Package ‘MAd’

February 19, 2015

Type Package
Title Meta-Analysis with Mean Differences
Version 0.8-2
Date 2014-12-23
Author AC Del Re & William T. Hoyt
Maintainer AC Del Re <acdelre@gmail.com>
Description A collection of functions for conducting a meta-
analysis with mean differences data. 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 metafor, R2wd, ggplot2
Enhances compute.es, irr
License GPL-2
URL http://acdelre.weebly.com
NeedsCompilation no
Repository CRAN
Date/Publication 2014-12-22 01:26:35

R topics documented:

MAd-package .................................................. 2
agg .......................................................... 7
ancova_to_d1 .............................................. 10
ancova_to_d2 .............................................. 11
atten ......................................................... 12
compute_dgs .............................................. 13
compute_ds ................................................. 14
compute_gs ............................................... 16
dat.cooper15.3 ........................................... 17
dat.cooperA2 .............................................. 17
MAd-package

Meta-Analysis with Mean Differences

Index 55
Description

The Mad package contains a variety of functions for conducting a mean differences 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 Mad functions to derive d (standardized mean differences) and g (unbiased d) from a variety of statistics/values reported in the primary studies (e.g., raw means and sd, t-test). 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), 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

<table>
<thead>
<tr>
<th>Package:</th>
<th>MAd</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type:</td>
<td>Package</td>
</tr>
<tr>
<td>Version:</td>
<td>0.8-2</td>
</tr>
<tr>
<td>Date:</td>
<td>2014-12-23</td>
</tr>
<tr>
<td>License:</td>
<td>GPL-2</td>
</tr>
<tr>
<td>LazyLoad:</td>
<td>yes</td>
</tr>
</tbody>
</table>

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

1. Computations to Calculate Mean Differences:

There are a variety of functions to compute d (standardized mean difference) and g (unbiased d) from various designs reported in the primary studies. Most functions were derived from Borenstein’s chapter in The Handbook of Research Synthesis and Meta-Analysis (Cooper, Hedges, & Valentine, 2009; pp. 228-234). For additional conversion formulas see the compute.es package: http://CRAN.R-project.org/package=compute.es

2. Within-Study Aggregation of Effect Sizes:

This function will simultaneously aggregate all within-study effect sizes while taking into account the correlations among the within-study outcome measures (Gleser & Olkin 2009; Gleser & Olkin 2009; Hedges & Olkin, 1985; Rosenthal et al., 2006). 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 and can vary between outcome types. This Mad aggregation function implements Gleser & Olkin (1994; 2009) and Borenstein et al. (2009) procedures for aggregating dependent effect sizes. To our knowledge, this is the first statistical package/program to explicitly utilize and automate this type of aggregation procedure, which has a dual effect of saving the researcher substantial time while improving 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)
AC Del Re & William T. Hoyt
Maintainer: AC Del Re <acdelre@gmail.com>

References


See Also
RcmdrPlugin.MA package: http://CRAN.R-project.org/package=RcmdrPlugin.MA;
MAc package: http://CRAN.R-project.org/package=MAc;
compute.es package: http://CRAN.R-project.org/package=compute.es;
metafor package: http://CRAN.R-project.org/package=metafor

Examples
## EXAMPLES FOR EACH BROAD AREA

# SAMPLE DATA:
MA <- data.frame(id=factor(rep(1:5, 3)),
  measure=c(rep("dep",5), rep("anx",5), rep("shy",5)),
  es=c(rnorm(5, 0.8,.2), rnorm(5, 0.5,.1), rnorm(5, 0.4,.1)),
  var_es=abs(rnorm(5*3, 0.05,.03)),
  nT=round(rnorm(5*3, 30, 5),0),
  nC=round(rnorm(5*3, 30, 5),0),
  mod1=factor(rep(c("a","b","c","d","e"),3)),
  mod2=rep(seq(20, 60, 10), 3))

# 1. COMPUTE MEAN DIFFERENCE STATISTIC FROM
# REPORTED STATS (GENERALLY FROM A PRIMARY STUDY):

# suppose the primary study reported an log odds ratio for different
# proportions between 2 groups. Then, running:

lor_to_d(.9070,.0676)

# reported log odds ratio (lor = .9070) and variance (.0676) will output the
# standardized mean difference (d) and its variance (var.d) that can be used in
# a meta-analysis.

## 2. ACCOUNT FOR DEPENDENCIES: WITHIN-STUDY EFFECT SIZES (ES):

## 2 EXAMPLES:
# EXAMPLE 1: AGGREGATING EFFECT SIZES FOR A DATA FRAME
# (MULTIPLE STUDIES AT LEAST SOME OF WHICH HAVE MULTIPLE DEPENDENT EFFECT SIZES)
# EXAMPLE 2: AGGREGATING EFFECT SIZES FOR SINGLE STUDY WITH THREE OR MORE
# EFFECT SIZES WHEN PAIRS OF DVS HAVE DIFFERENT CORRELATIONS

## EXAMPLE 1: MA IS A DATA FRAME CONTAINING MULTIPLE STUDIES (id),
## EACH WITH MULTIPLE EFFECT SIZES (CORRELATIONS BETWEEN ALL PAIRS OF DVS ARE r=.5.)

