

Package ‘MAc’

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Type Package

Title Meta-Analysis with Correlations

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Description This is an integrated meta-analysis package for conducting a correlational research synthesis. One of the unique features of this package is in its integration of user-friendly functions to facilitate statistical analyses at each stage in a meta-analysis with correlations. It uses recommended procedures as described in The Handbook of Research Synthesis and Meta-Analysis (Cooper, Hedges, & Valentine, 2009).

Depends R (>= 2.10.1)

Suggests ggplot2, R2wd, metafor

Enhances compute.es, irr

License GPL-2

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Description

This package contains a variety of functions relevant to conducting a correlational meta-analysis using recommended procedures as described in *The Handbook of Research Synthesis and Meta-Analysis* (Cooper, Hedges, and Valentine, 2009). The goal in creating this package was to provide user-friendly functions to assist researchers in the process of conducting a meta-analysis, from the initial to final stages of their analytic endeavor. The meta-analyst can begin their project by using MAc functions to derive correlation coefficients from the primary studies, when statistics other than correlations are reported (e.g., t-test, p-value, or Cohen's d). Then, the analyst can aggregate all within-study effect sizes (while accounting for within-study correlations among outcome measures

and eliminating any dependencies in the dataset) based on recommended procedures by Hunter & Schmidt (2004), calculate omnibus effect sizes under a fixed and random effects model, and assess for significant moderators (categorical and continuous, single and multi-predictor models) in the dataset. Finally, the meta-analyst can use one of several user-friendly graphics functions to visually represent their data.

Details

Package:	MAc
Type:	Package
Version:	1.1
Date:	2010-07-06
License:	GPL-2
LazyLoad:	yes

The MAc package has integrated functions to facilitate the meta-analytic process at nearly every analytical stage. There are five broad areas of analysis that the MAc package targets:

1. Computations to Calculate Correlations:

There are a variety of functions to compute r (correlation coefficients) from various designs reported in the primary studies. Most functions were derived from Borenstein's chapter (pp. 231-234) in *The Handbook of Research Synthesis and Meta-Analysis* (Cooper, Hedges, & Valentine, 2009). For additional conversion formulas see the **compute.es** package: <https://CRAN.R-project.org/package=compute.es>

2. Within-Study Aggregation of Effect Sizes:

This package contains functions that have automated (i.e., will compute for all studies simultaneously) the process of aggregating within-study effect sizes while taking into account the dependencies among the within-study effect sizes (Hunter & Schmidt, 2004; Hedges & Olkin, 1985; Rosenthal et al., 2006). These functions fix the correlation between within-study effect sizes at .50 (Wampold et al., 1997) and will compute the correct aggregated effect size for all studies. MAc functions implement Hunter and Schmidt's (2004) recommendations for aggregating dependent correlations (see chapter 10, pp. 435-8). To our knowledge, this is the first statistical package/program that has explicitly utilized and automated this aggregation procedure, which has a dual effect of saving the researcher **substantial** time while increasing the accuracy of their analyses.

3. Fixed and Random Effects Omnibus Analysis:

This package contains all the relevant functions to calculate fixed and random effects omnibus effect sizes, outputting the omnibus (i.e., overall) effect size, variance, standard error, upper and lower confidence intervals, and the Q-statistic (heterogeneity test).

4. Moderator Analyses:

There are user-friendly functions to compute fixed and random effects moderator analyses. These include single and multiple predictor models for both categorical and continuous moderator data.

5. Graphics:

This package has a variety of functions visually representing data. This includes boxplots and meta-regression scatterplots.

6. Sample of Additional Functions:
Export MA output to nicely formatted Word tables.

Author(s)

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References

Cooper, H., Hedges, L.V., & Valentine, J.C. (2009). *The handbook of research synthesis and meta-analysis* (2nd edition). New York: Russell Sage Foundation.

Hunter, J. E., Schmidt, F. L. (2004). *Methods of meta-analysis* (2nd edition). Thousand Oaks, CA: Sage.

Wampold, B. E., Mondin, G. W., Moody, M., Stich, F., Benson, K., & Ahn, H. (1997). A meta-analysis of outcome studies comparing bona fide psychotherapies: Empirically, 'all must have prizes.' *Psychological Bulletin*, 122(3), 203-215.

See Also

RcmdrPlugin.MAc package: <https://CRAN.R-project.org/package=RcmdrPlugin.MAd>;
MAd package: <https://CRAN.R-project.org/package=MAd>;
RcmdrPlugin.MAd package: <https://CRAN.R-project.org/package=RcmdrPlugin.MAc>;
compute.es package: <https://CRAN.R-project.org/package=compute.es>;
metafor package: <https://CRAN.R-project.org/package=metafor>

