Package ‘metadat’

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Description A collection of meta-analysis datasets for teaching purposes, illustrating/testing meta-
analytic methods, and validating published analyses.
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ByteCompile TRUE
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metadat-package

Description

The `metadat` package contains a large collection of meta-analysis datasets. These datasets are useful for teaching purposes, illustrating/testing meta-analytic methods, and validating published analyses.

Browsing and Searching for Datasets

A listing of all datasets in the package can be obtained with `help(package=metadat)`. Each dataset is also tagged with one or multiple concept terms. These concept terms refer to various aspects of a dataset, such as the field/topic of research, the outcome measure used for the analysis, the model(s) used for analyzing the data, and the methods/concepts that can be illustrated with the dataset. The `datsearch` function can be used to search among the existing datasets in the package based on their concept terms or based on a full-text search of their corresponding help files.

You can also read the documentation online at [https://wviechtb.github.io/metadat/](https://wviechtb.github.io/metadat/) (where the output from the example analyses corresponding to each dataset is provided).
Contributing New Datasets

We welcome contributions of new datasets to the package. For each dataset, there must be a citable reference, ideally in a peer-reviewed journal or publication. The general workflow for contributing a new dataset is as follows:

• Install the metadat package in R in the usual manner (i.e., install.packages("metadat")).

• If you are familiar with Git/GitHub and making pull requests, fork the package repository. Otherwise, download the source version of the package from GitHub and unzip the file to some directory on your computer.

• Place the raw data (in a non-binary format) in the data-raw directory. The file should be named dat.<author><year>.<ext>, where <author> is the last name of the first author of the publication from which the data come, <year> is the publication year, and <ext> is the file extension (e.g., .txt, .csv).

• Place a corresponding R script in the data-raw directory named dat.<author><year>.r that reads in the data, possibly does some data cleaning/processing, and then saves the dataset to the data directory (using save), with name dat.<author><year>.rda.

• Start R, load the metadat package (i.e., library(metadat)), and then run the prep_dat function (either set the working directory to the location of the source package beforehand or use the pkgdir argument of the prep_dat function to specify the source package location).

• For a new dataset, this should create a boilerplate template for a corresponding help file in the man directory, named dat.<author><year>.Rd. Edit the help file, adding the title and a short description of the dataset in general, a description of each variable in the dataset, further details on the dataset (e.g., the field of research, how the data was collected, the purpose of the dataset / what it was used for, the effect size or outcome measure used in the analysis, the types of analyses/models that can be illustrated with the dataset), a reference for the source of the dataset, one or multiple concept terms, the name and email address of the contributor of the dataset, and (optionally) example code to illustrate the analysis of the dataset.

• Either make a pull request (if you are familiar with this workflow) or zip up the dat.<author><year>.<ext>, dat.<author><year>.r, dat.<author><year>.rda, and dat.<author><year>.Rd files and open up a new issue at GitHub, attaching the zip file.

• If the above makes no sense to you, you can also email one of the package authors with a cleaned, raw data file in .txt or .csv format, along with a meta-data file (format doesn’t matter) that includes the information described above.

Citing the Package

If you use these data, please cite both the metadat package (see citation("metadat") for the reference) and the original source of the data as given under the help file of a dataset.

Bug/Error Reports

If you think you have found an error in an existing dataset or a bug in the package in general, please go to https://github.com/wviechtb/metadat/issues and open up a new issue.
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**dat.aloe2013**

*Studies on the Association Between Supervision Quality and Various Outcomes in Social, Mental Health, and Child Welfare Workers*

**Description**

Results from 5 studies examining the association between various measures of supervision quality and various work-related outcomes in social, mental health, and child welfare workers.

**Usage**

`dat.aloe2013`

**Format**

The data frame contains the following columns:

- `study`: character: study author(s) and year
- `n`: integer: sample size
- `tval`: numeric: t-statistic for the test of the association/predictor
- `preds`: integer: number of predictors included in the regression model
- `R2`: numeric: the coefficient of determination (i.e., R-squared value) of the regression model

**Details**

The dataset is based on studies that used regression models to examine the association between some measure of perceived supervision quality (e.g., the quality of the relationship with one’s supervisor) and some work-related outcome (e.g., job satisfaction) in social, mental health, and child welfare workers. The dataset was extracted from Aloe and Thompson (2013), which in turn is a subset of the studies included in the meta-analysis by Mor Barak et al. (2009).

The dataset can be used to illustrate the meta-analysis of regression models, using measures such as the (semi-)partial correlation coefficient. For this, the t-statistic from the regression model for the association (i.e., predictor) of interest was extracted from each regression model (tval), as well as the sample size (n), the number of predictors included in the regression model (preds), and the coefficient of determination (i.e., R-squared value) of the regression model (R2). Based on this information, the (semi-)partial correlation coefficient can be computed for each study, as well as its corresponding sampling variance. These values can then be meta-analyzed using standard methods.
Concepts

social work, (semi-)partial correlations, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.aloe2013
dat

### Not run:

### load metafor package
suppressPackageStartupMessages(library(metafor))

### compute the partial correlation coefficients and corresponding sampling variances
dat <- escalc(measure="PCOR", ti=tval, ni=n, mi=preds, data=dat)
dat

### random-effects model
res <- rma(yi, vi, data=dat)
res

### mixed-effects meta-regression model examining the relationship between the partial correlation coefficients and the number of predictors included in the models
res <- rma(yi, vi, mods = ~ preds, data=dat)
res

### compute the r-to-z transformed partial correlation coefficients and their variances
dat <- escalc(measure="ZPCOR", ti=tval, ni=n, mi=preds, data=dat)
dat

### random-effects model
res <- rma(yi, vi, data=dat)
res

### back-transformation to the partial correlation scale
predict(res, transf=transf.ztor)
```
### compute the semi-partial correlation coefficients and their variances
```r
dat <- escalc(measure="SPCOR", ti=tval, ni=n, mi=preds, r2i=R2, data=dat)
dat
```
### random-effects model
```r
res <- rma(yi, vi, data=dat)
res

# End(Not run)
```

---

**dat.anand1999**

*Studies on the Effectiveness of Oral Anticoagulants in Patients with Coronary Artery Disease*

---

**Description**

Results from 34 trials examining the effectiveness of oral anticoagulants in patients with coronary artery disease.

**Usage**

dat.anand1999

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>author(s) or trial name</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>intensity</td>
<td>character</td>
<td>intensity of anticoagulation (low, medium, or high)</td>
</tr>
<tr>
<td>asp.t</td>
<td>numeric</td>
<td>concomitant use of aspirin in the treatment group (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>asp.c</td>
<td>numeric</td>
<td>concomitant use of aspirin in the control group (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>ai</td>
<td>numeric</td>
<td>number of deaths in the treatment group</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of patients in the treatment group</td>
</tr>
<tr>
<td>ci</td>
<td>numeric</td>
<td>number of deaths in the control group</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of patients in the control group</td>
</tr>
</tbody>
</table>

**Details**

The dataset includes the results from 34 randomized clinical trials that examined the effectiveness of oral anticoagulants in patients with coronary artery disease. The results given here are focused on the total mortality in the treatment versus control groups.

**Concepts**

medicine, cardiology, odds ratios, Mantel-Haenszel method
Note

Strictly speaking, there are only 31 trials, since Breddin et al. (1980) and ATACS (1990) are multi-arm trials.

According to a correction, dat.anand1999$ci[29] should be 1. But then dat.anand1999$ci[21] would also have to be 1 (if these data indeed refer to the same control group). This appears contradictory, so this correction was not made.

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.anand1999
dat

## Not run:
### load metafor package
library(metafor)

### High-Intensity OA vs Control
rma.mh(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat,
       subset=(intensity=="high" & asp.t==0 & asp.c==0), digits=2)

### High- or Moderate-Intensity OA vs Aspirin
rma.mh(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat,
       subset=(intensity %in% c("high","moderate") & asp.t==0 & asp.c==1), digits=2)

### Moderate-Intensity OA vs Control
rma.mh(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat,
       subset=(intensity=="moderate" & asp.t==0 & asp.c==0), digits=2)

### High- or Moderate-Intensity OA and Aspirin vs Aspirin
rma.mh(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat,
       subset=(intensity %in% c("high","moderate") & asp.t==1 & asp.c==1), digits=2)

### Low-Intensity OA and Aspirin vs Aspirin
rma.mh(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat,
       subset=(intensity=="low" & asp.t==1 & asp.c==1), digits=2)

## End(Not run)
```
Description

Results from 17 studies on the association between recidivism and mental health in delinquent juveniles.

Usage
dat.assink2016

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study id number</td>
</tr>
<tr>
<td>esid</td>
<td>numeric</td>
<td>effect size within study id number</td>
</tr>
<tr>
<td>id</td>
<td>numeric</td>
<td>row id number</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>standardized mean difference</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
<tr>
<td>pubstatus</td>
<td>numeric</td>
<td>published study (0 = no; 1 = yes)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year of the study (approximately mean centered)</td>
</tr>
<tr>
<td>deltype</td>
<td>character</td>
<td>type of delinquent behavior in which juveniles could have recidivated (either general, overt, or covert)</td>
</tr>
</tbody>
</table>

Details

The studies included in this dataset (which is a subset of the data used in Assink et al., 2015) compared the difference in recidivism between delinquent juveniles with a mental health disorder and a comparison group of juveniles without a mental health disorder. Since studies differed in the way recidivism was defined and assessed, results are given in terms of standardized mean differences, with positive values indicating a higher prevalence of recidivism in the group of juveniles with a mental health disorder.

Multiple effect size estimates could be extracted from most studies (e.g., for different delinquent behaviors in which juveniles could have recidivated), necessitating the use of appropriate models/methods for the analysis. Assink and Wibbelink (2016) illustrate the use of multilevel meta-analysis models for this purpose.

Concepts

psychology, criminology, standardized mean differences, multilevel models, cluster-robust inference

Note

The year variable is not constant within study 3, as this study refers to two different publications using the same data.
### Examples

```r
### copy data into 'dat' and examine data
dat <- dat.assink2016
head(dat, 9)

## Not run:
### load metafor package
library(metafor)
### fit multilevel model
res <- rma.mv(yi, vi, random = ~ 1 | study/esid, data=dat)
res

### use cluster-robust inference methods
robust(res, cluster=study)

### LRTs for the variance components
res0 <- rma.mv(yi, vi, random = ~ 1 | study/esid, data=dat, sigma2=c(0,NA))
anova(res0, res)
res0 <- rma.mv(yi, vi, random = ~ 1 | study/esid, data=dat, sigma2=c(NA,0))
anova(res0, res)

### examine some potential moderators via meta-regression
rma.mv(yi, vi, mods = ~ pubstatus, random = ~ 1 | study/esid, data=dat)
rma.mv(yi, vi, mods = ~ year, random = ~ 1 | study/esid, data=dat)
dat$deltype <- relevel(factor(dat$deltype), ref="general")
rma.mv(yi, vi, mods = ~ deltype, random = ~ 1 | study/esid, data=dat)
rma.mv(yi, vi, mods = ~ year + deltype, random = ~ 1 | study/esid, data=dat)

### assume that the effect sizes within studies are correlated with rho=0.6
V <- vcalc(vi, cluster=study, obs=esid, data=dat, rho=0.6)
round(V[dat$study %in% c(1,2), dat$study %in% c(1,2)], 4)

### fit multilevel model using this approximate V matrix
res <- rma.mv(yi, V, random = ~ 1 | study/esid, data=dat)
res
```
### use cluster-robust inference methods
robust(res, cluster=study)

## End(Not run)

dat.axfors2021

**Mortality Outcomes with Hydroxychloroquine and Chloroquine in COVID-19 from an International Collaborative Meta-Analysis of Randomized Trials**

**Description**

Results from 33 trials examining the effectiveness of hydroxychloroquine or chloroquine in patients with COVID-19.

**Usage**

dat.axfors2021

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Variable</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>character</td>
<td>registry number</td>
</tr>
<tr>
<td>acronym</td>
<td>character</td>
<td>shortened registry number</td>
</tr>
<tr>
<td>patient_setting</td>
<td>character</td>
<td>patient setting</td>
</tr>
<tr>
<td>blinding_exact</td>
<td>character</td>
<td>study blinding</td>
</tr>
<tr>
<td>high_dose</td>
<td>character</td>
<td>high or low dose of medication</td>
</tr>
<tr>
<td>Published</td>
<td>character</td>
<td>publication status</td>
</tr>
<tr>
<td>hcq_cq</td>
<td>character</td>
<td>medication type (hcq = hydroxychloroquine or cq = chloroquine)</td>
</tr>
<tr>
<td>hcq_arm_event</td>
<td>numeric</td>
<td>number of deaths in the treatment group</td>
</tr>
<tr>
<td>hcq_arm_total</td>
<td>numeric</td>
<td>number of patients in the treatment group</td>
</tr>
<tr>
<td>control_arm_event</td>
<td>numeric</td>
<td>number of deaths in the control group</td>
</tr>
<tr>
<td>control_arm_total</td>
<td>numeric</td>
<td>number of patients in the control group</td>
</tr>
<tr>
<td>Control</td>
<td>character</td>
<td>control group type (Standard of Care or Placebo)</td>
</tr>
</tbody>
</table>

**Details**

The dataset includes the results from 33 published and unpublished randomized clinical trials that examined the effectiveness of hydroxychloroquine or chloroquine in patients with COVID-19. The results given here are focused on the total mortality in the treatment versus control groups.

**Concepts**

medicine, covid-19, odds ratios
Author(s)

W. Kyle Hamilton <whamilton@ucmerced.edu> https://kylehamilton.com

Source


References


Examples

# copy data into ‘dat’ and examine data
dat <- dat.axfors2021
dat

## Not run:

# load metafor package
library(metafor)

# calculate log odds ratios and corresponding sampling variances
dat <- escalc(measure="OR", ai=hcq_arm_event, n1i=hcq_arm_total, ci=control_arm_event, n2i=control_arm_total, data=dat)

# meta-analysis Hydroxychloroquine
res_hcq <- rma(yi, vi, subset=(hcq_cq=="hcq"), slab = id, data=dat)
print(res_hcq, digits=2)

# meta-analysis Chloroquine
res_cq <- rma(yi, vi, subset=(hcq_cq=="cq"), slab = id, data=dat)
print(res_cq, digits=2)

## End(Not run)
Description

Results from 77 papers with 678 effects evaluating associations among measures of situation awareness and task performance.

Usage
dat.bakdash2021

Format

The data frame contains the following columns:

- **Author** character  
  paper author(s)
- **Year** integer  
  year of paper publication
- **Title** character  
  title of paper
- **DOI** character  
  digital object identifier (DOI)
- **DTIC.link** character  
  permanent link for Defense Technical Information Collection (DITC) reports; see: https://www.dtic.mil
- **SA.measure.type** character  
  type of SA measure
- **Sample.size** integer  
  reported sample size
- **Sample.size.stats** integer  
  reported sample size based on reported statistics (this reflects excluded participants)
- **es.z** numeric  
  z-transformed correlation coefficient; includes ghost results (disclosed and undisclosed non-significant effects not reported in detail)
- **vi.z** numeric  
  variance for z-transformed correlation (calculated using Sample.size.stats, not Sample.size)
- **SampleID** character  
  unique identifier for each experiment/study
- **Outcome** integer  
  unique value for each effect size

Details

The dataset contains behavioral experiments from 77 papers/79 studies with a total of 678 effects, evaluating associations among measures of situation awareness (“knowing what is going on”) and task performance. Examples of situation awareness include knowledge of current vehicle speed in a simulated driving task and location and heading of aircraft in a simulated air traffic control task. Corresponding examples of task performance include “the number of collisions in a simulated driving task” and “subject matter expert rating of conflict management in a simulated air control task” (Bakdash et al. 2021a, p. 2). This dataset and the ‘Examples’ are a highly simplified version of the data and code in Bakdash et al. (2021b; 2021c). The journal article by Bakdash et al. (2021a) describes the systematic review and meta-analysis in detail.

This dataset is used to illustrate multilevel multivariate meta-analytic models for the overall pooled effect and pooled effects by situation awareness measure. We also adjust meta-analytic models using cluster-robust variance estimation / cluster-robust inference with the robust function in metafor. Results are shown graphically in a customized forest plot with a prediction interval (estimated plausible range of individual effects). Last, we create a table summarizing the estimated meta-analytic heterogeneity parameters.

The meta-analytic results show most pooled effect sizes in the positive medium range or less. There was also substantial meta-analytic heterogeneity (estimated systematic variance in true effects), nearing the magnitude of the overall pooled effect. We interpret the meta-analytic results as situation awareness typically having limited validity for task performance (i.e., good situation awareness does not tend to have strong probabilistic links with good performance and vice-versa). More formally, measures of situation awareness do not generally and meaningfully capture cognitive processes and
other relevant factors underlying task performance.

**Run-Time:**
The code run-time can be greatly sped-up using a linear algebra library with R that makes use of multiple CPU cores. See: https://www.metafor-project.org/doku.php/tips:speeding_up_model_fitting. To measure the run-time, uncomment these three lines: `start.time <- Sys.time()`, `end.time <- Sys.time()`, and `end.time - start.time`. Run-times on Windows 10 x64 with the Intel Math Kernel Library are:

<table>
<thead>
<tr>
<th>CPU</th>
<th>Run-Time (Minutes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>i7-11850H</td>
<td>2.49</td>
</tr>
<tr>
<td>i7-4770</td>
<td>5.38</td>
</tr>
</tbody>
</table>

**Concepts**
psychology, human factors, engineering, correlation coefficients, multilevel models, multivariate models, cluster-robust inference

**Author(s)**
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Laura Marusich, <laura.m.cooper20.civ@army.mil>, <lmarusich@gmail.com>

**Source**


**References**


**Examples**
```r
### copy data into ’dat’ and examine data
dat <- dat.bakdash2021
head(dat[c(1,2,6,8:12)])

### Not run:
#start.time <- Sys.time()

### load metafor
```
library(metafor)

### multilevel meta-analytic model to get the overall pooled effect
res.overall <- rma.mv(es.z, vi.z, mods = ~ 1,
                     random = ~ 1 | SampleID / Outcome,
                     data = dat,
                     test = "t")
res.overall

### get prediction interval
predict(res.overall)

### cluster-robust variance estimation (CRVE) / cluster-robust inference
res.overall.crve <- robust(res.overall, cluster = SampleID)
res.overall.crve

### get prediction interval
res.overall.crve.pred <- predict(res.overall.crve)
res.overall.crve.pred

### multilevel meta-analytic model for SA measures
res.sa <- rma.mv(es.z, vi.z, mods = ~ SA.measure.type - 1,
                random = ~ 1 | SampleID / Outcome,
                data = dat,
                test = "t")
res.sa

### cluster-robust variance estimation (CRVE) / cluster-robust inference
res.sa.crve <- robust(res.sa, cluster = SampleID)
res.sa.crve

### profile likelihood plots
par(mfrow=c(2,1))
profile(res.sa.crve, progbar = FALSE)

### format and combine output of meta-analytic models for the forest plot
all.z <- c(res.sa.crve$beta, # SA measures
           res.overall.crve$beta, # pooled effect for confidence interval (CI)
           res.overall.crve$beta) # pooled effect for prediction interval (PI)

all.ci.lower <- c(res.sa.crve$ci.lb, # SA measures
                   res.overall.crve$ci.lb, # pooled effect, lower CI
                   res.overall.crve$pi.lb) # pooled effect, lower PI

all.ci.upper <- c(res.sa.crve$ci.ub, # SA measures
                   res.overall.crve$ci.ub, # pooled effect, upper CI
                   res.overall.crve$pi.ub) # pooled effect, upper PI

### note: there is no p-value for the PI
all.pvals <- c(res.sa.crve$pval, res.overall.crve$pval)
all.labels <- c(sort(unique(dat$SA.measure.type)), "Overall", "95% Prediction Interval")

### function to round p-values for the forest plot
pvals.round <- function(input) {
  input <- ifelse(input < 0.001, "< 0.001",
    ifelse(input < 0.01, "< 0.01",
      ifelse(input < 0.05 & input >= 0.045, "< 0.05",
        ifelse(round(input, 2) == 1.00, "0.99",
          sprintf("%.2f", round(input, 2)))))))

all.pvals.rounded <- pvals.round(all.pvals)

### forest plot
plot.vals <- data.frame(all.labels, all.z, all.ci.lower, all.ci.upper)
par(mfrow=c(1,1), cex = 1.05)
forest(plot.vals$all.z,
  ci.lb = plot.vals$all.ci.lower,
  ci.ub = plot.vals$all.ci.upper,
  slab = plot.vals$all.labels,
  psize = 1,
  efac = 0, xlim = c(-1.8, 2.5), clim = c(-1, 1),
  transf = transf.ztor, # transform z to r
  at = seq(-0.5, 1, by = 0.25),
  xlab = expression("Correlation Coefficient"~"^\textit{r}\^\textsuperscript{\textprime}\tildafact{Var} r\tildafact{Var} p-value")
)

### keep trailing zero using sprintf
output <- cbind(sprintf("%.2f", round(transf.ztor(plot.vals$all.z), 2)),
  sprintf("%.2f", round(transf.ztor(plot.vals$all.ci.lower), 2)),
  sprintf("%.2f", round(transf.ztor(plot.vals$all.ci.upper), 2)))

### alignment kludge
annotext <- apply(output, 1, function(x) {paste0(" ", x[1], " [", x[2],",", x[3], "]")})
text( 1.05, 12:1, annotext, pos = 4, cex = 1.05)
text(-1.475, 14.00, "SA Measure", cex = 1.05)
text( 2.30, 14.00, substitute(paste(italic("p-value"))), cex = 1.05)
text( 1.55, 14.00, "Correlation [95% CI]", cex = 1.05)
abline(h = 1.5)

### black polygon for overall mean CIs
addpoly(all.z[11], ci.lb = all.ci.lower[11], ci.ub = all.ci.upper[11],
  rows = 2, annotate = FALSE, efac = 1.5, transf = transf.ztor)

### white polygon for PI
addpoly(all.z[12], ci.lb = all.ci.lower[12], ci.ub = all.ci.upper[12],
  rows = 1, col = "white", border = "black",
  annotate = FALSE, efac = 1.5, transf = transf.ztor)

par(mfrow=c(1,1), cex = 1) # reset graph parameters to default

### confidence intervals for the variance components
re.CI.variances <- confint(res.overall)
re.CI.variances
### fit model using alternative multivariate parameterization
res.overall.alt <- rma.mv(es.z, vi.z, mods = ~ 1,
  random = ~ factor(Outcome) | factor(SampleID),
  data = dat,
  test = "t")

### confidence intervals for the total amount of heterogeneity variance component
res.overall.alt.tau <- confint(res.overall.alt, tau2=1)$random

### I^2: http://www.metafor-project.org/doku.php/tips:i2_multilevel_multivariate
W <- diag(1/dat$vi.z)
X <- model.matrix(res.overall)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W

### I^2 (variance due to heterogeneity): 61%
I2 <- 100 * res.overall.alt$tau2 / (res.overall.alt$tau2 + (res.overall$k-res.overall$p)/sum(diag(P)))
I2

### 95% CI for I^2 using uncertainty around tau^2
I2.CI.lb <- 100 * res.overall.alt$tau[1,2] / (res.overall.alt$tau[1,2] + (res.overall$k-res.overall$p)/sum(diag(P)))
I2.CI.lb

I2.CI.ub <- 100 * res.overall.alt$tau[1,3] / (res.overall.alt$tau[1,3] + (res.overall$k-res.overall$p)/sum(diag(P)))
I2.CI.ub

### total amount of heterogeneity (tau)
sqrt(res.overall.alt$tau2)

### heterogeneity table
table.heterogeneity <- data.frame(matrix(ncol = 3, nrow = 4))
colnames(table.heterogeneity) <- c("Parameter Value",
  "Lower 95% CI",
  "Upper 95% CI")
rownames(table.heterogeneity) <- c("Tau (Total)",
  "Tau1 (Between paper)",
  "Tau2 (Within paper)",
  "I2 (%)")
table.heterogeneity[1,] <- res.overall.alt$tau2
table.heterogeneity[2,] <- sigma1.z[2,]
table.heterogeneity[3,] <- sigma2.z[2,]
table.heterogeneity[4,] <- c(I2, I2.CI.lb, I2.CI.ub)
round(table.heterogeneity, 2)

#end.time <- Sys.time()
dat.baker2009

Studies on Pharmacologic Treatments for Chronic Obstructive Pulmonary Disease

Description

Results from 39 trials examining pharmacologic treatments for chronic obstructive pulmonary disease (COPD).

Usage

dat.baker2009

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>study label</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>year of publication</td>
</tr>
<tr>
<td>id</td>
<td>numeric</td>
<td>study ID</td>
</tr>
<tr>
<td>treatment</td>
<td>character</td>
<td>treatment</td>
</tr>
<tr>
<td>exac</td>
<td>numeric</td>
<td>number of individuals with one or more COPD exacerbations</td>
</tr>
<tr>
<td>total</td>
<td>numeric</td>
<td>number of individuals</td>
</tr>
</tbody>
</table>

Details

This data set comes from a systematic review of randomized controlled trials on pharmacologic treatments for chronic obstructive pulmonary disease (COPD) (Baker et al., 2009).

The primary outcome, occurrence of one or more episodes of COPD exacerbation, is binary (yes / no). For this outcome, five drug treatments (fluticasone, budesonide, salmeterol, formoterol, tiotropium) and two combinations (fluticasone + salmeterol, budesonide + formoterol) were compared to placebo. The authors considered the two combinations as separate treatments instead of evaluating the individual components.

Concepts

- medicine, odds ratios, network meta-analysis, component network meta-analysis

Author(s)

Guido Schwarzer, <sc@imbi.uni-freiburg.de>, https://github.com/guido-s/
Source


See Also

pairwise, metabin, netmeta, netcomb, netmetabin

Examples

```r
### Show first 6 rows of the dataset
head(dat.baker2009)

## Not run:
### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print odds ratios and confidence limits with two digits
settings.meta(digits = 2)

### Transform data from long arm-based format to contrast-based
### format. Argument 'sm' has to be used for odds ratio as summary
### measure; by default the risk ratio is used in the metabin function
### called internally.
pw <- pairwise(treatment, exac, total, studlab = paste(study, year),
  data = dat.baker2009, sm = "OR")

### Conduct random effects network meta-analysis (NMA)
### with placebo as reference
net <- netmeta(pw, fixed = FALSE, ref = "plac")

### Show network graph
netgraph(net, seq = "optimal", start = "prcomp",
  labels = gsub("\"", " +\n", trts, fixed = TRUE),
  plastic = TRUE, thickness = "se.fixed", number = TRUE,
  points = TRUE, cex.points = 5, col.points = "red",
  offset = 0.025)

### Print and plot results for network meta-analysis
net
forest(net)

### Conduct component network meta-analysis (CNMA)
cnet <- netcomb(net)
cnet

### Compare results of NMA and additive CNMA
nb <- netbind(net, cnet, name = c("Standard NMA", "Additive CNMA"))
forest(nb)
```
## Description

Results from 48 studies on the effectiveness of school-based writing-to-learn interventions on academic achievement.

## Usage
dat.bangertdrowns2004

## Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>grade</td>
<td>numeric</td>
<td>grade level (1 = elementary; 2 = middle; 3 = high-school; 4 = college)</td>
</tr>
<tr>
<td>length</td>
<td>numeric</td>
<td>treatment length (in weeks)</td>
</tr>
<tr>
<td>minutes</td>
<td>numeric</td>
<td>minutes per assignment</td>
</tr>
<tr>
<td>wic</td>
<td>numeric</td>
<td>writing tasks were completed in class (0 = no; 1 = yes)</td>
</tr>
<tr>
<td>feedback</td>
<td>numeric</td>
<td>feedback on writing was provided (0 = no; 1 = yes)</td>
</tr>
<tr>
<td>info</td>
<td>numeric</td>
<td>writing contained informational components (0 = no; 1 = yes)</td>
</tr>
<tr>
<td>pers</td>
<td>numeric</td>
<td>writing contained personal components (0 = no; 1 = yes)</td>
</tr>
<tr>
<td>imag</td>
<td>numeric</td>
<td>writing contained imaginative components (0 = no; 1 = yes)</td>
</tr>
<tr>
<td>meta</td>
<td>numeric</td>
<td>prompts for metacognitive reflection (0 = no; 1 = yes)</td>
</tr>
<tr>
<td>subject</td>
<td>character</td>
<td>subject matter</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>total sample size of the study</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>standardized mean difference</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
</tbody>
</table>

## Details

In each of the studies included in this meta-analysis, an experimental group (i.e., a group of students that received instruction with increased emphasis on writing tasks) was compared against a control group (i.e., a group of students that received conventional instruction) with respect to some content-related measure of academic achievement (e.g., final grade, an exam/quiz/test score). The outcome measure for this meta-analysis was the standardized mean difference (with positive values indicating a higher mean level of academic achievement in the intervention group).

The standardized mean differences given here are bias-corrected and therefore differ slightly from the values reported in the article. Also, since only the total sample size is given in the article, the sampling variances were computed under the assumption that $n_{i1} = n_{i2} = n_i/2$. 
Concepts
education, standardized mean differences, meta-regression

Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

Examples
### copy data into 'dat' and examine data
dat <- dat.bangertdrowns2004
dat[1:10,-13]

## Not run:
### load metafor package
library(metafor)

### fit random-effects model
res <- rma(yi, vi, data=dat)
res

### some examples of mixed-effects meta-regression models
res <- rma(yi, vi, mods = ~ factor(grade), data=dat)
res
res <- rma(yi, vi, mods = ~ length, data=dat)
res
res <- rma(yi, vi, mods = ~ info + pers + imag + meta, data=dat)
res

## End(Not run)

---

**dat.baskerville2012**  *Studies on the Effectiveness of Practice Facilitation Interventions*

Description
Results from 23 studies on the effectiveness of practice facilitation interventions within the primary care practice setting.

Usage
dat.baskerville2012
Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>author</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>score</td>
<td>numeric</td>
<td>quality score (0 to 12 scale)</td>
</tr>
<tr>
<td>design</td>
<td>character</td>
<td>study design (cct = controlled clinical trial, rct = randomized clinical trial, crct = cluster randomized clinical trial)</td>
</tr>
<tr>
<td>alloconc</td>
<td>numeric</td>
<td>allocation concealed (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>blind</td>
<td>numeric</td>
<td>single- or double-blind study (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>itt</td>
<td>numeric</td>
<td>intention to treat analysis (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>fumonths</td>
<td>numeric</td>
<td>follow-up months</td>
</tr>
<tr>
<td>retention</td>
<td>numeric</td>
<td>retention (in percent)</td>
</tr>
<tr>
<td>country</td>
<td>character</td>
<td>country where study was conducted</td>
</tr>
<tr>
<td>outcomes</td>
<td>numeric</td>
<td>number of outcomes assessed</td>
</tr>
<tr>
<td>duration</td>
<td>numeric</td>
<td>duration of intervention</td>
</tr>
<tr>
<td>pperf</td>
<td>numeric</td>
<td>practices per facilitator</td>
</tr>
<tr>
<td>meetings</td>
<td>numeric</td>
<td>(average) number of meetings</td>
</tr>
<tr>
<td>hours</td>
<td>numeric</td>
<td>(average) hours per meeting</td>
</tr>
<tr>
<td>tailor</td>
<td>numeric</td>
<td>intervention tailored to the context and needs of the practice (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>smd</td>
<td>numeric</td>
<td>standardized mean difference</td>
</tr>
<tr>
<td>se</td>
<td>numeric</td>
<td>corresponding standard error</td>
</tr>
</tbody>
</table>

Details

Baskerville et al. (2012) describe outreach or practice facilitation as a "multifaceted approach that involves skilled individuals who enable others, through a range of intervention components and approaches, to address the challenges in implementing evidence-based care guidelines within the primary care setting". The studies included in this dataset examined the effectiveness of practice facilitation interventions for improving some relevant evidence-based practice behavior. The effect was quantified in terms of a standardized mean difference, comparing the change (from pre- to post-intervention) in the intervention versus the comparison group (or the difference from baseline in prospective cohort studies).

Concepts

medicine, primary care, standardized mean differences, publication bias, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

### copy data into 'dat' and examine data
dat <- dat.baskerville2012
dat

## Not run:
### load metafor package
library(metafor)

### random-effects model
res <- rma(smd, sei=se, data=dat, method="DL")
print(res, digits=2)

### funnel plot
funnel(res, xlab="Standardized Mean Difference", ylim=c(0,0.6))

### rank and regression tests for funnel plot asymmetry
ranktest(res)
regtest(res)

### meta-regression analyses examining various potential moderators
rma(smd, sei=se, mods = ~ score, data=dat, method="DL")
rma(smd, sei=se, mods = ~ alloconc, data=dat, method="DL")
rma(smd, sei=se, mods = ~ blind, data=dat, method="DL")
rma(smd, sei=se, mods = ~ itt, data=dat, method="DL")
rma(smd, sei=se, mods = ~ duration, data=dat, method="DL")
rma(smd, sei=se, mods = ~ tailor, data=dat, method="DL")
rma(smd, sei=se, mods = ~ pperf, data=dat, method="DL")
rma(smd, sei=se, mods = ~ I(meetings * hours), data=dat, method="DL")

## End(Not run)

### Studies on the Effectiveness of the BCG Vaccine Against Tuberculosis

**Description**

Results from 13 studies examining the effectiveness of the Bacillus Calmette-Guerin (BCG) vaccine against tuberculosis.

**Usage**

dat.bcg

**Format**

The data frame contains the following columns:

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>trial</td>
<td>numeric</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
</tr>
</tbody>
</table>

author(s)
The 13 studies provide data in terms of $2 \times 2$ tables in the form:

<table>
<thead>
<tr>
<th>vaccinated group</th>
<th>TB positive</th>
<th>TB negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>tpos</td>
<td>tneg</td>
<td></td>
</tr>
<tr>
<td>control group</td>
<td>cpos</td>
<td>cneg</td>
</tr>
</tbody>
</table>

The goal of the meta-analysis was to examine the overall effectiveness of the BCG vaccine for preventing tuberculosis and to examine moderators that may potentially influence the size of the effect.

The dataset has been used in several publications to illustrate meta-analytic methods (see ‘References’).

