Package ‘ConfoundedMeta’
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Title Sensitivity Analyses for Unmeasured Confounding in Meta-Analyses
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Description Conducts sensitivity analyses for unmeasured confounding in random-effects meta-analysis per Mathur & VanderWeele (in preparation). Given output from a random-effects meta-analysis with a relative risk outcome, computes point estimates and inference for: (1) the proportion of studies with true causal effect sizes more extreme than a specified threshold of scientific significance; and (2) the minimum bias factor and confounding strength required to reduce to less than a specified threshold the proportion of studies with true effect sizes of scientifically significant size. Creates plots and tables for visualizing these metrics across a range of bias values. Provides tools to easily scrape study-level data from a published forest plot or summary table to obtain the needed estimates when these are not reported.
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Description

Confounded meta estimates and inference for sensitivity analyses.

Confounded meta estimates the proportion of studies with true effect sizes above \( .q \) (or below \( .q \) for an apparently preventive \( .yr \)) as a function of the bias parameters; (2) the minimum bias factor on the relative risk scale (\( t_{\text{min}} \)) required to reduce to less than \( .r \) the proportion of studies with true effect sizes more extreme than \( .q \); and (3) the counterpart to (2) in which bias is parameterized as the minimum relative risk for both confounding associations (\( g_{\text{min}} \)).

Usage

```
confounded_meta(.q, .r = NULL, .muB = NULL, .sigB = 0, .yr, .vyr = NULL, .t2, .vt2 = NULL, CI.level = 0.95, .tail = NULL)
```

Arguments

- **.q**: True effect size that is the threshold for "scientific significance"
- **.r**: For \( t_{\text{min}} \) and \( g_{\text{min}} \), value to which the proportion of large effect sizes is to be reduced
- **.muB**: Mean bias factor on the log scale across studies
- **.sigB**: Standard deviation of log bias factor across studies
- **.yr**: Pooled point estimate (on log scale) from confounded meta-analysis
- **.vyr**: Estimated variance of pooled point estimate from confounded meta-analysis
- **.t2**: Estimated heterogeneity (\( \tau^2 \)) from confounded meta-analysis
- **.vt2**: Estimated variance of \( \tau^2 \) from confounded meta-analysis
- **CI.level**: Confidence level as a proportion
- **.tail**: above for the proportion of effects above \( .q \); below for the proportion of effects below \( .q \). By default, is set to above for relative risks above 1 and to below for relative risks below 1.

Details

To compute all three point estimates (\( \text{prop} \), \( t_{\text{min}} \), and \( g_{\text{min}} \)) and inference, all arguments must be non-NULL. To compute only a point estimate for \( \text{prop} \), arguments \( .r \), \( .vyr \), and \( .vt2 \) can be left NULL. To compute only point estimates for \( t_{\text{min}} \) and \( g_{\text{min}} \), arguments \( .muB \), \( .vyr \), and \( .vt2 \) can be left NULL. To compute inference for all point estimates, \( .vyr \) and \( .vt2 \) must be supplied.
Examples

d = metafor::escalc(measure="RR", ai=tpos, bi=tneg, 
    ci=cpos, di=cneg, data=metafor::dat.bcg)

m = metafor::rma.uni(yi=d$yi, vi=d$vi, knha=FALSE, 
    measure="RR", method="DL")

yr = as.numeric(m$b)  # metafor returns on log scale
vyr = as.numeric(m$vb)
t2 = m$tau2
vt2 = m$se.tau2^2

# obtaining all three estimators and inference
confounded_meta(.q=log(0.90), .r=0.20, .muB=log(1.5), .sigB=0.1, 
    .yr=yr, .vyr=vyr, .t2=t2, .vt2=vt2, 
    CI.level=0.95 )

# passing only arguments needed for prop point estimate
confounded_meta(.q=log(0.90), .muB=log(1.5),
    .yr=yr, .t2=t2, CI.level=0.95 )

# passing only arguments needed for Tmin, Gmin point estimates
confounded_meta(.q=log(0.90), .r=0.20, 
    .yr=yr, .t2=t2, CI.level=0.95 )

---

scrape_meta  
Convert forest plot or summary table to meta-analytic dataset

Description

Given relative risks (RR) and upper bounds of 95% confidence intervals (CI) from a forest plot or 
summary table, returns a dataframe ready for meta-analysis (e.g., via the metafor package) with the 
log-RRs and their variances. Optionally, the user may indicate studies for which the point estimate 
is to be interpreted as an odds ratios of a common outcome rather than a relative risk; for such 
studies, the function applies VanderWeele (2017)'s square-root transformation to convert the odds 
ratio to an approximate risk ratio.

