esci_estimate` object generated by the `estimate_r` function
- `rope` • A two-element vector defining the Region of Practical Equivalence (ROPE). Specify `c(0, 0)` to test a point null of exactly 0. Specify any two ascending values between -1 and 1 to test an interval null (e.g. `c(.25, .45)` to test the hypothesis that Pearson's  $r$  in the population ( $\rho$ ) is between .25 and .45).
- `output_html` • TRUE to return results in HTML; FALSE (default) to return standard output

**Details**

This function can be passed an `esci_estimate` object generated by `estimate_r()`.

It can test hypotheses about a specific value for the difference (a point null) or about a range of values (an interval null)

**Value**

Returns a list with 1-2 data frames

- **point\_null** - always returned
  - `test_type` - 'Nil hypothesis test', meaning a test against  $H_0 = 0$
  - `outcome_variable_name` - Name of the outcome variable
  - `effect` - Label for the effect being tested
  - `null_words` - Express the null in words
  - `confidence` - Confidence level, integer (95 for 95%, etc.)
  - `LL` - Lower boundary of the confidence% CI for the effect
  - `UL` - Upper boundary of the confidence% CI for the effect



- *CI* - Character representation of the CI for the effect
- *CI\_compare* - Text description of relation between CI and null
- *t* - If applicable, t value for hypothesis test
- *df* - If applicable, degrees of freedom for hypothesis test
- *p* - If applicable, p value for hypothesis test
- *p\_result* - Text representation of p value obtained
- *null\_decision* - Text representation of the decision for the null
- *conclusion* - Text representation of conclusion to draw
- *significant* - TRUE/FALSE if significant at alpha = 1-CI
- **interval\_null** - returned only if an interval null is specified
  - *test\_type* - 'Practical significance test', meaning a test against an interval null
  - *outcome\_variable\_name* -
  - *effect* - Name of the outcome variable
  - *rope* - Test representation of null interval
  - *confidence* - Confidence level, integer (95 for 95%, etc.)
  - *CI* - Character representation of the CI for the effect
  - *rope\_compare* - Text description of relation between CI and null interval
  - *p\_result* - Text representation of p value obtained
  - *conclusion* - Text representation of conclusion to draw
  - *significant* - TRUE/FALSE if significant at alpha = 1-CI

### Examples

```
# example code
estimate <- esci::estimate_r(r = 0.536, n = 50)

# Test against a point null of exactly 0
test_correlation(estimate)

# Test against an interval null (-0.1, 0.1)
test_correlation(estimate, rope = c(-0.1, 0.1))
```

---

test\_mdif

*Test a hypothesis about a difference in a continuous outcome variable.*

---

### Description

test\_mdif is suitable for conducting a testing a hypothesis about the magnitude of difference between two conditions for a continuous outcome variable. It can test hypotheses about differences in means or medians for both independent and paired designs.

**Usage**

```
test_mdifff(
  estimate,
  effect_size = c("mean", "median"),
  rope = c(0, 0),
  rope_units = c("raw", "sd"),
  output_html = FALSE
)
```

**Arguments**

- |             |  |
|-------------|--|
| estimate    | • An <code>esci_estimate</code> object generated by an <code>estimate_mdifff_</code> function  |
| effect_size | • One of 'mean' or 'median'. The effect size selected must be available in the <code>esci_estimate</code> object; medians are only available when the estimate was generated from raw data.  |
| rope        | • A two-element vector defining the Region of Practical Equivalence (ROPE). Specify <code>c(0, 0)</code> to test a point null of exactly 0. Specify any two ascending values to test an interval null (e.g. <code>c(-1, 1)</code> to test the hypothesis that the difference is between -1 and 1).                                       |
| rope_units  | • One of 'raw' (default) or 'sd', specifies the units of the ROPE. If 'sd' is specified, the rope is defined in standard deviation units (e.g. <code>c(-1, 1)</code> is taken as between -1 and 1 <i>standard deviations</i> from 0). When sd is used, the ROPE is converted to raw scores and then the test is conducted on raw scores. |
| output_html | • TRUE to return results in HTML; FALSE (default) to return standard output  |

**Details**

This function can be passed an `esci_estimate` object generated by `estimate_mdifff_one()`, `estimate_mdifff_two()`, `estimate_mdifff_paired()`, or `estimate_mdifff_ind_contrast()`.

