Package ‘vcmeta’

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Type Package

Title Varying Coefficient Meta-Analysis

Version 1.4.0

Description Implements functions for varying coefficient meta-analysis methods. These methods do not assume effect size homogeneity. Subgroup effect size comparisons, general linear effect size contrasts, and linear models of effect sizes based on varying coefficient methods can be used to describe effect size heterogeneity. Varying coefficient meta-analysis methods do not require the unrealistic assumptions of the traditional fixed-effect and random-effects meta-analysis methods.
For details see: Statistical Methods for Psychologists, Volume 5, <https://dgbonett.sites.ucsc.edu/>.

URL https://github.com/dgbonett/vcmeta

BugReports https://github.com/dgbonett/vcmeta/issues

License GPL-3

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Author Douglas G. Bonett [aut, cre],
Robert J. Calin-Jageman [ctb]

Maintainer Douglas G. Bonett <dgbonett@ucsc.edu>

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Contents

`cor.from.t` *Computes Pearson correlation between paired measurements from t statistic*

Description

This function computes the Pearson correlation between paired measurements using a reported paired-samples t statistic and other sample information. This correlation estimate is needed in several functions that analyze mean differences and standardized mean differences in paired-samples studies.

Usage

```
cor.from.t(m1, m2, sd1, sd2, t, n)
```

Arguments

`m1`	estimated mean for measurement 1
`m2`	estimated mean for measurement 2
`sd1`	estimated standard deviation for measurement 1
`sd2`	estimated standard deviation for measurement 2
`t`	value for paired-samples t-test
`n`	sample size

Value

Returns the sample Pearson correlation between the two paired measurements

Examples

```
cor.from.t(9.4, 9.8, 1.26, 1.40, 2.27, 30)

# Should return:
#                Estimate
# Correlation:  0.7415209
```

`meta.ave.agree` *Confidence interval for an average G-index agreement coefficient*

Description

Computes the estimate, standard error, and confidence interval for an average G-index of agreement from two or more studies. This function assumes that two raters each provide a dichotomous rating to a sample of objects. As a measure of agreement, the G-index is usually preferred to Cohen's kappa.

Usage

```
meta.ave.agree(alpha, f11, f12, f21, f22, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f11`	vector of frequency counts in cell 1,1
`f12`	vector of frequency counts in cell 1,2
`f21`	vector of frequency counts in cell 2,1
`f22`	vector of frequency counts in cell 2,2
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
f11 <- c(43, 56, 49)
f12 <- c(7, 2, 9)
f21 <- c(3, 5, 5)
f22 <- c(37, 54, 39)
meta.ave.agree(.05, f11, f12, f21, f22, bystudy = TRUE)

# Should return:
#          Estimate         SE        LL        UL
# Average 0.7843250 0.03540254 0.7149373 0.8537127
# Study 1 0.7446809 0.06883919 0.6097585 0.8796032
# Study 2 0.8512397 0.04770701 0.7577356 0.9447437
# Study 3 0.6981132 0.06954284 0.5618117 0.8344147
```

`meta.ave.cor` *Confidence interval for an average Pearson or partial correlation*

Description

Computes the estimate, standard error, and confidence interval for an average Pearson or partial correlation from two or more studies. The sample correlations must be all Pearson correlations or all partial correlations. Use the meta.ave.gen function to meta-analyze any combination of Pearson, partial, or Spearman correlations.

Usage

```
meta.ave.cor(alpha, n, cor, s, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`cor`	vector of estimated correlations
`s`	number of control variables (set to 0 for Pearson)
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2008). "Meta-analytic interval estimation for bivariate correlations." *Psychological Methods*, **13**(3), 173–181. ISSN 1939-1463, doi:10.1037/a0012868.

Examples

```
n <- c(55, 190, 65, 35)
cor <- c(.40, .65, .60, .45)
meta.ave.cor(.05, n, cor, 0, bystudy = TRUE)

# Should return:
#          Estimate         SE        LL        UL
# Average     0.525 0.05113361 0.4176678 0.6178816
# Study 1     0.400 0.11430952 0.1506943 0.6014699
# Study 2     0.650 0.04200694 0.5594086 0.7252465
# Study 3     0.600 0.08000000 0.4171458 0.7361686
# Study 4     0.450 0.13677012 0.1373507 0.6811071
```

---

meta.ave.cor.gen — *Confidence interval for an average correlation of any type*

Description

Computes the estimate, standard error, and confidence interval for an average correlation. Any type of correlation can be used (e.g., Pearson, Spearman, semipartial, factor correlation, Gamma coefficient, Somers d coefficient, tetrachoric, point-biserial, biserial, etc.).

Usage

```
meta.ave.cor.gen(alpha, cor, se, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`cor`	vector of estimated correlations
`se`	vector of standard errors
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2008). "Meta-analytic interval estimation for bivariate correlations." *Psychological Methods*, **13**(3), 173–181. ISSN 1939-1463, doi:10.1037/a0012868.

Examples

```
cor <- c(.396, .454, .409, .502, .350)
se <- c(.104, .064, .058, .107, .086)
meta.ave.cor.gen(.05, cor, se, bystudy = TRUE)

# Should return:
#         Estimate         SE        LL        UL
# Average   0.4222 0.03853362 0.3438560 0.4947070
# Study 1   0.3960 0.10400000 0.1753200 0.5787904
# Study 2   0.4540 0.06400000 0.3200675 0.5701415
# Study 3   0.4090 0.05800000 0.2893856 0.5160375
# Study 4   0.5020 0.10700000 0.2651183 0.6817343
# Study 5   0.3500 0.08600000 0.1716402 0.5061435
```

`meta.ave.cronbach` *Confidence interval for an average Cronbach alpha reliability*

Description

Computes the estimate, standard error, and confidence interval for an average Cronbach reliability coefficient from two or more studies.

Usage

```
meta.ave.cronbach(alpha, n, rel, r, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`rel`	vector of sample reliabilities
`r`	number of measurements (e.g., items) used to compute each reliability
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size

- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2010). "Varying coefficient meta-analytic methods for alpha reliability." *Psychological Methods*, **15**(4), 368–385. ISSN 1939-1463, doi:10.1037/a0020142.

Examples

```
n <- c(583, 470, 546, 680)
rel <- c(.91, .89, .90, .89)
meta.ave.cronbach(.05, n, rel, 10, bystudy = TRUE)

# Should return:
#          Estimate          SE        LL        UL
# Average    0.8975 0.003256081 0.8911102 0.9038592
# Study 1    0.9100 0.005566064 0.8985763 0.9204108
# Study 2    0.8900 0.007579900 0.8743616 0.9041013
# Study 3    0.9000 0.006391375 0.8868623 0.9119356
# Study 4    0.8900 0.006297549 0.8771189 0.9018203
```

`meta.ave.fisher` *Fisher confidence interval for an average correlation.*

Description

This function should be used with the meta.ave.gen function when the effect size is a correlation. Use the estimated average correlation and its standard error from meta.ave.gen in this function to obtain a more accurate confidence interval for the population average correlation.

Usage

```
meta.ave.fisher(alpha, cor, se)
```

Arguments

`alpha`	alpha value for 1-alpha confidence
`cor`	estimate of average correlation
`se`	standard error of average correlation

Value

Returns a 1-row matrix. The columns are:

- Estimate - estimate of average correlation (from input)
- LL - lower limit of the confidence interval
- UL - lower limit of the confidence interval

Examples

```
meta.ave.fisher(0.05, 0.376, .054)

# Should return:
# Estimate        LL        UL
#    0.376 0.2656039 0.4766632
```

`meta.ave.gen` *Confidence interval for an average of any parameter*

Description

Computes the estimate, standard error, and confidence interval for an average of any type of parameter from two or more studies.

Usage

```
meta.ave.gen(alpha, est, se, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`est`	vector of parameter estimates
`se`	vector of standard errors
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
est <- c(.022, .751, .421, .287, .052, .146, .562, .904)
se <- c(.124, .464, .102, .592, .864, .241, .252, .318)
meta.ave.gen(.05, est, se, bystudy = TRUE)

# Should return:
#           Estimate        SE          LL        UL
# Average  0.393125 0.1561622  0.08705266 0.6991973
# Study 1  0.022000 0.1240000 -0.22103553 0.2650355
# Study 2  0.751000 0.4640000 -0.15842329 1.6604233
# Study 3  0.421000 0.1020000  0.22108367 0.6209163
# Study 4  0.287000 0.5920000 -0.87329868 1.4472987
# Study 5  0.052000 0.8640000 -1.64140888 1.7454089
# Study 6  0.146000 0.2410000 -0.32635132 0.6183513
# Study 7  0.562000 0.2520000  0.06808908 1.0559109
# Study 8  0.904000 0.3180000  0.28073145 1.5272685
```

---

meta.ave.gen.cc — *Confidence interval for an average effect size using a constant coefficient model*

Description

Computes the estimate, standard error, and confidence interval for a weighted average effect from two or more studies using the constant coefficient (fixed-effect) meta-analysis model.

Usage

```
meta.ave.gen.cc(alpha, est, se, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`est`	vector of parameter estimates
`se`	vector of standard errors
`bystudy`	logical to also return each study estimate (TRUE) or not

Details

The weighted average estimate will be biased regardless of the number of studies or the sample size in each study. The actual confidence interval coverage probability can be much smaller than the specified confidence level when the population effect sizes are not identical across studies.

The constant coefficient model should be used with caution, and the varying coefficient methods in this package are the recommended alternatives. The varying coefficient methods do not require effect-size homogeneity across the selected studies. This constant coefficient meta-analysis function is included in the vcmeta package primarily for classroom demonstrations to illustrate the problematic characteristics of the constant coefficient meta-analysis model.

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

- Hedges LV, Olkin I (1985). *Statistical methods for meta-analysis*. Academic Press, New York. ISBN 01-233-63802.
- Borenstein M, Hedges LV, Higgins JP, Rothstein HR (2009). *Introduction to meta-analysis*. Wiley, New York.

See Also

meta.ave.gen

Examples

```
est <- c(.022, .751, .421, .287, .052, .146, .562, .904)
se <- c(.124, .464, .102, .592, .864, .241, .252, .318)
meta.ave.gen.cc(.05, est, se, bystudy = TRUE)

# Should return:
#              Estimate         SE          LL        UL
# Average     0.3127916 0.06854394  0.17844794 0.4471352
# Study 1     0.0220000 0.12400000 -0.22103553 0.2650355
# Study 2     0.7510000 0.46400000 -0.15842329 1.6604233
# Study 3     0.4210000 0.10200000  0.22108367 0.6209163
# Study 4     0.2870000 0.59200000 -0.87329868 1.4472987
# Study 5     0.0520000 0.86400000 -1.64140888 1.7454089
# Study 6     0.1460000 0.24100000 -0.32635132 0.6183513
# Study 7     0.5620000 0.25200000  0.06808908 1.0559109
# Study 8     0.9040000 0.31800000  0.28073145 1.5272685
```

---

meta.ave.gen.rc — *Confidence interval for an average effect size using a random coefficient model*

Description

Computes the estimate, standard error, and confidence interval for a weighted average effect from multiple studies using the random coefficient (random-effects) meta-analysis model. An estimate of effect-size heterogeneity (tau-squared) is also computed.

Usage

```
meta.ave.gen.rc(alpha, est, se, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`est`	vector of parameter estimates
`se`	vector of standard errors
`bystudy`	logical to also return each study estimate (TRUE) or not

Details

The random coefficient model assumes that the studies in the meta-analysis are a random sample from some definable superpopulation of studies. This assumption is very difficult to justify. The weighted average estimate will be biased regardless of the number of studies or the sample size in each study. The actual confidence interval coverage probability can much smaller than the specified confidence level if the effect sizes are correlated with the weights (which occurs frequently). The confidence interval for tau-squared assumes that the true effect sizes in the superpopulation of studies have a normal distribution. A large number of studies, each with a large sample size, is required to assess the superpopulation normality assumption and to accurately estimate tau-squared. The confidence interval for the population tau-squared is hypersensitive to very minor and difficult-to-detect violations of the superpopulation normality assumption.

The random coefficient model should be used with caution, and the varying coefficient methods in this package are the recommended alternatives. The varying coefficient methods allows the effect sizes to differ across studies but do not require the studies to be a random sample from a definable superpopoulation of studies. This random coefficient function is included in the vcmeta package primarily for classroom demonstrations to illustrate the problimatic characteristics of the random coefficient meta-analysis model.

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is true, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

- Hedges LV, Olkin I (1985). *Statistical methods for meta-analysis*. Academic Press, New York. ISBN 01-233-63802.
- Borenstein M, Hedges LV, Higgins JP, Rothstein HR (2009). *Introduction to meta-analysis*. Wiley, New York.

See Also

meta.ave.gen

Examples

```
est <- c(.022, .751, .421, .287, .052, .146, .562, .904)
se <- c(.124, .464, .102, .592, .864, .241, .252, .318)
meta.ave.gen.rc(.05, est, se, bystudy = TRUE)

# Should return:
#                Estimate        SE          LL        UL
# Tau-squared 0.03772628 0.0518109  0.00000000 0.1392738
# Average     0.35394806 0.1155239  0.12752528 0.5803708
# Study 1     0.02200000 0.1240000 -0.22103553 0.2650355
# Study 2     0.75100000 0.4640000 -0.15842329 1.6604233
# Study 3     0.42100000 0.1020000  0.22108367 0.6209163
# Study 4     0.28700000 0.5920000 -0.87329868 1.4472987
# Study 5     0.05200000 0.8640000 -1.64140888 1.7454089
# Study 6     0.14600000 0.2410000 -0.32635132 0.6183513
# Study 7     0.56200000 0.2520000  0.06808908 1.0559109
# Study 8     0.90400000 0.3180000  0.28073145 1.5272685
```

---

meta.ave.mean.ps — *Confidence interval for an average mean difference from paired-samples studies*

Description

Computes the estimate, standard error, and confidence interval for an average mean difference from two or more paired-samples studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence interval for the average effect size. Equality of variances within or across studies is not assumed.

Usage

```
meta.ave.mean.ps(alpha, m1, m2, sd1, sd2, cor, n, bystudy = TRUE)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for measurement 1
m2	vector of estimated means for measurement 2
sd1	vector of estimated SDs for measurement 1
sd2	vector of estimated SDs for measurement 2
cor	vector of estimated correlations for paired measurements
n	vector of sample sizes
bystudy	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(53, 60, 53, 57)
m2 <- c(55, 62, 58, 61)
sd1 <- c(4.1, 4.2, 4.5, 4.0)
sd2 <- c(4.2, 4.7, 4.9, 4.8)
cor <- c(.7, .7, .8, .85)
n <- c(30, 50, 30, 70)
meta.ave.mean.ps(.05, m1, m2, sd1, sd2, cor, n, bystudy = TRUE)

# Should return:
#         Estimate        SE        LL         UL      df
# Average    -3.25 0.2471557 -3.739691 -2.7603091 112.347
# Study 1    -2.00 0.5871400 -3.200836 -0.7991639  29.000
# Study 2    -2.00 0.4918130 -2.988335 -1.0116648  49.000
# Study 3    -5.00 0.5471136 -6.118973 -3.8810270  29.000
# Study 4    -4.00 0.3023716 -4.603215 -3.3967852  69.000
```

---

meta.ave.mean2 — *Confidence interval for an average mean difference from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for an average mean difference from two or more 2-group studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence intervals. Equality of variances within or across studies is not assumed.

Usage

```
meta.ave.mean2(alpha, m1, m2, sd1, sd2, n1, n2, bystudy = TRUE)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for group 1
m2	vector of estimated means for group 2
sd1	vector of estimated SDs for group 1
sd2	vector of estimated SDs for group 2
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
bystudy	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(7.4, 6.9)
m2 <- c(6.3, 5.7)
sd1 <- c(1.72, 1.53)
sd2 <- c(2.35, 2.04)
n1 <- c(40, 60)
n2 <- c(40, 60)
meta.ave.mean2(.05, m1, m2, sd1, sd2, n1, n2, bystudy = TRUE)

# Should return:
#          Estimate        SE        LL       UL        df
# Average      1.15 0.2830183 0.5904369 1.709563 139.41053
# Study 1      1.10 0.4604590 0.1819748 2.018025  71.46729
# Study 2      1.20 0.3292036 0.5475574 1.852443 109.42136
```

`meta.ave.meanratio.ps` *Confidence interval for an average mean ratio from paired-samples studies*

Description

Computes the estimate, standard error, and confidence interval for a geometric average mean ratio from two or more paired-samples studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence interval for the average effect size. Equality of variances within or across studies is not assumed.

Usage

```
meta.ave.meanratio.ps(alpha, m1, m2, sd1, sd2, cor, n, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for measurement 1
`m2`	vector of estimated means for measurement 2
`sd1`	vector of estimated SDs for measurement 1
`sd2`	vector of estimated SDs for measurement 2
`cor`	vector of estimated correlations for paired measurements
`n`	vector of sample sizes
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval
- df - degrees of freedom

Examples

```
m1 <- c(53, 60, 53, 57)
m2 <- c(55, 62, 58, 61)
sd1 <- c(4.1, 4.2, 4.5, 4.0)
sd2 <- c(4.2, 4.7, 4.9, 4.8)
cor <- c(.7, .7, .8, .85)
n <- c(30, 50, 30, 70)
meta.ave.meanratio.ps(.05, m1, m2, sd1, sd2, cor, n, bystudy = TRUE)

# Should return:
#            Estimate          SE          LL          UL
# Average -0.05695120 0.004350863 -0.06558008 -0.04832231
# Study 1 -0.03704127 0.010871086 -0.05927514 -0.01480740
# Study 2 -0.03278982 0.008021952 -0.04891054 -0.01666911
# Study 3 -0.09015110 0.009779919 -0.11015328 -0.07014892
# Study 4 -0.06782260 0.004970015 -0.07773750 -0.05790769
#         exp(Estimate)   exp(LL)   exp(UL)       df
# Average     0.9446402 0.9365240 0.9528266 103.0256
# Study 1     0.9636364 0.9424474 0.9853017  29.0000
# Study 2     0.9677419 0.9522663 0.9834691  49.0000
# Study 3     0.9137931 0.8956968 0.9322550  29.0000
# Study 4     0.9344262 0.9252073 0.9437371  69.0000
```

`meta.ave.meanratio2` *Confidence interval for an average mean ratio from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for a geometric average mean ratio from two or more 2-group studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence intervals. Equality of variances within or across studies is not assumed.