Examples

```
# Examples for each broad area:

id<-c(1:20)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,3,2,3,5,7,1)
dat<-data.frame(id,n,r,mod1)
dat$var.r <- var_r(dat$r, dat$n) # MAc function to derive variance
dat$z <- r_to_z(dat$r) # MAc function to convert to Fisher's z (z')
dat$var.z <- var_z(dat$n) # MAc function for variance of z'
dat$mods2 <- factor(rep(1:2, 10))
dat

# Note: for all the examples in this manual, we have made up data and manually
# created variables and datasets. If conducting your own meta-analysis,
# a more convenient way for using the functions is to import your data from
# a .csv file (with relevant variables in the dataset). One way to do this:
# dat <- read.csv(file.choose(), header = TRUE)
#
```

```
# Then, you can run the functions with this dataset and you do not need to
# manually create your dataset, as we have done above.

# 1. Computations to Calculate Correlations:

# For example, suppose the primary study reported a t-test value for differences
# between 2 groups and the total sample size. Then, running:

r_from_t (1.74, 30)

# reported t-value (1.74) and sample size (30) will output the
# correlation desired for use in the meta-analysis.

# 2. Within-Study Aggregation of Effect Sizes:

agg(id = id, r = r, n = n, data=dat)

# where data = data.frame with columns for id, r (correlation coefficient),
# and n (sample size) with multiple rows within each study (multiple
# correlations reported for each study). Outputs an aggregated data.frame
# with 1 effect size per study.

# 3. Fixed and Random Effects Omnibus Analysis

omni(es = z, var = var.z, data = dat, type="weighted", method = "random", ztor = TRUE)

# where data = data.frame with columns for id, es (r or z')
# , var (variance of r or z'), n (sample size). ztor = if using z', should
# it be converted back to r? see omni documentation for more details.

# 4. Moderator Analyses:

# Random effects
mareg(z~ mod1 + mods2, var = var.z, method = "REML", ztor = TRUE, data = dat)

# where data = data.frame with columns for es (r or z'),
# var (variance of r or z') and moderators.

# 5. Graphics:

## Not run: plotcon(es = r, var = var.r, mod = mod1, data = dat, method= "random",
modname= "Moderator")
## End(Not run)

# Additional Functions

# Export MA output to nicely formatted Word tables.

# install R2wd
# install.packages('R2wd', dependencies = TRUE)
```

```
# mareg fuction
temp <- mareg(z~ mod1 + mods2, var = var.z, method = "REML", ztor = TRUE, data = dat)
# Export data to Word in formatted table
# wd(temp, get = TRUE, new = TRUE)
```

agg *Meta-Analysis Aggregation*

Description

This fuction will simultaneously aggregate all within-study effect sizes while taking into account the correlations among the within-study outcome measures (Hunter and Schmidt, 2004). The default imputed correlation between within-study effect sizes is set at .50 (Wampold et al., 1997) and will compute an aggregated effect size for each study. This default of .50 is adjustable.

Usage

```
agg(id, r, n, cor = .50, mod=NULL, data)
```

Arguments

id	Study id with multiple rows of same id.
r	Correlation coefficient.
n	Sample size.
cor	Estimated correlation among within-study outcome variables. Default is .50 based on Wampold et al. (1997) recommended procedure.
mod	Default is NULL. To aggregate by id and one moderator. If there are multiple levels of a categorical moderator within study and one can in derive seperate effect size estimates for each level within and between studies. However, there will be dependency issues and one way to resolve is shown below in the examples.
data	data.frame with above values.

Value

Outputs a data.frame with aggregated effect sizes where each study is reduced to one row per study (unless aggregated by a moderator) by a weighted average formula. This formula is based on Hunter and Schmidt's (2004) approach to aggregation of dependent effect sizes (see chapter 10, pp. 435-8).

Author(s)

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Maintainer: AC Del Re <acdelre@gmail.com>

References

Hunter, J. E., Schmidt, F. L. (2004). *Methods of meta-analysis* (2nd edition). Thousand Oaks, CA: Sage.

Examples

```
id<-rep(1:5, 4)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-factor(rep(1:2, 10))
dat<-data.frame(id,n,r,mod1)

# Examples

# aggregate to 1 id per study (independent sample)
agg(id = id, r = r, n = n, data=dat)

# aggregate by id & a moderator (non-independent sample)
temp <- agg(id = id, r = r, n = n, mod = mod1, data=dat)

temp

# This function below will randomly select one within
# study level of the moderator (if there are more than one) and output an
# independent sample. Replace temp with the name of your data.
do.call(rbind, lapply(split(temp, temp$id),
function(.data) .data[sample(nrow(.data), 1),])))
```

ancova_to_d1

ANCOVA F-statistic to d

Description

Converts an ANCOVA F-statistic to d (standardized mean difference)

Usage

```
ancova_to_d1(m.1.adj, m.2.adj, sd.adj, n.1, n.2, R, q)
```

Arguments

m.1.adj	Adjusted mean of treatment group from ANCOVA.
m.2.adj	Adjusted mean of comparison group from ANCOVA.
sd.adj	Adjusted standard deviation.
n.1	Treatment group sample size.

n.2	Comparison group sample size.
R	Covariate outcome correlation or multiple correlation.
q	Number of covariates.

Value

d	Standardized mean difference (d).
var_d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

ancova_to_d2

ANCOVA F-statistic to d II

Description

Converts an ANCOVA F-statistic with pooled standard deviation to d (standardized mean difference)

Usage

```
ancova_to_d2(m.1.adj, m.2.adj, s.pooled, n.1, n.2, R, q)
```

Arguments

m.1.adj	Adjusted mean of treatment group from ANCOVA.
m.2.adj	Adjusted mean of comparison group from ANCOVA.
s.pooled	Pooled standard deviation.
n.1	Treatment group sample size.
n.2	Comparison group sample size.
R	Covariate outcome correlation or multiple correlation.
q	number of covariates.

Value

d Standardized mean difference (d).
 var_d Variance of d.

Author(s)

AC Del Re & William T. Hoyt
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References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

atten *Correction for Attenuation*

Description

Used to correct for attenuated effect sizes due to measurement unreliability.

Usage

atten(es, xx, yy, data)

Arguments

es r or z' effect size.
 xx Column for reliability of predictor variable ("independent variable").
 yy Column for reliability of outcome variable ("dependent variable").
 data data.frame with the above values.

Value

A new column for es corrected for attenuation (es.corrected) will be added to the data, for those xx & yy columns with complete data.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Hunter, J. E., Schmidt, F. L. (2004). *Methods of meta-analysis* (2nd edition). Thousand Oaks, CA: Sage.