Usage

scrape_meta(.type = "RR", .est, .hi, .sqrt = FALSE)

Arguments

.type  
RR if point estimates are RRs or ORs (to be handled on log scale); raw if point 
estimates are raw differences, standardized mean differences, etc. (such that 
they can be handled with no transformations)

.est  
Vector of study point estimates on RR or OR scale

.hi  
Vector of upper bounds of 95% CIs on RRs
Vector of booleans (TRUE/FALSE) for whether each study measured an odds ratio of a common outcome that should be approximated as a risk ratio via the square-root transformation

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**sens_plot**

*Plots for sensitivity analyses*

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**Description**

Produces line plots (.type="line") showing the bias factor on the relative risk (RR) scale vs. the proportion of studies with true RRs above .q (or below it for an apparently preventive relative risk). The plot secondarily includes a X-axis scaled based on the minimum strength of confounding to produce the given bias factor. The shaded region represents a 95% pointwise confidence band. Alternatively, produces distribution plots (.type="dist") for a specific bias factor showing the observed and true distributions of RRs with a red line marking exp(.q).

**Usage**

```r
sens_plot(.type, .q, .muB = NULL, .Bmin = log(1), .Bmax = log(5),
          .sigB = 0, .yr, .vyr = NULL, .t2, .vt2 = NULL, breaks.x1 = NULL,
          breaks.x2 = NULL, CI.level = 0.95)
```

**Arguments**

- **.type**: dist for distribution plot; line for line plot (see Details)
- **.q**: True effect size that is the threshold for "scientific significance"
- **.muB**: Single mean bias factor on log scale (only needed for distribution plot)
- **.Bmin**: Lower limit of lower X-axis on the log scale (only needed for line plot)
- **.Bmax**: Upper limit of lower X-axis on the log scale (only needed for line plot)
- **.sigB**: Standard deviation of log bias factor across studies (length 1)
- **.yr**: Pooled point estimate (on log scale) from confounded meta-analysis
- **.vyr**: Estimated variance of pooled point estimate from confounded meta-analysis
- **.t2**: Estimated heterogeneity (tau^2) from confounded meta-analysis
- **.vt2**: Estimated variance of tau^2 from confounded meta-analysis
- **breaks.x1**: Breaks for lower X-axis (bias factor) on RR scale
- **breaks.x2**: Breaks for upper X-axis (confounding strength) on RR scale
- **CI.level**: Pointwise confidence level as a proportion

**Details**

Arguments .vyr and .vt2 can be left NULL, in which case no confidence band will appear on the line plot.
Examples

# with variable bias and with confidence band
sens_plot(.type="line", .q=log(1.1), .Bmin=log(1), .Bmax=log(4), .sigB=0.1,
           .yr=log(1.3), .vyr=0.005, .t2=0.4, .vt2=0.03 )

# with fixed bias and without confidence band
sens_plot(.type="line", .q=log(1.1), .Bmin=log(1), .Bmax=log(4),
           .yr=log(1.3), .t2=0.4 )

# apparently preventive
sens_plot(.type="line", .q=log(0.90), .Bmin=log(1), .Bmax=log(4),
           .yr=log(0.6), .vyr=0.005, .t2=0.4, .vt2=0.04 )

# distribution plot: apparently causative
# commented out because takes 5-10 seconds to run
# sens_plot(.type="dist", .q=log(1.1), .muB=log(2),
#            .yr=log(1.3), .t2=0.4 )

# distribution plot: apparently preventive
# commented out because takes 5-10 seconds to run
# sens_plot(.type="dist", .q=log(0.90), .muB=log(1.5),
#            .yr=log(0.7), .t2=0.2 )

---

sens_table  
Tables for sensitivity analyses

Description

Produces table showing the proportion of true effect sizes more extreme than \( .q \) across a grid of bias parameters \( .\muB \) and \( .\sigmaB \) (for \( .\text{meas} == \text{"prop"} \)). Alternatively, produces a table showing the minimum bias factor (for \( .\text{meas} == \text{"Tmin"} \)) or confounding strength (for \( .\text{meas} == \text{"Gmin"} \)) required to reduce to less than \( .r \) the proportion of true effects more extreme than \( .q \).

