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

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Encoding UTF-8

LazyData true

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Estimate the diamond ratio for a meta-analytic effect, a measure of heterogeneity

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).
CI_diamond_ratio

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


Examples

```r
mydata <- esci::data_mccabemichael_brain

# Use esci to obtain effect sizes and sample variances, storing only raw_data
mydata <- esci::meta_mdiff_two(
  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,
)```
CI_smd_ind_contrast

\[
vi = \text{mydata}\$\text{sample\_variance}
\]

---

**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**

```r
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 statpsych
CI_smd_ind_contrast

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

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_pooled - used when assuming all groups have exact same variance
• sd_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_pooled
• d_avg - does not assume equal variance, standardized to sd_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
CI_smd_ind_contrast

References


• Cousineau & Goulet-Pelletier (2020) https://osf.io/preprints/psyarxiv/s2597

• Delacre et al., 2021, https://osf.io/preprints/psyarxiv/tu6mp/


See Also

• estimate_mdiff_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 [statpsych::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
```r
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

```r
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
**Data 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**

```r
data_altruism_happiness
```

**Examples**

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

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


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
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 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.
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:

<table>
<thead>
<tr>
<th>Study</th>
<th>Participants</th>
<th>N(Trials)</th>
<th>N(Hits)</th>
<th>Proportion Hits</th>
</tr>
</thead>
</table>

Source

**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

---

**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  

*BodyWellM - Ch12 - Body Satisfaction and Well-being data for males from Figure 11.24 left panel*

**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 Schon 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
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

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

**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
data_college_survey_2

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**

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

**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**

*EffronRaj fakenews - Ch8 - from Effron and Raj (2020)*

**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 Unethicallity 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
**data_emotion_heartrate**

**Format**

`data_effronraj_fakenews`:  
A data frame with 138 rows and 5 columns:  
- **ID** factor  
- **UnethOld** numeric  
- **UnethNew** numeric  
- **AccurOld** numeric  
- **AccurNew** numeric

**Source**


---

**data_emotion_heartrate**  
*Emotion heartrate - 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 heartrate data set from the book website.

**Usage**

`data_emotion_heartrate`

**Format**

`data_emotion_heartrate`:  
A data frame with 68 rows and 3 columns:  
- **ID** integer  
- **HR_baseline** numeric  
- **HR_anger** numeric

**Source**

data_exam_scores

**Exam Scores - Ch11 - for End-of-Chapter Exercise 11.2**

**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**

```r
data_exam_scores:
A data frame with 9 rows and 3 columns:

StudentID factor
First Exam numeric
Final Exam numeric
```

---

data_flag_priming_ma

**Flag Priming ma - Ch9 - Many Labs replications of Carter et al. (2011)**

**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) 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**

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

**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

data_halagappa

**Format**

data_halagappa:
A data frame with 6 rows and 4 columns:

- **Groups** factor
- **Mean** numeric
- **SD** numeric
- **n** integer

**Source**


**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 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. 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
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.co/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.
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

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) and 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
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_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**


---

**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
data_meditationbrain

Source


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
**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, 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
- **MoralJudgment** numeric

**Source**

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

Usage
data_penlaptop1

Format
data_penlaptop1:
A data frame with 65 rows and 2 columns:

<table>
<thead>
<tr>
<th>condition</th>
<th>transcription</th>
</tr>
</thead>
</table>

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

Source
https://journals.sagepub.com/doi/full/10.1177/0956797614524581

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
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
data_religionsharing

Format

data_rattanmotivation:
A data frame with 54 rows and 2 columns:

Group factor
Motivation numeric

Source


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`
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

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
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

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)

Usage

data_stickgold
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)
data_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

**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. This is a simplified version of the full data set.

**Usage**

data_videogameaggression

esci_plot_difference_axis_x

Format

data_videogameaggression:
A data frame with 223 rows and 3 columns:

Violence  factor
Difficulty factor
Aggression 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**