# AGGREGATION PROCEDURE:
# method="GO1"; GLESER AND OLKIN (1994) PROCEDURE WHEN d IS COMPUTED
# USING POOLED SD IN THE DENOMINATOR

MA1 <- agg(id=id, es=es, var=var.es, n.1=nT, n.2=nC, cor = .5, method="GO1", data=MA)

MA1

## EXAMPLE 2: STUDY 1 COMPARES A TREATMENT AND CONTROL GROUP ON
## THREE OUTCOME MEASURES (DEPRESSION, ANXIETY, AND SHYNESS).
## THE CORRELATION AMONG THE THREE PAIRS OF DVS ARE r12=.5, r13=.2, and r23=.3.

study1 <- data.frame( id=factor(rep(1, 3)),
  measure=c("dep", "anx", "shy"),
  es=c(0.8, 0.5, 0.4),
  var.es=c(0.01, 0.02, 0.1),
  nT=rep(30, 3),
  nC=rep(30, 3))

# ONE WOULD CONSTRUCT THE CORRELATION MATRIX AS FOLLOWS:
cors <- matrix(c(1,.5,2, .5,1,.3, .2,.3,1), nrow=3)

# AGGREGATION PROCEDURE:
# method="GO1", GLESER AND OLKIN (1994) PROCEDURE WHEN d
# IS COMPUTED USING POOLED SD IN THE DENOMINATOR

agg(id=id, es=es, var=var.es, n.1=nT, n.2=nC, cor=cor, method="GO1", mod = NULL, data=study1)

# where MA = data.frame with columns for id, es (standardized
# mean difference), var.es (variance of es), n.1 (sample size of group
# one), and n.2 (sample size of comparison group) with multiple rows per
# study. Outputs an aggregated data.frame with 1 effect size per study.

## 3.OMNIBUS ANALYSIS

# FIRST ADD MODERATORS TO THE AGGREGATED DATASET:

MODS <- data.frame(id=1:5,
    mod1=factor(c("a","b","a","b","b")),
    mod2=as.numeric(c(20, 30, 25, 35, 40)))

MA2 <- merge(MA1, MODS, by='id')

# Random Effects
m0 <- mareg(es~ 1, var = var1, method = "REML", data = MA2)

# where MA = data.frame with columns for id, es (standardized
# mean difference), var.es (variance of es), n.1 (sample size of group
# one), and n.2 (sample size of comparison group).

# view output:
summary(m0)

# 4. MODERATOR ANALYSIS:

# Random Effects
m1 <- mareg(es~ mod1 + mod2 , var = var1, method = "REML", data = MA2)

# view output:
summary(m1)

# 5. Graphics:

## Not run: plotcon(g = es1, var = var1, mod = mod1, data = MA2, method="random",
# modname= "Moderator")
## End(Not run)

# Additional Functions
# Export MA output to nicely formatted Word tables.

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

# Export data to Word in formatted table
# wd(m, get = TRUE, new = TRUE)

---

**agg**

**Aggregate Dependent Effect Sizes**

**Description**

This function will simultaneously aggregate all within-study effect sizes while taking into account the correlations among the within-study outcomes. The default correlation between outcome measures is set at .50 (Wampold et al., 1997), and can be adjusted as needed. An aggregate effect size and its variance is computed for each study. This MAd aggregation function implements Gleser & Olkin (1994) and Borenstein et al. (2009) procedures for aggregating dependent effect sizes.

**Usage**

```
agg(id, es, var, n.1=NULL, n.2=NULL, method = "BHHR", cor = .50, mod=NULL, data)
```

**Arguments**

- **id**: Study id with multiple rows of same id.
- **es**: Effect size. Use Cohen’s d for GO1 and GO2 method and use Hedges g for BHHR method.
- **var**: Variance of g.
- **n.1**: Sample size of group one. Only required if using method='GO1' or 'GO2'.
- **n.2**: Sample size of group two. Only required if using method='GO1' or 'GO2'.
- **cor**: Estimated correlation among within-study outcome variables. Input should either be a fixed correlation (default is r=.5) or a correlation matrix to allow different correlations between outcome types (in which case aggregation should typically be on one study at a time rather than the entire dataset–see examples below).
- **mod**: To aggregate by id and one moderator. If there are multiple levels of a categorical moderator within study and one can in derive separate effect size estimates for each level within and between studies. Default is NULL.
- **data**: data.frame with above values.
Value

Outputs a data frame with aggregated effect sizes and variances of effect sizes where each study is reduced to one row per study (unless aggregated by a moderator) by a weighted average formula.