Usage

```
meta.ave.meanratio2(alpha, m1, m2, sd1, sd2, n1, n2, bystudy = TRUE)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for group 1
m2	vector of estimated means for group 2
sd1	vector of estimated SDs for group 1
sd2	vector of estimated SDs for group 2
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
bystudy	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval
- df - degrees of freedom

References

Bonett DG, Price RM (2020). "Confidence intervals for ratios of means and medians." *Journal of Educational and Behavioral Statistics*, **45**(6), 750–770. ISSN 1076-9986, doi:10.3102/1076998620934125.

Examples

```
m1 <- c(7.4, 6.9)
m2 <- c(6.3, 5.7)
sd1 <- c(1.7, 1.5)
sd2 <- c(2.3, 2.0)
n1 <- c(40, 20)
n2 <- c(40, 20)
meta.ave.meanratio2(.05, m1, m2, sd1, sd2, n1, n2, bystudy = TRUE)

# Should return:
#          Estimate         SE          LL        UL  exp(Estimate)
# Average 0.1759928 0.05738065 0.061437186 0.2905484       1.192429
# Study 1 0.1609304 0.06820167 0.024749712 0.2971110       1.174603
# Study 2 0.1910552 0.09229675 0.002986265 0.3791242       1.210526
#          exp(LL)  exp(UL)       df
# Average 1.063364 1.337161 66.26499
# Study 1 1.025059 1.345965 65.69929
# Study 2 1.002991 1.461004 31.71341
```

`meta.ave.odds` *Confidence interval for average odds ratio from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for a geometric average odds ratio from two or more studies.

Usage

```
meta.ave.odds(alpha, f1, f2, n1, n2, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	vector of group 1 frequency counts
`f2`	vector of group 2 frequency counts
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - the exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

References

Bonett DG, Price RM (2015). "Varying coefficient meta-analysis methods for odds ratios and risk ratios." *Psychological Methods*, **20**(3), 394–406. ISSN 1939-1463, doi:10.1037/met0000032.

Examples

```
n1 <- c(204, 201, 932, 130, 77)
n2 <- c(106, 103, 415, 132, 83)
f1 <- c(24, 40, 93, 14, 5)
f2 <- c(12, 9, 28, 3, 1)
meta.ave.odds(.05, f1, f2, n1, n2, bystudy = TRUE)

# Should return:
#           Estimate        SE          LL        UL
# Average 0.86211102 0.2512852  0.36960107 1.3546210
# Study 1 0.02581353 0.3700520 -0.69947512 0.7511022
# Study 2 0.91410487 0.3830515  0.16333766 1.6648721
# Study 3 0.41496672 0.2226089 -0.02133877 0.8512722
# Study 4 1.52717529 0.6090858  0.33338907 2.7209615
# Study 5 1.42849472 0.9350931 -0.40425414 3.2612436
#         exp(Estimate)   exp(LL)   exp(UL)
# Average      2.368155 1.4471572  3.875292
# Study 1      1.026150 0.4968460  2.119335
# Study 2      2.494541 1.1774342  5.284997
# Study 3      1.514320 0.9788873  2.342625
# Study 4      4.605150 1.3956902 15.194925
# Study 5      4.172414 0.6674745 26.081952
```

`meta.ave.path` *Confidence interval for an average slope coefficient in a general linear model or a path model.*

Description

Computes the estimate, standard error, and confidence interval for an average slope coefficient in a general linear model (ANOVA, ANCOVA, multiple regression) or a path model from two or more studies.

Usage

```
meta.ave.path(alpha, n, slope, se, s, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`slope`	vector of slope estimates
`se`	vector of slope standard errors
`s`	number of predictors of the response variable
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
n <- c(75, 85, 250, 160)
slope <- c(1.57, 1.38, 1.08, 1.25)
se <- c(.658, .724, .307, .493)
meta.ave.path(.05, n, slope, se, 2, bystudy = TRUE)

#  Should return:
#         Estimate        SE          LL       UL       df
#  Average     1.32 0.2844334  0.75994528 1.880055 263.1837
#  Study 1     1.57 0.6580000  0.25830097 2.881699  72.0000
#  Study 2     1.38 0.7240000 -0.06026664 2.820267  82.0000
#  Study 3     1.08 0.3070000  0.47532827 1.684672 247.0000
#  Study 4     1.25 0.4930000  0.27623174 2.223768 157.0000
```

`meta.ave.pbcor` *Confidence interval for an average point-biserial correlation*

Description

Computes the estimate, standard error, and confidence interval for an average point-biserial correlation from two or more studies. Two types of point-biserial correlations can be meta-analyzed. One type uses an unweighted variance and is appropriate in 2-group experimental designs. The other type uses a weighted variance and is appropriate in 2-group nonexperimental designs with simple random sampling (but not stratified random sampling) within each study. This function requires all point-biserial correlations to be of the same type. Use the meta.ave.gen function to meta-analyze any combination of biserial correlation types.

Usage

```
meta.ave.pbcor(alpha, m1, m2, sd1, sd2, n1, n2, type, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for group 1
`m2`	vector of estimated means for group 2
`sd1`	vector of estimated SDs for group 1
`sd2`	vector of estimated SDs for group 2
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`type`	• set to 1 for weighted variance • set to 2 for unweighted variance
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2020). "Point-biserial correlation: Interval estimation, hypothesis testing, meta-analysis, and sample size determination." *British Journal of Mathematical and Statistical Psychology*, **73**(S1), 113–144. ISSN 0007-1102, doi:10.1111/bmsp.12189.

Examples

```
m1 <- c(21.9, 23.1, 19.8)
m2 <- c(16.1, 17.4, 15.0)
sd1 <- c(3.82, 3.95, 3.67)
sd2 <- c(3.21, 3.30, 3.02)
n1 <- c(40, 30, 24)
n2 <- c(40, 28, 25)
meta.ave.pbcor(.05, m1, m2, sd1, sd2, n1, n2, 2, bystudy = TRUE)

# Should return:
#          Estimate         SE        LL        UL
# Average 0.6159094 0.04363432 0.5230976 0.6942842
# Study 1 0.6349786 0.06316796 0.4842098 0.7370220
# Study 2 0.6160553 0.07776700 0.4255342 0.7380898
# Study 3 0.5966942 0.08424778 0.3903883 0.7283966
```

meta.ave.plot *Forest plot for average effect sizes*

Description

Generates a forest plot to visualize effect sizes estimates and overall averages from the meta.ave functions in vcmeta. If the column exp(Estimate) is present, this function plots the exponentiated effect size and CI found in columns exp(Estimate), exp(LL), and exp(UL). Otherwise, this function plots the effect size and CI found in the columns Estimate, LL, and UL.

Usage

```
meta.ave.plot(
  result,
  reference_line = NULL,
  diamond_height = 0.2,
  ggtheme = ggplot2::theme_classic()
)
```

Arguments

`result`	• a result matrix from any of the replicate functions in vcmeta
`reference_line`	Optional x-value for a reference line. Only applies if focuse is 'Difference' or 'Both'. Defaults to NULL, in which case a reference line is not drawn.
`diamond_height`	• Optional height of the diamond representing average effect size. Only applies if focus is 'Average' or 'Both'. Defaults to 0.2
`ggtheme`	• optional ggplot2 theme object; defaults to theme_classic()

Value

Returns a ggplot object. If stored, can be further customized via the ggplot API

Examples

```
# Plot results from meta.ave.mean2
m1 <- c(7.4, 6.9)
m2 <- c(6.3, 5.7)
sd1 <- c(1.72, 1.53)
sd2 <- c(2.35, 2.04)
n1 <- c(40, 60)
n2 <- c(40, 60)
result <- meta.ave.mean2(.05, m1, m2, sd1, sd2, n1, n2, bystudy = TRUE)
meta.ave.plot(result, reference_line = 0)


# Plot results from meta.ave.meanratio2
# Note that this plots the exponentiated effect size and CI
```

```
m1 <- c(53, 60, 53, 57)
m2 <- c(55, 62, 58, 61)
sd1 <- c(4.1, 4.2, 4.5, 4.0)
sd2 <- c(4.2, 4.7, 4.9, 4.8)
cor <- c(.7, .7, .8, .85)
n <- c(30, 50, 30, 70)
result <- meta.ave.meanratio.ps(.05, m1, m2, sd1, sd2, cor, n, bystudy = TRUE)
myplot <- meta.ave.plot(result, reference_line = 1)
myplot

# Change x-scale to log2
library(ggplot2)
myplot <- myplot + scale_x_continuous(
  trans = 'log2',
  limits = c(0.75, 1.25),
  name = "Estimated Ratio of Means, Log2 Scale"
)
myplot
```

---

meta.ave.prop.ps — *Confidence interval for an average proportion difference in paired-samples studies*

Description

Computes the estimate, standard error, and confidence interval for an average proportion difference from two or more studies.

Usage

```
meta.ave.prop.ps(alpha, f11, f12, f21, f22, bystudy = TRUE)
```

Arguments

alpha	alpha level for 1-alpha confidence
f11	vector of frequency counts in cell 1,1
f12	vector of frequency counts in cell 1,2
f21	vector of frequency counts in cell 2,1
f22	vector of frequency counts in cell 2,2
bystudy	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG, Price RM (2014). "Meta-analysis methods for risk differences." *British Journal of Mathematical and Statistical Psychology*, **67**(3), 371–387. ISSN 00071102, doi:10.1111/bmsp.12024.

Examples

```
f11 <- c(17, 28, 19)
f12 <- c(43, 56, 49)
f21 <- c(3, 5, 5)
f22 <- c(37, 54, 39)
meta.ave.prop.ps(.05, f11, f12, f21, f22, bystudy = TRUE)

# Should return:
#          Estimate         SE        LL        UL
# Average 0.3809573 0.03000016 0.3221581 0.4397565
# Study 1 0.3921569 0.05573055 0.2829270 0.5013867
# Study 2 0.3517241 0.04629537 0.2609869 0.4424614
# Study 3 0.3859649 0.05479300 0.2785726 0.4933572
```

`meta.ave.prop2` *Confidence interval for an average proportion difference in 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for an average proportion difference from two or more studies.

Usage

```
meta.ave.prop2(alpha, f1, f2, n1, n2, bystudy = TRUE)
```

Arguments

alpha	alpha level for 1-alpha confidence
f1	vector of group 1 frequency counts
f2	vector of group 2 frequency counts
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
bystudy	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG, Price RM (2014). "Meta-analysis methods for risk differences." *British Journal of Mathematical and Statistical Psychology*, **67**(3), 371–387. ISSN 00071102, doi:10.1111/bmsp.12024.

Examples

```
n1 <- c(204, 201, 932, 130, 77)
n2 <- c(106, 103, 415, 132, 83)
f1 <- c(24, 40, 93, 14, 5)
f2 <- c(12, 9, 28, 3, 1)
meta.ave.prop2(.05, f1, f2, n1, n2, bystudy = TRUE)

# Should return:
#             Estimate         SE            LL         UL
# Average 0.0567907589 0.01441216  2.854345e-02 0.08503807
# Study 1 0.0009888529 0.03870413 -7.486985e-02 0.07684756
# Study 2 0.1067323481 0.04018243  2.797623e-02 0.18548847
# Study 3 0.0310980338 0.01587717 -2.064379e-05 0.06221671
# Study 4 0.0837856174 0.03129171  2.245499e-02 0.14511624
# Study 5 0.0524199553 0.03403926 -1.429577e-02 0.11913568
```

`meta.ave.propratio2` *Confidence interval for an average proportion ratio from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for a geometric average proportion ratio from two or more studies.

Usage

```
meta.ave.propratio2(alpha, f1, f2, n1, n2, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	vector of group 1 frequency counts
`f2`	vector of group 2 frequency counts
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

References

Price RM, Bonett DG (2008). "Confidence intervals for a ratio of two independent binomial proportions." *Statistics in Medicine*, **27**(26), 5497–5508. ISSN 02776715, doi:10.1002/sim.3376.

Examples

```
n1 <- c(204, 201, 932, 130, 77)
n2 <- c(106, 103, 415, 132, 83)
f1 <- c(24, 40, 93, 14, 5)
f2 <- c(12, 9, 28, 3, 1)
meta.ave.propratio2(.05, f1, f2, n1, n2, bystudy = TRUE)

#  Should return:
#           Estimate        SE          LL        UL
# Average 0.84705608 0.2528742  0.35143178 1.3426804
# Study 1 0.03604257 0.3297404 -0.61023681 0.6823220
# Study 2 0.81008932 0.3442007  0.13546839 1.4847103
# Study 3 0.38746839 0.2065227 -0.01730864 0.7922454
# Study 4 1.49316811 0.6023296  0.31262374 2.6737125
# Study 5 1.50851199 0.9828420 -0.41782290 3.4348469
#     exp(Estimate)   exp(LL)   exp(UL)
# Average  2.332769 1.4211008  3.829294
# Study 1  1.036700 0.5432222  1.978466
# Study 2  2.248109 1.1450730  4.413686
# Study 3  1.473246 0.9828403  2.208350
# Study 4  4.451175 1.3670071 14.493677
# Study 5  4.520000 0.6584788 31.026662
```

---

meta.ave.semipart — *Confidence interval for an average semipartial correlation*

Description

Computes the estimate, standard error, and confidence interval for an average semipartial correlation from two or more studies.

Usage

```
meta.ave.semipart(alpha, n, cor, r2, bystudy = TRUE)
```

Arguments

alpha	alpha level for 1-alpha confidence
n	vector of sample sizes
cor	vector of estimated semipartial correlations
r2	vector of squared multiple correlations for a model that includes the IV and all control variables
bystudy	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
n <- c(128, 97, 210, 217)
cor <- c(.35, .41, .44, .39)
r2 <- c(.29, .33, .36, .39)
meta.ave.semipart(.05, n, cor, r2, bystudy = TRUE)

# Should return:
#          Estimate         SE        LL        UL
# Average    0.3975 0.03221240 0.3325507 0.4586965
# Study 1    0.3500 0.07175200 0.2023485 0.4820930
# Study 2    0.4100 0.07886080 0.2447442 0.5521076
# Study 3    0.4400 0.05146694 0.3338366 0.5351410
# Study 4    0.3900 0.05085271 0.2860431 0.4848830
```

---

meta.ave.slope — *Confidence interval for an average slope coefficient*

Description

Computes the estimate, standard error, and confidence interval for an average slope coefficient in a simple linear regression model from two or more studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence interval.

Usage

```
meta.ave.slope(alpha, n, cor, sdy, sdx, bystudy = TRUE)
```

Arguments

alpha	alpha level for 1-alpha confidence
n	vector of sample sizes
cor	vector of estimated correlations
sdy	vector of estimated SDs of y
sdx	vector of estimated SDs of x
bystudy	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

Examples

```
n <- c(45, 85, 50, 60)
cor <- c(.24, .35, .16, .20)
sdy <- c(12.2, 14.1, 11.7, 15.9)
sdx <- c(1.34, 1.87, 2.02, 2.37)
meta.ave.slope(.05, n, cor, sdy, sdx, bystudy = TRUE)

# Should return:
#          Estimate        SE         LL       UL       df
# Average 1.7731542 0.4755417  0.8335021 2.712806 149.4777
# Study 1 2.1850746 1.3084468 -0.4536599 4.823809  43.0000
# Study 2 2.6390374 0.7262491  1.1945573 4.083518  83.0000
# Study 3 0.9267327 0.8146126 -0.7111558 2.564621  48.0000
# Study 4 1.3417722 0.8456799 -0.3510401 3.034584  58.0000
```

`meta.ave.spear` *Confidence interval for an average Spearman correlation*

Description

Computes the estimate, standard error, and confidence interval for an average Spearman correlation from two or more studies. The Spearman correlation is preferred to the Pearson correlation if the relation between the two quantitative variables is monotonic rather than linear or if the bivariate normality assumption is not plausible.

Usage

```
meta.ave.spear(alpha, n, cor, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`cor`	vector of estimated Spearman correlations
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2008). "Meta-analytic interval estimation for bivariate correlations." *Psychological Methods*, **13**(3), 173–181. ISSN 1939-1463, doi:10.1037/a0012868.

Examples

```
n <- c(150, 200, 300, 200, 350)
cor <- c(.14, .29, .16, .21, .23)
meta.ave.spear(.05, n, cor, bystudy = TRUE)

# Should return:
#          Estimate         SE          LL        UL
# Average     0.206 0.02944265  0.14763960 0.2629309
# Study 1     0.140 0.08031750 -0.02151639 0.2943944
# Study 2     0.290 0.06492643  0.15476515 0.4145671
# Study 3     0.160 0.05635101  0.04689807 0.2690514
# Study 4     0.210 0.06776195  0.07187439 0.3402225
# Study 5     0.230 0.05069710  0.12690280 0.3281809
```

`meta.ave.stdmean.ps` *Confidence interval for an average standardized mean difference from paired-samples studies*

Description

Computes the estimate, standard error, and confidence interval for an average standardized mean difference from two or more paired-samples studies. Squrare root Unweighted variances and a single condition standard deviation are options for the standardizer. Equality of variances within or across studies is not assumed.

Usage

```
meta.ave.stdmean.ps(alpha, m1, m2, sd1, sd2, cor, n, stdzr, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for measurement 1
`m2`	vector of estimated means for measurement 2
`sd1`	vector of estimated SDs for measurement 1
`sd2`	vector of estimated SDs for measurement 2
`cor`	vector of estimated correlations for paired measurements
`n`	vector of sample sizes
`stdzr`	• set to 0 for square root unweighted average variance standardizer • set to 1 for measurement 1 SD standardizer • set to 2 for measurement 2 SD standardizer
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(23.9, 24.1)
m2 <- c(25.1, 26.9)
sd1 <- c(1.76, 1.58)
sd2 <- c(2.01, 1.76)
cor <- c(.78, .84)
n <- c(25, 30)
meta.ave.stdmean.ps(.05, m1, m2, sd1, sd2, cor, n, 1, bystudy = TRUE)

# Should return:
#           Estimate        SE        LL         UL
# Average -1.1931045 0.1568034 -1.500433 -0.8857755
# Study 1 -0.6818182 0.1773785 -1.029474 -0.3341628
# Study 2 -1.7721519 0.2586234 -2.279044 -1.2652594
```

`meta.ave.stdmean2` *Confidence interval for an average standardized mean difference from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for an average standardized mean difference from two or more 2-group studies. Square root unweighted variances, square root weighted variances, and single group standard deviation are options for the standardizer. Equality of variances within or across studies is not assumed.