Examples

```
# Sample data:

id <-c(1, 1:19)
n <-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r <-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
xx <-c(.88,.86,.83,.64,.89,.84,.89,.83,.99,.88,.81,.77,.86,.70,.79,
.71,.80,.74,.82,.86) # Reliability of "independent variable"
yy <-c(.99,.86,.83,.94,.89,.94,.89,.93,.99,.88,.81,.77,.86,.70,.79,
.71,.80,.94,.92,.96) # Reliability of "dependent variable"

dat<-data.frame(id, n, r, xx,yy)

# Example
atten(es= r, xx = xx, yy = yy, data= dat)
```

d_to_g	<i>Standardized Mean Difference (d) Statistic to Unbiased Standardized Mean Difference (g)</i>
--------	--

Description

Eliminates the small upward bias of d to provide an unbiased estimate of the population effect size parameter (g). This procedure will compute g for a single value of d.

Usage

```
d_to_g(d, var.d, n.1, n.2)
```

Arguments

d	Standardized mean difference statistic (d has a slight bias).
var.d	Variance of d.
n.1	Sample size of treatment group.
n.2	Sample size of comparison group.

Value

g	Unbiased Standardized mean difference statistic.
var.g	Variance of g.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

f.ancova_to_d	<i>ANCOVA F-statistic to Standardized Mean Difference (d)</i>
---------------	---

Description

Converts an ANCOVA F-statistic to d (standardized mean difference).

Usage

```
f.ancova_to_d(f, n.1, n.2, R, q)
```

Arguments

f	F-test value from ANCOVA.
n.1	Treatment group sample size.
n.2	Comparison group sample size.
R	Covariate outcome correlation or multiple correlation.
q	number of covariates.

Value

d	Standardized mean difference (d).
var_d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

fail_to_d

Failure groups to Standardized Mean Difference (d)

Description

Converts number of 'failure' groups reported in the primary study to standardized mean difference (d).

Usage

```
fail_to_d(B, D, n.1, n.0)
```

Arguments

B	Treatment failure.
D	Non-treatment failure.
n.1	Treatment sample size.
n.0	Control/comparison sample size.

Value

d	Standardized mean difference (d).
var_d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

f_to_d

*F-test to Standardized Mean Difference (d)***Description**

Converts F-test value to standardized mean difference (d).

Usage

```
f_to_d(f, n.1, n.2)
```

Arguments

f	F-value reported in primary study.
n.1	Sample size of treatment group.
n.2	Sample size of comparison group.

Value

d	Standardized mean difference (d).
var_d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt

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References

Borenstein, M. (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

icc	<i>Intraclass correlation coefficient (ICC) for oneway and twoway models</i>
-----	--

Description

Computes single score or average score ICCs as an index of interrater reliability of quantitative data. Additionally, F-test and confidence interval are computed.

Usage

```
icc(ratings, model = c("oneway", "twoway"),
    type = c("consistency", "agreement"),
    unit = c("single", "average"), r0 = 0, conf.level = 0.95)
```

Arguments

ratings	n*m matrix or dataframe, n subjects m raters.
model	a character string specifying if a oneway model (default) with row effects random, or a twoway model with column and row effects random should be applied. You can specify just the initial letter.
type	a character string specifying if "consistency" (default) or "agreement" between raters should be estimated. If a "oneway" model is used, only "consistency" could be computed. You can specify just the initial letter.
unit	a character string specifying the unit of analysis: Must be one of single (default) or average. You can specify just the initial letter.
r0	specification of the null hypothesis $r = r_0$. Note that a one sided test ($H_1: r > r_0$) is performed.
conf.level	confidence level of the interval.

Details

This function was created by Matthias Gamer for the irr package. For more details, see:

<http://rss.acs.unt.edu/Rdoc/library/irr/html/icc.html>

Details for the function:

Missing data are omitted in a listwise way. When considering which form of ICC is appropriate for an actual set of data, one has take several decisions (Shrout & Fleiss, 1979):

1. Should only the subjects be considered as random effects (oneway model) or are subjects and raters randomly chosen from a bigger pool of persons (twoway model).
2. If differences in judges' mean ratings are of interest, interrater agreement instead of consistency should be computed.
3. If the unit of analysis is a mean of several ratings, unit should be changed to average. In most cases, however, single values (unit = single) are regarded.

Value

A list with class `icclist` containing the following components:

<code>subjects</code>	the number of subjects examined.
<code>raters</code>	the number of raters.
<code>model</code>	a character string describing the selected model for the analysis.
<code>type</code>	a character string describing the selected type of interrater reliability.
<code>unit</code>	a character string describing the unit of analysis.
<code>icc.name</code>	a character string specifying the name of ICC according to McGraw & Wong (1996).
<code>value</code>	the intraclass correlation coefficient.
<code>r0</code>	the specified null hypothesis.
<code>Fvalue</code>	the value of the F-statistic.
<code>df1</code>	the numerator degrees of freedom.
<code>df2</code>	the denominator degrees of freedom.
<code>p.value</code>	the p-value for a two-sided test.
<code>conf.level</code>	the confidence level for the interval.
<code>lbound</code>	the lower bound of the confidence interval.
<code>ubound</code>	the upper bound of the confidence interval.

Author(s)

Matthias Gamer

References

- Bartko, J.J. (1966). The intraclass correlation coefficient as a measure of reliability. *Psychological Reports*, 19, 3-11.
- McGraw, K.O., & Wong, S.P. (1996), Forming inferences about some intraclass correlation coefficients. *Psychological Methods*, 1, 30-46.
- Shrout, P.E., & Fleiss, J.L. (1979), Intraclass correlation: uses in assessing rater reliability. *Psychological Bulletin*, 86, 420-428.