*Estimates for a continuous variable with no grouping (single-group design)*

**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**

```r
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_mdiff_one()`.
The estimated mean is from `statpsych::ci.mean1()` (renamed `ci.mean` as of statpsych 1.6).
The estimated median is from `statpsych::ci.median1()` (renamed `ci.median` as of statpsych 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`
Estimates for a 2x2 between-subjects design with a continuous outcome variable

- $ta_{LL}$ -
- $ta_{UL}$ -

• 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"
)
Description

Returns object estimate_mdiff_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_mdiff_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

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_A For raw data - The column name of the grouping variable, or a vector of group names, only 2 levels allowed

grouping_variable_B For raw data - The column name of the grouping variable, or a vector of group names, only 2 levels allowed


sds For summary data - A vector of 4 standard deviations, same order

ns For summary data - A vector of 4 sample sizes

grouping_variable_A_levels For summary data - An optional vector of 2 group labels

grouping_variable_B_levels For summary data - An optional vector of 2 group labels
estimate_mdiff_2x2_between

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_mdiff() and you can visualize the interaction specifically with plot_interaction(). You can test hypotheses with test_mdiff().

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 -
estimate_mdiff_2x2_between

- 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_mdiff_2x2_between(
  esci::data_videogameaggression, 
  Agression, 
  Violence, 
  Difficulty 
)

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

# To conduct a hypothesis test on the mean difference
res_htest_from_raw <- esci::test_mdiff(
  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_mdiff_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", 
)
estimate_mdiff_2x2_mixed

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

Description

Returns object estimate_mdiff_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_mdiff_2x2_mixed(
  data,
  outcome_variable_level1,
  outcome_variable_level2,
  grouping_variable,
  outcome_variable_name = "My outcome variable",
  repeated_measures_name = "Time"
estimate_mdif_2x2_mixed

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_mdiff() and you can visualize the interaction specifically with plot_interaction(). You can test hypotheses with test_mdiff().
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
estimate_mdiff_2x2_mixed

- 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_mdiff_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_mdiff(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_mdiff(
  estimates$interaction,
  effect_size = "mean"
)
**estimate_mdiff_ind_contrast**

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

**Description**

Returns object `estimate_mdiff_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_mdiff_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**

- **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

- **means**
  For summary data - A vector of 2 or more means

- **sds**
  For summary data - A vector of standard deviations, same length as means

- **ns**
  For summary data - A vector of sample sizes, same length as means

- **contrast**
  A vector of group weights, same length as number of groups.

- **grouping_variable_levels**
  For summary data - An optional vector of group labels, same length as means
estimate_mdiff_ind_contrast

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_mdiff() and you can test hypotheses with test_mdiff().
The estimated mean differences are from statpsych::ci.lc.mean.bs().
The estimated SMDs are from CI_smd_ind_contrast() which relies on statpsych::ci.lc.stdmean.bs() unless there are only 2 groups.
The estimated median differences are from statpsych::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_mdiff_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_mdiff(
  estimate_from_raw,
  effect_size = "median"
)

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

# From summary data
data("data_halagappa")

estimate_from_summary <- estimate_mdiff_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_mdiff(estimate_from_summary, effect_size = "mean")

# To conduct a hypothesis test
res_htest_from_raw <- esci::test_mdiff(
  estimate_from_summary,
  effect_size = "mean"
estimates for a single-group design with a continuous outcome variable compared to a reference or population value

Description

Returns object `estimate_mdiff_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

```r
estimate_mdiff_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_mdiff()` and you can test hypotheses with `test_mdiff()`.

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

The estimated SMDs are from `CI_smd_one()`.