Usage

```
meta.ave.stdmean2(alpha, m1, m2, sd1, sd2, n1, n2, stdzr, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for group 1
`m2`	vector of estimated means for group 2
`sd1`	vector of estimated SDs for group 1
`sd2`	vector of estimated SDs for group 2
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`stdzr`	• set to 0 for square root unweighted average variance standardizer • set to 1 for group 1 SD standardizer • set to 2 for group 2 SD standardizer • set to 3 for square root weighted average variance standardizer
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated effect size
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(21.9, 23.1, 19.8)
m2 <- c(16.1, 17.4, 15.0)
sd1 <- c(3.82, 3.95, 3.67)
sd2 <- c(3.21, 3.30, 3.02)
n1 <- c(40, 30, 24)
n2 <- c(40, 28, 25)
meta.ave.stdmean2(.05, m1, m2, sd1, sd2, n1, n2, 0, bystudy = TRUE)

# Should return:
#          Estimate        SE        LL       UL
# Average 1.526146 0.1734341 1.1862217 1.866071
# Study 1 1.643894 0.2629049 1.1286100 2.159178
# Study 2 1.566132 0.3056278 0.9671126 2.165152
# Study 3 1.428252 0.3289179 0.7835848 2.072919
```

`meta.ave.var` *Confidence interval for an average variance*

Description

Computes the estimate and confidence interval for an average variance from two or more studies. The estimated average variance or the upper confidence limit could be used as a variance planning value in sample size planning.

Usage

```
meta.ave.var(alpha, var, n, bystudy = TRUE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`var`	vector of sample variances
`n`	vector of sample sizes
`bystudy`	logical to also return each study estimate (TRUE) or not

Value

Returns a matrix. The first row is the average estimate across all studies. If bystudy is TRUE, there is 1 additional row for each study. The matrix has the following columns:

- Estimate - estimated variance
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
var <- c(26.63, 22.45, 34.12)
n <- c(40, 30, 50)
meta.ave.var(.05, var, n, bystudy = TRUE)

# Should return:
#          Estimate       LL       UL
# Average 27.73333 21.45679 35.84589
# Study 1 26.63000 17.86939 43.90614
# Study 2 22.45000 14.23923 40.57127
# Study 3 34.12000 23.80835 52.98319
```

---

meta.chitest *Computes a chi-square test of effect-size homogeneity*

Description

Computes a chi-square test of effect size homogeneity and p-value using effect-size estimates and their standard errors from two or more studies. This test should not be used to justify the use of a constant coeffient (fixed-effect) meta-analysis.

Usage

```
meta.chitest(est, se)
```

Arguments

est	vector of effect-size estimates
se	vector of effect-size standard errors

Value

Returns a one-row matrix:

- Q - chi-square test statitic
- df - degrees of freedom
- p - p-value

References

Borenstein M, Hedges LV, Higgins JP, Rothstein HR (2009). *Introduction to meta-analysis*. Wiley, New York.

Examples

```
est <- c(.297, .324, .281, .149)
se <- c(.082, .051, .047, .094)
meta.chitest(est, se)

# Should return:
#         Q df         p
#  2.706526  3 0.4391195
```

`meta.lc.agree` *Confidence interval for a linear contrast of G-index coefficients*

Description

Computes the estimate, standard error, and adjusted Wald confidence interval for a linear contrast of G-index of agreement coefficients from two or more studies. This function assumes that two raters each provide a dichotomous rating for a sample of objects.

Usage

```
meta.lc.agree(alpha, f11, f12, f21, f22, v)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f11`	vector of frequency counts in cell 1,1
`f12`	vector of frequency counts in cell 1,2
`f21`	vector of frequency counts in cell 2,1
`f22`	vector of frequency counts in cell 2,2
`v`	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the adjusted Wald confidence interval
- UL - upper limit of the adjusted Wald confidence interval

Examples

```
f11 <- c(43, 56, 49)
f12 <- c(7, 2, 9)
f21 <- c(3, 5, 5)
f22 <- c(37, 54, 39)
v <- c(.5, .5, -1)
meta.lc.agree(.05, f11, f12, f21, f22, v)

# Should return:
#           Estimate        SE         LL        UL
# Contrast 0.1022939 0.07972357 -0.05396142 0.2585492
```

---

meta.lc.gen *Confidence interval for a linear contrast of effect sizes*

Description

Computes the estimate, standard error, and confidence interval for a linear contrast of any type of effect size from two or more studies.

Usage

```
meta.lc.gen(alpha, est, se, v)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`est`	vector of parameter estimates
`se`	vector of standard errors
`v`	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
est <- c(.55, .59, .44, .48, .26, .19)
se <- c(.054, .098, .029, .084, .104, .065)
v <- c(.5, .5, -.25, -.25, -.25, -.25)
meta.lc.gen(.05, est, se, v)

# Should return:
#           Estimate         SE        LL        UL
# Contrast   0.2275 0.06755461 0.0950954 0.3599046
```

---

meta.lc.mean.ps *Confidence interval for a linear contrast of mean differences from paired-samples studies*

Description

Computes the estimate, standard error, and confidence interval for a linear contrast of paired-samples mean differences from two or more studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence interval. Equality of variances within or across studies is not assumed.

Usage

```
meta.lc.mean.ps(alpha, m1, m2, sd1, sd2, cor, n, v)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for measurement 1
m2	vector of estimated means for measurement 2
sd1	vector of estimated SDs for measurement 1
sd2	vector of estimated SDs for measurement 2
cor	vector of estimated correlations for paired measurements
n	vector of sample sizes
v	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(53, 60, 53, 57)
m2 <- c(55, 62, 58, 61)
sd1 <- c(4.1, 4.2, 4.5, 4.0)
sd2 <- c(4.2, 4.7, 4.9, 4.8)
cor <- c(.7, .7, .8, .85)
n <- c(30, 50, 30, 70)
v <- c(.5, .5, -.5, -.5)
meta.lc.mean.ps(.05, m1, m2, sd1, sd2, cor, n, v)

# Should return:
#          Estimate        SE       LL       UL      df
# Contrast      2.5 0.4943114 1.520618 3.479382 112.347
```

---

meta.lc.mean1 *Confidence interval for a linear contrast of means*

Description

Computes the estimate, standard error, and confidence interval for a linear contrast of means from two or more studies. This function will use either an unequal variance (recommended) or an equal variance method. A Satterthwaite adjustment to the degrees of freedom is used with the unequal variance method.

Usage

```
meta.lc.mean1(alpha, m, sd, n, v, eqvar = FALSE)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m`	vector of estimated means
`sd`	vector of estimated standard deviations
`n`	vector of sample sizes
`v`	vector of contrast coefficients
`eqvar`	• FALSE for unequal variance method • TRUE for equal variance method

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Snedecor GW, Cochran WG (1980). *Statistical methods*, 7th edition. ISU University Pres, Ames, Iowa.

Examples

```
m <- c(33.5, 37.9, 38.0, 44.1)
sd <- c(3.84, 3.84, 3.65, 4.98)
n <- c(10, 10, 10, 10)
v <- c(.5, .5, -.5, -.5)
meta.lc.mean1(.05, m, sd, n, v, eqvar = FALSE)

# Should return:
#          Estimate       SE        LL        UL       df
# Contrast    -5.35 1.300136 -7.993583 -2.706417 33.52169
```

`meta.lc.mean2` *Confidence interval for a linear contrast of mean differences from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for a linear contrast of 2-group mean differences from two or more studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence interval. Equality of variances within or across studies is not assumed.

Usage

```
meta.lc.mean2(alpha, m1, m2, sd1, sd2, n1, n2, v)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for group 1
m2	vector of estimated means for group 2
sd1	vector of estimated SDs for group 1
sd2	vector of estimated SDs for group 2
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
v	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2009). “Meta-analytic interval estimation for standardized and unstandardized mean differences.” *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(45.1, 39.2, 36.3, 34.5)
m2 <- c(30.0, 35.1, 35.3, 36.2)
sd1 <- c(10.7, 10.5, 9.4, 11.5)
sd2 <- c(12.3, 12.0, 10.4, 9.6)
n1 <- c(40, 20, 50, 25)
n2 <- c(40, 20, 48, 26)
v <- c(.5, .5, -.5, -.5)
meta.lc.mean2(.05, m1, m2, sd1, sd2, n1, n2, v)

# Should return:
#          Estimate       SE       LL       UL       df
# Contrast     9.95 2.837787 4.343938 15.55606 153.8362
```

meta.lc.meanratio.ps — *Confidence interval for a log-linear contrast of mean ratios from paired-samples studies*

Description

Computes the estimate, standard error, and confidence interval for a log-linear contrast of paired-sample mean ratios from two or more studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence interval. Equality of variances within or across studies is not assumed.

Usage

```
meta.lc.meanratio.ps(alpha, m1, m2, sd1, sd2, cor, n, v)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for measurement 1
`m2`	vector of estimated means for measurement 2
`sd1`	vector of estimated SDs for measurement 1
`sd2`	vector of estimated SDs for measurement 2
`cor`	vector of estimated correlations for paired measurements
`n`	vector of sample sizes
`v`	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimatedf log-linear contrast
- SE - standard error of log-linear contrast
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - exponentiated log-linear contrast
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval
- df - degrees of freedom

References

Bonett DG, Price RM (2020). "Confidence intervals for ratios of means and medians." *Journal of Educational and Behavioral Statistics*, **45**(6), 750–770. ISSN 1076-9986, doi:10.3102/1076998620934125.

Examples

```
m1 <- c(53, 60, 53, 57)
m2 <- c(55, 62, 58, 61)
sd1 <- c(4.1, 4.2, 4.5, 4.0)
sd2 <- c(4.2, 4.7, 4.9, 4.8)
cor <- c(.7, .7, .8, .85)
n <- c(30, 50, 30, 70)
v <- c(.5, .5, -.5, -.5)
meta.lc.meanratio.ps(.05, m1, m2, sd1, sd2, cor, n, v)

# Should return:
#           Estimate          SE         LL         UL exp(Estimate)
# Contrast 0.0440713 0.008701725 0.02681353 0.06132907      1.045057
#           exp(LL)  exp(UL)       df
# Contrast 1.027176 1.063249 103.0256
```

`meta.lc.meanratio2` *Confidence interval for a log-linear contrast of mean ratios from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for a log-linear contrast of 2-group mean ratios from two or more studies. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence interval. Equality of variances within or across studies is not assumed.

Usage

```
meta.lc.meanratio2(alpha, m1, m2, sd1, sd2, n1, n2, v)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for group 1
m2	vector of estimated means for group 2
sd1	vector of estimated SDs for group 1
sd2	vector of estimated SDs for group 2
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
v	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated log-linear contrast
- SE - standard error of log-linear contrast
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - exponentiated log-linear contrast
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval
- df - degrees of freedom

References

Bonett DG, Price RM (2020). "Confidence intervals for ratios of means and medians." *Journal of Educational and Behavioral Statistics*, **45**(6), 750–770. ISSN 1076-9986, doi:10.3102/1076998620934125.

Examples

```
m1 <- c(45.1, 39.2, 36.3, 34.5)
m2 <- c(30.0, 35.1, 35.3, 36.2)
sd1 <- c(10.7, 10.5, 9.4, 11.5)
sd2 <- c(12.3, 12.0, 10.4, 9.6)
n1 <- c(40, 20, 50, 25)
n2 <- c(40, 20, 48, 26)
v <- c(.5, .5, -.5, -.5)
meta.lc.meanratio2(.05, m1, m2, sd1, sd2, n1, n2, v)

# Should return:
#            Estimate         SE        LL        UL  exp(Estimate)
# Contrast 0.2691627 0.07959269 0.1119191 0.4264064      1.308868
#            exp(LL)  exp(UL)       df
# Contrast 1.118422 1.531743 152.8665
```

`meta.lc.odds` *Confidence interval for a log-linear contrast of odds ratios*

Description

Computes the estimate, standard error, and confidence interval for an exponentiated log-linear contrast of odds ratios from two or more studies.

Usage

```
meta.lc.odds(alpha, f1, f2, n1, n2, v)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	vector of group 1 frequency counts
`f2`	vector of group 2 frequency counts
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`v`	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated log-linear contrast
- SE - standard error of log-linear contrast
- exp(Estimate) - exponentiated log-linear contrast
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

References

Bonett DG, Price RM (2015). “Varying coefficient meta-analysis methods for odds ratios and risk ratios.” *Psychological Methods*, **20**(3), 394–406. ISSN 1939-1463, doi:10.1037/met0000032.

Examples

```
n1 <- c(50, 150, 150)
f1 <- c(16, 50, 25)
n2 <- c(50, 150, 150)
f2 <- c(7, 15, 20)
v <- c(1, -1, 0)
meta.lc.odds(.05, f1, f2, n1, n2, v)

# Should return:
#             Estimate        SE  exp(Estimate)   exp(LL)  exp(UL)
# Contrast -0.4596883 0.5895438      0.6314805 0.1988563 2.005305
```

`meta.lc.prop.ps` *Confidence interval for a linear contrast of proportion differences in paired-samples studies*

Description

Computes the estimate, standard error, and adjusted Wald confidence interval for a linear contrast of paired-samples proportion differences from two or more studies.

Usage

```
meta.lc.prop.ps(alpha, f11, f12, f21, f22, v)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f11`	vector of frequency counts in cell 1,1
`f12`	vector of frequency counts in cell 1,2
`f21`	vector of frequency counts in cell 2,1
`f22`	vector of frequency counts in cell 2,2
`v`	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the adjusted Wald confidence interval
- UL - upper limit of the adjusted Wald confidence interval

References

Bonett DG, Price RM (2014). "Meta-analysis methods for risk differences." *British Journal of Mathematical and Statistical Psychology*, **67**(3), 371–387. ISSN 00071102, doi:10.1111/bmsp.12024.

Examples

```
f11 <- c(17, 28, 19)
f12 <- c(43, 56, 49)
f21 <- c(3, 5, 5)
f22 <- c(37, 54, 39)
v <- c(.5, .5, -1)
meta.lc.prop.ps(.05, f11, f12, f21, f22, v)

# Should return:
```

```
#              Estimate         SE         LL       UL
#  Contrast -0.01436285 0.06511285 -0.1419817 0.113256
```

`meta.lc.prop1` *Confidence interval for a linear contrast of proportions*

Description

Computes the estimate, standard error, and an adjusted Wald confidence interval for a linear contrast of proportions from two or more studies.

Usage

```
meta.lc.prop1(alpha, f, n, v)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f`	vector of frequency counts
`n`	vector of sample sizes
`v`	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate -estimated linear contrast
- SE - standard error
- LL - lower limit of the adjusted Wald confidence interval
- UL - upper limit of the adjusted Wald confidence interval

References

Price RM, Bonett DG (2004). "An improved confidence interval for a linear function of binomial proportions." *Computational Statistics and Data Analysis*, **45**(3), 449–456. ISSN 01679473, doi:10.1016/S01679473(03)000070.

Examples

```
f <- c(26, 24, 38)
n <- c(60, 60, 60)
v <- c(-.5, -.5, 1)
meta.lc.prop1(.05, f, n, v)

# Should return:
#           Estimate         SE         LL        UL
# Contrast 0.2119565 0.07602892 0.06294259 0.3609705
```

---

meta.lc.prop2 — *Confidence interval for a linear contrast of proportion differences in 2-group studies*

Description

Computes the estimate, standard error, and adjusted Wald confidence interval for a linear contrast of 2-group proportion differences from two or more studies.

Usage

```
meta.lc.prop2(alpha, f1, f2, n1, n2, v)
```

Arguments

alpha	alpha level for 1-alpha confidence
f1	vector of group 1 frequency counts
f2	vector of group 2 frequency counts
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
v	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the adjusted Wald confidence interval
- UL - upper limit of the adjusted Wald confidence interval

References

Bonett DG, Price RM (2014). "Meta-analysis methods for risk differences." *British Journal of Mathematical and Statistical Psychology*, **67**(3), 371–387. ISSN 00071102, doi:10.1111/bmsp.12024.

Examples

```
n1 <- c(50, 150, 150)
n2 <- c(50, 150, 150)
f1 <- c(16, 50, 25)
f2 <- c(7, 15, 20)
v <- c(1, -1, 0)
meta.lc.prop2(.05, f1, f2, n1, n2, v)

# Should return:
#             Estimate         SE         LL        UL
# Contrast -0.05466931 0.09401019 -0.2389259 0.1295873
```

`meta.lc.propratio2` *Confidence interval for a log-linear contrast of proportion ratios from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for an exponentiated log-linear contrast of 2-group proportion ratios from two or more studies.

Usage

```
meta.lc.propratio2(alpha, f1, f2, n1, n2, v)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	vector of group 1 frequency counts
`f2`	vector of group 2 frequency counts
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`v`	vector of contrast coefficients

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated log-linear contrast
- SE - standard error of log-linear contrast
- exp(Estimate) - exponentiated log-linear contrast
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

References

Price RM, Bonett DG (2008). "Confidence intervals for a ratio of two independent binomial proportions." *Statistics in Medicine*, **27**(26), 5497–5508. ISSN 02776715, doi:10.1002/sim.3376.

Examples

```
n1 <- c(50, 150, 150)
f1 <- c(16, 50, 25)
n2 <- c(50, 150, 150)
f2 <- c(7, 15, 20)
v <- c(1, -1, 0)
meta.lc.propratio2(.05, f1, f2, n1, n2, v)

# Should return:
#             Estimate        SE  exp(Estimate)   exp(LL)  exp(UL)
# Contrast -0.3853396 0.4828218      0.6802196 0.2640405 1.752378
```

`meta.lc.stdmean.ps` *Confidence interval for a linear contrast of standardized mean differences from paired-samples studies*

Description

Computes the estimate, standard error, and confidence interval for a linear contrast of paired-samples standardized mean differences from two or more studies. Equality of variances within or across studies is not assumed.

Usage

```
meta.lc.stdmean.ps(alpha, m1, m2, sd1, sd2, cor, n, v, stdzr)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for measurement 1
`m2`	vector of estimated means for measurement 2
`sd1`	vector of estimated SDs for measurement 1
`sd2`	vector of estimated SDs for measurement 2
`cor`	vector of estimated correlations for paired measurements
`n`	vector of sample sizes
`v`	vector of contrast coefficients
`stdzr`	• set to 0 for square root unweighted average variance standardizer • set to 1 for measurement 1 SD standardizer • set to 2 for measurement 2 SD standardizer

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(53, 60, 53, 57)
m2 <- c(55, 62, 58, 61)
sd1 <- c(4.1, 4.2, 4.5, 4.0)
sd2 <- c(4.2, 4.7, 4.9, 4.8)
cor <- c(.7, .7, .8, .85)
n <- c(30, 50, 30, 70)
v <- c(.5, .5, -.5, -.5)
meta.lc.stdmean.ps(.05, m1, m2, sd1, sd2, cor, n, v, 0)

# Should return:
#             Estimate        SE        LL        UL
# Contrast  0.5127577 0.1392232 0.2398851 0.7856302
```

---

meta.lc.stdmean2 *Confidence interval for a linear contrast of standardized mean differences from 2-group studies*

Description

Computes the estimate, standard error, and confidence interval for a linear contrast of 2-group standardized mean differences from two or more studies. Equality of variances within or across studies is not assumed. Use the square root average variance standardizer (stdzr = 0) for 2-group experimental designs. Use the square root weighted variance standardizer (stdzr = 3) for 2-group nonexperimental designs with simple random sampling. The stdzr = 1 and stdzr = 2 options can be used with either experimental or nonexperimental designs.