Concepts

medicine, risk ratios, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.bcg
dat

## Not run:
### load metafor package
library(metafor)

### calculate log risk ratios and corresponding sampling variances
dat <- escalc(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, data=dat)
dat

### random-effects model
res <- rma(yi, vi, data=dat)
res

### average risk ratio with 95% CI
predict(res, transf=exp)

### mixed-effects model with absolute latitude and publication year as moderators
res <- rma(yi, vi, mods = ~ ablat + year, data=dat)
res

### predicted average risk ratios for 10-60 degrees absolute latitude
### holding the publication year constant at 1970
predict(res, newmods=cbind(seq(from=10, to=60, by=10), 1970), transf=exp)

### note: the interpretation of the results is difficult because absolute
### latitude and publication year are strongly correlated (the more recent
### studies were conducted closer to the equator)
plot(ablat ~ year, data=dat, pch=19, xlab="Publication Year", ylab="Absolute Lattitude")
cor(dat$ablat, dat$year)

## End(Not run)
```

---

**dat.begg1989**

*Studies on Bone-Marrow Transplantation versus Chemotherapy for the Treatment of Leukemia*

---

**Description**

Results from controlled and uncontrolled studies on the effectiveness of allogeneic bone-marrow transplantation (BMT) and conventional chemotherapy (CMO) in the treatment of acute nonlymphocytic leukemia.

**Usage**

`dat.begg1989`
The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>trt</td>
<td>character</td>
<td>treatment (BMT or CMO)</td>
</tr>
<tr>
<td>arms</td>
<td>numeric</td>
<td>number of arms in the study (1 = uncontrolled studies; 2 = controlled studies)</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>2-year disease-free survival rates</td>
</tr>
<tr>
<td>sei</td>
<td>numeric</td>
<td>corresponding standard errors</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variances</td>
</tr>
</tbody>
</table>

Details

The dataset includes the results from controlled and uncontrolled studies on the 2-year disease-free survival rate in patients with acute nonlymphocytic leukemia receiving either allogeneic bone-marrow transplantation (BMT) or conventional chemotherapy (CMO). In the controlled (two-arm) studies (studies 1-4), a cohort of patients in complete remission and potentially eligible for BMT was assembled, and those who consented and for whom a donor could be found received BMT, with the remaining patients used as controls (receiving CMO). In the uncontrolled (one-arm) studies (studies 5-16), only a single group was studied, receiving either BMT or CMO.

The data in this dataset were obtained from Table 1 in Begg and Pilote (1991, p. 902).

Concepts

medicine, oncology, single-arm studies, multilevel models

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```R
### copy data into `dat` and examine data
dat <- dat.begg1989
dat

## Not run:

### load metafor package
library(metafor)
```
### turn trt and arms into factors and set reference levels
```r
dat$trt <- relevel(factor(dat$trt), ref="CMO")
dat$arms <- relevel(factor(dat$arms), ref="2")
```

### create data frame with the treatment differences for the controlled studies
```r
dat2 <- data.frame(yi = dat$yi[c(1,3,5,7)] - dat$yi[c(2,4,6,8)],
                   vi = dat$vi[c(1,3,5,7)] + dat$vi[c(2,4,6,8)])
dat2
```

### DerSimonian and Laird method using the treatment differences
```r
res <- rma(yi, vi, data=dat2, method="DL", digits=2)
res
```

### Begg & Pilote (1991) model incorporating the uncontrolled studies
```r
res <- rma.mv(yi, vi, mods = ~ trt, random = ~ 1 | study,
               data=dat, method="ML", digits=2)
res
```

### model involving bias terms for the uncontrolled studies
```r
res <- rma.mv(yi, vi, mods = ~ trt + trt:arms, random = ~ 1 | study,
               data=dat, method="ML", digits=2)
res
```

### model with a random treatment effect
```r
res <- rma.mv(yi, vi, mods = ~ trt, random = list(~ 1 | study, ~ trt | study),
               struct="UN", tau2=c(0,NA), rho=0, data=dat, method="ML", digits=2)
res
```

### model with a random treatment effect, but with equal variances in both arms
```r
res <- rma.mv(yi, vi, mods = ~ trt, random = list(~ 1 | study, ~ trt | study),
               struct="CS", rho=0, data=dat, method="ML", digits=2)
res
```

### End(Not run)

---

**dat.berkey1998**

*Studies on Treatments for Periodontal Disease*

---

**Description**

Results from 5 trials comparing surgical and non-surgical treatments for medium-severity periodontal disease one year after treatment.

**Usage**

```
dat.berkey1998
```
Format
The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trial</td>
<td>numeric</td>
<td>trial number</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>number of patients</td>
</tr>
<tr>
<td>outcome</td>
<td>character</td>
<td>outcome (PD = probing depth; AL = attachment level)</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>observed mean difference in outcome (surgical versus non-surgical)</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
<tr>
<td>v1i</td>
<td>numeric</td>
<td>variances and covariances of the observed effects</td>
</tr>
<tr>
<td>v2i</td>
<td>numeric</td>
<td>variances and covariances of the observed effects</td>
</tr>
</tbody>
</table>

Details
The dataset includes the results from 5 trials that compared surgical and non-surgical methods for the treatment of medium-severity periodontal disease. Reported outcomes include the change in probing depth (PD) and attachment level (AL) one year after the treatment. The outcome measure used for this meta-analysis was the (raw) mean difference, calculated in such a way that positive values indicate that surgery was more effective than non-surgical treatment in decreasing the probing depth and increasing the attachment level (so, the results from the various trials indicate that surgery is preferable for reducing the probing depth, while non-surgical treatment is preferable for increasing the attachment level). Since each trial provides effect size estimates for both outcomes, the estimates are correlated. A multivariate model can be used to meta-analyze the two outcomes simultaneously.

The $v_{1i}$ and $v_{2i}$ values are the variances and covariances of the observed effects. In particular, for each study, variables $v_{1i}$ and $v_{2i}$ form a $2 \times 2$ variance-covariance matrix of the observed effects, with the diagonal elements corresponding to the sampling variances of the mean differences (the first for probing depth, the second for attachment level) and the off-diagonal value corresponding to the covariance of the two mean differences. Below, the full (block diagonal) variance-covariance for all studies is constructed from these two variables.

Concepts
medicine, dentistry, raw mean differences, multivariate models

Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source
Examples

```r
### copy data into 'dat' and examine data
dat <- dat.berkey1998
dat

## Not run:
### load metafor package
library(metafor)

### construct block diagonal var-cov matrix of the observed outcomes based on variables v1i and v2i
V <- vcalc(vi=1, cluster=author, rvars=c(v1i, v2i), data=dat)

### fit multiple outcomes (meta-regression) model (with REML estimation)
res <- rma.mv(yi, V, mods = ~ outcome - 1, random = ~ outcome | trial, struct="UN", data=dat)
print(res, digits=3)

### test/estimate difference between the two outcomes
anova(res, X=c(1,-1))

### fit model including publication year as moderator for both outcomes (with ML estimation)
res <- rma.mv(yi, V, mods = ~ outcome + outcome:I(year - 1983) - 1,
              random = ~ outcome | trial, struct="UN", data=dat, method="ML")
print(res, digits=3)

## End(Not run)
```

---

**dat.besson2016**

Dataset on How Maternal Diet Impacts Copying Styles in Rodents

**Description**

Results from 46 studies synthesising maternal nutritional effects on coping styles in rodents.

**Usage**

dat.besson2016

**Format**

The data frame contains the following columns:

- `comp_ID`: character, effect-size unique identifier
- `study_ID`: character, study unique identifier
- `dam_ID`: character, dam unique identifier (group of dams subjected to the same treatment)
- `animal_ID`: character, offspring unique identifier (group of offspring from the same dam group subjected to the same treatment)
- `Reference`: character, author's names and date
- `species`: character, species [rats or mice]
<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>strain</td>
<td>character strain</td>
</tr>
<tr>
<td>manip_type</td>
<td>character maternal nutritional manipulation type [protein or calorie]</td>
</tr>
<tr>
<td>manip_direction</td>
<td>character direction of maternal nutritional manipulation [- = restriction, + = overfeeding]</td>
</tr>
<tr>
<td>nom_manip_val</td>
<td>character degree of maternal nutritional manipulation as described in the original publications</td>
</tr>
<tr>
<td>exp</td>
<td>character percentage of caloric or protein maternal restriction or increase in caloric intake</td>
</tr>
<tr>
<td>control</td>
<td>character percentage of caloric or protein maternal restriction or increase in caloric intake</td>
</tr>
<tr>
<td>manip_type</td>
<td>character protein content, percentage fat or intake</td>
</tr>
<tr>
<td>adlib_con</td>
<td>character were maternal control groups fed ad libitum? [yes or no]</td>
</tr>
<tr>
<td>adlib_exp</td>
<td>character were maternal experimental groups fed ad libitum? [yes or no]</td>
</tr>
<tr>
<td>diet_con</td>
<td>character name of maternal control diet?</td>
</tr>
<tr>
<td>diet_exp</td>
<td>character name of maternal experimental diet?</td>
</tr>
<tr>
<td>dam_diet_start_dPC</td>
<td>numeric start of the dam diet [in days post-conception]</td>
</tr>
<tr>
<td>dam_diet_end_dPC</td>
<td>numeric end of the dam diet [in days post-conception]</td>
</tr>
<tr>
<td>diet_label</td>
<td>character period of maternal diet manipulation [pregestation = pre-gestation, pre = pre, lact = lactation, or pre+lact = pregnancy and lactation]</td>
</tr>
<tr>
<td>age_mating</td>
<td>numeric dam age at mating if known</td>
</tr>
<tr>
<td>n_con_dam</td>
<td>integer sample size of the control dam groups</td>
</tr>
<tr>
<td>n_exp_dam</td>
<td>integer sample size of the experimental dam groups</td>
</tr>
<tr>
<td>multi_use_con</td>
<td>character were control groups used multiple time? [yes or no]</td>
</tr>
<tr>
<td>dam_housing</td>
<td>character how were dams housed? [pair, group, or single]</td>
</tr>
<tr>
<td>temperature</td>
<td>numeric temperature during the experiment [°C]</td>
</tr>
<tr>
<td>photoperiod</td>
<td>integer photoperiod during the experiment [number of hours of light]</td>
</tr>
<tr>
<td>litter_size</td>
<td>integer size of the litter [number of pups per dam]</td>
</tr>
<tr>
<td>litter_size_equalized</td>
<td>character has litter size been equalized? [yes or no]</td>
</tr>
<tr>
<td>crossfostered</td>
<td>character have pups been cross-fostered? [yes or no]</td>
</tr>
<tr>
<td>sex</td>
<td>character sex of the offspring that were tested [m = male, f = female, both = mixed sex]</td>
</tr>
<tr>
<td>housing</td>
<td>character offspring housing during the test period [dam, pair, single, or group]</td>
</tr>
<tr>
<td>bodymass_mean_constr</td>
<td>numeric mean body mass of control offspring close to or during the testing period</td>
</tr>
<tr>
<td>bodymass_SE_constr</td>
<td>numeric S.E. for body mass of control offspring close to or during the testing period</td>
</tr>
<tr>
<td>bodymass_mean_exp</td>
<td>numeric mean body mass of experimental offspring close to or during the testing period</td>
</tr>
<tr>
<td>bodymass_SE_exp</td>
<td>numeric S.E. for body mass of experimental offspring close to or during the testing period</td>
</tr>
<tr>
<td>bm_N_constr</td>
<td>integer sample size for body mass of control offspring close to or during the testing period</td>
</tr>
<tr>
<td>bm_N_exp</td>
<td>integer sample size for body mass of experimental offspring close to or during the testing period</td>
</tr>
<tr>
<td>bm_dPP</td>
<td>integer age of offspring when body mass was measured [in days post-parturition]</td>
</tr>
<tr>
<td>offspring_diet</td>
<td>character offspring diet after weaning [type of control diet]</td>
</tr>
<tr>
<td>offspring_con_adlib</td>
<td>character were control offspring fed ad libitum after weaning? [yes or no]</td>
</tr>
<tr>
<td>offspring_diet_level</td>
<td>character name of offspring diet after weaning</td>
</tr>
<tr>
<td>offspring_diet_end_dPP</td>
<td>integer end of the offspring diet [in days post-parturition]</td>
</tr>
<tr>
<td>post_diet_adlib</td>
<td>character were experimental offspring fed ad libitum after weaning? [yes or no]</td>
</tr>
<tr>
<td>response_age_dPP</td>
<td>numeric offspring age when behavioural testing started [in days post-parturition]</td>
</tr>
<tr>
<td>authorsBehaviour_classification</td>
<td>character author’s classification of offspring behaviour [anxiety, exploration, or activity]</td>
</tr>
<tr>
<td>ourBehaviour_classification</td>
<td>character our classification of offspring behaviour [anxiety, exploration, or activity]</td>
</tr>
<tr>
<td>response_test</td>
<td>character type of test used [elevated T-maze (ETM), open field, etc.] to measure offspring behaviour</td>
</tr>
<tr>
<td>time_trial</td>
<td>integer duration of the testing [min]</td>
</tr>
<tr>
<td>measure</td>
<td>character measures taken during testing [total distance moved, time spent in open arm]</td>
</tr>
<tr>
<td>unit</td>
<td>character unit of the behavioural measure taken [min, s, m, number (#), etc.]</td>
</tr>
<tr>
<td>high_better</td>
<td>character for activity and exploration, a higher number is assumed to be better (i.e., activity scores)</td>
</tr>
<tr>
<td>night.day</td>
<td>character time of day when behaviours were measured [night or day]</td>
</tr>
</tbody>
</table>
Details

Data from experiments where dams were subject to caloric or protein restriction or were overfed around gestation were included. Offspring activity, exploration, or anxiety were measured outcomes variables from maternal experimental treatments. Multilevel meta-analysis and meta-regression models were used to analyze the meta-analytic data.

Concepts

ecology, evolution, standardized mean differences

Author(s)

Daniel Noble, <daniel.noble@anu.edu.au>

Source


Examples

```r
### copy data into `dat` and examine data
dat <- dat.besson2016
head(dat)

## Not run:

### load metafor
library(metafor)

### compute SD from SE
dat$sd_c <- with(dat, con_se * sqrt(con_n))
dat$sd_e <- with(dat, exp_se * sqrt(exp_n))
```
### compute standardized mean differences and corresponding sampling variances

```r
dat <- escalc(measure="SMD", m1i=exp_mean, m2i=con_mean, sd1i=sd_e, sd2i=sd_c, 
n1i=exp_n, n2i=con_n, data=dat, add.measure=TRUE)
```

### fit model

```r
mod1 <- rma.mv(yi ~ 1, V = vi, random = list(~ 1 | study_ID, ~ 1 | comp_ID), data = dat)
mod1
```

## End(Not run)

---

**dat.bonett2010**

**Studies on the Reliability of the CES-D Scale**

### Description

Results from 9 studies on the reliability of the Center for Epidemiologic Studies Depression (CES-D) Scale administered to children providing care to an elderly parent.

### Usage

```r
dat.bonett2010
```

### Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>source</td>
<td>character</td>
<td>source of data</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>sample size</td>
</tr>
<tr>
<td>mi</td>
<td>numeric</td>
<td>number of items in the scale</td>
</tr>
<tr>
<td>ai</td>
<td>numeric</td>
<td>observed value of Cronbach’s alpha</td>
</tr>
<tr>
<td>caregivers</td>
<td>character</td>
<td>gender of the children in the sample</td>
</tr>
</tbody>
</table>

### Details

The Center for Epidemiologic Studies Depression (CES-D) Scale is a 20-item questionnaire assessing various symptoms of depression, with each item scored on a 4-point scale. The scale has been used in several studies to examine depressive symptoms in children providing care to an elderly parent. The dataset includes information on the reliability of the scale as measured with Cronbach’s alpha in 9 such studies. Also, the gender composition of the children in each sample is indicated.

### Concepts

- psychology
- Cronbach’s alpha
- reliability generalization
- meta-regression
Examples

```r
### copy data into 'dat' and examine data
dat <- dat.bonett2010
dat

# Not run:

### load metafor package
library(metafor)

### meta-analysis using the raw alpha values
res <- rma(measure="ARAW", ai=ai, mi=mi, ni=ni, data=dat)
res

### meta-analysis using transformed alpha values (using the
### transformation suggested by Hakstian & Whalen, 1976)
res <- rma(measure="AHW", ai=ai, mi=mi, ni=ni, data=dat)
res
predict(res, transf=transf.iahw)

### meta-analysis using transformed alpha values (using the
### transformation suggested by Bonett, 2002)
res <- rma(measure="ABT", ai=ai, mi=mi, ni=ni, data=dat)
res
predict(res, transf=transf.iabt)

### forest plot
forest(res, slab=source, header=TRUE, atransf=transf.iabt, reline=coef(res))

### examine whether female/mixed samples yield different alphas (with raw alphas)
res <- rma(measure="ARAW", ai=ai, mi=mi, ni=ni, mods = ~ caregivers, data=dat)
res
predict(res, newmods=c(0,1), digits=2)
```
## dat.bornmann2007

### Description

Results from 21 studies on gender differences in grant and fellowship awards.

### Usage

dat.bornmann2007

### Format

The data frame contains the following columns:

- **study**: character study reference
- **obs**: numeric observation within study
- **doctype**: character document type
- **gender**: character gender of the study authors
- **year**: numeric (average) cohort year
- **org**: character funding organization / program
- **country**: character country of the funding organization / program
- **type**: character fellowship or grant application
- **discipline**: character discipline / field
- **waward**: numeric number of women who received a grant/fellowship award
- **wtotal**: numeric number of women who applied for an award
- **maward**: numeric number of men who received a grant/fellowship award
- **mtotal**: numeric number of men who applied for an award

### Details

The studies in this dataset examine whether the chances of receiving a grant or fellowship award differs for men and women. Note that many studies provide multiple comparisons (e.g., for different years / cohorts / disciplines). A multilevel meta-analysis model can be used to account for the multilevel structure in these data.

### Concepts

sociology, odds ratios, multilevel models

### Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)
**Source**

**References**

**Examples**
```r
### copy data into 'dat' and examine data
dat <- dat.bornmann2007
head(dat, 16)

### Not run:
### load metafor package
library(metafor)

### calculate log odds ratios and corresponding sampling variances
dat <- escalc(measure="OR", ai=waward, n1i=wtotal, ci=maward, n2i=mtotal, data=dat)

### fit multilevel meta-analysis model
res <- rma.mv(yi, vi, random = ~ 1 | study/obs, data=dat)
res

### estimated average odds ratio (with 95% CI/PI)
predict(res, transf=exp, digits=2)

### test for a difference between fellowship and grant applications
res <- rma.mv(yi, vi, mods = ~ type, random = ~ 1 | study/obs, data=dat)
res
predict(res, newmods=0:1, transf=exp, digits=2)
```

---

**dat.bourassa1996**  
*Studies on the Association between Handedness and Eye-Dominance*

**Description**
Results from 47 studies on the association between handedness and eye-dominance.

**Usage**
```r
dat.bourassa1996
```
Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>sample</td>
<td>numeric</td>
<td>sample number</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>(first) author</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>selection</td>
<td>character</td>
<td>selection of subjects on the basis of eyedness or handedness</td>
</tr>
<tr>
<td>investigator</td>
<td>character</td>
<td>investigator (psychologist, educationalist, or other)</td>
</tr>
<tr>
<td>hand_assess</td>
<td>character</td>
<td>method to assess handedness (questionnaire or performance based)</td>
</tr>
<tr>
<td>eye_assess</td>
<td>character</td>
<td>method to assess eyedness (see ‘Details’)</td>
</tr>
<tr>
<td>mage</td>
<td>numeric</td>
<td>mean age of sample</td>
</tr>
<tr>
<td>lh.le</td>
<td>numeric</td>
<td>number of left-handed left-eyed individuals</td>
</tr>
<tr>
<td>lh.re</td>
<td>numeric</td>
<td>number of left-handed right-eyed individuals</td>
</tr>
<tr>
<td>rh.le</td>
<td>numeric</td>
<td>number of right-handed left-eyed individuals</td>
</tr>
<tr>
<td>rh.re</td>
<td>numeric</td>
<td>number of right-handed right-eyed individuals</td>
</tr>
<tr>
<td>sex</td>
<td>character</td>
<td>sex of the sample (combined, male, or female)</td>
</tr>
</tbody>
</table>

Details

The 47 studies included in this meta-analysis examined the association between handedness and eye-dominance (ocular dominance or eyedness). Results are given in terms of $2 \times 2$ tables, indicating the number of left-handed left-eyed, left-handed right-eyed, right-handed left-eyed, and right-handed right-eyed individuals. Note that some studies included multiple (independent) samples, so that the meta-analysis included 54 samples in total. Also, for some studies, the combined data of the males and females are further broken down into the two subgroups.

In some studies, there was indication that the selection of subjects was not random with respect to handedness and/or eyedness. While this should not influence the size of the association as measured with the odds ratio, this invalidates those studies for assessing the overall percentage of left-eyed and left-handed individuals.

Handedness was assessed in the individual studies either based on a questionnaire or inventory or based on task performance. Eyedness was assessed based on various methods: E.1 methods are based on task performance, while E.2.a denotes assessment based on a questionnaire. The performance based methods could be further broken down into: E.1.a.i (monocular procedure with object/instrument held in one hand), E.1.a.ii (monocular procedure with object/instrument held in both hands), E.1.b (binocular procedure), E.1.c (a combination of the previous methods), and E.1.d (some other method).

Concepts

psychology, odds ratios

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org
**Source**


**Examples**

```r
### copy data into 'dat' and examine data
dat <- dat.bourassa1996
table(dat, 10)

### Not run:

### load metafor package
library(metafor)

### calculate log(OR) and corresponding sampling variance with 1/2 correction
dat <- escalc(measure="OR", ai=lh.le, bi=lh.re, ci=rh.le, di=rh.re, data=dat, add=1/2, to="all")
table(dat, 10)

### overall association between handedness and eyedness
res <- rma(yi, vi, data=dat, subset=sex="combined")
res
predict(res, transf=exp, digits=2)

### End(Not run)
```

**dat.cannon2006**

**Studies on the Effectiveness of Intensive Versus Moderate Statin Therapy for Preventing Coronary Death or Myocardial Infarction**

**Description**

Results from 4 trials examining the effectiveness of intensive (high dose) versus moderate (standard dose) statin therapy for preventing coronary death or myocardial infarction.

**Usage**

`dat.cannon2006`

**Format**

The data frame contains the following columns:

- **trial** character: trial name
- **pop** character: study population (post-ACS: post acute coronary syndrome; stable CAD: stable coronary artery disease)
- **nt** numeric: number of patients in the high dose group
- **nc** numeric: number of patients in the standard dose group
- **ep1t** numeric: number of events in the high dose group for end point 1: coronary death or non-fatal myocardial infarction
Details

The data were obtained from Figures 2, 3, 4, and 5 in Cannon et al. (2006). The authors used the Mantel-Haenszel method for combining the results from the 4 trials. This approach is implemented in the rma.mh function.

Concepts

medicine, cardiology, odds ratios, Mantel-Haenszel method

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

### copy data into 'dat' and examine data
dat <- dat.cannon2006
dat

### Not run:

### load metafor package
library(metafor)

### meta-analysis of log odds ratios using the MH method for endpoint 1
res <- rma.mh(measure="OR", ai=ep1t, n1i=nt, ci=ep1c, n2i=nc, data=dat, slab=trial)
print(res, digits=2)

### forest plot
forest(res, xlim=c(-.8,.8), atransf=exp, at=log(c(2/3, 1, 3/2)),
header=TRUE, top=2, cex=1.2, xlab="Odds Ratio")
mtext("(high dose better)", side=1, line=par("mgp")[1]-0.5, at=log(2/3), cex=1.2, font=3)
Studies on the Relationship between Course Instructor Ratings and Student Achievement

Description
Results from 20 studies on the correlation between course instructor ratings and student achievement.

Usage
dat.cohen1981

Format
The data frame contains the following columns:

<table>
<thead>
<tr>
<th>study</th>
<th>character</th>
<th>study author(s) and year</th>
</tr>
</thead>
<tbody>
<tr>
<td>sample</td>
<td>character</td>
<td>course type</td>
</tr>
<tr>
<td>control</td>
<td>character</td>
<td>ability control</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>sample size of the study (number of sections)</td>
</tr>
<tr>
<td>ri</td>
<td>numeric</td>
<td>observed correlation</td>
</tr>
</tbody>
</table>

Details
The studies included in this dataset examined to what extent students’ ratings of a course instructor correlated with their achievement in the course. Instead of correlating individual ratings and achievement scores, the studies were carried out in multisection courses, in which the sections had different instructors but all sections used a common achievement measure (e.g., a final exam). The correlation coefficients reflect the correlation between the mean instructor rating and the mean achievement score of each section. Hence, the unit of analysis are the sections, not the individuals.

Note that this dataset (extracted from Table A.3 in Cooper & Hedges, 1994) only contains studies with at least 10 sections.

Concepts
education, correlation coefficients

Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org
Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.cohen1981
dat[c(1,4,5)]

### Not run:

### load metafor package
library(metafor)

### calculate r-to-z transformed correlations and corresponding sampling variances
dat <- escalc(measure="ZCOR", ri=ri, ni=n1, data=dat[c(1,4,5)])
dat

### meta-analysis of the transformed correlations using a random-effects model
res <- rma(yi, vi, data=dat, digits=2)
res

### predicted average correlation with 95% CI
predict(res, transf=transf.ztor)

### End(Not run)
```

---

**dat.colditz1994**  
*Studies on the Effectiveness of the BCG Vaccine Against Tuberculosis*

Description

Results from 13 studies examining the effectiveness of the Bacillus Calmette-Guerin (BCG) vaccine against tuberculosis.

Usage

dat.colditz1994

Format

The data frame contains the following columns:
The 13 studies provide data in terms of $2 \times 2$ tables in the form:

<table>
<thead>
<tr>
<th></th>
<th>TB positive</th>
<th>TB negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>vaccinated group</td>
<td>tpos</td>
<td>tneg</td>
</tr>
<tr>
<td>control group</td>
<td>cpos</td>
<td>cneg</td>
</tr>
</tbody>
</table>

The goal of the meta-analysis was to examine the overall effectiveness of the BCG vaccine for preventing tuberculosis and to examine moderators that may potentially influence the size of the effect.

The dataset has been used in several publications to illustrate meta-analytic methods (see ‘References’).

Concepts

medicine, risk ratios, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.colditz1994
dat

## Not run:
### load metafor package
library(metafor)
### calculate log risk ratios and corresponding sampling variances
dat <- escalc(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, data=dat)
dat
### random-effects model
res <- rma(yi, vi, data=dat)
res
### average risk ratio with 95% CI
predict(res, transf=exp)
### mixed-effects model with absolute latitude and publication year as moderators
res <- rma(yi, vi, mods = ~ ablat + year, data=dat)
res
### predicted average risk ratios for 10-60 degrees absolute latitude
### holding the publication year constant at 1970
predict(res, newmods=cbind(seq(from=10, to=60, by=10), 1970), transf=exp)
### note: the interpretation of the results is difficult because absolute
### latitude and publication year are strongly correlated (the more recent
### studies were conducted closer to the equator)
plot(ablat ~ year, data=dat, pch=19, xlab="Publication Year", ylab="Absolute Lattitude")
cor(dat$ablat, dat$year)

### End(Not run)
```

---

**dat.collins1985a**

*Studies on the Treatment of Upper Gastrointestinal Bleeding by a Histamine H2 Antagonist*

---

**Description**

Results from studies examining the effectiveness of histamine H2 antagonists (cimetidine or ranitidine) in treating patients with acute upper gastrointestinal hemorrhage.

**Usage**

dat.collins1985a
Format

The data frame contains the following columns:

- **id**: numeric; study number
- **trial**: character; first author of trial
- **year**: numeric; year of publication
- **ref**: numeric; reference number
- **trt**: character; C = cimetidine, R = ranitidine
- **ctrl**: character; P = placebo, AA = antacids, UT = usual treatment
- **nti**: numeric; number of patients in treatment group
- **b.xti**: numeric; number of patients in treatment group with persistent or recurrent bleedings
- **o.xti**: numeric; number of patients in treatment group in need of operation
- **d.xti**: numeric; number of patients in treatment group that died
- **nci**: numeric; number of patients in control group
- **b.xci**: numeric; number of patients in control group with persistent or recurrent bleedings
- **o.xci**: numeric; number of patients in control group in need of operation
- **d.xci**: numeric; number of patients in control group that died

Details

The data were obtained from Tables 1 and 2 in Collins and Langman (1985). The authors used Peto’s (one-step) method for meta-analyzing the 27 trials. This approach is implemented in the `rma.peto` function. Using the same dataset, van Houwelingen, Zwinderman, and Stijnen (1993) describe some alternative approaches for analyzing these data, including fixed- and random-effects conditional logistic models. Those are implemented in the `rma.glmm` function.

Concepts

- medicine, odds ratios, Peto’s method, generalized linear models

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.collins1985a
dat
```
### Not run:

```r
## load metafor package
library(metafor)

### meta-analysis of log ORs using Peto's method (outcome: persistent or recurrent bleedings)
res <- rma.peto(ai=b.xti, n1i=nti, ci=b.xci, n2i=nci, data=dat)
print(res, digits=2)

### meta-analysis of log ORs using a conditional logistic regression model (FE model)
res <- rma.glmm(measure="OR", ai=b.xti, n1i=nti, ci=b.xci, n2i=nci, data=dat,
               model="CM.EL", method="FE")
summary(res)
predict(res, transf=exp, digits=2)

### plot the likelihoods of the odds ratios
llplot(measure="OR", ai=b.xti, n1i=nti, ci=b.xci, n2i=nci, data=dat,
       lwd=1, reline=NA, xlim=c(-4,4), drop00=FALSE)

### meta-analysis of log odds ratios using a conditional logistic regression model (RE model)
res <- rma.glmm(measure="OR", ai=b.xti, n1i=nti, ci=b.xci, n2i=nci, data=dat,
               model="CM.EL", method="ML")
summary(res)
predict(res, transf=exp, digits=2)

### meta-analysis of log ORs using Peto's method (outcome: need for surgery)
res <- rma.peto(ai=o.xti, n1i=nti, ci=o.xci, n2i=nci, data=dat)
print(res, digits=2)

### meta-analysis of log ORs using Peto's method (outcome: death)
res <- rma.peto(ai=d.xti, n1i=nti, ci=d.xci, n2i=nci, data=dat)
print(res, digits=2)
```

## End(Not run)

---

**dat.collins1985b**  
*Studies on the Effects of Diuretics in Pregnancy*

**Description**

Results from 9 studies examining the effects of diuretics in pregnancy on various outcomes.

**Usage**

```r
dat.collins1985b
```

**Format**

The data frame contains the following columns:
The 9 studies in this dataset examined the effects of diuretics in pregnancy on various outcomes, including the presence of any form of pre-eclampsia, perinatal death, stillbirth, and neonatal death.

Concepts

medicine, obstetrics, odds ratios, Peto’s method

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.collins1985b
dat

### Not run:

### load metafor package
library(metafor)

### calculate (log) odds ratio and sampling variance
dat <- escalc(measure="OR", n1i=pre.nti, n2i=pre.nci, ai=pre.xti, ci=pre.xci, data=dat)
summary(dat, digits=2, transf=exp)

### meta-analysis using Peto's method for any form of pre-eclampsia
```
dat.craft2003

Studies on the Relationship between the Competitive State Anxiety Inventory-2 and Sport Performance

Description

Results from 10 studies on the relationship between the Competitive State Anxiety Inventory-2 (CSAI-2) and sport performance.

Usage

dat.craft2003

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>sample size</td>
</tr>
<tr>
<td>sport</td>
<td>character</td>
<td>type of sport (T = team sport, I = individual sport)</td>
</tr>
<tr>
<td>ri</td>
<td>numeric</td>
<td>correlation coefficient</td>
</tr>
<tr>
<td>var1</td>
<td>character</td>
<td>variable 1 of the correlation coefficient (see ‘Details’)</td>
</tr>
<tr>
<td>var2</td>
<td>character</td>
<td>variable 2 of the correlation coefficient (see ‘Details’)</td>
</tr>
</tbody>
</table>

Details

The 10 studies included in this dataset are a subset of the studies included in the meta-analysis by Craft et al. (2003) on the relationship between the Competitive State Anxiety Inventory-2 (CSAI-2) and sport performance.

The CSAI-2 has three subscales: cognitive anxiety (acog), somatic anxiety (asom), and self-confidence (conf). The studies included in this dataset administered the CSAI-2 prior to some sport competition and then measured sport performance based on the competition. Most studies provided all 6 correlations (3 for the correlations among the 3 subscales and 3 for the correlations between the subscales and sport performance), but 2 studies (with study numbers 6 and 17) only provided a subset.
Concepts
psychology, correlation coefficients, multivariate models

Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

References

Examples
### copy data into 'dat' and examine data
dat <- dat.craft2003
head(dat, 18)

### load metafor package
library(metafor)

### construct dataset and var-cov matrix of the correlations
tmp <- rcalc(ri ~ var1 + var2 | study, ni=ni, data=dat)
V <- tmp$V
dat <- tmp$dat

### examine data for study 1
dat[dat$study == 1,]
V[dat$study == 1, dat$study == 1]

### examine data for study 6
dat[dat$study == 6,]
V[dat$study == 6, dat$study == 6]

### examine data for study 17
dat[dat$study == 17,]
V[dat$study == 17, dat$study == 17]

### multivariate random-effects model
res <- rma.mv(yi, V, mods = ~ var1.var2 - 1, random = ~ var1.var2 | study, struct="UN", data=dat)
res
dat.crede2010

## End(Not run)

| dat.crede2010 | Studies on the Relationship between Class Attendance and Grades in College Students |

### Description

Results from 68 studies on the relationship between class attendance and class performance and/or grade point average in college students.

### Usage

dat.crede2010

### Format

The data frame contains the following columns:

- **studyid**: numeric  
  study number
- **year**: numeric  
  publication year
- **source**: character  
  study source (journal, dissertation, other)
- **sampleid**: numeric  
  sample within study number
- **criterion**: character  
  criterion variable (grade, gpa)
- **class**: character  
  class type (science, nonscience)
- **ni**: numeric  
  sample size
- **ri**: numeric  
  observed correlation

### Details

The 68 studies included in this dataset provide information about the relationship between class attendance of college students and their performance (i.e., grade) in the class and/or their overall grade point average. Some studies included multiple samples and hence the dataset actually contains 97 correlation coefficients.