Author(s)

AC Del Re & William T. Hoyt

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

References


Examples

```r
## 2 EXAMPLES:

# EXAMPLE 1: Aggregating effect sizes for a data frame
# (multiple studies at least some of which have multiple
# effect sizes), assuming equal correlations (r=.5) between
# pairs of DVs.
# EXAMPLE 2: Aggregating effect sizes for a single study
# with 3 or more effect sizes when pairs of DVs have
# different correlations.

# LOAD DATA (EXAMPLE DATA FROM HOYT & DEL RE, 2015 SIMULATION):
data(dat.hoyt)

## EXAMPLE 1: dat.hoyt is a data frame with multiple studies identified
## by variable 'id'. Each study has multiple effect sizes based on
## multiple DVs. Correlations between all pairs of DVs are r=.5.

# NOTE: Based on a simulation study by Hoyt & Del Re (2015), it is
# recommended that methods "G01" and "G02" (Gleser and Olkin)
# should aggregate Cohen’s d, without using Hedges & Olkin’s
# recommended bias correction. (Studies providing only a single
# effect size should still be corrected for bias, after aggregation.)
```
# Method "BHHR" should aggregate Hedges' g, after bias correction.

# Option 1: method="BHHR"; Borenstein et al. (2009) procedure. # Use with Hedges' g; can also be used with any other effect # size (e.g., z', LOR).
agg(id=id, es=g, var=vg, cor=.5, 
    method="BHHR", mod=NULL, data=dat.hoyt)

# Option 2: method="G01"; Gleser & Olkin (1994) procedure when 
# d is computed using pooled sd in denominator.
agg(id=id, es=d, var=vd, n.1=n.T, n.2=n.C, cor = .5, 
    method="G01", mod = NULL, data=dat.hoyt)

# Option 3: method="G02"; Gleser & Olkin (1994) procedure when 
# d is computed using sd.2 (typically control group sd) 
# in denominator
agg(id=id, es=d, var=vd, n.1=n.T, n.2=n.C, cor = .5, 
    method="G02", mod = NULL, data=dat.hoyt)

## EXAMPLE 2: Single study comparing T and C group 
## on three DVs: depression, anxiety, and shyness 
## r12=.5; r13=.2; r23=.3

data <- dat.hoyt[20:22,]

# Step 1: Create the correlation matrix, based on r12, r13, and r23:
cors <- matrix(c(1,.5,.2,  
                  .5,1,.3,  
                  .2,.3,1), nrow=3)

# Step 2: Aggregate using agg() function.

# Option 1: method="BHHR"; Borenstein et al. (2009) procedure. # Use with Hedges' g; can also be used with any other effect # size (e.g., z', LOR).
agg(id=id, es=g, var=vg, cor=cors, 
    method="BHHR", mod=NULL, data=data)

# Option 2: method="G01"; Gleser & Olkin (1994) procedure when 
# d is computed using pooled sd in denominator.
agg(id=id, es=d, var=vd, n.1=n.T, n.2=n.C, cor = cors, 
    method="G01", mod = NULL, data=data)

# Option 3: method="G02"; Gleser & Olkin (1994) procedure when
# d is computed using sd.2 (typically control group sd)
# in denominator

agg(id=id, es=d, var=vd, n.1=n.T, n.2=n.C, cor = cors,
   method="G02", mod = NULL, data=data)

## Citation ##
# Hoyt, W. T., & Del Re, A. C. (2013). Comparison of methods for
# aggregating dependent effect sizes in meta-analysis.
# Manuscript submitted for publication.

---

**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 <acdrlre@gmail.com>
ancova_to_d2

References


See Also
d_to_g, mean_to_d, mean_to_d2, t_to_d, f_to_d, p_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

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.

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

Value

Author(s)
AC Del Re & William T. Hoyt
Maintainer: AC Del Re <acdelre@gmail.com>
Correction for Attenuation

Description

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

Usage

atten(g, xx, yy, data)

Arguments

- g: Hedges g (unbiased estimate of d) 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 g corrected for attenuation (g_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

Examples

```r
# 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)
g <- c(.68, .56, .23, .64, .49, -.04, .49, .33, .58, .18, -.11, .27, .26, .40, .49,
       .51, .40, .34, .42, .16)
var.g <- c(.08, .06, .03, .04, .09, .04, .009, .033, .0058, .018, .011, .027, .026, .0040,
         .049, .0051, .040, .034, .0042, .016)
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"

df <- data.frame(id, n, g, var.g, xx, yy)

# Example

atten(g = g, xx = xx, yy = yy, data = df)
```

compute_dgs

**Computes Vector of Standardized Mean Differences**

Description

Adds d & g (standardized mean difference) to a data.frame. Required inputs are: n.1 (sample size of group one), m.1 (raw post-mean value of group one), sd.1 (standard deviation of group one), n.2 (sample size of group two), m.2 (raw post-mean value of group two), sd.2 (standard deviation of group two).