Usage

```
meta.lc.stdmean2(alpha, m1, m2, sd1, sd2, n1, n2, v, stdzr)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for group 1
m2	vector of estimated means for group 2
sd1	vector of estimated SDs for group 1
sd2	vector of estimated SDs for group 2
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
v	vector of contrast coefficients
stdzr	• set to 0 for square root unweighted average variance standardizer • set to 1 for group 1 SD standardizer • set to 2 for group 2 SD standardizer • set to 3 for square root weighted average variance standardizer

Value

Returns 1-row matrix with the following columns:

- Estimate - estimated linear contrast
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
m1 <- c(45.1, 39.2, 36.3, 34.5)
m2 <- c(30.0, 35.1, 35.3, 36.2)
sd1 <- c(10.7, 10.5, 9.4, 11.5)
sd2 <- c(12.3, 12.0, 10.4, 9.6)
n1 <- c(40, 20, 50, 25)
n2 <- c(40, 20, 48, 26)
v <- c(.5, .5, -.5, -.5)
meta.lc.stdmean2(.05, m1, m2, sd1, sd2, n1, n2, v, 0)

# Should return:
#           Estimate        SE        LL       UL
# Contrast 0.8557914 0.2709192 0.3247995 1.386783
```

`meta.lm.agree` *Meta-regression analysis for G agreement indices*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a G-index of agreement. The estimates are OLS estimates with robust standard errors that accomodate residual heteroscedasticity.

Usage

```
meta.lm.agree(alpha, f11, f12, f21, f22, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f11`	vector of frequency counts in cell 1,1
`f12`	vector of frequency counts in cell 1,2
`f21`	vector of frequency counts in cell 2,1
`f22`	vector of frequency counts in cell 2,2
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
f11 <- c(40, 20, 25, 30)
f12 <- c(3, 2, 2, 1)
f21 <- c(7, 6, 8, 6)
f22 <- c(26, 25, 13, 25)
x1 <- c(1, 1, 4, 6)
x2 <- c(1, 1, 0, 0)
X <- matrix(cbind(x1, x2), 4, 2)
meta.lm.agree(.05, f11, f12, f21, f22, X)
```

```
# Should return:
#     Estimate         SE         z     p          LL        UL
# b0 0.1904762 0.38772858 0.4912617 0.623 -0.56945786 0.9504102
# b1 0.0952381 0.07141957 1.3335013 0.182 -0.04474169 0.2352179
# b2 0.4205147 0.32383556 1.2985438 0.194 -0.21419136 1.0552207
```

---

meta.lm.cor *Meta-regression analysis for Pearson or partial correlations*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a Fisher-transformed Pearson or partial correlation. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The correlations are Fisher-transformed and hence the parameter estimates do not have a simple interpretation. However, the hypothesis test results can be used to decide if a population slope is either positive or negative.

Usage

```
meta.lm.cor(alpha, n, cor, s, X)
```

Arguments

alpha	alpha level for 1-alpha confidence
n	vector of sample sizes
cor	vector of estimated Pearson or partial correlations
s	number of control variables
X	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - Standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
n <- c(55, 190, 65, 35)
cor <- c(.40, .65, .60, .45)
q <- 0
x1 <- c(18, 25, 23, 19)
X <- matrix(x1, 4, 1)
meta.lm.cor(.05, n, cor, q, X)

# Should return:
#       Estimate         SE         z     p           LL         UL
# b0 -0.47832153 0.48631509 -0.983563 0.325 -1.431481595 0.47483852
# b1  0.05047154 0.02128496  2.371231 0.018  0.008753794 0.09218929
```

`meta.lm.cor.gen` *Meta-regression analysis for correlations*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a Fisher-transformed correlation. The correlations can be of different types (e.g., Pearson, partial, Spearman). The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. This function uses estimated correlations and their standard errors as input. The correlations are Fisher-transformed and hence the parameter estimates do not have a simple interpretation. However, the hypothesis test results can be used to decide if a population slope is either positive or negative.

Usage

```
meta.lm.cor.gen(alpha, cor, se, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`cor`	vector of estimated correlations
`se`	number of control variables
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value

- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
cor <- c(.40, .65, .60, .45)
se <- c(.182, .114, .098, .132)
x1 <- c(18, 25, 23, 19)
X <- matrix(x1, 4, 1)
meta.lm.cor.gen(.05, cor, se, X)

# Should return:
#       Estimate         SE          z     p
# b0 -0.47832153 0.63427931 -0.7541181 0.451
# b1  0.05047154 0.02879859  1.7525699 0.080
```

---

meta.lm.cronbach *Meta-regression analysis for Cronbach reliabilities*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a log-complement Cronbach reliablity. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The exponentiated slope estimate for a predictor variable describes a multiplicative change in non-reliability associated with a 1-unit increase in that predictor variable, controlling for all other predictor variables in the model.

Usage

```
meta.lm.cronbach(alpha, n, rel, r, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`rel`	vector of estimated reliabilities
`r`	number of measurements (e.g., items)
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - exponentiated OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the exponentiated confidence interval
- UL - upper limit of the exponentiated confidence interval

References

Bonett DG (2010). "Varying coefficient meta-analytic methods for alpha reliability." *Psychological Methods*, **15**(4), 368–385. ISSN 1939-1463, doi:10.1037/a0020142.

Examples

```
n <- c(583, 470, 546, 680)
rel <- c(.91, .89, .90, .89)
x1 <- c(1, 0, 0, 0)
X <- matrix(x1, 4, 1)
meta.lm.cronbach(.05, n, rel, 10, X)

# Should return:
#      Estimate         SE          z     p        LL          UL
# b0 -2.2408328 0.03675883 -60.960391 0.000 -2.3128788 -2.16878684
# b1 -0.1689006 0.07204625  -2.344336 0.019 -0.3101087 -0.02769259
```

`meta.lm.gen` *Meta-regression analysis for any type of effect size*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is any type of effect size. The estimates are OLS estimates with robust standard errors that accomodate residual heteroscedasticity.

Usage

```
meta.lm.gen(alpha, est, se, X)
```

Arguments

alpha	alpha level for 1-alpha confidence
est	vector of parameter estimates
se	vector of standard errors
X	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
est <- c(4.1, 4.7, 4.9, 5.7, 6.6, 7.3)
se <- c(1.2, 1.5, 1.3, 1.8, 2.0, 2.6)
x1 <- c(10, 20, 30, 40, 50, 60)
x2 <- c(1, 1, 1, 0, 0, 0)
X <- matrix(cbind(x1, x2), 6, 2)
meta.lm.gen(.05, est, se, X)

# Should return:
#      Estimate         SE           z     p         LL         UL
# b0  3.5333333 4.37468253  0.80767766 0.419 -5.0408869 12.1075535
# b1  0.0600000 0.09058835  0.66233679 0.508 -0.1175499  0.2375499
# b2 -0.1666667 2.81139793 -0.05928249 0.953 -5.6769054  5.3435720
```

---

meta.lm.mean.ps *Meta-regression analysis for paired-samples mean differences*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a paired-samples mean difference. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity.

Usage

```
meta.lm.mean.ps(alpha, m1, m2, sd1, sd2, cor, n, X)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for measurement 1
m2	vector of estimated means for measurement 2
sd1	vector of estimated SDs for measurement 1
sd2	vector of estimated SDs for measurement 2
cor	vector of estimated correlations for paired measurements
n	vector of sample sizes
X	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- t - t-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
n <- c(65, 30, 29, 45, 50)
cor <- c(.87, .92, .85, .90, .88)
m1 <- c(20.1, 20.5, 19.3, 21.5, 19.4)
m2 <- c(10.4, 10.2, 8.5, 10.3, 7.8)
sd1 <- c(9.3, 9.9, 10.1, 10.5, 9.8)
sd2 <- c(7.8, 8.0, 8.4, 8.1, 8.7)
x1 <- c(2, 3, 3, 4, 4)
X <- matrix(x1, 5, 1)
meta.lm.mean.ps(.05, m1, m2, sd1, sd2, cor, n, X)

# Should return:
#    Estimate        SE        t     p        LL        UL  df
# b0     8.00 1.2491990 6.404104 0.000 5.5378833 10.462117 217
# b1     0.85 0.3796019 2.239188 0.026 0.1018213  1.598179 217
```

meta.lm.mean1 — *Meta-regression analysis for 1-group means*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a mean from one group. The estimates are OLS estimates with robust standard errors that accomodate residual heteroscedasticity.

Usage

```
meta.lm.mean1(alpha, m, sd, n, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m`	vector of estimated means
`sd`	vector of estimated standard deviations
`n`	vector of sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- t - t-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

Examples

```
n <- c(25, 15, 30, 25, 40)
m <- c(20.1, 20.5, 19.3, 21.5, 19.4)
sd <- c(10.4, 10.2, 8.5, 10.3, 7.8)
x1 <- c(1, 1, 0, 0, 0)
x2 <- c( 12, 13, 11, 13, 15)
X <- matrix(cbind(x1, x2), 5, 2)
meta.lm.mean1(.05, m, sd, n, X)

# Should return:
```

```
#       Estimate        SE          t     p         LL        UL  df
# b0 19.45490196 6.7873381 2.86635227 0.005  6.0288763 32.880928 132
# b1  0.25686275 1.9834765 0.12950128 0.897 -3.6666499  4.180375 132
# b2  0.04705882 0.5064693 0.09291544 0.926 -0.9547876  1.048905 132
```

`meta.lm.mean2` *Meta-regression analysis for 2-group mean differences*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a 2-group mean difference. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity.

Usage

```
meta.lm.mean2(alpha, m1, m2, sd1, sd2, n1, n2, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for group 1
`m2`	vector of estimated means for group 2
`sd1`	vector of estimated SDs for group 1
`sd2`	vector of estimated SDs for group 2
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- t - t-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
n1 <- c(65, 30, 29, 45, 50)
n2 <- c(67, 32, 31, 20, 52)
m1 <- c(31.1, 32.3, 31.9, 29.7, 33.0)
m2 <- c(34.1, 33.2, 30.6, 28.7, 26.5)
sd1 <- c(7.1, 8.1, 7.8, 6.8, 7.6)
sd2 <- c(7.8, 7.3, 7.5, 7.2, 6.8)
x1 <- c(4, 6, 7, 7, 8)
x2 <- c(1, 0, 0, 0, 1)
X <- matrix(cbind(x1, x2), 5, 2)
meta.lm.mean2(.05, m1, m2, sd1, sd2, n1, n2, X)

# Should return:
#    Estimate        SE         t     p         LL        UL  df
# b0   -15.20 3.4097610 -4.457791 0.000 -21.902415 -8.497585 418
# b1     2.35 0.4821523  4.873979 0.000   1.402255  3.297745 418
# b2     2.85 1.5358109  1.855697 0.064  -0.168875  5.868875 418
```

---

meta.lm.meanratio.ps *Meta-regression analysis for paired-samples log mean ratios*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a paired-samples log mean ratio. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The exponentiated slope estimate for a predictor variable describes a multiplicative change in the mean ratio associated with a 1-unit increase in that predictor variable, controlling for all other predictor variables in the model.

Usage

```
meta.lm.meanratio.ps(alpha, m1, m2, sd1, sd2, cor, n, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for measurement 1
`m2`	vector of estimated means for measurement 2
`sd1`	vector of estimated SDs for measurement 1
`sd2`	vector of estimated SDs for measurement 2

`cor`	vector of estimated correlations for paired measurements
`n`	vector of sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - the exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

Examples

```
n <- c(65, 30, 29, 45, 50)
cor <- c(.87, .92, .85, .90, .88)
m1 <- c(20.1, 20.5, 19.3, 21.5, 19.4)
m2 <- c(10.4, 10.2, 8.5, 10.3, 7.8)
sd1 <- c(9.3, 9.9, 10.1, 10.5, 9.8)
sd2 <- c(7.8, 8.0, 8.4, 8.1, 8.7)
x1 <- c(2, 3, 3, 4, 4)
X <- matrix(x1, 5, 1)
meta.lm.meanratio.ps(.05, m1, m2, sd1, sd2, cor, n, X)

# Should return:
#      Estimate         SE           LL        UL        z     p
# b0 0.50957008 0.13000068  0.254773424 0.7643667 3.919749 0.000
# b1 0.07976238 0.04133414 -0.001251047 0.1607758 1.929697 0.054
#     exp(Estimate)   exp(LL)  exp(UL)
# b0       1.664575 1.2901693 2.147634
# b1       1.083030 0.9987497 1.174422
```

meta.lm.meanratio2 *Meta-regression analysis for 2-group log mean ratios*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a 2-group log mean ratio. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The exponentiated slope estimate for a predictor variable describes a multiplicative change in the mean ratio associated with a 1-unit increase in that predictor variable, controlling for all other predictor variables in the model.

Usage

```
meta.lm.meanratio2(alpha, m1, m2, sd1, sd2, n1, n2, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for group 1
`m2`	vector of estimated means for group 2
`sd1`	vector of estimated SDs for group 1
`sd2`	vector of estimated SDs for group 2
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - the exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

Examples

```
n1 <- c(65, 30, 29, 45, 50)
n2 <- c(67, 32, 31, 20, 52)
m1 <- c(31.1, 32.3, 31.9, 29.7, 33.0)
m2 <- c(34.1, 33.2, 30.6, 28.7, 26.5)
sd1 <- c(7.1, 8.1, 7.8, 6.8, 7.6)
sd2 <- c(7.8, 7.3, 7.5, 7.2, 6.8)
x1 <- c(4, 6, 7, 7, 8)
X <- matrix(x1, 5, 1)
meta.lm.meanratio2(.05, m1, m2, sd1, sd2, n1, n2, X)

# Should return:
#       Estimate         SE          LL          UL         z p
# b0 -0.40208954 0.09321976 -0.58479692 -0.21938216 -4.313351 0
# b1  0.06831545 0.01484125  0.03922712  0.09740377  4.603078 0
#    exp(Estimate)  exp(LL)   exp(UL)
# b0     0.6689208 0.557219 0.8030148
# b1     1.0707030 1.040007 1.1023054
```

`meta.lm.odds` *Meta-regression analysis for odds ratios*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a log odds ratio. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The exponentiated slope estimate for a predictor variable describes a multiplicative change in the odds ratio associated with a 1-unit increase in that predictor variable, controlling for all other predictor variables in the model.

Usage

```
meta.lm.odds(alpha, f1, f2, n1, n2, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	vector of group 1 frequency counts
`f2`	vector of group 2 frequency counts
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - the exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

References

Bonett DG, Price RM (2015). "Varying coefficient meta-analysis methods for odds ratios and risk ratios." *Psychological Methods*, **20**(3), 394–406. ISSN 1939-1463, doi:10.1037/met0000032.

Examples

```
n1 <- c(204, 201, 932, 130, 77)
n2 <- c(106, 103, 415, 132, 83)
f1 <- c(24, 40, 93, 14, 5)
f2 <- c(12, 9, 28, 3, 1)
x1 <- c(4, 4, 5, 3, 26)
x2 <- c(1, 1, 1, 0, 0)
X <- matrix(cbind(x1, x2), 5, 2)
meta.lm.odds(.05, f1, f2, n1, n2, X)

# Should return:
#        Estimate         SE           z     p         LL         UL
# b0  1.541895013 0.69815801  2.20851868 0.027  0.1735305 2.91025958
# b1 -0.004417932 0.04840623 -0.09126784 0.927 -0.0992924 0.09045653
# b2 -1.071122269 0.60582695 -1.76803337 0.077 -2.2585213 0.11627674
#    exp(Estimate)   exp(LL)   exp(UL)
# b0     4.6734381 1.1894969 18.361564
# b1     0.9955918 0.9054779  1.094674
# b2     0.3426238 0.1045049  1.123307
```

`meta.lm.prop.ps` *Meta-regression analysis for paired-samples proportion differences*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a paired-samples proportion difference. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity.

Usage

```
meta.lm.prop.ps(alpha, f11, f12, f21, f22, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f11`	vector of frequency counts in cell 1,1
`f12`	vector of frequency counts in cell 1,2
`f21`	vector of frequency counts in cell 2,1
`f22`	vector of frequency counts in cell 2,2
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG, Price RM (2014). "Meta-analysis methods for risk differences." *British Journal of Mathematical and Statistical Psychology*, **67**(3), 371–387. ISSN 00071102, doi:10.1111/bmsp.12024.

Examples

```
f11 <- c(40, 20, 25, 30)
f12 <- c(3, 2, 2, 1)
f21 <- c(7, 6, 8, 6)
f22 <- c(26, 25, 13, 25)
x1 <- c(1, 1, 4, 6)
x2 <- c(1, 1, 0, 0)
X <- matrix(cbind(x1, x2), 4, 2)
meta.lm.prop.ps(.05, f11, f12, f21, f22, X)

# Should return:
#       Estimate         SE          z     p          LL         UL
# b0 -0.21113402 0.21119823 -0.9996960 0.317 -0.62507494 0.20280690
# b1  0.02185567 0.03861947  0.5659236 0.571 -0.05383711 0.09754845
# b2  0.12575138 0.17655623  0.7122455 0.476 -0.22029248 0.47179524
```

`meta.lm.prop1` *Meta-regression analysis for 1-group proportions*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a proportion from one group. The estimates are OLS estimates with robust standard errors that accomodate residual heteroscedasticity.

Usage

```
meta.lm.prop1(alpha, f, n, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f`	vector of frequency counts
`n`	vector of sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
f <- c(38, 26, 24, 15, 45, 38)
n <- c(80, 60, 70, 50, 180, 200)
x1 <- c(10, 15, 18, 22, 24, 30)
X <- matrix(x1, 6, 1)
meta.lm.prop1(.05, f, n, X)

# Should return:
#       Estimate         SE         z p          LL           UL
# b0  0.63262816 0.06845707  9.241239 0  0.49845477  0.766801546
# b1 -0.01510565 0.00290210 -5.205076 0 -0.02079367 -0.009417641
```

---

meta.lm.prop2 — *Meta-regression analysis for 2-group proportion differences*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a 2-group proportion difference. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity.