The dataset was obtained via personal communication. Note that this dataset differs just slightly from the one used by Credé et al. (2010).

### Concepts

- education, correlation coefficients, multilevel models

### Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)
Source

Personal communication.

References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.crede2010
head(dat, 18)

### load metafor package
library(metafor)

### calculate r-to-z transformed correlations and corresponding sampling variances
dat <- escalc(measure="ZCOR", ri=ri, ni=ni, data=dat)

### meta-analysis for the relationship between attendance and grades
res <- rma(yi, vi, data=dat, subset=criterion="grade")
res

### estimated average correlation with 95% CI/PI
predict(res, transf=transf.ztor, digits=2)

### examine if relationship between attendance and grades differs for nonscience/science classes
res <- rma(yi, vi, mods = ~ class, data=dat, subset=criterion="grade")
res

### estimated average correlations for nonscience and science classes
predict(res, newmods=c(0,1), transf=transf.ztor, digits=2)

### examine if relationship between attendance and grades has changed over time
res <- rma(yi, vi, mods = ~ year, data=dat, subset=criterion="grade")
res

### meta-analysis for the relationship between attendance and GPA
res <- rma(yi, vi, data=dat, subset=criterion="gpa")
res

### estimated average correlation with 95% CI/PI
predict(res, transf=transf.ztor, digits=2)
```
### examine if relationship between attendance and GPA has changed over time
res <- rma(yi, vi, mods = ~ year, data=dat, subset=criterion=="gpa")
res

### use a multilevel model to examine the relationship between attendance and grades
res <- rma.mv(yi, vi, random = ~ 1 | studyid/sampleid, data=dat, subset=criterion=="grade")
res
predict(res, transf=transf.ztor, digits=2)

### use a multilevel model to examine the relationship between attendance and GPA
res <- rma.mv(yi, vi, random = ~ 1 | studyid/sampleid, data=dat, subset=criterion=="gpa")
res
predict(res, transf=transf.ztor, digits=2)

## End(Not run)

---

**dat.curtis1998**  
*Studies on the Effects of Elevated CO2 Levels on Woody Plant Mass*

**Description**

Results from studies examining the effects of elevated CO2 levels on woody plant mass.

**Usage**

dat.curtis1998

**Format**

The data frame contains the following columns:

- **id**: numeric, observation number
- **paper**: numeric, paper number
- **genus**: character, genus name
- **species**: character, species name
- **fungrp**: character, plant functional group
- **co2.ambi**: numeric, ambient CO2 level (control group)
- **co2.elev**: numeric, elevated CO2 level (treatment group)
- **units**: character, units for CO2 exposure levels
- **time**: numeric, maximum length of time (days) of CO2 exposure
- **pot**: character, growing method (see ‘Details’)
- **method**: character, CO2 exposure facility (see ‘Details’)
- **stock**: character, planting stock code
- **xtrt**: character, interacting treatment code (see ‘Details’)
- **level**: character, interacting treatment level codes (see ‘Details’)
- **m1i**: numeric, mean plant mass under elevated CO2 level (treatment group)
Details

The studies included in this dataset compared the total above- plus below-ground biomass (in grams) for plants that were either exposed to ambient (around 35 Pa) and elevated CO2 levels (around twice the ambient level). The co2ambi and co2elev variables indicate the CO2 levels in the control and treatment groups, respectively (with the units variable specifying the units for the CO2 exposure levels). Many of the studies also varied one or more additional environmental variables (defined by the xtrt and level variables):

- NONE = no additional treatment factor
- FERT = soil fertility (either a CONTROL, HIGH, or LOW level)
- LIGHT = light treatment (always a LOW light level)
- FERT+L = soil fertility and light (a LOW light and soil fertility level)
- H2O = well watered vs drought (either a WW or DRT level)
- TEMP = temperature treatment (either a HIGH or LOW level)
- OZONE = ozone exposure (either a HIGH or LOW level)
- UVB = ultraviolet-B radiation exposure (either a HIGH or LOW level)

In addition, the studies differed with respect to various design variables, including CO2 exposure duration (time), growing method (pot: number = pot size in liters; GRND = plants rooted in ground; HYDRO = solution or aeroponic culture), CO2 exposure facility (method: GC = growth chamber; GH = greenhouse; OTC = field-based open-top chamber), and planting stock (stock: SEED = plants started from seeds; SAP = plants started from cuttings). The goal of the meta-analysis was to examine the effects of elevated CO2 levels on plant physiology and growth and the interacting effects of the environmental (and design) variables.

Concepts

ecology, ratios of means

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.curtis1998
head(dat)

### Not run:

### load metafor package
library(metafor)

### calculate (log transformed) ratios of means and corresponding sampling variances
dat <- escalc(measure="ROM", m1i=m1i, sd1i=sd1i, n1i=n1i,
m2i=m2i, sd2i=sd2i, n2i=n2i, data=dat)
head(dat)

### meta-analysis using a random-effects model
res <- rma(yi, vi, method="DL", data=dat)
res

### average ratio of means with 95% CI
predict(res, transf=exp, digits=2)

### meta-analysis for plants grown under nutrient stress
res <- rma(yi, vi, method="DL", data=dat, subset=(xtrt=="FERT" & level=="LOW"))
predict(res, transf=exp, digits=2)

### meta-analysis for plants grown under low light conditions
res <- rma(yi, vi, method="DL", data=dat, subset=(xtrt=="LIGHT" & level=="LOW"))
predict(res, transf=exp, digits=2)

### End(Not run)
```

---

dat.dagostino1998  
*Studies on the Effectiveness of Antihistamines in Reducing Symptoms of the Common Cold*

Description

Results from 9 studies on the effectiveness of antihistamines in reducing the severity of runny nose and sneezing in the common cold.

Usage

dat.dagostino1998
Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study id</td>
</tr>
<tr>
<td>cold</td>
<td>character</td>
<td>natural or induced cold study</td>
</tr>
<tr>
<td>scale.rn</td>
<td>character</td>
<td>scale for measuring runny nose severity</td>
</tr>
<tr>
<td>scale.sn</td>
<td>character</td>
<td>scale for measuring sneezing severity</td>
</tr>
<tr>
<td>drug</td>
<td>character</td>
<td>type of antihistamine studied</td>
</tr>
<tr>
<td>tnt</td>
<td>numeric</td>
<td>total sample size of the treatment group</td>
</tr>
<tr>
<td>tnc</td>
<td>numeric</td>
<td>total sample size of the control (placebo) group</td>
</tr>
<tr>
<td>outcome</td>
<td>character</td>
<td>outcome variable (see ‘Details’)</td>
</tr>
<tr>
<td>mt</td>
<td>numeric</td>
<td>mean in the treatment group</td>
</tr>
<tr>
<td>sdt</td>
<td>numeric</td>
<td>SD in the treatment group</td>
</tr>
<tr>
<td>mc</td>
<td>numeric</td>
<td>mean in the control group</td>
</tr>
<tr>
<td>sdc</td>
<td>numeric</td>
<td>SD in the control group</td>
</tr>
<tr>
<td>xt</td>
<td>numeric</td>
<td>number of patients reaching the therapy goal in the treatment group</td>
</tr>
<tr>
<td>xc</td>
<td>numeric</td>
<td>number of patients reaching the therapy goal in the control (placebo) group</td>
</tr>
<tr>
<td>nt</td>
<td>numeric</td>
<td>sample size of the treatment group for measuring the outcome</td>
</tr>
<tr>
<td>nc</td>
<td>numeric</td>
<td>sample size of the control group for measuring the outcome</td>
</tr>
</tbody>
</table>

Details

The studies for this meta-analysis were assembled to examine the effectiveness of antihistamines in reducing the severity of runny nose and sneezing in the common cold. Effectiveness was measured after one and two days of treatment in terms of 4 different outcome variables:

1. \( rnic1 \) and \( rnic2 \) (continuous): incremental change (improvement) in runny nose severity at day 1 and day 2,
2. \( rngoal1 \) and \( rngoal2 \) (dichotomous): reaching the goal of therapy (of at least a 50% reduction in runny nose severity) at day 1 and day 2,
3. \( snic1 \) and \( snic2 \) (continuous): incremental change (improvement) in sneezing severity at day 1 and day 2, and
4. \( rngoal1 \) and \( rngoal2 \) (dichotomous): reaching the goal of therapy (of at least a 50% reduction in sneezing severity) at day 1 and day 2.

For the continuous outcomes, standardized mean differences can be computed to quantify the difference between the treatment and control groups. For the dichotomous outcomes, one can compute (log) odds ratios to quantify the difference between the treatment and control groups.

Concepts

medicine, standardized mean differences, odds ratios, multivariate models

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org
Source


Examples

```r
### copy data into 'dat' and examine data
data <- dat.dagostino1998
deep(dat, 16)

# Not run:

### load metafor package
library(metafor)

### compute standardized mean differences and corresponding sampling variances
data <- escalc(measure="SMD", m1i=mt, m2i=mc, sd1i=sdt, sd2i=sdc, n1i=nt, n2i=nc, data=dat,
add.measure=TRUE)

### compute log odds ratios and corresponding sampling variances
data <- escalc(measure="OR", ai=xt, ci=xc, n1i=nt, n2i=nc, data=dat,
replace=FALSE, add.measure=TRUE, add=1/2, to="all")

### inspect data for the first study
head(dat, 8)

### fit a random-effects model for incremental change in runny nose severity at day 1
data <- rma(yi, vi, data=dat, subset=outcome=="rnic1")
res

### fit a random-effects model for reaching the goal of therapy for runny nose severity at day 1
data <- rma(yi, vi, data=dat, subset=outcome=="rngoal1")
res
predict(res, transf=exp)

### construct approximate V matrix assuming a correlation of 0.7 for sampling errors within studies
data$esid <- ave(dat$study, dat$study, FUN=seq)
V <- vcalc(vi, cluster=study, obs=esid, rho=0.7, data=dat)

### fit a model for incremental change in runny nose severity at day 1 and at day 2, allowing for
### correlated sampling errors (no random effects added, since there does not appear to be any
### noteworthy heterogeneity in these data)
data <- rma.mv(yi, V, mods = ~ outcome - 1, data=dat, subset=outcome %in% c("rnic1", "rnic2"))
res

### test if there is a difference in effects at day 1 and day 2
anova(res, X=c(1,-1))

# End(Not run)
```
Description

Results from 16 studies examining the effectiveness of topical plus systemic antibiotics to prevent respiratory tract infections (RTIs).

Usage
dat.damico2009

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>study</th>
<th>character</th>
<th>year</th>
<th>numeric</th>
<th>first author</th>
<th>publication year</th>
<th>numeric</th>
<th>number of RTIs in the treatment group</th>
<th>numeric</th>
<th>number of patients in the treatment group</th>
<th>numeric</th>
<th>number of RTIs in the control group</th>
<th>numeric</th>
<th>number of patients in the control group</th>
<th>numeric</th>
<th>allocation concealment (0 = not adequate, 1 = adequate)</th>
<th>numeric</th>
<th>blinding (0 = open, 1 = double-blind)</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>year</td>
<td>numeric</td>
<td>first author</td>
<td>publication year</td>
<td>numeric</td>
<td>number of RTIs in the treatment group</td>
<td>numeric</td>
<td>number of patients in the treatment group</td>
<td>numeric</td>
<td>number of RTIs in the control group</td>
<td>numeric</td>
<td>number of patients in the control group</td>
<td>numeric</td>
<td>allocation concealment (0 = not adequate, 1 = adequate)</td>
<td>numeric</td>
<td>blinding (0 = open, 1 = double-blind)</td>
</tr>
</tbody>
</table>

Details

The dataset includes the results from 16 studies that examined the effectiveness of topical plus systemic antibiotics versus no prophylaxis to prevent respiratory tract infections (RTIs).

Concepts

medicine, odds ratios

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

### copy data into 'dat' and examine data
dat <- dat.damico2009
dat

## Not run:

### load metafor package
library(metafor)

### meta-analysis of the (log) odds ratios using the Mantel-Haenszel method
rma.mh(measure="OR", ai=xt, n1i=nt, ci=xc, n2i=nc, data=dat, digits=2)

### calculate log odds ratios and corresponding sampling variances
dat <- escalc(measure="OR", ai=xt, n1i=nt, ci=xc, n2i=nc, data=dat)

### meta-analysis using a random-effects model
res <- rma(yi, vi, data=dat, method="DL")
res
predict(res, transf=exp, digits=2)

## End(Not run)

dat.debruin2009

Studies on Standard Care Quality and HAART-Adherence

Description

Results from 13 trials providing information about standard care quality and HAART-adherence in control groups.

Usage

dat.debruin2009

Format

The data frame contains the following columns:

- **author**: character (first) author of study
- **year**: numeric publication year
- **scq**: numeric standard care quality
- **ni**: numeric number of patients in the standard care group
- **xi**: numeric number of patients with an undetectable viral load in standard care group
- **mi**: numeric number of patients with a detectable viral load in standard care group
- **ethnicity**: character dominant ethnicity of the patients in the standard care group
- **patients**: character inclusion of patients continuing or starting (a new) treatment
- **select**: character baseline selection of patients with adherence problems or no selection
- **sens**: character sensitivity of viral load assessments (<400 vs. >=400 copies/ml)
Details

Highly active antiretroviral therapy (HAART) refers to a combination of multiple antiretroviral drugs that can effectively suppress the HIV virus. However, achieving viral suppression (to the point that the virus becomes essentially undetectable in a blood sample) requires high levels of adherence to an often complicated medication regimen. A number of trials have examined various interventions that aim to increase adherence levels. In each trial, patients receiving the intervention are compared to patients in a control group receiving standard care (often referred to as ‘care as usual’). However, the quality of standard care can vary substantially between these studies. de Bruin et al. (2009) assessed the quality of standard care provided (based on a quantification of the number of behavior change techniques applied) and examined to what extent the quality of standard care was related to the proportion of patients achieving effective viral suppression in the control groups.

Concepts

psychology, medicine, proportions, single-arm studies, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.debruin2009
dat

### load metafor package
library(metafor)

### calculate proportions and corresponding sampling variances
dat <- escalc(measure="PR", xi=xi, ni=ni, data=dat)
dat

### random-effects model
res <- rma(yi, vi, data=dat)
print(res, digits=2)

### mixed-effects meta-regression model with all predictors/covariates
res <- rma(yi, vi, mods = ~ scq + ethnicity + patients + select + sens, data=dat)
print(res, digits=3)
```
mixed-effects meta-regression model with scq and ethnicity as predictors/covariates
res <- rma(yi, vi, mods = ~ scq + ethnicity, data=dat)
print(res, digits=3)

## End(Not run)

---

**dat.dogliotti2014**  
*Studies on Antithrombotic Treatments to Prevent Strokes*

**Description**

Results from 20 trials examining the effectiveness of antithrombotic treatments to prevent strokes in patients with non-valvular atrial fibrillation.

**Usage**

dat.dogliotti2014

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>study label</td>
</tr>
<tr>
<td>id</td>
<td>numeric</td>
<td>study ID</td>
</tr>
<tr>
<td>treatment</td>
<td>character</td>
<td>treatment</td>
</tr>
<tr>
<td>stroke</td>
<td>numeric</td>
<td>number of strokes</td>
</tr>
<tr>
<td>total</td>
<td>numeric</td>
<td>number of individuals</td>
</tr>
</tbody>
</table>

**Details**

This data set comes from a systematic review aiming to estimate the effects of eight antithrombotic treatments including placebo in reducing the incidence of major thrombotic events in patients with non-valvular atrial fibrillation (Dogliotti et al., 2014).

The review included 20 studies with 79,808 participants, four studies are three-arm studies. The primary outcome is stroke reduction (yes / no).

**Concepts**

medicine, odds ratios, network meta-analysis, Mantel-Haenszel method

**Author(s)**

Guido Schwarzer, <sc@imbi.uni-freiburg.de>, [https://github.com/guido-s/](https://github.com/guido-s/)
Source

See Also
pairwise, metabin, netmeta, netmetabin

Examples
### Show first 7 rows / 3 studies of the dataset
head(dat.dogliotti2014, 7)

### Not run:
### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print odds ratios and confidence limits with two digits
settings.meta(digits = 2)

### Change appearance of confidence intervals
cilayout("", "-")

### Transform data from long arm-based format to contrast-based
### format. Argument 'sm' has to be used for odds ratio as summary
### measure; by default the risk ratio is used in the metabin function
### called internally.
pw <- pairwise(treat = treatment, n = total, event = stroke,
        studlab = study, data = dat.dogliotti2014, sm = "OR")

### Print log odds ratios (TE) and standard errors (seTE)
head(pw, 5)[, 1:5]

### Conduct network meta-analysis (NMA) with placebo as reference
net <- netmeta(pw, ref = "plac")

### Details on excluded study
selvars <- c("studlab", "event1", "n1", "event2", "n2")
subset(pw, studlab == "WASPO, 2007")[, selvars]

### Show network graph
netgraph(net, seq = "optimal", number = TRUE)

### Conduct Mantel-Haenszel NMA
net.mh <- netmetabin(pw, ref = "plac")

### Compare results of inverse variance and Mantel-Haenszel NMA
nb <- netbind(net, net.mh, random = FALSE,
        name = c("Inverse variance", "Mantel-Haenszel"))
forest(nb, xlim = c(0.15, 2), at = c(0.2, 0.5, 1, 2))
### Print and plot results for inverse variance NMA
net
forest(net)

## End(Not run)

dat.dong2013

### Studies on Safety of Inhaled Medications for Chronic Obstructive Pulmonary Disease

#### Description
Results from 41 trials examining the safety of inhaled medications in patients with chronic obstructive pulmonary disease.

#### Usage
dat.dong2013

#### Format
The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>integer</td>
<td>study ID</td>
</tr>
<tr>
<td>treatment</td>
<td>character</td>
<td>treatment</td>
</tr>
<tr>
<td>death</td>
<td>integer</td>
<td>mortality</td>
</tr>
<tr>
<td>randomized</td>
<td>integer</td>
<td>number of individuals</td>
</tr>
</tbody>
</table>

#### Details
This network meta-analysis compared the safety of inhaled medications in patients with chronic obstructive pulmonary disease (Dong et al., 2013).

Mortality was reported in 41 randomized trials, with a total of 52,462 patients. Mortality was low, with 2,408 deaths (4.6%) reported across all studies. There were nine studies that reported zero events in at least one of the treatment arms and three additional studies had zero events in all treatment arms.

This data set was used in Efthimiou et al. (2019) to illustrate the Mantel-Haenszel method for network meta-analysis.

#### Concepts
medicine, odds ratios, network meta-analysis, Mantel-Haenszel method

#### Author(s)
Guido Schwarzer, <sc@imbi.uni-freiburg.de>, https://github.com/guido-s/
Source


References


See Also

`pairwise`, `metabin`, `netmetabin`

Examples

```r
### Show first 6 rows / 3 studies of the dataset
head(dat.dong2013)

## Not run:
### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print odds ratios and confidence limits with two digits
settings.meta(digits = 2)

### Change appearance of confidence intervals
cilayout("("", "-")

### Transform data from long arm-based format to contrast-based
### format. Argument 'sm' has to be used for odds ratio as summary
### measure; by default the risk ratio is used in the metabin function
### called internally.
pw <- pairwise(treatment, death, randomized, studlab = id,
data = dat.dong2013, sm = "OR")

### Calculated log odds ratios (TE) and standard errors (seTE)
pw[1:3, 1:9]

### Conduct Mantel-Haenszel network meta-analysis (NMA)
net <- netmetabin(pw, ref = "plac")

### Network graph
netgraph(net, seq = "optimal", col = "black", plastic = FALSE,
points = TRUE, pch = 21, cex.points = 3, col.points = "black",
bg.points = "gray", thickness = "se.fixed",
number.of.studies = TRUE)
```
### Show results for Mantel-Haenszel NMA
net
forest(net)

### League table with network estimates in lower triangle and direct
### estimates in upper triangle
netleague(net)

### Assess inconsistency
print(netsplit(net), show = "both", ci = TRUE, overall = FALSE,
nchar.trts = 6)

## End(Not run)

dat.dorn2007

---

**Studies on Complementary and Alternative Medicine for Irritable Bowel Syndrome**

---

**Description**

Results from 19 trials examining complementary and alternative medicine (CAM) for irritable bowel syndrome (IBS).

**Usage**

dat.dorn2007

**Format**

The data frame contains the following columns:

- **id**: numeric, trial id number
- **study**: character, (first) author
- **year**: numeric, publication year
- **country**: character, country where trial was conducted
- **ibs.crit**: character, IBS diagnostic criteria (Manning, Rome I, Rome II, or Other)
- **days**: numeric, number of treatment days
- **visits**: numeric, number of practitioner visits
- **jada**: numeric, Jadad score
- **x.a**: numeric, number of responders in the active treatment group
- **n.a**: numeric, number of participants in the active treatment group
- **x.p**: numeric, number of responders in the placebo group
- **n.p**: numeric, number of participants in the placebo group
Details

The dataset includes the results from 19 randomized clinical trials that examined the effectiveness of complementary and alternative medicine (CAM) for irritable bowel syndrome (IBS).

Concepts

medicine, alternative medicine, risk ratios

Note

The data were extracted from Table I in Dorn et al. (2009). Comparing the funnel plot in Figure 1 with the one obtained below indicates that the data for study 5 (Davis et al., 2006) in the table were not the ones that were used in the actual analyses.

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.dorn2007
dat

## Not run:
### load metafor package
library(metafor)

### calculate log risk ratios and corresponding sampling variances
dat <- escalc(measure="RR", ai=x.a, n1i=n.a, ci=x.p, n2i=n.p, data=dat)

### random-effects model
res <- rma(yi, vi, data=dat, digits=2, method="DL")
res

### estimated average risk ratio
predict(res, transf=exp)

### funnel plot with study 5 highlighted in red
funnel(res, atransf=exp, at=log(c(.1, .2, .5, 1, 2, 5, 10)),
    ylim=c(0,1), steps=6, las=1, col=ifelse(id == 5, "red", "black"))

### change log risk ratio for study 5
```
dat$yi[5] <- -0.44
### results are now more in line with what is reported in the paper
### (although the CI in the paper is not wide enough)
res <- rma(yi, vi, data=dat, digits=2, method="DL")
predict(res, transf=exp)

### funnel plot with study 5 highlighted in red
funnel(res, atransf=exp, at=log(c(.1,.2,.5, 1, 2, 5, 10)),
       ylim=c(0,1), steps=6, las=1, col=ifelse(id == 5, "red", "black"))

## End(Not run)

---

**dat.egger2001**

*Studies on the Effectiveness of Intravenous Magnesium in Acute Myocardial Infarction*

**Description**

Results from 16 trials examining the effectiveness of intravenous magnesium in the prevention of death following acute myocardial infarction.

**Usage**

`dat.egger2001`

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>numeric</td>
<td>trial id number</td>
</tr>
<tr>
<td>study</td>
<td>character</td>
<td>first author or trial name</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>ai</td>
<td>numeric</td>
<td>number of deaths in the magnesium group</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of patients in the magnesium group</td>
</tr>
<tr>
<td>ci</td>
<td>numeric</td>
<td>number of deaths in the control group</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of patients in the control group</td>
</tr>
</tbody>
</table>

**Details**

The dataset includes the results from 16 randomized clinical trials that examined the effectiveness of intravenous magnesium in the prevention of death following acute myocardial infarction. Studies 1-7 were included in the meta-analyses by Teo et al. (1991) and Horner (1992) and were combined with the results from the LIMIT-2 trial (Woods et al., 1992) in Yusuf et al. (1993), suggesting that magnesium is an effective treatment for reducing mortality. However, the results from the ISIS-4 mega trial (ISIS-4 Collaborative Group, 1995) indicated no reduction in mortality with magnesium treatment. Publication bias has been suggested as one possible explanation for the conflicting find-
The present dataset includes some additional trials and are based on Table 18.2 from Egger, Davey Smith, and Altman (2001).

Concepts

medicine, cardiology, Peto’s method, publication bias

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


See Also

dat.li2007

Examples

```r
### copy data into 'dat' and examine data
dat <- dat.egger2001
dat
```
## Not run:

### load metafor package
library(metafor)

### meta-analysis of trials 1-7 using Peto's method (as in Teo et al., 1991)
res <- rma.peto(ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, subset=1:7)
print(res, digits=2)

### meta-analysis of trials 1-7 and LIMIT-2 (as in Yusuf et al., 1993)
res <- rma.peto(ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, subset=c(1:7,14))
print(res, digits=2)

### meta-analysis of all trials except ISIS-4
res <- rma.peto(ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, subset=-16)
print(res, digits=2)
predict(res, transf=exp, digits=2)

### meta-analysis of all trials including ISIS-4
res <- rma.peto(ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat)
print(res, digits=2)
predict(res, transf=exp, digits=2)

### contour-enhanced funnel plot centered at 0
funnel(res, refline=0, level=c(90, 95, 99), shade=c("white", "gray", "darkgray")

## End(Not run)

dat.fine1993

### Studies on Radiation Therapy with or without Adjuvant Chemotherapy in Patients with Malignant Gliomas

---

**Description**

Results from 17 trials comparing post-operative radiation therapy with and without adjuvant chemotherapy in patients with malignant gliomas.

**Usage**

dat.fine1993

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Event</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>nei</td>
<td>numeric</td>
<td>sample size in the experimental group receiving radiotherapy plus adjuvant chemotherapy</td>
</tr>
<tr>
<td>nci</td>
<td>numeric</td>
<td>sample size in the control group receiving radiotherapy alone</td>
</tr>
<tr>
<td>e1i</td>
<td>numeric</td>
<td>number of survivors at 6 months in the experimental group</td>
</tr>
</tbody>
</table>
Details

The 17 trials report the post-operative survival of patients with malignant gliomas receiving either radiation therapy with adjuvant chemotherapy or radiation therapy alone. Survival was assessed at 6, 12, 18, and 24 months in all but one study (which assessed survival only at 12 and at 24 months). The data were reconstructed by Trikalinos and Olkin (2012) based on Table 2 in Fine et al. (1993) and Table 3 in Dear (1994). The data can be used to illustrate how a meta-analysis can be conducted of effect sizes reported at multiple time points using a multivariate model.

Concepts

medicine, oncology, odds ratios, longitudinal models

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.fine1993
dat

## Not run:

### load metafor package
library(metafor)
```
### calculate log(ORs) and sampling variances for each time point
```
dat <- escalc(measure="OR", ai=e1i, n1i=nei, ci=c1i, n2i=nci, data=dat, var.names=c("y1i","v1i"))
dat <- escalc(measure="OR", ai=e2i, n1i=nei, ci=c2i, n2i=nci, data=dat, var.names=c("y2i","v2i"))
dat <- escalc(measure="OR", ai=e3i, n1i=nei, ci=c3i, n2i=nci, data=dat, var.names=c("y3i","v3i"))
dat <- escalc(measure="OR", ai=e4i, n1i=nei, ci=c4i, n2i=nci, data=dat, var.names=c("y4i","v4i"))
```

### calculate the covariances (equations in Appendix of Trikalinos & Olkin, 2012)
```
dat$v12i <- with(dat, nei / (e1i * (nei - e2i)) + nci / (c1i * (nci - c2i)))
dat$v13i <- with(dat, nei / (e1i * (nei - e3i)) + nci / (c1i * (nci - c3i)))
dat$v14i <- with(dat, nei / (e1i * (nei - e4i)) + nci / (c1i * (nci - c4i)))
dat$v23i <- with(dat, nei / (e2i * (nei - e3i)) + nci / (c2i * (nci - c3i)))
dat$v24i <- with(dat, nei / (e2i * (nei - e4i)) + nci / (c2i * (nci - c4i)))
dat$v34i <- with(dat, nei / (e3i * (nei - e4i)) + nci / (c3i * (nci - c4i)))
```

### create dataset in long format
```
dat.long <- data.frame(study=rep(1:nrow(dat), each=4), time=1:4,
yi=c(t(dat[c("y1i","y2i","y3i","y4i")])),
vi=c(t(dat[c("v1i","v2i","v3i","v4i")])))
```

### var-cov matrices of the studies
```
V <- lapply(split(dat, dat$study),
  function(x) matrix(c( x$v1i, x$v12i, x$v13i, x$v14i,
                      x$v12i, x$v2i, x$v23i, x$v24i,
                      x$v13i, x$v23i, x$v3i, x$v34i,
                      x$v14i, x$v24i, x$v34i, x$v4i), nrow=4, ncol=4, byrow=TRUE))
```

### remove rows for the missing time points in study 17
```
dat.long <- na.omit(dat.long)
```

### remove corresponding rows/columns from var-cov matrix
```
V[[17]] <- V[[17]][c(2,4),c(2,4)]
```

### make a copy of V
```
Vc <- V
```

### replace any (near) singular var-cov matrices with ridge corrected versions
```
repl.Vi <- function(Vi) {
  res <- eigen(Vi)
  if (any(res$values <= .08)) {
    round(res$vectors %*% diag(res$values + .08) %*% t(res$vectors), 12)
  } else {
    Vi
  }
}
Vc <- lapply(Vc, repl.Vi)
```

### do not correct var-cov matrix of study 17
```
Vc[[17]] <- V[[17]]
```

### construct block diagonal matrix
```
Vc <- bldiag(Vc)
```

### multivariate fixed-effects model
res <- rma.mv(yi, Vc, mods = ~ factor(time) - 1, method="FE", data=dat.long)
print(res, digits=3)

### multivariate random-effects model with heteroscedastic AR(1) structure for the true effects
res <- rma.mv(yi, Vc, mods = ~ factor(time) - 1, random = ~ time | study,
struct="HAR", data=dat.long, control=list(optimizer="hjk"))
print(res, digits=3)

### profile the variance components
par(mfrow=c(2,2))
profile(res, tau2=1, xlim=c(0,.2))
profile(res, tau2=2, xlim=c(0,.2))
profile(res, tau2=3, xlim=c(0,.2))
profile(res, tau2=4, xlim=c(.1,.3))

### profile the autocorrelation coefficient
par(mfrow=c(1,1))
profile(res, rho=1)

## End(Not run)

---

**dat.franchini2012**

**Studies on Dopamine Agonists to Reduce “Off-Time” in Patients with Advanced Parkinson Disease**

**Description**

Results from 7 trials examining the effectiveness of four dopamine agonists and placebo to reduce “off-time” in patients with advanced Parkinson disease.

**Usage**

dat.franchini2012

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Study</td>
<td>character</td>
<td>study label</td>
</tr>
<tr>
<td>Treatment1</td>
<td>character</td>
<td>treatment 1</td>
</tr>
<tr>
<td>y1</td>
<td>numeric</td>
<td>treatment effect arm 1</td>
</tr>
<tr>
<td>sd1</td>
<td>numeric</td>
<td>standard deviation arm 2</td>
</tr>
<tr>
<td>n1</td>
<td>integer</td>
<td>sample size arm 1</td>
</tr>
<tr>
<td>Treatment2</td>
<td>character</td>
<td>treatment 2</td>
</tr>
<tr>
<td>y2</td>
<td>numeric</td>
<td>treatment effect arm 2</td>
</tr>
<tr>
<td>sd2</td>
<td>numeric</td>
<td>standard deviation arm 2</td>
</tr>
<tr>
<td>n2</td>
<td>integer</td>
<td>sample size arm 1</td>
</tr>
<tr>
<td>Treatment3</td>
<td>character</td>
<td>treatment 3</td>
</tr>
</tbody>
</table>
Details

This network meta-analysis compared the effectiveness of four active treatments and placebo in patients with advanced Parkinson disease (Franchini et al., 2012). The outcome is mean lost work-time reduction in patients given dopamine agonists as adjunct therapy. The data are given as sample size, mean, and standard deviation in each trial arm.

This data set was used as an example in the supplemental material of Dias et al. (2013) where placebo is coded as 1 and the four active drugs as 2 to 5.

Examples

```r
### Show results from first three studies; third study is a three-arm study
head(dat.franchini2012, 3)

## Not run:
### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print mean differences with two digits
settings.meta(digits = 2)

### Transform data from wide arm-based format to contrast-based format. Argument 'sm' must not be provided as the mean difference is the default in R function metacont() called internally.
pw <- pairwise(list(Treatment1, Treatment2, Treatment3),
    n = list(n1, n2, n3),
    mean = list(y1, y2, y3),
...
dat.frank2008

Studies on the Association Between the CASP8 -652 6N del Promoter Polymorphism and Breast Cancer Risk

Description

Results from 4 case-control studies examining the association between the CASP8 -652 6N del promoter polymorphism and breast cancer risk.

Usage

dat.frank2008

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>study</th>
<th>character</th>
<th>study identifier</th>
</tr>
</thead>
<tbody>
<tr>
<td>bc.ins.ins</td>
<td>numeric</td>
<td>number of cases who have a homozygous insertion polymorphism</td>
</tr>
<tr>
<td>bc.ins.del</td>
<td>numeric</td>
<td>number of cases who have a heterozygous insertion/deletion polymorphism</td>
</tr>
<tr>
<td>bc.del.del</td>
<td>numeric</td>
<td>number of cases who have a homozygous deletion polymorphism</td>
</tr>
<tr>
<td>ct.ins.ins</td>
<td>numeric</td>
<td>number of controls who have a homozygous insertion polymorphism</td>
</tr>
<tr>
<td>ct.ins.del</td>
<td>numeric</td>
<td>number of controls who are heterozygous insertion/deletion polymorphism</td>
</tr>
<tr>
<td>ct.del.del</td>
<td>numeric</td>
<td>number of controls who have a homozygous deletion polymorphism</td>
</tr>
</tbody>
</table>

Details

The 4 studies included in this dataset are case-control studies that have examined the association between the CASP8 -652 6N del promoter polymorphism and breast cancer risk. Breast cancer cases and controls were genotyped and either had a homozygous insertion, a heterozygous insertion/deletion, or a homozygous deletion polymorphism.
Ziegler et al. (2011) used the same dataset to illustrate the use of meta-analytic methods to examine deviations from Hardy-Weinberg equilibrium across multiple studies. The relative excess heterozygosity (REH) is the proposed measure for such a meta-analysis, which can be computed by setting measure="REH".