Usage

```r
compute_dgs(n.1, m.1, sd.1, n.2, m.2, sd.2, data, denom = "pooled.sd")
```

Arguments

- **n.1**: sample size of group one.
- **m.1**: raw post-mean value of group one.
- **sd.1**: standard deviation of group one.
- **n.2**: sample size of group two.
- **m.2**: raw post-mean value of group two.
- **sd.2**: standard deviation of group two.
- **data**: data.frame with above values
- **denom**: Value in the denominator to standardize the means by. pooled.sd will pool together both groups in deriving d. control.sd uses the standard deviation of group two (typically the control condition) to calculate d.
compute_ds

Computes Vector of Standardized Mean Differences

Adds d (standardized mean difference) to a data.frame. Required inputs are: n.1 (sample size of group one), m.1 (raw post-mean value of group one), sd.1 (standard deviation of group one), n.2 (sample size of group two), m.2 (raw post-mean value of group two), sd.2 (standard deviation of group two).
compute_ds

Usage
compute_ds(n.1, m.1, sd.1, n.2, m.2, sd.2, data, denom = "pooled.sd")

Arguments
n.1 sample size of group one.
m.1 raw post-mean value of group one.
sd.1 standard deviation of group one.
n.2 sample size of group two.
m.2 raw post-mean value of group two.
sd.2 standard deviation of group two.
data data.frame with values above.
denom Value in the denominator to standardize the means by. pooled.sd will pool together both groups in deriving d. control.sd uses the standard deviation of group two (typically the control condition) to calculate d.

Value
d Standardized mean difference.
var.d Variance of d.
se.d Standard error of d.

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

References

See Also
compute_ds, compute_dgs

Examples
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)
m.1 <- c(0.68,0.56,0.23,0.64,0.49,0.4,0.49,0.53,0.58,1.18,1.1,1.27,0.26,0.40,0.49,0.51,0.40,0.34,0.42,0.66)
m.2 <- c(0.38,0.36,0.23,0.34,0.29,0.4,1.9,0.33,0.28,1.1,1.11,1.27,0.21,0.140,0.149,0.51,0.140,0.134,0.42,0.16)
sd.1 <- c(0.28,0.26,0.23,0.44,0.49,0.34,0.39,0.33,0.58,0.38,0.31,0.27,0.26,0.40,
compute_gs

Converts Vector of Standardized Mean Differences

Description

Adds g (unbiased standardized mean difference) to a data.frame. Required inputs are: n.1 (sample size of group one), sd.1 (standard deviation of group one), n.2 (sample size of group two).

Usage

compute_gs(d, var.d, n.1, n.2, data)

Arguments

d Standardized mean difference (biased).
var.d Variance of d.
n.1 sample size of group one.
n.2 sample size of group two.
data data.frame with standardized mean difference, variance of d, sample size of group one, sample size of group two.

Value

g Unbiased standardized mean difference.
var.g Variance of g.
se.g Standard error of g.

Author(s)

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

References

See Also

compute_ds, compute_dgs

Examples

```r
id <- c(1:20)
n.1 <- c(10, 20, 13, 22, 28, 12, 12, 16, 16, 19, 36, 12, 36, 75, 33, 121, 37, 14, 14, 40, 16, 14, 20)
n.2 <- c(11, 12, 20, 15, 12, 12, 16, 19, 11, 34, 75, 33, 120, 37, 14, 40, 16, 10, 21)
m.1 <- c(0.68, 0.56, 0.23, 0.64, 0.49, 1.49, 0.53, 0.58, 1.18, 0.11, 1.27, 0.26, 0.40, 0.49, 0.51, 0.40, 0.34, 0.42, 0.66)
m.2 <- c(0.38, 0.36, 0.23, 0.34, 0.29, 0.4, 1.9, 0.33, 0.39, 0.33, 28, 0.11, 27, 0.21, 1.40, 1.49, 0.51, 1.40, 1.34, 0.42, 0.16)
sd.1 <- c(0.28, 0.26, 0.23, 0.44, 0.49, 0.34, 0.39, 0.33, 0.58, 0.38, 0.31, 0.27, 0.26, 0.40, 0.49, 0.51, 1.40, 1.34, 0.42, 0.46)
sd.2 <- c(0.28, 0.26, 0.23, 0.44, 0.49, 0.44, 0.39, 0.33, 0.58, 0.38, 0.51, 0.27, 0.26, 0.40, 0.49, 0.51, 1.40, 1.34, 1.42, 0.36)
mod1 <- c(1, 2, 3, 4, 1, 2, 8, 7, 5, 3, 9, 7, 5, 4, 3, 2, 3, 5, 7, 1)
mod2 <- factor(c(rep(1, 2, 3, 4), 5))
dfs <- data.frame(id, n.1, m.1, sd.1, n.2, m.2, sd.2, mod1, mod2)

# Example

# first compute d
dfs2 <- compute_ds(n.1, m.1, sd.1, n.2, m.2, sd.2, data = dfs)

# now, compute g
compute_gs(d, var.d, n.1, n.2, dfs2)
```

**Description**

Data from Table 15.3 in The Handbook for Research Synthesis and Meta-Analysis (Cooper et al., 2009)

**dat.cooper15.3**

Data from Table A2 in The Handbook for Research Synthesis and Meta-Analysis (Cooper et al., 2009)

**dat.cooperA2**

Data from Table A2 in The Handbook for Research Synthesis and Meta-Analysis (Cooper et al., 2009)
dat.hoyt  
*Subset of simulated data to demonstrate aggregation for dependent effect sizes*

**Description**  
Subset of simulated data to demonstrate aggregation for dependent effect sizes. This data comes from: Hoyt, W. T., & Del Re, A. C. (2013). Comparison of methods for aggregating dependent effect sizes in meta-analysis. Manuscript submitted for publication.