Usage

```
meta.lm.prop2(alpha, f1, f2, n1, n2, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	vector of group 1 frequency counts
`f2`	vector of group 2 frequency counts
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG, Price RM (2014). "Meta-analysis methods for risk differences." *British Journal of Mathematical and Statistical Psychology*, **67**(3), 371–387. ISSN 00071102, doi:10.1111/bmsp.12024.

Examples

```
f1 <- c(24, 40, 93, 14, 5)
f2 <- c(12, 9, 28, 3, 1)
n1 <- c(204, 201, 932, 130, 77)
n2 <- c(106, 103, 415, 132, 83)
x1 <- c(4, 4, 5, 3, 26)
x2 <- c(1, 1, 1, 0, 0)
X <- matrix(cbind(x1, x2), 5, 2)
meta.lm.prop2(.05, f1, f2, n1, n2, X)

# Should return:
#        Estimate          SE          z     p          LL          UL
# b0  0.089756283 0.034538077  2.5987632 0.009  0.02206290 0.157449671
# b1 -0.001447968 0.001893097 -0.7648672 0.444 -0.00515837 0.002262434
# b2 -0.034670988 0.034125708 -1.0159786 0.310 -0.10155615 0.032214170
```

`meta.lm.propratio2` *Meta-regression analysis for proportion ratios*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a log proportion ratio. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The exponentiated slope estimate for a predictor variable describes a multiplicative change in the proportion ratio associated with a 1-unit increase in that predictor variable, controlling for all other predictor variables in the model.

Usage

```
meta.lm.propratio2(alpha, f1, f2, n1, n2, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	vector of group 1 frequency counts
`f2`	vector of group 2 frequency counts
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- exp(Estimate) - the exponentiated estimate
- exp(LL) - lower limit of the exponentiated confidence interval
- exp(UL) - upper limit of the exponentiated confidence interval

References

Price RM, Bonett DG (2008). "Confidence intervals for a ratio of two independent binomial proportions." *Statistics in Medicine*, **27**(26), 5497–5508. ISSN 02776715, doi:10.1002/sim.3376.

Examples

```
n1 <- c(204, 201, 932, 130, 77)
n2 <- c(106, 103, 415, 132, 83)
f1 <- c(24, 40, 93, 14, 5)
f2 <- c(12, 9, 28, 3, 1)
x1 <- c(4, 4, 5, 3, 26)
x2 <- c(1, 1, 1, 0, 0)
X <- matrix(cbind(x1, x2), 5, 2)
meta.lm.propratio2(.05, f1, f2, n1, n2, X)

# Should return:
#         Estimate         SE           z     p          LL         UL
# b0  1.4924887636 0.69172794  2.15762393 0.031  0.13672691 2.84825062
# b1  0.0005759509 0.04999884  0.01151928 0.991 -0.09741998 0.09857188
# b2 -1.0837844594 0.59448206 -1.82307345 0.068 -2.24894789 0.08137897
#     exp(Estimate)   exp(LL)   exp(UL)
# b0      4.4481522 1.1465150 17.257565
# b1      1.0005761 0.9071749  1.103594
# b2      0.3383128 0.1055102  1.084782
```

meta.lm.semipart *Meta-regression analysis for semipartial correlations*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a Fisher-transformed semipartial correlation. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The correlations are Fisher-transformed and hence the parameter estimates do not have a simple interpretation. However, the hypothesis test results can be used to decide if a population slope is either positive or negative.

Usage

```
meta.lm.semipart(alpha, n, cor, r2, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`cor`	vector of estimated semipartial correlations
`r2`	vector of squared multiple correlations for a model that includes the IV and all control variables
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
n <- c(128, 97, 210, 217)
cor <- c(.35, .41, .44, .39)
r2 <- c(.29, .33, .36, .39)
x1 <- c(18, 25, 23, 19)
X <- matrix(x1, 4, 1)
meta.lm.semipart(.05, n, cor, r2, X)
```

```
# Should return:
#      Estimate        SE         z     p          LL         UL
# b0 0.19695988 0.3061757 0.6432905 0.520 -0.40313339 0.79705315
# b1 0.01055584 0.0145696 0.7245114 0.469 -0.01800004 0.03911172
```

`meta.lm.spear` *Meta-regression analysis for Spearman correlations*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a Fisher-transformed Spearman correlation. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. The correlations are Fisher-transformed and hence the parameter estimates do not have a simple interpretation. However, the hypothesis test results can be used to decide if a population slope is either positive or negative.

Usage

```
meta.lm.spear(alpha, n, cor, X)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`cor`	vector of estimated Spearman correlations
`X`	matrix of predictor values

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
n <- c(150, 200, 300, 200, 350)
cor <- c(.14, .29, .16, .21, .23)
x1 <- c(18, 25, 23, 19, 24)
X <- matrix(x1, 5, 1)
meta.lm.spear(.05, n, cor, X)

# Should return:
#       Estimate         SE          z     p           LL         UL
# b0 -0.08920088 0.26686388 -0.3342561 0.738 -0.612244475 0.43384271
# b1  0.01370866 0.01190212  1.1517825 0.249 -0.009619077 0.03703639
```

---

meta.lm.stdmean.ps — *Meta-regression analysis for paired-samples standardized mean differences*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a paired-samples standardized mean difference. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity.

Usage

```
meta.lm.stdmean.ps(alpha, m1, m2, sd1, sd2, cor, n, X, stdzr)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for measurement 1
m2	vector of estimated means for measurement 2
sd1	vector of estimated SDs for measurement 1
sd2	vector of estimated SDs for measurement 2
cor	vector of estimated correlations for paired measurements
n	vector of sample sizes
X	matrix of predictor values
stdzr	• set to 0 for square root unweighted average variance standardizer • set to 1 for measurement 1 SD standardizer • set to 2 for measurement 2 SD standardizer

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- t - t-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
n <- c(65, 30, 29, 45, 50)
cor <- c(.87, .92, .85, .90, .88)
m1 <- c(20.1, 20.5, 19.3, 21.5, 19.4)
m2 <- c(10.4, 10.2, 8.5, 10.3, 7.8)
sd1 <- c(9.3, 9.9, 10.1, 10.5, 9.8)
sd2 <- c(7.8, 8.0, 8.4, 8.1, 8.7)
x1 <- c(2, 3, 3, 4, 4)
X <- matrix(x1, 5, 1)
meta.lm.stdmean.ps(.05, m1, m2, sd1, sd2, cor, n, X, 0)

# Should return:
#      Estimate         SE         z     p         LL        UL
# b0 1.01740253 0.25361725 4.0115667 0.000  0.5203218 1.5144832
# b1 0.04977943 0.07755455 0.6418635 0.521 -0.1022247 0.2017836
```

---

meta.lm.stdmean2 *Meta-regression analysis for 2-group standardized mean differences*

Description

This function estimates the intercept and slope coefficients in a meta-regression model where the dependent variable is a 2-group standardized mean difference. The estimates are OLS estimates with robust standard errors that accommodate residual heteroscedasticity. Use the unweighted variance standardizer for 2-group experimental designs, and use the weighted variance standardizer for 2-group nonexperimental designs. A single-group standardizer can be used in either experimental or nonexperimental designs.

Usage

```
meta.lm.stdmean2(alpha, m1, m2, sd1, sd2, n1, n2, X, stdzr)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	vector of estimated means for group 1
m2	vector of estimated means for group 2
sd1	vector of estimated SDs for group 1
sd2	vector of estimated SDs for group 2
n1	vector of group 1 sample sizes
n2	vector of group 2 sample sizes
X	matrix of predictor values
stdzr	• set to 0 for square root unweighted average variance standardizer • set to 1 for group 1 SD standardizer • set to 2 for group 2 SD standardizer • set to 3 for square root weighted average variance standardizer

Value

Returns a matrix. The first row is for the intercept with one additional row per predictor. The matrix has the following columns:

- Estimate - OLS estimate
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
n1 <- c(65, 30, 29, 45, 50)
n2 <- c(67, 32, 31, 20, 52)
m1 <- c(31.1, 32.3, 31.9, 29.7, 33.0)
m2 <- c(34.1, 33.2, 30.6, 28.7, 26.5)
sd1 <- c(7.1, 8.1, 7.8, 6.8, 7.6)
sd2 <- c(7.8, 7.3, 7.5, 7.2, 6.8)
x1 <- c(4, 6, 7, 7, 8)
X <- matrix(x1, 5, 1)
```

```
meta.lm.stdmean2(.05, m1, m2, sd1, sd2, n1, n2, X, 0)

# Should return:
#      Estimate        SE         z p         LL         UL
# b0 -1.6988257 0.4108035 -4.135373 0 -2.5039857 -0.8936657
# b1  0.2871641 0.0649815  4.419167 0  0.1598027  0.4145255
```

`meta.sub.cor` *Confidence interval for a subgroup difference in average Pearson or partial correlations*

Description

Computes the estimate, standard error, and confidence interval for a difference in average Pearson or partial correlations for two mutually exclusive subgroups of studies. Each subgroup can have one or more studies. All of the correlations must be either Pearson correlations or partial correlations.

Usage

```
meta.sub.cor(alpha, n, cor, s, group)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`cor`	vector of estimated correlations
`s`	number of control variables (set to 0 for Pearson)
`group`	vector of group indicators: • 1 for set A • 2 for set B • 0 to ignore

Value

Returns a matrix with three rows:

- Row 1 - estimate for Set A
- Row 2 - estimate for Set B
- Row 3 - estimate for difference, Set A - Set B

The columns are:

- Estimate - estimated average correlation or difference
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2008). "Meta-analytic interval estimation for bivariate correlations." *Psychological Methods*, **13**(3), 173–181. ISSN 1939-1463, doi:10.1037/a0012868.

Examples

```
n <- c(55, 190, 65, 35)
cor <- c(.40, .65, .60, .45)
group <- c(1, 1, 2, 0)
meta.sub.cor(.05, n, cor, 0, group)

# Should return:
#                 Estimate         SE         LL        UL
# Set A:             0.525 0.06195298  0.3932082 0.6356531
# Set B:             0.600 0.08128008  0.4171458 0.7361686
# Set A - Set B:    -0.075 0.10219894 -0.2645019 0.1387283
```

`meta.sub.cronbach` *Confidence interval for a subgroup difference in average Cronbach reliabilities*

Description

Computes the estimate, standard error, and confidence interval for a difference in average Cronbach reliability coefficients for two mutually exclusive subgroups of studies. Each set can have one or more studies. The number of measurements used to compute the sample reliablity coefficient is assumed to be the same for all studies.

Usage

```
meta.sub.cronbach(alpha, n, rel, r, group)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`rel`	vector of estimated Cronbach reliabilities
`r`	number of measurements (e.g., items)
`group`	vector of group indicators: • 1 for set A • 2 for set B • 0 to ignore

Value

Returns a matrix with three rows:

- Row 1 - estimate for Set A
- Row 2 - estimate for Set B
- Row 3 - estimate for difference, Set A - Set B

The columns are:

- Estimate - estimated average correlation or difference
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2010). "Varying coefficient meta-analytic methods for alpha reliability." *Psychological Methods*, **15**(4), 368–385. ISSN 1939-1463, doi:10.1037/a0020142.

Examples

```
n <- c(120, 170, 150, 135)
rel <- c(.89, .87, .73, .71)
group <- c(1, 1, 2, 2)
r <- 10
meta.sub.cronbach(.05, n, rel, r, group)

# Should return:
#                Estimate         SE        LL        UL
# Set A:             0.88 0.01068845 0.8581268 0.8999386
# Set B:             0.72 0.02515130 0.6684484 0.7668524
# Set A - Set B:     0.16 0.02732821 0.1082933 0.2152731
```

`meta.sub.gen` *Confidence interval for a subgroup difference in average effect size*

Description

Computes the estimate, standard error, and confidence interval for a difference in the average effect size (any type of effect size) for two mutually exclusive subgroups of studies. Each subgroup can have one or more studies. All of the effects sizes should be compatible.

Usage

```
meta.sub.gen(alpha, est, se, group)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`est`	vector of estimated effect sizes
`se`	vector of effect size standard errors
`group`	vector of group indicators: • 1 for set A • 2 for set B • 0 to ignore

Value

Returns a matrix with three rows:

- Row 1 - estimate for Set A
- Row 2 - estimate for Set B
- Row 3 - estimate for difference, Set A - Set B

The columns are:

- Estimate - estimated average effect size or difference
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
est <- c(.920, .896, .760, .745)
se <- c(.098, .075, .069, .055)
group <- c(1, 1, 2, 2)
meta.sub.gen(.05, est, se, group)

# Should return:
#                 Estimate         SE          LL        UL
# Set A:            0.9080 0.06170292 0.787064504 1.0289355
# Set B:            0.7525 0.04411916 0.666028042 0.8389720
# Set A - Set B:    0.1555 0.07585348 0.006829917 0.3041701
```

`meta.sub.pbcor` *Confidence interval for a subgroup difference in average point-biserial correlations*

Description

Computes the estimate, standard error, and confidence interval for a difference in average point-biserial correlations for two mutually exclusive subgroups of studies. Each subgroup can have one or more studies. Two types of point-biserial correlations can be analyzed. One type uses an unweighted variance and is recommended for 2-group experimental designs. The other type uses a weighted variance and is recommended for 2-group nonexperimental designs with simple random sampling (but not stratified random sampling) within each study. Equality of variances within or across studies is not assumed.

Usage

```
meta.sub.pbcor(alpha, m1, m2, sd1, sd2, n1, n2, type, group)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m1`	vector of estimated means for group 1
`m2`	vector of estimated means for group 2
`sd1`	vector of estimated SDs for group 1
`sd2`	vector of estimated SDs for group 2
`n1`	vector of group 1 sample sizes
`n2`	vector of group 2 sample sizes
`type`	• set to 1 for weighted variance • set to 2 for unweighted variance
`group`	vector of group indicators: • 1 for set A • 2 for set B • 0 to ignore

Value

Returns a matrix with three rows:

- Row 1 - estimate for Set A
- Row 2 - estimate for Set B
- Row 3 - estimate for difference, Set A - Set B

The columns are:

- Estimate - estimated average correlation or difference

- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2020). "Point-biserial correlation: Interval estimation, hypothesis testing, meta-analysis, and sample size determination." *British Journal of Mathematical and Statistical Psychology*, **73**(S1), 113–144. ISSN 0007-1102, doi:10.1111/bmsp.12189.

Examples

```
m1 <- c(45.1, 39.2, 36.3, 34.5)
m2 <- c(30.0, 35.1, 35.3, 36.2)
sd1 <- c(10.7, 10.5, 9.4, 11.5)
sd2 <- c(12.3, 12.0, 10.4, 9.6)
n1 <- c(40, 20, 50, 25)
n2 <- c(40, 20, 48, 26)
group <- c(1, 1, 2, 2)
meta.sub.pbcor(.05,  m1, m2, sd1, sd2, n1, n2, 2, group)

# Should return:
#                    Estimate         SE         LL        UL
# Set A:           0.36338772 0.08552728  0.1854777 0.5182304
# Set B:          -0.01480511 0.08741322 -0.1840491 0.1552914
# Set A - Set B:   0.37819284 0.12229467  0.1320530 0.6075828
```

`meta.sub.semipart` *Confidence interval for a subgroup difference in average semipartial correlations*

Description

Computes the estimate, standard error, and confidence interval for a difference in average semipartial correlations for two subgroups of mutually exclusive studies. Each subgroup can have one or more studies.

Usage

```
meta.sub.semipart(alpha, n, cor, r2, group)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`cor`	vector of estimated semi-partial correlations

r2 vector of squared multiple correlations for a model that includes the IV and all control variables

group vector of group indicators:
- 1 for set A
- 2 for set B
- 0 to ignore

Value

Returns a matrix with three rows:

- Row 1 - estimate for Set A
- Row 2 - estimate for Set B
- Row 3 - estimate for difference, Set A - Set B

The columns are:

- Estimate - estimated average correlation or difference
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

Examples

```
n <- c(55, 190, 65, 35)
cor <- c(.40, .65, .60, .45)
r2 <- c(.25, .41, .43, .39)
group <- c(1, 1, 2, 0)
meta.sub.semipart(.05, n, cor, r2, group)

# Should return:
#                Estimate         SE         LL        UL
# Set A:            0.525 0.05955276  0.3986844 0.6317669
# Set B:            0.600 0.07931155  0.4221127 0.7333949
# Set A - Set B:   -0.075 0.09918091 -0.2587113 0.1324682
```

---

meta.sub.spear *Confidence interval for a subgroup difference in average Spearman correlations*

Description

Computes the estimate, standard error, and confidence interval for a difference in average Spearman correlations for two mutually exclusive subgroups of studies. Each subgroup can have one or more studies.

Usage

```
meta.sub.spear(alpha, n, cor, group)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`n`	vector of sample sizes
`cor`	vector of estimated Spearman correlations
`group`	vector of group indicators: • 1 for set A • 2 for set B • 0 to ignore

Value

Returns a matrix with three rows:

- Row 1 - estimate for Set A
- Row 2 - estimate for Set B
- Row 3 - estimate for difference, Set A - Set B

The columns are:

- Estimate - estimated average correlation or difference
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2008). "Meta-analytic interval estimation for bivariate correlations." *Psychological Methods*, **13**(3), 173–181. ISSN 1939-1463, doi:10.1037/a0012868.

Examples

```
n <- c(55, 190, 65, 35)
cor <- c(.40, .65, .60, .45)
group <- c(1, 1, 2, 0)
meta.sub.spear(.05, n, cor, group)

# Should return:
#                Estimate         SE         LL        UL
# Set A:            0.525 0.06483629  0.3865928 0.6402793
# Set B:            0.600 0.08829277  0.3992493 0.7458512
# Set A - Set B:   -0.075 0.10954158 -0.2760700 0.1564955
```

`replicate.cor` *Compares and combines Pearson or partial correlations in original and follow-up studies*

Description

This function can be used to compare and combine Pearson or partial correlations from an original study and a follow-up study. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.cor(alpha, cor1, n1, cor2, n2, s)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`cor1`	estimated correlation in original study
`n1`	sample size in original study
`cor2`	estimated correlation in follow-up study
`n2`	sample size in follow-up study
`s`	number of control variables in each study (0 for Pearson)

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in correlations
- Row 4 estimates the average correlation

The columns are:

- Estimate -correlation estimate (single study, difference, average)
- SE - standard error
- z - t-value for rows 1 and 2; z-value for rows 3 and 4
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). “Design and analysis of replication studies.” *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.cor(.05, .598, 80, .324, 200, 0)

# Should return:
#                          Estimate         SE        z            p        LL        UL
# Original:                   0.598 0.07320782 6.589418 4.708045e-09 0.4355043 0.7227538
# Follow-up:                  0.324 0.06376782 4.819037 2.865955e-06 0.1939787 0.4428347
# Original - Follow-up:       0.274 0.09708614 2.633335 8.455096e-03 0.1065496 0.4265016
# Average:                    0.461 0.04854307 7.634998 2.264855e-14 0.3725367 0.5411607
```

`replicate.cor.gen` *Compares and combines any type of correlation in original and follow-up studies*

Description

This function can be used to compare and combine any type of correlation from an original study and a follow-up study. The confidence level for the difference is $1 - 2$*alpha, which is recommended for equivalence testing.