It can test hypotheses about a specific value for the difference (a point null) or about a range of values (an interval null)

**Value**

Returns a list with 1-2 data frames

- **point\_null** - always returned
  - *test\_type* - 'Nil hypothesis test', meaning a test against  $H_0 = 0$
  - *outcome\_variable\_name* - Name of the outcome variable
  - *effect* - Label for the effect being tested
  - *null\_words* - Express the null in words
  - *confidence* - Confidence level, integer (95 for 95%, etc.)
  - *LL* - Lower boundary of the confidence% CI for the effect
  - *UL* - Upper boundary of the confidence% CI for the effect
  - *CI* - Character representation of the CI for the effect

- *CI\_compare* - Text description of relation between CI and null
- *t* - If applicable, t value for hypothesis test
- *df* - If applicable, degrees of freedom for hypothesis test
- *p* - If applicable, p value for hypothesis test
- *p\_result* - Text representation of p value obtained
- *null\_decision* - Text representation of the decision for the null
- *conclusion* - Text representation of conclusion to draw
- *significant* - TRUE/FALSE if significant at alpha = 1-CI
- **interval\_null** - returned only if an interval null is specified
  - *test\_type* - 'Practical significance test', meaning a test against an interval null
  - *outcome\_variable\_name* -
  - *effect* - Name of the outcome variable
  - *rope* - Test representation of null interval
  - *confidence* - Confidence level, integer (95 for 95%, etc.)
  - *CI* - Character representation of the CI for the effect
  - *rope\_compare* - Text description of relation between CI and null interval
  - *p\_result* - Text representation of p value obtained
  - *conclusion* - Text representation of conclusion to draw
  - *significant* - TRUE/FALSE if significant at alpha = 1-CI

## Examples

```
# example code
data("data_penlaptop1")

estimate <- esci::estimate_mdif_two(
  data = data_penlaptop1,
  outcome_variable = transcription,
  grouping_variable = condition,
  switch_comparison_order = TRUE,
  assume_equal_variance = TRUE
)

# Test mean difference against point null of 0
esci::test_mdif(
  estimate,
  effect_size = "mean"
)

# Test median difference against point null of 0
# Note that t, df, p return NA because test is completed
# by interval.
esci::test_mdif(
  estimate,
  effect_size = "median"
)

# Test mean difference against interval null of -10 to 10
```

```
esci::test_mdifff(
  estimate,
  effect_size = "mean",
  rope = c(-10, 10)
)

# Test mean difference against interval null of d (-0.20, 0.20) d = 0.2 is often
# thought of as a small effect, so this test examines if the effect is
# negligible (clearly between negligible and small), substantive (clearly more
# than small), or unclear. The d boundaries provided are converted to raw scores
# and then the CI of the observed effect is compared to the raw-score boundaries
esci::test_mdifff(
  estimate,
  effect_size = "mean",
  rope = c(-0.2, 0.2),
  rope_units = "sd"
)
```

---

test\_pdiff

*Test a hypothesis about a difference in proportion*


---

## Description

test\_pdiff is suitable for testing a hypothesis about a difference in proportions between two conditions with a categorical outcome variable. It can test hypotheses for both independent and paired designs.

## Usage

```
test_pdiff(estimate, rope = c(0, 0), output_html = FALSE)
```

## Arguments

- |             |   |
|-------------|---|
| estimate    | • An esci_estimate object generated by an estimate_pdiff_ function  |
| rope        | • A two-element vector defining the Region of Practical Equivalence (ROPE). Specify c(0, 0) to test a point null of exactly 0. Specify any two ascending values between -1 and 1 to test an interval null (e.g. c(-.25, .25) to test the hypothesis that the difference in proportion is between -.25 and .25). |
| output_html | • TRUE to return results in HTML; FALSE (default) to return standard output   |

## Details

This function can be passed an esci\_estimate object generated by [estimate\\_pdiff\\_one\(\)](#), [estimate\\_pdiff\\_two\(\)](#), [estimate\\_pdiff\\_paired\(\)](#), or [estimate\\_pdiff\\_ind\\_contrast\(\)](#).

It can test hypotheses about a specific value for the difference (a point null) or about a range of values (an interval null)