---

dat.sim.es  
*Subset of simulated psychotherapy treatment studies (k=8) with dependent effect sizes*

**Description**  
This data set includes effect sizes for treatment vs control groups for a random subset of 8 simulated psychotherapy treatment studies (total population k = 1000). The known population standardized mean difference for outcome one is \( g = 0.50 \) and for outcome two \( g = 0.80 \). The data set also includes two correlated study-level variables (i.e., moderators): treatment duration (dose) and average participant distress (stress).

This data accompanies a tutorial for meta-analysis:  

---

dat.sim.final  
*Final aggregated dataset of simulated psychotherapy treatment studies (k=8)*

**Description**  
This data set includes aggregated effect sizes for treatment vs control groups for a random subset of 8 simulated psychotherapy treatment studies (total population k = 1000). The known population standardized mean difference for outcome one is \( g = 0.50 \) and for outcome two \( g = 0.80 \). The data set also includes two correlated study-level variables (i.e., moderators): treatment duration (dose) and average participant distress (stress).

This data accompanies a tutorial for meta-analysis:  

### dat.sim.raw

**Subset of simulated psychotherapy treatment studies (k=8) with means and SD**

**Description**

This data set includes means and standard deviations for treatment and control groups for a subset of k = 8 simulated psychotherapy treatment studies from a population of k = 1000 (see dat.sim1 and dat.sim2 for the k = 1000 studies for outcome 1 and 2, respectfully). Although effect sizes are not calculated in this dataset, the known population standardized mean difference for outcome one is d=0.50 and for outcome two g=0.80. The data set also includes two correlated study-level variables (i.e., moderators): treatment duration (dose) and average participant distress (stress).

This data accompanies a tutorial for meta-analysis:


---

### dat.sim1

**Simulated psychotherapy treatment studies for 'outcome one’**

**Description**

This data set includes 1000 simulated psychotherapy treatment studies. The population standardized mean difference for outcome one is d=0.50. The data set also includes two correlated study-level variables (i.e., moderators): treatment duration (dose) and average participant distress (stress).

This data accompanies a tutorial for meta-analysis:


---

### dat.sim2

**Simulated psychotherapy treatment studies for 'outcome two’**

**Description**

This data set includes 1000 simulated psychotherapy treatment studies. The population standardized mean difference for outcome two is d=0.80. The data set also includes two correlated study-level variables (i.e., moderators): treatment duration (dose) and average participant distress (stress).

This data accompanies a tutorial for meta-analysis:

**d_to_g**  

*Standardized Mean Difference (d) Statistic to Unbiased Standardized Mean Difference (g)*

---

**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**

```r
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**

f.ancova_to_d

**ANCOVA F-statistic to Standardized Mean Difference (d)**

**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**


**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

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


See Also

d_to_g, mean_to_d, mean_to_d2, t_to_d, f_to_d, p_to_d, p_to_d1, p_to_d2, ancova_to_d, ancova_to_d1, ancova_to_d2, tt_ancova_to_d, f_ancova_to_d, r_to_d, p_ancova_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

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

References

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
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
```r
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 = r0. Note that a one sided test (H1: r > r0) 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:
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:

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

Author(s)

Matthias Gamer

References


Examples

```r
# 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:

```r
# 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  8  
#  3  2 12  9  8
# the data will need to be reshaped to be processed by the
# icc function:
```

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

# icc function (created by Matthias Gamer for the 'irr' package)
icc(cbind(wide$Code.1, wide$Code.2), type = "consistency")
```

---

### Kappa

#### Description

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

#### Usage

```r
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>
lor_to_d

Examples

# sample data

```r
study <- c(1,1,2,2,3) # 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 1 8 10 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.
Description

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

Usage

macat(g, var, mod, data, method = "random")

Arguments

g Hedges g (unbiased estimate of d) 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.

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.

I2
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, Qb + Qw != Q in the random effects output.

Qw
Q-within (or error). Measure of within-group heterogeneity.

Qw.df
Degrees of freedom for Q-within.

Qw.p
Q-within p-value (for homogeneity).

Qb
Q-between (or model). Measure of model fit.

Qb.df
Degrees of freedom for Q-between.