Usage

```
replicate.cor.gen(alpha, cor1, se1, cor2, se2)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`cor1`	estimated correlation in original study
`se1`	standard error of correlation in original study
`cor2`	estimated correlation in follow-up study
`se2`	standard error of correlation in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in correlations
- Row 4 estimates the average correlation

The columns are:

- Estimate - correlation estimate (single study, difference, average)

- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.cor.gen(.05, .454, .170, .318, .098)

# Should return:
#                       Estimate         SE         z            p          LL        UL
# Original:                0.454 0.17000000 2.2869806 0.0221969560  0.06991214 0.7208577
# Follow-up:               0.318 0.09800000 3.0215123 0.0025151541  0.11522137 0.4953353
# Original - Follow-up:    0.136 0.19622436 0.6671281 0.5046902807 -0.21543667 0.4237240
# Average:                 0.386 0.09811218 3.4089419 0.0006521538  0.19606750 0.5480170
```

`replicate.gen` *Compares and combines effect sizes in original and follow-up studies*

Description

This function can be used to compare and combine any effect size using the effect size estimate and its standard error from the original study and the follow-up study. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.gen(alpha, est1, se1, est2, se2)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`est1`	estimated effect size in original study
`se1`	effect size standard error in original study
`est2`	estimated effect size in follow-up study
`se2`	effect size standard error in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in effect sizes
- Row 4 estimates the average effect size

Columns are:

- Estimate - effect size estimate (single study, difference, average)
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.gen(.05, .782, .210, .650, .154)

# Should return:
#                       Estimate        SE         z            p         LL        UL
#  Original:               0.782 0.2100000 3.7238095 1.962390e-04  0.3704076 1.1935924
#  Follow-up:              0.650 0.1540000 4.2207792 2.434593e-05  0.3481655 0.9518345
#  Original - Follow-up:   0.132 0.2604151 0.5068831 6.122368e-01 -0.2963446 0.5603446
#  Average:                0.716 0.1302075 5.4989141 3.821373e-08  0.4607979 0.9712021
```

`replicate.mean.ps` *Compares and combines paired-samples mean differences in original and follow-up studies*

Description

This function computes confidence intervals from an original study and a follow-up study where the effect size is a paired-samples mean difference. Confidence intervals for the difference and average effect size are also computed. Equality of variances within or across studies is not assumed. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence intervals for the difference and average. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.mean.ps(
  alpha,
  m11,
  m12,
  sd11,
  sd12,
  cor1,
  n1,
  m21,
  m22,
  sd21,
  sd22,
  cor2,
  n2
)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m11`	estimated mean for measurement 1 in original study
`m12`	estimated mean for measurement 2 in original study
`sd11`	estimated SD for measurement 1 in original study
`sd12`	estimated SD for measurement 2 in original study
`cor1`	estimated correlation of paired measurements in orginal study
`n1`	sample size in original study
`m21`	estimated mean for measurement 1 in follow-up study
`m22`	estimated mean for measurement 2 in follow-up study
`sd21`	estimated SD for measurement 1 in follow-up study
`sd22`	estimated SD for measurement 2 in follow-up study
`cor2`	estimated correlation of paired measurements in follow-up study
`n2`	sample size in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in mean differences
- Row 4 estimates the average mean difference

The columns are:

- Estimate - mean difference estimate (single study, difference, average)

- SE - standard error
- df - degrees of freedom
- t - t-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.mean.ps(.05, 86.22, 70.93, 14.89, 12.32, .765, 20,
                       84.81, 77.24, 15.68, 16.95, .702, 75)

#  Should return:
#                      Estimate       SE        t            p
# Original:               15.29 2.154344 7.097288 9.457592e-07
# Follow-up:               7.57 1.460664 5.182575 1.831197e-06
# Original - Follow-up:    7.72 2.602832 2.966000 5.166213e-03
# Average:                11.43 1.301416 8.782740 1.010232e-10
#                             LL       UL       df
# Original:              10.780906 19.79909 19.00000
# Follow-up:              4.659564 10.48044 74.00000
# Original - Follow-up:   3.332885 12.10712 38.40002
# Average:                8.796322 14.06368 38.40002
```

`replicate.mean1` *Compares and combines single mean in original and follow-up studies*

Description

This function computes confidence intervals for a single mean from an original study and a follow-up study. Confidence intervals for the difference between the two means and average of the two means are also computed. Equality of variances across studies is not assumed. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence intervals for the difference and average. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.mean1(alpha, m1, sd1, n1, m2, sd2, n2)
```

Arguments

alpha	alpha level for 1-alpha confidence
m1	estimated mean in original study
sd1	estimated SD in original study
n1	sample size in original study
m2	estimated mean in follow-up study
sd2	estimated SD in follow-up study
n2	sample size for in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in means
- Row 4 estimates the average mean

The columns are:

- Estimate - mean estimate (single study, difference, average)
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.mean1(.05, 21.9, 3.82, 40, 25.2, 3.98, 75)

# Should return:
#                        Estimate        SE        LL        UL       df
# Original:                 21.90 0.6039950 20.678305 23.121695 39.00000
# Follow-up:                25.20 0.4595708 24.284285 26.115715 74.00000
# Original - Follow-up:     -3.30 0.7589567 -4.562527 -2.037473 82.63282
# Average:                  23.55 0.3794784 22.795183 24.304817 82.63282
```

`replicate.mean2` *Compares and combines 2-group mean differences in original and follow-up studies*

Description

This function computes confidence intervals from an original study and a follow-up study where the effect size is a 2-group mean difference. Confidence intervals for the difference and average effect size are also computed. Equality of variances within or across studies is not assumed. A Satterthwaite adjustment to the degrees of freedom is used to improve the accuracy of the confidence intervals. The same results can be obtained using the meta.lc.mean2 function with appropriate contrast coefficients. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.mean2(
  alpha,
  m11,
  m12,
  sd11,
  sd12,
  n11,
  n12,
  m21,
  m22,
  sd21,
  sd22,
  n21,
  n22
)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m11`	estimated mean for group 1 in original study
`m12`	estimated mean for group 2 in original study
`sd11`	estimated SD for group 1 in original study
`sd12`	estimated SD for group 2 in original study
`n11`	sample size for group 1 in original study
`n12`	sample size for group 2 in original study
`m21`	estimated mean for group 1 in follow-up study
`m22`	estimated mean for group 2 in follow-up study
`sd21`	estimated SD for group 1 in follow-up study

sd22	estimated SD for group 2 in follow-up study
n21	sample size for group 1 in follow-up study
n22	sample size for group 2 in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in mean differences
- Row 4 estimates the average mean difference

The columns are:

- Estimate - mean difference estimate (single study, difference, average)
- SE - standard error
- t - t-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.mean2(.05, 21.9, 16.1, 3.82, 3.21, 40, 40,
                     25.2, 19.1, 3.98, 3.79, 75, 75)

# Should return:
#                      Estimate        SE          t            p
# Original:                5.80 0.7889312  7.3517180 1.927969e-10
# Follow-up:               6.10 0.6346075  9.6122408 0.000000e+00
# Original - Follow-up:   -0.30 1.0124916 -0.2962988 7.673654e-01
# Average:                 5.95 0.5062458 11.7531843 0.000000e+00
#                             LL       UL        df
# Original:                4.228624 7.371376  75.75255
# Follow-up:               4.845913 7.354087 147.64728
# Original - Follow-up:   -1.974571 1.374571 169.16137
# Average:                 4.950627 6.949373 169.16137
```

`replicate.oddsratio` *Compares and combines odds ratios in original and follow-up studies*

Description

This function computes confidence intervals for an odds ratio from an original study and a follow-up study. Confidence intervals for the ratio of odds ratios and geometric average odds ratio are also computed. The confidence level for the ratio of ratios is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.oddsratio(alpha, est1, se1, est2, se2)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`est1`	estimate of log odds ratio in original study
`se1`	standard error of log odds ratio in original study
`est2`	estimate of log odds ratio in follow-up study
`se2`	standard error of log odds ratio in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the ratio of odds ratios
- Row 4 estimates the geometric average odds ratio

The columns are:

- Estimate - odds ratio estimate (single study, ratio, average)
- SE - standard error
- z - z-value
- p - p-value
- LL - exponentiated lower limit of the confidence interval
- UL - exponentiated upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.oddsratio(.05, 1.39, .302, 1.48, .206)

# Should return:
#                          Estimate        SE          z            p
# Original:              1.39000000 0.3020000  4.6026490 4.171509e-06
# Follow-up:             1.48000000 0.2060000  7.1844660 6.747936e-13
# Original/Follow-up:   -0.06273834 0.3655681 -0.1716188 8.637372e-01
# Average:               0.36067292 0.1827840  1.9732190 4.847061e-02
#                         exp(LL)  exp(UL)
# Original:             2.2212961 7.256583
# Follow-up:            2.9336501 6.578144
# Original/Fllow-up:    0.5147653 1.713551
# Average:              1.0024257 2.052222
```

`replicate.plot` *Plot to compare estimates from original and follow-up studies*

Description

Generates a basic plot using ggplot2 to visualize the estimates from and original and follow-up studies.

Usage

```
replicate.plot(
  result,
  focus = c("Both", "Difference", "Average"),
  reference_line = NULL,
  diamond_height = 0.2,
  difference_axis_ticks = 5,
  ggtheme = ggplot2::theme_classic()
)
```

Arguments

`result`	• a result matrix from any of the replicate functions in vcmeta
`focus`	• Optional specification of the focus of the plot; defaults to 'Both' • Both - plots each estimate, differencence, and average • Difference - plot each estimate and difference between them • Average - plot each estimate and the average effect size
`reference_line`	• Optional x-value for a reference line. Only applies if focus is 'Difference' or 'Both'. Defaults to NULL, in which case a reference line is not drawn.
`diamond_height`	• Optional height of the diamond representing average effect size. Only applies if focus is 'Average' or 'Both'. Defaults to 0.2

difference_axis_ticks
- Optional requested number of ticks on the difference axis. Only applies if focus is 'Difference' or 'Both'. Defaults to 5.

ggtheme
- optional ggplot2 theme object; defaults to theme_classic()

Value

Returns a ggplot object. If stored, can be further customized via the ggplot API

Examples

```
# Compare Damisch et al., 2010 to Calin-Jageman & Caldwell 2014
# Damisch et al., 2010, Exp 1, German participants made 10 mini-golf putts.
# Half were told they had a 'lucky' golf ball; half were not.
# Found a large but uncertain improvement in shots made in the luck condition
# Calin-Jageman & Caldwell, 2014, Exp 1, was a pre-registered replication with
# input from Damisch, though with English-speaking participants.
#
# Here we compare the effect sizes, in original units, for the two studies.
# Use the replicate.mean2 function because the design is a 2-group design.

library(ggplot2)
damisch_v_calinjageman_raw <- replicate.mean2(
  alpha = 0.05,
  m11 = 6.42,
  m12 = 4.75,
  sd11 = 1.88,
  sd12 = 2.15,
  n11 = 14,
  n12 = 14,
  m21 = 4.73,
  m22 = 4.62,
  sd21 = 1.958,
  sd22 = 2.12,
  n21 = 66,
  n22 = 58
)

# View the comparison:
damisch_v_calinjageman_raw


# Now plot the comparison, focusing on the difference
replicate.plot(damisch_v_calinjageman_raw, focus = "Difference")

# Plot the comparison, focusing on the average
replicate.plot(damisch_v_calinjageman_raw,
  focus = "Average",
  reference_line = 0,
  diamond_height = 0.1
)
```

```
# Plot the comparison with both difference and average.
# In this case, store the plot for manipulation
myplot <- replicate.plot(
  damisch_v_calinjageman_raw,
  focus = "Both",
  reference_line = 0
)

# View the stored plot
myplot

# Change x-labels and study labels
myplot <- myplot + xlab("Difference in Putts Made, Lucky - Control")
myplot <- myplot + scale_y_discrete(
    labels = c(
      "Average",
      "Difference",
      "Calin-Jageman & Caldwell, 2014",
      "Damisch et al., 2010"
      )
  )

# View the updated plot
myplot
```

`replicate.prop.ps` *Compares and combines paired-samples proportion differences in original and follow-up studies*

Description

This function computes confidence intervals from an original study and a follow-up study where the effect size is a paired-samples proportion difference. Confidence intervals for the difference and average of effect sizes are also computed. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.prop.ps(alpha, f1, f2)
```

Arguments

alpha	alpha level for 1-alpha confidence
f1	vector of frequency counts for 2x2 table in original study
f2	vector of frequency counts for 2x2 table in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in proportion differences
- Row 4 estimates the average proportion difference

The columns are:

- Estimate - proportion difference estimate (single study, difference, average)
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
f1 <- c(42, 2, 15, 61)
f2 <- c(69, 5, 31, 145)
replicate.prop.ps(.05, f1, f2)

# Should return:
#                           Estimate         SE           z            p
# Original:              0.106557377 0.03440159  3.09745539 1.951898e-03
# Follow-up:             0.103174603 0.02358274  4.37500562 1.214294e-05
# Original - Follow-up:  0.003852359 0.04097037  0.09402793 9.250870e-01
# Average:               0.105511837 0.02048519  5.15064083 2.595979e-07
#                                LL         UL
# Original:              0.03913151 0.17398325
# Follow-up:             0.05695329 0.14939592
# Original - Follow-up: -0.06353791 0.07124263
# Average:               0.06536161 0.14566206
```

`replicate.prop1` *Compares and combines single proportion in original and follow-up studies*

Description

This function computes confidence intervals for a single proportion from an original study and a follow-up study. Confidence intervals for the difference between the two proportions and average of the two proportions are also computed. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.prop1(alpha, f1, n1, f2, n2)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f1`	frequency count in original study
`n1`	sample size in original study
`f2`	frequency count in follow-up study
`n2`	sample size for in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in proportions
- Row 4 estimates the average proportion

The columns are:

- Estimate - proportion estimate (single study, difference, average)
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). “Design and analysis of replication studies.” *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.prop1(.05, 21, 300, 35, 400)

# Should return:
#                          Estimate         SE          LL         UL
# Original:              0.07565789 0.01516725  0.04593064 0.10538515
# Follow-up:             0.09158416 0.01435033  0.06345803 0.11971029
# Original - Follow-up: -0.01670456 0.02065098 -0.05067239 0.01726328
# Average:               0.08119996 0.01032549  0.06096237 0.10143755
```

`replicate.prop2` *Compares and combines 2-group proportion differences in original and follow-up studies*

Description

This function computes confidence intervals from an original study and a follow-up study where the effect size is a 2-group proportion difference. Confidence intervals for the difference and average effect size are also computed. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.prop2(alpha, f11, f12, n11, n12, f21, f22, n21, n22)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f11`	frequency count for group 1 in original study
`f12`	frequency count for group 2 in original study
`n11`	sample size for group 1 in original study
`n12`	sample size for group 2 in original study
`f21`	frequency count for group 1 in follow-up study
`f22`	frequency count for group 2 in follow-up study
`n21`	sample size for group 1 in follow-up study
`n22`	sample size for group 2 in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study

- Row 3 estimates the difference in proportion differences
- Row 4 estimates the average proportion difference

The columns are:

- Estimate - proportion difference estimate (single study, difference, average)
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.prop2(.05, 21, 16, 40, 40, 19, 13, 60, 60)

# Should return:
#                          Estimate         SE         z         p
# Original:              0.11904762 0.10805233 1.1017590 0.2705665
# Follow-up:             0.09677419 0.07965047 1.2149858 0.2243715
# Original - Follow-up:  0.02359056 0.13542107 0.1742016 0.8617070
# Average:               0.11015594 0.06771053 1.6268656 0.1037656
#                                LL        UL
# Original:              -0.09273105 0.3308263
# Follow-up:             -0.05933787 0.2528863
# Original - Follow-up:  -0.19915727 0.2463384
# Average:               -0.02255427 0.2428661
```

`replicate.ratio.prop2` *Compares and combines 2-group proportion ratios in original and follow-up studies*

Description

This function computes confidence intervals from an original study and a follow-up study where the effect size is a 2-group proportion ratio. Confidence intervals for the ratio and geometric average of effect sizes are also computed. The confidence level for the ratio of ratios is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.ratio.prop2(alpha, f11, f12, n11, n12, f21, f22, n21, n22)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`f11`	frequency count for group 1 in original study
`f12`	frequency count for group 2 in original study
`n11`	sample size for group 1 in original study
`n12`	sample size for group 2 in original study
`f21`	frequency count for group 1 in follow-up study
`f22`	frequency count for group 2 in follow-up study
`n21`	sample size for group 1 in follow-up study
`n22`	sample size for group 2 in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the ratio of proportion ratios
- Row 4 estimates the geometric average proportion ratio

The columns are:

- Estimate - proportion difference estimate (single study, ratio, average)
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). “Design and analysis of replication studies.” *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.ratio.prop2(.05, 21, 16, 40, 40, 19, 13, 60, 60)

# Should return:
#                      Estimate        LL       UL
# Original:           1.3076923 0.8068705 2.119373
# Follow-up:          1.4528302 0.7939881 2.658372
# Original/Follow-up: 0.9000999 0.4703209 1.722611
# Average:            1.3783522 0.9362893 2.029132
```

`replicate.slope` *Compares and combines slope coefficients in original and follow-up studies*

Description

This function computes confidence intervals for a slope from the original and follow-up studies, the difference in slopes, and the average of the slopes. Equality of error variances across studies is not assumed. The confidence interval for the difference uses a 1 - 2*alpha confidence level, which is recommended for equivalence testing. Use the replicate.gen function for slopes in other types of models (e.g., binary logistic, ordinal logistic, SEM).

Usage

```
replicate.slope(alpha, b1, se1, n1, b2, se2, n2, s)
```

Arguments

`alpha`	alpha level for 1-alpha or 1 - 2alpha confidence
`b1`	sample slope in original study
`se1`	standard error of slope in original study
`n1`	sample size in original study
`b2`	sample slope in follow-up study
`se2`	standard error of slope in follow-up study
`n2`	sample size in follow-up study
`s`	number of predictor variables in model

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in slopes
- Row 4 estimates the average slope

The columns are:

- Estimate - slope estimate (single study, difference, average)
- SE - standard error
- t - t-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval
- df - degrees of freedom

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.slope(.05, 23.4, 5.16, 50, 18.5, 4.48, 90, 4)

# Should return:
#                        Estimate       SE         t            p
# Original:                 23.40 5.160000 4.5348837 4.250869e-05
# Follow-up:                18.50 4.480000 4.1294643 8.465891e-05
# Original - Follow-up:      4.90 6.833447 0.7170612 4.749075e-01
# Average:                  20.95 3.416724 6.1316052 1.504129e-08
#                               LL       UL       df
# Original:              13.007227 33.79277  45.0000
# Follow-up:              9.592560 27.40744  85.0000
# Original - Follow-up: -6.438743 16.23874 106.4035
# Average:               14.176310 27.72369 106.4035
```

---

replicate.spear — *Compares and combines Spearman correlations in original and follow-up studies*

Description

This function can be used to compare and combine Spearman correlations from an original study and a follow-up study. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing.