Usage

sens_table(.meas, .q, .r = seq(0.1, 0.9, 0.1), .muB = NULL, .sigB = NULL,
           .yr, .t2)

Arguments

- \( .\text{meas} \)  prop, Tmin, or Gmin
- \( .q \)  True effect size that is the threshold for "scientific significance"
- \( .r \)  For Tmin and Gmin, vector of values to which the proportion of large effect sizes is to be reduced
- \( .\muB \)  Mean bias factor on the log scale across studies
- \( .\sigmaB \) Standard deviation of log bias factor across studies
- \( .yr \)  Pooled point estimate (on log scale) from confounded meta-analysis
- \( .t2 \)  Estimated heterogeneity (\( \tau^2 \)) from confounded meta-analysis
Details
For \(\text{meas}==\text{"Tmin"}\) or \(\text{meas}==\text{"Gmin"}\), arguments \(\text{muB}\) and \(\text{sigB}\) can be left NULL; \(\text{r}\) can also be NULL as it will default to a reasonable range of proportions. Returns a data.frame whose rows are values of \(\text{muB}\) (for \(\text{meas}==\text{"prop"}\)) or of \(\text{r}\) (for \(\text{meas}==\text{"Tmin"}\) or \(\text{meas}==\text{"Gmin"}\)). Its columns are values of \(\text{sigB}\) (for \(\text{meas}==\text{"prop"}\)) or of \(\text{q}\) (for \(\text{meas}==\text{"Tmin"}\) or \(\text{meas}==\text{"Gmin"}\)). Tables for \(\text{Gmin}\) will display NaN for cells corresponding to \(\text{Tmin}<1\), i.e., for which no bias is required to reduce the effects as specified.

Examples

\[
\text{sens_table}( \text{.meas=\text{"prop"}}, \text{.q=log(1.1)}, \text{.muB=c( log(1.1), log(1.5), log(2.0))}, \text{.sigB=c(0, 0.1, 0.2)}, \text{.yr=log(2.5)}, \text{.t2=0.1})
\]
\[
\text{sens_table}( \text{.meas=\text{"Tmin"}}, \text{.q=c( log(1.1), log(1.5))}, \text{.yr=log(1.3)}, \text{.t2=0.1})
\]

\# will have NaNs in cells with Tmin < 1 (no bias needed)
\[
\text{sens_table}( \text{.meas=\text{"Gmin"}}, \text{.r=0.8}, \text{.q=c( log(1.1))}, \text{.yr=log(1.3)}, \text{.t2=0.1})
\]

---

stronger_than

Estimate proportion of population effect sizes above or below a threshold

Description
This is a wrapper for \text{confounded_meta} that estimates, without any adjustment for confounding bias, the proportion of effect sizes above or below a specified threshold. Effect sizes may be of any type (they need not be relative risks).

Usage

\[
\text{stronger_than(.q, .yr, .vyr = NULL, .t2, .vt2 = NULL, CI.level = 0.95, .tail)}
\]

Arguments

- \(.q\) True effect size that is the threshold for "scientific significance"
- \(.yr\) Pooled point estimate from meta-analysis
- \(.vyr\) Estimated variance of pooled point estimate from meta-analysis
- \(.t2\) Estimated heterogeneity (\(\tau^2\)) from meta-analysis
- \(.vt2\) Estimated variance of \(\tau^2\) from meta-analysis
- \(\text{CI.level}\) Confidence level as a proportion
- \(.tail\) above for the proportion of effects above \(\text{.q}\); below for the proportion of effects below \(\text{.q}\).
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