Examples

```
# sample data

study <- c(1,1,2,2,3,3)
rater <- c(rep(1:2,3))
mod1 <- round(rnorm(6, 10, 1))
mod2 <- c(5,5, 9, 9, 8, 8)
mod3 <- c(10,10, 9, 9, 8, 8)
w <-data.frame(study, rater, mod1, mod2, mod3)
w
```

```

# if data is in this format:

# study rater mod1 mod2 mod3
#   1   1   9   9  10
#   1   2  11   8  10
#   2   1   9  10  11
#   2   2   9  10  11
#   3   1   9   9   8
#   3   2  12   9   8
#
# the data will need to be reshaped to be processed by the
# icc function:

long <- reshape(w, varying=colnames(w)[3:5], v.names="Code",
               idvar=c('study', 'rater'), timevar="mods", direction='long')
wide <- reshape(long, idvar=c('mods', 'study'), timevar='rater')

# icc function (created by Matthias Gamer for the 'irr' package)

icc(cbind(wide$Code.1, wide$Code.2), type= "consistency")

```

Kappa

Inter-Rater Agreement

Description

Kappa coefficients for assessing inter-rater agreement between two coders (for categorical variables/moderators).

Usage

```
Kappa(rater1, rater2)
```

Arguments

rater1	First rater of categorical variable to be analyzed. This vector needs to be in a separate column if in a data.frame.
rater2	Second rater on same categorical variable to be analyzed. This vector needs to be in a separate column if in a data.frame.

Value

Kappa coefficients for inter-rater reliability (categorical variables).

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

Examples

```

# sample data

study <- c(1,1,2,2,3,3) # study coded
rater <- rep(1:2, 3) # 2 raters
mod1 <- as.factor(round(rnorm(6, 10, 1))) # values coded for mod 1
mod2 <- as.factor(round(rnorm(6, 10, 1)))
mod3 <- as.factor(round(rnorm(6, 10, 1)))
mod4 <- as.factor(round(rnorm(6, 10, 1)))
mod5 <- as.factor(round(rnorm(6, 10, 1)))
mod6 <- as.factor(round(rnorm(6, 10, 1)))
w <- data.frame(study, rater, mod1, mod2, mod3, mod4, mod5, mod6)
w

# if data is in this format:
# study rater mod1 mod2 mod3 mod4 mod5 mod6
# 1 1 8 10 9 9 10 10
# 1 2 10 11 10 10 13 12
# 2 1 11 10 11 11 10 12
# 2 2 13 10 10 11 12 9
# 3 1 11 10 11 10 10 9
# 3 2 10 10 11 9 10 11
#
# the data will need to be reshaped to be processed by the
# Kappa function:

long <- reshape(w, varying=colnames(w)[3:8], v.names="code",
                idvar=c('study', 'rater'), timevar= 'mods', direction='long')
wide <- reshape(long, idvar=c('mods', 'study'), timevar='rater')
wide

# running the function:

Kappa(wide$code.1, wide$code.2)

```

lor_to_d

Log Odds Ratio to Standardized Mean Difference (d)

Description

Converts a log odds ratio reported in the primary study to a standardized mean difference (d).

Usage

```
lor_to_d(lor, var.lor)
```

Arguments

lor Log odds ratio reported in the primary study.
var.lor Variance of the log odds ratio.

Value

d Standardized mean difference (d).
var_d Variance of d.

Author(s)

AC Del Re & William T. Hoyt
Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

macat

Categorical Moderator Analysis

Description

Computes single predictor categorical moderator analysis under a fixed or random effects model.

Usage

```
macat(es, var, mod, data, method= "random", ztor = FALSE)
```

Arguments

es r or z' effect size.
var Variance of es.
mod Categorical moderator variable used for moderator analysis.
method Default is random. For fixed effects, use fixed.
ztor Default is FALSE. If TRUE, this assumes z' (Fisher's z) was used in the es argument and the analyst would like z' to be converted to r (for interpretive purposes) after analyzing in z'.
data data.frame with values above.

Details

See Konstantopoulos & Hedges (2009; pp. 280-288) for the computations used in this function.

Value

mod	Level of the categorical moderator.
k	Number of studies for each level of the moderator.
estimate	Mean effect size of each level of the moderator.
ci.l	Lower 95% confidence interval.
ci.u	Upper 95% confidence interval.
z	z-score (standardized value).
p	Significance level.
var	Variance of effect size.
se	Square root of variance.
Q	Q-statistic (measure of homogeneity).
df	Degrees of freedom for Q-statistic.
p.h	p-value for homogeneity within that level of the moderator.
I ²	Proportion of total variation in effect size that is due to heterogeneity rather than chance (see Shadish & Haddock, 2009; pp. 263).
Q	Q-statistic overall. Note: Whether fixed or random effects analyses are conducted, the Q statistic reported is for the fixed effect model. Therefore, Q _b + Q _w != Q in the random effects output.
Q _w	Q-within (or error). Measure of within-group heterogeneity.
Q _w .df	Degrees of freedom for Q-within.
Q _w .p	Q-within p-value (for homogeneity).
Q _b	Q-between (or model). Measure of model fit.
Q _b .df	Degrees of freedom for Q-between.
Q _b .p	Q-between p-value (for homogeneity). Q _b and Q _b .p provide the test of whether the moderator variable(s) account for significant variance among effect sizes.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Konstantopoulos & Hedges (2009). Analyzing effect sizes: Fixed-effects models. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

Shadish & Haddock (2009). Analyzing effect sizes: Fixed-effects models. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 257-278). New York: Russell Sage Foundation.