Usage

```
replicate.spear(alpha, cor1, n1, cor2, n2)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`cor1`	estimated Spearman correlation in original study
`n1`	sample size in original study
`cor2`	estimated Spearman correlation in follow-up study
`n2`	sample size in follow-up study

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in correlations
- Row 4 estimates the average correlation

The columns are:

- Estimate - Spearman correlation estimate (single study, difference, average)
- SE - standard error
- z - z-value
- p - p-value
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.spear(.05, .598, 80, .324, 200)

# Should return:
#                        Estimate         SE        z            p         LL        UL
# Original:                 0.598 0.07948367 5.315140 1.065752e-07 0.41985966 0.7317733
# Follow-up:                0.324 0.06541994 4.570582 4.863705e-06 0.19049455 0.4457384
# Original - Follow-up:     0.274 0.10294378 3.437975 5.860809e-04 0.09481418 0.4342171
# Average:                  0.461 0.05147189 9.967944 0.000000e+00 0.36695230 0.5457190
```

`replicate.stdmean.ps` *Compares and combines paired-samples standardized mean differences in original and follow-up studies*

Description

This function computes confidence intervals from an original study and a follow-up study where the effect size is a paired-samples standardized mean difference. Confidence intervals for the difference and average effect size are also computed. Equality of variances within or across studies is not assumed. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing. Square root unweighted variances and single-condition standard deviation are options for the standardizer.

Usage

```
replicate.stdmean.ps(
  alpha,
  m11,
  m12,
  sd11,
  sd12,
  cor1,
  n1,
  m21,
  m22,
  sd21,
  sd22,
  cor2,
  n2,
  stdzr
)
```

Arguments

`alpha`	alpha level for 1-alpha confidence
`m11`	estimated mean for group 1 in original study
`m12`	estimated mean for group 2 in original study
`sd11`	estimated SD for group 1 in original study
`sd12`	estimated SD for group 2 in original study
`cor1`	estimated correlation of paired observations in orginal study
`n1`	sample size in original study
`m21`	estimated mean for group 1 in follow-up study
`m22`	estimated mean for group 2 in follow-up study
`sd21`	estimated SD for group 1 in follow-up study
`sd22`	estimated SD for group 2 in follow-up study
`cor2`	estimated correlation of paired observations in follow-up study
`n2`	sample size in follow-up study
`stdzr`	• set to 0 for square root unweighted average variance standardizer • set to 1 for measurement 1 SD standardizer • set to 2 for measurement 2 SD standardizer

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in standardized mean differences

- Row 4 estimates the average standardized mean difference

The columns are:

- Estimate - standardized mean difference estimate (single study, difference, average)
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.stdmean.ps(alpha = .05, 86.22, 70.93, 14.89, 12.32, .765, 20,
                                  84.81, 77.24, 15.68, 16.95, .702, 75, 0)

# Should return:
#                          Estimate         SE        LL        UL
#  Orginal:              1.0890300 0.22915553 0.6697353 1.5680085
#  Follow-up:            0.4604958 0.09590506 0.2756687 0.6516096
#  Original - Follow-up: 0.6552328 0.24841505 0.2466264 1.0638392
#  Average:              0.7747629 0.12420752 0.5313206 1.0182052
```

`replicate.stdmean2` *Compares and combines 2-group standardized mean differences in original and follow-up studies*

Description

This function computes confidence intervals from an original study and a follow-up study where the effect size is a 2-group standardized mean difference. Confidence intervals for the difference and average effect size are also computed. Equality of variances within or across studies is not assumed. The confidence level for the difference is 1 – 2*alpha, which is recommended for equivalence testing. Square root unweighted variances, square root weighted variances, and single-group standard deviation are options for the standardizer.

Usage

```
replicate.stdmean2(
  alpha,
  m11,
  m12,
  sd11,
```

```
  sd12,
  n11,
  n12,
  m21,
  m22,
  sd21,
  sd22,
  n21,
  n22,
  stdzr
)
```

Arguments

alpha	alpha level for 1-alpha confidence
m11	estimated mean for group 1 in original study
m12	estimated mean for group 2 in original study
sd11	estimated SD for group 1 in original study
sd12	estimated SD for group 2 in original study
n11	sample size for group 1 in original study
n12	sample size for group 2 in original study
m21	estimated mean for group 1 in follow-up study
m22	estimated mean for group 2 in follow-up study
sd21	estimated SD for group 1 in follow-up study
sd22	estimated SD for group 2 in follow-up study
n21	sample size for group 1 in follow-up study
n22	sample size for group 2 in follow-up study
stdzr	• set to 0 for square root unweighted average variance standardizer • set to 1 for group 1 SD standardizer • set to 2 for group 2 SD standardizer • set to 3 for square root weighted average variance standardizer

Value

A 4-row matrix. The rows are:

- Row 1 summarizes the original study
- Row 2 summarizes the follow-up study
- Row 3 estimates the difference in standardized mean differences
- Row 4 estimates the average standardized mean difference

The columns are:

- Estimate - standardized mean difference estimate (single study, difference, average)
- SE - standard error
- LL - lower limit of the confidence interval
- UL - upper limit of the confidence interval

References

Bonett DG (2021). "Design and analysis of replication studies." *Organizational Research Methods*, **24**(3), 513–529. ISSN 1094-4281, doi:10.1177/1094428120911088.

Examples

```
replicate.stdmean2(.05, 21.9, 16.1, 3.82, 3.21, 40, 40,
                        25.2, 19.1, 3.98, 3.79, 75, 75, 0)

# Should return:
#                           Estimate        SE         LL        UL
#  Original:              1.62803662 0.2594668  1.1353486 2.1524396
#  Follow-up:             1.56170447 0.1870576  1.2030461 1.9362986
#  Original - Follow-up:  0.07422178 0.3198649 -0.4519092 0.6003527
#  Average:               1.59487055 0.1599325  1.2814087 1.9083324
```

`se.ave.cor.nonover` *Computes the standard error for the average of two Pearson correlations with no variables in common that have been estimated from the same sample*

Description

In a study that reports the sample size and six correlations (cor12, cor34, cor13, cor14, cor23, and cor24) where variables 1 and 3 are different measurements of one attribute and variables 2 and 4 are different measurements of a second attribute, this function can be used to compute the average of cor12 and cor34 and its standard error. Note that cor12 and cor34 have no variable in common (i.e., no "overlapping" variable). The average correlation and the standard error from this function can be used as input in the meta.ave.cor.gen function in a meta-analysis where some studies have reported cor12 and other studies have reported cor34.

Usage

```
se.ave.cor.nonover(cor12, cor34, cor13, cor14, cor23, cor24, n)
```

Arguments

`cor12`	estimated correlation between variables 1 and 2
`cor34`	estimated correlation between variables 3 and 4
`cor13`	estimated correlation between variables 1 and 3
`cor14`	estimated correlation between variables 1 and 4
`cor23`	estimated correlation between variables 2 and 3
`cor24`	estimated correlation between variables 2 and 4
`n`	sample size

Value

Returns a two-row matrix. The first row gives results for the average correlation and the second row gives the results with a Fisher transformation. The columns are:

- Estimate - estimated average of cor12 and cor34
- SE - standard error
- VAR(cor12) - variance of cor12
- VAR(cor34) - variance of cor34
- COV(cor12,cor34) - covariance of cor12 and cor34

Examples

```
se.ave.cor.nonover(.357, .398, .755, .331, .347, .821, 100)

# Should return:
#               Estimate         SE VAR(cor12)  VAR(cor34) COV(cor12,cor34)
# Correlation:  0.377500 0.07768887 0.00784892 0.007301895      0.004495714
# Fisher:       0.397141 0.09059993 0.01030928 0.010309278      0.006122153
```

`se.ave.cor.over` *Computes the standard error for the average of two Pearson correlations with one variable in common that have been estimated from the same sample*

Description

In a study that reports the sample size and three correlations (cor12, cor13, and cor23 where variable 1 is called the "overlapping" variable), and variables 2 and 3 are different measurements of the same attribute, this function can be used to compute the average of cor12 and cor13 and its standard error. The average correlation and the standard error from this function can be used as input in the meta.ave.cor.gen function in a meta-analysis where some studies have reported cor12 and other studies have reported cor13.

Usage

```
se.ave.cor.over(cor12, cor13, cor23, n)
```

Arguments

`cor12`	estimated correlation between variables 1 and 2
`cor13`	estimated correlation between variables 1 and 3
`cor23`	estimated correlation between variables 2 and 3
`n`	sample size

Value

Returns a two-row matrix. The first row gives results for the average correlation and the second row gives the results with a Fisher transformation. The columns are:

- Estimate - estimated average of cor12 and cor13
- SE - standard error
- VAR(cor12) - variance of cor12
- VAR(cor13) - variance of cor13
- COV(cor12,cor13) - covariance of cor12 and cor13

Examples

```
se.ave.cor.over(.462, .518, .755, 100)

# Should return:
#                Estimate         SE  VAR(cor12) VAR(cor13) COV(cor12,cor13)
# Correlation:  0.4900000 0.07087351 0.006378045 0.00551907      0.004097553
# Fisher:       0.5360603 0.09326690 0.010309278 0.01030928      0.007119936
```

`se.ave.mean2.dep` *Computes the standard error for the average of 2-group mean differences from two parallel measurement response variables in the same sample*

Description

In a study that reports a 2-group mean difference for two response variables that satisfy the conditions of parallel measurments, this function can be used to compute the standard error of the average of the two mean differences using the two estimated means, estimated standard deviations, estimated within-group correlation between the two response variables, and the two sample sizes. The average mean difference and standard error output from this function can then be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in a meta-analysis where some studies have used one of the two parallel response variables and other studies have used the other parallel response variable. Equality of variances is not assumed.

Usage

```
se.ave.mean2.dep(m1A, m2A, sd1A, sd2A, m1B, m2B, sd1B, sd2B, rAB, n1, n2)
```

Arguments

m1A	estimated mean for variable A in group 1
m2A	estimated mean for variable A in group 2
sd1A	estimated standard deviation for variable A in group 1

sd2A	estimated standard deviation for variable A in group 2
m1B	estimated mean for variable B in group 1
m2B	estimated mean for variable B in group 2
sd1B	estimated standard deviation for variable B in group 1
sd2B	estimated standard deviation for variable B in group 2
rAB	estimated within-group correlation between variables A and B
n1	sample size for group 1
n2	sample size for group 2

Value

Returns a one-row matrix:

- Estimate - estimated average mean difference
- SE - standard error
- VAR(A) - variance of mean difference for variable A
- VAR(B) - variance of mean difference for variable B
- COV(A,B) - covariance of mean differences for variables A and B

Examples

```
se.ave.mean2.dep(21.9, 16.1, 3.82, 3.21, 24.8, 17.1, 3.57, 3.64, .785, 40, 40)

# Should return:
#                           Estimate        SE    VAR(A)    VAR(B)  COV(A,B)
# Average mean difference:     6.75 0.7526878 0.6224125 0.6498625 0.4969403
```

---

se.biphi — *Computes the standard error for a biserial-phi correlation*

Description

This function computes an estimate of a biserial-phi correlation and its standard error using the frequency counts from a 2 x 2 contingency table where one variable is naturally dichotomous and the other variable is artifically dichotomous. A biserial-phi correlation could be compatible with a point-biserial correlation in a meta-analysis. The biserial-phi estimate and the standard error from this function can be used as input in the meta.ave.cor.gen function in a meta-analysis where a point-biserial correlation has been obtained in some studies and a biserial-phi correlation has been obtained in other studies.

Usage

```
se.biphi(f1, f2, n1, n2)
```

Arguments

`f1`	number of participants in group 1 who have the attribute
`f2`	number of participants in group 2 who have the attribute
`n1`	sample size for group 1
`n2`	sample size for group 2

Value

Returns a 1-row matrix. The columns are:

- Estimate - estimated biserial-phi correlation
- SE - standard error

Examples

```
se.biphi(34, 22, 50, 50)

# Should return:
#                Estimate        SE
# Biserial-phi:  0.27539 0.1074594
```

`se.bscor` *Computes the standard error for a biserial correlation*

Description

This function computes a biserial correlation and its standard error. A biserial correlation can be used when one variable is quantitative and the other variable has been artifically dichotmized. The biserial correlation estimates the correlation between an observable quantitative variable and an unobserved quantitative variable that is measured on a dichotomous scale. This function requires the estimated mean, estimated standard deviation, and samples size from each level of the dichotomized variable. This function is useful in a meta-analysis of Pearson correlations where some studies report a Pearson correlation and other studies report the information needed to compute a biserial correlation. The biserial correlation and standard error output from this function can be used as input in the meta.ave.cor.gen function.

Usage

```
se.bscor(m1, m2, sd1, sd2, n1, n2)
```

Arguments

`m1`	estimated mean for level 1
`m2`	estimated mean for level 2
`sd1`	estimated standard deviation for level 1
`sd2`	estimated standard deviation for level 2
`n1`	sample size for level 1
`n2`	sample size for level 2

Details

This function computes a point-biserial correlation and its standard error as a function of a standardized mean difference with a weighted variance standardizer. Then the point-biserial estimate is transformed into a biserial correlation using the traditional adjustment. The adjustment is also applied to the point-biserial standard error to obtain the standard error for the biserial correlation.

The biserial correlation assumes that the observed quantitative variable and the unobserved quantitative variable have a bivariate normal distribution. Bivariate normality is a crucial assumption underlying the transformation of a point-biserial correlation to a biserial correlation. Bivariate normality also implies equal variances of the observed quantitative variable at each level of the dichotomized variable, and this assumption is made in the computation of the standard error.

Value

Returns a one-row matrix:

- Estimate - estimated biserial correlation
- SE - standard error

References

Bonett DG (2020). "Point-biserial correlation: Interval estimation, hypothesis testing, meta-analysis, and sample size determination." *British Journal of Mathematical and Statistical Psychology*, **73**(S1), 113–144. ISSN 0007-1102, doi:10.1111/bmsp.12189.

Examples

```
se.bscor(21.9, 16.1, 3.82, 3.21, 40, 40)

#  Should return:
#                          Estimate         SE
#  Biserial correlation:  0.8018318 0.07451665
```

se.cohen — *Computes the standard error for Cohen's d*

Description

This function computes the standard error of Cohen's d using only the two sample sizes and an estimate of Cohen's d. Cohen's d and its standard error assume equal variances. The estimate of Cohen's d, with the standard error output from this function, can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where different types of compatible standardized mean differences are used in the meta-analysis.

Usage

```
se.cohen(d, n1, n2)
```

Arguments

d	estimated Cohen's d
n1	sample size for group 1
n2	sample size for group 2

Value

Returns a one-row matrix:

- Estimate - Cohen's d (from input)
- SE - standard error

See Also

se.stdmean2

Examples

```
se.cohen(.78, 35, 50)

# Should return:
#            Estimate        SE
# Cohen's d:     0.78 0.2288236
```

se.cor — *Computes the standard error for a Pearson or partial correlation*

Description

This function computes the standard error of a Pearson or partial correlation using the estimated correlation, sample size, and number of control variables. The correlation, along with the standard error output from this function, can be used as input in the meta.ave.cor.gen function in applications where a combination of different types of correlations are used in the meta-analysis.

Usage

```
se.cor(cor, s, n)
```

Arguments

`cor`	estimated Pearson or partial correlation
`s`	number of control variables (set to 0 for Pearson)
`n`	sample size

Value

Returns a one-row matrix:

- Estimate - Pearson or partial correlation (from input)
- SE - standard error

References

Bonett DG (2008). "Meta-analytic interval estimation for bivariate correlations." *Psychological Methods*, **13**(3), 173–181. ISSN 1939-1463, doi:10.1037/a0012868.

Examples

```
se.cor(.40, 0, 55)

# Should return:
#               Estimate       SE
# Correlation:       0.4 0.116487
```

se.mean.ps *Computes the standard error for a paired-samples mean difference*

Description

This function computes the standard error of a paired-samples mean difference using the estimated means, estimated standard deviations, estimated Pearson correlation, and sample size. The effect size estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where compatible mean differences from a combination of 2-group and paired-samples experiments are used in the meta-analysis. Equality of variances is not assumed.

Usage

```
se.mean.ps(m1, m2, sd1, sd2, cor, n)
```

Arguments

m1	estimated mean for measurement 1
m2	estimated mean for measurement 2
sd1	estimated standard deviation for measurement 1
sd2	estimated standard deviation for measurement 2
cor	estimated correlation for measurements 1 and 2
n	sample size

Value

Returns a one-row matrix:

- Estimate - estimated mean difference
- SE - standard error

References

Snedecor GW, Cochran WG (1980). *Statistical methods*, 7th edition. ISU University Pres, Ames, Iowa.

Examples

```
se.mean.ps(23.9, 25.1, 1.76, 2.01, .78, 25)

# Should return:
#                    Estimate        SE
# Mean difference:       -1.2 0.2544833
```

`se.mean2` *Computes the standard error for a 2-group mean difference*

Description

This function computes the standard error of a 2-group mean difference using the estimated means, estimated standard deviations, and sample sizes. The effect size estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where compatible mean differences from a combination of 2-group and paired-samples experiments are used in the meta-analysis. Equality of variances is not asumed.

Usage