The estimated median differences are from `statpsych::ci.median1()` (renamed `ci.median` as of `statpsych 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 -
Examples

# From raw data
data("data_penlaptop1")
estimate_from_raw <- esci::estimate_mdiff_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_mdiff(estimate_from_raw, effect_size = "mean")

# To conduct a hypothesis test
res_h testim <- esci::test_mdiff(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_mdiff_one(
comparison_mean = mymean,
comparison_sd = mysd,
comparison_n = myn,
reference_mean = 12
)

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

# To conduct a hypothesis test
res_h testim <- esci::test_mdiff(estimate_from_summary,
effect_size = "mean",
rope = c(-2, 2)
)
**estimate_mdiff_paired**  
*Estimates for a repeated-measures study with two measures of a continuous variable*

**Description**

Returns object `estimate_mdiff_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**

```r
estimate_mdiff_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_mdiff() and you can test hypotheses with test_mdiff().

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

The estimated SMDs are from CI_smd_ind_contrast().

The estimated median differences are from statpsych::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


estimate_mdiff_paired

- 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_htest_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_mdiff_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_mdiff(
  estimate_from_summary,
  effect_size = "mean"
)

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

---

**estimate_mdiff_two**

*Estimates for a two-group study with a continuous outcome variable*

**Description**

Returns object `estimate_mdiff_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_mdiff_two()`
```r
estimate_mdiff_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_mdiff() and you can test hypotheses with test_mdiff().
The estimated mean differences are from statpsych::ci.mean2().
The estimated SMDs are from CI_smd_ind_contrast().
The estimated median differences are from statpsych::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 -
estimate_mdiff_two

- $q_1$ -
- $q_3$ -
- $n$ -
- missing -
- $df$ -
- $mean\_SE$ -
- $median\_SE$ -

• raw_data
  - grouping_variable -
  - outcome_variable -

Examples

# From raw data
data("data_penlaptop1")

estimate_from_raw <- esci::estimate_mdiff_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_mdiff(
estimate_from_raw,
effect_size = "median"
)

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

# From summary data
estimate_from_summary <- esci::estimate_mdiff_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)
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,
ccase_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
>= 0

ns
For summary data - A numeric vector of sample sizes, same length as counts,
each an integer >= 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. De-
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_mdiff() and you
can test hypotheses with test_mdiff().

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**

```r
# 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_htest_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_htest_from_summary <- esci::test_pdiff(estimate_from_summary)
```

---

**estimate_pdiff_one**  
Estimates for a single-group design with a categorical outcome variable compared to a reference or population value.

**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

```r
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

- **data**
  For raw data - a dataframe 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

- **comparison_cases**
  For summary data, a numeric integer > 0

- **comparison_n**
  For summary data, a numeric integer >= count

- **reference_p**
  Reference proportion, numeric >=0 and <=1

- **case_label**
  An optional numeric or character label for the count level.

- **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_pdiff()` and you can test hypotheses with `test_pdiff()`.

The estimated proportion differences are from `statpsych::ci.prop1()` (renamed ci.prop as of statpsych 1.6).

Value

Returns an object of class `esci_estimate`

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

- **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_htest_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_hptest_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 of a vector.

reference_measure
  For raw data - The reference measure, a factor. Can be the column name of a data frame of 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_hitest_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 >= 0

comparison_n
For summary data, a numeric integer >= comparison_events

reference_cases
For summary data, a numeric integer >= 0

reference_n
For summary data, a numeric integer >= 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_mdiff() and you can test hypotheses with test_mdiff().

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

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

The estimated correlation (phi) is from statpsych::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 -
• **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**

```r
data("data_campus_involvement")

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

Estimates for a categorical variable with no grouping (single-group design)

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
)

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

# To conduct a hypothesis test
res_htest_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_hptest_from_summary <- esci::test_pdiff(estimate_from_summary)
**estimate_proportion**

**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 `statpsych::ci.prop1()` (renamed `ci.prop` as of `statpsych` 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`
estimate_r

- 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.
estimate_r

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 statpsych::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

Estimates the difference in correlation for a design with two groups and two continuous outcome variables