Concepts
medicine, oncology, genetics, odds ratios

Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

References

Examples
```r
### copy data into 'dat' and examine data
dat <- dat.frank2008
dat

### load metafor package
library(metafor)

### calculate log odds ratios comparing ins/del versus ins/ins
dat <- escalc(measure="OR", ai=bc.ins.del, bi=bc.ins.ins,
              ci=ct.ins.del, di=ct.ins.ins, data=dat)

### fit random-effects model and get the pooled odds ratio (with 95% CI)
res <- rma(yi, vi, data=dat)
res
predict(res, transf=exp, digits=2)

### calculate log odds ratios comparing del/del versus ins/ins
dat <- escalc(measure="OR", ai=bc.del.del, bi=bc.ins.ins,
```

### fit random-effects model and get the pooled odds ratio (with 95% CI)
res <- rma(yi, vi, data=dat)
res
predict(res, transf=exp, digits=2)

### calculate log odds ratios comparing ins/del+del/del versus ins/ins
dat <- escalc(measure="OR", ai=bc.ins.del+bc.del.del, bi=bc.ins.ins, 
    ci=ct.ins.del+ct.del.del, di=ct.ins.ins, data=dat)

### fit random-effects model and get the pooled odds ratio (with 95% CI)
res <- rma(yi, vi, data=dat)
res
predict(res, transf=exp, digits=2)

### compute the relative excess heterozygosity in the controls
dat <- escalc(measure="REH", ai=ct.ins.ins, bi=ct.ins.del, ci=ct.del.del, 
    slab=study, data=dat)

### fit random-effects model and get the pooled REH value (with 90% CI)
res <- rma(yi, vi, data=dat, level=90)
res
predict(res, transf=exp, digits=2)

### draw forest plot
forest(res, atransf=exp, header=TRUE, xlim=c(-1.5,1.5), at=log(c(0.5,5/7,1,7/5,2))
segments(log(5/7), -2, log(5/7), res$k+1, lty="dotted")
segments(log(7/5), -2, log(7/5), res$k+1, lty="dotted")

## End(Not run)

---

**dat.gibson2002**  
*Studies on the Effectiveness of Self-Management Education and Regular Medical Review for Adults with Asthma*

---

**Description**

Results from 15 trials examining the effectiveness of self-management education and regular medical review for adults with asthma.

**Usage**

dat.gibson2002
Format

The data frame contains the following columns:
Asthma management guidelines typically recommend for patients to receive education and regular medical review. While self-management programs have been shown to increase patient knowledge, it is less clear to what extent they actually impact health outcomes. The systematic review by Gibson et al. (2002) examined the effectiveness of self-management education and regular medical review for adults with asthma. In each study, participants receiving a certain management intervention were compared against those in a control/comparison group with respect to a variety of health outcomes. One of the outcomes examined in a number of studies was the number of days off work/school.

The majority of studies reporting this outcome provided means and standard deviations allowing a meta-analysis of standardized mean differences. Seven studies also reported the number of participants who had one or more days off work/school in each group. These studies could be meta-analyzed using, for example, (log) risk ratios. Finally, one could also consider a combined analysis based on standardized mean differences computed from the means and standard deviations where available and using probit transformed risk differences (which also provide estimates of the standardized mean difference) for the remaining studies.

Some degree of patient education was provided in all studies. In addition, the type variable indicates what additional intervention components were included in each study:

1. optimal self-management (writing action plan, self-monitoring, regular medical review),
2. self-monitoring and regular medical review,
3. self-monitoring only,
4. regular medical review only,
5. written action plan only.

Concepts

medicine, primary care, risk ratios, standardized mean differences

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org
### Example

#### Data Importing

```r
# load data
dat <- dat.gibson2002

dat
```

#### Data Exploration

```r
# load metafor package
library(metafor)

# compute standardized mean differences and corresponding sampling variances
dat <- escalc(measure="SMD", m1i=m1i, sd1i=sd1i, n1i=n1i, m2i=m2i, sd2i=sd2i, n2i=n2i, data=dat)
dat

# fit an equal-effects model to the standardized mean differences (as in Gibson et al., 2002)
res <- rma(yi, vi, data=dat, method="EE")
print(res, digits=2)

# compute log risk ratios and corresponding sampling variances
dat <- escalc(measure="RR", ai=ai, bi=bi, ci=ci, di=di, data=dat)
dat

# fit an equal-effects model to the log risk ratios
res <- rma(yi, vi, data=dat, method="EE")
print(res, digits=2)
predict(res, transf=exp, digits=2)

# note: Gibson et al. (2002) used the Mantel-Haenszel method for their analysis
rma.mh(measure="RR", ai=ai, bi=bi, ci=ci, di=di, data=dat, digits=2)

# compute standardized mean differences where possible and otherwise probit transformed
# risk differences (which also provide estimates of the standardized mean differences)
dat <- escalc(measure="SMD", m1i=m1i, sd1i=sd1i, n1i=n1i,
             m2i=m2i, sd2i=sd2i, n2i=n2i, data=dat, add.measure=TRUE)
dat <- escalc(measure="PBIT", ai=ai, bi=bi, ci=ci, di=di, data=dat, replace=FALSE, add.measure=TRUE)
dat

# fit a random-effects model to these estimates
res <- rma(yi, vi, data=dat)
print(res, digits=2)

# meta-regression model examining if there are systematic differences based on the
# type of measure used (there are only 2 studies where measure="PBIT", so this isn't
# very conclusive here, but shown for illustration purposes)
res <- rma(yi, vi, mods = ~ measure, data=dat)
## dat.graves2010

### Studies on the Effectiveness of Injected Cholera Vaccines

**Description**

Results from 17 studies on the effectiveness of injected vaccines against cholera.

**Usage**

```R
dat.graves2010
```

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>study</th>
<th>character</th>
</tr>
</thead>
<tbody>
<tr>
<td>ai</td>
<td>numeric</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
</tr>
<tr>
<td>ci</td>
<td>numeric</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
</tr>
</tbody>
</table>

**Details**

Cholera is an infection caused by certain strains of the bacterium *Vibrio cholerae*. When untreated, mortality rates can be as high as 50-60%. Proper sanitation practices are usually effective in preventing outbreaks, but a number of oral and injectable vaccines have also been developed. The Cochrane review by Graves et al. (2010) examined the effectiveness of injectable vaccines for preventing cholera cases and death. The present dataset includes results from 17 studies that reported the number of cholera cases in vaccinated and placebo/comparison groups up to 7 months after the treatment.

**Concepts**

medicine, risk ratios, Mantel-Haenszel method

**Author(s)**

Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)

**Source**

Examples

```r
### copy data into 'dat' and examine data
dat <- dat.graves2010
dat

### Not run:

### load metafor package
library(metafor)

### analysis using the Mantel-Haenszel method
rma.mh(measure="RR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, digits=2)

### End(Not run)
```

---

**dat.gurusamy2011**  
*Studies on Interventions to Reduce Mortality after Liver Transplantation*

**Description**

Results from 14 trials examining the mortality risk of interventions for decreasing blood loss and blood transfusion requirements during liver transplantation.

**Usage**

dat.gurusamy2011

**Format**

The data frame contains the following columns:

- **study**: character, study information
- **treatment**: character, treatment
- **death**: integer, mortality at 60 days post-transplantation
- **n**: integer, number of individuals

**Details**

This network meta-analysis compared the effectiveness of seven interventions for decreasing blood loss and blood transfusion requirements during liver transplantation (Gurusamy et al., 2011).

Fourteen studies reported mortality at 60 days, in 1,002 patients. Forty-five deaths were reported across all studies (4.5%). Six studies observed deaths in all treatment arms while three studies did not observe any deaths.
This data set was used in Efthimiou et al. (2019) to introduce the Mantel-Haenszel method for network meta-analysis.

One of the treatments (solvent detergent plasma) was only included in one study with zero events in both treatment arms; this study was excluded from all network meta-analyses. In addition, no death was observed in the antithrombin III arm of the only study evaluating this treatment which was excluded from the Mantel-Haenszel network meta-analysis.

Concepts

medicine, odds ratios, network meta-analysis, Mantel-Haenszel method

Author(s)

Guido Schwarzer, <sc@imbi.uni-freiburg.de>, https://github.com/guido-s/

Source


References


See Also

pairwise, metabin, netmetabin

Examples

```r
### Show first 6 rows of the dataset
head(dat.gurusamy2011)

### Only study evaluating solvent detergent plasma
subset(dat.gurusamy2011, study == "Williamson 1999")

### Only study evaluating antithrombin III
subset(dat.gurusamy2011, study == "Baudo 1992")

## Not run:
### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print odds ratios and confidence limits with two digits
settings.meta(digits = 2)

### Change appearance of confidence intervals
```
Transform data from long arm-based format to contrast-based format. Argument 'sm' has to be used for odds ratio as summary measure; by default the risk ratio is used in the metabin function called internally.

```r
pw <- pairwise(treatment, death, n, studlab = study, data = dat.gurusamy2011, sm = "OR")
```

### Conduct Mantel-Haenszel network meta-analysis (NMA)
```r
net.MH <- netmetabin(pw, ref = "cont")
```

### Conduct inverse variance (IV) network meta-analysis
```r
net.IV <- netmeta(pw, ref = "cont")
```

### Network graph (Mantel-Haenszel NMA)
```r
netgraph(net.MH, seq = "optimal", col = "black", plastic = FALSE, points = TRUE, pch = 21, cex.points = 3, col.points = "black", bg.points = "gray", thickness = "se.fixed", number.of.studies = TRUE)
```

### Full network graph (based on inverse variance method, including study comparing Antithrombin III with Control/Placebo)
```r
netgraph(net.IV, seq = "optimal", col = "black", plastic = FALSE, points = TRUE, pch = 21, cex.points = 3, col.points = "black", bg.points = "gray", thickness = "se.fixed", number.of.studies = TRUE)
```

### Compare results for Mantel-Haenszel and IV NMA
```r
forest(netbind(net.MH, net.IV, random = FALSE, name = c("MH NMA", "IV NMA")))
```

### Show results for Mantel-Haenszel NMA
```r
net.MH
forest(net.MH)
```

### League table with network estimates in lower triangle and direct estimates in upper triangle
```r
netleague(net.MH)
```

### Assess inconsistency
```r
print(netsplit(net.MH), show = "both", ci = TRUE, overall = FALSE, nchar.trts = 6)
```

```r
## End(Not run)
```
Description

Results from 37 studies on the risk of lung cancer in women exposed to environmental tobacco smoke (ETS) from their smoking spouse.

Usage
dat.hackshaw1998

Format

The data frame contains the following columns:

```
<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>first author of study</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>country</td>
<td>character</td>
<td>country where study was conducted</td>
</tr>
<tr>
<td>design</td>
<td>character</td>
<td>study design (either cohort or case-control)</td>
</tr>
<tr>
<td>cases</td>
<td>numeric</td>
<td>number of lung cancer cases</td>
</tr>
<tr>
<td>or</td>
<td>numeric</td>
<td>odds ratio</td>
</tr>
<tr>
<td>or.lb</td>
<td>numeric</td>
<td>lower bound of 95% CI for the odds ratio</td>
</tr>
<tr>
<td>or.ub</td>
<td>numeric</td>
<td>upper bound of 95% CI for the odds ratio</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>log odds ratio</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
</tbody>
</table>
```

Details

The dataset includes the results from 37 studies (4 cohort, 33 case-control) examining if women (who are lifelong nonsmokers) have an elevated risk for lung cancer due to exposure to environmental tobacco smoke (ETS) from their smoking spouse. Values of the log odds ratio greater than 0 indicate an increased risk of cancer in exposed women compared to women not exposed to ETS from their spouse.

Note that the log odds ratios and corresponding sampling variances were back-calculated from the reported odds ratios and confidence interval (CI) bounds (see ‘Examples’). Since the reported values were rounded to some extent, this introduces some minor inaccuracies into the back-calculations. The overall estimate reported in Hackshaw et al. (1997) and Hackshaw (1998) can be fully reproduced though.

Concepts

medicine, oncology, epidemiology, smoking, odds ratios

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

# Examples

```r
### copy data into `dat` and examine data
dat <- dat.hackshaw1998
head(dat, 10)

### Not run:

### load metafor package
library(metafor)

### random-effects model using the log odds ratios
res <- rma(yi, vi, data=dat, method="DL")
res

### estimated average odds ratio with CI (and prediction interval)
predict(res, transf=exp, digits=2)

### illustrate how the log odds ratios and corresponding sampling variances
### were back-calculated based on the reported odds ratios and CI bounds
dat$yi <- log(dat$or)
dat$vi <- ((log(dat$or.ub) - log(dat$or.lb)) / (2*qnorm(.975)))^2

### End(Not run)
```

---

# dat.hahn2001

**Studies on the Effectiveness of Different Rehydration Solutions for the Prevention of Unscheduled Intravenous Infusion in Children with Diarrhoea**

---

**Description**

Results from 12 trials examining the effectiveness of a reduced versus standard rehydration solution for the prevention of unscheduled intravenous infusion in children with diarrhoea.

**Usage**

`dat.hahn2001`

**Format**

The data frame contains the following columns:

- **study**: character  trial name and year
- **ai**: numeric  number of children requiring unscheduled intravenous infusion in the reduced rehydration solution group
- **nli**: numeric  number of children in the reduced rehydration solution group
The dataset includes the results from 12 randomized clinical trials that examined the effectiveness of a reduced osmolarity oral rehydration solution (total osmolarity <250 mmol/l with reduced sodium) with a standard WHO oral rehydration solution (sodium 90 mmol/l, glucose 111mmol/l, total osmolarity 311 mmol/l) for the prevention of unscheduled intravenous infusion in children with diarrhoea.

**Concepts**

medicine, odds ratios, Mantel-Haenszel method

**Author(s)**

Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)

**Source**


**Examples**

```r
### copy data into 'dat' and examine data
dat <- dat.hahn2001
dat

## Not run:
### load metafor package
library(metafor)

### meta-analysis of (log) odds rations using the Mantel-Haenszel method
res <- rma.mh(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, digits=2, slab=study)
res

### forest plot (also show studies that were excluded from the analysis)
options(na.action="na.pass")
forest(res, atransf=exp, at=log(c(.01, .1, 1, 10, 100)), header=TRUE)
options(na.action="na.omit")

## End(Not run)```
Description

Results from 35 studies measuring olfactory loss in COVID-19 patients using either objective or subjective measures.

Usage
dat.hannum2020

Format

The data frame contains the following columns:

- **authorName**: character (first) author of study
- **DOI**: character article DOI number
- **ni**: numeric number of Covid-19 positive patients in the study
- **xi**: numeric number of Covid-19 positive patients in the study with olfactory loss
- **percentOlfactoryLoss**: numeric percent of the sample with olfactory loss
- **objectivity**: character objective or subjective measure used
- **measured**: character outcome measure
- **testType**: character type of test used
- **country**: character country where patients were treated
- **patientType**: character type of patient information and location where being treated

Details

One of the symptoms of COVID-19 infection is olfactory loss (loss of smell) either recently acquired anosmia (complete loss of smell) or hyposmia (partial loss of smell). One challenge to reaching this symptom is the wide range of reported prevalence for this symptom ranging from 5 percent to 98 percent. In this dataset studies were grouped into one of two groups based on the type of method used to measure smell loss (either subjective measures, such as self-reported smell loss, or objective measures using rated stimuli).

Concepts

- medicine, covid-19, proportions

Author(s)

W. Kyle Hamilton <whamilton@ucmerced.edu> [https://kylehamilton.com](https://kylehamilton.com)
Source

Ramirez VA, Hannum ME, Lipson SJ, Herriman RD, Toskala AK, Lin C, Joseph PV, Reed DR.

References


Examples

# copy data into 'dat' and examine data
dat <- dat.hannum2020
dat

## Not run:

# load metafor package
library(metafor)

# compute effect size
dat <- escalc(measure="PR", xi=xi, ni=ni, data=dat)

# split data into objective and subjective datasets
dat_split <- split(dat, dat$objectivity)
dat_objective <- dat_split["Objective"]
dat_subjective <- dat_split["Subjective"]

# random-effects model all studies
res_all <- rma(yi, vi, data=dat)
print(res_all, digits=2)

# random-effects model objective
res_objective <- rma(yi, vi, data=dat_objective)
print(res_objective, digits=2)

# random-effects model subjective
res_subjective <- rma(yi, vi, data=dat_subjective)
print(res_subjective, digits=2)

## End(Not run)
Description

Results from 6 clinical trials examining the effectiveness of adjusted-dose warfarin for preventing strokes in patients with atrial fibrillation.

Usage

dat.hart1999

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trial</td>
<td>numeric</td>
<td>trial number</td>
</tr>
<tr>
<td>study</td>
<td>character</td>
<td>study name (abbreviated)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>x1i</td>
<td>numeric</td>
<td>number of strokes in the warfarin group</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of patients in the warfarin group</td>
</tr>
<tr>
<td>t1i</td>
<td>numeric</td>
<td>total person-time (in years) in the warfarin group</td>
</tr>
<tr>
<td>x2i</td>
<td>numeric</td>
<td>number of strokes in the placebo/control group</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of patients in the placebo/control group</td>
</tr>
<tr>
<td>t2i</td>
<td>numeric</td>
<td>total person-time (in years) in the placebo/control group</td>
</tr>
<tr>
<td>compgrp</td>
<td>character</td>
<td>type of comparison group (placebo or control)</td>
</tr>
<tr>
<td>prevtype</td>
<td>character</td>
<td>type of prevention (primary or secondary)</td>
</tr>
<tr>
<td>trinr</td>
<td>character</td>
<td>target range for the international normalized ratio (INR)</td>
</tr>
</tbody>
</table>

Details

The 6 studies provide data with respect to the number of strokes in the warfarin and the comparison (placebo or control) group. In addition, the number of patients and the total person-time (in years) is provided for the two groups. The goal of the meta-analysis was to examine the effectiveness of adjusted-dose warfarin for preventing strokes in patients with atrial fibrillation.

Concepts

medicine, cardiology, incidence rates

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

### copy data into ‘dat’ and examine data
dat <- dat.hart1999
dat.hartmannboyce2018

Studies on the Effectiveness of Nicotine Replacement Therapy for Smoking Cessation

Description

Results from 133 studies examining the effectiveness of nicotine replacement therapy (NRT) for smoking cessation at 6+ months of follow-up.

Usage

dat.hartmannboyce2018
Format

The data frame contains the following columns:

- **study**: numeric, study identifier
- **x.nrt**: numeric, number of participants in the NRT group who were abstinent at the follow-up
- **n.nrt**: numeric, number of participants in the NRT group
- **x.ctrl**: numeric, number of participants in the control group who were abstinent at the follow-up
- **n.ctrl**: numeric, number of participants in the control group
- **treatment**: character, type of NRT provided in the treatment group

Details

The dataset includes the results from 133 studies examining the effectiveness of nicotine replacement therapy (NRT) for smoking cessation. The results given in this dataset pertain to abstinence at 6+ months of follow-up. NRT was provided to participants in the treatment groups in various forms as indicated by the treatment variable (e.g., gum, patch, inhalator). Note that the dataset includes 136 rows, since a few studies included multiple treatments.

Concepts

- medicine, smoking, risk ratios, Mantel-Haenszel method

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.hartmannboyce2018
head(dat, 10)

### load metafor package
library(metafor)

### turn treatment into a factor with the desired ordering
dat$treatment <- factor(dat$treatment, levels=unique(dat$treatment))

### meta-analysis per treatment using the M-H method
lapply(split(dat, dat$treatment), function(x)
  rma.mh(measure="RR", ai=x.nrt, n1i=n.nrt,
         ci=x.ctrl, n2i=n.ctrl, data=x, digits=2))
```
### all combined
```r
rma.mh(measure="RR", ai=x.nrt, n1i=n.nrt, ci=x.ctrl, n2i=n.ctrl, data=dat, digits=2)
```

## End(Not run)

---

**dat.hasselblad1998**  
*Studies on the Effectiveness of Counseling for Smoking Cessation*

#### Description

Results from 24 studies on the effectiveness of various counseling types for smoking cessation.

#### Usage

dat.hasselblad1998

#### Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>numeric</td>
<td>id number for each treatment arm</td>
</tr>
<tr>
<td>study</td>
<td>numeric</td>
<td>study id number</td>
</tr>
<tr>
<td>authors</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>trt</td>
<td>character</td>
<td>intervention group</td>
</tr>
<tr>
<td>xi</td>
<td>numeric</td>
<td>number of individuals abstinent</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>number of individuals in group</td>
</tr>
</tbody>
</table>

#### Details

The dataset includes the results from 24 studies on the effectiveness of various counseling types for smoking cessation (i.e., self-help, individual counseling, group counseling, and no contact). The dataset indicates the total number of individuals within each study arm and the number that were abstinent from 6 to 12 months. The majority of the studies compared two interventions types against each other, while 2 studies compared three types against each other simultaneously.

The data can be used for a 'network meta-analysis' (also called a 'mixed treatment comparison'). The code below shows how such an analysis can be conducted using an arm-based and a contrast-based model (see Salanti et al., 2008, for more details).

#### Concepts

medicine, psychology, smoking, odds ratios, network meta-analysis
Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

References


Examples
```r
### copy data into 'dat' and examine data
dat <- dat.hasselblad1998
dat

### Not run:

### load metafor package
library(metafor)

### create network graph ('igraph' package must be installed)
library(igraph, warn.conflicts=FALSE)
pairs <- data.frame(do.call(rbind, 
  sapply(split(dat$trt, dat$study), function(x) t(combn(x,2)))), stringsAsFactors=FALSE)
lvls <- c("no_contact", "self_help", "ind_counseling", "grp_counseling")
pairs$X1 <- factor(pairs$X1, levels=lvls)
pairs$X2 <- factor(pairs$X2, levels=lvls)
tab <- table(pairs[,1], pairs[,2])
tab # adjacency matrix
g <- graph_from_adjacency_matrix(tab, mode = "plus", weighted=TRUE, diag=FALSE)
vertex_attr(g, "name") <- c("No Contact", "Self-Help", 
  "Individual\nCounseling", "Group\nCounseling")
plot(g, edge.curved=FALSE, edge.width=E(g)$weight, layout=layout_on_grid,
  vertex.size=45, vertex.color="lightgray", vertex.label.color="black", vertex.label.font=2)

### calculate log odds for each study arm
dat <- escalc(measure="PLO", xi=xi, ni=ni, add=1/2, to="all", data=dat)
dat

### convert trt variable to factor with desired ordering of levels
```
dat$hasselblad1998

```r
dat$trt <- factor(dat$trt, levels=c("no_contact", "self_help", "ind_counseling", "grp_counseling"))

### add a space before each level (this makes the output a bit more legible)
levels(dat$trt) <- paste0(" ", levels(dat$trt))

### network meta-analysis using an arm-based model with fixed study effects
### by setting rho=1/2, tau^2 reflects the amount of heterogeneity for all treatment comparisons
res <- rma.mv(yi, vi, mods = ~ factor(study) + trt - 1,
               random = ~ trt | study, rho=1/2, data=dat, btt="trt")

### all pairwise odds ratios of interventions versus no contact
predict(res, newmods=cbind(matrix(0, nrow=3, ncol=24), diag(3)),
         intercept=FALSE, transf=exp, digits=2)

### all pairwise odds ratios comparing interventions (ic vs sh, gc vs sh, and gc vs ic)
predict(res, newmods=cbind(matrix(0, nrow=3, ncol=24), rbind(c(-1,1,0), c(-1,0,1), c(0,-1,1))),
         intercept=FALSE, transf=exp, digits=2)

### forest plot of ORs of interventions versus no contact
dev.new(width=7, height=4)
par(mar=c(5,4,1,2))
forest(c(0,res$beta[25:27]), sei=c(0,res$se[25:27]), psize=1, xlim=c(-3,4), digits=c(2,1), efac=2,
      slab=c("No Contact", "Self-Help", "Individual Counseling", "Group Counseling"),
      atransf=exp, at=log(c(.5, 1, 2, 4, 8)), xlab="Odds Ratio for Intervention vs. No Contact",
      header=c("Intervention", "Odds Ratio [95% CI]"))

########################################################################
### restructure dataset to a contrast-based format
dat <- to.wide(dat.hasselblad1998, study="study", grp="trt", ref="no_contact", grpvars=6:7)

### calculate log odds ratios for each treatment comparison
dat <- escalc(measure="OR", ai=xi.1, n1i=ni.1,
              ci=xi.2, n2i=ni.2, add=1/2, to="all", data=dat)

dat

### calculate the variance-covariance matrix of the log odds ratios for multitreatment studies
### see Gleser & Olkin (2009), equation (19.11), for the covariance equation
calc.v <- function(x) {
  v <- matrix(1/(x$xi.2[1] + 1/2) + 1/(x$ni.2[1] - x$xi.2[1] + 1/2), nrow=nrow(x), ncol=nrow(x))
  diag(v) <- x$vi
  v
}
V <- bldiag(lapply(split(dat, dat$study), calc.v))

### add contrast matrix to dataset
dat <- contrmat(dat, grp1="trt.1", grp2="trt.2")

dat

### network meta-analysis using a contrast-based random-effects model
### by setting rho=1/2, tau^2 reflects the amount of heterogeneity for all treatment comparisons
res <- rma.mv(yi, V, mods = ~ self_help + ind_counseling + grp_counseling - 1,
               random = ~ trt | study, rho=1/2, data=dat, btt="trt")
```
random = ~ comp | study, rho=1/2, data=dat)  
res

### predicted odds ratios of interventions versus no contact
predict(res, newmods=diag(3), transf=exp, digits=2)

### fit random inconsistency effects model (see Law et al., 2016)
res <- rma.mv(yi, V, mods = ~ self_help + ind_counseling + grp_counseling - 1,  
              random = list(~ comp | study, ~ comp | design), rho=1/2, phi=1/2, data=dat)  
res

## End(Not run)

---

**dat.hine1989**  
*Studies on Prophylactic Use of Lidocaine After a Heart Attack*

**Description**

Results from 6 studies evaluating mortality from prophylactic use of lidocaine in acute myocardial infarction.

**Usage**

dat.hine1989

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>source</td>
<td>character</td>
<td>source of data</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of patients in lidocaine group</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of patients in control group</td>
</tr>
<tr>
<td>ai</td>
<td>numeric</td>
<td>number of deaths in lidocaine group</td>
</tr>
<tr>
<td>ci</td>
<td>numeric</td>
<td>number of deaths in control group</td>
</tr>
</tbody>
</table>

**Details**

Hine et al. (1989) conducted a meta-analysis of death rates in randomized controlled trials in which prophylactic lidocaine was administered to patients with confirmed or suspected acute myocardial infarction. The dataset describes the mortality at the end of the assigned treatment period for control and intravenous lidocaine treatment groups for six studies. The question of interest is whether there is a detrimental effect of lidocaine. Because the studies were conducted to compare rates of arrhythmias following a heart attack, the studies, taken individually, are too small to detect important differences in mortality rates.

The data in this dataset were obtained from Table I in Normand (1999, p. 322).
dat.ishak2007

Concepts

medicine, cardiology, risk differences

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.hine1989
dat

## Not run:
### load metafor package
library(metafor)

### calculate risk differences and corresponding sampling variances
dat <- escalc(measure="RD", n1i=n1i, n2i=n2i, ai=ai, ci=ci, data=dat)
dat

### meta-analysis of risk differences using a random-effects model
res <- rma(yi, vi, data=dat)
res

## End(Not run)
```

---

dat.ishak2007  Studies on Deep-Brain Stimulation in Patients with Parkinson’s disease

Description

Results from 46 studies examining the effects of deep-brain stimulation on motor skills of patients with Parkinson’s disease.
Usage
dat.ishak2007

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>(first) author and year</td>
</tr>
<tr>
<td>y1i</td>
<td>numeric</td>
<td>observed mean difference at 3 months</td>
</tr>
<tr>
<td>v1i</td>
<td>numeric</td>
<td>sampling variance of the mean difference at 3 months</td>
</tr>
<tr>
<td>y2i</td>
<td>numeric</td>
<td>observed mean difference at 6 months</td>
</tr>
<tr>
<td>v2i</td>
<td>numeric</td>
<td>sampling variance of the mean difference at 6 months</td>
</tr>
<tr>
<td>y3i</td>
<td>numeric</td>
<td>observed mean difference at 12 months</td>
</tr>
<tr>
<td>v3i</td>
<td>numeric</td>
<td>sampling variance of the mean difference at 12 months</td>
</tr>
<tr>
<td>y4i</td>
<td>numeric</td>
<td>observed mean difference at long-term follow-up</td>
</tr>
<tr>
<td>v4i</td>
<td>numeric</td>
<td>sampling variance of the mean difference at the long-term follow-up</td>
</tr>
<tr>
<td>mdur</td>
<td>numeric</td>
<td>mean disease duration (in years)</td>
</tr>
<tr>
<td>mbase</td>
<td>numeric</td>
<td>mean baseline UPDRS score</td>
</tr>
</tbody>
</table>

Details

Deep-brain stimulation (DBS), which is delivered through thin surgically implanted wires in specific areas of the brain and controlled by the patient, is meant to provide relief of the debilitating symptoms of Parkinson’s disease. The dataset includes the results from 46 studies examining the effects of DBS of the subthalamic nucleus on motor functioning, measured with the Unified Parkinson’s Disease Rating Scale (UPDRS). The effect size measure for this meta-analysis was the mean difference of the scores while the stimulator is active and the baseline scores (before implantation of the stimulator). Since lower scores on the UPDRS indicate better functioning, negative numbers indicate improvements in motor skills. Effects were generally measured at 3, 6, and 12 months after implantation of the stimulator, with some studies also including a further long-term follow-up. However, the number of measurements differed between studies - hence the missing data on some of the measurement occasions.

Since the same patients were followed over time within a study, effect size estimates from multiple measurement occasions are likely to be correlated. A multivariate model accounting for the correlation in the effects can be used to meta-analyze these data. A difficulty with this approach is the lack of information about the correlation of the measurements over time in the individual studies. The approach taken by Ishak et al. (2007) was to assume an autoregressive (AR1) structure for the estimates within the individual studies. In addition, the correlation in the true effects was modeled, again using an autoregressive structure.

Concepts

medicine, raw mean differences, longitudinal models

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org
### Source

### Examples
```r
### copy data into 'dat' and examine data
dat <- dat.ishak2007
head(dat, 5)

## Not run:
### load metafor package
library(metafor)

### create long format dataset
dat <- reshape(dat, direction="long", idvar="study", v.names=c("yi","vi"),
               varying=list(c(2,4,6,8), c(3,5,7,9)))
dat <- dat[order(study, time),]

### remove missing measurement occasions from dat.long
dat <- dat[!is.na(yi),]
rownames(dat) <- NULL
head(dat, 8)

### construct the full (block diagonal) V matrix with an AR(1) structure
### assuming an autocorrelation of 0.97 as estimated by Ishak et al. (2007)
V <- vcalc(vi, cluster=study, time1=time, phi=0.97, data=dat)

### plot data
with(dat, interaction.plot(time, study, yi, type="b", pch=19, lty="solid", xaxt="n",
                        legend=FALSE, xlab="Time Point", ylab="Mean Difference", bty="l")
axis(side=1, at=1:4, lab=c("1 (3 months)", "2 (6 months)", "3 (12 months)", "4 (12+ months)"))

### multivariate model with heteroscedastic AR(1) structure for the true effects
res <- rma.mv(yi, V, mods = ~ factor(time) - 1, random = ~ time | study,
              struct = "HAR", data = dat)
print(res, digits=2)

## End(Not run)
```

---

**dat.kalaian1996**

---

**Studies on the Effectiveness of Coaching for the SAT**

---

**Description**

Results from studies examining the effectiveness of coaching on the performance on the Scholastic Aptitude Test (SAT).
Usage

dat.kalaian1996

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Variable</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>numeric</td>
<td>row (effect) id</td>
</tr>
<tr>
<td>study</td>
<td>character</td>
<td>study identifier</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of participants in the coached group</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of participants in the uncoached group</td>
</tr>
<tr>
<td>outcome</td>
<td>character</td>
<td>subtest (verbal or math)</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>standardized mean difference</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
<tr>
<td>hrs</td>
<td>numeric</td>
<td>hours of coaching</td>
</tr>
<tr>
<td>ets</td>
<td>numeric</td>
<td>study conducted by the Educational Testing Service (ETS) (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>homework</td>
<td>numeric</td>
<td>assignment of homework outside of the coaching course (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>type</td>
<td>numeric</td>
<td>study type (1 = randomized study, 2 = matched study, 3 = nonequivalent comparison study)</td>
</tr>
</tbody>
</table>

Details

The effectiveness of coaching for the Scholastic Aptitude Test (SAT) has been examined in numerous studies. This dataset contains standardized mean differences comparing the performance of a coached versus uncoached group on the verbal and/or math subtest of the SAT. Studies may report a standardized mean difference for the verbal subtest, the math subtest, or both. In the latter case, the two standardized mean differences are not independent (since they were measured in the same group of subjects). The number of hours of coaching (variable hrs), whether the study was conducted by the Educational Testing Service (variable ets), whether homework was assigned outside of the coaching course (variable homework), and the study type (variable type) may be potential moderators of the treatment effect.

Concepts

education, standardized mean differences, multivariate models, meta-regression

Note

The dataset was obtained from Table 1 in Kalaian and Raudenbush (1996). However, there appear to be some inconsistencies between the data in the table and those that were actually used for the analyses (see ‘Examples’).