See Also

[plotcat, wd](#)

Examples

```
id<-c(1:20)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,3,2,3,5,7,1)
dat<-data.frame(id,n,r,mod1)
dat$var.r <- var_r(dat$r, dat$n) # MAC function to derive variance
dat$z <- r_to_z(dat$r) # MAC function to convert to Fisher's z (z')
dat$var.z <- var_z(dat$n) # MAC function for variance of z'
dat$mods2 <- factor(rep(1:2, 10))
dat

# Example

# Random effects
macat(es = z, var= var.z, mod = mods2, data = dat, ztor = TRUE, method= "random")
```

macatC

Direct Categorical Moderator Comparison

Description

Function for a planned comparison between two levels of a moderator under a fixed or random effects model.

Usage

```
macatC(x1, x2, es, var, mod, data, method= "random", type= "post.hoc", ztor = FALSE)
```

Arguments

x1	One level of categorical moderator.
x2	Comparison level of same categorical moderator.
es	r or z' effect size.
var	Variance of es.
mod	Categorical moderator variable used for moderator analysis.
method	Default is random. For fixed effects, use fixed.
type	post.hoc assumes the comparison was not planned prior to conducting the meta analysis. The a priori option, planned, assumes the researcher planned to conduct the analysis a priori. Default is post.hoc using the Scheffe post hoc statistical method.

ztor	Default is FALSE. If TRUE, this assumes z' (Fisher's z) was used in the <code>es</code> argument and the analyst would like z' to be converted to r (for interpretive purposes) after analyzing in z' .
data	<code>data.frame</code> with values above.

Details

See Konstantopoulos & Hedges (2009; pp. 280-288) for the computations used in this function.

Value

<code>diff</code>	Mean difference between the two levels.
<code>var.diff</code>	Variance of <code>diff</code> .
<code>p</code>	Significance level.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Konstantopoulos & Hedges (2009). Analyzing effect sizes: Fixed-effects models. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

Shadish & Haddock (2009). Analyzing effect sizes: Fixed-effects models. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 257-278). New York: Russell Sage Foundation.

See Also

[macat](#),

Examples

```
id<-c(1:20)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,3,2,3,5,7,1)
dat<-data.frame(id,n,r,mod1)
dat$var.r <- var_r(dat$r, dat$n) # MAC function to derive variance
dat$z <- r_to_z(dat$r) # MAC function to convert to Fisher's z (z')
dat$var.z <- var_z(dat$n) # MAC function for variance of z'
dat$mods2 <- factor(rep(1:4, 5))
dat

# Example
macatC(1, 2, es=r, var=var.r, mod=mods2, data=dat, method= "random",
```

```
type= "post.hoc", ztor = FALSE)
```

 mareg

Meta-Regression

Description

Meta-regression function for a single or multiple predictor model. This function is a wrapper for the `rma()` function in the `metafor` package (Viechtbauer, W, 2010). Please see <https://CRAN.R-project.org/package=metafor> for details or for more advanced functionality with the `rma()` function.

Usage

```
mareg(formula, var, data, ztor = FALSE, method = "REML", subset, ...)
```

Arguments

formula	This is a formula based function, similar to other functions in R (e.g., <code>lm</code>), where the criterion variable (e.g., <code>r</code> or <code>z'</code>) is dependent on (<code>~</code>) the predictor variables (e.g., moderators). The formula for two moderators would take this form: <code>mareg(r ~ mod1 + mod2, var.r, data)</code> , where <code>r</code> is the criterion variable predicted by <code>mod1</code> and <code>mod2</code> . The variance (<code>var</code>) of each <code>r</code> is <code>var.r</code> in this case.
var	Variance of <code>r</code> or <code>z'</code> .
data	Aggregated data.frame (see <code>agg</code> function for setting up the dataset for these analyses) with <code>id</code> , <code>es</code> (<code>r</code> or <code>z'</code>), <code>var</code> (variance of <code>r</code> or <code>z'</code>) for each study.
method	Default is REML (Restricted-Maximal Likelihood), which is the standard random effects method. For fixed effects, use FE. Other options are specified in the <code>metafor</code> package manual (<code>'rma'</code> function).
ztor	Default is FALSE. If TRUE, this assumes <code>z'</code> (Fisher's <code>z</code>) was used in the <code>es</code> argument and the analyst would like <code>z'</code> to be converted to <code>r</code> (for interpretive purposes) after analyzing in <code>z'</code> .
subset	an optional vector specifying a subset of observations to be used in the fitting process.
...	Additional arguments to be passed to <code>rma()</code> .

Details

See Wolfgang Viechtbauer (2010). `metafor`: Meta-Analysis Package for R. R package version 1.1-0. for the details of the `rma()` function. <https://CRAN.R-project.org/package=metafor>

Value

estimate	Unstandardized regression coefficient estimate.
se	Standard error of the estimate coefficient.
z	z-value.
ci.l	Lower 95% confidence interval.
ci.u	Upper 95% confidence interval.
Pr(> z)	p-value (significance level).
QE	Q-error. Measure of error in the model.
QE.df	Degrees of freedom for Q-error.
QEp	Q-error p-value (for homogeneity).
QM	Q-model. Measure of model fit.
QM.df	Degrees of freedom for Q-model.
QMp	Q-between p-value (for homogeneity). QM and QMp provide the test of whether the moderator variable(s) account for significant variance among effect sizes.

References

Wolfgang Viechtbauer (2010). metafor: Meta-Analysis Package for R. R package version 1.1-0. <https://CRAN.R-project.org/package=metafor>

See Also

[wd](#), [plotcon](#)

Examples

```
# install metafor
# install.packages('metafor', dependencies = TRUE)

# Sample data
id<-c(1:20)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,3,2,3,5,7,1)
dat<-data.frame(id,n,r,mod1)
dat$var.r <- var_r(dat$r, dat$n) # MAC function to derive variance
dat$z <- r_to_z(dat$r) # MAC function to convert to Fisher's z (z')
dat$var.z <- var_z(dat$n) # MAC function for variance of z'
dat$mods2 <- factor(rep(1:2, 10))
dat

# Examples

# Random Effects
```

```

mareg(r~ mod1 + mods2, var = var.r, method = "REML", data = dat)

# Fixed Effects
mareg(r~ mod1 + mods2, var = var.r, method = "FE", data = dat)

```

mean_to_d

Means to Standardized Mean Difference

Description

Converts raw mean scores reported in the primary study to a standardized mean difference (d).