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

```r
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

data For raw data - a dataframe 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
grouping_variable For raw data, a vector that is a factor or the name of a factor column from data
comparison_r For summary data, a pearson’s r correlation coefficient
comparison_n For summary data - An integer > 0
reference_r For summary data, a pearson’s r correlation coefficient
reference_n For summary data - An integer > 0
grouping_variable_levels For summary data - An optional vector of 2 group labels
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.
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.
save_raw_data 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 `statpsych::ci.cor()`.

The difference in r values is from `statpsych::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 -
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_htest_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 `aes()`. If specified and `inherit.aes = TRUE` (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
The data to be displayed in this layer. There are three options:
If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a `formula` (e.g. `~ head(.x, 10)`).

stat
The statistical transformation to use on the data for this layer. When using a `geom_*()` function to construct a layer, the stat argument can be used to override the default coupling between geoms and stats. The stat argument accepts the following:
• A `Stat ggproto subclass, for example `StatCount`.
• A string naming the stat. To give the stat as a string, strip the function name of the `stat_` prefix. For example, to use `stat_count()`, give the stat as "count".
• For more information and other ways to specify the stat, see the layer stat documentation.

position
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 position argument accepts the following:
• The result of calling a position function, such as `position_jitter()`. This method allows for passing extra arguments to the position.
• A string naming the position adjustment. To give the position as a string, strip the function name of the `position_` prefix. For example, to use `position_jitter()`, give the position as "jitter".
• For more information and other ways to specify the position, see the layer position documentation.

...
Other arguments passed to the geom. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `lineweight = 3` (see Aesthetics, below).

##Aesthetics##
`geom_meta_diamond_h` understands the following aesthetics (required are in bold):
• x - The horizontal center of the diamond
• y - The vertical placement of the diamond
• xmin - The left-side start of the diamond
• xmax - The right-side start of the diamond
• height - The vertical span of the diamond
jamovicorrelation

Correlations: Single Group

**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",
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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 .

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<tr>
<td>sp_alpha_PI</td>
</tr>
</tbody>
</table>
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:

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

---

jamovidescribe  Describe

---

Description

Describe

Usage

```r
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",
)```
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
jamovimagnitude

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"
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
cnf_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
jamovimdiff2x2

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

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

---

**jamovimdiffindcontrast**

*Means and Medians: Independent Groups Contrast*

**Description**

Means and Medians: Independent Groups Contrast

**Usage**

```r
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

.
s

ns

grouping_variable_levels

.

outcome_variable_name

.
jamovimdiffindcontrast

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
jamovimdiffindcontrast

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)
jamovimdifpaired  Means and Medians: Paired

Description

Means and Medians: Paired

Usage

jamovimdifpaired(
    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)

jamovimidifftwo  Means and Medians: Two Groups

Description
Means and Medians: Two Groups

Usage

jamovimidifftwo(
  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_comparision = "circle filled",
shape_summary_reference = "circle filled",
shape_summary_comparison = "circle filled",
shape_summary_difference = "triangle filled",
color_raw_reference = "#008DF9",
color_raw_comparision = "#009F81",
color_summary_reference = "#008DF9",
color_summary_comparision = "#009F81",
color_summary_difference = "black",
fill_raw_reference = "NA",
fill_raw_comparision = "NA",
fill_summary_reference = "#008DF9",
fill_summary_comparision = "#009F81",
fill_summary_difference = "black",
size_raw_reference = 2,
size_raw_comparision = 2,
size_summary_reference = 4,
size_summary_comparision = 4,
size_summary_difference = 4,
alpha_raw_reference = 1,
alpha_raw_comparision = 1,
alpha_summary_reference = 1,
alpha_summary_comparision = 1,
linetype_summary_reference = "solid",
linetype_summary_comparision = "solid",
linetype_summary_difference = "solid",
color_interval_reference = "black",
color_interval_comparision = "black",
color_interval_difference = "black",
size_interval_reference = 3,
size_interval_comparision = 3,
size_interval_difference = 3,
alpha_interval_reference = 1,
alpha_interval_comparision = 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:

```r
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 = "0.50",
size_interval_comparison = "0.50",
size_interval_difference = "0.50",
size_interval_unused = "0.50",
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    .
m/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$debug: an html
- results$help: an html
- results$raw_data: a table
- results$es_meta: a table
- results$es_heterogeneity: a table
- results$es_meta_difference: a table
- results$estimation_plot_warnings: an html
- results$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  