Qb.p
Q-between p-value (for homogeneity). Qb and Qb.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


See Also

plotcat, wd
Examples

```r
id <- c(1:20)
n.1 <- c(10, 20, 13, 22, 28, 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(0.68, 0.56, 0.23, 0.64, -0.04, 1.49, 1.33, 0.58, 1.18, -0.11, 1.27, 0.26, 0.40, 0.49, 0.51, 0.40, 0.34, 0.42, 1.16)
var.g <- c(0.08, 0.06, 0.03, 0.04, 0.09, 0.04, 0.009, 0.033, 0.0058, 0.018, 0.011, 0.027, 0.026, 0.0040, 0.049, 0.0051, 0.040, 0.034, 0.0042, 0.016)
mod <- factor(c(rep(c(1, 2, 3), 5)))
df <- data.frame(id, n.1, n.2, g, var.g, mod)

# Example

# Random effects
macat(g = g, var = var.g, mod = mod, data = df, 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**

```r
macatC(x1, x2, g, var, mod, data, method = "random", type = "post.hoc")
```

**Arguments**

- `x1` One level of categorical moderator.
- `x2` Comparison level of same categorical moderator.
- `g` Hedges g (unbiased estimate of d) effect size.
- `var` Variance of g.
- `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.
- `data` `data.frame` with values above.

**Details**

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

diff Mean difference between the two levels.
var.diff Variance of diff.
p Significance level.

Author(s)

AC Del Re & William T. Hoyt

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

References


See Also

macat,

Examples

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, 25, 12, 12, 36, 19, 11, 34, 75, 33, 120, 37, 14, 40, 16, 10, 21)
g <- c(88, .56, .23, .64, -.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, .0033, .0058, .018, .011, .027, .026, .0040, .049, .0051, .040, .034, .0042, .016)
mod<factor(c(rep(c(1, 2, 3), 5)))
df<--data.frame(id, n.1,n.2, g, var.g,mod)

# Example
macatC(1, 2, g=g, var=var.g, mod=mod, data=df, method= "random",
type= "post.hoc")
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 http://CRAN.R-project.org/package=metafor for details or for more advanced functionality with the rma() function.

Usage

mareg(formula, var, data, method = "REML", subset, digits = 3, ...)

Arguments

- **formula**: This is a formula based function, similar to other functions in R (e.g., lm), where the criterion variable (e.g., Hedges g in this case) is dependent on ("~") the predictor variables (e.g., moderators). The formula for two moderators would take this form: mareg(g ~ mod1 + mod2, var.g, data), where g is the criterion variable predicted by mod1 and mod2. The variance (var) of each g is var.g in this case.
- **var**: Variance of g.
- **data**: Aggregated data.frame (see agg function for setting up the dataset for these analyses) with id, g (unbiased standardized mean difference), var.g (variance of g) 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 metafor package manual ("rma" function).
- **subset**: an optional vector specifying a subset of observations to be used in the fitting process.
- **digits**: Number of digits to output. Default is 3.
- **...**: Additional arguments to be passed to rma().

Details


Value

- **estimate**: Meta-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-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


See Also

wd, plotcon

Examples

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

# Sample data
data(dat.sim.final)

# Examples

# OMNIBUS
m0 <- mareg(es~1, var=var, data=dat.sim.final)
summary(m0)

# META-REGRESSION
m1 <- mareg(es~dose, var=var, data=dat.sim.final)
summary(m1)  # SINGLE MODERATOR

m2 <- mareg(es~stress, var=var, data=dat.sim.final)
summary(m2)  # SINGLE MODERATOR

m3 <- mareg(es~dose + stress, var=var, data=dat.sim.final)
summary(m3)  # MULTIPLE MODERATOR
**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**

**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`
**Description**

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

**Usage**

```r
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**


**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`
or_to_d

Odds Ratio to Standardized Mean Difference (d)

Description

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

Usage

or_to_d(or)

Arguments

or        Odds ratio.

Value

d        Standardized mean difference (d).

Author(s)

AC Del Re & William T. Hoyt

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

References


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
**Description**

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

**Usage**

```r
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**


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

Description

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

Usage

```r
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


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 boxplot graphic for each level of the specified moderator.

**Usage**

`plotcat(g, var, mod, data, modname=NULL, title=NULL, ...)`

**Arguments**

- `g`: Hedges g (unbiased estimate of d) effect size.
- `var`: Variance of g.
- `mod`: Categorical moderator variable used for moderator analysis.
- `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**


**See Also**

`macat`, `plotcon`
Examples

```r
id <- c(1, 19)
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(rep(c(1, 1, 2, 3), 5))
df <- data.frame(id, n.1, n.2, g, var.g, mod)

# Example

## Not run: plotcat(g = g, var = var.g, mod = mod, data = df, 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

```r
plotcon(g, var, mod, data, method = "random", modname = NULL, 
title = NULL, ...)
```

Arguments

- **g**: Hedges g (unbiased estimate of d) effect size.
- **var**: Variance of g.
- **mod**: Categorical moderator variable used for moderator analysis.
- **method**: Default is random (Restricted-Maximal Likelihood), which is the standard random effects method. 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

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.
**PubBias**

**Author(s)**

AC Del Re & William T. Hoyt

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

**References**


**See Also**

`mareg, plotcat`

**Examples**