Usage

```
mean_to_d(m.1, m.2, sd.1, sd.2, n.1, n.2)
```

Arguments

m.1	Mean of group one.
m.2	Mean of group two.
sd.1	Standard deviation of group one.
sd.2	Standard deviation of group two.
n.1	Sample size of group one.
n.2	Sample size of group two.

Value

d	Standardized mean difference (d).
var.d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

 mean_to_d2

Means with Pooled SD to Standardized Mean Difference

Description

Converts raw mean scores with pooled standard deviation from the primary study to a standardized mean difference (d).

Usage

```
mean_to_d2(m.1, m.2, s.pooled, n.1, n.2)
```

Arguments

m.1	Mean of group one.
m.2	Mean of group two.
s.pooled	Pooled standard deviation.
n.1	Sample size of group one.
n.2	Sample size of group two.

Value

d	Standardized mean difference (d).
var.d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

d_to_g, mean_to_d, t_to_d, f_to_d, p_to_d1, p_to_d2, ancova_to_d1, ancova_to_d2, tt.ancova_to_d, f.ancova_to_d, r_to_d, p.ancova_to_d1, p.ancova_to_d2, lor_to_d, prop_to_or, prop_to_d, r_from_chi, r_from_d, r_from_d1, r_from_t

 omni

Omnibus Effect Size (Fixed and Random Effects)

Description

Computes fixed and random effects omnibus effect size for correlations.

Usage

```
omni(es, var, data, type="weighted", method = "random", ztor = FALSE)
```

Arguments

es	r or z' effect size.
var	Variance of es.
type	weighted or unweighted. Default is weighted. Use the unweighted variance method only if Q is rejected and is very large relative to the number of studies in the meta-analysis.
method	Default is random. For fixed effects, use fixed.
ztor	Default is FALSE. If TRUE, this assumes z' (Fisher's z) was used in the es argument and the analyst would like z' to be converted to r (for interpretive purposes) after analyzing in z'.
data	data.frame with above values.

Value

Fixed and random effects:

k	Number of studies in the meta-analysis.
estimate	Unstandardized regression coefficient estimate.
se	Standard error of the estimate coefficient.
z	z-value.
ci.l	Lower 95% confidence interval.
ci.u	Upper 95% confidence interval.
p	Significance level.
Q	Q-statistic (measure of homogeneity).
df.Q	Degrees of freedom for Q-statistic.
Qp	Q-statistic p-value (assesses overall homogeneity between studies).
I2	Proportion of total variation in effect size that is due to systematic differences between effect sizes rather than by chance (see Shadish & Haddock, 2009; pp. 263).

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

p.ancova_to_d1	<i>One-tailed p-value from ANCOVA to Standardized Mean Difference (d)</i>
----------------	---

Description

Converts a one-tailed p-value from ANCOVA reported in the primary study to a standardized mean difference (d)

Usage

p.ancova_to_d1(p, n.1, n.2, R, q)

Arguments

p	One-tailed p-value reported in primary study.
n.1	Treatment group sample size.
n.2	Comparison group sample size.
R	Covariate outcome correlation or multiple correlation.
q	number of covariates.

Value

d	Standardized mean difference (d).
var_d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

p.ancova_to_d2	<i>Two-tailed p-value from ANCOVA to Standardized Mean Difference (d)</i>
----------------	---

Description

Converts a two-tailed p-value from ANCOVA reported in the primary study to a standardized mean difference (d)

Usage

```
p.ancova_to_d2(p, n.1, n.2, R, q)
```

Arguments

p	Two-tailed p-value reported in primary study.
n.1	Treatment group sample size.
n.2	Comparison group sample size.
R	Covariate outcome correlation or multiple correlation.
q	number of covariates.

Value

d	Standardized mean difference (d).
var_d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

 plotcat

Categorical Moderator Graph

Description

Outputs a rich and detailed boxplot graphic for each level of the specified moderator (under a fixed or random effects model).

Usage

```
plotcat(es, var, mod, data, method="random", modname=NULL, title=NULL, ...)
```

Arguments

es	r or z' effect size.
var	Variance of es.
mod	Categorical moderator variable used for moderator analysis.
method	Default is random. For fixed effects, use fixed.
data	data.frame with values above.
modname	Name of moderator to appear on x axis of plot. Default is NULL.
title	Plot title. Default is NULL.
...	Additional arguments to be passed to ggplot.

Value

Boxplot graph with median, max, min, and outliers from a fixed or random effects categorical moderator analysis. Places jitter points (for each study) on the boxplots. The size of each point (representing a study in the analysis) are based on study weights where more precise studies have larger points. The ggplot2 package outputs the graphics.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Cooper, H., Hedges, L.V., & Valentine, J.C. (2009). *The handbook of research synthesis and meta-analysis* (2nd edition). New York: Russell Sage Foundation.

See Also[macat](#), [plotcon](#)**Examples**

```

id<-c(1:20)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,3,2,3,5,7,1)
dat<-data.frame(id,n,r,mod1)
dat$var.r <- var_r(dat$r, dat$n) # MAC function to derive variance
dat$z <- r_to_z(dat$r) # MAC function to convert to Fisher's z (z')
dat$var.z <- var_z(dat$n) # MAC function for variance of z'
dat$mods2 <- factor(rep(1:2, 10))

# Example

## Not run: plotcat(es = r, var = var.r, mod = mods2, data = dat, method= "random",
  modname= "Moderator")
## End(Not run)

```

plotcon

*Meta Regression Scatterplot***Description**

Outputs a scatterplot from a fixed or random effects meta regression (continuous and/or categorical).