Description
Meta-Analysis: Means

Usage

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


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",
mlab = "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 .
dlables .
d moderator .
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
<table>
<thead>
<tr>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>color_summary_difference</code></td>
</tr>
<tr>
<td><code>color_summary_overall</code></td>
</tr>
<tr>
<td><code>fill_raw_reference</code></td>
</tr>
<tr>
<td><code>fill_raw_comparison</code></td>
</tr>
<tr>
<td><code>fill_raw_unused</code></td>
</tr>
<tr>
<td><code>fill_summary_reference</code></td>
</tr>
<tr>
<td><code>fill_summary_comparison</code></td>
</tr>
<tr>
<td><code>fill_summary_unused</code></td>
</tr>
<tr>
<td><code>fill_summary_difference</code></td>
</tr>
<tr>
<td><code>fill_summary_overall</code></td>
</tr>
<tr>
<td><code>alpha_raw_reference</code></td>
</tr>
<tr>
<td><code>alpha_raw_comparison</code></td>
</tr>
<tr>
<td><code>alpha_raw_unused</code></td>
</tr>
<tr>
<td><code>alpha_summary_reference</code></td>
</tr>
<tr>
<td><code>alpha_summary_comparison</code></td>
</tr>
<tr>
<td><code>alpha_summary_unused</code></td>
</tr>
<tr>
<td><code>alpha_summary_difference</code></td>
</tr>
<tr>
<td><code>alpha_summary_overall</code></td>
</tr>
<tr>
<td><code>linetype_raw_reference</code></td>
</tr>
<tr>
<td><code>linetype_raw_comparison</code></td>
</tr>
<tr>
<td><code>linetype_summary_difference</code></td>
</tr>
<tr>
<td><code>linetype_raw_unused</code></td>
</tr>
<tr>
<td><code>color_interval_reference</code></td>
</tr>
<tr>
<td><code>color_interval_comparison</code></td>
</tr>
</tbody>
</table>
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",
)
Arguments

```r
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
  .
Values

A results object containing:

```r
results$debug
results$help
results$raw_data
results$es_meta
results$es_heterogeneity
results$es_meta_difference
results$estimation_plot_warnings
results$estimation_plots
```

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

```r
results$raw_data$asDF
as.data.frame(results$raw_data)
```
jamovimetar  

Meta-Analysis: Correlations

Description

Meta-Analysis: Correlations

Usage

```r
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:

```r
results$debug
results$help
results$raw_data
results$es_meta
results$es_heterogeneity
results$es_meta_difference
results$estimation_plot_warnings
results$estimation_plots
```

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

```r
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$debug
results$help
results$overview
results$es_proportion_difference
results$point_null
results$interval_null
results$estimation_plot_warnings
results$estimation_plots
```

A preformatted

A html

A table

A table

A table

A html

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_comparision = "4",
size_summary_difference = "4",
alpha_summary_reference = "1",
alpha_summary_comparision = "1",
alpha_summary_difference = "1",
linetype_summary_reference = "solid",
linetype_summary_comparision = "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 .
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:

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

Correlations: Two Groups

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

color_summary_reference
fill_summary_reference
fill_summary_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)
**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**

```r
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

```r
# 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)
```
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

```r
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: (mean - reference) / 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 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(
      454 ,
      317 ,
      430 ,
      525 ,
      479 ,
      387 ,
      531
    ))
)
meta_d2

```
"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)
```
**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**

```r
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: \( \frac{(\text{comparison\_mean} - \text{reference\_mean})}{\text{sd\_pooled}} \) or Cohen’s d_avg: \( \frac{(\text{comparison\_mean} - \text{reference\_mean})}{\text{sd\_avg}} \)

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**

```r
# 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",
```
### meta_mdiff_two

Estimate meta-analytic difference in means across multiple two-group studies.

#### Description

`meta_mdiff_two` 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