```
se.mean2(m1, m2, sd1, sd2, n1, n2)
```

Arguments

`m1`	estimated mean for group 1
`m2`	estimated mean for group 2
`sd1`	estimated standard deviation for group 1
`sd2`	estimated standard deviation for group 2
`n1`	sample size for group 1
`n2`	sample size for group 2

Value

Returns a one-row matrix:

- Estimate - estimated mean difference
- SE - standard error

References

Snedecor GW, Cochran WG (1980). *Statistical methods*, 7th edition. ISU University Pres, Ames, Iowa.

Examples

```
se.mean2(21.9, 16.1, 3.82, 3.21, 40, 40)

#                  Estimate        SE
# Mean difference:       5.8 0.7889312
```

se.meanratio.ps *Computes the standard error for a paired-samples log mean ratio*

Description

This function computes the standard error of a paired-samples log mean ratio using the estimated means, estimated standard deviations, estimated Pearson correlation, and sample size. The log-mean estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where compatible mean ratios from a combination of 2-group and paired-samples experiments are used in the meta-analysis. Equality of variances is not assumed.

Usage

```
se.meanratio.ps(m1, m2, sd1, sd2, cor, n)
```

Arguments

`m1`	estimated mean for measurement 1
`m2`	estimated mean for measurement 2
`sd1`	estimated standard deviation for measurement 1
`sd2`	estimated standard deviation for measurement 2
`cor`	estimated correlation for measurements 1 and 2
`n`	sample size

Value

Returns a one-row matrix:

- Estimate - estimated log mean ratio
- SE - standard error

References

Bonett DG, Price RM (2020). "Confidence intervals for ratios of means and medians." *Journal of Educational and Behavioral Statistics*, **45**(6), 750–770. ISSN 1076-9986, doi:10.3102/1076998620934125.

Examples

```
se.meanratio.ps(21.9, 16.1, 3.82, 3.21, .748, 40)

# Should return:
#                   Estimate         SE
# Log mean ratio:  0.3076674 0.02130161
```

`se.meanratio2` *Computes the standard error for a 2-group log mean ratio*

Description

This function computes the standard error of a 2-group log mean ratio using the estimated means, estimated standard deviations, and sample sizes. The log mean estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in application where compatible mean ratios from a combination of 2-group and paired-samples experiments are used in the meta-analysis. Equality of variances is not assumed.

Usage

```
se.meanratio2(m1, m2, sd1, sd2, n1, n2)
```

Arguments

`m1`	estimated mean for group 1
`m2`	estimated mean for group 2
`sd1`	estimated standard deviation for group 1
`sd2`	estimated standard deviation for group 2
`n1`	sample size for group 1
`n2`	sample size for group 2

Value

Returns a one-row matrix:

- Estimate - estimated log mean ratio
- SE - standard error

References

Bonett DG, Price RM (2020). "Confidence intervals for ratios of means and medians." *Journal of Educational and Behavioral Statistics*, **45**(6), 750–770. ISSN 1076-9986, doi:10.3102/1076998620934125.

Examples

```
se.meanratio2(21.9, 16.1, 3.82, 3.21, 40, 40)

# Should return:
#                    Estimate       SE
# Log mean ratio:  0.3076674 0.041886
```

se.odds *Computes the standard error for a log odds ratio*

Description

This function computes a log odds ratio and its standard error using the frequency counts and sample sizes in a 2-group design. These frequency counts and sample sizes can be obtained from a 2x2 contingency table. This function is useful in a meta-analysis of odds ratios where some studies report the sample odds ratio and its standard error and other studies only report the frequency counts or a 2x2 contingency table. The log odds ratio and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions.

Usage

```
se.odds(f1, n1, f2, n2)
```

Arguments

f1	number of participants who have the outcome in group 1
n1	sample size for group 1
f2	number of participants who have the outcome in group 2
n2	sample size for group 2

Value

Returns a one-row matrix:

- Estimate - estimated log odds ratio
- SE - standard error

References

Bonett DG, Price RM (2015). "Varying coefficient meta-analysis methods for odds ratios and risk ratios." *Psychological Methods*, **20**(3), 394–406. ISSN 1939-1463, doi:10.1037/met0000032.

Examples

```
se.odds(36, 50, 21, 50)

# Should return:
#                  Estimate        SE
# Log odds ratio:  1.239501 0.4204435
```

`se.pbcor` *Computes the standard error for a point-biserial correlation*

Description

This function computes a point-biserial correlation and its standard error for two types of point-biserial correlations in 2-group designs using the estimated means, estimated standard deviations, and samples sizes. Equality of variances is not assumed. One type of point-biserial correlation uses an unweighted average of variances and is recommended for 2-group experimental designs. The other type of point-biserial correlation uses a weighted average of variances and is recommended for 2-group nonexperimental designs with simple random sampling (but not stratified random sampling). This function is useful in a meta-analysis of compatible point-biserial correlations where some studies used a 2-group experimental design and other studies used a 2-group nonexperimental design. The effect size estimate and standard error output from this function can be used as input in the meta.ave.cor.gen function.

Usage

```
se.pbcor(m1, m2, sd1, sd2, n1, n2, type)
```

Arguments

`m1`	estimated mean for group 1
`m2`	estimated mean for group 2
`sd1`	estimated standard deviation for group 1
`sd2`	estimated standard deviation for group 2
`n1`	sample size for group 1
`n2`	sample size for group 2
`type`	• set to 1 for weighted variance average • set to 2 for unweighted variance average

Value

Returns a one-row matrix:

- Estimate - estimated point-biserial correlation
- SE - standard error

References

Bonett DG (2020). "Point-biserial correlation: Interval estimation, hypothesis testing, meta-analysis, and sample size determination." *British Journal of Mathematical and Statistical Psychology*, **73**(S1), 113–144. ISSN 0007-1102, doi:10.1111/bmsp.12189.

Examples

```
se.pbcor(21.9, 16.1, 3.82, 3.21, 40, 40, 1)

#  Should return:
#                                Estimate         SE
#  Point-biserial correlation:  0.6349786 0.05981325
```

`se.prop.ps` *Computes the estimate and standard error for a paired-samples proportion difference*

Description

This function computes the Bonett-Price standard error of a paired-samples proportion difference using the frequency counts from a 2 x 2 contingency table. The effect size estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where compatible proportion differences from a combination of 2-group and paired-samples studies are used in the meta-analysis.

Usage

```
se.prop.ps(f00, f01, f10, f11)
```

Arguments

`f00`	number of participants with y = 0 and x = 0
`f01`	number of participants with y = 0 and x = 1
`f10`	number of participants with y = 1 and x = 0
`f11`	number of participants with y = 1 and x = 1

Value

Returns a one-row matrix:

- Estimate - estimated proportion difference
- SE - standard error

References

Bonett DG, Price RM (2012). "Adjusted wald confidence interval for a difference of binomial proportions based on paired data." *Journal of Educational and Behavioral Statistics*, **37**(4), 479–488. ISSN 1076-9986, doi:10.3102/1076998611411915.

Examples

```
se.prop.ps(16, 64, 5, 15)

# Should return:
#                          Estimate         SE
# Proportion difference:  0.5784314 0.05953213
```

---

se.prop2 *Computes the estimate and standard error for a 2-group proportion difference*

Description

This function computes the Agresti-Caffo standard error of a 2-group proportion difference using the frequency counts and sample sizes. The effect size estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where compatible proportion differences from a combination of 2-group and paired-samples studies are used in the meta-analysis.

Usage

```
se.prop2(f1, f2, n1, n2)
```

Arguments

f1	number of participants in group 1 who have the outcome
f2	number of participants in group 2 who have the outcome
n1	sample size for group 1
n2	sample size for group 2

Value

Returns a one-row matrix:

- Estimate - estimated proportion difference
- SE - standard error

References

Agresti A, Caffo B (2000). "Simple and Effective Confidence Intervals for Proportions and Differences of Proportions Result from Adding Two Successes and Two Failures." *The American Statistician*, **54**(4), 280-288. doi:10.1080/00031305.2000.10474560.

Examples

```
se.prop2(31, 16, 40, 40)

# Should return:
#                           Estimate        SE
# Proportion difference:  0.3571429 0.1002777
```

---

se.semipartial *Computes the standard error for a semipartial correlation*

Description

This function computes the standard error of a semipartial correlation using the estimated correlation, sample size, and squared multiple correlation for the full model. The full model includes the independent variable of interest and all control variables. The effect size estimate and standard error output from this function can be used as input in the meta.ave.cor.gen function in applications where a combination of different types of correlations are used in the meta-analysis.

Usage

```
se.semipartial(cor, r2, n)
```

Arguments

cor	estimated semipartial correlation
r2	estimated squared multiple correlation for a model that includes the IV and all control variables
n	sample size

Value

Returns a one-row matrix:

- Estimate - semipartial correlation (from input)
- SE - standard error

Examples

```
se.semipartial(.40, .25, 60)

# Should return:
#                             Estimate        SE
# Semipartial correlation:        0.4 0.1063262
```

se.slope — *Computes a slope and standard error*

Description

This function computes a slope and its standard error for a simple linear regression model (random-x model) using the estimated Pearson correlation and the estimated standard deviations of the response variable and predictor variable. This function is useful in a meta-analysis of slopes of a simple linear regression model where some studies report the Pearson correlation but not the slope.

Usage

```
se.slope(cor, sdy, sdx, n)
```

Arguments

`cor`	estimated Pearson correlation
`sdy`	estimated standard deviation of the response variable
`sdx`	estimated standard deviation of the predictor variable
`n`	sample size

Value

Returns a one-row matrix:

- Estimate - estimated slope
- SE - standard error

References

Snedecor GW, Cochran WG (1980). *Statistical methods*, 7th edition. ISU University Pres, Ames, Iowa.

Examples

```
se.slope(.392, 4.54, 2.89, 60)

# Should return:
#          Estimate        SE
# Slope:  0.6158062 0.1897647
```

`se.spear` *Computes the standard error for a Spearman correlation*

Description

This function computes the Bonett-Wright standard error of a Spearman correlation using the estimated correlation and sample size. The standard error from this function can be used as input in the meta.ave.cor.gen function in applications where a combination of different types of correlations are used in the meta-analysis.

Usage

```
se.spear(cor, n)
```

Arguments

`cor`	estimated Spearman correlation
`n`	sample size

Value

Returns a one-row matrix:

- Estimate - Spearman correlation (from input)
- SE - standard error

References

Bonett DG, Wright TA (2000). "Sample size requirements for estimating Pearson, Kendall and Spearman correlations." *Psychometrika*, **65**(1), 23–28. ISSN 0033-3123, doi:10.1007/BF02294183.

Examples

```
se.spear(.40, 55)

# Should return:
#                        Estimate        SE
# Spearman correlation:       0.4 0.1210569
```

`se.stdmean.ps` *Computes the standard error for a paired-samples standardized mean difference*

Description

This function computes the standard error of a paired-samples standardized mean difference using the sample size and estimated means, standard deviations, and estimated correlation. The effect size estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where compatible standardized mean differences from a combination of 2-group and paired-samples experiments are used in the meta-analysis. Equality of variances is not assumed.

Usage

```
se.stdmean.ps(m1, m2, sd1, sd2, cor, n, stdzr)
```

Arguments

`m1`	estimated mean for measurement 1
`m2`	estimated mean for measurement 2
`sd1`	estimated standard deviation for measurement 1
`sd2`	estimated standard deviation for measurement 2
`cor`	estimated correlation for measurements 1 and 2
`n`	sample size
`stdzr`	• set to 0 for square root average variance standardizer • set to 1 for measurement 1 SD standardizer • set to 2 for measurement 2 SD standardizer

Value

Returns a one-row matrix:

- Estimate - estimated standardized mean difference
- SE - standard error

References

Bonett DG (2009). “Meta-analytic interval estimation for standardized and unstandardized mean differences.” *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

Examples

```
se.stdmean.ps(23.9, 25.1, 1.76, 2.01, .78, 25, 0)

# Should return:
#                                     Estimate        SE
# Standardizedd mean difference:   -0.6352097 0.1602852
```

`se.stdmean2` *Computes the standard error for a 2-group standardized mean difference*

Description

This function computes the standard error of a 2-group standardized mean difference using the sample sizes and the estimated means standardizer (stdzr = 0) for 2-group experimental designs. Use the square root weighted variance standardizer (stdzr = 3) for 2-group nonexperimental designs with simple random sampling. The single-group standardizers (stdzr = 1 and stdzr = 2) can be used with either 2-group experimental or nonexperimental designs. The effect size estimate and standard error output from this function can be used as input in the meta.ave.gen, meta.lc.gen, and meta.lm.gen functions in applications where compatible standardized mean differences from a combination of 2-group and paired-samples experiments are used in the meta-analysis. Equality of variances is not assumed.

Usage

```
se.stdmean2(m1, m2, sd1, sd2, n1, n2, stdzr)
```

Arguments

m1	estimated mean for group 1
m2	estimated mean for group 2
sd1	estimated standard deviation for group 1
sd2	estimated standard deviation for group 2
n1	sample size for group 1
n2	sample size for group 2
stdzr	• set to 0 for square root average variance standardizer • set to 1 for group 1 SD standardizer • set to 2 for group 2 SD standardizer • set to 3 for square root weighted variance standardizer

Value

Returns a one-row matrix:

- Estimate - estimated standardized mean difference
- SE - standard error

References

Bonett DG (2009). "Meta-analytic interval estimation for standardized and unstandardized mean differences." *Psychological Methods*, **14**(3), 225–238. ISSN 1939-1463, doi:10.1037/a0016619.

See Also

se.cohen

Examples

```
se.stdmean2(21.9, 16.1, 3.82, 3.21, 40, 40, 0)

# Should return:
#                                 Estimate        SE
# Standardized mean difference:  1.643894 0.2629049
```

---

se.tetra — *Computes the standard error for a tetrachoric correlation approximation*

Description

This function computes an estimate of a tetrachoric correlation approximation and its standard error using the frequency counts from a 2 x 2 contingency table for two artifically dichotomous variables. A tetrachoric approximation could be compatible with a Pearson correlation in a meta-analysis. The tetrachoric approximation and the standard error from this function can be used as input in the meta.ave.cor.gen function in a meta-analysis where some studies have reported Pearson correlations between quantitative variables x and y and other studies have reported a 2 x 2 contingency table for dichotomous measurements of variables x and y.

Usage

```
se.tetra(f00, f01, f10, f11)
```

Arguments

f00	number of participants with y = 0 and x = 0
f01	number of participants with y = 0 and x = 1
f10	number of participants with y = 1 and x = 0
f11	number of participants with y = 1 and x = 1

Value

Returns a 1-row matrix. The columns are:

- Estimate - estimated tetrachoric approximation
- SE - standard error

References

Bonett DG, Price RM (2005). “Inferential methods for the tetrachoric correlation coefficient.” *Journal of Educational and Behavioral Statistics*, **30**(2), 213–225. ISSN 1076-9986, doi:10.3102/10769986030002213.

Examples

```
se.tetra(46, 15, 54, 85)

# Should return:
#                Estimate         SE
# Tetrachoric:  0.5135167 0.09358336
```

---

stdmean2.from.t — *Computes Cohen’s d from pooled-variance t statistic*

Description

This function computes Cohen’s d for a 2-group design (which is a standardized mean difference with a weighted variance standardizer) using a pooled-variance independent-samples t statistic and the two sample sizes. This function also computes the standard error for Cohen’s d. The Cohen’s d estimate and standard error assume equality of population variances.

Usage

```
stdmean2.from.t(t, n1, n2)
```

Arguments

`t`	pooled-variance t statistic
`n1`	sample size for group 1
`n2`	sample size for group 2

Value

Returns Cohen’s d and its equal-variance standard error

Examples

```
stdmean2.from.t(3.27, 25, 25)

# Should return:
#             Estimate       SE
# Cohen's d  0.9439677 0.298801
```

`table.from.odds` *Computes the cell frequencies in a 2x2 table using the marginal proportions and odds ratio*

Description

This function computes the cell proportions and frequencies in a 2x2 contingency table using the reported marginal proportions, estimated odds ratio, and total sample size. The cell frequncies could then be used to compute other measures of effect size. In the output, "cell ij" refers to row i and column j.

Usage

```
table.from.odds(p1row, p1col, or, n)
```

Arguments

`p1row`	marginal proportion for row 1
`p1col`	marginal proportion for column 1
`or`	estimated odds ratio
`n`	total sample size

Value

A 2-row matrix. The rows are:

- Row 1 gives the four computed cell proportions
- Row 2 gives the four computed cell frequencies

The columns are:

- cell 11 - proportion and frequency for cell 11
- cell 12 - proportion and frequency for cell 12
- cell 21 - proportion and frequency for cell 21
- cell 22 - proportion and frequency for cell 22

References

Bonett DG (2007). “Transforming odds ratios into correlations for meta-analytic research.” *American Psychologist*, **62**(3), 254–255. doi:10.1037/0003066X.62.3.254.

Examples

```
table.from.odds(.17, .5, 3.18, 100)

# Should return:
#                cell 11    cell 12    cell 21    cell 22
# Proportion:  0.1233262 0.04667383  0.3766738  0.4533262
# Frequency:  12.0000000 5.00000000 38.0000000 45.0000000
```

`table.from.phi` *Computes the cell frequencies in a 2x2 table using the marginal proportions and phi correlation*

Description

This function computes the cell proportions and frequencies in a 2x2 contingency table using the reported marginal proportions, estimated phi correlation, and total sample size. The cell frequncies could then be used to compute other measures of effect size. In the output, "cell ij" refers to row i and column j.

Usage

```
table.from.phi(p1row, p1col, phi, n)
```

Arguments

`p1row`	marginal proportion for row 1
`p1col`	marginal proportion for column 1
`phi`	estimated phi correlation
`n`	total sample size

Value

A 2-row matrix. The rows are:

- Row 1 gives the four computed cell proportions
- Row 2 gives the four computed cell frequencies

The columns are:

- cell 11 - proportion and frequency for cell 11
- cell 12 - proportion and frequency for cell 12
- cell 21 - proportion and frequency for cell 21
- cell 22 - proportion and frequency for cell 22

Examples

```
table.from.phi(.28, .64, .38, 200)

# Should return:
#                cell 11   cell 12    cell 21    cell 22
# Proportion:  0.2610974 0.0189026  0.3789026  0.3410974
# Frequency   52.0000000 4.0000000 76.0000000 68.0000000
```

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