Usage

```
plotcon(es, var, mod, data, method= "random", modname=NULL,
  title=NULL, ylim=c(0, 1), ...)
```

Arguments

es	r or z' effect size.
var	Variance of g.
mod	Categorical moderator variable used for moderator analysis.
method	Default is random. For fixed effects, use fixed.
data	data.frame with values above.
modname	Name of moderator to appear on x axis of plot. Default is NULL.
title	Plot title. Default is NULL.
ylim	Limits of y-axis with the first argument for the minimum y-value and the second for the maximum y value. Default is c(0, 1).
...	Additional arguments to be passed to ggplot.

Value

Scatterplot with fixed or random effects regression line with size of visual points based on study weights, where the more precise studies have larger points. The ggplot2 package outputs the rich graphics.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Cooper, H., Hedges, L.V., & Valentine, J.C. (2009). *The handbook of research synthesis and meta analysis* (2nd edition). New York: Russell Sage Foundation.

See Also

[mareg](#), [plotcat](#)

Examples

```
id<-c(1:20)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,3,2,3,5,7,1)
dat<-data.frame(id,n,r,mod1)
dat$var.r <- var_r(dat$r, dat$n) # MAC function to derive variance
dat$z <- r_to_z(dat$r) # MAC function to convert to Fisher's z (z')
dat$var.z <- var_z(dat$n) # MAC function for variance of z'
dat$mods2 <- factor(rep(1:2, 10))

# Example

## Not run: plotcon(es = r, var = var.r, mod = mod1, data = dat, method= "random",
modname= "Moderator")
## End(Not run)
```

PubBias

Assess for Publication Bias

Description

Assess for publication bias in the meta-analytic data

Usage

```
PubBias(data)
```


Value

d Standardized mean difference (d).
var_d Variance of d.

Author(s)

AC Del Re & William T. Hoyt
Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

p_to_d2

Two-tailed p-value to Standardized Mean Difference (d)

Description

One-tailed p-value reported in primary study to Standardized Mean Difference (d)

Usage

p_to_d2(p, n.1, n.2)

Arguments

p Two-tailed p-value reported in primary study.
n.1 Sample size of treatment group.
n.2 Sample size of comparison group.

Value

d Standardized mean difference (d).
var_d Variance of d.

Author(s)

AC Del Re & William T. Hoyt
Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

<i>r2</i>	<i>Explained Variance</i>
-----------	---------------------------

Description

Compares tau-squared from empty model (omnibus or overall weighted mean) to model with moderators and provides percentage of explained variance.

Usage

```
r2(x)
```

Arguments

x Will take either a `mareg` (meta-regression), or `macat` (single predictor categorical moderator analysis) object and evaluate.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

Examples

```
# Sample data
id<-c(1:20)
n.1<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
n.2 <- c(11,22,10,20,25,12,12,36,19,11,34,75,33,120,37,14,40,16,10,21)
g <- c(.68,.56,.23,.64,.49,-.04,1.49,1.33,.58,1.18,-.11,1.27,.26,.40,.49,
.51,.40,.34,.42,1.16)
var.g <- c(.08,.06,.03,.04,.09,.04,.009,.033,.0058,.018,.011,.027,.026,.0040,
.049,.0051,.040,.034,.0042,.016)
mod<-factor(c(rep(c(1,1,2,3),5)))
mods2<-c(rep(1:5,4))
df<-data.frame(id, n.1,n.2, g, var.g,mod, mods2)
```

```
# Examples

# mareg fuction
temp <- mareg(g~ mod + mods2, var = var.g, method = "REML", data = df)

r2(temp)
```

r_from_chi

Chi-Squared to Correlation

Description

Converting Chi-squared statistic (with 1 degree of freedom) reported in primary study to r

Usage

```
r_from_chi(chi.sq, n)
```

Arguments

chi.sq	Chi squared statistic from primary study.
n	Sample size in primary study.

Value

Computes correlation coefficient (r).

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

r_from_d	<i>Correlation from Mean Difference</i>
----------	---

Description

Converts d (mean difference) to r where $n.tmt = n.comparison$ (see section 12.5.4, Borenstein, 2009; pp. 234).

Usage

```
r_from_d(d, var.d, a = 4)
```

Arguments

d	Mean difference statistic (d) reported in primary study.
$var.d$	Variance of d reported in primary study.
a	Used to compute correlation. Default is 4.

Value

Outputs a correlation coefficient (r).

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d1](#), [r_from_t](#)

 r_from_d1

Correlation from Mean Difference II

Description

Converts d (mean difference) reported in primary study to r (correlation coefficient) where sample size of the treatment group is not equal to the sample size of the comparison group (see section 12.5.4, Borenstein, 2009; pp. 234).

Usage

```
r_from_d1(d, n.1, n.2, var.d)
```

Arguments

<code>d</code>	Mean difference statistic (d) reported in primary study.
<code>n.1</code>	sample size of group one reported in primary study.
<code>n.2</code>	sample size of group two reported in primary study.
<code>var.d</code>	variance of d reported in primary study.

Value

Computes a correlation coefficient (r).

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_t](#)

r_from_t	<i>Correlation from t-test</i>
----------	--------------------------------

Description

Compute correlation from t-value reported in the primary study (see section 12.5.4, Borenstein, 2009; pp. 234).

Usage

```
r_from_t(t, n)
```

Arguments

t	t-statistic value reported in primary study.
n	Sample size reported in primary study.

Value

Outputs the correlation coefficient (r).