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

Examples

### copy data into 'dat' and examine data

dat <- dat.kalaian1996
head(dat, 12)

### load metafor package

library(metafor)

### check ranges

range(dat$yi[dat$outcome == "verbal"])[1] # -0.35 to 0.74 according to page 230
range(dat$yi[dat$outcome == "math"])[1] # -0.53 to 0.60 according to page 231

### comparing this with Figure 1 in the paper reveals some discrepancies

par(mfrow=c(1,2), mar=c(5,4,1,1))

plot(log(dat$hrs[dat$outcome == "verbal"]), dat$yi[dat$outcome == "verbal"],
     pch=19, xlab="Log(Coaching Hours)", ylab="Effect Size (verbal)",
     ylim=c(-0.5,1), xaxs="i", yaxs="i")
abline(h=c(-0.5,0,0.5), lty="dotted")
abline(v=log(c(5,18)), lty="dotted")

plot(log(dat$hrs[dat$outcome == "math"], dat$yi[dat$outcome == "math"],
     pch=19, xlab="Log(Coaching Hours)", ylab="Effect Size (math)",
     ylim=c(-1.0,1), xaxs="i", yaxs="i")
abline(h=c(-0.5,0,0.5), lty="dotted")
abline(v=log(c(5,18)), lty="dotted")

### construct variance-covariance matrix assuming rho = 0.66 for effect sizes
### corresponding to the 'verbal' and 'math' outcome types

V <- vcalc(vi, cluster=study, type=outcome, data=dat, rho=0.66)

### fit multivariate random-effects model

res <- rma.mv(yi, V, mods = ~ outcome - 1,
               random = ~ outcome | study, struct="UN",
               data=dat, digits=3)

res

### test whether the effect differs for the math and verbal subtest

anova(res, X=c(1,-1))

### log-transform and mean center the hours of coaching variable

dat$loghrs <- log(dat$hrs) - mean(log(dat$hrs), na.rm=TRUE)

### fit multivariate model with log(hrs) as moderator

res <- rma.mv(yi, V, mods = ~ outcome + outcome:loghrs - 1,
               random = ~ outcome | study, struct="UN",
               data=dat, digits=3)

res

### fit model with tau2 = 0 for outcome verbal (which also constrains rho = 0)

res <- rma.mv(yi, V, mods = ~ outcome + outcome:loghrs - 1,
               random = ~ outcome | study, struct="UN", tau2=c(NA,0),
               data=dat, digits=3)
dat.kearon1998

Studies on the Accuracy of Venous Ultrasonography for the Diagnosis of Deep Venous Thrombosis

Description

Results from diagnostic accuracy studies examining the accuracy of venous ultrasonography for the diagnosis of deep venous thrombosis.

Usage

dat.kearon1998

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>numeric</td>
<td>study id</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>patients</td>
<td>character</td>
<td>patient group (either symptomatic or asymptomatic patients)</td>
</tr>
<tr>
<td>tp</td>
<td>numeric</td>
<td>number of true positives</td>
</tr>
<tr>
<td>np</td>
<td>numeric</td>
<td>number of positive patients (cases)</td>
</tr>
<tr>
<td>tn</td>
<td>numeric</td>
<td>number of true negatives</td>
</tr>
<tr>
<td>nn</td>
<td>numeric</td>
<td>number of negative patients (non-cases)</td>
</tr>
</tbody>
</table>

Details

The studies included in the dataset examined the accuracy of venous ultrasonography for the diagnosis of a first deep venous thrombosis in symptomatic and asymptomatic patients. Cases and non-cases were determined based on contrast venography. Venous ultrasonography was then used to make a diagnosis, leading to a given number of true positives and negatives.

A subset of this dataset (using only the studies with asymptomatic patients) was used by Deeks et al. (2005) to illustrate methods for detecting publication bias (or small-study effects) in meta-analyses of diagnostic accuracy studies.

Concepts

medicine, odds ratios, diagnostic accuracy studies, multivariate models, publication bias
Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.kearon1998
head(dat)

### Not run:

### load metafor package
library(metafor)

### calculate diagnostic log odds ratios and corresponding sampling variances
dat <- escalc(measure="OR", ai=tp, n1i=np, ci=nn-tn, n2i=nn, data=dat, add=1/2, to="all")
head(dat)

### fit random-effects model for the symptomatic patients
res <- rma(yi, vi, data=dat, subset=patients=="symptomatic")
res

### fit random-effects model for the asymptomatic patients
res <- rma(yi, vi, data=dat, subset=patients=="asymptomatic")
res

### estimated average diagnostic odds ratio (with 95% CI)
predict(res, transf=exp, digits=2)

### regression test for funnel plot asymmetry using SE as predictor
reg <- regtest(res, model="lm")
reg

### corresponding funnel plot
funnel(res, atransf=exp, xlim=c(0,7), at=log(c(1,10,100,1000)), ylim=c(0,1.5), steps=4)
ys <- seq(0, 2, length=100)
lines(coef(reg$fit)[1] + coef(reg$fit)[2]*ys, ys, lwd=2, lty=3)

### regression test for funnel plot asymmetry using total sample size as predictor
```
### regression test for funnel plot asymmetry using 1/sqrt(ESS) as predictor (Deeks et al., 2005)

```
dat$invessi <- 1/(4*dat$np) + 1/(4*dat$nn)
tmp <- rma(yi, invessi, data=dat, subset=patients=="asymptomatic")
reg <- regtest(tmp, model="lm")
reg
```

### corresponding funnel plot

```
funnel(tmp, at=log(c(1,10,100,1000)), ylim=c(0,0.15), steps=4,
      refline=coef(reg), level=0, ylab="1/root(ess)"
ys <- seq(0, .20, length=100)
lines(coef(reg$fit)[1] + coef(reg$fit)[2]*ys, ys, lwd=2, lty=3)
```

### convert data to long format

```
dat <- to.long(measure="OR", ai=tp, n1i=np, ci=tn, n2i=nn,
               data=dat.kearon1998, subset=patients=="asymptomatic")
dat <- dat[9:12]
levels(dat$group) <- c("sensitivity", "specificity")
dat
```

### calculate logit-transformed sensitivities

```
dat <- escalc(measure="PLO", xi=out1, mi=out2, data=dat, add=1/2, to="all",
              include=group=="sensitivity")
dat
```

### calculate logit-transformed specificities

```
dat <- escalc(measure="PLO", xi=out1, mi=out2, data=dat, add=1/2, to="all",
              include=group=="specificity")
dat
```

### bivariate random-effects model for logit sensitivity and specificity

```
res <- rma.mv(yi, vi, mods = ~ group - 1, random = ~ group | study, struct="UN", data=dat)
res
```

### estimated average sensitivity and specificity based on the model

```
predict(res, newmods = rbind(c(1,0),c(0,1)), transf=transf.ilogit, tau2.levels=c(1,2), digits=2)
```

### estimated average diagnostic odds ratio based on the model

```
predict(res, newmods = c(1,1), transf=exp, digits=2)
```

```
## End(Not run)
```
Description

Results from 31 studies examining differences in planning performance in schizophrenia patients versus healthy controls.

Usage
dat.knapp2017

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>author</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>study</td>
<td>numeric</td>
<td>study id number</td>
</tr>
<tr>
<td>task</td>
<td>character</td>
<td>type of task</td>
</tr>
<tr>
<td>difficulty</td>
<td>numeric</td>
<td>task difficulty</td>
</tr>
<tr>
<td>group1</td>
<td>character</td>
<td>identifier for patient group within studies</td>
</tr>
<tr>
<td>group2</td>
<td>character</td>
<td>identifier for control group within studies</td>
</tr>
<tr>
<td>comp</td>
<td>numeric</td>
<td>identifier for comparisons within studies</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>standardized mean difference for planning performance</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
<tr>
<td>n_sz</td>
<td>numeric</td>
<td>number of schizophrenic patients</td>
</tr>
<tr>
<td>n_hc</td>
<td>numeric</td>
<td>number of healthy controls</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>standardized mean difference for IQ</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
</tbody>
</table>

Details

The studies included in this dataset examined differences between schizophrenia patients and healthy controls with respect to their performance on the tower of London test (https://en.wikipedia.org/wiki/Tower_of_London_test) or a similar cognitive task measuring planning ability. The outcome measure for this meta-analysis was the standardized mean difference (with positive values indicating better performance in the healthy controls compared to the schizophrenia patients).

The dataset has a more complex structure for several reasons:

1. Studies 2, 3, 9, and 20 included more than one schizophrenia patient group and the standardized mean differences were computed by comparing these groups against a single healthy control group.
2. Studies 6, 12, 14, 15, 18, 19, 22, and 26 had the patients and controls complete different tasks of varying complexity (essentially the average number of moves required to complete a task). Study 6 also included two different task types.
3. Study 24 provides two standardized mean differences, one for men and the other for women.
4. Study 29 provides three standardized mean differences, corresponding to the three different COMT Val158Met genotypes (val/val, val/met, and met/met).

All 4 issues described above lead to a multilevel structure in the dataset, with multiple standardized mean differences nested within some of the studies. Issues 1. and 2. also lead to correlated sampling errors.

Concepts

psychology, standardized mean differences, multilevel models, multivariate models, cluster-robust inference, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.knapp2017
dat[-c(1:2)]

### load metafor package
library(metafor)

### fit a standard random-effects model ignoring the issues described above
res <- rma(yi, vi, data=dat)
res

### fit a multilevel model with random effects for studies and comparisons within studies
### (but this ignored the correlation in the sampling errors)
res <- rma.mv(yi, vi, random = ~ 1 | study/comp, data=dat)
res

### create variable that indicates the task and difficulty combination as increasing integers
dat$task.diff <- unlist(lapply(split(dat, dat$study), function(x) {
  task.int <- as.integer(factor(x$task))
  diff.int <- as.integer(factor(x$difficulty))
  diff.int[is.na(diff.int)] <- 1
  paste0(task.int, ".", diff.int))})

### construct correlation matrix for two tasks with four different difficulties where the correlation is 0.4 for different difficulties of the same task, 0.7 for the same difficulty of different tasks, and 0.28 for different difficulties of different tasks
```
R <- matrix(0.4, nrow=8, ncol=8)
R[5:8,1:4] <- R[1:4,5:8] <- 0.28
diag(R[1:4,5:8]) <- 0.7
diag(R[5:8,1:4]) <- 0.7
diag(R) <- 1
rownames(R) <- colnames(R) <- paste0(rep(1:2, each=4), ".", 1:4)
R

### construct an approximate V matrix accounting for the use of shared groups and
### for correlations among tasks/difficulties as specified in the R matrix above
V <- vcalc(vi, cluster=study, grp1=group1, grp2=group2, w1=n_sz, w2=n_hc,
          obs=task.diff, rho=R, data=dat)

### correlation matrix for study 3 with four patient groups and a single control group
round(cov2cor(V[dat$study == 3, dat$study == 3]), 2)

### correlation matrix for study 6 with two tasks with four difficulties
cov2cor(V[dat$study == 6, dat$study == 6])

### correlation matrix for study 24 with two independent groups
cov2cor(V[dat$study == 24, dat$study == 24])

### correlation matrix for study 29 with three independent groups
cov2cor(V[dat$study == 29, dat$study == 29])

### fit multilevel model as above, but now use this V matrix in the model
res <- rma.mv(yi, V, random = ~ 1 | study/comp, data=dat)
res
predict(res, digits=2)

### use cluster-robust inference methods based on this model
robust(res, cluster=study)

### use methods from clubSandwich package
robust(res, cluster=study, clubSandwich=TRUE)

### examine if task difficulty is a potential moderator of the effect
res <- rma.mv(yi, V, mods = ~ difficulty, random = ~ 1 | study/comp, data=dat)
res
sav <- robust(res, cluster=study)
sav
sav <- robust(res, cluster=study, clubSandwich=TRUE)
sav

### draw bubble plot
regplot(sav, xlab="Task Difficulty", ylab="Standardized Mean Difference", las=1, digits=1, bty="l")

## End(Not run)
**dat.konstantopoulos2011**

*Studies on the Effects of Modified School Calendars on Student Achievement*

---

**Description**

Results from 56 studies on the effects of modified school calendars on student achievement.

**Usage**

`dat.konstantopoulos2011`

**Format**

The data frame contains the following columns:

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>district</strong></td>
<td>numeric</td>
<td>district id number</td>
</tr>
<tr>
<td><strong>school</strong></td>
<td>numeric</td>
<td>school id number (within district)</td>
</tr>
<tr>
<td><strong>study</strong></td>
<td>numeric</td>
<td>study id number</td>
</tr>
<tr>
<td><strong>yi</strong></td>
<td>numeric</td>
<td>standardized mean difference</td>
</tr>
<tr>
<td><strong>vi</strong></td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
<tr>
<td><strong>year</strong></td>
<td>numeric</td>
<td>year of the study</td>
</tr>
</tbody>
</table>

**Details**

Instead of following the more traditional school calendar with a long summer break (in addition to a short winter and spring break), some schools have switched to a modified school calendar comprising more frequent but shorter intermittent breaks (e.g., 9 weeks of school followed by 3 weeks off), while keeping the total number of days at school approximately the same. The effects of using such a modified calendar on student achievement have been examined in a number of studies and were meta-analyzed by Cooper et al. (2003).

The dataset (taken from Konstantopoulos, 2011) contains the results from 56 studies, each comparing the level of academic achievement in a group of students following a modified school calendar with that of a group of students following a more traditional school calendar. The difference between the two groups was quantified in terms of a standardized mean difference (with positive values indicating a higher mean level of achievement in the group following the modified school calendar).

The studies were conducted at various schools that were clustered within districts. The data therefore have a multilevel structure, with schools nested within districts. A multilevel meta-analysis of these data can be used to estimate and account for the amount of heterogeneity between districts and between schools within districts.

**Concepts**

education, standardized mean differences, multilevel models
Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.konstantopoulos2011
dat

### load metafor package
library(metafor)

### regular random-effects model
res <- rma(yi, vi, data=dat)
print(res, digits=3)

### regular random-effects model using rma.mv()
res <- rma.mv(yi, vi, random = ~ 1 | study, data=dat)
print(res, digits=3)

### multilevel random-effects model
res.ml <- rma.mv(yi, vi, random = ~ 1 | district/school, data=dat)
print(res.ml, digits=3)

### profile variance components
profile(res.ml, progbar=FALSE)

### multivariate parameterization of the model
res.mv <- rma.mv(yi, vi, random = ~ school | district, data=dat)
print(res.mv, digits=3)

### tau^2 from multivariate model = sum of the two variance components from the multilevel model
round(sum(res.ml$sigma2), 3)

### rho from multivariate model = intraclass correlation coefficient based on the multilevel model
round(res.ml$sigma2[1] / sum(res.ml$sigma2), 3)

### End(Not run)
```
Description

Results from 58 studies on the effectiveness of cognitive-behavioral therapy (CBT) for reducing recidivism in juvenile and adult offenders.

Usage
dat.landenberger2005

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>(first) author and year</td>
</tr>
<tr>
<td>pubtype</td>
<td>character</td>
<td>publication type (book chapter, journal article, report, or thesis)</td>
</tr>
<tr>
<td>country</td>
<td>character</td>
<td>country where study was carried out (Canada, New Zealand, UK, or USA)</td>
</tr>
<tr>
<td>design</td>
<td>character</td>
<td>study design (matched groups, nonequivalent groups, or randomized trial)</td>
</tr>
<tr>
<td>program</td>
<td>character</td>
<td>purpose of setting up the CBT program (for demonstration, practice, or research purposes)</td>
</tr>
<tr>
<td>setting</td>
<td>character</td>
<td>treatment setting (community or prison)</td>
</tr>
<tr>
<td>designprob</td>
<td>character</td>
<td>indication of study design problems (no, favors the control group, or favors the treatment group)</td>
</tr>
<tr>
<td>n.ctrl.rec</td>
<td>numeric</td>
<td>number of recidivists in the control group</td>
</tr>
<tr>
<td>n.ctrl.non</td>
<td>numeric</td>
<td>number of non-recidivists in the control group</td>
</tr>
<tr>
<td>n.cbt.rec</td>
<td>numeric</td>
<td>number of recidivists in the CBT group</td>
</tr>
<tr>
<td>n.cbt.non</td>
<td>numeric</td>
<td>number of non-recidivists in the CBT group</td>
</tr>
<tr>
<td>interval</td>
<td>numeric</td>
<td>recidivism interval (in months)</td>
</tr>
<tr>
<td>group</td>
<td>numeric</td>
<td>study group (adults or juveniles)</td>
</tr>
<tr>
<td>age</td>
<td>numeric</td>
<td>mean age of the study group</td>
</tr>
<tr>
<td>male</td>
<td>numeric</td>
<td>percentage of males in the study group</td>
</tr>
<tr>
<td>minority</td>
<td>numeric</td>
<td>percentage of minorities in the study group</td>
</tr>
<tr>
<td>length</td>
<td>numeric</td>
<td>treatment length (in weeks)</td>
</tr>
<tr>
<td>sessions</td>
<td>numeric</td>
<td>number of CBT sessions per week</td>
</tr>
<tr>
<td>hrs_week</td>
<td>numeric</td>
<td>treatment hours per week</td>
</tr>
<tr>
<td>hrs_total</td>
<td>numeric</td>
<td>total hours of treatment</td>
</tr>
<tr>
<td>cbt.cogskills</td>
<td>character</td>
<td>CBT component: cognitive skills (yes, no)</td>
</tr>
<tr>
<td>cbt.cogrestruct</td>
<td>character</td>
<td>CBT component: cognitive restructuring (yes, no)</td>
</tr>
<tr>
<td>cbt.intpprbsolv</td>
<td>character</td>
<td>CBT component: interpersonal problem solving (yes, no)</td>
</tr>
<tr>
<td>cbt.socskills</td>
<td>character</td>
<td>CBT component: social skills (yes, no)</td>
</tr>
<tr>
<td>cbt.angerctrl</td>
<td>character</td>
<td>CBT component: anger control (yes, no)</td>
</tr>
<tr>
<td>cbt.victimimpact</td>
<td>character</td>
<td>CBT component: victim impact (yes, no)</td>
</tr>
<tr>
<td>cbt.subabuse</td>
<td>character</td>
<td>CBT component: substance abuse (yes, no)</td>
</tr>
<tr>
<td>cbt.behavmod</td>
<td>character</td>
<td>CBT component: behavior modification (yes, no)</td>
</tr>
<tr>
<td>cbt.relapseprev</td>
<td>character</td>
<td>CBT component: relapse prevention (yes, no)</td>
</tr>
<tr>
<td>cbt.moralrsng</td>
<td>character</td>
<td>CBT component: moral reasoning (yes, no)</td>
</tr>
<tr>
<td>cbt.roletaking</td>
<td>character</td>
<td>CBT component: role taking (yes, no)</td>
</tr>
<tr>
<td>cbt.other</td>
<td>character</td>
<td>CBT component: other (yes, no)</td>
</tr>
</tbody>
</table>
Details

Landenberger and Lipsey (2005) conducted a meta-analysis of 58 experimental and quasi-experimental studies of the effects of cognitive-behavioral therapy (CBT) on the recidivism rates of adult and juvenile offenders (see also Lipsey et al., 2007). The present dataset includes the results of these studies and a range of potential moderator variables to identify factors associated with variation in treatment effects.

Concepts

psychology, criminology, odds ratios, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

Personal communication.

References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.landenberger2005
head(dat)

### Not run:

### load metafor package
library(metafor)

### calculate log odds ratios (for non-recidivism in CBT vs. control groups) and sampling variances
dat <- escalc(measure="OR", ai=n.cbt.non, bi=n.cbt.rec, ci=n.ctrl.non, di=n.ctrl.rec, data=dat)

### fit random-effects model
res <- rma(yi, vi, data=dat)

### estimated average OR and corresponding 95% CI/PI
predict(res, transf=exp, digits=2)

### examine if number of treatment sessions per week is a potential moderator
res <- rma(yi, vi, mods = ~ sessions, data=dat)
```
### predicted ORs for 1, 2, 5, or 10 sessions per week

```r
predict(res, newmods=c(1,2,5,10), transf=exp, digits=2)
```

```r
## End(Not run)
```

---

**dat.laopaiboon2015**  
*Studies on the Effectiveness of Azithromycin for Treating Lower Respiratory Tract Infections*

**Description**

Results from 15 studies on the effectiveness of azithromycin versus amoxycillin or amoxycillin/clavulanic acid (amoxyclav) in the treatment of acute lower respiratory tract infections.

**Usage**

```r
dat.laopaiboon2015
```

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>author</td>
<td>character</td>
<td>author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>ai</td>
<td>numeric</td>
<td>number of clinical failures in the group treated with azithromycin</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of patients in the group treated with azithromycin</td>
</tr>
<tr>
<td>ci</td>
<td>numeric</td>
<td>number of clinical failures in the group treated with amoxycillin or amoxyclav</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of patients in the group treated with amoxycillin or amoxyclav</td>
</tr>
<tr>
<td>age</td>
<td>character</td>
<td>whether the trial included adults or children</td>
</tr>
<tr>
<td>diag.ab</td>
<td>numeric</td>
<td>trial included patients with a diagnosis of acute bacterial bronchitis</td>
</tr>
<tr>
<td>diag.cb</td>
<td>numeric</td>
<td>trial included patients with a diagnosis of chronic bronchitis with acute exacerbation</td>
</tr>
<tr>
<td>diag.pn</td>
<td>numeric</td>
<td>trial included patients with a diagnosis of pneumonia</td>
</tr>
<tr>
<td>ctrl</td>
<td>character</td>
<td>antibiotic in control group (amoxycillin or amoxyclav)</td>
</tr>
</tbody>
</table>

**Details**

Azithromycin is an antibiotic useful for the treatment of a number of bacterial infections. Laopaiboon et al. (2015) conducted a meta-analysis of trials comparing the effectiveness of azithromycin versus amoxycillin or amoxycillin/clavulanic acid (amoxyclav) in the treatment of acute lower respiratory tract infections, including acute bacterial bronchitis, acute exacerbations of chronic bronchitis, and pneumonia. The results from 15 trials are included in this dataset.

**Concepts**

- medicine, risk ratios
### Examples

```r
### copy data into 'dat' and examine data
dat <- dat.laopaiboon2015
dat

### Not run:

### load metafor package
library(metafor)

### analysis using the Mantel-Haenszel method
rma.mh(measure="RR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, digits=3)

### calculate log risk ratios and corresponding sampling variances
dat <- escalc(measure="RR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat)

### random-effects model
res <- rma(yi, vi, data=dat)
res

### average risk ratio with 95% CI
predict(res, transf=exp)

### End(Not run)
```

## Description

Results from 33 trials comparing intravenous streptokinase versus placebo or no therapy in patients who had been hospitalized for acute myocardial infarction.

## Usage

dat.lau1992

## Format

The data frame contains the following columns:
In the paper by Lau et al. (1992), the data are used to illustrate the idea of a cumulative meta-analysis, where the results are updated as each trial is added to the dataset. See ‘Examples’ for code that replicates the results and shows corresponding forest plots.

Details

The data include:

- **trial**: character, trial name
- **year**: numeric, publication year
- **ai**: numeric, number of deaths in the streptokinase group
- **n1i**: numeric, number of patients in the streptokinase group
- **ci**: numeric, number of deaths in the control group
- **n2i**: numeric, number of patients in the control group

Concepts

- medicine, cardiology, odds ratios, cumulative meta-analysis

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.lau1992
dat

### Not run:

### load metafor package
library(metafor)

### meta-analysis of log odds ratios using the MH method
res <- rma.mh(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, slab=trial)
print(res, digits=2)

### forest plot
forest(res, xlim=c(-10,9), atransf=exp, at=log(c(.01, 0.1, 1, 10, 100)),
       header=TRUE, top=2, ilab=dat$year, ilab.xpos=-6)
text(-6, 35, "Year", font=2)

### cumulative meta-analysis
sav <- cumul(res)

### forest plot of the cumulative results
```
Studies on Acupoint P6 Stimulation for Preventing Nausea

Description

Results from studies examining the effectiveness of wrist acupuncture point P6 stimulation for preventing postoperative nausea.

Usage

dat.lee2004

Format

The data frame contains the following columns:

- id: numeric trial id number
- study: character first author
- year: numeric study year
- ai: numeric number of patients experiencing nausea in the treatment group
- n1i: numeric total number of patients in treatment group
- ci: numeric number of patients experiencing nausea in the sham group
- n2i: numeric total number of patients in the sham group

Details

Postoperative nausea and vomiting are common complications following surgery and anaesthesia. As an alternative to drug therapy, acupuncture has been studied as a potential treatment in several trials. The dataset contains the results from 16 clinical trials examining the effectiveness of wrist acupuncture point P6 stimulation for preventing postoperative nausea.

Concepts

- medicine, alternative medicine, risk ratios

Author(s)

Wolfgang Viechtbauer, \texttt{<wvb@metafor-project.org>}, \url{https://www.metafor-project.org}
### dat.lehmann2018

**Source**


**Examples**

```r
### copy data into 'dat' and examine data
dat <- dat.lee2004
dat

### Not run:

### load metafor package
library(metafor)

### meta-analysis based on log risk ratios
res <- rma(measure="RR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat)
res
predict(res, transf=exp, digits=2)

### End(Not run)
```

---

**dat.lehmann2018**

*The Effect of Red on Perceived Attractiveness*

**Description**

Results from studies in which participants rated the attractiveness of photos that featured red or a control color. See OSF project at https://osf.io/xy47p/.

**Usage**

`dat.lehmann2018`

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Short_Title</td>
<td>character</td>
<td>Shortened citation formatted Author name(s), year of publication - Experiment number</td>
</tr>
<tr>
<td>Full_Citation</td>
<td>character</td>
<td>Full citation in APA format.</td>
</tr>
<tr>
<td>Short_Citation</td>
<td>character</td>
<td>Shortened citation of different format, exactly as it would appear in an in-text citation.</td>
</tr>
<tr>
<td>Year</td>
<td>numeric</td>
<td>Year study published (whether in journal or published online).</td>
</tr>
<tr>
<td>Study</td>
<td>character</td>
<td>Experiment number. If only one experiment presented in a paper, then ‘Exp 1’, otherwise numbered accordingly.</td>
</tr>
<tr>
<td>Peer_Reviewed</td>
<td>character</td>
<td>Whether the experiment was published in a peer-reviewed journal or not. ‘Yes’ = peer-reviewed.</td>
</tr>
<tr>
<td>Source_Type</td>
<td>character</td>
<td>Location where experiment is available, including journal articles, conference proceedings, online-only, pre-registered, etc.</td>
</tr>
<tr>
<td>Preregistered</td>
<td>character</td>
<td>Whether experiment was pre-registered or not.</td>
</tr>
</tbody>
</table>
Details

This is data from a meta-analysis of studies that test the red-romance hypothesis, which is that the color red enhances heterosexual attraction in romantic contexts. Analyzing male participants only, the meta-analysis should show a small, statistically significant effect (d = 0.26 [0.12, 0.40], p = .0004, N = 2,961). Analyzing female participants only should show a very small effect (d = 0.13

<table>
<thead>
<tr>
<th>Variable</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Moderator_Group</td>
<td>character</td>
<td>In some studies, a moderator was intentionally investigated that was meant to reduce the red-romance effect.</td>
</tr>
<tr>
<td>Gender</td>
<td>character</td>
<td>Gender of rater (male or female). In all cases, gender of stimuli will be opposite.</td>
</tr>
<tr>
<td>Color_Contrast</td>
<td>character</td>
<td>The color used as the contrast against red. In some cases, not every contrast color was used.</td>
</tr>
<tr>
<td>Color_Form</td>
<td>character</td>
<td>Location of color in photo. Background = background or border color manipulated; red = color of manipulated object.</td>
</tr>
<tr>
<td>Photo_Type</td>
<td>character</td>
<td>Amount of body visible in photo. Head Shot = head only; Bust = head, shoulders, some torso.</td>
</tr>
<tr>
<td>DV_Type</td>
<td>character</td>
<td>Scale used for DV. ‘Perceived attractiveness’ = the perceived attractiveness scale used.</td>
</tr>
<tr>
<td>DV_Items</td>
<td>numeric</td>
<td>Number of items in DV.</td>
</tr>
<tr>
<td>DV_Scale</td>
<td>character</td>
<td>Full length of DV scale, if clear.</td>
</tr>
<tr>
<td>DV_ScaleBottom</td>
<td>numeric</td>
<td>Lower anchor of DV scale.</td>
</tr>
<tr>
<td>DV_ScaleTop</td>
<td>numeric</td>
<td>Upper anchor of DV scale.</td>
</tr>
<tr>
<td>Location</td>
<td>character</td>
<td>Country where study took place, if clear. ‘Worldwide’ in some cases of online participation.</td>
</tr>
<tr>
<td>Continent</td>
<td>character</td>
<td>Continent where study took place, for the sake of creating larger categories for analysis.</td>
</tr>
<tr>
<td>Participants</td>
<td>character</td>
<td>Basic notes about participants. Students = high school, undergraduate, or graduate students; online = internet; adult = no other common identifying factor given.</td>
</tr>
<tr>
<td>Participant_Notes</td>
<td>character</td>
<td>A finer grained description of participant characteristics.</td>
</tr>
<tr>
<td>Design</td>
<td>character</td>
<td>Whether study was a between- or within-subjects design.</td>
</tr>
<tr>
<td>Eth_Majority</td>
<td>character</td>
<td>Basic notes about participant ethnicity for ease of analysis. This represents the ethnicity of the people pictured in the stimulus materials.</td>
</tr>
<tr>
<td>Eth_Majority_Detail</td>
<td>character</td>
<td>A finer grained description of participant characteristics, including in some cases participant counts when the ethnic majority was close to another category.</td>
</tr>
<tr>
<td>Eth_Stim</td>
<td>character</td>
<td>Ethnicity of the people pictured in the stimuli materials.</td>
</tr>
<tr>
<td>Eth_Match</td>
<td>character</td>
<td>Whether the ethnic majority of the participant pool matched the ethnicity of stimuli.</td>
</tr>
<tr>
<td>Red_Age</td>
<td>numeric</td>
<td>Mean age of participants in red group. If not given for specific group, then mean age overall.</td>
</tr>
<tr>
<td>Control_Age</td>
<td>numeric</td>
<td>Mean age of participants in control group. If not given for specific group, then mean age overall.</td>
</tr>
<tr>
<td>Color_Red</td>
<td>character</td>
<td>Specific values of the color used in the study.</td>
</tr>
<tr>
<td>Color_Control</td>
<td>character</td>
<td>Specific values of control color, if given. ‘No data’ if not given or unclear.</td>
</tr>
<tr>
<td>Red_Original</td>
<td>character</td>
<td>Whether the red color used in the study is within 5 units of the LCh values for red in the original study.</td>
</tr>
<tr>
<td>Color_Match</td>
<td>character</td>
<td>Whether the color used in the study is within 5 units of the red color on the LCh scale.</td>
</tr>
<tr>
<td>Presentation_Control</td>
<td>character</td>
<td>Whether the color of the stimulus viewed by each participant was consistent, as in participants viewing everything on paper, versus uncontrolled presentation of the stimulus, as in viewing stimulus on different computers.</td>
</tr>
<tr>
<td>Stimuli_Presentation</td>
<td>character</td>
<td>Method for presenting stimuli. ‘Paper’ = stimuli printed on paper, shown in-person; ‘Screen’ = stimuli shown on-screen, not carefully controlled; ‘Screen Control’ = stimuli shown on-screen, but screen carefully color-matched.</td>
</tr>
<tr>
<td>Red_N</td>
<td>numeric</td>
<td>Number of participants in red group.</td>
</tr>
<tr>
<td>Red_M</td>
<td>numeric</td>
<td>Mean rating of DV in red group.</td>
</tr>
<tr>
<td>Red_SD</td>
<td>numeric</td>
<td>Standard deviation of DV in red group.</td>
</tr>
<tr>
<td>Control_N</td>
<td>numeric</td>
<td>Number of participants in control group.</td>
</tr>
<tr>
<td>Control_M</td>
<td>numeric</td>
<td>Mean rating of DV in control group.</td>
</tr>
<tr>
<td>Control_SD</td>
<td>numeric</td>
<td>Standard deviation of DV in control group.</td>
</tr>
<tr>
<td>SD_diff</td>
<td>numeric</td>
<td>Calculated for within-subjects studies, standard deviation of difference scores.</td>
</tr>
<tr>
<td>RM_r</td>
<td>numeric</td>
<td>Calculated for within-subjects studies, correlation between participant ratings of red and control attractiveness.</td>
</tr>
<tr>
<td>Control_Attractiveness</td>
<td>numeric</td>
<td>Attractiveness of stimuli in control condition, calculated as (Control_M - DV_ScaleBottom) / DV_ScaleTop.</td>
</tr>
<tr>
<td>Notes</td>
<td>character</td>
<td>Any additional notes on the study.</td>
</tr>
<tr>
<td>Total.SampleSize</td>
<td>numeric</td>
<td>Total unique participants in the study.</td>
</tr>
<tr>
<td>pooled</td>
<td>numeric</td>
<td>Pooled standard deviation for within-subjects studies.</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>Standardized mean difference.</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>Corresponding sampling variance.</td>
</tr>
</tbody>
</table>
The analyses in the published meta-analysis found clear evidence of upward bias in the estimate for female participants and equivocal evidence for male participants. Moderator analyses suggest effect sizes may have declined over time (both genders), may be largest when an original shade of red is used (men only), and may be smaller in pre-registered studies (women only).

**Concepts**

psychology, attraction, standardized mean differences

**Author(s)**

Robert Calin-Jageman, <rcalinjageman@dom.edu>, [https://calin-jageman.net](https://calin-jageman.net)

**Source**


**Examples**

```r
### copy data into 'dat' and examine data
dat <- dat.lehmann2018
head(dat)

## Not run:
### load metafor package
library(metafor)

### meta-analyses for male and female participants
red_romance_malep <- dat[dat$Gender == "Males", ]
red_romance_femalep <- dat[dat$Gender == "Females", ]

res_malep <- rma(yi, vi, data=red_romance_malep, test="knha")
res_malep
res_femalep <- rma(yi, vi, data=red_romance_femalep, test="knha")
res_femalep

## End(Not run)
```

---

**dat.li2007**

*Studies on the Effectiveness of Intravenous Magnesium in Acute Myocardial Infarction*
Description

Results from 22 trials examining the effectiveness of intravenous magnesium in the prevention of death following acute myocardial infarction.

Usage

dat.li2007

Format

The data frame contains the following columns:

- id: numeric, trial id number
- study: character, first author or trial name
- year: numeric, publication year
- ai: numeric, number of deaths in the magnesium group
- n1i: numeric, number of patients in the magnesium group
- ci: numeric, number of deaths in the control group
- n2i: numeric, number of patients in the control group

Details

The dataset includes the results from 22 randomized clinical trials that examined the effectiveness of intravenous magnesium in the prevention of death following acute myocardial infarction. It is similar to the dataset dat.egger2001, with some slight differences in the included trials and data used.

Concepts

medicine, cardiology, odds ratios, publication bias

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


See Also

dat.egger2001

Examples

```r
### copy data into 'dat' and examine data
dat <- dat.li2007
dat
```
## Not run:

### load metafor package
library(metafor)

### meta-analysis of all trials except ISIS-4
res <- rma(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, method="EE", subset=-14)
print(res, digits=2)
predict(res, transf=exp, digits=2)

### meta-analysis of all trials including ISIS-4
res <- rma(measure="OR", ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, method="EE")
print(res, digits=2)
predict(res, transf=exp, digits=2)

### contour-enhanced funnel plot centered at 0
funnel(res, refline=0, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"))

## End(Not run)

---

**dat.lim2014**

*Studies on the Association Between Maternal Size, Offspring Size, and Number of Offsprings*

### Description

Results from studies examining the association between maternal size, offspring size, and number of offsprings.

### Usage

dat.lim2014

### Format

The object is a list containing data frames `m_o_size`, `m_o_fecundity`, `o_o_unadj`, and `o_o_adj` that contain the following columns and the corresponding phylogenetic trees called `m_o_size_tree`, `m_o_fecundity_tree`, `o_o_unadj_tree`, and `o_o_adj_tree`:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>article</td>
<td>numeric</td>
<td>article id</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>species</td>
<td>character</td>
<td>species</td>
</tr>
<tr>
<td>amniotes</td>
<td>character</td>
<td>whether the species was amniotic</td>
</tr>
<tr>
<td>environment</td>
<td>character</td>
<td>whether the species were wild or captive</td>
</tr>
<tr>
<td>reprodunit</td>
<td>character</td>
<td>whether the data were based on lifetime reproductive output or a single reproductive event (only in <code>m_o_size</code> and <code>m_o_fecundity</code>)</td>
</tr>
<tr>
<td>ri</td>
<td>numeric</td>
<td>correlation coefficient</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>sample size</td>
</tr>
</tbody>
</table>
Details

The object dat.lim2014 includes 4 datasets:

- **m_o_size** on the correlation between maternal size and offspring size
- **m_o_fecundity** on the correlation between maternal size and number of offsprings
- **o_o_unadj** on the correlation between offspring size and number of offsprings
- **o_o_adj** on the correlation between offspring size and number of offsprings adjusted for maternal size

Objects **m_o_size_tree**, **m_o_fecundity_tree**, **o_o_unadj_tree**, and **o_o_adj_tree** are the corresponding phylogenetic trees for the species included in each of these datasets.

Concepts

- ecology
- evolution
- correlation coefficients
- multilevel models
- phylogeny

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.lim2014$o_o_unadj
dat[1:14, -c(2:3)]

# Not run:

### load metafor package
library(metafor)

### load ape package
library(ape, warn.conflicts=FALSE)
```
### calculate r-to-z transformed correlations and corresponding sampling variances
dat <- escalc(measure="ZCOR", ri=ri, ni=ni, data=dat)

### copy tree to 'tree'
tree <- dat.lim2014$o_o_unadj_tree

### compute branch lengths
tree <- compute.brlen(tree)

### compute phylogenetic correlation matrix
A <- vcv(tree, corr=TRUE)

### make copy of the species variable
dat$species.phy <- dat$species

### create effect size id variable
dat$esid <- 1:nrow(dat)

### fit multilevel phylogenetic meta-analytic model
res <- rma.mv(yi, vi,
  random = list(~ 1 | article, ~ 1 | esid, ~ 1 | species, ~ 1 | species.phy),
  R=list(species.phy=A), data=dat)
res

## End(Not run)

---

**dat.linde2005**

*Studies on the Effectiveness of St. John’s Wort for Treating Depression*

**Description**

Results from 26 studies on the effectiveness of Hypericum perforatum extracts (St. John’s wort) for treating depression.