```r
# SAMPLE DATA
MA2 <- read.table(textConnection("id es1 var1 n.1 n.2 mod1 mod2
1 1 0.5695938 0.04906967 26 30 a 20
2 2 0.4123667 0.04362541 28 34 b 30
3 3 0.4884333 0.04458363 34 28 a 25
4 4 0.5014756 0.04186354 37 29 b 35
5 5 0.5540745 0.0439382 31 32 b 40
6 6 0.5695938 0.04906967 26 30 a 20
7 7 0.4123667 0.04362541 28 34 b 30
8 8 0.4884333 0.04458363 34 28 a 25
9 9 0.5014756 0.04186354 37 29 b 35
10 10 0.5540745 0.0439382 31 32 b 40"))
```

```r
# EXAMPLE
plotcon(es1, var1, mod2, data=MA2, method= "fixed", modname="NULL", title="NULL")
```

---

**PubBias**

**Assess for Publication Bias**

**Description**

Assess for publication bias in the meta-analytic data

**Usage**

`PubBias(data)`

**Arguments**

- `data` data.frame having been analyzed by the `weights` function with id and z.score (standardized z-value).
**Value**

- **k** Number of studies.
- **Z** Overall z-value for data set.
- **K0** Number of studies needed to include with effect size = 0 (null) in order for the p > .05 (null hypothesis retained).
- **K.per** Number of missing studies for every observed study for the overall effect to be nullified.

**Author(s)**

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

**References**


**See Also**

weights

---

**p_to_d1**

*One-tailed p-value to Standardized Mean Difference (d)*

**Description**

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

**Usage**

```
p_to_d1(p, n.1, n.2)
```

**Arguments**

- **p** One-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.
**p_to_d2**

**Author(s)**

AC Del Re & William T. Hoyt

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

**References**


**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**

```r
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


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

r2  

---

Explained Variance

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(11,22,10,20,25,12,12,36,19,11,34,53,33,120,37,14,40,16,10,21)
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(1,2,3),5)))
mods2<-'c(rep(1:5,4))
df<-'data.frame(id, n.1,n.2, g, var.g,mod, mods2)
# Examples

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

r2(temp)
```

---

**robustSE**

*Robust standard error*

---

**Description**

When the correlation between dependent effect sizes are unknown, one approach is to conduct the meta-analysis by assuming that the effect sizes are independent. Then, Hedges et al. (2010) robust standard error procedure can be calculated to adjust for dependence.

**Usage**

```r
robustSE(model, cluster=NULL, CI=.95, digits=3)
```

**Arguments**

- `model`: omnibus or moderator model object fitted from `mareg()` function.
- `cluster`: Name of variable where the dependencies are present. This will typically be the variable for `study id` where `length(unique(study_id))>1`.
- `CI`: Confidence interval. Defaults to .95.
- `digits`: Number of digits to output. Defaults to 3.

**Value**

- `estimate`: Meta-regression coefficient estimate.
- `se`: Adjusted Standard error of the estimate coefficient.
- `t`: t-value.
- `ci.l`: Adjusted Lower 95% confidence interval.
- `ci.u`: Adjusted Upper 95% confidence interval.
- `p`: p-value.

**Author(s)**

Mike Cheung with modifications by AC Del Re

**References**


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).
r_from_d

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).

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

Author(s)

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

References


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

**Arguments**

- **d**: Mean difference statistic (d) reported in primary study.
- **n.1**: sample size of group one reported in primary study.
- **n.2**: sample size of group two reported in primary study.
- **var.d**: 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**


**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`
Description

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

Usage

\[ r_{\text{from}\_t}(t, n) \]

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


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, t_toancova_d1, 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.
Correlation (r) to Standardized Mean Difference (d)

Description

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

Usage

```r
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


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
tt.ancova_to_d

\textit{t-test Value from ANCOVA to Standardized Mean Difference (d)}

\textbf{Description}

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

\textbf{Usage}

\texttt{tt.ancova_to_d(t, n.1, n.2, R, q)}

\textbf{Arguments}

t \hspace{1em} t-test value reported in primary study.

n.1 \hspace{1em} Treatment group sample size.

n.2 \hspace{1em} Comparison group sample size.

R \hspace{1em} Covariate outcome correlation or multiple correlation.

q \hspace{1em} number of covariates.

\textbf{Value}

d \hspace{1em} Standardized mean difference (d)

\texttt{var_d} \hspace{1em} Variance of d

\textbf{Author(s)}

AC Del Re & William T. Hoyt

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

\textbf{References}


\textbf{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
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


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
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


Author(s)

AC Del Re & William T. Hoyt

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

References


See Also

omni, mareg, macat

Examples

```r
# 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,.49,.133,.58,1.18,-.11,.27,.26,.40,.49,.51,.40,.34,.42,.16)
var.g<-c(.08,.06,.03,.04,.09,.04,.009,.009,0058,.018,.011,.027,.026,.0040,
```
wgts

Weights added to Meta Data

Description

Adds weights to the meta-analysis data set.