```r
meta_mdiff_two(
  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

data A data frame or tibble
comparison_means Set of comparison_group means, 1 per study
comparison_sds Set of comparison_group standard deviations, 1 per study, all > 0
comparison_ns Set of comparison_group sample sizes, positive integers, 1 for each study
reference_means Set of reference_group means, 1 per study
reference_sds Set of comparison_group standard deviations, 1 per study, all > 0
reference_ns Set of reference_group sample sizes, positive integers, 1 for each study
r Optional correlation between measures for w-s studies, NA otherwise
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 '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 mean_difference.
assume_equal_variance Defaults to FALSE
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 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

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

# Meta-analysis: random effects, no moderator
estimate <- esci::meta_mdiff_two(
  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_mdiff_two(
  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_mdiff_two(
  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",
)
meta_mean

    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**

```r
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
meta_mean

**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
  - **I^2** - I^2 measure of heterogeneity
  - **I^2_LL** - Lower bound of conf_level% confidence interval for I^2
  - **I^2_UL** - upper bound of conf_level% confidence interval for I^2
  - **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**

```r
# 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 d
estimate_moderator_d <- esci::meta_mean(
  data = esci::data_mccabemichael_brain,
  means = "M Brain",
  sds = "s Brain",
  ns = "n Brain",
  moderator_variable_name = "moderator",
  moderator_level = "Level",
  random_effects = FALSE
)

myplot_forest_moderator <- esci::plot_meta(estimate_moderator_d)
```

---

**Notes:**

- The `meta_mean` function calculates the meta-analytic effect size and heterogeneity estimates.
- The `raw_data` argument is used to provide a data frame with one row per study.
- The `es_heterogeneity` output includes heterogeneity estimates and confidence intervals.
- The `moderator` option allows for the inclusion of moderators in the analysis.
- The `random_effects` argument determines whether to use random effects modeling.

---

**Example Usage:**

```r
# 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 d
est_mod <- esci::meta_mean(
  data = esci::data_mccabemichael_brain,
  means = "M Brain",
  sds = "s Brain",
  ns = "n Brain",
  measure = "Cohen's d",
  moderator_variable_name = "moderator",
  moderator_level = "Level",
  random_effects = FALSE
)

myplot_forest_mod <- esci::plot_meta(est_mod)
```
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**

*Estimate meta-analytic difference in proportions over multiple studies with two independent groups and a categorical outcome variable.*

**Description**

`meta_pdiff_two` is suitable for synthesizing across multiple two-group studies with a categorical outcome variable. It takes as input 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**

```r
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 >= 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 metafor::escalc() 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 frame 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**

```r
# 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,
Estimate a meta-analytic proportion of outcomes over multiple studies with a categorical outcome variable.

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

```r
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
  - **I^2** - I^2 measure of heterogeneity
  - **I^2_LL** - Lower bound of conf_level% confidence interval for I^2
  - **I^2_UL** - upper bound of conf_level% confidence interval for I^2
  - **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
meta_proportion

- `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**

```r
# 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(
```
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),
)


meta_r

91

178,
64,
19,
135
),
subsets = as.factor(
  c(
    'Strings',
    'Strings',
    'Piano',
    'Piano',
    'Piano',
    'Piano',
    'Piano',
    'Piano',
    'Strings',
    'Strings',
    'Strings'
  )
)
)
)

# Meta-analysis, random effects, no moderator
estimate <- esci::meta_r(
  escl_single_r,
  rvalues,
  sample_size,
  studies,
  random_effects = TRUE
)

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

# Meta-analysis, random effects, moderator (subsets)
estimate_moderator <- esci::meta_r(
  escl_single_r,
  rvalues,
  sample_size,
  studies,
  subsets,
  random_effects = TRUE
)