**Usage**

dat.linde2005

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>study</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>country</td>
<td>character</td>
<td>study location</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>total sample size</td>
</tr>
<tr>
<td>major</td>
<td>numeric</td>
<td>sample restricted to patients who met criteria for major depression</td>
</tr>
</tbody>
</table>
The dataset includes the results from 26 double-blind placebo-controlled trials on the effectiveness of Hypericum perforatum extracts (St. John’s wort) for treating depression (note that 2 studies did not provide sufficient response information).

Data were extracted from Table 1 and Figure 3 from Linde et al. (2005). For study duration, the assessment week (instead of the total study duration) was coded for Philipp et al. (1999) and Montgomery et al. (2000). For dosage, the midpoint was coded when a range of values was given.

The definition of what constitutes a response differed across studies and is coded as follows:

1. HRSD score reduction of at least 50% or HRSD score after therapy <10,
2. HRSD reduction of at least 50%,
3. based on HRSD scale but exact definition not reported,
4. global patient assessment of efficacy,
5. at least ‘much improved’ on the Clinical Global Impression sub-scale for global improvement.

The group variable corresponds to the variable used by Linde et al. (2005) to stratify their analyses and is coded as follows:

1. smaller trials restricted to major depression,
2. larger trials restricted to major depression,
3. smaller trials not restricted to major depression,
4. larger trials not restricted to major depression.

Concepts

medicine, psychiatry, risk ratios

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.linde2005
head(dat)

### Not run:

### load metafor package
library(metafor)

### remove studies with no response information and study with no responses in either group
dat <- dat[-c(5,6,26),]

### calculate log risk ratios and corresponding sampling variances
dat <- escalc(measure="RR", ai=ai, ci=ci, n1i=n1i, n2i=n2i, data=dat)
head(dat)

### meta-analysis of the log risk ratios using a random-effects model
res <- rma(yi, vi, data=dat, method="DL")
res

### mixed-effects meta-regression model with stratification variable
res <- rma(yi, vi, mods = ~ factor(group) - 1, data=dat, method="DL")
res

### predicted average risk ratio for each level of the stratification variable
predict(res, newmods=diag(4), transf=exp, digits=2)

### End(Not run)

---

dat.linde2015   Studies on Classes of Antidepressants for the Primary Care Setting

Description

Results from 66 trials examining eight classes of antidepressants and placebo for the primary care setting.

Usage

dat.linde2015
Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>integer</td>
<td>study ID</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>first author</td>
</tr>
<tr>
<td>year</td>
<td>integer</td>
<td>year of publication</td>
</tr>
<tr>
<td>treatment1</td>
<td>character</td>
<td>treatment 1</td>
</tr>
<tr>
<td>treatment2</td>
<td>character</td>
<td>treatment 2</td>
</tr>
<tr>
<td>treatment3</td>
<td>character</td>
<td>treatment 3</td>
</tr>
<tr>
<td>n1</td>
<td>integer</td>
<td>number of patients (arm 1)</td>
</tr>
<tr>
<td>resp1</td>
<td>integer</td>
<td>number of early responder (arm 1)</td>
</tr>
<tr>
<td>remi1</td>
<td>integer</td>
<td>number of early remissions (arm 1)</td>
</tr>
<tr>
<td>loss1</td>
<td>integer</td>
<td>number of patients loss to follow-up (arm 1)</td>
</tr>
<tr>
<td>loss.ae1</td>
<td>integer</td>
<td>number of patients loss to follow-up due to adverse events (arm 1)</td>
</tr>
<tr>
<td>ae1</td>
<td>integer</td>
<td>number of patients with adverse events (arm 1)</td>
</tr>
<tr>
<td>n2</td>
<td>integer</td>
<td>number of patients (arm 2)</td>
</tr>
<tr>
<td>resp2</td>
<td>integer</td>
<td>number of early responder (arm 2)</td>
</tr>
<tr>
<td>remi2</td>
<td>integer</td>
<td>number of early remissions (arm 2)</td>
</tr>
<tr>
<td>loss2</td>
<td>integer</td>
<td>number of patients loss to follow-up (arm 2)</td>
</tr>
<tr>
<td>loss.ae2</td>
<td>integer</td>
<td>number of patients loss to follow-up due to adverse events (arm 2)</td>
</tr>
<tr>
<td>ae2</td>
<td>integer</td>
<td>number of patients with adverse events (arm 2)</td>
</tr>
<tr>
<td>n3</td>
<td>integer</td>
<td>number of patients (arm 3)</td>
</tr>
<tr>
<td>resp3</td>
<td>integer</td>
<td>number of early responder (arm 3)</td>
</tr>
<tr>
<td>remi3</td>
<td>integer</td>
<td>number of early remissions (arm 3)</td>
</tr>
<tr>
<td>loss3</td>
<td>integer</td>
<td>number of patients loss to follow-up (arm 3)</td>
</tr>
<tr>
<td>loss.ae3</td>
<td>integer</td>
<td>number of patients loss to follow-up due to adverse events (arm 3)</td>
</tr>
<tr>
<td>ae3</td>
<td>integer</td>
<td>number of patients with adverse events (arm 3)</td>
</tr>
</tbody>
</table>

Details

This data set comes from a systematic review of 8 pharmacological treatments of depression and placebo in primary care with 66 studies (8 of which were 3-arm studies) including 14,785 patients.

The primary outcome is early response, defined as at least a 50% score reduction on a depression scale after completion of treatment. Secondary outcomes (also measured as dichotomous) were early remission (defined as having a symptom score below a fixed threshold after completion of treatment), lost to follow-up, lost to follow-up due to adverse events, and any adverse event. The odds ratio was used as effect measure.

This data set was used as an example in Rücker and Schwarzer (2017) who introduced methods to resolve conflicting rankings of outcomes in network meta-analysis.

Concepts

medicine, psychiatry, odds ratios, network meta-analysis

Author(s)

Guido Schwarzer, <sc@imbi.uni-freiburg.de>, https://github.com/guido-s/
Source


References


See Also

pairwise, metabin, netmeta, netrank

Examples

```r
### Show results from first three studies (including three-arm study
### Lecrubier 1997)
head(dat.linde2015, 3)

### Not run:

### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print odds ratios and confidence limits with two digits
settings.meta(digits = 2)

### Change appearance of confidence intervals
cilayout(“(“, “-“)

### Define order of treatments in printouts
          “NaSSa”, “rMAO-A”, “Hypericum”, “Placebo”)

### Transform data from wide arm-based format to contrast-based format
### (outcome: early response). Argument ‘sm’ has to be used for odds
### ratio as summary measure; by default the risk ratio is used in the
### metabin function called internally.
pw1 <- pairwise(list(treatment1, treatment2, treatment3),
    event = list(resp1, resp2, resp3),
    n = list(n1, n2, n3),
    studlab = id, data = dat.linde2015, sm = “OR”)

### Conduct random effects network meta-analysis for primary outcome
### (early response); small number of early responses is bad (argument
### small.values)
net1 <- netmeta(pw1, fixed = FALSE, reference = “Placebo”, seq = trts,
    small.values = “bad”)
```
### Random effects NMA for early remission

```r
pw2 <- pairwise(treat = list(treatment1, treatment2, treatment3),
    event = list(remi1, remi2, remi3),
    n = list(n1, n2, n3),
    studlab = id, data = dat.linde2015, sm = "OR")
net2 <- netmeta(pw2, fixed = FALSE,
    seq = trts, ref = "Placebo", small.values = "bad")
net2
```

### Ranking of treatments

```r
nr1 <- netrank(net1)
nr2 <- netrank(net2)
nr1
nr2
```

### Partial order of treatment rankings (two outcomes)

```r
outcomes <- c("Early response", "Early remission")
po12 <- netposet(nr1, nr2, outcomes = outcomes)
plot(po12)
```

## End(Not run)

---

### Description

Results from 93 trials examining 22 interventions (including placebo and usual care) for the primary care of depression.

### Usage

```r
dat.linde2016
```

### Format

The data frame contains the following columns:

- `id` integer study ID
- `lnOR` numeric response after treatment (log odds ratio)
- `selnOR` numeric standard error of log odds ratio
- `treat1` character first treatment
- `treat2` character second treatment
Details

This data set comes from a network meta-analysis of 22 treatments of depression in primary care (Linde et al., 2016), based on 93 trials (79 two-arm trials, 13 three-arm trials, and one four-arm trial). The primary outcome was response after treatment (yes/no), defined as a reduction from baseline by at least 50% on a depression scale. The data set contains log odds ratios with standard errors for all pairwise comparisons.

The interventions comprised both medical and psychological treatments, also in combination, including placebo and usual care (UC) (Linde et al., 2016). Pharmacological interventions were tricyclic antidepressants (TCA), selective serotonin reuptake inhibitors (SSRI), serotonin-noradrenaline reuptake inhibitors (SNRI), noradrenaline reuptake inhibitors (NRI), low-dose serotonin (5-HT2) antagonists and reuptake inhibitors (low-dose SARI), noradrenergic and specific serotonergic agents (NaSSa), reversible inhibitors of monoaminoxidase A (rMAO-A), hypericum extracts, and an individualized drug. Psychological interventions were cognitive behavioral therapy (CBT; four forms: face-to-face CBT, remote therapist-led CBT, guided self-help CBT, and no or minimal contact CBT), face-to-face problem-solving therapy (PST), face-to-face interpersonal psychotherapy, face-to-face psychodynamic therapy, and “other face-to-face therapy”. Combination therapies were face-to-face CBT + SSRI, face-to-face PST + SSRI, and face-to-face interpersonal psychotherapy + SSRI.

The data set was used as an example in Rücker et al. (2020) to illustrate component network meta-analysis using frequentist methods.

Concepts

medicine, psychiatry, odds ratios, network meta-analysis, component network meta-analysis

Author(s)

Guido Schwarzer, <sc@imbi.uni-freiburg.de>, https://github.com/guido-s/

Source


References


See Also

netmeta

Examples

```r
### Show results of first three studies (first study has three treatment arms)
head(dat.linde2016, 5)
```
## Not run:

### Load netmeta package

dat.lopez2019

### Print odds ratios and confidence limits with two digits

dat.lopez2019

### Define order of treatments in printouts and forest plots

dat.lopez2019

### Conduct random effects network meta-analysis

dat.lopez2019

### Network graph

dat.lopez2019

### Show results

dat.lopez2019

### Additive component network meta-analysis with placebo as inactive treatment

dat.lopez2019

## Not run:

### Load netmeta package

```r
suppressPackageStartupMessages(library(netmeta))
```

### Print odds ratios and confidence limits with two digits

```r
settings.meta(digits = 2)
```

### Define order of treatments in printouts and forest plots

```r
trts <- c("SSRI", 
  "Face-to-face CBT", "Face-to-face interpsy", "Face-to-face PST", 
  "Face-to-face CBT + SSRI", "Face-to-face interpsy + SSRI", 
  "Face-to-face PST + SSRI", 
  "Face-to-face psychodyn", "Other face-to-face", 
  "TCA", "SNRI", "NRI", "Low-dose SARI", "NaSSa", "rMAO-A", "Ind drug", 
  "Hypericum", 
  "Remote CBT", "Self-help CBT", "No contact CBT", 
  "UC", "Placebo")
```

### Conduct random effects network meta-analysis

```r
net <- netmeta(lnOR, selnOR, treat1, treat2, id, 
  data = dat.linde2016, reference.group = "placebo", 
  seq = trts, sm = "OR", fixed = FALSE)
```

### Network graph

```r
netgraph(net, seq = "o", number = TRUE)
```

### Show results

```r
net
```

```r
forest(net, xlim = c(0.2, 50))
```

### Additive component network meta-analysis with placebo as inactive treatment

```r
nc <- netcomb(net, inactive = "placebo")
```

```r
nc
```

```r
forest(nc, xlim = c(0.2, 50))
```

## Not run:

---

**dat.lopez2019**

**Studies on the Effectiveness of CBT for Depression**

---

**Description**

Results from 76 studies examining the effectiveness of cognitive behavioral therapy (CBT) for depression in adults.
Usage
dat.lopez2019

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>(first) author and year of study</td>
</tr>
<tr>
<td>treatment</td>
<td>character</td>
<td>treatment provided (see ‘Details’)</td>
</tr>
<tr>
<td>scale</td>
<td>character</td>
<td>scale used to measure depression symptoms</td>
</tr>
<tr>
<td>n</td>
<td>numeric</td>
<td>group size</td>
</tr>
<tr>
<td>diff</td>
<td>numeric</td>
<td>standardized mean change</td>
</tr>
<tr>
<td>se</td>
<td>numeric</td>
<td>corresponding standard error</td>
</tr>
<tr>
<td>group</td>
<td>numeric</td>
<td>type of therapy (0 = individual, 1 = group therapy)</td>
</tr>
<tr>
<td>tailored</td>
<td>numeric</td>
<td>whether the intervention was tailored to each patient (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>sessions</td>
<td>numeric</td>
<td>number of sessions</td>
</tr>
<tr>
<td>length</td>
<td>numeric</td>
<td>average session length (in minutes)</td>
</tr>
<tr>
<td>intensity</td>
<td>numeric</td>
<td>product of sessions and length</td>
</tr>
<tr>
<td>multi</td>
<td>numeric</td>
<td>intervention included multimedia elements (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>cog</td>
<td>numeric</td>
<td>intervention included cognitive techniques (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>ba</td>
<td>numeric</td>
<td>intervention included behavioral activation (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>psed</td>
<td>numeric</td>
<td>intervention included psychoeducation (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>home</td>
<td>numeric</td>
<td>intervention included homework (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>prob</td>
<td>numeric</td>
<td>intervention included problem solving (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>soc</td>
<td>numeric</td>
<td>intervention included social skills training (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>relax</td>
<td>numeric</td>
<td>intervention included relaxation (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>goal</td>
<td>numeric</td>
<td>intervention included goal setting (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>final</td>
<td>numeric</td>
<td>intervention included a final session (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>mind</td>
<td>numeric</td>
<td>intervention included mindfulness (0 = no, 1 = yes)</td>
</tr>
<tr>
<td>act</td>
<td>numeric</td>
<td>intervention included acceptance and commitment therapy (0 = no, 1 = yes)</td>
</tr>
</tbody>
</table>

Details

The dataset includes the results from 76 studies examining the effectiveness of cognitive behavioral therapy (CBT) for treating depression in adults. Studies included two or more of the following treatments/conditions:

1. treatment as usual (TAU),
2. no treatment,
3. wait list,
4. psychological or attention placebo,
5. face-to-face CBT,
6. multimedia CBT,
7. hybrid CBT (i.e., multimedia CBT with one or more face-to-face sessions).

Multimedia CBT was defined as CBT delivered via self-help books, audio/video recordings, telephone, computer programs, apps, e-mail, or text messages.
Variable `diff` is the standardized mean change within each group, with negative values indicating a decrease in depression symptoms.

**Concepts**

psychiatry, standardized mean changes, network meta-analysis

**Author(s)**

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

**Source**

Personal communication.

**References**


**Examples**

```r
### copy data into 'dat' and examine data
dat <- dat.lopez2019
dat[1:10,1:6]

### load metafor package
library(metafor)

### create network graph ('igraph' package must be installed)
library(igraph, warn.conflicts=FALSE)
pairs <- data.frame(do.call(rbind, sapply(split(dat$treatment, dat$study), function(x) t(combn(x,2)))), stringsAsFactors=FALSE)
pairs$X1 <- factor(pairs$X1, levels=sort(unique(dat$treatment)))
pairs$X2 <- factor(pairs$X2, levels=sort(unique(dat$treatment)))
tab <- table(pairs[,1], pairs[,2])
tab # adjacency matrix
g <- graph_from_adjacency_matrix(tab, mode = "plus", weighted=TRUE, diag=FALSE)
plot(g, edge.curved=FALSE, edge.width=E(g)$weight/2,
     layout=layout_in_circle(g, order=c("Wait list", "No treatment", "TAU", "Multimedia CBT", "Hybrid CBT", "F2F CBT", "Placebo")),
     vertex.size=45, vertex.color="lightgray", vertex.label.color="black", vertex.label.font=2)

### restructure data into wide format
dat <- to.wide(dat, study="study", grp="treatment", ref="TAU",
grpvars=c("diff","se","n"), postfix=c("1","2"))

### compute contrasts between treatment pairs and corresponding sampling variances
```
dat$yi <- with(dat, diff1 - diff2)
dat$vi <- with(dat, se1^2 + se2^2)

### calculate the variance-covariance matrix for multitreatment studies
calc.v <- function(x) {
  v <- matrix(x$se2[1]^2, nrow=nrow(x), ncol=nrow(x))
  diag(v) <- x$vi
  v
}
V <- bldiag(lapply(split(dat, dat$study), calc.v))

### add contrast matrix to the dataset
dat <- contrmat(dat, grp1="treatment1", grp2="treatment2")

### network meta-analysis using a contrast-based random-effects model
### by setting rho=1/2, tau^2 reflects the amount of heterogeneity for all treatment comparisons
### the treatment left out (TAU) becomes the reference level for the treatment comparisons
res <- rma.mv(yi, V, data=dat,
  mods = ~ No.treatment + Wait.list + Placebo + F2F.CBT + Hybrid.CBT + Multimedia.CBT - 1,
  random = ~ comp | study, rho=1/2)
res

### forest plot of the contrast estimates (treatments versus TAU)
forest(coef(res), diag(vcov(res)), slab=sub('.', '', names(coef(res)), fixed=TRUE),
  xlim=c(-5,5), ylim=c(-3,3), psize=1, header="Treatment",
  xlab="Difference in Standardized Mean Change (compared to TAU)"

### fit random inconsistency effects model
res <- rma.mv(yi, V, data=dat,
  mods = ~ No.treatment + Wait.list + Placebo + F2F.CBT + Hybrid.CBT + Multimedia.CBT - 1,
  random = list(~ comp | study, ~ comp | design), rho=1/2, phi=1/2)
res

## End(Not run)

dat.maire2019

Studies on Temporal Trends in Fish Community Structures in French Rivers

Description

Results from studies examining changes in the abundance of fish species in French rivers.

Usage

dat.maire2019
Format

The object is a list containing a data frame called dat that contains the following columns and distance matrix called dmat:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>site</td>
<td>character</td>
<td>study site</td>
</tr>
<tr>
<td>station</td>
<td>character</td>
<td>sampling station at site</td>
</tr>
<tr>
<td>site_station</td>
<td>character</td>
<td>site and station combined</td>
</tr>
<tr>
<td>s1</td>
<td>numeric</td>
<td>Mann-Kendal trend statistic for relative abundance of non-local species</td>
</tr>
<tr>
<td>vars1</td>
<td>numeric</td>
<td>corresponding sampling variance (corrected for temporal autocorrelation)</td>
</tr>
<tr>
<td>s2</td>
<td>numeric</td>
<td>Mann-Kendal trend statistic for relative abundance of northern species</td>
</tr>
<tr>
<td>vars2</td>
<td>numeric</td>
<td>corresponding sampling variance (corrected for temporal autocorrelation)</td>
</tr>
<tr>
<td>s3</td>
<td>numeric</td>
<td>Mann-Kendal trend statistic for relative abundance of non-native species</td>
</tr>
<tr>
<td>vars3</td>
<td>numeric</td>
<td>corresponding sampling variance (corrected for temporal autocorrelation)</td>
</tr>
<tr>
<td>const</td>
<td>numeric</td>
<td>constant value of 1</td>
</tr>
</tbody>
</table>

Details

The dataset includes the results from 35 sampling stations (at 11 sites along various French rivers) examining the abundance of various fish species over time (i.e., over 19-37 years, all until 2015). The temporal trend in these abundance data was quantified in terms of Mann-Kendal trend statistics, with positive values indicating monotonically increasing trends. The corresponding sampling variances were corrected for the temporal autocorrelation in the data (Hamed & Rao, 1998).

The distance matrix dmat indicates the distance of the sampling stations (1-423 river-km). For stations not connected through the river network, a high distance value of 10,000 river-km was set (effectively forcing the spatial correlation to be 0 for such stations).

The dataset can be used to illustrate a meta-analysis allowing for spatial correlation in the outcomes.

Concepts

ecology, climate change, spatial correlation

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References

Examples

### copy data into 'dat' and examine data

```r
dat <- dat.maire2019$dat
dat[-10]
```

### copy distance matrix into 'dmat' and examine first 5 rows/columns

```r
dmat <- dat.maire2019$dmat
dmat[1:5,1:5]
```

# Not run:

### load metafor package

```r
library(metafor)
```

### fit a standard random-effects model ignoring spatial correlation

```r
res1 <- rma.mv(s1, vars1, random = ~ 1 | site_station, data=dat)
res1
```

### fit model allowing for spatial correlation

```r
res2 <- rma.mv(s1, vars1, random = ~ site_station | const, struct="SPGAU",
               data=dat, dist=list(dmat), control=list(rho.init=10))
res2
```

### add random effects for sites and stations within sites

```r
res3 <- rma.mv(s1, vars1, random = list(~ 1 | site/station, ~ site_station | const), struct="SPGAU",
               data=dat, dist=list(dmat), control=list(rho.init=10))
res3
```

### likelihood ratio tests comparing the models

```r
anova(res1, res2)
anova(res2, res3)
```

### profile likelihood plots for model res2

```r
profile(res2, cline=TRUE)
```

### effective range (river-km for which the spatial correlation is >= .05)

```r
sqrt(3) * res2$rho
```

### note: it was necessary to adjust the starting value for rho in models

```r
res2 and res3 so that the optimizer does not get stuck in a local maximum
profile(res2, rho=1, xlim=c(0,200), steps=100)
```

### End(Not run)

---

dat.mccurdy2020

### Studies on the Generation Effect

Description

Results from 126 articles that examined the so-called ‘generation effect’.
Usage

The data frame contains the following columns:

- **article**: numeric  
  - article identifier
- **experiment**: character  
  - experiment (within article) identifier
- **sample**: numeric  
  - sample (within experiment) identifier
- **id**: numeric  
  - row identifier
- **pairing**: numeric  
  - identifier to indicate paired conditions within experiments
- **yi**: numeric  
  - mean recall rate for the condition
- **vi**: numeric  
  - corresponding sampling variance
- **ni**: numeric  
  - number of participants for the condition
- **stimuli**: numeric  
  - number of stimuli for the condition
- **condition**: factor  
  - condition ('read' or 'generate')
- **gen_difficulty**: factor  
  - generation difficulty ('low' or 'high')
- **manip_type**: factor  
  - manipulation type of the generate versus read condition (using a ‘within’ or ‘between’ subjects design)
- **present_style**: factor  
  - presentation style ('mixed' or 'pure' list presentation)
- **word_status**: factor  
  - word status ('words', 'non-words', or 'numbers')
- **memory_test**: factor  
  - memory test ('recognition', 'cued recall', or 'free recall')
- **memory_type**: factor  
  - memory type ('item', 'source', 'font color', 'font type', 'order', 'cue word', 'background color')
- **gen_constraint**: factor  
  - generation constraint ('low', 'medium', or 'high')
- **learning_type**: factor  
  - learning type ('incidental' or 'intentional')
- **stimuli_relation**: factor  
  - stimuli relation ('semantic', 'category', 'antonym', 'synonym', 'rhyme', 'compound words', 'definitions', or 'unrelated')
- **gen_mode**: factor  
  - generation mode ('verbal/speaking', 'covert/thinking', or 'writing/typing')
- **gen_task**: factor  
  - generation task ('anagram', 'letter transposition', 'word fragment', 'sentence completion', 'word stem', 'calculation', or 'cue only')
- **attention**: factor  
  - attention ('divided' or 'full')
- **pacing**: factor  
  - pacing ('self-paced' or 'timed')
- **filler_task**: factor  
  - filler task ('yes' or 'no')
- **age_grp**: factor  
  - age group ('younger' or 'older' adults)
- **retention_delay**: factor  
  - retention delay ('immediate', 'short', or 'long')

Details

The generation effect is the memory benefit for self-generated compared with read or experimenter-provided information (Jacoby, 1978; Slamecka & Graf, 1978). In a typical study, participants are presented with a list of stimuli (usually words or word pairs). For half of the stimuli, participants self-generate a target word (e.g., open–cl_____), while for the other half, participants simply read an intact target word (e.g., above–below). On a later memory test for the target words, the common finding is that self-generated words are better remembered than read words (i.e., the generation effect).

Although several theories have been proposed to explain the generation effect, there is still some debate on the underlying memory mechanism(s) contributing to this phenomenon. The meta-analysis by McCurdy et al. (2020) translated various theories on the generation effect into hypotheses that could then be tested in moderator analyses based on a dataset containing 126 articles.
ments, and 1653 mean recall estimates collected under various conditions.

Detailed explanations of the various variables coded (and how these can be used to test various hypotheses regarding the generation effect) can be found in the article. The most important variable is condition, which denotes whether a particular row of the dataset corresponds to the results of a ‘read’ or a ‘generate’ condition.

The data structure is quite complex. Articles may have reported the findings from multiple experiments involving one or multiple samples that were examined under various conditions. The pairing variable indicates which rows of the dataset represent a pairing of a read condition with one or multiple corresponding generate conditions within an experiment. A pairing may involve the same sample of subjects (when using a within-subjects design for comparing the conditions) or different samples (when using a between-subjects design).

Concepts

psychology, memory, proportions, raw means, multilevel models, cluster-robust inference

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.mccurdy2020
head(dat)

### load metafor package
library(metafor)

### fit multilevel mixed-effects meta-regression model
res <- rma.mv(yi, vi, mods = ~ condition, 
               random = list(~ 1 | article/experiment/sample/id, ~ 1 | pairing),
               data=dat, sparse=TRUE, digits=3)
```
dat.mcdaniel1994

### proportion of total amount of heterogeneity due to each component
```r
data.frame(source=res$s.names, sigma2=round(res$sigma2, 3),
prop=round(res$sigma2 / sum(res$sigma2), 2))
```

### apply cluster-robust inference
```r
sav <- robust(res, cluster=article)
sav
```

### estimated average recall rate in read and generate conditions
```r
predict(sav, newmods = c(0,1), digits=3)
```

### use methods from clubSandwich package
```r
dsav <- robust(res, cluster=article, clubSandwich=TRUE)
dsav
```

## End(Not run)

---

**dat.mcdaniel1994 Studies on the Validity of Employment Interviews**

### Description

Results from 160 studies on the correlation between employment interview assessments and job performance.

### Usage

```r
dat.mcdaniel1994
```

### Format

The data frame contains the following columns:

- **study**: numeric, study number
- **ni**: numeric, sample size of the study
- **ri**: numeric, observed correlation
- **type**: character, interview type (j = job-related, s = situational, p = psychological)
- **struct**: character, interview structure (u = unstructured, s = structured)

### Details

The 160 studies provide data in terms of the correlation between employment interview performance and actual job performance. In addition, the interview type and the interview structure are indicated.

McDaniel et al. (1994) describe the interview type and structure variables as follows. "Questions in situational interviews [...] focus on the individual’s ability to project what his or her behavior
would be in a given situation. [...] Job-related interviews are those in which the interviewer is a personnel officer or hiring authority and the questions attempt to assess past behaviors and job-related information, but most questions are not considered situational. Psychological interviews are conducted by a psychologist, and the questions are intended to assess personal traits, such as dependability." In structured interviews, "the questions and acceptable responses were specified in advance and the responses were rated for appropriateness of content. [...] Unstructured interviews gather applicant information in a less systematic manner than do structured interviews. Although the questions may be specified in advance, they usually are not, and there is seldom a formalized scoring guide. Also, all persons being interviewed are not typically asked the same questions."

The goal of the meta-analysis was to examine the overall criterion-related validity of employment interviews and to examine whether the validity depends on the type and structure of the interview.

The data in this dataset were obtained from Table A.2 in Rothstein, Sutton, and Borenstein (2005, p. 325-329). Note that the type and struct variables contain some NAs.

Concepts

psychology, correlation coefficients, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.mcdaniel1994
head(dat)

### Not run:

### load metafor package
library(metafor)

### calculate r-to-z transformed correlations and corresponding sampling variances
dat <- escalc(measure="ZCOR", ri=ri, ni=ni, data=dat)
head(dat)

### meta-analysis of the transformed correlations using a random-effects model
res <- rma(yi, vi, data=dat)
```
### Average correlation with 95% CI
`predict(res, transf=transf.ztor)`

### Mixed-effects model with interview type as factor
### Note: Job-related interviews is the reference level
`rma(yi, vi, mods = ~ factor(type), data=dat)`

### Mixed-effects model with interview structure as factor
### Note: Structured interviews is the reference level
`rma(yi, vi, mods = ~ factor(struct), data=dat)`

### Note: The interpretation of the results is difficult since all
### Situational interviews were structured, almost all psychological
### Interviews were unstructured, and actually for the majority of
### The psychological interviews it was unknown whether the interview
### Was structured or unstructured
`table(dat$type, dat$struct, useNA="always")`

### Meta-analysis of raw correlations using a random-effects model
`res <- rma(measure="COR", ri=ri, ni=ni, data=dat.mcdaniel1994)`
`res`

## End(Not run)
Details

The dataset contains the data from the meta-analysis by Michael et al. (2013) of experiments on the persuasive power of a brain image. The meta-analysis analyzed an original study by McCabe and Castel (2008) as well as 10 replication attempts conducted by the authors of the meta-analysis. In each study, participants read an article about using brain imaging as a lie detector. The article either included a superfluous fMRI image of a brain (brain) or not (no_brain). After reading the article, all participants responded to the statement “Do you agree or disagree with the conclusion that brain imaging can be used as a lie detector?” on a scale from 1 (strongly disagree) to 4 (strongly agree).

The original study by McCabe and Castel (2008) reported a relatively large increase in agreement due to the presence of brain images. Meta-analysis of the original study with the 10 replications suggests, however, a small, possibly null effect: an estimated average raw mean difference of 0.07 points, 95% CI [-0.00, 0.14], under a random-effects model.

In some studies, the article included a passage critiquing the primary claims made in the article; this is coded in the Included_Critique column for analysis as a possible moderator. Note that Experiment 3 by McCabe and Castel (2008) was a 2x2 between subjects design: brain image presence was manipulated as well as the inclusion of a critique. The two different critique conditions are recorded as separate rows in this dataset. Analysis of this dataset with metafor yields the same results (given rounding) reported in the manuscript.