Usage

wgts(g, var.g, data)

Arguments

g Hedges g (unbiased standardized mean difference estimate).
var.g Variance of g.
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>
Index

*Topic **aggregation**
  agg, 7

*Topic **aplot**
  plotcat, 39
  plotcon, 40

*Topic **arith**
  ancova_to_d1, 10
  ancova_to_d2, 11
  d_to_g, 20
  f.ancova_to_d, 21
  f_to_d, 23
  fail_to_d, 22
  lor_to_d, 27
  mean_to_d, 34
  mean_to_d2, 35
  or_to_d, 36
  p.ancova_to_d1, 37
  p.ancova_to_d2, 38
  p_to_d1, 42
  p_to_d2, 43
  r_from_chi, 46
  r_from_d, 47
  r_from_d1, 48
  r_from_t, 49
  r_to_d, 50
  t_to_d, 52
  tt.ancova_to_d, 51

*Topic **data**
  atten, 12
  compute_dgs, 13
  compute_ds, 14
  compute_gs, 16
  dat.cooper15.3, 17
  dat.cooper2, 17
  dat.hoyt, 18
  dat.sim.es, 18
  dat.sim.final, 18
  dat.sim.raw, 19
  dat.sim1, 19
  dat.sim2, 19
  dat.sim, 19

  agg, 7
  ancova_to_d1, 10, 11, 12, 21–23, 28, 34–38, 43, 44, 47–52
  ancova_to_d2, 11, 12, 21–23, 28, 34–38, 43, 44, 47–52
  atten, 12

  compute_dgs, 13, 15, 17
  compute_ds, 14, 14, 15, 17
  compute_gs, 14, 16

  d_to_g, 11, 12, 20, 21–23, 28, 34–38, 43, 44, 47–52
  dat.cooper15.3, 17
  dat.cooper2, 17
  dat.hoyt, 18
  dat.sim.es, 18
  dat.sim.final, 18
  dat.sim.raw, 19
  dat.sim1, 19
  dat.sim2, 19

  f.ancova_to_d, 11, 12, 21, 22, 23, 28, 34–38, 43, 44, 47–52
  f_to_d, 11, 12, 21, 22, 23, 28, 34–38, 43, 44, 47–52
  fail_to_d, 22

  icc, 24

  PubBias, 41
  wgts, 54

*Topic **models**
  macat, 28
  macatC, 30

*Topic **package**
  Mad-package, 2

*Topic **word**
  r2, 44
  wd, 53

agg, 7
ancova_to_d1, 10, 11, 12, 21–23, 28, 34–38, 43, 44, 47–52
ancova_to_d2, 11, 12, 21–23, 28, 34–38, 43, 44, 47–52
atten, 12
compute_dgs, 13, 15, 17
compute_ds, 14, 14, 15, 17
compute_gs, 14, 16
d_to_g, 11, 12, 20, 21–23, 28, 34–38, 43, 44, 47–52
dat.cooper15.3, 17
dat.cooper2, 17
dat.hoyt, 18
dat.sim.es, 18
dat.sim.final, 18
dat.sim.raw, 19
dat.sim1, 19
dat.sim2, 19
f.ancova_to_d, 11, 12, 21, 22, 23, 28, 34–38, 43, 44, 47–52
f_to_d, 11, 12, 21, 22, 23, 28, 34–38, 43, 44, 47–52
fail_to_d, 22
icc, 24
Kappa, 26
lor_to_d, 11, 12, 21–23, 27, 34–38, 43, 44, 47–52
macat, 28, 31, 39, 53
macatC, 30
MAd (MAd-package), 2
MAd-package, 2
mareg, 32, 41, 46, 53
mean_to_d, 11, 12, 21–23, 28, 34, 35–38, 43, 44, 47–52
mean_to_d2, 11, 12, 21–23, 28, 34, 35, 36, 37, 43, 44, 47–52
omni, 53
or_to_d, 36
p.ancova_to_d1, 11, 12, 21–23, 28, 34–36, 37, 38, 43, 44, 47–52
p.ancova_to_d2, 11, 12, 21–23, 28, 34–38, 38, 43, 44, 47–52
p_to_d1, 11, 12, 21–23, 28, 34–38, 42, 44, 47–52
p_to_d2, 11, 12, 21–23, 28, 34–38, 43, 43, 47–52
plotcat, 29, 39, 41
plotcon, 33, 39, 40
prop_to_d, 11, 12, 21–23, 28, 34, 35, 37, 38, 43, 44, 47–52
prop_to_or, 11, 12, 21–23, 28, 34–38, 43, 44, 47–52
PubBias, 41
r2, 44
r_from_chi, 11, 12, 21–23, 28, 34–38, 43, 44, 46, 47–52
r_from_d, 11, 12, 21–23, 28, 34–38, 43, 44, 47, 48–52
r_from_d1, 11, 12, 21–23, 28, 34–38, 43, 44, 47, 48, 49–52
r_from_t, 11, 12, 21–23, 28, 34–38, 43, 44, 47, 48, 49, 50–52
r_to_d, 11, 12, 21–23, 28, 34–38, 43, 44, 47–49, 50, 51, 52
robustSE, 45
t_to_d, 11, 12, 21–23, 28, 34–38, 43, 44, 47–51, 52

tt.ancova_to_d, 11, 12, 21–23, 28, 34–38, 43, 44, 47–50, 51, 52
wd, 29, 33, 53
weights, 42
wgts, 54