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

data • for raw data, a data frame or tibble
outcome_variable • for raw data, either a vector containing numerical data or the name of a data-frame column containing a factor
grouping_variable • optional; for raw data either a vector containing a factor or the name of a data frame column containing a factor
means For summary data - A vector of 1 or more numerical means
sds For summary data - A vector of standard deviations, same length as means
ns For summary data - A vector of sample sizes, same length as means
grouping_variable_levels For summary data - An optional vector of group labels, same length as means. 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.
overview

  grouping_variable_name
       Optional friendly name for the grouping variable. If a data frame is passed, this argument is ignored.
  conf_level       The confidence level for the confidence interval. Given in decimal form. Defaults to 0.95.
  assume_equal_variance       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 \texttt{statpsych::ci.mean1()}, and the estimated median, CI, and SE is from \texttt{statpsych::ci.median1()}. If equal variance is assumed, each group CI is calculated as with respect to all group data, using \texttt{statpsych::ci.lc.mean.bs()} and \texttt{statpsych::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  
Calculates descriptive statistics for a numerical variable

**Description**

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

**Usage**

```r
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)
plot_correlation

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

Plot an estimated Pearson’s r value

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 esci_estimate object generated by `estimate_r()`
- **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(-0.1, 1))
- **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

```r
# From raw data
data("data_thomason_1")
estimate_from_raw <- esci::estimate_r(
estici::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):
```

plot_correlation
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)
)

---

plot_describe

**Plot a histogram or dotplot of an estimated magnitude with raw data**

**Description**

The `plot_describe` function takes an estimate produced from the `estimate_magnitude` function 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**

```r
plot_describe(
    estimate,  # Estimate of the magnitude
    type = c("histogram", "dotplot"),  # Type of plot: histogram or dotplot
    mark_mean = FALSE,  # Mark mean
    mark_median = FALSE,  # Mark median
    mark_sd = FALSE,  # Mark standard deviation
    mark_quartiles = FALSE,  # Mark quartiles
    mark_z_lines = FALSE,  # Mark z lines
    mark_percentile = NULL,  # Mark percentile
    histogram_bins = 12,  # Number of bins for histogram
    ylim = c(0, NA),  # Y-limits
    ybreaks = NULL,  # Y-breaks
    xlim = c(NA, NA),  # X-limits
    xbreaks = NULL,  # X-breaks
    fill_regular = "#008DF9",  # Fill color for regular
    fill_highlighted = "#E20134"  # Fill color for highlighted
)
```
plot_describe

```r
  color = "black",
  marker_size = 5,
  ggtheme = NULL
```

Arguments

- **estimate**: A esci_estimate object with raw data and es_mean
- **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 >= 1
- **xlim**: 2-length numeric vector
- **xbreaks**: numeric >= 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
plot_interaction

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

Plot the interaction from a 2x2 design

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_mdiff_2x2_between()` or `estimate_mdiff_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_mdiff_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 ggplot2::theme_classic()
plot_interaction

line_count  Optional integer > 0 to specify the number of lines used to visualize the simple-effect confidence intervals; defaults to 100

line_alpha  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 textbook 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_mdiff_2x2_between(
estaci::data_videogameaggression,
Aggression,
Violence,
Difficulty
)

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

# To conduct a hypothesis test on the mean difference
res_htest_from_raw <- esci::test_mdiff(
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)
sns <- 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_mdiff_2x2_between(
plot_magnitude

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"),
)
```r
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 esci_estimate object generated by `estimate_magnitude()`

- **effect_size**
  - Optional; One of 'mean' (default) or 'median'; specifies which measure of central tendency to highlight; note medians are only available if the esci_estimate 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. c(0, 0) to test a point null of exactly 0); for an interval null pass ascending values (e.g. c(-1, 1))

- **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 textbook 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
plot_mdiff

Plots for comparing continuous outcome variables between conditions

plot_mdiff 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_mdiff_one(), estimate_mdiff_two(), estimate_mdiff_paired(), estimate_mdiff_ind_contrast().
estimate_mdiff_2x2_between(), and estimate_mdiff_2x2_mixed(). This function returns a ggplot2 object.