Concepts

psychology, persuasion, raw mean differences

Author(s)

Robert Calin-Jageman, <rcalinjageman@dom.edu>, https://calin-jageman.net

Source


References

Examples

```r
### copy data into 'dat' and examine data
dat <- dat.michael2013
dat

### Not run:

### load metafor package
library(metafor)

### Data prep
# yi and vi are already provided, but here's how you would use escalc() to obtain
# a raw-mean difference and its variance.
# Note the measure parameter is "MD" for 'raw mean difference'
dat <- metafor::escalc(
  measure = "MD",
  m1i = Brain_m,
  m2i = No_brain_m,
  sd1i = Brain_s,
  sd2i = No_brain_s,
  n1i = Brain_n,
  n2i = No_brain_n,
  data = dat
)

### meta-analysis using a random-effects model of the raw mean differences
res <- rma(yi, vi, data=dat)
print(res, digits=2)

### examine if Included_Critique is a potential moderator
res <- rma(yi, vi, mods = ~ Included_Critique, data=dat)
print(res, digits=2)

### End(Not run)
```

---

dat.molloy2014

*Studies on the Relationship between Conscientiousness and Medication Adherence*

Description

Results from 16 studies on the correlation between conscientiousness and medication adherence.

Usage

`dat.molloy2014`
Format

The data frame contains the following columns:
Conscientiousness, one of the big-5 personality traits, can be defined as “socially prescribed impulse control that facilitates task- and goal-directed behaviour, such as thinking before acting, delaying gratification, following norms and rules and planning, organising and prioritising tasks” (John & Srivastava, 1999). Conscientiousness has been shown to be related to a number of health-related behaviors (e.g., tobacco/alcohol/drug use, diet and activity patterns, risky behaviors). A recent meta-analysis by Molloy et al. (2014) examined to what extent conscientiousness is related to medication adherence, that is, the extent to which (typically chronically ill) patients follow a prescribed medication regimen (e.g., taking a daily dose of a cholesterol lowering drug in patients with high LDL serum cholesterol levels). The results from the 16 studies included in this meta-analysis are provided in this dataset.

Variable a_measure indicates whether adherence was measured based on self-reports or a more ‘objective’ measure (e.g., electronic monitoring of pill bottle openings, pill counts). Variable c_measure indicates whether conscientiousness was measured with some version of the NEO personality inventory or some other scale. Methodological quality was scored by the authors on a 1 to 4 scale with higher scores indicating higher quality (see article for details on how this score was derived).

Concepts

psychology, medicine, correlation coefficients

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References

Examples

```r
### copy data into 'dat' and examine data
dat <- dat.molloy2014
dat[-c(5:6)]

### Not run:

### load metafor package
library(metafor)

### calculate r-to-z transformed correlations and corresponding sampling variances
dat <- escalc(measure="ZCOR", ri=ri, ni=ni, data=dat, slab=paste(authors, year, sep=" ", "))
dat[-c(5:6)]

### meta-analysis of the transformed correlations using a random-effects model
res <- rma(yi, vi, data=dat)
res

### average correlation with 95% CI
predict(res, digits=3, transf=transf.ztor)

### forest plot
forest(res, addpred=TRUE, xlim=c(-1.6,1.6), atransf=transf.ztor,
at=transf.rtoz(c(-.4,-.2,0,.2,.4,.6)), digits=c(2,3), cex=.8,
header="Author(s), Year")

### funnel plot
funnel(res)

### End(Not run)
```

---

dat.moura2021  

**Studies on Assortative Mating**

**Description**

Results from 457 studies on assortative mating in various species.

**Usage**

dat.moura2021

**Format**

The object is a list containing a data frame called `dat` that contains the following columns and a phylogenetic tree called `tree`:

- `study.id`: character, study id
The 457 studies included in this dataset provide 1828 correlation coefficients describing the similarity in some measure of body size in mating couples in 341 different species.

Concepts

ecology, evolution, correlation coefficients, multivariate models, phylogeny, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.moura2021$dat
```
## Not run:
### load metafor package
library(metafor)

### load ape package
library(ape, warn.conflicts=FALSE)

### calculate r-to-z transformed correlations and corresponding sampling variances
dat <- escalc(measure="ZCOR", ri=ri, ni=ni, data=dat)

### copy tree to 'tree'
tree <- dat.moura2021$tree

### turn tree into an ultrametric one
tree <- compute.brlen(tree)

### compute phylogenetic correlation matrix
A <- vcv(tree, corr=TRUE)

### make copy of the species.id variable
dat$species.id.phy <- dat$species.id

### fit multilevel phylogenetic meta-analytic model
res <- rma.mv(yi, vi,
               random = list(~1 | study.id, ~1 | effect.size.id, ~1 | species.id, ~1 | species.id.phy),
               R=list(species.id.phy=A), data=dat)
res

### examine if spatial and/or temporal pooling of data tends to yield larger correlations
res <- rma.mv(yi, vi,
              mods = ~ spatially.pooled * temporally.pooled,
              random = list(~1 | study.id, ~1 | effect.size.id, ~1 | species.id, ~1 | species.id.phy),
              R=list(species.id.phy=A), data=dat)
res

### estimated average correlation without pooling, when pooling spatially,
### when pooling temporally, and when pooling spatially and temporally
predict(res, newmods = rbind(c(0,0,0),c(1,0,0),c(0,1,0),c(1,1,1)), transf=transf.ztor, digits=2)

## End(Not run)
Description

A meta-analysis on the association between the size of a male’s bib and their social status in house sparrows (*Passer domesticus*).

Usage
dat.nakagawa2007

Format

The data frame contains the following columns:

- **StudyID** character identity of primary study
- **Place** character location of study population
- **Correlation** numeric correlation coefficient
- **SampleSize** integer sample size of population

Details

Each study measures the association between a sparrows bib size and its social status. Effects are quantified as correlation coefficients.

Concepts

ecology, correlation coefficients

Author(s)

Daniel Noble, <daniel.noble@anu.edu.au>

Source


Examples

```r
# Example code
### copy data into 'dat' and examine data
dat <- dat.nakagawa2007
dat

### Not run:

### load metafor package
library(metafor)

### calculate Zr
dat <- escalc(measure="ZCOR", ri=Correlation, ni=SampleSize, data=dat)
```
### fit meta-analytic model
res <- rma.mv(yi, vi, random = list(~ 1 | StudyID), data=dat)
res

## End(Not run)

---

dat.nielweise2007

*Studies on Anti-Infective-Treated Central Venous Catheters for Prevention of Catheter-Related Bloodstream Infections*

#### Description
Results from 18 studies comparing the risk of catheter-related bloodstream infection when using anti-infective-treated versus standard catheters in the acute care setting.

#### Usage
dat.nielweise2007

#### Format
The data frame contains the following columns:

<table>
<thead>
<tr>
<th>study</th>
<th>numeric</th>
<th>study number</th>
</tr>
</thead>
<tbody>
<tr>
<td>author</td>
<td>character</td>
<td>(first) author</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>ai</td>
<td>numeric</td>
<td>number of CRBSIs in patients receiving an anti-infective catheter</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of patients receiving an anti-infective catheter</td>
</tr>
<tr>
<td>ci</td>
<td>numeric</td>
<td>number of CRBSIs in patients receiving a standard catheter</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of patients receiving a standard catheter</td>
</tr>
</tbody>
</table>

#### Details
The use of a central venous catheter may lead to a catheter-related bloodstream infection (CRBSI), which in turn increases the risk of morbidity and mortality. Anti-infective-treated catheters have been developed that are meant to reduce the risk of CRBSIs. Niel-Weise et al. (2007) conducted a meta-analysis of studies comparing infection risk when using anti-infective-treated versus standard catheters in the acute care setting. The results from 18 such studies are included in this dataset.

The dataset was used in the article by Stijnen et al. (2010) to illustrate various generalized linear mixed-effects models for the meta-analysis of proportions and odds ratios (see ‘References’).

#### Concepts
medicine, odds ratios, generalized linear models
Description

Results from 18 studies comparing the risk of catheter-related bloodstream infection when using anti-infective-treated versus standard catheters for total parenteral nutrition or chemotherapy.
Usage
dat.nielweise2008

Format
The data frame contains the following columns:

- **study** numeric: study number
- **authors** character: study authors
- **year** numeric: publication year
- **x1i** numeric: number of CRBSIs in patients receiving an anti-infective catheter
- **t1i** numeric: total number of catheter days for patients receiving an anti-infective catheter
- **x2i** numeric: number of CRBSIs in patients receiving a standard catheter
- **t2i** numeric: total number of catheter days for patients receiving a standard catheter

Details
The use of a central venous catheter may lead to a catheter-related bloodstream infection (CRBSI), which in turn increases the risk of morbidity and mortality. Anti-infective-treated catheters have been developed that are meant to reduce the risk of CRBSIs. Niel-Weise et al. (2008) conducted a meta-analysis of studies comparing infection risk when using anti-infective-treated versus standard catheters for total parenteral nutrition or chemotherapy. The results from 9 such studies are included in this dataset.

The dataset was used in the article by Stijnen et al. (2010) to illustrate various generalized linear mixed-effects models for the meta-analysis of incidence rates and incidence rate ratios (see ‘References’).

Concepts
medicine, incidence rates, generalized linear models

Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

References
Examples

```r
### copy data into 'dat' and examine data
dat <- dat.nielweise2008
dat

## Not run:

### load metafor package
library(metafor)

### standard (inverse-variance) random-effects model
res <- rma(measure="IRR", x1i=x1i, t1i=t1i, x2i=x2i, t2i=t2i, data=dat)
print(res, digits=3)
predict(res, transf=exp, digits=2)

### random-effects conditional Poisson model
res <- rma.glmm(measure="IRR", x1i=x1i, t1i=t1i, x2i=x2i, t2i=t2i, data=dat, model="CM.EL")
print(res, digits=3)
predict(res, transf=exp, digits=2)

## End(Not run)
```

---

**dat.normand1999**  
*Studies on the Length of Hospital Stay of Stroke Patients*

**Description**

Results from 9 studies on the length of the hospital stay of stroke patients under specialized care and under conventional/routine (non-specialist) care.

**Usage**

`dat.normand1999`

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>source</td>
<td>character</td>
<td>source of data</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>number of patients under specialized care</td>
</tr>
<tr>
<td>m1i</td>
<td>numeric</td>
<td>mean length of stay (in days) under specialized care</td>
</tr>
<tr>
<td>sd1i</td>
<td>numeric</td>
<td>standard deviation of the length of stay under specialized care</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>number of patients under routine care</td>
</tr>
<tr>
<td>m2i</td>
<td>numeric</td>
<td>mean length of stay (in days) under routine care</td>
</tr>
<tr>
<td>sd2i</td>
<td>numeric</td>
<td>standard deviation of the length of stay under routine care</td>
</tr>
</tbody>
</table>
Details

The 9 studies provide data in terms of the mean length of the hospital stay (in days) of stroke patients under specialized care and under conventional/routine (non-specialist) care. The goal of the meta-analysis was to examine the hypothesis whether specialist stroke unit care will result in a shorter length of hospitalization compared to routine management.

Concepts

medicine, raw mean differences, standardized mean differences

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.normand1999
dat

## Not run:
### load metafor package
library(metafor)

### calculate mean differences and corresponding sampling variances
dat <- escalc(measure="MD", m1i=m1i, sd1i=sd1i, n1i=n1i, m2i=m2i, sd2i=sd2i, n2i=n2i, data=dat)
dat

### meta-analysis of mean differences using a random-effects model
res <- rma(yi, vi, data=dat)
res

### meta-analysis of standardized mean differences using a random-effects model
res <- rma(measure="SMD", m1i=m1i, sd1i=sd1i, n1i=n1i, m2i=m2i, sd2i=sd2i, n2i=n2i, data=dat, slab=source)
res

### draw forest plot
forest(res, xlim=c(-7,5), ylim=c(-3,1), header="Study/Source")

### calculate (log transformed) ratios of means and corresponding sampling variances
dat <- escalc(measure="ROM", m1i=m1i, sd1i=sd1i, n1i=n1i, m2i=m2i, sd2i=sd2i, n2i=n2i, data=dat)
dat
```
### meta-analysis of the (log transformed) ratios of means using a random-effects model

```r
res <- rma(yi, vi, data=dat)
res
predict(res, transf=exp, digits=2)
```

## End(Not run)

---

**dat.obrien2003**  
*Studies on the Relationship Between BMI and Risk of Preeclampsia*

**Description**

Results from 13 studies on the relationship between maternal body mass index (BMI) and the risk of preeclampsia.

**Usage**

`dat.obrien2003`

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study id</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>(first) author of the study</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>ref</td>
<td>numeric</td>
<td>reference number</td>
</tr>
<tr>
<td>ch</td>
<td>character</td>
<td>exclusion due to chronic hypertension (yes/no)</td>
</tr>
<tr>
<td>dm</td>
<td>character</td>
<td>exclusion due to diabetes mellitus (yes/no)</td>
</tr>
<tr>
<td>mg</td>
<td>character</td>
<td>exclusion due to multiple gestation (yes/no)</td>
</tr>
<tr>
<td>bmi.lb</td>
<td>numeric</td>
<td>lower bound of the BMI interval</td>
</tr>
<tr>
<td>bmi.ub</td>
<td>numeric</td>
<td>upper bound of the BMI interval</td>
</tr>
<tr>
<td>bmi</td>
<td>numeric</td>
<td>midpoint of the BMI interval</td>
</tr>
<tr>
<td>cases</td>
<td>numeric</td>
<td>number of preeclampsia cases in the BMI group</td>
</tr>
<tr>
<td>total</td>
<td>numeric</td>
<td>number of individuals in the BMI group</td>
</tr>
</tbody>
</table>

**Details**

The dataset includes the results from 13 studies examining the relationship between maternal body mass index (BMI) and the risk of preeclampsia. For each study, results are given in terms of the number of preeclampsia cases within two or more groups defined by the lower and upper BMI bounds as shown in the dataset (NA means that the interval is either open to the left or right). The `bmi` variable is the interval midpoint as defined by O’Brien et al. (2003).

**Concepts**

medicine, obstetrics, risk ratios, proportions, multilevel models, dose-response models
### Examples

```r
### copy data into 'dat' and examine data
dat <- dat.obrien2003
dat

### Not run:

### load metafor package
library(metafor)

### restructure the data into a wide format
dat2 <- to.wide(dat, study="study", grp="grp", ref=1, grpvars=c("bmi","cases","total"),
    addid=FALSE, adddesign=FALSE, postfix=c(1,2))
dat2[1:10, -c(2:3)]

### calculate log risk ratios and corresponding sampling variances
dat2 <- escalc(measure="RR", ai=cases1, n1i=total1, ci=cases2, n2i=total2, data=dat2)
dat2[1:10, -c(2:7)]

### forest plot of the risk ratios
dd <- c(0,diff(dat2$study))
dd[dd > 0] <- 1
rows <- (1:nrow(dat2)) + cumsum(dd)
rows <- 1 + max(rows) - rows
slabs <- mapply(function(x,y,z) as.expression(bquote(.(x)^.(y)~.(z))),
    dat2$author, dat2$ref, dat2$year)
with(dat2, forest(yi, vi, header=TRUE, slab=slabs, xlim=c(-7,5.5), fonts="mono", cex=0.8,
    psize=1, pch=19, efac=0, rows=rows, ylim=c(0,max(rows)+3), yaxs="i",
    atransf=exp, at=log(c(.05,.1,.2,.5,1,2,5,10,20)), ilab=comp, ilab.pos=4))
text(-4.4, max(rows)+2, "Comparison", font=2, cex=0.8, pos=4)

### within-study mean center the BMI variable
dat$bmicent <- with(dat, bmi - ave(bmi, study))

### compute the proportion of preeclampsia cases and corresponding sampling variances
dat <- escalc(measure="PR", xi=cases, ni=total, data=dat)

### convert the proportions to percentages (and convert the variances accordingly)
dat$yi <- dat$yi*100
dat$vi <- dat$vi*100^2
dat[1:10, -c(2:3)]
```
### fit multilevel meta-regression model to examine the relationship between the centered BMI variable and the risk of preeclampsia

```r
res <- rma.mv(yi, vi, mods = ~ bmicent, random = ~ 1 | study/grp, data=dat)
res
```

### draw scatterplot with regression line

```r
res$slab <- dat$ref
regplot(res, xlab=expression("Within-Study Mean Centered BMI"~(kg/m^2)), ylab="Preeclampsia Prevalence (%)", las=1, bty="l", at=seq(0,18,by=2), olim=c(0,100), psize=2, bg="gray90", label=TRUE, offset=0, labsize=0.6)
```

### fit model using a random slope for bmicent

```r
res <- rma.mv(yi, vi, mods = ~ bmicent, random = ~ bmicent | study, struct="GEN", data=dat)
res
```

### load rms package

```r
library(rms)
```

### fit restricted cubic spline model

```r
res <- rma.mv(yi, vi, mods = ~ rcs(bmicent, 4), random = ~ 1 | study/grp, data=dat)
res
```

### get knot positions

```r
knots <- attr(rcs(model.matrix(res)[,2], 4), "parms")
```

### computed predicted values based on the model

```r
xs <- seq(-10, 10, length=1000)
sav <- predict(res, newmods=rcspline.eval(xs, knots, inclx=TRUE))
```

### draw scatterplot with regression line based on the model

```r
tmp <- regplot(res, mod=2, pred=sav, xvals=xs, xlab=expression("Within-Study Mean Centered BMI"~(kg/m^2)), ylab="Preeclampsia Prevalence (%)", las=1, bty="l", at=seq(0,18,by=2), olim=c(0,100), psize=2, bg="gray90", label=TRUE, offset=0, labsize=0.6)
abline(v=knots, lty="dotted")
points(tmp)
```

## End(Not run)

---

**dat.pagliaro1992**

*Studies on the Effectiveness of Nonsurgical Treatments in Cirrhosis*

---

**Description**

Results from 26 trials examining the effectiveness of beta-blockers and sclerotherapy for the prevention of first bleeding in patients with cirrhosis
Usage

dat.pagliaro1992

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study id</td>
</tr>
<tr>
<td>trt</td>
<td>character</td>
<td>either beta-blockers, sclerotherapy, or control</td>
</tr>
<tr>
<td>xi</td>
<td>numeric</td>
<td>number of patients with first bleeding</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>number of patients treated</td>
</tr>
</tbody>
</table>

Details

The dataset includes the results from 26 randomized controlled trials examining the effectiveness of nonsurgical treatments for the prevention of first bleeding in patients with cirrhosis. Patients were either treated with beta-blockers, endoscopic sclerotherapy, or with a nonactive treatment (control). Two trials included all three treatment conditions, 7 trials compared beta-blockers against control, and 17 trials compared sclerotherapy against control. The dataset has been used in various papers to illustrate methods for conducting a network meta-analysis / mixed treatment comparison.

Concepts

medicine, odds ratios, Mantel-Haenszel method, network meta-analysis

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.pagliaro1992
dat

## Not run:

### load metafor package
library(metafor)

### restructure dataset to a contrast-based format
dat.c <- to.wide(dat, study="study", grp="trt", grpvars=3:4)
dat.c
```
### Mantel-Haenszel results for beta-blockers and sclerotherapy versus control, respectively
rma.mh(measure="OR", ai=xi.1, n1i=ni.1, ci=xi.2, n2i=ni.2, data=dat.c, subset=(trt.1=="beta-blockers"), digits=2)

rma.mh(measure="OR", ai=xi.1, n1i=ni.1, ci=xi.2, n2i=ni.2, data=dat.c, subset=(trt.1=="sclerotherapy"), digits=2)

### calculate log odds for each study arm
dat <- escalc(measure="PLO", xi=xi, ni=ni, data=dat)
dat

### turn treatment variable into factor and set reference level
dat$trt <- relevel(factor(dat$trt), ref="control")

### add a space before each level (this makes the output a bit more legible)
levels(dat$trt) <- paste0(" ", levels(dat$trt))

### network meta-analysis using an arm-based random-effects model with fixed study effects
### (by setting rho=1/2, tau^2 reflects the amount of heterogeneity for all treatment comparisons)
res <- rma.mv(yi, vi, mods = ~ factor(study) + trt - 1, random = ~ trt | study, rho=1/2, data=dat)
res

### average odds ratio comparing beta-blockers and sclerotherapy versus control, respectively
predict(res, newmods=c(rep(0,26), 1, 0), transf=exp, digits=2)
predict(res, newmods=c(rep(0,26), 0, 1), transf=exp, digits=2)

### average odds ratio comparing beta-blockers versus sclerotherapy
predict(res, newmods=c(rep(0,26), 1, -1), transf=exp, digits=2)

## End(Not run)

---

dat.pignon2000

Studies on the Effectiveness of Locoregional Treatment plus Chemotherapy for Head and Neck Squamous-Cell Carcinoma

---

**Description**

Results from studies examining mortality risk in patients with nonmetastatic head and neck squamous-cell carcinoma receiving either locoregional treatment plus chemotherapy versus locoregional treatment alone.

**Usage**

dat.pignon2000

**Format**

The data frame contains the following columns:
The purpose of this meta-analysis was to examine the mortality risk in patients with nonmetastatic head and neck squamous-cell carcinoma receiving either locoregional treatment plus chemotherapy versus locoregional treatment alone. For 65 trials, the dataset provides the observed minus expected number of deaths and corresponding variances in the locoregional treatment plus chemotherapy group. Based on these values, we can estimate the log hazard ratios with \( \frac{\text{OmE}}{\text{V}} \) and the corresponding sampling variance with \( \frac{1}{\text{V}} \).

The trials were also divided according to the timing of the chemotherapy: (1) adjuvant, after the locoregional treatment, (2) neoadjuvant, before the locoregional treatment, and (3) concomitant, chemotherapy given concomitantly or alternating with radiotherapy.

### Concepts
- medicine
- oncology
- hazard ratios

### Author(s)
Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)

### Source

### Examples
```r
### copy data into 'dat' and examine data
dat <- dat.pignon2000
define data

### load metafor package
library(metafor)

### calculate log hazard ratios and sampling variances
dat$yi <- with(dat, OmE/V)
dat$vi <- with(dat, 1/V)
define data

### meta-analysis based on all 65 trials
res <- rma(yi, vi, data=dat, method="EE", digits=2)
define data
```
res
predict(res, transf=exp)

### only adjuvant trials
res <- rma(yi, vi, data=dat, method="EE", subset=grp==1, digits=2)
res
predict(res, transf=exp)

### only neoadjuvant trials
res <- rma(yi, vi, data=dat, method="EE", subset=grp==2, digits=2)
res
predict(res, transf=exp)

### only concomitant trials
res <- rma(yi, vi, data=dat, method="EE", subset=grp==3, digits=2)
res
predict(res, transf=exp)

## End(Not run)

dat.pritz1997

Studies on the Effectiveness of Hyperdynamic Therapy for Treating Cerebral Vasospasm

Description

Results from 14 studies on the effectiveness of hyperdynamic therapy for treating cerebral vasospasm.

Usage
dat.pritz1997

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>authors</td>
<td>character</td>
<td>study authors</td>
</tr>
<tr>
<td>xi</td>
<td>numeric</td>
<td>number of patients that improved with hyperdynamic therapy</td>
</tr>
<tr>
<td>ni</td>
<td>numeric</td>
<td>total number of patients treated</td>
</tr>
</tbody>
</table>

Details

As described in Zhou et al. (1999), "hyperdynamic therapy refers to induced hypertension and hypervolaemia (volume expansion) to treat ischaemic symptoms due to vasospasm, and the success of this therapy is defined as clinical improvement in terms of neurologic deficits." For each study that was included in the meta-analysis, the dataset includes information on the number of patients
that improved under this form of therapy and the total number of patients that were treated. The goal of the meta-analysis is to estimate the true (average) success rate of hyperdynamic therapy.

Concepts

medicine, single-arm studies, proportions

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.pritz1997
dat

## Not run:
### load metafor package
library(metafor)

### computation of "weighted average" in Zhou et al. (1999), Table IV
dat <- escalc(measure="PR", xi=xi, ni=ni, data=dat, add=0)
theta.hat <- sum(dat$ni * dat$yi) / sum(dat$ni)
se.theta.hat <- sqrt(sum(dat$ni^2 * dat$vi) / sum(dat$ni)^2)
ci.lb <- theta.hat - 1.96 * se.theta.hat
ci.ub <- theta.hat + 1.96 * se.theta.hat
round(c(estimate = theta.hat, se = se.theta.hat, ci.lb = ci.lb, ci.ub = ci.ub), 4)

### this is identical to an equal-effects model with sample size weights
rma(yi, vi, weights=ni, method="EE", data=dat)

### random-effects model with raw proportions
dat <- escalc(measure="PR", xi=xi, ni=ni, data=dat)
res <- rma(yi, vi, data=dat)
predict(res)
```
dat.raudenbush1985

Studies on Assessing the Effects of Teacher Expectations on Pupil IQ

Description

Results from 19 studies examining how teachers’ expectations about their pupils can influence actual IQ levels.

Usage

dat.raudenbush1985

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>numeric</td>
<td>study number</td>
</tr>
<tr>
<td>author</td>
<td>character</td>
<td>study author(s)</td>
</tr>
<tr>
<td>year</td>
<td>numeric</td>
<td>publication year</td>
</tr>
<tr>
<td>weeks</td>
<td>numeric</td>
<td>weeks of contact prior to expectancy induction</td>
</tr>
<tr>
<td>setting</td>
<td>character</td>
<td>whether tests were group or individually administered</td>
</tr>
<tr>
<td>tester</td>
<td>character</td>
<td>whether test administrator was aware or blind</td>
</tr>
<tr>
<td>n1i</td>
<td>numeric</td>
<td>sample size of experimental group</td>
</tr>
<tr>
<td>n2i</td>
<td>numeric</td>
<td>sample size of control group</td>
</tr>
<tr>
<td>yi</td>
<td>numeric</td>
<td>standardized mean difference</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
</tbody>
</table>

Details

In the so-called ‘Pygmalion study’ (Rosenthal & Jacobson, 1968), “all of the predominantly poor children in the so-called Oak elementary school were administered a test pretentiously labeled the ‘Harvard Test of Inflected Acquisition.’ After explaining that this newly designed instrument had identified those children most likely to show dramatic intellectual growth during the coming year, the experimenters gave the names of these ‘bloomers’ to the teachers. In truth, the test was a traditional IQ test and the ‘bloomers’ were a randomly selected 20% of the student population. After retesting the children 8 months later, the experimenters reported that those predicted to bloom
had in fact gained significantly more in total IQ (nearly 4 points) and reasoning IQ (7 points) than the control group children. Further, at the end of the study, the teachers rated the experimental children as intellectually more curious, happier, better adjusted, and less in need of approval than their control group peers” (Raudenbush, 1984).

In the following years, a series of studies were conducted attempting to replicate this rather controversial finding. However, the great majority of those studies were unable to demonstrate a statistically significant difference between the two experimental groups in terms of IQ scores. Raudenbush (1984) conducted a meta-analysis based on 19 such studies to further examine the evidence for the existence of the ‘Pygmalion effect’. The dataset includes the results from these studies.

The outcome measure used for the meta-analysis was the standardized mean difference ($y_i$), with positive values indicating that the supposed ‘bloomers’ had, on average, higher IQ scores than those in the control group. The weeks variable indicates the number of weeks of prior contact between teachers and students before the expectancy induction. Testing was done either in a group setting or individually, which is indicated by the setting variable. Finally, the tester variable indicates whether the test administrators were either aware or blind to the researcher-provided designations of the children’s intellectual potential.

The data in this dataset were obtained from Raudenbush and Bryk (1985) with information on the setting and tester variables extracted from Raudenbush (1984).

Concepts

education, standardized mean differences, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


Examples

```r
# copy data into 'dat' and examine data
dat <- dat.raudenbush1985
dat

# Not run:

# load metafor package
library(metafor)

# random-effects model
res <- rma(yi, vi, data = dat)
res
```
### create weeks variable where values larger than 3 are set to 3
```r
dat$weeks.c <- ifelse(dat$weeks > 3, 3, dat$weeks)
```

### mixed-effects model with weeks.c variable as moderator
```r
res <- rma(yi, vi, mods = ~ weeks.c, data = dat, digits = 3)
res
```

## End(Not run)

---

**dat.riley2003**  
**Studies on MYC-N as a Prognostic Marker for Neuroblastoma**

### Description

Results from 81 studies examining overall and disease-free survival in neuroblastoma patients with amplified versus normal MYC-N protein levels.

### Usage

```r
dat.riley2003
```

### Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>study</th>
<th>numeric</th>
<th>study number</th>
</tr>
</thead>
<tbody>
<tr>
<td>yi</td>
<td>numeric</td>
<td>log hazard ratio of the outcome in those with amplified versus normal MYC-N protein levels</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>sampling variance of the log hazard ratio</td>
</tr>
<tr>
<td>sei</td>
<td>numeric</td>
<td>standard error of the log hazard ratio</td>
</tr>
<tr>
<td>outcome</td>
<td>character</td>
<td>outcome (OS = overall survival; DFS = disease-free survival)</td>
</tr>
</tbody>
</table>

### Details

The meta-analysis by Riley et al. (2003) examined a variety of prognostic markers for overall and disease-free survival in patients with neuroblastoma. One of the markers examined was amplified levels of the MYC-N protein, with is associated with poorer outcomes.

The dataset given here was extracted from Riley (2011) and has been used in several other publications (e.g., Riley et al., 2004, 2007). The dataset provides the (log) hazard ratios (and corresponding standard errors) with respect to these two outcomes in 81 studies, with positive values indicating a greater risk of death (for OS) or disease recurrence/death (for DFS) for patients with high MYC-N levels compared to those with normal/low levels. Note that information on both outcomes could only be extracted from 17 studies (39 studies only provided sufficient information to extract the OS estimate, while 25 studies only allowed for extraction of the DFS estimate).
Concepts

medicine, oncology, hazard ratios

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source


References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.riley2003
dat

### Not run:

### load metafor package
library(metafor)

### random-effects model analysis for outcome DFS
res <- rma(yi, sei=sei, data=dat, subset=(outcome == "DFS"), method="DL")
res
predict(res, transf=exp, digits=2)

### random-effects model analysis for outcome OS
res <- rma(yi, sei=sei, data=dat, subset=(outcome == "OS"), method="DL")
res
predict(res, transf=exp, digits=2)

### End(Not run)
```
Description

Results from 26 trials examining the effectiveness of glucose-lowering agents in patients with type 2 diabetes

Usage
dat.senn2013

Format

The data frame contains the following columns:

- **study**: character (first) author and year of study
- **ni**: numeric sample size of the study arm
- **treatment**: character treatment given
- **comment**: character whether figures given are based on raw values at outcome or on change from baseline
- **mi**: numeric raw mean or mean change
- **sdi**: numeric standard deviation

Details

The dataset includes the results from 26 randomized controlled trials examining the effectiveness of adding various oral glucose-lowering agents to a baseline sulfonylurea therapy in patients with type 2 diabetes. The outcome measured in the studies was either the mean HbA1c level at follow-up or the mean change in HbA1c level from baseline to follow-up. A total of 10 different treatment types were examined in these studies: acarbose, benfluorex, metformin, miglitol, pioglitazone, placebo, rosiglitazone, sitagliptin, sulfonylurea alone, and vildagliptin. One study included three treatment arms (Willms, 1999), while the rest of the studies included two treatment arms (hence, the dataset includes the results from 53 treatment arms).

The data can be used for a network meta-analysis, either using an arm-based or a contrast-based model. See ‘Examples’ below.

Concepts

- medicine
- raw mean differences
- network meta-analysis

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

References


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.senn2013
dat

# Not run:

### load metafor package
library(metafor)

### create network graph ('igraph' package must be installed)
library(igraph, warn.conflicts=FALSE)
pairs <- data.frame(do.call(rbind,
  sapply(split(dat$treatment, dat$study), function(x) t(combn(x,2))), stringsAsFactors=FALSE)
pairs$X1 <- factor(pairs$X1, levels=sort(unique(dat$treatment)))
pairs$X2 <- factor(pairs$X2, levels=sort(unique(dat$treatment)))
tab <- table(pairs[,1], pairs[,2])
tab # adjacency matrix
g <- graph_from_adjacency_matrix(tab, mode = "plus", weighted=TRUE, diag=FALSE)
plot(g, edge.curved=FALSE, edge.width=E(g)$weight, layout=layout_as_star(g, center="placebo"),
  vertex.size=45, vertex.color="lightgray", vertex.label.color="black", vertex.label.font=2)

### table of studies versus treatments examined
print(addmargins(table(dat$study, dat$treatment)), zero.print="")

### table of frequencies with which treatment pairs were studied
print(as.table(crossprod(table(dat$study, dat$treatment))), zero.print="")

### add means and sampling variances of the means to the dataset
dat <- escalc(measure="MN", mi=mi, sdi=sdi, ni=ni, data=dat)

### turn treatment variable into factor and set reference level
dat$treatment <- relevel(factor(dat$treatment), ref="placebo")

### add a space before each level (this makes the output a bit more legible)
levels(dat$treatment) <- paste0(" ", levels(dat$treatment))

### network meta-analysis using an arm-based fixed-effects model with fixed study effects
res.fe <- rma.mv(yi, vi, mods = ~ study + treatment - 1, data=dat, slab=paste0(study, treatment))
res.fe

### test if treatment factor as a whole is significant
```
### forest plot of the contrast estimates (treatments versus placebos)

```r
data <- dat.senn2013[c(1,4:2,5:6)]  # reorder variables first
data <- to.wide(data, study="study", grp="treatment", ref="placebo", grpvars=4:6)
data
```

### calculate mean difference and corresponding sampling variance for each treatment comparison

```r
dat <- escalc(measure="MD", m1i=mi.1, sd1i=sdi.1, n1i=n1i, n2i=n2i, y1i=y1i, y2i=y2i, data=data, slab=paste0(study, treatment), reflevel="placebo")
```
### calculate the variance-covariance matrix of the mean differences for the multitreatment studies

```
calc.v <- function(x) {
  v <- matrix(x$sdi.2[1]^2 / x$ni.2[1], nrow=nrow(x), ncol=nrow(x))
  diag(v) <- x$vi
  v
}
```

```
V <- bldiag(lapply(split(dat, dat$study), calc.v))
```

### add contrast matrix to dataset

```
dat <- contrmat(dat, grp1="treatment.1", grp2="treatment.2")
```

### network meta-analysis using a contrast-based random-effects model

#### by setting $rho=\frac{1}{2}$, $tau^2$ reflects the amount of heterogeneity for all treatment comparisons

#### the treatment left out (placebo) becomes the reference level for the treatment comparisons

```
res <- rma.mv(yi, V, mods = ~ acarbose + benfluorex + metformin + miglitol + pioglitazone +
              rosiglitazone + sitagliptin + sulfonylurea + vildagliptin - 1,
              random = ~ comp | study, rho=1/2, tau2=tau2, data=dat)
```

### forest plot of the contrast estimates (treatments versus placebos)

```
forest(coef(res), diag(vcov(res)), slab=names(coef(res)), order="obs",
       xlim=c(-3.0, 2.5), alim=c(-1.5, 0.5), psize=1, xlab="Estimate", header="Treatment")
```

### estimate all pairwise differences between treatments

```
contr <- data.frame(t(combn(names(coef(res)), 2)))
contr <- contrmat(contr, "X1", "X2", last="vildagliptin")
rownames(contr) <- paste(contr$X1, "-", contr$X2)
contr <- as.matrix(contr[-c(1:2)])
sav <- predict(res, newmods=contr)
sav["slab"] <- rownames(contr)
sav
```

### estimate all pairwise differences between treatments

```
inc <- rma.mv(yi, V, mods = ~ acarbose + benfluorex + metformin + miglitol + pioglitazone +
              rosiglitazone + sitagliptin + sulfonylurea + vildagliptin - 1,
              random = list(~ comp | study, ~ comp | design), rho=1/2, phi=1/2, data=dat)
```

### compute P-scores (see Rücker & Schwarzer, 2015)

```
contr <- data.frame(t(combn(c(names(coef(res)),"placebo"), 2))) # add 'placebo' to contrast matrix
contr <- contrmat(contr, "X1", "X2", last="placebo", append=FALSE)
b <- c(coef(res),0) # add 0 for 'placebo' (the reference treatment)
vb <- bldiag(vcov(res),0) # add 0 row/column for 'placebo' (the reference treatment)
pvals <- apply(contr, 1, function(x) pnorm((x%*%b) / sqrt(t(x)%*%vb%*%x)))
tab <- vec2mat(pvals, corr=FALSE)
tab[upper.tri(tab)] <- t((1 - tab)[upper.tri(tab)])
rownames(tab) <- colnames(tab) <- colnames(contr)
```
round(tab, 2) # like Table 2 in the article
cbind(pscore=round(sort(apply(tab, 1, mean, na.rm=TRUE), decreasing=TRUE), 3))

# note: the values are slightly different from the ones given in Table 3 of Rücker and
# Schwarzer (2015) since model 'res' above is fitted using REML estimation while the
# results shown in the article are based on the 'netmeta' package, which uses a DL-type
# estimator for the amount of heterogeneity by default

############################################################################
## End(Not run)

---

### dat.stowe2010

#### Studies on Adjuvant Treatments to Levodopa Therapy for Parkinson disease

**Description**

Results from 29 trials assessing efficacy of three drug classes as adjuvant treatment to levodopa therapy in patients with Parkinson disease and motor complications.