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#),

r_to_d	<i>Correlation (r) to Standardized Mean Difference (d)</i>
--------	--

Description

Converts a correlation (r) to standardized mean difference (d).

Usage

r_to_d(r, N)

Arguments

r	Correlation coefficient.
N	Total sample size.

Value

d	Standardized mean difference (d).
---	-----------------------------------

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

r_to_z	<i>Correlation to Fisher's z</i>
--------	----------------------------------

Description

Computes Fisher's z from correlation coefficient.

Usage

r_to_z(r)

Arguments

r Correlation coefficient value.

Value

Outputs Fisher's z statistic.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Cooper, H., Hedges, L.V., & Valentine, J.C. (2009). *The handbook of research synthesis and meta-analysis* (2nd edition). New York: Russell Sage Foundation.

tt.ancova_to_d	<i>t-test Value from ANCOVA to Standardized Mean Difference (d)</i>
----------------	---

Description

Converts a t-test value from ANCOVA to a standardized mean difference (d)

Usage

tt.ancova_to_d(t, n.1, n.2, R, q)

Arguments

t	t-test value reported in primary study.
n.1	Treatment group sample size.
n.2	Comparison group sample size.
R	Covariate outcome correlation or multiple correlation.
q	number of covariates.

Value

d	Standardized mean difference (d)
var_d	Variance of d

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [t_to_d](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

t_to_d	<i>t-test Value to Standardized Mean Difference (d)</i>
--------	---

Description

Converts a t-test value reported in the primary study to a standardized mean difference (d).

Usage

```
t_to_d(t, n.1, n.2)
```

Arguments

t	t-test value reported in primary study.
n.1	Sample size of treatment group.
n.2	Sample size of comparison group.

Value

d	Standardized mean difference (d).
var_d	Variance of d.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Borenstein (2009). Effect sizes for continuous data. In H. Cooper, L. V. Hedges, & J. C. Valentine (Eds.), *The handbook of research synthesis and meta analysis* (pp. 279-293). New York: Russell Sage Foundation.

See Also

[d_to_g](#), [mean_to_d](#), [mean_to_d2](#), [f_to_d](#), [p_to_d1](#), [p_to_d2](#), [ancova_to_d1](#), [ancova_to_d2](#), [tt.ancova_to_d](#), [f.ancova_to_d](#), [r_to_d](#), [p.ancova_to_d1](#), [p.ancova_to_d2](#), [lor_to_d](#), [prop_to_or](#), [prop_to_d](#), [r_from_chi](#), [r_from_d](#), [r_from_d1](#), [r_from_t](#)

var_r

Correlation Variance

Description

Computes variance of a correlation coefficient (r).

Usage

```
var_r(r, n)
```

Arguments

r	correlation coefficient.
n	Study sample size.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Cooper, H., Hedges, L.V., & Valentine, J.C. (2009). *The handbook of research synthesis and meta-analysis* (2nd edition). New York: Russell Sage Foundation.

var_z

Fisher's z Variance

Description

Computes the variance of a Fisher's z transformation

Usage

```
var_z(n)
```

Arguments

n Study sample size.

Value

Computes the variance of Fisher's z.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

References

Cooper, H., Hedges, L.V., & Valentine, J.C. (2009). *The handbook of research synthesis and meta-analysis* (2nd edition). New York: Russell Sage Foundation.

wd

Output to Word in formatted tables

Description

Function for exporting MA output to nicely formatted Word tables.

Usage

```
wd(object, get = FALSE, new = FALSE, ...)
```

Arguments

object	Will take either an omni (Omnibus), mareg (meta-regression), or macat (single predictor categorical moderator analysis) object and export to Word in a formatted table.
get	Start up the Word program? TRUE if an instance of Word is not currently open.
new	Output data into a new Word document? TRUE or FALSE.
...	Additional arguments to be passed to R2wd functions.

Details

This function depends of the R2wd package. See Christian Ritter (2010). R2wd: Write MS-Word documents from R. R package version 1.3 for the details of the R2wd package.

Author(s)

AC Del Re & William T. Hoyt
 Maintainer: AC Del Re <acdelre@gmail.com>

References

Christian Ritter (2010). R2wd: Write MS-Word documents from R. R package version 1.3.

See Also

[omni](#), [mareg](#), [macat](#)

Examples

```
# Sample data
id<-c(1:20)
n<-c(10,20,13,22,28,12,12,36,19,12,36,75,33,121,37,14,40,16,14,20)
r<-c(.68,.56,.23,.64,.49,-.04,.49,.33,.58,.18,-.11,.27,.26,.40,.49,
.51,.40,.34,.42,.16)
mod1<-c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,3,2,3,5,7,1)
dat<-data.frame(id,n,r,mod1)
dat$var.r <- var_r(dat$r, dat$n) # MAC function to derive variance
dat$z <- r_to_z(dat$r) # MAC function to convert to Fisher's z (z')
dat$var.z <- var_z(dat$n) # MAC function for variance of z'
dat$mods2 <- factor(rep(1:2, 10))
dat

# Examples

# install R2wd
# install.packages('R2wd', dependencies = TRUE)

# mareg fuction
temp <- mareg(r~ mod1 + mods2, var = var.r, method = "REML", data = dat)

# Export data to Word in formatted table
```

```
## Not run: wd(temp, get = TRUE, new = TRUE)
```

wgts

Weights added to Meta Data

Description

Adds weights to the meta-analysis data set.

Usage

```
wgts(es, var.es, data)
```

Arguments

es	r or z' effect size.
var.es	Variance of es
data	data.frame with values above.

Value

Adds fixed and random-effects weights and confidence intervals to meta data set.

Author(s)

AC Del Re & William T. Hoyt

Maintainer: AC Del Re <acdelre@gmail.com>

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