Usage

```r
plot_mdiff(
  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

- `estimate` An esci-estimate object generated by an estimate_mdiff_ 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`
- `data_layout` Optional; one of `random`, `swarm`, or `none` to determine how raw data (if available) will be displayed. Defaults to `random`
- `data_spread` Optional numeric determining width raw data will use in each condition. Defaults to 0.15 (relative to 1 unit per condition)
- `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_nudge` Optional numeric determining degree to which measures of central tendency will be shifted to the right of the raw data; defaults to 0.4
- `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
plot_mdiff

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 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_penlaptop1")
estimate_from_raw <- esci::estimate_mdiff_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_mdiff(
  estimate_from_raw,
  effect_size = "median"
)

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

# From summary data
estimate_from_summary <- esci::estimate_mdiff_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_mdiff(
  estimate_from_summary,
  effect_size = "mean"
)

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

generate a forest plot displaying results of a meta-analysis
plot_meta

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_mdiff_two(), meta_mean(), meta_pdiff_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 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
plot_meta

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_mdiff_two(
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_mdiff_two(
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_mdiff_two(
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
)
plot_pdiff

Plots for comparing categorical outcome variables between conditions

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 \texttt{estimate_pdiff\_one()}, \texttt{estimate_pdiff\_two()}, \texttt{estimate_pdiff\_paired()}, \texttt{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

- \texttt{estimate} An esci-estimate object generated by an \texttt{estimate_pdiff\_function}
- \texttt{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 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

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_htest_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_htest_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**

```r
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 textbook *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

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

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

# 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)

---

**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**

```r
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
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

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 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_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_htest_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 esci_estimate object generated by `estimate_r()
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 r 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 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
print.esci_estimate

**Examples**

```r
# 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

---

test_correlation  
*Test a hypothesis about the strength of a Pearson’s r correlation*

Description

test_correlation is suitable for testing a hypothesis about 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 H0 = 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
test_mdiff

- 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_mdiff**

Test a hypothesis about a difference in a continuous outcome variable.

**Description**

`test_mdiff` 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_mdiff(
  estimate,
  effect_size = c("mean", "median"),
  rope = c(0, 0),
  rope_units = c("raw", "sd"),
  output_html = FALSE
)

Arguments

- estimate
  • An esci_estimate object generated by an estimate_mdiff_ function
- effect_size
  • One of 'mean' or 'median'. The effect size selected must be available in the esci_estimate 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 c(0, 0) to test a point null of exactly 0. Specify any two ascending values to test an interval null (e.g. c(-1, 1) 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. c(-1, 1) is taken as between -1 and 1 standard deviations 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_mdiff_one(), estimate_mdiff_two(), estimate_mdiff_paired(), or estimate_mdiff_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 H0 = 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_mdiff_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_mdiff(
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_mdiff(
estimate,
effect_size = "median"
)

# Test mean difference against interval null of -10 to 10
esci::test_mdiff(
    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_mdiff(
    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).
test_pdiff

Value

Returns a list with 1-2 data frames

- **point_null** - always returned
  - `test_type` - 'Nil hypothesis test', meaning a test against H0 = 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

```r
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)

```r
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**

```r
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
- \( p_{\text{result}} \) - Text representation of p value obtained
- \( \text{null\_decision} \) - Text representation of the decision for the null
- \( \text{conclusion} \) - Text representation of conclusion to draw
- \( \text{significant} \) - TRUE/FALSE if significant at alpha = 1-CI

- **interval\_null** - returned only if an interval null is specified
  - \( \text{test\_type} \) - 'Practical significance test', meaning a test against an interval null
  - \( \text{outcome\_variable\_name} \) -
  - \( \text{effect} \) - Name of the outcome variable
  - \( \text{rope} \) - Test representation of null interval
  - \( \text{confidence} \) - Confidence level, integer (95 for 95%, etc.)
  - \( \text{CI} \) - Character representation of the CI for the effect
  - \( \text{rope\_compare} \) - Text description of relation between CI and null interval
  - \( p_{\text{result}} \) - Text representation of p value obtained
  - \( \text{conclusion} \) - Text representation of conclusion to draw
  - \( \text{significant} \) - TRUE/FALSE if significant at alpha = 1-CI

**Examples**

```r
# 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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