**Usage**

dat.stowe2010

**Format**

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>character</td>
<td>study label</td>
</tr>
<tr>
<td>id</td>
<td>integer</td>
<td>study id</td>
</tr>
<tr>
<td>t1</td>
<td>character</td>
<td>treatment 1</td>
</tr>
<tr>
<td>y1</td>
<td>numeric</td>
<td>treatment effect arm 1</td>
</tr>
<tr>
<td>sd1</td>
<td>numeric</td>
<td>standard deviation arm 1</td>
</tr>
<tr>
<td>n1</td>
<td>integer</td>
<td>sample size arm 1</td>
</tr>
<tr>
<td>t2</td>
<td>character</td>
<td>treatment 2</td>
</tr>
<tr>
<td>y2</td>
<td>numeric</td>
<td>treatment effect arm 2</td>
</tr>
<tr>
<td>sd2</td>
<td>numeric</td>
<td>standard deviation arm 2</td>
</tr>
<tr>
<td>n2</td>
<td>integer</td>
<td>sample size arm 2</td>
</tr>
<tr>
<td>t3</td>
<td>character</td>
<td>treatment 3</td>
</tr>
<tr>
<td>y3</td>
<td>numeric</td>
<td>treatment effect arm 3</td>
</tr>
<tr>
<td>sd3</td>
<td>numeric</td>
<td>standard deviation arm 3</td>
</tr>
<tr>
<td>n3</td>
<td>integer</td>
<td>sample size arm 3</td>
</tr>
</tbody>
</table>
Details

This data set contains data from a Cochrane review assessing efficacy and safety of three drug classes as adjuvant treatment to levodopa therapy in patients with Parkinson disease and motor complications (Stowe et al., 2010).

The authors conducted three pairwise meta-analyses comparing dopamine agonists, catechol-O-methyl transferase inhibitors (COMTI), and monoamine oxidase type B inhibitors (MAOBI) with placebo. The primary outcome was the mean reduction of the time spent in a relatively immobile ‘off’ phase (mean off-time), calculated in hours per day. Relative treatment effects were expressed as mean difference. Data on this outcome were available for 5,331 patients from 28 studies comparing an active treatment with placebo and one three-arm study comparing two active treatments with placebo.

Concepts

medicine, raw mean differences, network meta-analysis

Author(s)

Guido Schwarzer, <sc@imbi.uni-freiburg.de>, https://github.com/guido-s/

Source


See Also

pairwise, metacont, netmeta, netrank, rankogram, netleague

Examples

```r
### Show results from three studies (including three-arm study LARGO)
dat.stowe2010[18:20, ]

### Not run:

### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print mean differences with two digits and standard errors with 3 digits
settings.meta(digits = 2, digits.se = 3)

### Transform data from wide arm-based format to contrast-based format. Argument 'sm' must not be provided as the mean difference is the default in R function metacont() called internally.
pw <- pairwise(treat = list(t1, t2, t3), n = list(n1, n2, n3),
               mean = list(y1, y2, y3), sd = list(sd1, sd2, sd3),
```
### Show calculated mean differences (TE) for three studies

```r
selstudy <- c("COMTI(E) INT-OZ", "LARGO", "COMTI(E) Nomecomt")
subset(pw, studlab %in% selstudy)[, c(3:7, 10, 1)]
```

### Conduct random effects network meta-analysis (NMA)

```r
net <- netmeta(pw, fixed = FALSE, ref = "plac")
```

### Show network graph

```r
netgraph(net, number = TRUE, multiarm = TRUE,
cex = 1.25, offset = 0.025,
cex.number = 1, pos.number.of.studies = 0.3)
```

### Print NMA results

```r
net
```

### Forest plot with NMA results

```r
forest(net)
```

### Forest plot showing all network estimates of active treatments

```r
forest(net, ref = c("C", "D", "M"), baseline = FALSE, drop = TRUE)
```

### Treatment ranking using P-scores

```r
netrank(net)
```

### Rankogram with all ranking probabilities

```r
set.seed(1909)
ran <- rankogram(net)
ran
plot(ran)
```

### Treatment ranking using SUCRAs

```r
netrank(ran)
```

### League table showing network and direct estimates

```r
netleague(net, seq = netrank(net), ci = FALSE)
```

---

**dat.tannersmith2016**  
*Studies on the Relationship between School Motivation and Criminal Behavior*

---

**Description**

Results from 17 studies on the correlation between school motivation/attitudes and subsequent delinquent/criminal behavior.
Usage

dat.tannersmith2016

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>studyid</th>
<th>numeric</th>
<th>study identifier</th>
</tr>
</thead>
<tbody>
<tr>
<td>yi</td>
<td>numeric</td>
<td>r-to-z transformed correlation coefficient</td>
</tr>
<tr>
<td>vi</td>
<td>numeric</td>
<td>corresponding sampling variance</td>
</tr>
<tr>
<td>sei</td>
<td>numeric</td>
<td>corresponding standard error</td>
</tr>
<tr>
<td>aget1</td>
<td>numeric</td>
<td>age at which the school motivation/attitudes were assessed</td>
</tr>
<tr>
<td>aget2</td>
<td>numeric</td>
<td>age at which the delinquent/criminal behavior was assessed</td>
</tr>
<tr>
<td>propmale</td>
<td>numeric</td>
<td>proportion of male participants in the sample</td>
</tr>
<tr>
<td>sexmix</td>
<td>character</td>
<td>whether the sample consisted only of males, only of females, or a mix</td>
</tr>
</tbody>
</table>

Details

The dataset includes 113 r-to-z transformed correlation coefficients from 17 prospective longitudinal studies that examined the relationship between school motivation/attitudes and subsequent delinquent/criminal behavior.

Multiple coefficients could be extracted from the studies “given the numerous ways in which school motivation/attitudes variables could be operationalized (e.g., academic aspirations, academic self-efficacy) as well as the numerous ways in which crime/delinquency could be operationalized (e.g., property crime, violent crime)” (Tanner-Smith et al., 2016).

Since information to compute the covariance between multiple coefficients within studies is not available, Tanner-Smith et al. (2016) illustrate the use of cluster-robust inference methods for the analysis of this dataset.

Note that this dataset is only meant to be used for pedagogical and demonstration purposes and does not constitute a proper review or synthesis of the complete and current research evidence on the given topic.

Concepts

psychology, criminology, correlation coefficients, multilevel models, cluster-robust inference, meta-regression

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

### Examples

```r
### copy data into 'dat' and examine data
dat <- dat.tannersmith2016
head(dat)

### Not run:

### load metafor package
library(metafor)

### compute mean age variables within studies
dat$aget1 <- ave(dat$aget1, dat$studyid)
dat$aget2 <- ave(dat$aget2, dat$studyid)

### construct an effect size identifier variable
dat$esid <- 1:nrow(dat)

### construct an approximate var-cov matrix assuming a correlation of 0.8
### for multiple coefficients arising from the same study
V <- vcalc(vi, cluster=studyid, obs=esid, rho=0.8, data=dat)

### fit a multivariate random-effects model using the approximate var-cov matrix V
res <- rma.mv(yi, V, random = ~ esid | studyid, data=dat)
res

### use cluster-robust inference methods
robust(res, cluster=studyid, clubSandwich=TRUE)

### note: the results obtained above and below are slightly different compared
### to those given by Tanner-Smith et al. (2016) since the approach illustrated
### here makes use a multivariate random-effects model for the 'working model'
### before applying the cluster-robust inference methods, while the results given
### in the paper are based on a somewhat simpler working model

### examine the main effects of the age variables
res <- rma.mv(yi, V, mods = ~ aget1 + aget2,
              random = ~ 1 | studyid/esid, data=dat)
robust(res, cluster=studyid, clubSandwich=TRUE)

### also examine their interaction
res <- rma.mv(yi, V, mods = ~ aget1 * aget2,
              random = ~ 1 | studyid/esid, data=dat)
robust(res, cluster=studyid, clubSandwich=TRUE)

### add the sexmix factor to the model
res <- rma.mv(yi, V, mods = ~ aget1 * aget2 + sexmix,
              random = ~ 1 | studyid/esid, data=dat)
robust(res, cluster=studyid, clubSandwich=TRUE)

### End(Not run)
```
Description

Results from 33 studies examining the association between male circumcision and HIV infection.

Usage
dat.vanhowe1999

Format

The data frame contains the following columns:

<table>
<thead>
<tr>
<th>Study</th>
<th>Character</th>
<th>Study Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>Category</td>
<td>Character</td>
<td>Study Type (high-risk group, partner study, or population survey)</td>
</tr>
<tr>
<td>Non.pos</td>
<td>Numeric</td>
<td>Number of non-circumcised HIV positive cases</td>
</tr>
<tr>
<td>Non.neg</td>
<td>Numeric</td>
<td>Number of non-circumcised HIV negative cases</td>
</tr>
<tr>
<td>Cir.pos</td>
<td>Numeric</td>
<td>Number of circumcised HIV positive cases</td>
</tr>
<tr>
<td>Cir.neg</td>
<td>Numeric</td>
<td>Number of circumcised HIV negative cases</td>
</tr>
</tbody>
</table>

Details

The 33 studies provide data in terms of $2 \times 2$ tables in the form:

\[
\begin{array}{ccc}
\text{HIV positive} & \text{HIV negative} \\
\text{non-circumcised} & \text{non.pos} & \text{non.neg} \\
\text{circumcised} & \text{cir.pos} & \text{cir.neg}
\end{array}
\]

The goal of the meta-analysis was to examine if the risk of an HIV infection differs between non-circumcised versus circumcised men.

The dataset is interesting because it can be used to illustrate the difference between naively pooling results by summing up the counts across studies and then computing the odds ratio based on the aggregated table (as was done by Van Howe, 1999) and conducting a proper meta-analysis (as illustrated by O’Farrell & Egger, 2000). In fact, a proper meta-analysis shows that the HIV infection risk is on average higher in non-circumcised men, which is the opposite of what the naive pooling approach yields (which makes this an illustration of Simpson’s paradox).

Concepts

medicine, epidemiology, odds ratios

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org
Source

References

Examples
```r
### copy data into 'dat' and examine data
dat <- dat.vanhowe1999
dat

## Not run:
### load metafor package
library(metafor)

### naive pooling by summing up the counts within categories and then
### computing the odds ratios and corresponding confidence intervals
cat1 <- with(dat[dat$category=='high-risk group',],
  escalc(measure="OR", ai=sum(non.pos), bi=sum(non.neg), ci=sum(cir.pos), di=sum(cir.neg)))
cat2 <- with(dat[dat$category=='partner study',],
  escalc(measure="OR", ai=sum(non.pos), bi=sum(non.neg), ci=sum(cir.pos), di=sum(cir.neg)))
cat3 <- with(dat[dat$category=='population survey',],
  escalc(measure="OR", ai=sum(non.pos), bi=sum(non.neg), ci=sum(cir.pos), di=sum(cir.neg)))
summary(cat1, transf=exp, digits=2)
summary(cat2, transf=exp, digits=2)
summary(cat3, transf=exp, digits=2)

### naive pooling across all studies
all <- escalc(measure="OR", ai=sum(dat$non.pos), bi=sum(dat$non.neg),
  ci=sum(dat$cir.pos), di=sum(dat$cir.neg))
summary(all, transf=exp, digits=2)

### calculate log odds ratios and corresponding sampling variances
dat <- escalc(measure="OR", ai=non.pos, bi=non.neg, ci=cir.pos, di=cir.neg, data=dat)
dat

### random-effects model
res <- rma(yi, vi, data=dat, method="DL")
res
predict(res, transf=exp, digits=2)

### random-effects model within subgroups
res <- rma(yi, vi, data=dat, method="DL", subset=category=="high-risk group")
predict(res, transf=exp, digits=2)
res <- rma(yi, vi, data=dat, method="DL", subset=category=="partner study")
predict(res, transf=exp, digits=2)
res <- rma(yi, vi, data=dat, method="DL", subset=category=="population survey")
```
predict(res, transf=exp, digits=2)

## End(Not run)

dat.viechtbauer2021  

### Description

Results from 20 hypothetical randomized clinical trials examining the effectiveness of a medication for treating some disease.

### Usage

dat.viechtbauer2021

### Format

The data frame contains the following columns:

- **trial**: numeric  
  trial number
- **nTi**: numeric  
  number of patients in the treatment group
- **nCi**: numeric  
  number of patients in the control group
- **xTi**: numeric  
  number of patients in the treatment group with remission
- **xCi**: numeric  
  number of patients in the control group with remission
- **dose**: numeric  
  dosage of the medication provided to patients in the treatment group (in milligrams per day)

### Details

The dataset was constructed for the purposes of illustrating the model checking and diagnostic methods described in Viechtbauer (2021). The code below provides the results for many of the analyses and plots discussed in the book chapter.

### Concepts

- medicine, odds ratios, outliers, model checks

### Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, [https://www.metafor-project.org](https://www.metafor-project.org)

### Source

Examples

### copy data into 'dat' and examine data
dat <- dat.viechtbauer2021
dat

## Not run:
### load metafor package
library(metafor)
### calculate log odds ratios and corresponding sampling variances
dat <- escalc(measure="OR", ai=xTi, n1i=nTi, ci=xCi, n2i=nCi, add=1/2, to="all", data=dat)
dat
### number of studies
k <- nrow(dat)
### fit models
res.CE <- rma(yi, vi, data=dat, method="CE") # same as method="EE"
res.CE
res.RE <- rma(yi, vi, data=dat, method="DL")
res.RE
res.MR <- rma(yi, vi, mods = dose, data=dat, method="FE")
res.MR
res.ME <- rma(yi, vi, mods = dose, data=dat, method="DL")
res.ME
### forest and bubble plot
par(mar=c(5,4,1,2))
forest(dat$yi, dat$vi, psize=0.8, efac=0, xlim=c(-4,6), ylim=c(-3,23),
   cex=1, width=c(5,5,5), xlab="Log Odds Ratio (LnOR)"
addpoly(res.CE, row=-1.5, mlab="CE Model")
addpoly(res.RE, row=-2.5, mlab="RE Model")
text(-4, 22, "Trial", pos=4, font=2)
text( 6, 22, "LnOR [95% CI]", pos=2, font=2)
abline(h=0)
tmp <- regplot(res.ME, xlim=c(0,250), ylim=c(-1,1.5), predlim=c(0,250), shade=FALSE, digits=1,
   xlab="Dosage (mg per day)" , psize="seinv", plim=NA,5, bty="l", las=1,
   lty=c("solid", "dashed"), label=TRUE, labsize=0.8, offset=c(1,0.7))
res.sub <- rma(yi, vi, mods = dose, data=dat, method="DL", subset=-6)
abline(res.sub, lty="dotted")
points(tmp$xi, tmp$yi, pch=21, cex=tmp$psize, col="black", bg="darkgray")
par(mar=c(5,4,4,2))

### number of standardized deleted residuals larger than ±1.96 in each model

sum(abs(rstudent(res.CE)$z) >= qnorm(.975))
sum(abs(rstudent(res.MR)$z) >= qnorm(.975))
sum(abs(rstudent(res.RE)$z) >= qnorm(.975))
sum(abs(rstudent(res.ME)$z) >= qnorm(.975))

### plot of the standardized deleted residuals for the RE and ME models

plot(NA, NA, xlim=c(1,20), ylim=c(-4,4), xlab="Study", ylab="Standardized (Deleted) Residual", xaxt="n", main="Random-Effects Model", las=1)
axis(side=1, at=1:20)
abline(h=c(-1.96,1.96), lty="dotted")
abline(h=0)
points(1:20, rstandard(res.RE)$z, type="o", pch=19, col="gray70")
points(1:20, rstudent(res.RE)$z, type="o", pch=19)
legend("top", pch=19, col=c("gray70","black"), lty="solid",
       legend=c("Standardized Residuals","Standardized Deleted Residuals"), bty="n")

plot(NA, NA, xlim=c(1,20), ylim=c(-4,4), xlab="Study", ylab="Standardized (Deleted) Residual", xaxt="n", main="Mixed-Effects Model", las=1)
axis(side=1, at=1:20)
abline(h=c(-1.96,1.96), lty="dotted")
abline(h=0)
points(1:20, rstandard(res.ME)$z, type="o", pch=19, col="gray70")
points(1:20, rstudent(res.ME)$z, type="o", pch=19)
legend("top", pch=19, col=c("gray70","black"), lty="solid",
       legend=c("Standardized Residuals","Standardized Deleted Residuals"), bty="n")

### Baujat plots

baujat(res.CE, main="Common-Effects Model", xlab="Squared Pearson Residual", ylim=c(0,5), las=1)
baujat(res.ME, main="Mixed-Effects Model", ylim=c(0,2), las=1)

### GOSH plots (skipped because this takes quite some time to run)

if (FALSE) {
  res.GOSH.CE <- gosh(res.CE, subsets=10^7)
  plot(res.GOSH.CE, cex=0.2, out=6, xlim=c(-0.25,1.25), breaks=c(200,100))

  res.GOSH.ME <- gosh(res.ME, subsets=10^7)
  plot(res.GOSH.ME, het="tau2", out=6, breaks=50, adjust=0.6, las=1)
}

### plot of treatment dosage against the standardized residuals

plot(dat$dose, rstandard(res.ME)$z, pch=19, xlab="Dosage (mg per day)", ylab="Standardized Residual", xlim=c(0,250), ylim=c(-2.5,2.5), las=1)
abline(h=c(-1.96,1.96), lty="dotted", lwd=2)
### quadratic polynomial model

```r
rma(yi, vi, mods = ~ dose + I(dose^2), data=dat, method="DL")
```

### lack-of-fit model

```r
resLOF <- rma(yi, vi, mods = ~ dose + factor(dose), data=dat, method="DL", btt=3:9)
resLOF
```

### scatter plot to illustrate the lack-of-fit model

```r
regplot(res.ME, xlim=c(0,250), ylim=c(-1.0,1.5), xlab="Dosage (mg per day)", ci=FALSE, predlim=c(0,250), psize=1, pch=19, col="gray60", digits=1, lwd=1, bty="l", las=1)
dosages <- sort(unique(dat$dose))
lines(dosages, fitted(resLOF)[match(dosages, dat$dose)], type="o", pch=19, cex=2, lwd=2)
points(dat$dose, dat$yi, pch=19, col="gray60")
legend("bottomright", legend=c("Linear Model", "Lack-of-Fit Model"), pch=c(NA,19), col=c("black", lty="solid", lwd=c(1,2), pt.cex=c(1,2), seg.len=4, bty="n")
```

### checking normality of the standardized deleted residuals

```r
qqnorm(res.ME, type="rstudent", main="Standardized Deleted Residuals", pch=19, label="out", lwd=2, pos=24, ylim=c(-4.3), lty=c("solid", "dotted"), las=1)
```

### checking normality of the random effects

```r
sav <- qqnorm(ranef(res.ME)$pred, main="BLUPs of the Random Effects", cex=1, pch=19, xlab=c(-2.2,2.2), ylim=c(-0.6,0.6), las=1)
abline(a=0, b=sd(ranef(res.ME)$pred), lwd=2)
text(sav$x[6], sav$y[6], "6", pos=4, offset=0.4)
```

### hat values for the CE and RE models

```r
plot(NA, NA, xlim=c(1,20), ylim=c(0,0.21), xaxt="n", las=1, xlab="Study", ylab="Hat Value")
axis(1, 1:20, cex.axis=1)
points(hatvalues(res.CE), type="o", cex=1)
points(hatvalues(res.RE), type="o")
abline(h=1/20, lty="dotted", lwd=2)
title("Hat Values for the CE/RE Models")
legend("topright",pch=19, col=c("gray70","black"), lty="solid",
       legend=c("Common-Effects Model", "Random-Effects Model"), bty="n")
```

### heatmap of the hat matrix for the ME model

```r
cols <- colorRampPalette(c("blue", "white", "red"))(101)
h <- hatvalues(res.ME, type="matrix")
image(1:nrow(h), 1:ncol(h), t(h[nrow(h):1,]), axes=FALSE, xlab="Influence of the Observed Effect of Study ...", ylab="On the Fitted Value of Study ...", col=cols, ylim=c(-max(abs(h)),max(abs(h)))
```
axis(1, 1:20, tick=FALSE)
axis(2, 1:20, labels=20:1, las=1, tick=FALSE)
abline(h=seq(0.5,20.5,by=1), col="white")
abline(v=seq(0.5,20.5,by=1), col="white")
points(1:20, 20:1, pch=19, cex=0.4)
title("Heatmap for the Mixed-Effects Model")

### plot of leverages versus standardized residuals for the ME model
plot(hatvalues(res.ME), rstudent(res.ME)$z, pch=19, cex=0.2+3*sqrt(cooks.distance(res.ME)),
  las=1, xlab="Leverage (Hat Value)", ylab="Standardized Deleted Residual",
  xlim=c(0,0.35), ylim=c(-3.5,2.5))
abline(h=c(-1.96,1.96), lty="dotted", lwd=2)
abline(h=0, lwd=2)
ids <- c(3,6,9)
text(hatvalues(res.ME)[ids] + c(0,0.013,0.010), rstudent(res.ME)$z[ids] - c(0.18,0,0), ids)
title("Leverage vs. Standardized Deleted Residuals")

### plot of the Cook's distances for the ME model
plot(1:20, cooks.distance(res.ME), ylim=c(0,1.6), type="o", pch=19, las=1, xaxt="n", yaxt="n",
  xlab="Study", ylab="Cook's Distance")
axis(1, 1:20, cex.axis=1)
axis(2, seq(0,1.6,by=0.4), las=1)
title("Cook's Distances")

### plot of the leave-one-out estimates of tau^2 for the ME model
x <- influence(res.ME)
plot(1:20, x$inf$tau2.del, ylim=c(0,0.15), type="o", pch=19, las=1, xaxt="n", yaxt="n",
  xlab="Study", ylab=expression(paste("Estimate of \( \tau^2 \) without the \( i \)th study")))
abline(h=res.ME$tau2, lty="dashed")
axis(1, 1:20)
title("Residual Heterogeneity Estimates")

### plot of the covariance ratios for the ME model
plot(1:20, x$inf$cov.r, ylim=c(0,2.0), type="o", pch=19, las=1, xaxt="n", yaxt="n",
  xlab="Study", ylab="Covariance Ratio")
abline(h=1, lty="dashed")
axis(1, 1:20)
title("Covariance Ratios")

### fit mixed-effects model without studies 3 and/or 6
rma(yi, vi, mods=~dose, data=dat, method="DL", subset=-3)
rma(yi, vi, mods=~dose, data=dat, method="DL", subset=-6)
rma(yi, vi, mods=~dose, data=dat, method="DL", subset=-c(3,6))

## End(Not run)
Description

Results from 41 studies examining the relationship between measures of individual quality and the expression of structurally coloured sexual signals.

Usage

dat.white2020

Format

The object is a data frame which contains the following columns:

- **study_id**: character, study-level ID
- **obs**: character, observation-level ID
- **exp_obs**: character, whether the study is observational or experimental
- **control**: numeric, whether the study did (1) or did not (0) include a non-sexual control trait
- **class**: character, class of the study organisms
- **genus**: character, class of the study organisms
- **species**: character, species of the study organisms
- **sex**: character, sex of the study organisms
- **iridescent**: numeric, whether the colour signals were iridescent (1) or not (0)
- **col_var**: character, the colour variable quantified
- **col_component**: character, whether the colour variable is chromatic or achromatic
- **quality_measure**: character, the measure of individual quality used
- **region**: character, the body region from which colour was sampled
- **n**: numeric, study sample size
- **r**: numeric, Pearson’s correlation coefficient

Details

The 186 rows in this dataset come from 41 experimental and observational studies reporting on the correlation between measures of individual quality (age, body condition, immune function, parasite resistance) and the expression of structurally coloured sexual signals across 28 species. The purpose of this meta-analysis was to test whether structural colour signals show heightened condition-dependent expression, as predicted by evolutionary models of 'honest' signalling.

Concepts

ecology, evolution, correlation coefficients
Author(s)

Thomas E. White, <thomas.white@sydney.edu.au>

Source


Examples

```r
### copy data into 'dat' and examine data
dat <- dat.white2020
head(dat, 10)

## Not run:
### load metafor package
library(metafor)

### calculate r-to-z transformed correlations and corresponding sampling variances
dat <- escalc(measure="ZCOR", ri=r, ni=n, data=dat)

### fit multilevel meta-analytic model
res <- rma.mv(yi, vi, random = list(~ 1 | study_id, ~ 1 | obs), data=dat)
res

## End(Not run)
```

---

**dat.woods2010**

*Studies on Treatments for Chronic Obstructive Pulmonary Disease*

**Description**

Results from 3 trials examining the mortality risk of three treatments and placebo in patients with chronic obstructive pulmonary disease.

**Usage**

dat.woods2010

**Format**

The data frame contains the following columns:

- **author**: character - first author / study name
- **treatment**: character - treatment
- **r**: integer - number of deaths
- **N**: integer - number of patients
Details
Count mortality statistics in randomised controlled trials of treatments for chronic obstructive pulmonary disease (Woods et al., 2010, Table 1).

Concepts
medicine, odds ratios, network meta-analysis

Author(s)
Guido Schwarzer, <sc@imbi.uni-freiburg.de>, https://github.com/guido-s/

Source

Examples
```r
### Show full data set
dat.woods2010

### Not run:

### Load netmeta package
suppressPackageStartupMessages(library(netmeta))

### Print odds ratios and confidence limits with two digits
settings.meta(digits = 2)

### Change appearance of confidence intervals
cilayout("(", ")")

### Transform data from long arm-based format to contrast-based
### format. Argument 'sm' has to be used for odds ratio as summary
### measure; by default the risk ratio is used in the metabin function
### called internally.
pw <- pairwise(treatment, event = r, n = N,
   studlab = author, data = dat.woods2010, sm = "OR")
pw

### Conduct network meta-analysis
net <- netmeta(pw)
net

### Show forest plot
forest(net, ref = "Placebo", drop = TRUE,
   leftlabs = "Contrast to Placebo")
```

## End(Not run)
Description

Results from studies examining the effectiveness of beta blockers for reducing mortality and reinfarction.

Usage

dat.yusuf1985

Format

The data frame contains the following columns:

- **table**: character (table number)
- **id**: character (trial id number)
- **trial**: character (trial name or first author)
- **ai**: numeric (number of deaths/reinfarctions in treatment group)
- **n1i**: numeric (number of patients in treatment group)
- **ci**: numeric (number of deaths/reinfarctions in control group)
- **n2i**: numeric (number of patients in control group)

Details

The dataset contains table 6 (total mortality from short-term trials of oral beta blockers), 9 (total mortality at one week from trials with an initial IV dose of a beta blocker), 10 (total mortality from long-term trials with treatment starting late and mortality from day 8 onwards in long-term trials that began early and continued after discharge), 11 (nonfatal reinfarction from long-term trials of beta blockers), 12a (sudden death in long-term beta blocker trials), and 12b (nonsudden death in long-term beta blocker trials) from the meta-analysis by Yusuf et al. (1985) on the effectiveness of beta blockers for reducing mortality and reinfarction.

The article also describes what is sometimes called Peto’s one-step method for meta-analyzing $2 \times 2$ table data. This method is implemented in the `rma.peto` function.

Concepts

medicine, cardiology, odds ratios, Peto’s method

Author(s)

Wolfgang Viechtbauer, <wvb@metafor-project.org>, https://www.metafor-project.org

Source

Examples

```r
### copy data into 'dat'
dat <- dat.yusuf1985
dat[dat$table == 6,]

### Not run:

### load metafor package
library(metafor)

### to select a table for the analysis
tab <- "6" # either: 6, 9, 10, 11, 12a, 12b

### to double-check total counts as reported in article
apply(dat[dat$table==tab,4:7], 2, sum, na.rm=TRUE)

### meta-analysis using Peto's one-step method
res <- rma.peto(ai=ai, n1i=n1i, ci=ci, n2i=n2i, data=dat, subset=(table==tab))
res
predict(res, transf=exp, digits=2)

### End(Not run)
```

---

**datsearch**

*Search Function for the Datasets*

**Description**

Function to search among the existing datasets.

**Usage**

```r
datsearch(pattern, concept=TRUE, matchall=TRUE, fixed=TRUE, pkgdown=FALSE)
```

**Arguments**

- **pattern**: character string or vector of strings specifying the terms to search for within the datasets. Can also be left unspecified to start the function in an interactive mode.
- **concept**: logical indicating whether the search should be confined to the concept terms (TRUE by default) or whether a full-text search should be conducted.
- **matchall**: logical indicating whether only the datasets matching all terms (if multiple are specified) are returned (TRUE by default) or whether datasets matching any one of the terms are returned.
**datsearch**

`datsearch()` logical indicating whether a term is a string to be matched as is (TRUE by default). If FALSE, a search term is a regular expression that `grep` will search for. Only relevant when concept=FALSE (i.e., when doing a full-text search).

`pkgdown` logical indicating whether the standard help file or the pkgdown docs (at [https://wviechtb.github.io/metadat/](https://wviechtb.github.io/metadat/)) should be shown for a chosen dataset (FALSE by default).

**Details**

The function can be used to search all existing datasets in the `metadat` package based on their concept terms (see below) or based on a full-text search of their corresponding help files.

When running `datsearch()` without the pattern argument specified, the function starts in an interactive mode and prompts for one or multiple search terms.

Alternatively, one can specify a single search term via the pattern argument or multiple search terms by using a string vector as the pattern or by separating multiple search terms in a single string with ‘;’, ‘:’, or ‘and’.

If matchall=TRUE (the default), only datasets matching all search terms (if multiple are specified) are returned. If matchall=FALSE, datasets matching any one of the search terms are returned.

If a single match is found, the corresponding help file is directly shown. If multiple matches are found, the user is prompted to choose one of the matching datasets of interest.

**Concept Terms**

Each dataset is tagged with one or multiple concept terms that refer to various aspects of a dataset, such as the field/topic of research, the outcome measure used for the analysis, the model(s) used for analyzing the data, and the methods/concepts that can be illustrated with the dataset.

- In terms of ‘fields/topics’, the following terms have been used at least once: alternative medicine, attraction, cardiology, climate change, covid-19, criminology, dentistry, ecology, education, engineering, epidemiology, evolution, genetics, human factors, medicine, memory, obstetrics, oncology, persuasion, primary care, psychiatry, psychology, smoking, social work, sociology.
- In terms of ‘outcome measures’, the following terms have been used at least once: correlation coefficients, Cronbach’s alpha, hazard ratios, incidence rates, raw mean differences, odds ratios, proportions, ratios of means, raw means, risk differences, risk ratios, (semi-)partial correlations, standardized mean changes, standardized mean differences.
- In terms of ‘models/methods/concepts’, the following terms have been used at least once: cluster-robust inference, component network meta-analysis, cumulative meta-analysis, diagnostic accuracy studies, dose response models, generalized linear models, longitudinal models, Mantel-Haenszel method, meta-regression, model checks, multilevel models, multivariate models, network meta-analysis, outliers, Peto’s method, phylogeny, publication bias, reliability generalization, single-arm studies, spatial correlation.

**Author(s)**

Daniel Noble, <daniel.noble@anu.edu.au>
Wolfgang Viechtbauer, <wvb@metafor-project.org>
# Examples

# note: the examples below are not run since they require interactivity

if (FALSE) {

# start the function in the interactive mode
datsearch()

# find all datasets tagged with the concept term 'standardized mean differences'
datsearch("standardized mean differences")

# find all datasets tagged with the concept terms 'odds ratio' and 'multilevel'
datsearch("odds ratio, multilevel")

# do a full-text search for the term 'infarct'
datsearch("infarct", concept=FALSE)

# do a full-text search for 'rma.mv(' (essentially finds all datasets where
# the rma.mv() function was used in the examples section of a help file)
datsearch("rma.mv(" , concept=FALSE)
}
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