**Value**

Returns a list with 1-2 data frames

- **point\_null** - always returned
  - *test\_type* - 'Nil hypothesis test', meaning a test against  $H_0 = 0$
  - *outcome\_variable\_name* - Name of the outcome variable
  - *effect* - Label for the effect being tested
  - *null\_words* - Express the null in words
  - *confidence* - Confidence level, integer (95 for 95%, etc.)
  - *LL* - Lower boundary of the confidence% CI for the effect
  - *UL* - Upper boundary of the confidence% CI for the effect
  - *CI* - Character representation of the CI for the effect
  - *CI\_compare* - Text description of relation between CI and null
  - *t* - If applicable, t value for hypothesis test
  - *df* - If applicable, degrees of freedom for hypothesis test
  - *p* - If applicable, p value for hypothesis test
  - *p\_result* - Text representation of p value obtained
  - *null\_decision* - Text representation of the decision for the null
  - *conclusion* - Text representation of conclusion to draw
  - *significant* - TRUE/FALSE if significant at  $\alpha = 1 - CI$
- **interval\_null** - returned only if an interval null is specified
  - *test\_type* - 'Practical significance test', meaning a test against an interval null
  - *outcome\_variable\_name* -
  - *effect* - Name of the outcome variable
  - *rope* - Test representation of null interval
  - *confidence* - Confidence level, integer (95 for 95%, etc.)
  - *CI* - Character representation of the CI for the effect
  - *rope\_compare* - Text description of relation between CI and null interval
  - *p\_result* - Text representation of p value obtained
  - *conclusion* - Text representation of conclusion to draw
  - *significant* - TRUE/FALSE if significant at  $\alpha = 1 - CI$

**Examples**

```
estimate <- estimate_pdiff_two(
  comparison_cases = 10,
  comparison_n = 20,
  reference_cases = 78,
  reference_n = 252,
  grouping_variable_levels = c("Original", "Replication"),
  conf_level = 0.95
)

# Test against null of exactly
test_pdiff(estimate)
```

```
# Test against null of (-0.1, 0.1)
test_pdiff(estimate, rope = c(-0.1, 0.1))
```

---

test\_rdiff

*Test a hypothesis about a difference in correlation strength*


---

## Description

test\_rdiff is suitable for testing a hypothesis about a difference in correlation ( $r$ ) between two conditions. At the moment, it can only test hypotheses for independent-group designs.

## Usage

```
test_rdiff(estimate, rope = c(0, 0), output_html = FALSE)
```

## Arguments

- |             |  |
|-------------|--|
| estimate    | • An esci_estimate object generated by an estimate_rdiff_ function   |
| rope        | • A two-element vector defining the Region of Practical Equivalence (ROPE). Specify $c(0, 0)$ to test a point null of exactly 0. Specify any two ascending values between -1 and 1 to test an interval null (e.g. $c(-.25, .25)$ to test the hypothesis that the difference in correlation is between -.25 and .25). |
| output_html | • TRUE to return results in HTML; FALSE (default) to return standard output  |

## Details

This function can be passed an esci\_estimate object generated by `estimate_rdiff_two()`.

It can test hypotheses about a specific value for the difference (a point null) or about a range of values (an interval null)

## Value

Returns a list with 1-2 data frames

- **point\_null** - always returned
  - *test\_type* - 'Nil hypothesis test', meaning a test against  $H_0 = 0$
  - *outcome\_variable\_name* - Name of the outcome variable
  - *effect* - Label for the effect being tested
  - *null\_words* - Express the null in words
  - *confidence* - Confidence level, integer (95 for 95%, etc.)
  - *LL* - Lower boundary of the confidence% CI for the effect
  - *UL* - Upper boundary of the confidence% CI for the effect
  - *CI* - Character representation of the CI for the effect
  - *CI\_compare* - Text description of relation between CI and null

- *t* - If applicable, t value for hypothesis test
- *df* - If applicable, degrees of freedom for hypothesis test
- *p* - If applicable, p value for hypothesis test
- *p\_result* - Text representation of p value obtained
- *null\_decision* - Text representation of the decision for the null
- *conclusion* - Text representation of conclusion to draw
- *significant* - TRUE/FALSE if significant at alpha = 1-CI
- **interval\_null** - returned only if an interval null is specified
  - *test\_type* - 'Practical significance test', meaning a test against an interval null
  - *outcome\_variable\_name* -
  - *effect* - Name of the outcome variable
  - *rope* - Test representation of null interval
  - *confidence* - Confidence level, integer (95 for 95%, etc.)
  - *CI* - Character representation of the CI for the effect
  - *rope\_compare* - Text description of relation between CI and null interval
  - *p\_result* - Text representation of p value obtained
  - *conclusion* - Text representation of conclusion to draw
  - *significant* - TRUE/FALSE if significant at alpha = 1-CI

### Examples

```
# example code
estimate <- esci::estimate_rdiff_two(
  comparison_r = .53,
  comparison_n = 45,
  reference_r = .41,
  reference_n = 59,
  grouping_variable_levels = c("Females", "Males"),
  x_variable_name = "Satisfaction with life",
  y_variable_name = "Body satisfaction",
  grouping_variable_name = "Gender",
  conf_level = .95
)
test_rdiff(estimate)
```

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